Evolutionary and Biogeographic Studies in the genus *Kniphofia* Moench (Asphodelaceae)

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Dedication

To my wife, Sandhayia Kanhaye

Durgam Kaaj Jagat Ke Jeete,
Sugam Anugrah Tumhre Te Te

Goswami Tulsidas (1532-1623)

Abstract

Kniphofia, a genus of approximately 71 species, is almost entirely African with two species occurring in Madagascar and one in Yemen. Commonly known as ‘red hot pokers’ they are popular among horticulturists. The genus is also well known for its complex alpha taxonomy. To date, no studies have examined the phylogenetic relationships among species or the evolutionary history of the genus, and little work has been done on their biogeography. The main focus of this study was (i) to review the alpha taxonomy, (ii) to assess diversity and endemism in *Kniphofia*, (iii) to use DNA sequence data to reconstruct a species-level phylogeny to understand intra-generic species relationships and evolutionary processes (iv) to use phylogeographic approaches to study the biogeography and evaluate biogeographical patterns, and (v) to assess anatomical variation and determine if anatomical characters are useful for species delimitation.

It was found that the genus has six centres of diversity, five of which are centres of endemism. The South African Centre is the most speciose and is also the largest centre of endemism. *Kniphofia* shows a strong Afromontane grassland affinity in Tropical and East Africa. In South Africa, it is found from high altitudes to coastal habitats, with the most speciose regions being Afromontane grasslands. It is thus not considered to be an Afromontane element, but rather an Afromontane associate.

Five major evolutionary lineages were identified using cpDNA sequence data (*trnT-L* spacer), four of which are southern African. The fifth lineage is represented by material from Madagascar, East and Tropical Africa. The nuclear *ITS* region failed to provide resolution, as many sequences were identical. The five lineages recovered using cpDNA showed some congruence with geographic origin rather than the taxonomic arrangement based on morphology. All of the

species with multiple samples were non-monophyletic. This could be due to hybridisation and/or incomplete lineage sorting.

The nested clade analysis, although preliminary, did not completely agree with the phylogenetic analyses. One of the three third level nested clades appears to show fragmentation between the Cape Region, KwaZulu-Natal and northern parts of southern Africa. Furthermore, another nested clades recovered suggest a range expansion and radiation from the Drakensberg into the adjacent Drakensberg-Maputoland-Pondoland transition.

Morphological species of *Kniphofia* exhibited substantial leaf anatomical variation and anatomical characters do not cluster samples into their morphological species. The anatomical results do not fit any geographic pattern, nor do they correspond to the lineages recovered using molecular markers or the nested clades. Leaf anatomical variation does not appear to be influenced by geographical or environmental factors. However, hybridisation may play a role but was not tested in this study.

In light of the above findings it is proposed that the evolutionary and biogeographic history of *Kniphofia* is strongly linked to tectonic events, and Quaternary climatic cycles and vegetation changes. Tectonic events (viz. uplifts) may have resulted in vicariance events that may account for the five cpDNA lineages recovered in phylogenetic analyses, while Quaternary climatic cycles and vegetation changes may have had a more recent impact on evolution and biogeography. It is hypothesised that the ancestral area for *Kniphofia* was much more widespread when Afromontane grasslands were more extensive during cooler and drier glacial episodes. *Kniphofia* on the high mountains of Tropical and East Africa would have tracked Afromontane grasslands as they expanded their ranges in cooler periods. While during wetter and warmer interglacial periods *Kniphofia* would have retreated into refugia on the mountains of Tropical and East Africa, with no gene flow possible between these refugia. In South

Africa, where latitude compensates for altitude, *Kniphofia* may have maintained a distribution that extended into the lowlands even during interglacials.

A cyclic climate change hypothesis implies that populations of *Kniphofia* (at different phases of the climatic cycle) would have experienced periods of contractions and fragmentation followed by periods of range expansion and coalescence or secondary contact. Altitudinal shifting is proposed to be the most likely mechanism for fragmentation and range expansion, and would would possibly promoted hybridisation. Within the five lineages there is evidence for recent differentiation as the branch lengths are short, there are numerous non-monophyletic species and numerous identical haplotypes (cpDNA and *ITS*) which collectively indicate a recent radiation in southern Africa. A recent radiation would also account for the taxonomic confusion and difficulty in differentiating morpho-species. These climatic events may also account for the substantial anatomical variation in southern African *Kniphofia* species.

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Preface

Some of the work presented in this study has been published previously:

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Declaration

This thesis is the result is the result of the author's original work except where acknowledged or specifically stated in the text. It has not been submitted for any other degree or examination at any other university or academic institution.

……………………………………..
Syd Ramdhani

Chapter 1: Introduction

1.1. The genus *Kniphofia* Moench (Asphodelaceae)

The genus *Kniphofia* Moench, commonly known as ‘red hot pokers’, comprises approximately 71 species. *Kniphofia* is an asphodelaceous genus characterised by a perennial, rhizomatous, usually acaulescent and herbaceous habit. Leaves are rosulate, linear and usually keeled. Inflorescences are subspicate racemes with a bract at the base of pedicels. Flowers are tubular and range from white, yellow to various shades of red which are more conspicuous at the apex of the inflorescence producing a bicolourous appearance. Flowers are three-merous, with six tepals and a hypogynous three chambered sessile ovary. Fruits are globose to ovoid capsules that house seeds that are usually flattened.

The genus is almost entirely African with two species from Madagascar and one from Yemen. *Kniphofia* is chiefly distributed in southern and eastern Africa, preferring temperate mountainous grassland and moist habitats (Ramdhani *et al*., 2006). In South Africa (SA) 48 species are currently recognised (Codd, 2005). The centre of diversity is the Drakensberg region of the KwaZulu-Natal and Eastern Cape provinces of South Africa. The genus is known for its complex alpha-taxonomy and contains several species complexes (Codd, 1968, 2005).

Kniphofia has considerable horticultural appeal because of the charismatic and conspicuous inflorescences of many members (Fig. 1.1.) and the ease with which taxa hybridise in cultivation (Taylor, 1985; Baijnath, 2004). It is a frequent subject in popular horticultural and botanical publications (McMaster, 1999; Van Jaarsveld, 2003; Baijnath, 2004; Dold and McMaster, 2005). Despite the popularity of the genus, phylogenetic relationships amongst the different species within *Kniphofia* have not been explored previously. The complex alpha-taxonomy and poorly understood phylogenetic relationships within *Kniphofia*

Fig. 1.1. Some representatives of *Kniphofia*. A. *K. caulescens* (N.P. Barker 1821, Sani Pass). B. *K. acraea* (T. Dold 4626, Mount Zebra National Park). C. *K. fibrosa* (P.B. Phillipson 5579, Dohne Hill). D. *K. pauciflora* (clone from Natal National Botanical Garden). E. *K. splendida* (SR 548, Haentersberg; photo by E.A. Kellogg). F. *K. uvaria* (SR 471, Dimbiza). G. *K. schimperi* (SR 391, Bale Mountains). H. *K. typhoides* formerly placed in *Notosceptrum* [portrait from www.smgrowers.com]. I. *K. linearifolia* (T. Dold 4638, Satans Nek).

1.2. Previous systematics studies in *Kniphofia*

The pre- and post-Linnean taxonomic history of the genus was discussed in great detail by Codd (1968), who gave an excellent overview of taxonomic work prior to his revision and it would be pointless to repeat it herein. The salient publications which have a direct bearing on the present study are dealt with below.

Bentham and Hooker (1883) described the segregate genus *Notosceptrum* Benth. based on floral characters. Characters used to separate *Notosceptrum* from *Kniphofia* were very long slender inflorescences bearing numerous ascending or patent flowers and a short, subcampanulate perianth, which is relatively deeply lobed in *Notosceptrum* (Codd, 1967).

Berger (1908) monographed *Kniphofia*, recognising 67 species with 13 varieties. He upheld *Notosceptrum* with five species. Berger divided *Kniphofia* into 14 formal sections. This monograph brought together the information on the genus available at the time including a comprehensive list of hybrids and garden cultivars. According to Codd (1968), Berger's work suffers two main weaknesses. Firstly, the nomenclature was not acceptable according to the International Code of Botanical Nomenclature, a criticism that is not completely justified as Berger's work was published at a time when the Code was still in early developmental stages. The second weakness was that Berger did not study the plants in the field, which made his treatment unrealistic in several respects. Codd (1968, p. 387) noted that Berger showed "no grasp of geographical distribution of species and little concept of the variation, which occurs within a taxonomic group, resulting in too many 'species' (amongst those known to him) being upheld on unreliable 'differences'".

Subsequent to Berger's (1908) monograph there was a large accumulation of collections in South Africa. However, little work was done until after the Second

World War. In 1947 Miss Eileen Bruce started a revision on the genus in South Africa. She worked actively on the genus between 1947 to 1952. She recognised three new species namely *Kniphofia splendida* E.A. Bruce, *Kniphofia rigidifolia* E.A. Bruce and *Kniphofia coralligemma* E.A. Bruce (Bruce, 1955). Unfortunately, her career was cut short by her death in 1955 (Codd, 1968).

During the 1950's and 1960's, Dr. L.E. Codd of the National Herbarium (PRE) contributed significantly to the taxonomy of the genus describing numerous species and resolved taxonomic problems such as typification and correct identification (Codd, 1959, 1961, 1963, 1964, 1965). Codd (1967) re-examined the status of *Notosceptrum* and found that the floral characters used to separate *Notosceptrum* and *Kniphofia* break down when all the known species (at that time) were considered. He thus merged *Notosceptrum* into *Kniphofia*. Codd's work on the genus culminated in a revision of the South African species in 1968. He recognised 45 species and eight subspecies. An updated revision of Codd (1968) was published posthumously in 2005 which documented 48 species and six subspecies from southern Africa. Codd passed away in 1999 but had completed the manuscript of the second revision in the late 1980's. By this time Codd was a very experienced taxonomist who had worked on a number of diverse plant groups. Codd's approach was not strictly herbarium based. He did extensive field work with numerous collections and had an excellent knowledge of *Kniphofia*. Despite Codd's (1968, 2005) revisionary efforts there still remain many taxonomic problems which require further investigation and his works are testament to the complex taxonomy and evolutionary history of this genus.

Codd's (1968, 2005) revisions are of vital importance, as these were used as the taxonomic framework in this study and his species delimitations were followed for southern African representatives of *Kniphofia*.

1.2.1. Problems encountered by Codd

1.2.1.1. The *Kniphofia uvaria* (L.) Oken complex

Codd (1968) did not resolve *K. uvaria* and its allies [*Kniphofia rooperi* (T. Moore) Lem., *Kniphofia tysonii* Baker, *Kniphofia citrina* Baker and *Kniphofia linearifolia* Baker] completely. This complex is widespread and variable. Nevertheless, he delimited five species (*K. uvaria*, *K. rooperi*, *K. tysonii*, *K. citrina* and *K. linearifolia*) on the basis of inflorescence shape and perianth length. This group varies in size and degree of variability of inflorescences and species delimitations are not clear cut, but are linked by intermediates. However, each group had a fairly well-defined geographical distribution range (Codd, 1968).

Codd (2005) retained the species in this complex but provided additional information. Overlap in distribution and intergradation of characters between *K. uvaria* and other species of the complex (except *K. tysonsii*) in the Eastern Cape (especially in the King Williams Town and Albany area) were noted. *K. tysonii* shows no intergradation with *K. uvaria* but does intergrade with *K. linearifolia*. Codd (2005) also postulated that *K. linearifolia* is possibly the 'parent' form of the complex. The evidence above suggests extensive hybridisation in the evolutionary history of the complex. Furthermore, a specimen from the Bouwershoekberge (Graff-Reinet, Bayliss 3917) has some unusual morphological features which requires further investigation to better understand its placement (Codd, 2005).

K. uvaria sensu stricto

K. uvaria sensu stricto has a wide distribution from the Cape Region, extending as far north as the Kamiesberg, east towards the Albany district and inland into the foothills of the Drakensberg. Four forms were noted by Codd (2005), with slightly different morphologies and each with a fairly distinct distribution with some overlap and intergradation. No formal rank was awarded to these forms (Codd, 2005).

K. rooperi

Poor material of this species can be confused with *K. drepanophylla* and *K. littoralis*. Several collections between Komga and Knysna, and inland (King Williams Town and Stutterheim) appear to be intermediate between *K. rooperi* and *K. uvaria*. Also specimens from Albany, Port Elizabeth and Humansdorp link *K. rooperi* with *K. citrina* (Codd, 2005).

K. citrina

K. citrina has a distribution that overlaps with *K. uvaria* and intermediate collections have been reported (Codd, 2005). Despite Codd's (2005) opinion that 'separate species rank for *K. citrina* is scarcely justified' he retained it as a separate species.

K. linearifolia

This is the most widespread *Kniphofia* species in southern Africa. Specimens that are small in stature are not easily distinguished from *Kniphofia baurii* Baker. *K. linearifolia*, *K. rooperi* and *K. uvaria* are closely related and intermediate specimens have been reported in sympatric distributions. Intermediate collections have also been reported for *K. linearifolia* and *K. tysonii*. Racemes of *Kniphofia praecox* Baker show close resemblance to *K. linearifolia* and it has been implicated in the hybrid ancestry of *K. praecox* (Codd, 2005).

K. tysonii

Codd (1968, 2005) recognised two subspecies of *K. tysonii*. *Kniphofia tysonii* Baker subsp. *tysonii* Codd is related to *K. linearifolia*. Intermediate specimens are also known that are difficult to place with certainty. Some specimens of *Kniphofia tysonii* Baker subsp. *lebobomboensis* Codd are difficult to separate from *K. tysonii* subsp. *tysonii* in the herbarium, although the two subspecies do not overlap in distribution (Codd, 2005). Codd (2005) speculated that *K. tysonii* subsp. *lebobomboensis* was derived from *K. linearifolia* rather than *K. tysonii* subsp. *tysonii.* This implies a closer relation to a separate species rather than it sister subspecies i.e. *K. tysonii* is not monophyletic. Intermediates between *K. tysonii* subsp. *lebobomboensis* and *K. linearifolia* have been reported (Codd, 2005).

The above situation in the *K. uvaria* complex and *K. uvaria sensu stricto* poses complications for workers not familiar with the plants and can easily result in erroneous identifications. Thus, an intensive study on the *K. uvaria* complex is required before a satisfactory classification is achieved. This will entail extensive field work, identification of additional taxonomic characters and further exploration with multiple approaches.

1.2.1.2. *Kniphofia baurii* Baker

Codd (1968, 2005) found that the typical form of *K. baurii* may be confused in the herbarium with *Kniphofia drepanophylla* Baker. *K. baurii* occurs in two disjunct areas. One form is from Engcobo towards southern KwaZulu-Natal. The other form occurs in northern KwaZulu-Natal (Dundee inland towards the foothills of the Drakensberg and northwards towards Wakkerstroom) and is more robust.

Codd (1968) included in *K. baurii* a group of specimens that deviated from typical *K. baurii*. These specimens originate mainly from the Eastern Cape and East Griqualand. This group was characterised by a later flowering time (which is spring flowering for typical *K. baurii*) and greenish flowers with dull red buds. Apart from these differences, the plants compared well with *K. baurii* morphologically (Codd, 1968). Codd (2005) considered this group to belong to *K. linaerifolia*.

During this study difficulty was experienced at times in keying out *K. baurii* and *K. uvaria* as the two taxa are similar in many respects. This might indicate that *K. baurii* should be treated as part of the *K. uvaria* complex.

1.2.1.3. *Kniphofia praecox* Baker

The species concept of *K. praecox* is in doubt. The *K. uvaria* and *K. praecox* complexes have largely contributed to the cultivation of 'red hot pokers' in Europe. The early history of the genus is confused by the application and misinterpretation of species names within these species complexes (Codd, 1968). Until 1800 apparently only *K. uvaria* was known to botanists in Europe. The typification of this species is not in doubt. *K. uvaria* was easily available to early collectors. As botanical exploration proceeded further eastwards in South Africa, more robust Kniphofias were collected and made their way to Europe (Codd, 1968).

In the early 1800's robust hybrids of *Kniphofia* started to appear in Europe (Codd, 1968, 2005). Jacquin (1809) included an illustration of a *Kniphofia* under the name *Veltheimia uvaria* Willd. The identity of the plant in this illustration was uncertain until Codd (1968) matched it with naturally occurring plants with restricted distributions in the Komga and Knysna areas [now recognised as *Kniphofia bruceae* (Codd) Codd, see below]. It has narrow, long-acuminate bracts that make it clearly different from members of the *K. uvaria* complex, which has ovate-oblong, obtuse to rounded bracts. It seems probable that these plants (i.e. *K. bruceae*) were widely available in Europe during the early 1800's and superficially resembled members of the *K. uvaria* complex.

Baker (1870) tentatively described *K. praecox*. He separated *K. praecox* from *K. uvaria* mainly on the earlier flowering time of *K. praecox*. However, in subsequent revisions he included *K. praecox* under *K. uvaria.* Codd (1968) found that the type of *K. praecox* preserved in Kew Herbarium was allied to the plant illustrated by Jacquin (1809), but was not an exact match with known wild populations associated with the plant in Jacquin's plate (i.e. *K. bruceae*). At the time he found it appropriate to include the wild plants (*K. bruceae*) under the broad concept of *K. praecox*. Codd (1968) also questioned whether the type might be of hybrid origin, as it did not match exactly with any known plants from the wild. One must take into account the history of this type, which was from garden material cultivated by W. W. Saunders. He supposedly obtained the plants from Thomas Cooper. Although Cooper made herbarium specimens of the material he collected from the wild, Codd did not trace or examine this material. Codd also suspected that the type specimen of *K. praecox* was possibly obtained from another source. Despite this confusion concerning the type of *K. praecox*, Codd (1968) maintained *K. praecox* as a separate species with two subspecies. *Kniphofia praecox* Baker subsp. *bruceae* Codd was erected based on its affinity with and possible parentage of *K. praecox*. He noted that the two subspecies could be separated on several characters, notably the narrower and more acuminate bracts, longer pedicels, the shorter perianth, which tends to be constricted above the ovary, and the well-exserted stamens in *K. praecox* subsp. *bruceae*. Codd (1987) raised *K. praecox* subsp. *bruceae* to species rank (= *K. bruceae*) for specimens from the Komga area. He also considered the specimens from the Knysna-Willowmore area to belong to *K. bruceae*, although they differed amongst themselves. Codd (1987) could still not locate plants in the wild that matched to the type of *K. praecox*. He further found that narrow bracts were recorded from three small disjunct areas (near Komga, between Plettenberg Bay and Knysna, and near Kouga).

According to Codd (2005) the species concept of *K. praecox* appears to be derived from *K. bruceae* crossed with another showy species (possibly *K. uvaria* or *K. linearifolia*) along the lines of his earlier work. These hybrids produced several derivatives, which became widely accepted in cultivation under epithets such as *K. uvaria*. The true *K. uvaria* was either lost or regarded as inferior to the above mentioned hybrids. Plants of this mixed nature are still grown in gardens today but have become modified to varying degrees due to a long history of cultivation in Europe. It is evident that hybridisation with other additional species in cultivation has produced numerous horticultural and ornamental forms (C. Whitehouse, pers. comm.).

The bract shape is the only character that can separate these hybrids from *K. linearifolia*. Many illustrations published over the years cannot be confidently placed as bract characters are not depicted. The plants described as *K. praecox* appears to be one of these hybrids as no material collected in the wild thus far match the type of *K. praecox*. Despite the dubious and complicated history of *K. praecox*, Codd (2005) retained this species.

Furthermore, the name *K. praecox* still appears to be used for the Knysna-Willowmore specimens and *K. bruceae* exclusively for the Komga populations. The concept of *K. praecox sensu* Codd in the wild is unresolved, if such plants do exist. Although Codd (1987) regarded the Knysna-Willowmore specimens as belonging to *K. bruceae*, the name *K. praecox* persists and is being applied to material from the Knysna-Willowmore area (e.g. Goldblatt and Manning, 2000). It seems that this broad concept of *K. praecox* has been a dumping ground for material that does not key out well or fails to key out to members of the *K. uvaria* complex (taxa with superficially similar morphologies), but fits the geographical distribution and flowering time based on Codd's (1968, 2005) concept of *K. praecox*. At this point in time it is uncertain if these wild plants of so-called *K. praecox* represent a mixture of different forms. More material will have to be gathered and critically compared. A detailed study will help resolve the problems in delimiting *K. praecox* or validate its inclusion with the presently accepted concept of *K. bruceae sensu stricto*. I have not attempted to solve this problem in this study due to time constraints and limited field work done in the Cape Region.

1.2.1.4. *Kniphofia brachystachya* (Zahlbr.) Codd

An intermediate collection (Nicholson *sn*) from Karkloof between *K. brachystachya* and *Kniphofia buchananii* Baker was noted by Codd (2005). Codd (2005) treated it as a form of *K. brachystachya* until more material becomes available. This may represent a hybrid between *K. brachystachya* and *K. buchananii*.

1.2.1.5. *Kniphofia buchananii* Baker

K. buchananii is closely related to *Kniphofia breviflora* Harv. ex Baker. There are occasional intermediates suggesting that *K. buchananii* should be treated as a subspecies of *K. breviflora* (Codd, 2005). However, these intermediates may represent hybrids.

1.2.1.6. *Kniphofia breviflora* Harv. ex Baker

Two colour forms associated with distribution have been recorded by Codd (2005). As mentioned above *K. breviflora* and *K. buchananii* are closely related. *K. breviflora* also shows a close relationship with *K. albescens* Codd (see below).

1.2.1.7. *Kniphofia albescens* Codd

Codd (1968, 2005) noted that *K. albescens* and *K. breviflora* overlap in northern KwaZulu-Natal and it is sometimes difficult to distinguish them with certainty. *K. albescens* is a more robust plant usually growing in clusters with longer flowers and bracts.

1.2.1.8. *Kniphofia evansii* Baker

A specimen of *K. evansii* (Trauseld 741) from Giants Castle Game Reserve has a combination of characters of *K. evansii* and *Kniphofia porphyrantha* Baker. It may represent a hybrid and requires further investigation (Codd, 1968, 2005).

1.2.1.9. *Kniphofia ichopensis* Baker ex Schinz

Codd (1968) recognised this species with no infra-specific taxa. Codd (1986) described a variety of *K. ichopensis* viz. *Kniphofia ichopensis* Baker ex Schinz var. *aciformis* Codd. It is identical in perianth and bract characters to *Kniphofia ichopensis* Baker ex Schinz var. *ichopensis* Codd and was therefore considered to be a variety of *K. ichopensis*. However, it does have unique leaves which require further investigation and may represent a separate species (Codd, 2005). The two varieties overlap in distribution but no intermediates have been found (Codd, 2005).

1.2.1.10. *Kniphofia fibrosa* Baker

Hybrid swarms presumably derived from *K. fibrosa* and *Kniphofia triangularis* Kunth subsp. *triangularis* Codd have been reported from the Bushmans Nek, Upper Pholela Cave, Siponweni, Ndloveni (Hilliard and Burtt, 1987) and Mahwaqa Mountain (Anne Rennie, pers. comm.), where the putative parents are found (Codd, 1986, 2005). Both species also flower at the same time in sympatric situations on the Sunset Farm part of the Mahwaqa Mountain (personal observation).

Hilliard and Burtt (1987) also noted that *Kniphofia angustifolia* (Baker) Codd (= *K. rufa* Baker) forms hybrids with *K. fibrosa* and *K. triangularis*. *K. angustifolia* may have also contributed to the range of variation in *K. fibrosa* (Codd, 2005).

1.2.1.11. *Kniphofia laxiflora* Kunth

Codd (1968, 2005) found that *K. laxiflora* was a variable species with a wide distribution from Port St. Johns inland into the Drakensberg and as far north as southern Mpumalanga. He recognised three main forms (Forms A, B and C). Each form has a somewhat distinct geographical distribution but it is difficult to separate these forms in the herbarium (Codd, 2005). Thus, Codd did not award these separate formal taxonomic rank. In southern KwaZulu-Natal *K. laxiflora* tends to grade with *K. gracilis* (especially in perianth length) making placement difficult (Codd, 2005). Codd (1968, 2005) found a few specimens with bracts of intermediate shape between *K. laxiflora* and other lax-flowering species e.g. *K. ichopensis*. These may represent hybrids.

1.2.1.12. *Kniphofia gracilis* Baker

Codd (1968, 2005) noted that variation within *K. gracilis* required further investigation. This includes examination of characters such as length and density of the inflorescences, and degree of constriction of the perianth above the ovary. In typical *K. gracilis* the inflorescence is short and flowers relatively dense with the perianth 14-20 mm long and more or less parallel-sided, expanding at the mouth. Other plants considered to belong to *K. gracilis* have lax, elongated inflorescences with the perianth 11-16 mm long, constricted above the ovary and expanding at about the midpoint, and varying in colour from white to yellow. Codd (1968) found several herbarium specimens that are intermediate in these inflorescence and perianth characters, making it impossible to separate the material satisfactorily into infra-specific groups in the herbarium.

In southern KwaZulu-Natal, *K. laxiflora* tends to intergrade with *K. gracilis* (especially in perianth length) (Codd, 2005). Codd (1968) found specimens of *K. gracilis* with perianths about 20 mm long, which he regarded as intermediate between *K. gracilis* and *K. laxiflora* (perianth usually 24-32 mm long). This renders the distinction between *K. gracilis* and *K. laxiflora* somewhat arbitrary and merging the two species would create a heterogeneous assemblage of material, which Codd considered unfavourable. Thus, Codd (1968, 2005) maintained the two species. These problematic specimens may possibly be hybrids.

1.2.1.13. *Kniphofia angustifolia* (Baker) Codd

The type of *Kniphofia rufa* Baker is a plant of uncertain origin. Furthermore, it could not be exactly matched with any material collected in the wild by Codd (1968) and may be of hybrid origin, but the evidence was inconclusive (Codd, 1968). Based on the above Codd (1968) considered discarding the name *K. rufa*, but found it necessary at the time to reluctantly uphold the name.

Codd (1968) found that *K. rufa* varies in colour from white to yellow or coral-red. However, colours cannot be discerned in most herbarium specimens. Thus, no attempt was made to subdivide the species into varieties. Some specimens of the 'coral-red' flowering form have inflorescences that are more compact than usual and are difficult to distinguish from the Natal form of *K. triangularis* subsp. *triangularis*. Codd speculated that *K. triangularis* might have played a part in the evolution of the lax, coral-red inflorescences. However, colour is not easily observed in herbarium specimens, whereas delimitation can be made on relative inflorescence density. Thus, he included these plants as a colour form of *K. rufa*.

Subsequently, Codd (1986) could not find a good match of the type of *K. rufa* with wild material and proposed that *K. rufa* should be considered as an insufficiently known entity until matching material from the wild was found. All the other entities that did not match the type perfectly but fell under the name *K. rufa sensu* Codd (1968) were placed in *K. angustifolia.* Furthermore, Codd (1968) mentioned plants with longer flowers which are coral-red to orange-red may be due to hybridisation with *K. triangularis* (see above notes with regard to *K. rufa*). Thus, Codd (2005) considered *K. rufa* to be of doubtful application.

Codd (2005) noted that *K. angustifolia* exhibits some localised variation which was attributed to hybrid swarms with possibly *K. triangularis* subsp. *triangularis*. Hilliard and Burtt (1987) also noted that *K. augustifolia* (*K. rufa*) forms hyrids with *K. fibrosa* and *K. triangularis*. Some specimens may also be confused with *K. ichopensis* var. *ichopensis* but can be separated by leaf width.

1.2.1.14. *Kniphofia ensifolia* Baker

Codd (1968) recognised two subspecies based on flowering time (*Kniphofia ensifolia* Baker subsp. *ensifolia* Codd and *Kniphofia ensifolia* Baker subsp. *autumnalis* Codd). It appears that in the eastern Free State, *K. linearifolia* forms hybrids with *K. ensifolia* subspecies *autumnalis* (Codd, 2005).

1.2.1.15. *Kniphofia coralligemma* E.A. Bruce

Codd (1968) recorded three forms, which differed mainly in inflorescence colour and geographical distribution. More research is required before a decision can be reached regarding the status of these forms. Codd (2005) still recognised the three forms without formal rank being awarded.

1.2.1.16. *Kniphofia northiae* Baker

Codd (1968) noted that there were two colour forms and two leaf forms. In the typical form from the Eastern Cape, Lesotho and the Drakensberg the leaves lacked a distinct keel and were crescentiform in transverse section. In the second form (from Bergville, Estcourt and Lesotho) the leaves were broadly V-shaped with a distinct mid-rib. Codd (1968) suggested that further studies should be done in order to determine whether this species should be divided into separate taxa. Baijnath (1987) subsequently described *Kniphofia albomontana* Baijnath to accommodate taxa of *K. northiae* with V-shaped leaves using anatomical data (Baijnath, 1980) to support his decision. He also noted that *K. albomontana* was closely related to *K. caulescens*.

1.2.1.17. *Kniphofia galpinii* Baker

Codd (1968) noted the strong similarities between *K. galpinii* and *K. triangularis*. He considered treating *K. galpinii* as a subspecies of *K. triangularis*. However, many small differences justified retaining it as a separate species. Mention is made of specimens that needed further investigation from Jessievale Plantation (Carolina) and the Pasture Station (Ermelo) that do not entirely match *K. galpinii*. Although Codd (1968) excluded these specimens from *K. galpinii*, he thought that they were closely related to *K. galpinii* and suggested that further data was needed to determine their taxonomic status. Also, some specimens cited from KwaZulu-Natal differed slightly from typical *K. galpinii*, but these differences were insufficient to warrant a separate status. Codd (1968) considered these to represent a form that required further investigation. Poor specimens of *K. linearifolia* may be confused with *K. galpinii* (Codd, 2005).

1.2.1.18. *Kniphofia thodei* Baker

Herbarium specimens of *K. thodei* may be confused with *Kniphofia prophyrantha* Baker or *K. triangularis* but in fresh material the floral colour of *K. thodei* (buds are coral red to dull red often tipped with white, while open flowers are white) helps to easily identify this species (Codd, 1968).

1.2.1.19 *Kniphofia triangularis* Kunth

Reference has already been made to *K. triangularis* subsp. *triangularis* under *K. angustifolia* (and *K. rufa*). It may have contributed to the evolution of the lax, coral-red inflorescences in the latter species. However, at times the distinction between lax and dense inflorescences are not clear cut and specimens may be difficult to place. Codd (1968) found that collections of *Kniphofia triangularis* Kunth subsp. *obtusiloba* Berger (Codd) are not clearly distinct from *K. galpinii*, which also occurs in Mpumalanga. Hybrid swarms presumably derived from *K. triangularis* subsp. *triangularis* and *K. fibrosa* have been reported above under *K. fibrosa* (Codd, 1986, 2005). In the herbarium, specimens of *K. triangularis* may be confused with *K. porphyrantha* (Codd, 2005).

1.2.1.20. *Kniphofia porphyrantha* Baker

In the herbarium it is not always easy to distinguish between specimens of *K. porphyrantha* and certain allied species with acute to acuminate bracts. However, with fresh material *K. porphyrantha* can easily be separated from *K. triangularis* subsp. *obtusiloba*, *K. galpinii*, *K. thodei* and *Kniphofia fluviatilis* Codd (Codd, 1968, 2005). Also, the closely related *K. fluviatilis* resembles *K. porphyrantha* in some respects.

1.2.1.21. *Kniphofia littoralis* Codd

This species has characteristically large fruits. When capsules are present, *K. littoralis* can be distinguished from all other species of the genus (Codd, 1968, 2005). In general appearance it resembles *K. baurii*, *Kniphofia drepanophylla* Baker and forms of *K. rooperi*. Smaller and depauperate specimens of *K rooperi* may easily be confused with *K. littoralis* if fruits are lacking, but Codd (1968) enumerated several morphological differences. According to Codd (1968) intermediate specimens may give the impression of being hybrids, but are best considered variants of *K. rooperi*.

1.2.1.22. *Kniphofia drepanophylla* Baker

As noted above, the typical form of *K. baurii* may be confused in the herbarium with *K. drepanophylla* (Codd, 1968, 2005). Codd (2005) reported an intermediate between *K. baurii* and *K. drepanophylla* (Killick and Marais 2014) from Weza which needs further investigation.

1.2.2. Codd’s Key

The artificial keys to species of *Kniphofia* that Codd (1968, 2005) constructed are problematic. Apart from the problems associated with the taxa discussed above, it is highly ambiguous at many dichotomies. There are at least 13 taxa that key out in more than a single couplet in the latest key (Codd, 2005). Furthermore, Codd

(2005) made extensive use of flowering times, which although useful, can be problematic as flowering periods fluctuate depending on weather patterns, especially rainfall. *K. linearifolia* is not in Codd's (2005) key which appears to be a typographical error. *Kniphofia leucocephala* Baijnath described by Baijnath (1992a) is wrongly placed in 'couplet 61b' which seems to best fit *K. linearifolia*.

1.2.3. Other systematic studies in *Kniphofia*

Cufodontis (1971) described *K. hildebrandtii* Cufod. He also changed the invalid name *Kniphofia elegans* Codd to *Kniphofia coddiana* Cufod.

Marais (1973) revised the remaining tropical African species recognising 22 species which include:

1. *Kniphofia thomsonii* Baker
2. *Kniphofia schimperi* Baker
3. *Kniphofia hildebrandtii* Cufod.
4. *Kniphofia princeae* (Berger) Marais
5. *Kniphofia pumila* (Ait.) Kunth
6. *Kniphofia foliosa* Hochst.
7. *Kniphofia splendida* E.A. Bruce
8. *Kniphofia dubia* De Wild.
9. *Kniphofia bequaertii* De Wild.
10. *Kniphofia linearifolia* Baker
11. *Kniphofia kirkii* Baker
12. *Kniphofia grantii* Baker
13. *Kniphofia nana* Marais
14. *Kniphofia isoetifolia* Hochst.
15. *Kniphofia insignis* Rendle
16. *Kniphofia reynoldsii* Codd
17. *Kniphofia benguellensis* Baker
18. *Kniphofia reflexa* Codd

19. *Kniphofia pallidiflora* Baker
20. *Kniphofia ankaratrensis* Baker
21. *Kniphofia sumarae* Deflers
22. *Kniphofia nubigena* Mildbr.

Marais (1973) did not group taxa into infrageneric sections. Marais (1973), like Codd (1968, 2005), found difficulty with some taxa. He recognised two varieties of *K. thomsonii*. Marais considered *K. ankaratrensis* (Madagascar) to be related to *K. splendida* (southern Africa and Malawi) and may represent the same species. He also noted that *K. sumarae* from Yemen was an excellent link between taxa placed in *Notosceptrum* and African species such as *K. pumila* and *K. foliosa*.

Blackmore (1981a, 1981b) described *Kniphofia mulanjeana* Blackmore and *Kniphofia monticola* Blackmore from Malawi. Lavranos (1983) noted that *K. sumarae* from Yemen was closely affiliated to *Kniphofia acraea* Codd, *K. brachystachya*, *Kniphofia typhoides* Codd and *K. umbrina* from southern Africa. He also supported Marais' view that *K. sumarae* is a good link between taxa placed in *Notosceptrum* and African species such as *K. pumila* and *K. foliosa*. Codd (1985) lectotypified the type species of *Notosceptrum*. This was done to ensure that if at a later date the genus *Notosceptrum* was restored, a generic name and type species would be available. This exercise raises doubt over his earlier decision to lump *Notosceptrum* into *Kniphofia*.

Kativu (1996) treated eight species for the *Flora Zambesiaca* area. These included *K. benguellensis*, *K. reynoldsii*, *K. dubia*, *K. grantii*, *K. mulanjeana*, *K. princeae*, *K. linearifolia* and *K. splendida*. However, he failed to include *K. monticola* in this treatment. Demissew and Nordal (1997) treated seven species for the Flora of Ethiopia and Eritrea viz. *K. pumila*, *K. foliosa*, *K. hildebrandtii*, *K. isoetifolia*, *K. insignis*, *K. schimperi* and *K. thomsonii*. Whitehouse (2002a) recorded eight species of *Kniphofia* from the Flora of Tropical East Africa region.

His treatment included *K. thomsonii*, *Kniphofia goetzei* Engl., *K. princeae*, *K. pumila*, *K. grantii*, *K. bequaertii*, *Kniphofia paludosa* Engl. and *K. reynoldsii*. He maintained *K. goetzei*, which Marais (1973) sunk under *K. thomsonii*, and noted that there were taxonomic problems between these two species. Furthermore, Whitehouse (2002a) maintained *K. paludosa*, which Marais (1973) considered a synonym of *K. kirkii*. Whitehouse (2002a) relegated the name *K. kirkii* to *nomen dubium*.

Thus the genus *Kniphofia*, as conceived at present, contains approximately 71 species (Table 1.1.), of which 48 are southern African

Table 1.1. Currently recognised *Kniphofia* species with distributions. Southern African taxa are assigned to their provisional species groups proposed by Codd (1968). Author citations follow Codd (2005) for southern African representatives, and Whitehouse (2002a) and Marais (1973) for representatives from Tropical Africa, Yemen and Madagascar. Abbreviations: DRC= Democratic Republic of Congo.

Taxon	**Distribution**	**Informal species group recognised by Codd (1968)**
1. *Kniphofia acraea* Codd	South Africa	2
2. *Kniphofia albescens* Codd	South Africa	3
3. *Kniphofia albomontana* Baijnath	South Africa	5
4. *Kniphofia angustifolia* (Baker) Codd	South Africa	4
5. *Kniphofia ankaratrensis* Baker	Madagascar	
6. *Kniphofia baurii* Baker	South Africa	9
7. *Kniphofia benguellensis* Baker	Angola, Zambia	
8. *Kniphofia bequaertii* De Wild.	DRC, Tanzania, Burundi, Rwanda, Uganda	
9. *Kniphofia brachystachya* (Zahlbr.) Codd	South Africa, Lesotho	2
10. *Kniphofia breviflora* Baker	South Africa, Swaziland	3
11. *Kniphofia bruceae* (Codd) Codd	South Africa	5
12. *Kniphofia buchananii* Baker	South Africa	3
13. *Kniphofia caulescens* Baker ex Hook. *f*.	South Africa, Lesotho	5

Table 1.1. continued

Taxon	**Distribution**	**Informal species group recognised by Codd (1968)**
14. *Kniphofia citrina* Baker	South Africa	10
15. *Kniphofia coddiana* Cufod.	South Africa	9
16. *Kniphofia coralligemma* E.A. Bruce	South Africa	5
17. *Kniphofia crassifolia* Baker	South Africa	3
18. *Kniphofia drepanophylla* Baker	South Africa	5
19. *Kniphofia dubia* De Wild.	DRC, Tanzania, Zambia, Angola	
20. *Kniphofia ensifolia* Baker	South Africa	5
21. *Kniphofia evansii* Baker	South Africa	7
22. *Kniphofia fibrosa* Baker	South Africa	3
23. *Kniphofia flammula* Codd	South Africa	3
24. *Kniphofia fluviatilis* Codd	South Africa	8
25. *Kniphofia foliosa* Hochst.	Ethiopia	
26. *Kniphofia galpinii* Baker	South Africa, Swaziland	8
27. *Kniphofia goetzei* Engl.	Tanzania	
28. *Kniphofia gracilis* Harv. ex Baker	South Africa	4

Table 1.1. continued

Taxon	**Distribution**	**Informal species group recognised by Codd (1968)**
29. *Kniphofia grantii* Baker	DRC, Rwanda, Burundi, Tanzania, Malawi, Zambia, Uganda	
30. *Kniphofia hildebrandtii* Cufod.	Ethiopia	
31. *Kniphofia hirsuta* Codd	South Africa, Lesotho	5
32. *Kniphofia ichopensis* Baker ex Schinz	South Africa	4
33. *Kniphofia isoetifolia* Hochst.	Ethiopia	
34. *Kniphofia insignis* Rendle	Ethiopia	
35. *Kniphofia latifolia* Codd	South Africa	10
36. *Kniphofia laxiflora* Kunth	South Africa	4
37. *Kniphofia leucocephala* Baijnath	South Africa	3
38. *Kniphofia linearifolia* Baker	South Africa, Malawi, Swaziland, Zimbabwe, Mozambique	10
39. *Kniphofia littoralis* Codd	South Africa	9
40. *Kniphofia monticola* Blackmore	Malawi	
41. *Kniphofia mulanjeana* Blackmore	Malawi	

Table 1.1. continued

Taxon	**Distribution**	**Informal species group recognised by Codd (1968)**
42. *Kniphofia multiflora* J.M. Wood & M.S. Evans	South Africa, Swaziland	1
43. *Kniphofia nana* Marais	DRC	
44. *Kniphofia northiae* Baker	South Africa, Lesotho	6
45. *Kniphofia nubigena* Mildbr.	Sudan	
46. *Kniphofia pallidiflora* Baker	Madagascar	
47. *Kniphofia paludosa* Engl. (= *K. kirkii* Baker)	Tanzania	
48. *Kniphofia parviflora* Kunth	South Africa	2
49. *Kniphofia pauciflora* Baker	South Africa	4
50. *Kniphofia porphyrantha* Baker	South Africa, Swaziland, Lesotho	8
51. *Kniphofia praecox* Baker	South Africa	5
52. *Kniphofia princeae* (Berger) Marais	DRC, Tanzania, Malawi, Rwanda	
53. *Kniphofia pumila* (Ait.) Kunth	DRC, Ethiopia, Sudan, Uganda, Kenya, Sudan, Eritrea	
54. *Kniphofia reflexa* Codd	Cameroon	
55. *Kniphofia reynoldsii* Codd	Tanzania, Malawi, Zambia	
56. *Kniphofia rigidifolia* E.A. Bruce	South Africa	10

Table 1.1. continued

Taxon	**Distribution**	**Informal species group recognised by Codd (1968)**
57. *Kniphofia ritualis* Codd	South Africa, Lesotho	5
58. *Kniphofia rooperi* (T. Moore) Lem.	South Africa	10
59. *Kniphofia sarmentosa* (Andrews) Kunth	South Africa	5
60. *Kniphofia schimperi* Baker	Ethiopia, Eritrea	
61. *Kniphofia splendida* E.A. Bruce	South Africa, Swaziland, Zimbabwe, Malawi	5
62. *Kniphofia stricta* Codd	South Africa, Lesotho	6
63. *Kniphofia sumarae* Deflers	Yemen	
64. *Kniphofia tabularis* Marloth	South Africa	4
65. *Kniphofia thodei* Baker	South Africa, Lesotho	8
66. *Kniphofia thomsonii* Baker	DRC, Kenya, Tanzania, Uganda, Ethiopia	
67. *Kniphofia triangularis* Kunth	South Africa, Lesotho	7
68. *Kniphofia typhoides* Codd	South Africa	2
69. *Kniphofia tysonii* Baker	South Africa, Swaziland	10
70. *Kniphofia umbrina* Codd	Swaziland	2
71. *Kniphofia uvaria* (L.) Oken	South Africa	10

1.2.4. Attempts at Infra-generic Classification

Berger (1908) divided *Kniphofia* into 14 sections and maintained the genus *Notosceptrum*. These sections were based on floral, leaf, inflorescence and bract morphology as well as caulescence and geography (viz. Section *Arabicae* for *K. sumarae*). Codd (1968) grouped southern African taxa into ten informal infra-generic groups of no formal rank based on probable affinity. These sections were based on leaf, floral, inflorescence and bract morphology, stature and flowering times. He saw no advantage in Berger's (1908) sections, although he viewed them as sound, and did not support *Notosceptrum* as a separate genus. Codd (2005) made no mention of infra-generic groupings.

1.2.5. Anatomy

Baijnath (1980) investigated the leaf anatomy of 18 *Kniphofia* species to assess the taxonomic value of leaf anatomical characters. He found that leaf surface and internal anatomy (vascular bundles and crystals) proved to be useful characters. Anatomical data did not support *Notosceptrum* as a separate genus. However, in most cases multiple samples of a single species were not examined to assess intra-specific anatomical variation.

1.2.6. Ethnobotany

The Basutos use *K. ritualis* to prepare a decoction to cure shoulder pains. It is also used by women when girls undergo sacred initiation rites, hence the epithet '*ritualis*'. *K. caulescens* is frequently planted around Basuto huts as a charm against lightning (Codd, 1968). Several taxa are used by the Zulus but have limited medicinal value. Infusions made from rhizomes of *K. laxiflora* and *K. rooperi* are used to treat chest aliments, while crushed roots and rhizomes of *K. uvaria* are included in enemas administered for painful menstruation. Also, infusions *of K. buchananii* and *K. parviflora* are used as snake deterrents (Hutchings *et al*., 1996). The tough fibrous leaves of some species (e.g. *K. albescens*) are used as twine (Baijnath, 2004). Infusions of *K. uvaria* are taken orally by Xhosa women to treat infertility (Matsiliza and Barker, 2001). Xhosa mothers use pieces of dried rhizome of *K. rooperi* in necklaces to bring good fortune to their children (Baijnath, 2004).

1.2.7. Conservation

Many *Kniphofia* species are in need of conservation. A high number of South African species (25) are included in the Red Data List of Hilton-Taylor (1996). Scott-Shaw (1999) documented 17 *Kniphofia* taxa considered to be under threat in KwaZulu-Natal and neighbouring regions. Taxa under threat are listed in Table 1.2. Witkowski *et al*. (2001) examined the conservation biology of *K. umbrina* and found it to be critically endangered.

1.3. Systematic position of *Kniphofia* within Asphodelaceae

Asphodelaceae was placed in the order Asparagales (APG, 1998) and considered a family of the lower asparagoids, which are characterised by simultaneous microsporogenesis (Chase *et al*., 1995; Rudall *et al*., 1997, Fay *et al*., 2000). The Angiosperm Phylogeny Group (APG, 2003) in an apparent effort to simplify Asparagales classification, have proposed that Asphodelaceae and Hemerocallidaceae be included in Xanthorrhoeaceae *sensu lato*. This proposal was partly put forward to facilitate and simplify teaching asparagoid families as there are difficulties experienced by non-specialists in the group (APG, 2003; Peter Stevens, pers. comm.). In this scenario Asphodelaceae would fall into Xanthorrhoeaceae and would have to be awarded a subordinate rank. The APG classification is in a state of continual refinement and future changes are anticipated judging from the uncertainties and complexity in the classification of Asparagales.

Table 1.2. List of *Kniphofia* species under threat in southern African.

Taxon	**Conservation Status**	**Source**
1. *K. acraea*	Rare	Hilton-Taylor (1996)
2. *K. angustifolia*	Not threatened; Lower risk (Least concern)	Hilton-Taylor (1996); Scott-Shaw (1999)
3. *K. brachystachya*	Lower risk (Least concern)	Scott-Shaw (1999)
4. *K. breviflora*	Lower risk (Least concern)	Scott-Shaw (1999)
5. *K. bruceae*	Rare	Hilton-Taylor (1996)
6. *K. buchananii*	Lower risk (Least concern)	Scott-Shaw (1999)
7. *K. citrina*	Indeterminate	Hilton-Taylor (1996)
8. *K. coddiana*	Rare; Lower risk (Near threatened)	Hilton-Taylor (1996); Scott-Shaw (1999)
9. *K. coralligemma*	Rare	Hilton-Taylor (1996)
10. *K. crassifolia*	Indeterminate	Hilton-Taylor (1996)
11. *K. drepanophylla*	Insufficiently known; Vulnerable	Hilton-Taylor (1996); Scott-Shaw (1999)
12. *K. ensifolia* subsp. *autumnalis*	Rare	Hilton-Taylor (1996)
13. *K. evansii*	Rare; Lower risk (Near threatened)	Hilton-Taylor (1996); Scott-Shaw (1999)
14. *K. fibrosa*	Not threatened	Hilton-Taylor (1996)
15. *K. flammula*	Vulnerable	Hilton-Taylor (1996); Scott-Shaw (1999)
16. *K. hirsuta*	Vulnerable	Hilton-Taylor (1996)

Table 1.2. continued

Taxon	**Conservation Status**	**Source**
17. *K. ichopensis*	Lower risk (Least concern)	Scott-Shaw (1999)
18. *K. latifolia*	Endangered	Hilton-Taylor (1996); Scott-Shaw (1999)
19. *K. leucocephala*	Endangered; Critically endangered	Hilton-Taylor (1996); Scott-Shaw (1999)
20. *K. littoralis*	Not threatened; Lower risk (Near threatened)	Hilton-Taylor (1996); Scott-Shaw (1999)
21. *K. northiae*	Lower risk (Least concern)	Scott-Shaw (1999)
22. *K. pauciflora*	Extinct; Extinct in wild	Hilton-Taylor (1996); Scott-Shaw (1999)
23. *K. rigidifolia*	Rare	Hilton-Taylor (1996)
24. *K. rooperi*	Not threatened; Lower risk (Least concern)	Hilton-Taylor (1996); Scott-Shaw (1999)
25. *K. sarmentosa*	Rare	Hilton-Taylor (1996)
26. *K. thodei*	Not threatened	Hilton-Taylor (1996)
27. *K. triangularis* subsp. *obtusiloba*	Rare	Hilton-Taylor (1996)
28. *K. typhoides*	Insufficiently known	Hilton-Taylor (1996)
29. *K. tysonii* subsp. *lebomboensis*	Not threatened; Data deficient	Hilton-Taylor (1996); Scott-Shaw (1999)
30. *K. umbrina*	Endangered; Critically endangered	Hilton-Taylor (1996); Witkowski *et al.* (1999)

The above proposal to recognise Xanthorrhoeaceae *s.l.* (including Asphodelaceae and Hemerocallidaceae) has not gained wide acceptance yet. Thus, I have taken a conservative approach and retain Asphodelaceae.

Chase *et al.* (2000) using chloroplast DNA sequence data found that Asphodelaceae *sensu* Dahlgren *et al.* (1985) is monophyletic, and more closely related to Hemerocallidaceae and Xanthorrhoeaceae than the morphologically similar Anthericaceae. McPherson *et al.* (2004) found that an intron from the 3' *rps12* locus is absent in all Asphodelaceae examined and some representatives of the closely related Hemerocallidaceae. This loss can be treated as a strong molecular marker for the monophyly of Asphodelaceae.

Asphodelaceae is separated from other lilioid monocot groups by the combination of the following characters: general presence of anthraquinones, lack of saponins, simultaneous microsporogenesis, atypical ovular morphology and the presences of an aril. Each of these occurs in other asparagoid groups but the above combinational features distinctively define Asphodelaceae (Chase *et al.*, 2000). Additionally several combinational seed characters that might be useful in distinguishing Asphodelaceae include presence of an aril, an endosperm with lipids and aleurone instead of starch, and an embryo that is three-quarter of the length of the endosperm. However, all the above characters except the presence of an aril are not useful for field identifications.

Morphologically, Asphodelaceae is divided into two more or less clearly delimited subfamilies, Alooideae and Asphodeloideae. Alooideae has a distinct southern African centre of radiation with outliers in Saudi Arabia, Madagascar and the Mascarene Islands. Asphodeloideae has a predominantly Eurasian distribution with significant outliers in Africa, Australia and New Zealand (Treutlein *et al.*, 2003). Currently, the most accepted morphological treatment of Asphodelaceae is the framework of Dahlgren *et al.* (1985). Although this treatment is widely accepted, there have been varying and different views on the relationships of the genera in Asphodelaceae. Despite various attempts to stabilise classification of Asphodelaceae, generic relationships remain unresolved (Treutlein *et al.*, 2003).

Kniphofia represents a monophyletic lineage within the Asphodelaceae. However, its subfamilial affinity has been disputed. Some workers have placed *Kniphofia* within Alooideae based on floral morphology and inflorescence structure (Cronquist, 1981, 1988). However, other studies using different approaches have shown that *Kniphofia* is best placed in Asphodeloideae, supporting the Dahlgren *et al.* (1985) classification. Van Staden and Drewes (1994) and Van-Wyk *et al*. (1995) found phytochemical evidence for a close relationship between *Kniphofia* and other Asphodeloideae genera (viz. *Bulbine* Wolf and *Bulbinella* Kunth). Chase *et al.* (2000) investigated generic relationships in Asphodelaceae using chloroplast DNA (cpDNA) sequence data and found that *Kniphofia* is better placed in the subfamily Asphodeloideae (with *Bulbinella* Kunth, *Bulbine* Wolf, *Jodrellia* Baijnath, *Trachyandra* Kunth, *Eremurus* M. Beib., *Asphodeline* Reichenb. and *Asphodelus* L.). These workers support the basic framework of Dahlgren *et al.* (1985). However, support for two separate subfamilies is lacking. Alooideae appears to be monophyletic, while Asphodeloideae is paraphyletic (Fig. 1.2.).

Molecular studies using cpDNA sequences by Treultein *et al.* (2003) concentrated on subfamily Alooideae. Increased sampling of Alooideae revealed that *Aloe* and *Haworthia* are non-monophyletic (Treultein *et al*., 2003). Like Chase *et al*. (2000), Treultein *et al.* (2003), found Alooideae to monophyletic while Asphodeloideae was paraphyletic. Both studies (Chase *et al.*, 2000; Treultein *et al*., 2003) revealed that *Bulbine* was sister to *Jodrellia* supporting the separation of the latter from *Bulbine*. The segregation was originally proposed based on floral morphology by Baijnath (1976). The *Bulbine-Jodrellia* clade is sister to the Alooideae clade (Fig. 1.2.). Immediately sister to the above clades is a lineage composed of *Kniphofia* and *Bulbinella* i.e. *Bulbinella* is sister to *Kniphofia* (Chase *et al*., 2000; Treultein *et al*., 2003) (Fig. 1.2.).

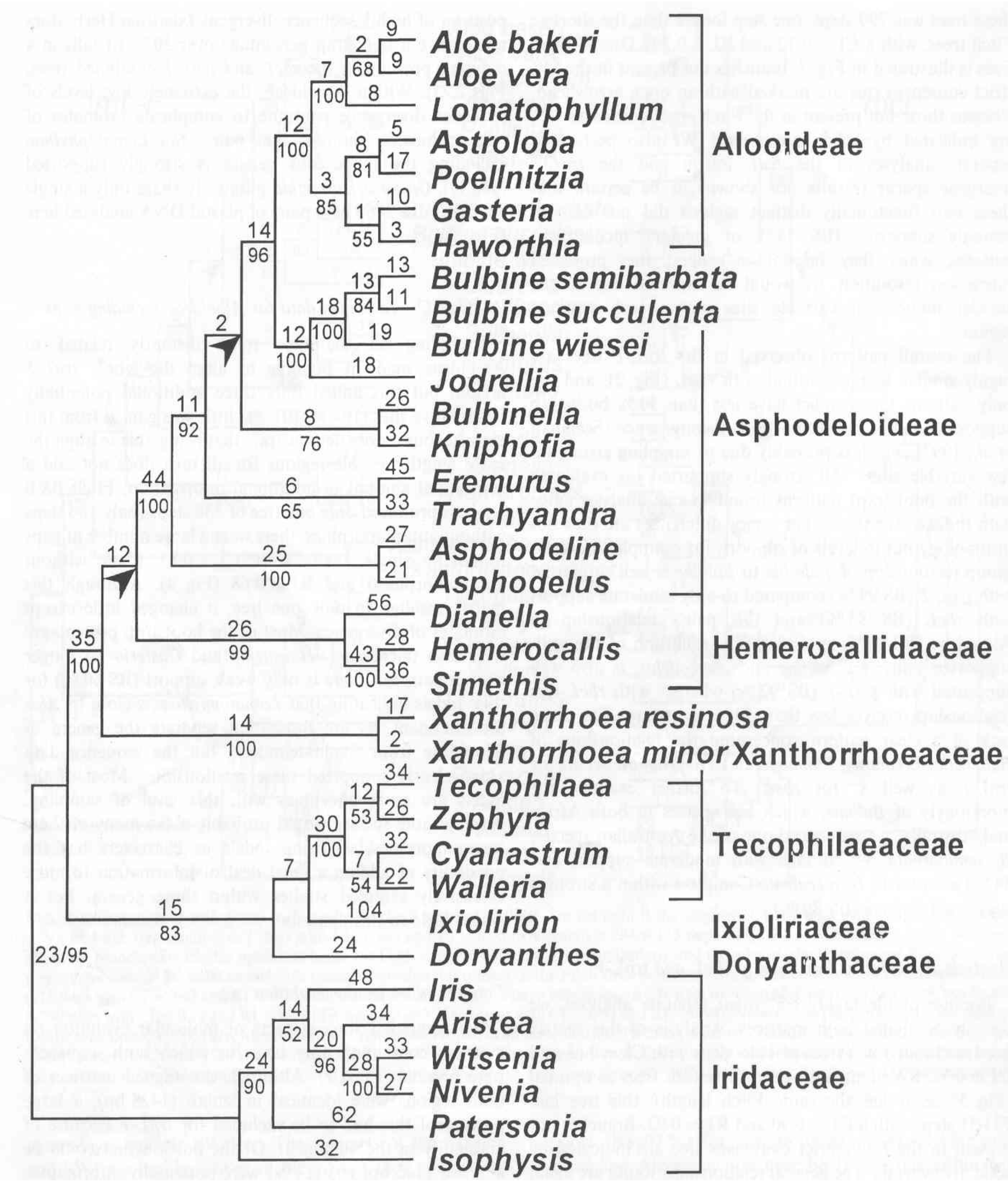


Fig. 1.2. Phylogenetic tree showing relationships between Asphodelaceae and closely related asparagoid families based on chloroplast DNA (*rbcL* and *trnL-F*) (from Chase *et al.*, 2000).

This is a surprising result as one would expect *Kniphofia* to be more closely placed to the morphologically similar Alooideae and *Bulbinella* to be more closely placed to other morphologically similar Asphodeloideae genera e.g. *Bulbine*. Further research may explain the close relationship between *Kniphofia* and *Bulbinella*.

1.4. The present study

Even with the vast taxonomic background that currently exists for the genus, a contemporary and cohesive revision for the entire genus does not exist. The monographic work of Berger (1908) is outdated.

Most past workers examined the genus in parts based on regional limits e.g. Codd (2005). The number of specimens collected has increased considerably, and some previously poorly collected areas have received more attention over the past few decades (e.g. Tanzania). This has not only meant that knowledge of species limits has improved, but also a number of new species have been discovered and additional distributional data has accumulated (Kativu, 1996; Demissew and Nordal, 1997; Whitehouse, 2002a).

A revision of the entire genus is thus a very difficult undertaking. It will require extensive field work (on a continental scale) to understand the biology of these plants in their natural habitats. Due to limits imposed by time and resources a revision of the entire genus was not attempted in this study. *Kniphofia* has a complicated taxonomic history, with numerous taxonomic problems that remain unresolved. The complex taxonomic history and problematic morphological delimitation of many taxa makes additional research necessary.

In past studies of the genus limited attempts were made to examine evolutionary relationships or produce a phylogenetic classification. Thus, phylogenetic relationships within *Kniphofia* (and many other genera of Asphodelaceae) are still unsettled and continue to be disputed. Furthermore, no work has been done on the biogeography or phylogeography of the genus.

1.5. Aims of the present study

There are four main aims of the present study:

1. To undertake a genus level, Africa-wide, assessment of diversity and endemism in the genus (Chapter 2).
2. To use DNA sequence data from chloroplast and nuclear markers to reconstruct a species-level phylogeny for the genus *Kniphofia* in order to better understand intra-generic species relationships and evolutionary processes (Chapter 3).
3. To use the phylogenies and nested clades (a phylogeographic approach) generated from DNA sequence data to study the biogeography and evaluate the biogeographical patterns in the genus (Chapter 4).
4. To assess anatomical variation and determine if anatomical characters are useful for species delimitation (Chapter 5).

A synthesis of this study and conclusions are presented in Chapter 6.

Chapter 2: Chorology and Centres of Diversity

2.1. Introduction

Despite its horticultural popularity of *Kniphofia*, no general account of its biogeography is available. Geographic patterns combined with molecular data can provide important insights into evolutionary processes (e.g. McKinnon *et al*., 1999; Schaal and Olsen, 2000). In *Kniphofia* knowledge of geographic patterns is essential in understanding its evolution and to interpret the DNA sequence data results. Thus, it is necessary to review the biogeographical patterns in *Kniphofia*.

2.1.1. *Kniphofia* in African plant biogeography

According to White (1978) *Kniphofia* is one of several genera that are centred in southern Africa and is essentially Afromontane. Others include *Alepidea* F.Delaroche (Apiaceae), *Bowkeria* Harvey (Scrophulariaceae), *Lotononis* (DC) Eckl. & Zeyh. (= *Buchenroedera* Eckl. & Zeyh., Fabaceae), *Styppeiochloa* De Winter (= *Crinipes* Hochst., Poaceae), *Macowania* Oliv. (Asteraceae) and *Rendlia* Chiov. (Poaceae). Of these, *Styppeiochloa*, *Kniphofia*, *Macowania* and *Rendlia* are more or less exclusively Afromontane north of the Limpopo River (White, 1978). Furthermore, *Kniphofia* is centered in the eastern part of southern Africa and decreases northwards on the African mountains into south-western Arabia (Yemen) with two species from Madagascar. Other genera that have a similar distribution pattern are *Alepidia*, *Freesia* Klatt (= *Anomatheca* Ker Gawl., Iridaceae), *Dierama* K.Koch (Iridaceae), *Dietes* Salisb. ex Klatt (Iridaceae), *Knowltonia* Salisb. (Ranunculaceae) and *Merxmuellera* Conert (Poaceae) (Goldblatt, 1978). Beyond these general trends, no research has focused on biogeographic aspects of *Kniphofia*.

The findings above indicate that *Kniphofia* is not an Afromontane element *sensu stricto*. It does show a strong association with the Afromontane Region but extends beyond the boundaries of this vegetation, especially in southern Africa. Consequently it is worth examining the Afromontane Region briefly.

2.1.2. The Afromontane Region: a brief overview

The Afromontane Region is an archipelago-like regional centre of endemism, consisting of c. 4 000 species with 75% endemism (White, 1978, 1981, 1983) and is a hot spot of diversity (Burgoyne *et al.*, 2005). White’s figures are probably an under estimate since Hilliard and Burtt (1987) found c. 1 261 species from the southern KwaZulu-Natal Drakensberg alone. Although many species are local endemics, the majority, especially the dominants, are widely distributed within the Afromontane Region (White, 1981).

Relationships to other phytochoria are considered to be complex and White (1981) considered the flora to be more complex in origin and evolutionary history than any other in the world. The ‘islands’ that make up the Afromontane archipelago are widely distributed over Africa. These islands extend from the Lome Mountains and Tingi Hills (Sierra Leone) in the west to the Alh Mescat Mountains (Somalia) to the east, the Red Sea Hills to the north and the Cape Region (South Africa) in the south (White, 1978, 1983). The region is very diverse in lithology and physiography. Some islands of volcanic origin are of different laval ages (White, 1983). Seven regional mountain systems are recognised (White, 1978, 1983):

1. West African
2. Ethiopian
3. Kivu-Ruwenzori
4. Imatongs-Usambara
5. Uluguru-Mulanje
6. Chimanimani
7. Drakensberg

The West African system is the most isolated and some of the mountains within it are more isolated from each other than are most mountains in other systems (White, 1978, 1983). Despite the complexity and wide distances separating the islands of the archipelago, the collective flora of the region exhibits remarkable continuity, uniformity and internal cohesiveness, making it distinct enough to separate from other adjacent phytochoria (White,1978, 1981, 1983). This high degree of homogeneity across the distributional range of the Afromontane Region is reflected ecologically and phytogeographically (Linder, 1990). The Afromontane Region was not recovered by Linder (1998) as a homogeneous unit in his study testing Frank White's phytochoria, but the importance of the Afromontane Region in contributing to species richness and endemism was demonstrated. Linder (2001) examined plant diversity and endemism in sub-Saharan Tropical Africa. He did not recover an Afromontane centre or centres *per se*, because of the coarse sampling approach but reference to the Afromontane Region is made in several instances.

On most African mountains the vegetation diminishes in stature from the lower slopes to the summit but is often modified by local features of aspect, exposure, frost, soil depth and local climatic patterns which are determined by the size and configuration of the mountain in relation to the distance from the sea or other sources of moisture (White, 1978, 1983). Climate for the region is variable. The mean rainfall in the Forest Belt is usually more than 1 000 mm per year. Rainfall is lower in the drier types transitional to the lowlands. In the Afroalpine Belt above the forests, some mountains have much less than 1 000 mm per year. Cloud is a feature of most mountains and frost varies considerably (White, 1983).

Each massif has a unique ecology (White, 1981). On any given mountain there is a wide range of vegetation types with a corresponding change in floristic composition (White, 1983). The vegetation may have few species in common but all the types are connected by complex series of intermediates (White, 1981). The floristic differences between the extreme vegetation types on a single mountain are usually greater than the differences between the Afromontane assemblages as a whole on the mountain and the assemblage found on nearby or distant mountains (White, 1981, 1983). On most of the islands the vegetation consists almost predominantly of Afromontane endemic or near endemic species, but in some areas the Afromontane Region is diluted by lowland species (White, 1981).

In general the African mountains show ecological and altitudinal zonation. Three broad belts are widely recognised: the Alpine Belt, the Subalpine (Ericaceous) Belts and the Forest Belt (e.g. Hedberg, 1970; White, 1983; Linder, 1990). The mountains of Africa have large spatial separation with latitudinal influence on zonation (Linder, 1990) and each massif with its own peculiarities (White, 1978). The recognition of distinct zones is often arbitrary (White, 1978). In the tropics these belts are more or less well demarcated, but further south altitudinal belts become confusing and difficult to interpret (Linder, 1990). Zonation is more defined in the mountains of East Africa where the Forest and Ericaceous belts are reasonably distinct (White, 1978). Beneath the Forest Belt there is usually a transition zone connecting the Afromontane and lower phytochoria. In Malawi, Zimbabwe and Mozambique most of the mountains lie within the Forest Belt and in these countries the mountains are surrounded by a sea of Miombo woodland, generally with no intermingling of vegetation (White, 1978).

Extensive transitional conditions occur only in South Africa, where latitude compensates for altitude. The Afromontane vegetation transcends to almost sea level and relationships with surrounding phytochoria are complex (White, 1978). This is also because of the rich surrounding flora, the great diversity of biomes and climatic provinces (summer and winter rainfall) that the Afromontane Region transects. In the equatorial regions the Alpine Belt starts between 3 300-4 000 m. In the Drakensberg it is between 2 800 m to the summit (3 484 m). In the Cape Region the Alpine Belt is reported to be above 1 700 m, but is ‘scarcely known’ (Linder, 1990). The Subalpine (Ericaceous) Belt lies between the upper reaches of the forest margin and the transitional to the Alpine Belt. In the tropics the

Ericaceous Belt penetrates into the forest with no clear altitudinal zonation (Linder, 1990). The Forests Belt begin at c. 2 000 m in Tropical Africa, c. 800 m in Zimbabwe and reaches sea level in South Africa (Linder, 1990). There is a significant amount of mixing with the surrounding lower vegetation (Linder, 1990) and the Forest Belt is a dynamic mosaic of forests and grassland (Meadows and Linder, 1993).

Data on the distribution of *Kniphofia* obtained from previous revisions (Codd, 1968, 2005; Marais, 1973; Kativu, 1996; Whitehouse, 2002a; Demissew and Nordal, 1997), the Pretoria Computerised Information System (PRECIS) database and collections made during this study revealed the following patterns: in East and Tropical Africa, *Kniphofia* is predominantly found in the Afromontane Region supporting White's (1978) observation. Furthermore, *Kniphofia* exhibits a strong Afromontane Grassland affinity being found predominantly but not exclusively in Afromontane grasslands. It also occasionally occurs in lower surrounding vegetation that has a grassland element (e.g. Miombo woodland) and in higher Subalpine vegetation e.g. Bale Mountains, Ethiopia (personal observation).

Kniphofia is confined mostly to the Afromontane Region in Tropical and East Africa especially the Afromontane grasslands but occasionally occurs at lower altitudes. White (1978) noted that Afromontane species which descend into lower phytochoria are marginal intruders or do so as distant satellite populations. The distribution of *Kniphofia* beyond the Forest Belt in Tropical and East Africa is considered to be a marginal intrusion. This is expected when the complexity of zonation on these mountains are taken into account.

The Afromontane Region in southern Africa is centered in Lesotho and the Drakensberg Region (Cowling and Hilton-Taylor, 1997). The Drakensberg forms part of the great escarpment at the eastern periphery of the southern Africa plateau, extending from the central Eastern Cape (Barkly East) in the south to the

Wolkberg (south-east Northern Province) in the north. This spans a distance of c. 1 050 km with an estimated c. 2 200 angiosperms in the core of the region (*sensu* van Wyk and Smith, 2001). The Afromontane Region in southern Africa is unique as latitude compensates for altitude and the Afromontane vegetation descends to almost sea level with intermingling and transitional conditions between Afromontane and surrounding vegetation (White, 1978). In the Cape Region enclaves of forests are found close to sea level (White, 1978, 1983). The compensation effects of latitude results in many Afromontane species descend to sea level and the lower level of the Afromontane Region becomes blurred (Moll and White, 1978).

A few *Kniphofia* species are found in the Subalpine Belt e.g. *K. porphyrantha* and three species (*K. caulescens*, *K. northiae* and *K. ritualis*) were noted from the Alpine Belt in the Drakensberg (Killick, 1978). In South Africa, *Kniphofia* occurs from the Alpine Belt in the Drakensberg and descends to the coastal regions. It appears that the compensational effects of latitude for altitude has resulted in *Kniphofia* spreading to lower altitudes in southern Africa.

A high number of *Kniphofia* species (18 species; 38% of *Kniphofia* species in SA, 25% for the entire genus) prefer high altitudes of more than 1 500 m (Codd, 1968, 2005). An altitude of 1500 m in this case is used as a conservative lower altitudinal limit value for the Afromontane vegetation, considering the intermingling of vegetation in southern Africa and that the Forest Belt mostly ranges from 1 280-1 830 m in the Drakensberg (White, 1978). Thirty species (63% of *Kniphofia* species in SA, 42% for the entrie genus) occur from 0-1 500 m i.e. a substantial number of *Kniphofia* species occur in the Drakensberg-Maputoland-Pondoland transition. Additionally six species (13% of *Kniphofia* species in SA, 9% for the entire genus) are strictly coastal endemics (i.e. Maputoland-Pondoland coastal endemics). The six coastal endemics include *K. littoralis*, *K. pauciflora*, *K. coddiana*, *K. drepanophylla*, *K. rooperi* and *K. leucocephala*.

The Afromontane (Drakensberg) and Tongoland (i.e. Maputoland)-Pondoland (Drakensberg-Maputoland-Pondoland) transition is unique in that it is the only region in Africa where the Afromontane and lowland species intermingle over an extensive area (White, 1978). The Maputoland-Pondoland Region is a mosaic that displays great physiographic diversity with steep climatic gradients. It is a mosaic of forest, thicket, savanna, grassland, fynbos and swamp vegetation (Moll and White, 1978). It interfingers with elements of the Afromontane Region (Goldblatt, 1978) especially along river valleys (Cowling and Hilton-Taylor, 1997). The borders of this region are difficult to demarcate as it includes tropical, subtropical and afromontane elements. It is considered as an artifical rather than a natural floristic unit (van Wyk and Smith, 2001).

2.1.2.1. Afromontane Grasslands: a brief overview

Kniphofia shows a strong association with Afromontane grasslands. Thus it is worth examining these grasslands in more detail. The most extensive vegetation in the Afromontane Region is fire-maintained grassland consisting predominantly of species which are also abundant in the lowlands (White, 1978). The grasslands are perennial tussock grasslands subject to regular burning and are associated with a rich herbaceous flora. Afromontane grasslands are more extensive on the drier mountains with frequent fire (Meadows and Linder, 1993).

Evidence suggests that Afromontane grasslands are not recent (Ellery *et al.*, 1991; Meadows and Linder, 1993), contradicting earlier views of White (1978) and Acocks (1953) who believed that these grasslands were of recent origin due to anthropogenic activity. There is a growing consensus that the current distribution of grasslands predates intensive farming by thousands of years (Ellery and Mentis, 1992; Meadows and Linder, 1993). High levels of endemism amongst herbaceous flora of grasslands (especially geophytes) also indicates a long history for this component in the Afromontane Region (Meadows and Linder, 1993; O'Connor and Bredenkamp, 1997; Burgoyne *et al.*, 2005).

In Tropical and East Africa most Afromontane vegetation occurs above 2 000 m (White, 1983). At high altitudes Afromontane species become increasingly numerous and lowland forest gives way to transitional forest and, ultimately where massifs are high enough, to montane forests (Moll and White, 1978). The secondary grasslands of the Afroalpine Belt differ from those of the Forest Belt in both composition and chorological relationship. Grasses of the Afroalpine belts are usually confined to the high mountains (White, 1978).

The most extensive vegetation of the Forest Belt in South Africa is *Themeda triandra* grassland. This grassland consists predominately of species which are also abundant in the lowlands (White, 1978). In South Africa patterns are obscured because 'temperate' grasses descend much lower and the most abundant tropical grass (*Tremeda triandra*) ascends relatively high (White, 1983). In the Afromontane regions of southern Africa most of the endemics are associated with grasslands (Hilliard and Burtt, 1987; Meadows and Linder, 1993; Cowling and Hilton-Taylor, 1997).

Since *Kniphofia* has a strong Afromontane grassland affinity, factors influencing grassland distributions are presumed to influence the distribution of *Kniphofia* to some degree. The distribution of grasslands is the result of the subtle interplay of climate, topology, fire, and grazing. The overall extent of grasslands seems to be strongly determined by climatic variables, while fire and grazing exert considerable influence on the boundaries of the biome (O'Connor and Bredenkamp, 1997). Ellery *et al.* (1991) demonstrated that climate is the overriding determinant of grassland biome distribution as a whole in southern Africa. A number of grassland and savanna sites have the potential to support forest but are prevented from doing so by fire or some other disturbance. As the degree of seasonality of rainfall increases, vegetation is susceptible to burning due to the prolonged or intense dry period. Ellery *et al*. (1991) have suggested that climate contributes to the maintenance of grasslands by promoting a disturbance regime that excludes woody plants. Meadows and Linder (1993) have found that for afromontane grasslands seasonality and not total rainfall is important in the shift towards grassland from forest.

Bond *et al.* (2003) believe that the vegetation of South Africa could be very different if fires were infrequent. The eastern half of the country could be covered with trees in the absence of fire. It appears that most of the higher rainfall south-western and eastern parts of the country owe their current vegetation to high fire frequencies (Bond *et al*., 2003).

The aim of this chapter was to study the chorology of *Kniphofia* and to determine centres of diversity and endemism for *Kniphofia*. Several approaches were used to determine diversity and endemism. An Africa-wide chorological assessment was done for the entire genus. These were used to delimit centres of diversity and endemism. Subsequently, southern African was studied in greater detail. A chorological assessment was done for southern African to delimit areas of diversity and endemism. A numerical analysis was done to find areas of diversity. Additionally endemism in southern Africa was assessed using a parsimony analysis of endemicity approach and mapping of range restricted taxa.

2.2. Materials and Methods

Chorology in a broad sense is the study of the distribution of taxa and floristic regions and their history (see van Wyk and Smith, 2001). In a more restricted botanical sense it applies to the study of the distribution of a specific group of plants (e.g. a family or genus). A basic tenet of such a study is to determine the number of species and distribution thereof within a given area. These in turn assists in delimiting areas of diversity and endemism.

Numerical analyses can also be used to determine centres of diversity. Species richness and diversity per unit area (e.g. quarter degree grids) provides a rapid assessment of species rich areas. This data is then used to determine areas of diversity. In this approach areas with similar species composition are located by a clustering method (e.g. Linder and Mann, 1998). Clusters/groups of areas (typically grids) are then delimited and these groups are mapped to determine areas of diversity.

Areas of endemism can be located using a parsimony analysis of endemicity approach (Morrone, 1994) by subjecting distributional data to a parsimony analysis. The results are then used to determine areas of endemism. Areas of endemism can also be located by plotting the distribution of range restricted species. The distribution outlines for these taxa are mapped and areas of overlap are used to delimit areas of endemism (e.g. Linder and Mann, 1998).

2.2.1. Africa-wide chorological assessment for *Kniphofia*

Distribution data were obtained from previous revisions (Codd, 1968, 2005; Marais, 1973; Kativu, 1996; Whitehouse, 2002a; Demissew and Nordal, 1997), the PRECIS database and collections made during this study. These were plotted onto maps of Africa. Based on these distribution patterns several more or less geographically isolated distribution areas were delimited for Africa, Madagascar and Yemen. Distribution patterns were then used to produce a chorological map of Africa and Madagascar which depicted species richness by means of isochores. Centres of endemism, overlap regions and outliers were determined for these regions by comparing species lists of these areas following the method of Linder (1983). Centres of diversity were also determined from these lists. Centres of endemism are defined as regions having more than 30% endemism, outliers are areas with less than 30% endemism and where the majority of the species are held in common with a nearby centre. In overlap regions endemism is less than 30% and the non-endemic species are held in common with two other centres (Linder, 1983). Subcentres (within centres) were also determined for diversity and endemism. Subcentres of diversity were determined from species lists and areas with more than four species were delimited as subcentres. The requirement of a minimum of four species to define a subcentre is subjective. However, it is the most convenient way of defining subcentres for *Kniphofia* especially in Tropical Africa were species richness is not as high as southern Africa. Subcentres of endemism were defined as areas that have ≥30% endemism for that centre.

2.2.2. Studies in Southern Africa

A more detailed phytogeographic analysis was done for southern Africa (South Africa, Swaziland and Lesotho) because of the large amount of distributional data accumulated for the region. The PRECIS data was provided in 1/16th degree square (i.e. quarter degree) grids for 46 of the 48 taxa. The two exceptions were *K. crassifolia* and *K. praecox*. *K. crassifolia* is only known from the type collection with vague locality details. This species most likely falls within the quarter degree grid 2329DD (Houtbosch, Limpopo Province; Pieter Winter, pers. comm.). All collections of *K. praecox* were placed under *K. bruceae* in PRECIS, viz. collections from the Western Cape. The problems associated with *K. praecox* were outlined in Chapter 1. Codd (2005) in his latest revision upheld *K. praecox*, which is followed in this study. The necessary addition and modifications were done for *K. crassifolia* and *K. praecox* respectively.

2.2.2.1. Numerical analysis of distribution data to determine areas of diversity

Quarter degree grid (QDG) diversity or species richness which is the number of species per QDG was obtained from the PRECIS data and collections made during this study to determine species rich areas.

The data above was used to create a matrix for southern African *Kniphofia* taxa with species as characters and QDGs as terminal units (Appendix 1). Areas with similar species composition were located by using the method of Linder and Mann (1998). The data set was analysed using NT-SYS version 2.0. (Rohlf, 1998). A similarity matrix was generated using the Jaccard similarity (J) co-efficient and clustering of grids was performed using UPGMA (Unweighted Pair Group Method, Arithmetic Average) clustering method. The Jaccard co-efficient disregards shared absences and is therefore suitable for biogeographical analysis where absences may either be due to 'real' absences or a result of under collection. Grids with a single species (singletons) show either 0% or 100% similarity to other grids, thus accentuating errors and distorting results (Linder and Mann, 1998). Consequently, these grids were removed prior to the analysis. Clusters/groups of grids were arbitrarily delimited by a phenon line and these groups were mapped to determine areas of diversity. This approach was also advocated at the half degree grid (HDG) scale. The data set showing *Kniphofia* species as characters and HDGs as terminal units (with singleton HDGs removed) is given in Appendix 2.

2.2.2.2. Parsimony analysis of endemicity (PAE)

Areas of endemism i.e. those grids which have at least some species resticted to them were located using a parsimony approach (Morrone, 1994). The QDG data set (Appendix 1) was subjected to a parsimony analysis conducted using PAUP* 4.0b10 (Swofford, 2002). Uninformative characters (i.e. species) were excluded and all characters were equally weighted and unordered. A randon input analysis was performed to determine if there were multiple islands of equally most parsimonious trees (Maddison, 1991). A full heuristic search was conducted on the trees found by this method with TBR branch swapping and MAXTREES set at 1 000. A strict consensus tree was constructed from all the most parsimonious trees. Groups of grids were mapped and those which have at least two species unique to them are regarded as areas of endemism. The distribution boundaries of these endemic species are mapped to delineate the boundaries of each area (Morrone, 1994; Morrone and Crisci, 1995). This technique was also applied at the HDG scale.

2.2.2.3. Areas of endemism based on mapping of range restricted species

Areas of endemism were located by plotting the distribution of range restricted species which are defined as species with a distribution area of ten QDGs or less (Linder and Mann, 1998). The distribution outlines for these taxa are overlaid on a map and areas of overlap are used to delimit centres of endemism (Linder and Mann, 1998).

2.3. Results and Discussion

2.3.1. Africa-wide chorological assessment for *Kniphofia*

Six centres of diversity were delimited from the chorological analysis (Fig. 2.1.). These are Madagascar, Cameroon, Rift Valley, South-central Africa, Zimbabwe and South Africa (including Lesotho and Swaziland). These areas are based on geographic limits and species assemblages rather than political boundaries. The Rift Valley Centre includes species from Yemen, Sudan, Ethiopia, Kenya, North-eastern parts of the Democratic Republic of Congo (DRC), Uganda, Burundi, Rwanda and northern Tanzania. The South-central African Centre includes species from Angola, South-eastern parts of the DRC, Zambia, Malawi, Mozambique and south-central Tanzania. The Zimbabwe Centre includes species from Zimbabwe and a species from Mozambique. The South Africa (SA) Centre includes species from Lesotho, Swaziland and a single species from Mozambique. The number of species within these centres were represented by means of isochores (Fig. 2.1.).

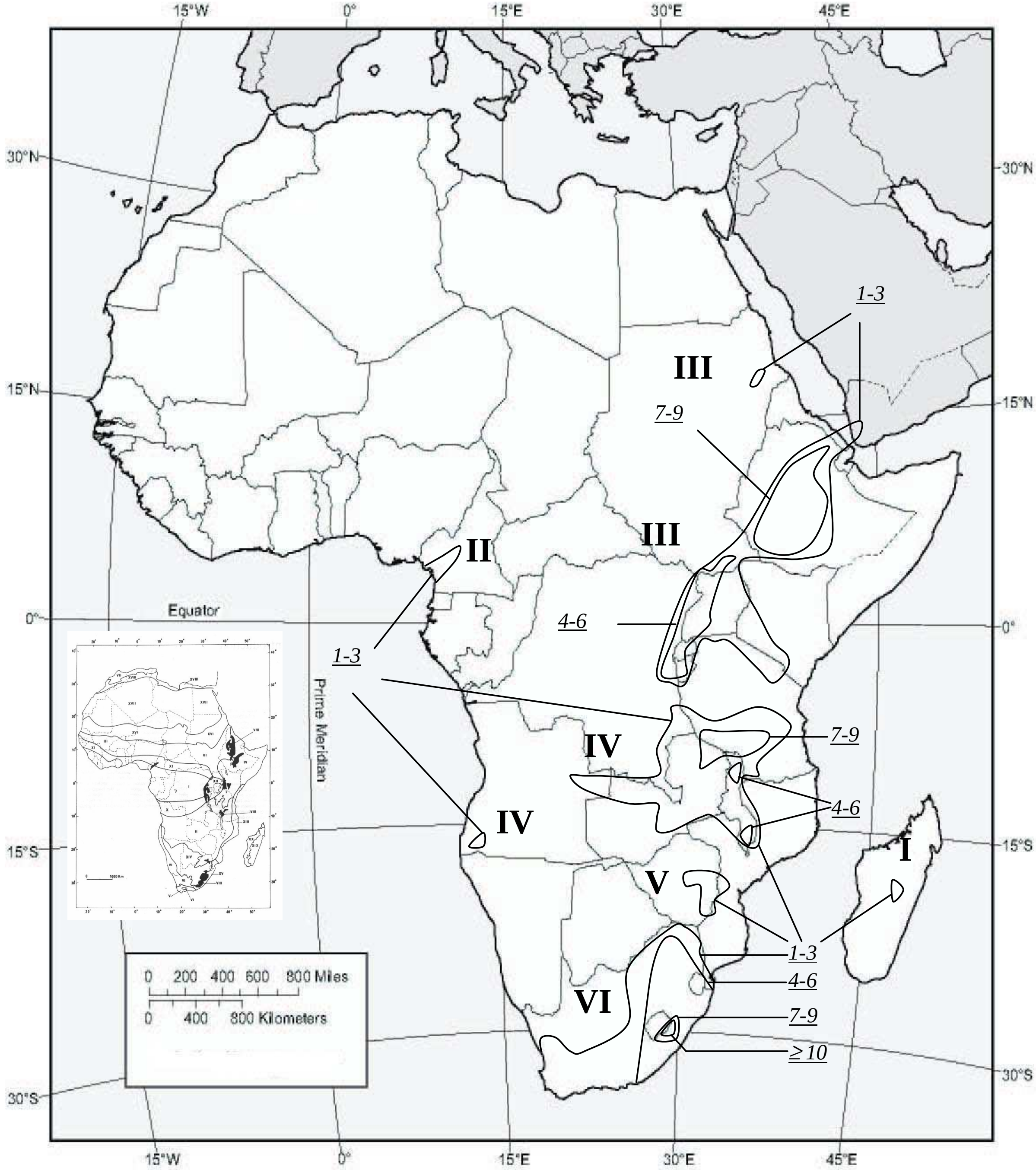


Fig. 2.1. Centres of diversity recognised for *Kniphofia* with number of species (underlined and italised) represented by isochores. Bold numbers represent the centres of diversity: I= Madagascar, II= Cameroon, III= Rift Valley, IV= South-central Africa, V= Zimbabwe, VI= South Africa. The insert shows the vegetation map of Africa and Madagascar (White, 1978) with black areas representing the Afromontane Region. (Map source: T. Dorschied, Arizona State University ©).

The most diverse centres in descending order are: South Africa (48 species), South-central Africa (14 species), Rift Valley (11 species), Zimbabwe and Madagascar (both with two species) and Cameroon (one species). South Africa represents the centre of diversity for the genus. A summary of the results for species diversity, endemism and patterns of overlap are presented in Table 2.1.

Table 2.1. Species richness, levels of endemism and patterns of overlap among the centres of diversity for *Kniphofia*.

	Madagascar	Cameroon	Rift Valley	South-central Africa	Zimbabwe	South Africa
Madagascar	2					
Cameroon	0	1				
Rift Valley	0	0	11			
South-central Africa	0	0	5	14		
Zimbabwe	0	0	0	2	2	
South Africa	0	0	0	2	2	48
Percentage of species in genus	3	1.5	16	18	3	68
No. of endemics (% endemics)	2 (100)	1 (100)	7 (64)	7 (50)	0 (0)	46 (96)

Five of the six centres are considered to represent centres of diversity and endemism for *Kniphofia*. The exception is the Zimbabwe Centre which has no endemics. The two species (*K. linearifolia* and *K. splendida*) of this centre are found in the South Africa Centre and the South-central Africa Centre. Zimbabwe is best treated as a region of overlap. Linder (1983) also found a lack of endemism in the Chimanimani Mountains for Disinae and regarded Zimbabwe to be an overlap region.

The centres of diversity and endemism for *Kniphofia* have a strong Afromontane affinity. A comparison of the centres of diversity for *Kniphofia* with the Afromontane centres of White (1978) and the centres of diversity for Disinae recovered by Linder (1983) is given in Table 2.2.

Table 2.2. Comparisons between the centres of diversity for *Kniphofia* with the Afromontane centres of White (1978) and the centres of diversity for Disinae recovered by Linder (1983).

***Kniphofia*: centres of divesity**	**Afromontane centres of White (1978) (RMS= regional mountain system)**	**Disinae: centres of diversity (Linder, 1983)**
South Africa	Drakensberg RMS found within SA Centre for *Kniphofia*	Cape and Natal-Transvaal Centres of Linder (1983) within SA Centre for *Kniphofia*
Zimbabwe	corresponds to Chimanimani RMS	corresponds to Zimbabwe Centre of Linder (1983)
South-cental Africa	includes entire Uluguru-Mulanje RMS and part of Kivu-Ruwenzori RMS	mostly within South-central Africa Centre of Linder (1983)
Rift Valley	includes part of Kivu-Ruwenzori RMS, and entire Imatongs-Usambara and Ethiopian RMS	corresponds mostly to Linder’s (1983) East Africa Centre
Cameroon	found within part of West African RMS	found within Linder’s (1983) West Africa Centre
Madagascar	mountains of Madagascar not considered as an island of the Afromontane archipelago	found within Linder’s (1983) Madagascar Centre

2.3.2. Subcentres of diversity and endemism

A summary of species richness and levels of endemism for subcentres within designated centres of diversity and endemism (using the chorological approach) are presented in Table 2.3. Eight subcentres of diversity (Fig. 2.2.) and two subcentres of endemism are proposed within the six centres of diversity. Subcentres for southern Africa are not discussed in detail in this section. It is more appropriate to discuss the subcentres for SA in section 2.3.3. (Studies in the South African Centre). Other subcentres are discussed below.

Table 2.3. Species richness and levels of endemism for subcentres of *Kniphofia*.

Centre: Subcentre	Total no. of species	No. of endemics	Percentage endemism (*= subcentre of endemism)
Rift Valley	11	7	64%
Ruwenzori	5	0	0
Ethiopia	7	5	46*
South Central Africa	14	7	50%
Mulanje	5	2	14
Nyika	4	0	0
South-central Tanzania	7	2	14
South Africa	48	46	96%
Cape-Karoo	8	3	6
Extended Drakensberg	40	26	54*
Northern South Africa	15	5	10

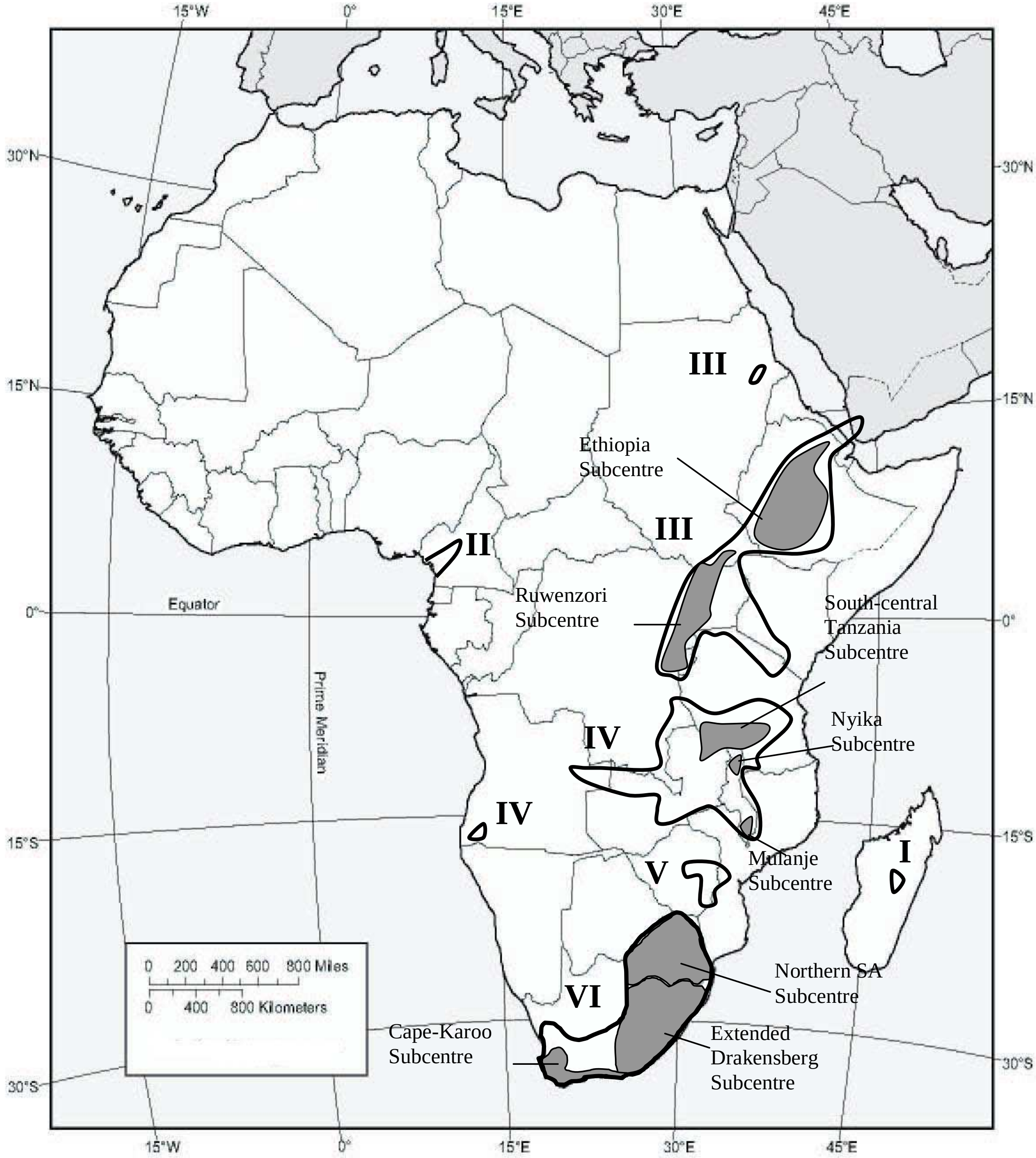


Fig. 2.2. Subcentres of diversity (shaded grey) within centres of diversity recognised for *Kniphofia*. Bold numbers represent the centres of diversity: I= Madagascar, II= Cameroon, III= Rift Valley, IV= South-central Africa, V= Zimbabwe, VI= South Africa (Map source: T. Dorschied, Arizona State University ©).

2.3.2.1. Subcentres in the Rift Valley Centre

Two areas were delimited as subcentres of diversity: the Ruwenzori and Ethiopia subcentres. The Ruwenzori Subcentre corresponds to the Kivu-Ruwenzori regional mountain system of White (1978).

The Ruwenzori Subcentre includes the boundary regions of the following countries: DRC, Burundi, Rwanda, Uganda and Sudan. None of the species found in this subcentre are endemics as all species (*K. grantii*, *K. pumila*, *K. thomsonii*, *K. princeae* and *K. bequaertii*) are found in the South-central Centre and this region is considered as an area of overlap. Most of this subcentre is in the Lake Victoria Regional Mosaic. This mosaic is a junction of five distinct floras viz. Guinea-Congolian, Sudanian, Zambezian, Somali-Masai and Afromontane. The vegetation is a mosaic of improvised variants of the first four floras, in some cases with an admixture of Afromontane species (White, 1983). This may account for its overlap status.

The Ethiopia Subcentre corresponds to the Ethiopian regional mountain system of White (1978). It is also a subcentre for endemism (46% endemism) for *Kniphofia*. Only one other subcentre of endemism (the Extended Drakensberg Subcentre) was recovered for *Kniphofia*. The geology of Ethiopia is varied. It is a tectonically active area with the Rift Valley transecting through. About 50.4% of land above 2 000 m and 79.9% landmass above 3 000 m in Africa occurs in Ethiopia (Yalden, 1983). According to Brenan (1978) the size of Ethiopia (c. 1 200 000 km^2) and the topodiversity accounts for the rich endemic element of the flora. The tectonics of the region may also play a role. These factors may also explain the regional diversity and endemism for *Kniphofia* in Ethiopia

2.3.2.2. Subcentres in South-central Africa

Three areas were delimited as subcentres of diversity: Mulanje, the Nyika Plateau and the South-central Tanzania Subcentres (Fig. 2.2). The Mulanje Subcentre represents Mount Mulanje (southern Malawi). This area is not considered a subcentre of endemism (14% endemism). Most of the non-endemics are found in the in the nearby Nyika Plateau Subcentre. Furthermore, *K. linearifolia* and *K. splendida* are found in the South Africa and Zimbabwe, and the region is best treated as a region of overlap. None of the species of the Nyika Plateau are endemics and most of the species are found in other subcentres of the South-central Africa Centre, therefore, it is considered to be a region of overlap.

The South-central Tanzania Subcentre represents south-central Tanzania, the northern tip of Malawi and part of northern Zambia. This area is not considered a subcentre of endemism (14% endemism). Some species (*K. grantii*, *K. thomsonii* and *K. princeae*) are found in the East Africa Centre, while other species (*K. renoldsii*, *K. grantii* and *K. princeae*) are found in other subcentres of the South-central Africa Centre. Additionally *K. dubia* is widespread in Zambia, in areas that do not fall into a designated subcentre. It is thus best to consider this region as an area of overlap.

2.3.3. Studies in the South African Centre

2.3.3.1. Subcentres of diversity and endemism based on chorology

Three areas were subjectively delimited as subcentres of diversity in SA based on distribution patterns of species viz. the Cape-Karoo, the Extended Drakensberg and the Northern South Africa subcentres (Table 2.3., Fig. 2.2.). The Cape-Karoo Subcentre did not show much QDG diversity i.e. no grids had more than three species. Despite this lack of diversity, the entire area was analysed to assess endemism of *Kniphofia* within this region. This was done for two reasons. Firstly the Fynbos and karooid biomes are unique within Africa, and secondly numerous workers have found links between the Cape Region and the Afromontane Region (discussed later). When the entire Cape-Karoo Subcentre is considered, eight species in total are distributed within the area of which three are endemic. It does not represent a subcentre of endemism (6% endemism) but rather an outlier as most of the non-endemics are found in the in the nearby Extended Drakensberg Subcentre. It is found within the Cape Floristic and Succulent Karoo regions and extends eastwards into the Albany Centre (*sensu* van Wyk and Smith, 2001). It is also interesting to note that while *Kniphofia* is not widespread in the Fynbos and karooid biomes other Asphodelaceae genera (*Aloe*, *Haworthia*, *Bulbine, Bulbinella, Trachyandra*) are common in these regions. Also, the Disinae is most speciose in the Cape Region while *Kniphofia* has poor representation for this region.

Two Afromontane regions have been noted as hot spots in SA: the Drakensberg and its associated uplands falls into the Eastern Mountain Centre, and the Wolkberg Centre (Cowling and Hilton-Taylor, 1997). The two other SA subcentres for *Kniphofia* broadly correspond to these regions. The Extended Drakensberg Subcentre represents the Drakensberg and extended areas in Lesotho, Free State (FS), Eastern Cape (EC) and KwaZulu-Natal (KZN). This extended area represents the major diversity of the genus and is better treated as a single unit. It is also a subcentre for endemism (54% endemism) for *Kniphofia*. It mostly corresponds to the Eastern Mountain Centre (Cowling and Hilton-Taylor, 1997). It covers almost the entire Drakensberg Alpine Centre and most of the Maputoland-Pondoland Region of van Wyk and Smith (2001). It also extends into the Albany Centre (van Wyk and Smith, 2001) in the south.

The Northern South Africa Subcentre represents the area that covers the former Transvaal Province of SA, Swaziland and the southern tip of Mozambique. Additionally several endemic *Kniphofia* species are from this area. This area is not considered a subcentre of endemism (10% endemism). Most of the non-endemics are found in the nearby Extended Drakensberg Subcentre with two species (*K. linearifolia* and *K. splendida*) extending north to the Zimbabwe Centre and the South-central Africa Centre (Malawi). It is therefore considered to be a region of overlap. This includes the entire Wolkberg Centre (*sensu* Cowling and Hilton-Taylor, 1997). This region includes the entire Soutpansberg Centre, Wolkberg Centre, Sekhukhuneland Centre, Barberton Centre and northern parts of the Maputoland-Pondoland Region of van Wyk and Smith (2001).

2.3.3.2. Areas of diversity using numerical analyses

Grid diversity and species richness were based on the quarter degree scale for the SA region and is shown in Fig. 2.3.

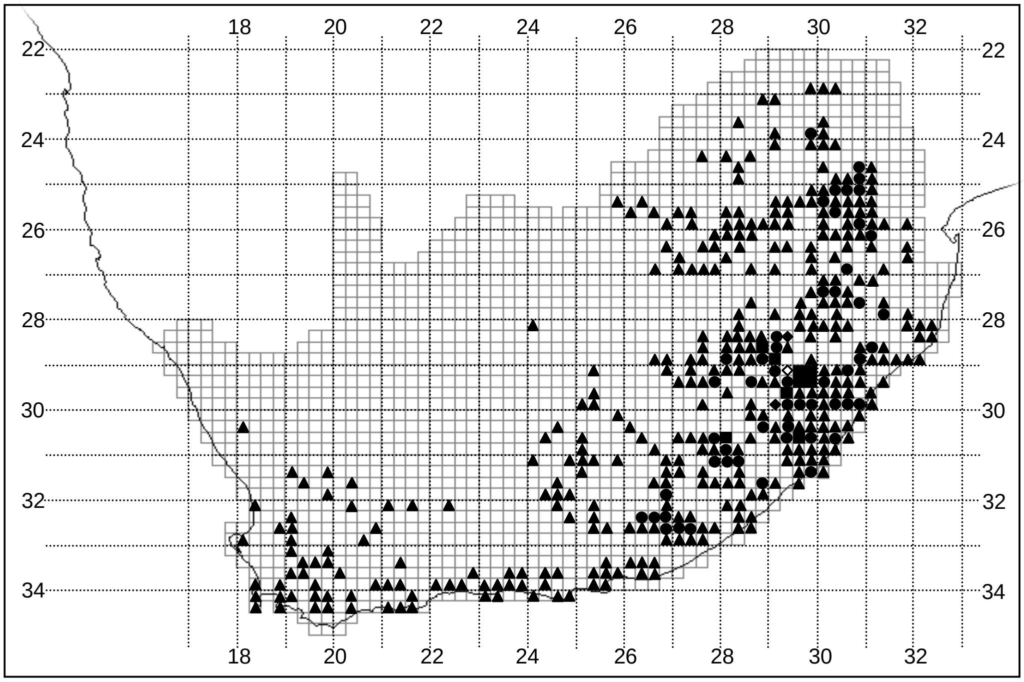


Fig. 2.3. Quarter degree grid species richness of *Kniphofia* within the South Africa Centre (▲= 1-3 species, ●= 4-6 species, ■= 7-9 species, ♦= 10-12 species, ◊= 13 species).

The 12 most species rich QDGs in descending order are:

- Champagne Castle (2929AB): n= 13
- Bushmans Nek (2929CC): n= 11
- Van Reenen (2829AD): n= 10
- Sani Pass (2929CB), Ntabamhlope (2929BA) and Witsieshoek (2828DB): n= 9
- Naudes Nek (3028CA), Estcourt (2929BB) and Cathedral Peak (2829CC): n= 8
- Weza (3029DA), Nottingham Road (2929BC) and Kamberg (2929BC): n= 7

The QDG data set (excluding singleton QDGs) used for the numerical analysis using the Jaccard similarity (J) co-efficient and UPGMA clustering contained 191 QDGs and 48 taxa. The phenogram generated is not shown as the patterns were difficult to interpret. A half degree grid approach was explored to determine if patterns were more evident at this scale. The HDG data set (excluding singleton HDGs) used for the numerical analysis using the Jaccard similarity (J) co-efficient and UPGMA clustering contained 121 HDGs and 48 taxa.

The overall patterns recovered by the QDG and HDG analysis revealed similar patterns. However, distinct patterns especially within the main clusters were recovered for the HDG analysis. A possible reason for this result is that the large amount of QDG grids are too small in geographical cover and contain a fewer number of species. This results in too many QDGs with similar species composition and clustering of grids that do not necessarily reflect close proximity. At this scale there was a high degree of geographical scattering of clusters which in turn appears to reflect much geographical overlap. Consequently, this makes patterns difficult to infer. The HDG approach takes into account species in four neighbouring QDGs. Increasing the spatial area is more likely to increase the number of taxa in a HDG and also increased the likelihood that the species composition of grids in close proximity are similar. At this scale scattering and overlap are reducded as the grids appears to reflect similar species compositions in close proximity. The HDG approach phenogram generated is shown in Fig. 2.4. Four clusters (A-D) were delimited and mapped (Fig. 2.5.).

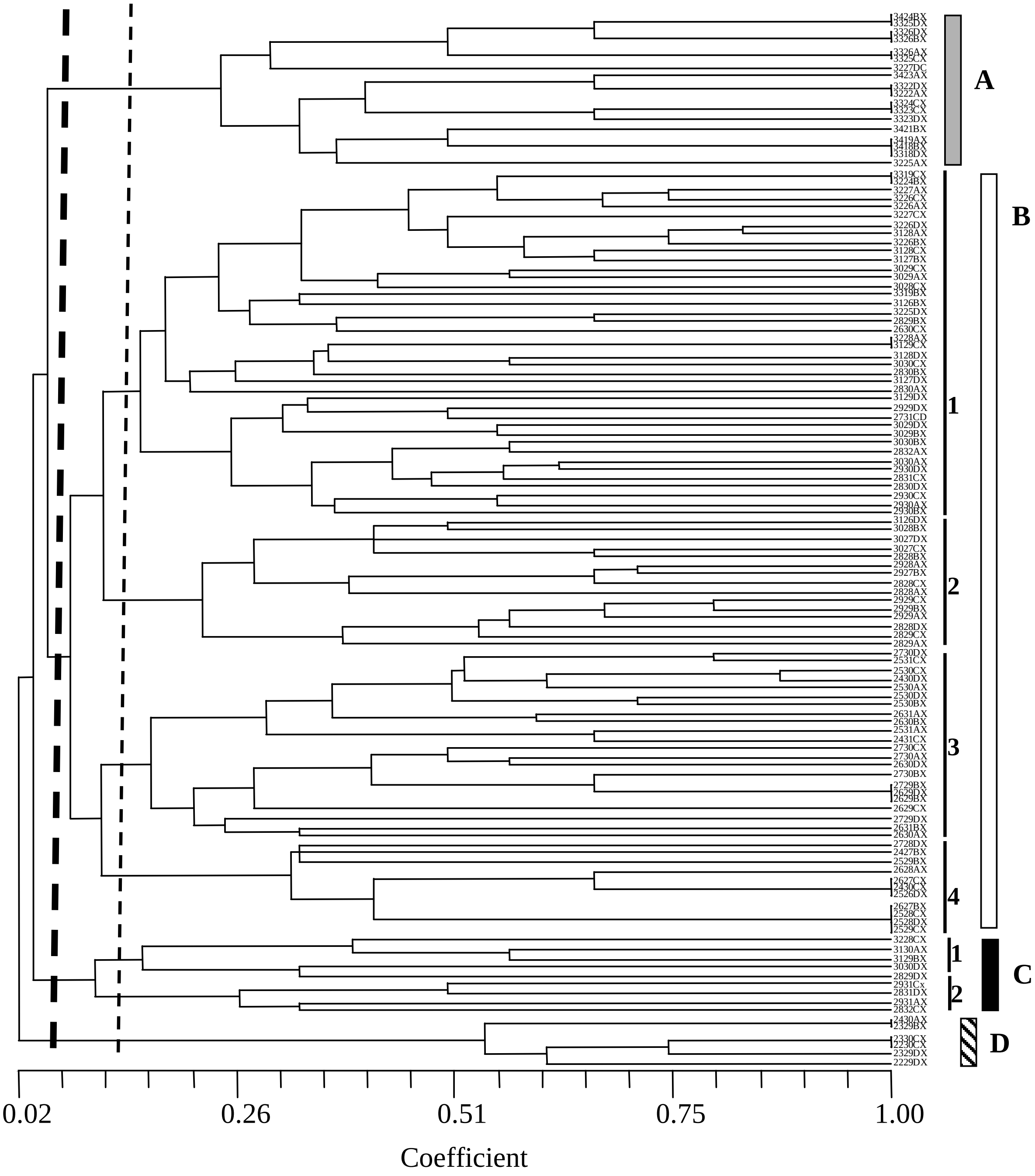


Fig. 2.4. The phenogram of half degree grids derived from the Jaccard analysis of the data set excluding singleton HDGs. The dense black phenon line shows the main clusters while the less dense phenon line shows sub clusters. Main clusters are labeled A-D and sub clusters are numerically depicted.

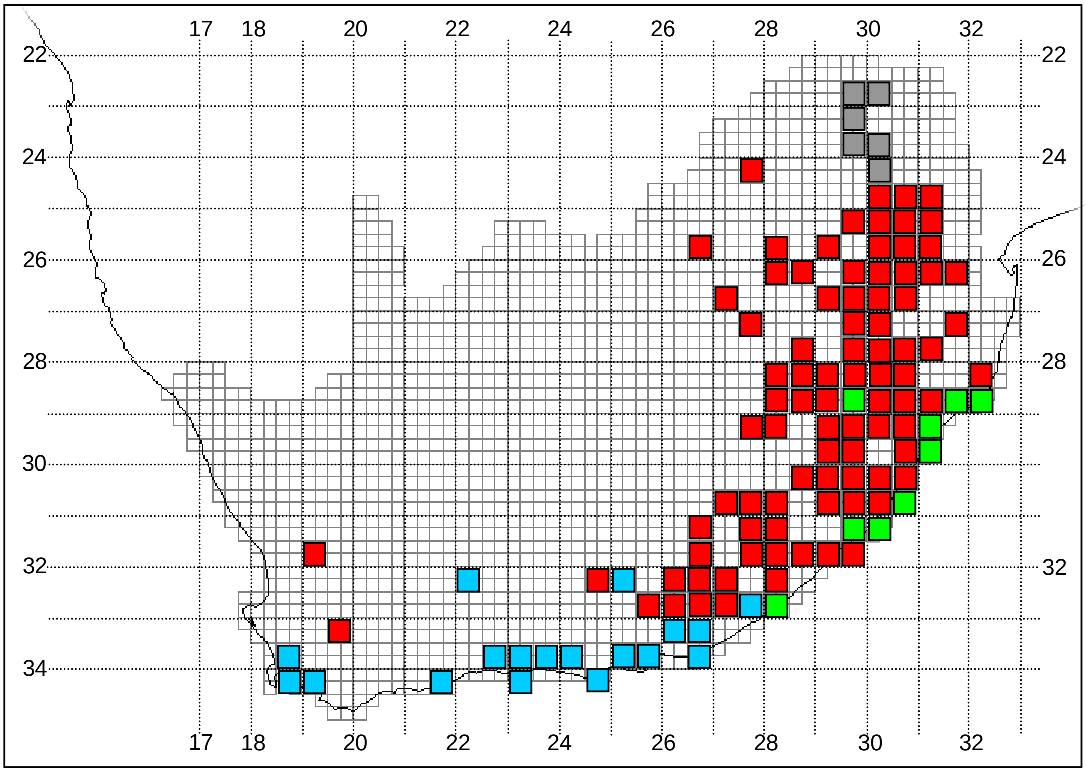


Fig. 2.5. Map showing the distribution of main clusters of the phenogram derived from the Jaccard analysis of the data set excluding singleton HDGs. Main clusters are color coded: Cluster A= blue, Cluster B= red, Cluster C= green and Cluster D= grey (see text for details).

Cluster A has a distinct Cape-Karoo distribution. It is found within the Cape Floristic and Succulent Karoo regions and extends eastwards into the Albany Centre (*sensu* van Wyk and Smith, 2001).

Cluster B has a distribution that covers much of northern, eastern and partly central SA, and extends into the Cape-Karoo Region in the south were it overlaps with Cluster A. An outlier of Cluster B is found in the Cape-Karoo Region. Cluster B is divided into four sub clusters (Fig. 2.6.A.).

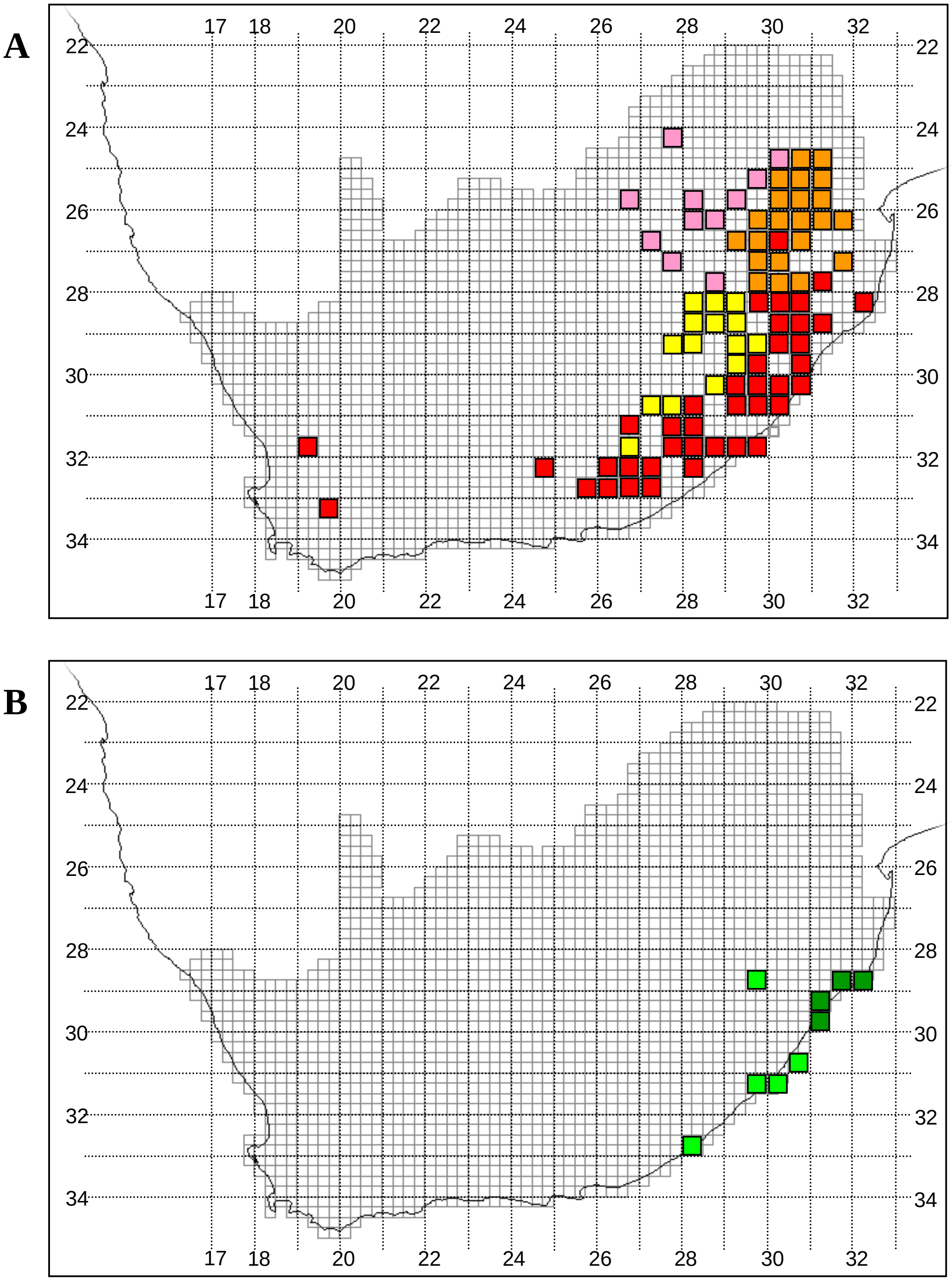


Fig. 2.6. Map showing the distribution of main clusters with sub clusters derived from Jaccard analysis of the data set excluding singleton HDGs. A. Cluster B with sub clusters B1 (red), B2 (yellow), B3 (orange) and B4 (pink). B. Cluster C with sub clusters C1 (bright green) and C2 (dark green).

Cluster B1 is found mostly with the Maputoland-Pondoland Region of van Wyk and Smith (2001). It also extends into the Albany Centre (van Wyk and Smith, 2001) in the south. The outlier of Cluster B found in the Cape-Karoo Region is also from this sub cluster (B1). It extends from Calvinia south east to the De Doorns region. It is found within the Cape Floristic and Succulent Karoo regions of van Wyk and Smith (2001). This may represent remnants an ancestral escarpment track for *Kniphofia* and/or the Afromontane vegetation. Cluster B2 is found mostly with the Drakensberg Alpine Centre of van Wyk and Smith (2001). Most of western distribution of Cluster B3 is in no regions or centres of endemism as defined by van Wyk and Smith (2001). In the north and north east of its distribution, it extends partly into the Wolkberg and Sekhukhuneland centres of van Wyk and Smith (2001). In the south and south east it is found partly in the Barberton Centre and the Maputoland-Pondoland Region of van Wyk and Smith (2001). Most of the entire distribution of Cluster B4 is in no regions or centres of endemism as defined by van Wyk and Smith (2001). In the north east of the distribution of this sub cluster, it extends only partly into the Wolkberg and Sekhukhuneland centres of van Wyk and Smith (2001).

Cluster C has an eastern coast distribution with a single outlier in the Winterton region. It extends south and abuts Cluster A. The Winterton outlier has two species in the HDG (*K. brachystachya* and *K. gracilis*) and may be an artifact of under collecting. Cluster C is divided into two sub clusters (Fig. 2.6.B.). The entire distribution of Cluster C is found in the Maputoland-Pondoland Region of van Wyk and Smith (2001). Only two HDGs (in the Mkambati region) of C1 are strictly in the Pondoland Centre of van Wyk and Smith (2001). Also only the two northern most HDGs (in the Richards Bay area) of C2 are strictly in the Maputoland Centre. All the others regions of Cluster C are in the Maputoland-Pondoland Region of van Wyk and Smith (2001).

Cluster D has a distinct extreme northern SA distribution. Cluster D transects through the Soutpansberg Centre of van Wyk and Smith (2001). It also marginally penetrates into the Wolkberg and Sekhukhuneland centres of van Wyk and Smith (2001) in the south.

2.3.3.3. Areas of endemism using parsimony analysis of endemicity (PAE)

A PAE approach was attempted for South African *Kniphofia* species. The HDG PAE analysis did not recover any areas of endemism as the consensus tree was a single large polytomy (not shown). Thus the discussion below concentrates on the QDG analysis. The data matix included 419 QDGs and 48 species. Four species were found to be parsimony uninformative viz. *K. acraea*, *K. crassifolia*, *K. flammula* and *K. leucocephala* and excluded from the analysis. A strict consensus tree based on the distribution of *Kniphofia* at the quarter degree scale is presented in Fig. 2.7. which is also a large polytomy. Three small clades were delimited and mapped (Fig. 2.8.). Clade A has a Cape-Karoo distribution (from Calvinia in the north extending south to Ceres, and from Citrusdal in the west towards the Sutherland region in the east). Clade B is distributed from the Underberg region northwards to Frere. Clade C is distributed from Iswepe south-east to the Wakkerstroom-Vredehof region.

Clades A and B had only one unique species and using PAE excludes these regions. Clade C had six unique species viz. *K. albescens*, *K. baurii*, *K. fluvialitis*, *K. linearifolia*, *K. multiflora* and *K. porphyrantha*. The distribution of these species were then mapped within the distribution of the clade to delimit an area of endemism (C in Fig. 2.8.) and is termed the Iswepe-Wakkerstroom-Vredehof area of endemism. The Iswepe-Wakkerstroom-Vredehof area of endemism does not fall into any major regions or centres delimited by van Wyk and Smith (2001). It lies outside the western boundary of Maputoland-Pondoland Region. It is also in close proximity to the Barberton Centre which is to the north. This area is within the Northern SA Subcentre (of the chorological approach).

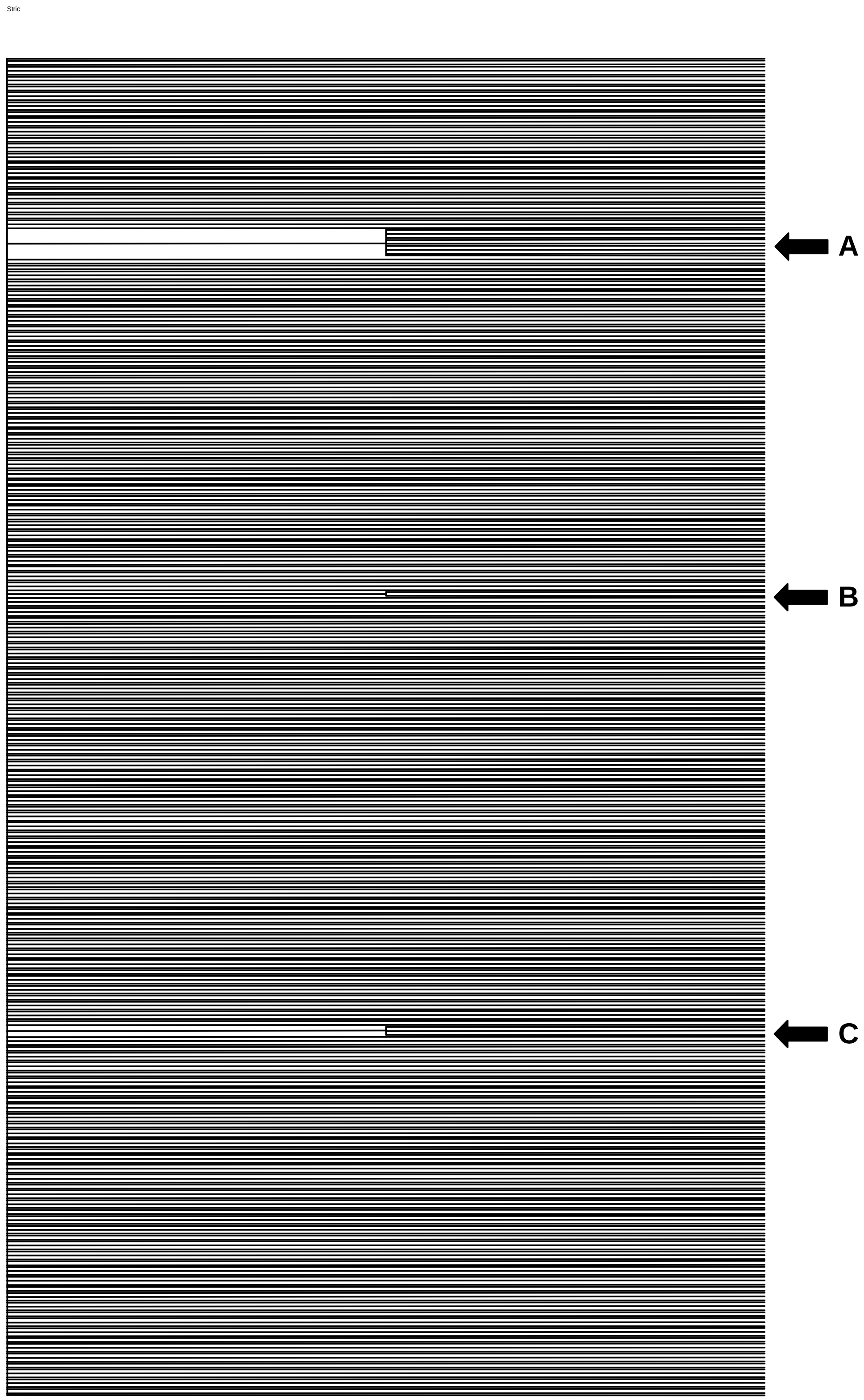


Fig. 2.7. Stict consensus tree of 1 000 most parsimonious tree based on distribution of *Kniphofia* species at the quarter degree scale. The actual grids are not shown for each terminal as it was not possible to visually depict them in the above tree. Main clades are labeled A-C.

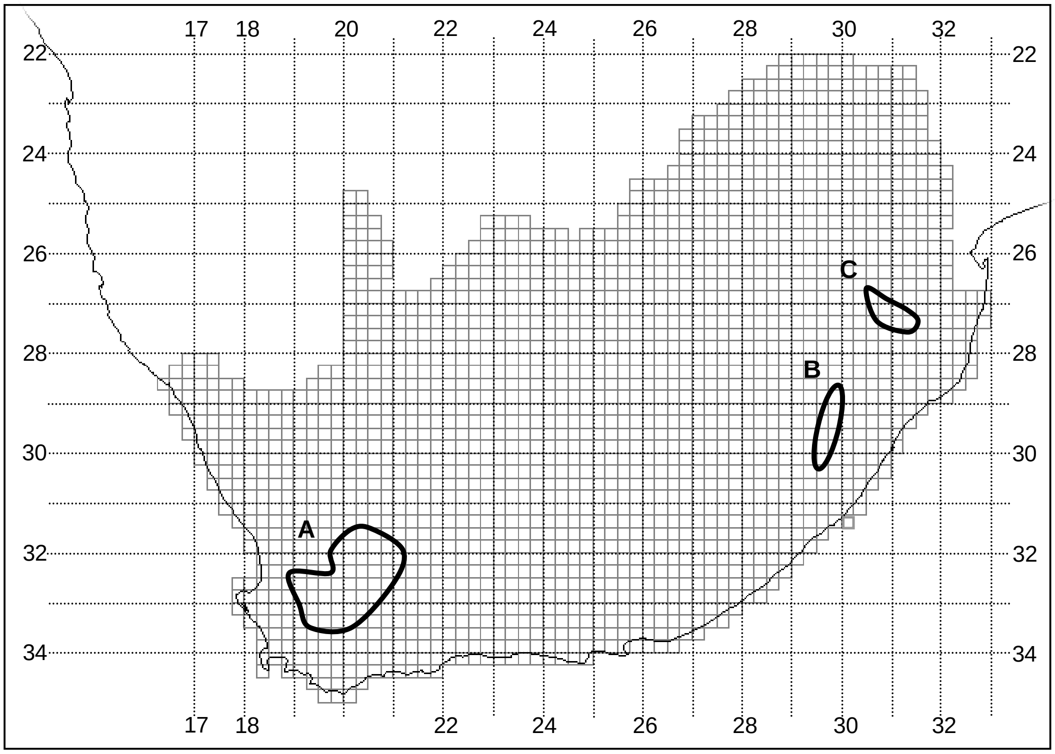


Fig. 2.8. Map showing the distribution of main clades of stict consensus tree based on distribution of *Kniphofia* species at the QDG scale. Main clades are labeled A-C (see text for details).

The PAE approach has major disadvantages as it excludes highly localised endemics confined to a single QDG that may not share this grid with other nearby endemics and/or conspecifics. These taxa are autoapomorphies which are not parsimony informative and are thus excluded from the analysis. This could potentially under estimate endemism.

K. baurii and *K. linearifolia* have wide distributions in SA, while *K. fluvialitis* and *K. porphyrantha* are also considered to be wides with a more restricted distribution. Thus these four species are not ‘true’ endemics to the Iswepe-Wakkerstroom-Vredehof area of endemism. However, *K. multiflora* and *K. albescens* are confined to the northern parts of SA. If the strict consensus tree (as above) is not well resolved then many areas rich in endemics are excluded.

Linder and Mann (1998) also found that PAE excluded regions rich in endemism. QDGs were used as infomation units and depend on presence data only. Under collection may result in grids being excluded from endemic areas (Linder and Mann, 1998). Additionally scale may be an important factor to consider. In this study the HDG PAE analysis did not recover any areas of endemism. The HDG scale may be too coarse to detect areas of endemism. The use of larger areas (e.g. whole degree grids) may reduce the noise caused by many smaller empty units and also reduces resolution (Linder and Mann, 1998).

2.3.3.4. Areas of endemism found by mapping of range restricted species

Twenty-one *Kniphofia* species are found in ten or less QDGs and were considered to be range restricted (Table 2.4).

Table 2.4. *Kniphofia* species occurring in ten or less QDGs.

Number of	***Kniphofia* species**
1	*K. acreae, K. crassifolia, K. leucocephala, K. flammula*
2	*K. bruceae, K. drepanophylla, K. evansii, K. pauciflora, K. umbrina*
4	*K. hirsuta, K. latifolia*
5	*K. coddiana*
7	*K. praecox, K. tabularis*
8	*K. brachystachya, K. breviflora, K. rigidifolia*
9	*K. albomontana, K. angustifolia, K. sarmentosa*
10	*K. fibrosa*

The mapped distribution of these range restricted species are shown in Fig. 2.9.A. Areas of endemism were determined from this map and are defined by contours of overlapping distributions (Fig. 2.9.B.).

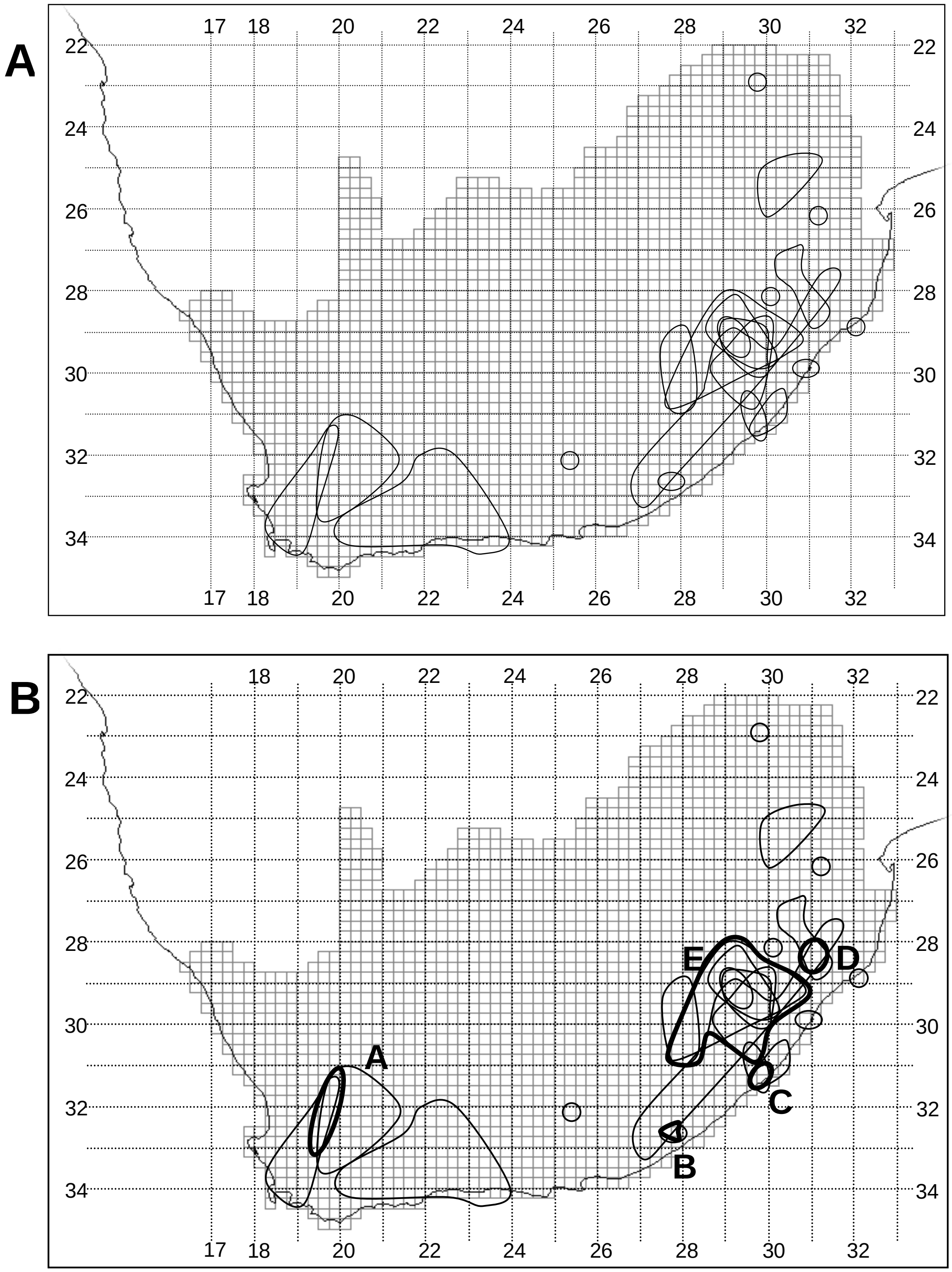


Fig. 2.9. A. Map showing the outlines of distribution of range restricted *Kniphofia* species. B. The dense black out lines show areas of endemism (A-E) which are defined by the overlapping distributions of range restricted *Kniphofia* species (see text for details).

Five areas of endemism (Fig. 2.9.B.) were determined using this method viz.:

A. Cape area of endemism (defined by *K. sarmentosa* and *K. tabularis*): extends from Calvinia to Groenfontein in the south.

B. Albany area of endemism (defined by *K. fibrosa* and *K. bruceae*): centred in the Kei Road-Komga region.

C. Pondoland Coast area of endemism (defined by *K. coddiana* and *K. drepanophylla*): centred in the Mkambati-Kanyayo region.

D. Northern KZN area of endemism (defined by *K. fibrosa* and *K. latifolia*): distributed in the Nkandla-Bobanango region.

E. Drakensberg-Maputoland-Pondoland area of endemism (defined by *K. drepanophylla*, *K. hirsuta*, *K. fibrosa*, *K. albomontana*, *K. brachystachya*, *K. angustifolia*, *K. breviflora* and *K. evansii*) is the largest area. It extends from the southern Free Sate into the Eastern Cape (including parts of Lesotho) in a southern direction, and eastwards into KZN and the Eastern Cape.

The Cape area of endemism is found within the Cape Floristic and Succulent Karoo regions of van Wyk and Smith (2001) and does not fall into any areas of diversity and endemism found by Linder and Mann (1998) for *Thamnochortus*. The Albany area of endemism falls into a very small part of the Albany Centre of van Wyk and Smith (2001). The Pondoland Coast area of endemism represents a small portion of the Pondoland Centre of van Wyk and Smith (2001). The Northern KZN area of endemism represents a very small area of the Maputoland-Pondoland Region of van Wyk and Smith (2001). The Drakensberg-Maputoland-Pondoland area of endemism covers a large part of the Drakensberg Alpine Centre and the Maputoland-Pondoland Region of van Wyk and Smith (2001).

This approach also has disadvantages. Range restricted species are considered to be taxa within ten or less QDGs. Under collecting may result in a taxon to be considered range restricted. Range restricted status may not be due to ‘real’ absences but a result of under collection. Highly localised range restricted taxa that are not sympatric in QDGs with other range restricted species are also not taken into account as overlapping of range restricted species defines this method. Eight species (*K. acreae, K. crassifolia, K. flammula, K. latifolia, K. leucocephala, K. pauciflora, K. praecox* and *K. rigidifolia*) with restricted ranges do not have distributions that overlap with other range restricted taxa and were not used to define areas of endemism. Furthermore taxa within ten or less QDGs may have a wide distribution and are not a ‘true’ range restricted species. In this study, *K. fibrosa* which is present in ten QDGs has a range from northern KZN to the Albany region. Excluding this species results in only three areas of endemism (Cape, Pondoland Coast and Drakensberg-Maputoland-Pondoland).

2.3.3.5. Comparison of areas of diversity and endemism in the South African Centre

Several approaches were explored to determine areas of diversity and endemism in SA. Areas of diversity were found by plotting distributions of species and then subjectively delimiting subcentres of diversity (chorological approach). A numerical analysis was also done to find areas of diversity. Delimiting areas of diversity in the SA region presented a formidable challenge.

The Cape-Karoo Region was recovered as an area of diversity in both approaches viz. Cluster A of the numerical analysis and the Cape-Karoo of the chorological approach. Furthemore an outlier of Cluster B (B1) is found in the Cape-Karoo Region.

A Northern SA area of diversity was also recovered by both approaches. The area delimited by the numerical approach (Cluster D) was far smaller in geographical cover and at the extreme north when compared with the chorological approach (Northern SA Centre). The rest of the Northern SA Centre is represented by two sub clusters from Cluster B (B3 and B4) which are north of the 28°S latitude.

This is very interesting as the 28°S latitude is also the approximate southern boundary of the Northern SA Centre (chorological approach).

The Extended Drakensberg Subcentre (chorological approach) is represented by Cluster C and two sub clusters of Cluster B (viz. B1 and B2) of the numerical approach. Cluster B1 (excluding the Cape-Karoo outlier) fits a Maputoland-Pondoland Region distribution but extends into the Albany Centre (van Wyk and Smith, 2001) in the south. Cluster B2 fits a Drakensberg Alpine Centre distribution of van Wyk and Smith (2001). While Cluster C (excluding the Winterton outlier) is found in the coastal regions of the Maputoland-Pondoland Region of van Wyk and Smith (2001).

It is difficult to delimit clear cut and distinct areas of diversity as there is a high degree of overlap using the two approaches (above). The transitional nature of southern African grasslands, the many ecotones and altitudinal transgression of Afromontane Grassland may be responsible for large number of overlapping *Kniphofia* distributions. These factors (especially in the greater Afromontane and Maputoland-Pondoland regions) may account for the above results.

Endemism was determined by three methods. In the first approach the subcentres of diversity from the chorological approach were analysed for levels of endemism. Using this approach only the Extended Drakensberg Subcentre (with 54% endemism within SA) was recognised as a subcentre of endemism. The second approach using PAE recovered only one area of endemism. The Iswepe-Wakkerstroom-Vredehof area of endemism is defined by six species i.e. 13% endemism within SA. The third approach entailed mapping range restricted species and using overlapping distributions to determine areas of endemism. This approach recovered five areas of endemism viz. a Cape, Albany, Pondoland Coast, Northern KZN and a Drakensberg-Maputoland-Pondoland area. The Cape, Albany, Pondoland Coast and Northern KZN areas of endemism were each defined by two endemics i.e. each has 4% endemism within SA. The

Drakensberg-Maputoland-Pondoland area of endemism was defined by eight endemics i.e. 17% endemism within SA.

The PAE approach recovered the Iswepe-Wakkerstroom-Vredehof area of endemism which is within the Northern SA Subcentre (of the chorlogical approach). The mapping of range restricted approach recovered a Cape area of endemism falls in a small part of the Cape-Karoo Subcentre found in the chorological approach. Additionally the Albany, Pondoland Coast, Northern KZN and Drakensberg-Maputoland-Pondoland areas of endemism are found within the boundaries of the Extended Drakensberg Subcentre recovered in the chorological approach.

The PAE and mapping of range restricted species approaches did not recover exactly the same centres but some interesting patterns are worth noting. The Cape, Albany and Pondoland Coast areas of endemism are too far south and with a different suite of species for a detailed comparison with the Iswepe-Wakkerstroom-Vredehof area of endemism i.e. only the Drakensberg-Maputoland-Pondoland and Northern KZN areas of endemism are worth considering with the Iswepe-Wakkerstroom-Vredehof area of endemism.

The Drakensberg-Maputoland-Pondoland area of endemism (obtained using the mapping of range restricted species method) is the largest of the three areas and covers a large part of the Drakensberg Alpine Centre and the Maputoland-Pondoland Region of van Wyk and Smith (2001). The Northern KZN area of endemism (mapping of range restricted species method) represents a very small area of the Maputoland-Pondoland Region of van Wyk and Smith (2001) and is the smallest of the three areas of endemism under consideration. The Iswepe-Wakkerstroom-Vredehof area of endemism (PAE approach) lies outside the extreme inland (western) boundary of the Maputoland-Pondoland Region and the Barberton Centre is in close proximity to the north. The boundaries of the Barberton Centre have not been mapped in detail (van Wyk and Smith, 2001) and the possibility that the Iswepe-Wakkerstroom-Vredehof area of endemism is within this centre cannot be ruled out. The Barberton Centre has a strong afromontane affinity in terms of the vegetation and flora (van Wyk and Smith, 2001) and has been treated as part of the Drakenberg Regional Mountain System by White (1978). Floristically the Barberton Centre is part of the Afromontane Region and mountainous areas in the Barberton Centre may have served as afromontane refugia (van Wyk and Smith, 2001). The Iswepe-Wakkerstroom-Vredehof area of endemism appears to reflect this afromontane affinity.

The Drakensberg-Maputoland-Pondoland area of endemism is defined by *K. drepanophylla*, *K. hirsuta*, *K. fibrosa*, *K. albomontana*, *K. brachystachya*, *K. angustifolia*, *K. breviflora* and *K. evansii*. The Northern KZN area of endemism is defined by *K. fibrosa* and *K. latifolia*. The Iswepe-Wakkerstroom-Vredehof area is defined by *K. albescens*, *K. baurii*, *K. fluvialitis*, *K. linearifolia*, *K. multiflora* and *K. porphyrantha*. Suprisingly not a single species is shared by all three regions of endemism. Only *K. fibrosa* is shared by the Drakensberg-Maputoland-Pondoland and the Northern KZN areas of endemism. Also none of the areas of endemism recovered by PAE and mapping of range-restricted taxa show any degree of overlap. These patterns are indeed very hard to comprehend.

It is difficult to assess the above findings in a broader context as no studies exist that have defined areas of diversity endemism in the Drakensberg, the Maputoland-Pondoland Region, the Drakensberg-Maputoland-Pondoland transition and northern parts of SA. Also no studies could be found on a particular plant group that has examined areas of diversity and endemism on a fine scale (as above) for these particular regions. Delimiting areas of diversity and endemism for *Kniphofia* in SA presents an arduous task as shown above. Perhaps it may be more convenient to express areas of diversity and endemism in terms of a core area, regions of overlap and outlier regions. In this scenario the Drakensberg-Maputoland-Pondoland region will be designated as the core area of diversity and endemism, with the Northern SA and Cape-Karoo regions as outliers and the regions in between treated as regions of overlap.

2.4. Conclusions

Kniphofia has a strong Afromontane Grassland affinity in Tropical and East Africa but occasionally extends beyond the boundary of the Afromontane vegetation. In South Africa it is found from high altitudes to coastal habitats but the most speciose regions for *Kniphofia* are Afromontane grasslands. The compensation of latitude for altitude may largely explain this pattern in southern Africa. It is thus not considered to be an Afromontane element, but rather an Afromontane associate. Other factors such as fire and climate which influence grassland distribution in southern Africa may also influence the distribution of *Kniphofia*. In the Drakensberg-Maputoland-Pondoland transition soil and geology may be more important factors to understand distribution patterns in *Kniphofia*. However, this will entail a detailed study of soil and lithology that are required for the different species of *Kniphofia*.

Kniphofia has six centres of diversity, five of these are centres of endemism. The South African Centre is the most diverse, species rich and the largest centre of endemism for *Kniphofia*. Delimitation of areas of diversity and endemism within these centres is more challenging as demonstrated by a more detailed study of the SA region. However, eight subcentres of diversity are proposed of which only two are considered subcentres of endemism (the Extended Drakensberg and Ethiopia subcentres) at this stage. A more comprehensive study for the entire genus will require the loan of material from southern Africa, African and international herbaria to verify identifications and locality data. This could not be done in this study due to time limitations. Thus, the data presented here should be regarded as preliminary attempt to better understand the biogeographical patterns for the entire genus.

The different approaches used to study diversity and endemism of *Kniphofia* in SA produced varying results. PRECIS data is known to have a 10% error factor. Specimen identifications and locality data were not checked and verified for the PRECIS data. Hence the data and results presented here may have some degree of error and may partly account for the results obtained. Another major issue in these studies, especially endemism, is collecting intensity. The PRECIS data may not include collections from smaller regional herbaria that may have a higher localised collecting intensity and more local *Kniphofia* collections. Also there may be over collecting in accessible areas and more importantly under collecting in areas that are inaccessible for which data is critically needed. This is of particular importance in *Kniphofia*. Although the genus has a wide distribution in SA, endemic species frequently occurs in mountainous terrain in areas that are not well collected. The lack of appropropraite data may partly account for the differing results.

Chapter 3: Phylogenetic Reconstruction

3.1. Introduction

Phylogeny reconstruction using DNA sequence data provides plant systematists with unrivaled scope for investigating relationships and evolutionary processes. Since the 1980's the molecular phylogenetic approach has re-shaped and revolutionised our understanding of relationships and evolution at all taxonomic levels in plants (Crawford, 2000; Soltis and Soltis, 2000a; Borsch *et al.*, 2005). Initial molecular systematic studies focussed on resolving higher level (supra-generic) relationships (e.g. Chase *et al.*, 1993). However, more recently species-level molecular phylogenies of plants have become more common in the literature as DNA regions suitably variable at the species level have been found for various groups (e.g. van der Niet *et al*., 2005; Archibald *et. al*., 2005).

DNA sequence data can be obtained from three sources in angiosperms: chloroplast DNA (cpDNA), nuclear DNA (nDNA) and mitochondrial DNA (mtDNA). These sources each have advantages and disadvantages for the taxonomic level of study and the nature of the evolutionary problem (Soltis and Soltis, 1998). Numerous regions of the chloroplast and nuclear genomes are routinely used for phylogenetic inference in plants. Mitochondrial DNA sequences are also now being used more frequently (Chat *et al*., 2004; Bakker *et al*., 2005; Guo and Ge, 2005). Plant molecular systematists have relied heavily on the chloroplast genome. Chloroplast markers are still the primary source of data for inferring phylogenies followed by the nuclear ribosomal internal transcribed spacer (*ITS*) region (Shaw *et al*., 2005).

Genomes are composed of different segments of DNA (genes, introns, spacers). These regions mutate at different rates due to functional constraints and each region generally has a typical taxonomic range of application. However, rates of evolution for a specific marker may vary between groups (Doebley *et al*., 1990;

Bousquet *et al*., 1992) and the range of application may vary vastly from group to group (Soltis and Soltis, 1998). Thus, the mode and tempo of DNA sequence evolution varies for different markers.

3.1.1. The Chloroplast Genome

The chloroplast genome is circular, ranging in size from 120-217 kilobase pairs (Kbp) (Palmer, 1987; Dowling *et al*., 1990). The chloroplast genome contains (with few exceptions) two duplicate regions in reverse orientation, called the inverted repeats (IR). The inverted repeats range from 12-25 Kbp in length, is structurally conserved and accounts for length variation between different groups (Kim and Lee, 2005). The occurence of insertions or deletions (indels) of nucleotides which results in length mutations are common in cpDNA. The majority of these length mutations are extremely short (1-10 bp) and occur mostly in non-coding regions (Palmer, 1987). The two IR regions separate the remainder of the molecule into the large single-copy (LSC) and the small single copy (SSC) regions (Kim and Lee, 2005).

The chloroplast genome shows a high degree of conservation in size, structure, gene content and linear order of genes (Palmer, 1987; Downie and Palmer, 1992; Kim and Lee, 2005). Despite the general assumption that the chloroplast genome is conservative, some studies have shown that its composition is not static. It can lose segments over time by gene deletion and intron loss. For example McPherson *et al.* (2004) have found that an intron from the 3’ *rps12* locus is absent in all Asphodelaceae examined (including *Kniphofia*) and some representatives of the closely related Hemerocallidaceae. This loss can be treated as a marker supporting the monophyly for Asphodelaceae and these Hemerocallidaceae representatives.

The abundance of cpDNA in leaf cells, its ability to be isolated easily, its small size and the highly conserved mode of cpDNA evolution have made cpDNA useful for systematic comparisons (Palmer, 1987). The technical ease of working with cpDNA is another advantage and many molecular phylogenies for plants are still based solely on chloroplast markers (e.g. Scheen *et al*., 2004). Consequently, this has created a bias towards the use of cpDNA in molecular systematic studies (Harrison, 1991; Morton, 2000). The extensive use of the chloroplast genome has led to the construction of many primers for both coding and non-coding regions of this genome (e.g. Taberlet *et al*., 1991; Sang *et al*., 1997; Shaw *et al.*, 2005), which has greatly facilitated phylogenetic studies.

The chloroplast genome evolves slowly at the nucleotide sequence level and generally evolves more slowly than nuclear DNA. In some cases the rates of substitution are so slow that data from multiple regions have to be combined to gain phylogenetic insights at lower levels (Goldblatt *et al*., 2002; Butterworth and Wallace, 2004; Barfuss *et al*., 2005; Shaw *et al*., 2005).

Different parts of the chloroplast genome evolve at different rates (Palmer, 1987). As a result, a wide range of possibilities exist for resolving relationships using data from the chloroplast genome, from the level of species to family, and even higher levels (Soltis and Soltis, 1998). The conservative nature of the chloroplast genome limits applicability, potentially excluding studies of closely related species and intra-specific populations. However, several studies have successfully used cpDNA variation to examine population-level relationships and evolutionary processes within species (e.g. Saltonstall, 2002; Huang *et al.*, 2002; Honjo *et al*., 2004; Zhang *et al.*, 2005).

The genetic data present in cpDNA is of great interest in phylogeny and population genetics mainly because of the non-mendelian mode of inheritance of the genome. Chloroplasts are usually maternally inherited in angiosperms (Palmer, 1987; Harris and Ingram, 1991; Korpelainen, 2004). Uniparental transmission of cpDNA provides information unavailable from the nuclear genome, which is bi-parentally inherited.

Hybridisation is an important phenomenon in angiosperm evolution and speciation (Vriesendorp and Bakker, 2005). Hybridisation has played a vital role in the evolution of many plant lineages throughout their histories (Church and Taylor, 2005; Okuyama *et al*., 2005) and it is becoming more apparent that reticulate evolution is more frequent than previously thought (Ainouche *et al*., 2003). As the chloroplast genome is uniparentally inherited and haploid, it reveals only half the parentage in angiosperms. If hybridisation is followed by introgression and subsequent fixation of alien cpDNA, then the phylogeny will resolve the maternal lineage (Small *et al.*, 2004). A central assumption in phylogenetics is that terminal taxa are the product of bifurcating lineage splitting events, rather than the products of reticulation. The uniparental, usually maternal inheritance of the chloroplast genome is bifurcating rather than reticulate. The chloroplast genome is also haploid with no intra-individual allelic variation (Small *et al.*, 2004).

If chloroplast capture (the movement of a chloroplast genome from one species to another by introgression) is undetected it will bias phylogenetic estimates. It can lead to erroneous phylogenetic conclusions, as only the maternal lineage is reconstructed (Rieseberg and Soltis, 1991; Cronn *et al*., 2002), but when recognised it can be very informative about evolutionary processes (Soltis and Soltis, 1998). At higher taxonomic levels, where hybridisation is unlikely, organellar and nuclear phylogenies should be concordant (Palmer, 1987). Thus, any conclusions drawn from cpDNA phylogenies have to be preliminary and tentative until they are compared with nuclear data (Cronn *et al*., 2002).

3.1.1.1. Non-coding regions in the chloroplast genome

In general non-coding DNA regions [introns and intergenic spacers (*IGS*)] have been viewed as more variable than coding regions due to fewer functional constraints (Taberlet *et al*., 1991; Gielly and Taberlet, 1994). Non-coding regions tend to evolve more rapidly than coding regions, by the accumulation of indels at a rate equal to that for nucleotide substitution and have become very useful below the family level (Gielly and Taberlet, 1994). Gielly and Taberlet (1994) found that non-coding cpDNA (*trnL-F* region) evolved faster than coding cpDNA (*rbcL*). Studies of coding and non-coding regions show that the variable sites in *rbcL* change faster than those of the non-coding *trnL-trnF* region, however, the *trnL-trnF* region has more variable sites than *rbcL* (Chase *et al.*, 2000; Richardson *et al.,* 2000). Reeves *et al.* (2001) found that protein coding regions (*rbcL* and *rps4*) had fewer variable sites overall but those present changed more frequently than the more numerous variable sites in the *trnL-F* region. These results may be explained by non-coding regions being constrained by their own secondary structures (Asmussen and Chase, 2001).

However, in some cases non-coding regions do not have enough variation and have to be combined with coding regions to provide desired resolution (Goldblatt *et al*., 2002; Butterworth and Wallace, 2004; Barfuss *et al*., 2005). Also Sauquet *et al.* (2003) reported that coding *ndhF* and *matK* regions were as or more variable than non-coding regions in Magnoliales and Myristicaceae. Third codon positions in coding regions like *rbcL* have been shown to be under less functional constraint as they change more often than first and second codon positions (Kellog and Juliano, 1998).

Despite all the research on non-coding cpDNA evolution, we still know very little (Bremer *et al.,* 2002). Non-coding cpDNA regions have been thought to be unsuitable for resolving deep level phylogenies because of high mutational and evolutionary rates (Nickrent *et al*., 2004). The fast rate of evolution has lead to the notion that most of the sites in non-coding DNA will be saturated when used at higher levels in phylogenetic reconstruction (Borsch *et al*., 2003). However, Bremer *et al.* (2002) have shown that non-coding regions are almost as good as coding regions in higher ranks of the asterids. Borsch *et al.* (2003) demonstrated that a large number of variable sites change only once in non-coding regions and these regions could be used at higher levels to infer basal angiosperm relationships. Non-coding DNA can have secondary structures, regulating regions and different functions that constrain DNA. It consists of independently and randomly evolving parts as well as constrained parts (Bremer *et al.*, 2002). Knowledge of these features could optimise phylogenetic reconstruction.

Choosing an appropriate non-coding region for a particular taxonomic level is essential for maximising its utility as a phylogenetic tool (Kelchner, 2000). Shaw *et al.* (2005) compared relative rates of evolution among non-coding regions between broad taxonomic groups. The phylogenetic utility of different non-coding cpDNA regions within a group can vary tremendously (Shaw *et al*., 2005). In some plant groups that have undergone recent radiation it may be difficult to generate sufficient phylogenetic signal due to the relatively slow rate at which mutations accumulate, even for rapidly evolving non-coding regions (Small *et al*., 1998).

In non-coding cpDNA microstructural changes of four to six nucleotides are frequent (Kelchner, 2000; Borsch *et al*., 2003). Many of these are simple sequence repeats (SSR). In some positions these changes can occur repeatedly, completely or partly. These require attention in homology assessment (Borsch *et al*., 2005). Slipped-stranded mispairing, stem-loop secondary structures and mutational triggers should be recognised. Kim and Lee (2005) have reported the widespread presence of many small inversions in non-coding regions of cpDNA of many land plants. These should also be recognised in phylogenetic reconstruction (Kim and Lee, 2005). Presently, phylogenetic approaches do not routinely take these factors into account even though these phenomena could enhance the phylogenetic utility and accuracy of non-coding cpDNA data (Kelchner, 2000).

Despite these drawbacks, Shaw *et al.* (2005) found that since 1995 studies using non-coding cpDNA are increasing every year, with the continued reliance on a few selective regions. Most of these studies have employed some portion of the *trnL-F* region or the *trnK-matK* region despite these markers having fewer potentially informative characters than other options. Very few investigators are using other non-coding cpDNA regions from the numerous possibilities that exist. Shaw *et al.* (2005) attributes this trend to the lack of knowledge of the relative evolutionary rates of different non-coding cpDNA regions.

3.1.2. The Nuclear Genome

Plants have nuclear genomes that are complex. This genome has extensive structural variation in size, chromosome number, number and arrangement of genes and number of genome copies per nucleus (Kellogg and Bennetzen, 2004). Nuclear DNA other than ribosomal DNA (rDNA) exists either as high copy repetitive DNA or low to moderate copy DNA elements. Distinguishing sequences related by descent (orthologues) from a massive pool of related but non-orthologous sequences is challenging. Low copy nDNA typically evolves independently of paralogous sequences and tend to be stable in position and copy number facilitating identification and isolation of orthologous sequences (Small *et al.,* 2004).

In land plants rRNA genes are organised into two distinct tandem arrays. One is composed of 5S rRNA genes and intergenic spacers in tandem arrays at one or more chromosomal loci. The second is the 18S-5.8S-26S rDNA cistron (Small *et al*., 2004). This marker is by far the most frequently used nuclear marker (Álvarez and Wendel, 2003; Small *et al*. 2004). Recently more studies are beginning to use low copy nuclear genes because of the problems and limitations imposed by cpDNA and nDNA (Mort and Crawford, 2004; Small *et al.*, 2004). Low copy nuclear genes are limitless and generally evolve faster than cpDNA and *ITS* sequences (Small *et al.*, 1998; Cronn *et al.*, 2002). Faster evolutionary rates result in greater reward for sequencing effort as more variation is found per unit sequence than in organellar genes. In numerous studies low copy nuclear genes have proven to be more useful than chloroplast and/or *ITS* sequence data (Baumel, *et al.* 2002; Ingram and Doyle, 2003; Levin *et al*., 2005).

Nuclear genes also provide numerous independent unlinked loci for comparative phylogenetic inference with cpDNA markers. The combination of maternally inherited cytoplasmic markers with biparentally inherited nuclear markers provides a more precise and accurate determination of parentage (Ainouche *et al*., 2003). This can assist with inference of hybridisation, introgression and lineage sorting (Doyle *et al*., 2003; Small *et al*., 2004).

However, even at this early stage of usage, several limitations of nDNA have been noted (see Small *et al*., 2004 for review). These included complex architecture and dynamics. Genes have a tendency to exist as a family, which leads to difficulty in identifying and isolating orthologous genes.

Plants hybridise and undergo polyploidy processes that are frequent modes of evolution in plants (Baumel, *et al.* 2002, Ainouche *et al*., 2003, Soltis *et al.* 2003; Doyle *et al.* 2003). It is well known that hybridisation can result in polyploidy. Polyploidy is common in plants with estimates ranging from 30-80% of angiosperms being polyploid (Hegarty and Hiscock, 2005). Polyploidisation can have major effects on genome structure and function (Soltis *et al*., 2003; Adams and Wendel, 2005). It can also have major effects on the evolution and ecology of taxa involved (Soltis *et al*., 2003). The results from nuclear markers may be more complex than those of chloroplast markers in cases of polyploidy because nuclear markers can reflect multiple donors to a polyploid taxon (Mason-Gramer, 2004). The complex architecture and dynamics of the nuclear genome coupled with factors such as hybridisation and polyploidy could make identification and isolation of orthologous genes difficult.

Other issues (that to varying degrees may be compounded by hybridisation and/or polyploidy) include concerted evolution, paralogous sequences and the presence of intra-specific, intra-populational and intra-individual variation (heterozygosity). Moverover, the target nDNA occurs in relatively low quantities, consequently the amplification of single-copy genes can be problematic.

3.1.3. Regions of DNA employed in this study

It is often necessary to use multiple independent data sets to gain insights on phylogenetic relationships (Cronn *et al*., 2002). Independent sources of data improve the tracking of species rather than gene phylogenies. This approach allows for phylogenies generated from independent data sources to be compared and to test for congruency. Comparing phylogenies at lower taxonomic levels can be invaluable to explain evolutionary processes that cannot be achieved by either genome alone (Baumel *et al*., 2002; Cronn *et al*., 2002; Doyle *et al.* 2003; Ingram and Doyle, 2003). DNA sequence data from both the chloroplast and nuclear genome were utilised for this study. It was also necessary to ensure that gene regions sampled had adequate variation, to produce informative phylogenies.

Choosing an appropriate marker for molecular phylogenetics is of fundamental importance (Knoop, 2005). *A priori* selection of appropriate markers for phylogenetic studies is often difficult (Gielly and Taberlet, 1994; Pelser *et al*., 2003, Knoop, 2005). There is a paucity of information on the relative tempo of evolution among different regions (Shaw *et al*., 2005) and the phylogenetic resolution of different markers is highly dependent on the taxonomic group (Nickrent *et al*., 2004). Furthermore, it is difficult to predict from character variability or sequence divergence what or how much sequence data will be adequate for any given phylogenetic problem (Bohs, 2004) as variability alone does not always constitute phylogenetic usefulness. For the purposes of this study, four non-coding chloroplast regions (*trnT-L* spacer, *trnL* intron, *rps16* intron and *psbA-trnH* spacer) and one nuclear region (*ITS*) were screened for phylogenetic usefulness.

3.1.3.1. The *trnT-trnF* (*trnT-F*) region

Among the first non-coding regions to be exploited for lower level systematic studies was the *trnT-F* region. The *trnT-F* region is located in the large single copy region of the cp genome, about eight Kbp downstream from *rbcL*. Three highly conserved transfer RNA (tRNA) genes are found in this region: threonine (UGU), leucine (UAA) and phenylalanine (GAA). These genes are separated by intergenic spacers of several hundred base pairs (Taberlet *et al.*, 1991). The entire *trnT-F* region is composed of seven units (Taberlet *et al.*, 1991):

(i) a small portion of the 3' end of the threonine (UGU) gene
(ii) the *trnT-L* intergenic spacer (*IGS*)
(iii) the 5' exon of *trnL*
(iv) the *trnL* intron
(v) the 3' exon of *trnL*
(vi) the *trnL-F IGS*
(vii) a small portion of the phenylalanine (GAA) gene

The primers designed by Taberlet *et al.* (1991) were situated in conserved regions and demonstrated amplification in diverse land plants ranging from mosses (e.g. Stech, 2004) to angiosperms. The non-coding portions are the *trnL* intron, as well as two intergenic spacers between *trnT-L* and *trnL-F*.

The *trnL* intron and *trnL-F* spacer have become the most popular and widely used non-coding cpDNA markers in plant systematics (Shaw *et al.*, 2005; Kim and Lee, 2005). Initial comparisons suggest that these regions evolve at rates similar to *rbcL*, but can evolve at rates up to three times faster than *rbcL*, depending on the study group (Soltis and Soltis, 1998).

Bakker *et al.* (2000) found that nucleotide substitutions in the *trnL* intron accumulated in a more uniform pattern than the *trnL-F* spacer in angiosperms, suggesting differing functional constraints between the two regions. The *trnL* intron showed sequence conservation in the regions flanking the *trnL* exons while the central part was variable. Bakker *et al.* (2000) assumed that since the *trnL-F* spacer had no secondary structural elements, the *trnL* intron and *trnL-F* spacer where probably co-transcribed. Bakker *et al.* (2000) concluded that in the *trnL-F* region there was neutrality in substitutions i.e. the *trnL* intron and *trnL-F* spacer evolve neutrally. The spacers of the *trnT-F* region are not required for processing of tRNA and the *trnL* gene maintains secondary structure and sequence elements critical for self-splicing from precursor RNAs. No promoter elements were found in the *trnT-L* and *trnL-F* spacer regions in Gnetales (Won and Renner, 2005). The absence of conserved promoter elements for tRNA genes from these spacer regions suggests that these spacers are not under functional constraint. This contradicts Bakker *et al.* (2000) suggestions that the *trnL-F* spacer (but not the *trnT-L* spacer) is under differing functional constraint. Won and Renner (2005) suggested that the absence of promoter elements upstream of the genes relieves the spacers from functional constraint that would otherwise be necessary if promoters were present. Release from the tRNA promoting/processing mechanism may explain why the spacers are less conserved with many indels and point mutations (Won and Renner, 2005). No studies of this nature were found for angiosperms where a similar scenario may apply.

Usually these regions are used in studies of closely related species or genera. However, Bremer *et al.* (2002) and Borsch *et al.* (2003) demonstrated that the *trnT-F* region could infer relationships at higher levels. Fay *et al.* (2000) used a combined analysis of four plastid regions (*rbcL*, *atpB*, *trnL* intron and *trnL-trnF* spacer) to resolve relationships in the Order Asparagales. Renner and Chanderbali (2000) used the *trnT-L* region in a combined approach to resolve relationships in Hernandiaceae, Lauraceae and Monimiaceae (Order Laurales).

Sauquet *et al.* (2003) examined relationships in Magnoliales using multiple cpDNA regions including the *trnT-F* region.

This region has also been found to be informative at the family level. Bayer and Starr (1998) used the *trnL* intron and the *trnL-F* intergenic spacer to resolve relationships among tribes of Asteraceae. Bayer *et al.* (2000) used *trnL-F* sequences to reconstruct the phylogenetic relationships in Gnaphalieae (Asteraceae). Chase *et al.* (2000) investigated generic relationships in Asphodelaceae using chloroplast DNA (*rbcL* and *trnL-trnF*) sequence data. These authors found that *trnL-F* region only marginally out-performed *rbcL*. In a comparative study of coding and non-coding regions in palms, Asmussen and Chase (2001) found that *trnL-F* sequences were almost as useful as the *rps16* intron sequences in phylogenetic inferences. This study focussed on subfamilial and tribal delimitations in Arecaceae.

The presence of many small inversions appears to be a common feature of the *trnT-F* region, which may account for a large number of sequence differences. A single inversion (i.e. a single evolutionary event) may be interpreted as many point mutations. This could lead to erroneous phylogenetic reconstruction (Kim and Lee, 2005). Indels, which are characteristic of non-coding regions, are also common in this region (Bakker *et al.*, 2000; Borsch *et al.,* 2003). These are derived from either deletion or duplication of adjacent sequences or occur in non-repetitive regions of the spacer (Goldenberg *et al.*, 1993). Borsch *et al.* (2003) examined numerous basal angiosperm families and had to first assess the primary homology of indels. Thereafter substitutions in indels and overlapping indels were treated.

3.1.3.1.1. The *trnT-L* spacer

The *trnT-L* spacer is not as frequently used as the *trnL-F* regions (Perret *et al.*, 2003; Shaw *et al.*, 2005), although it is the most variable of the three markers

(Small *et al*., 1998, Neves *et al*., 2005), with the *trnL-F* spacer generally more variable than the *trnL* intron (e.g. Bayer and Starr, 1998; Bayer *et al*., 2000). The *trnT-L* spacer varies in plants from c. 400 to 1 500 bp. The unpopularity of the *trnT-L* spacer is due to difficulties associated with amplification. It also frequently has large AT rich regions that may be difficult to align (Shaw *et al*., 2005).

Despite the limited application of the *trnT-L* spacer, it was found to be variable in *Kniphofia* and is thus reviewed in detail here. In many studies this spacer has been used in combination with sequences from other cpDNA regions (particularly adjacent *trnL-F* sequences) to infer phylogenetic relationships at various levels. The high variability of the spacer has resulted in the application of this region to inferring relationships at the species and genus level. However, it has been used at higher levels in several combinational studies (Bremer *et al*., 2002; Borsch *et al.*; 2003; Fay *et al*., 2000; Renner and Chanderbali, 2000; Sauquet *et al*., 2003).

The *trnT-L* spacer has also proven useful at various infra-familial levels (generic, tribal and subtribal limits) in Apocynaceae (Liede, 2001; Liede and Täuber, 2002; Liede *et al*., 2002; Liede and Kunze, 2002; Meve and Liede, 2004a; Meve and Liede, 2004b; Liede-Schumann *et al*., 2005), Cactaceae (Applequist and Wallace, 2002), Cyperaceae (Roalson *et al*., 2001), Atherospermataceae (Renner *et al*., 2000), Gesneriaceae (Perret *et al*., 2003); Rubiaceae (Razafimandimbison and Bremer, 2002; Lantz and Bremer, 2004; Alejandro *et al*., 2005; Lantz and Bremer, 2005) and Scrophulariaceae (Kornall and Bremer, 2004).

It has been used in many species level studies to gain insights into phylogenetic relationships at the species level. Some of these are summarised in Table 3.1.

It has also proven in some instances to be variable at intra-specific level e.g. *Cyclobalanopsis glauca* [Fagaceae, Huang *et al.* (2002)], *Phragmites australis*

[Poaceae, Saltonstall (2002)] and *Primula sieboldii* [Primulaceae, Honjo *et al.* (2004)]. Mason-Gamer (2004) used the *trnT-F* region (along with other markers) to examine the evolutionary history of *Elymus repens* (Poaceae). Zhang *et al.* (2005) found the *trnT-F* region useful in inferring the phylogeography of *Juniperus przewalskii* (Cupressaceae).

Nickrent *et al.* (2004) could not obtain sequences in *trnT-F* regions (regions not specified) for many taxa in *Arceuthobium*. This problem was attributed to sequence divergence at the primer binding sites caused by either substitutional mutations or deletions. Thus, these workers have questioned the universal applicability of the primers of Taberlet *et al.* (1991).

Table 3.1. Examples of phylogenetic studies that have utilised the *trnT-L* spacer at the species level.

Study	**Genus studied**	**Makers used**	**Comments**
Böhle *et al.* (1996)	*Echium*	*ITS*, *trnT-L*, *trnL*, *trnL-F*	*ITS* most divergent; *trnT-F* treated as a single unit, combined analysis used to infer relationships
Small *et al.* (1998)	*Gossypium*	Seven cpDNA markers & *Adh*	*Adh* most informative, only two cpDNA markers (*trnT-L* & *rpl16*) with informative characters
Fukuda *et al.* (2001)	*Lycium*	*matK*, *trnT-L*, *trnL*, *trnL-F*	*trnL-F* most informative, but *trnT-L* evolving more rapidly, combined analysis used to infer relationships
Mummenhoff *et al.* (2001)	*Lepidium*	*trnT-L*, *trnL*, *trnL-F*	*trnT-L* most informative
Baumel *et al.* (2002)	*Spartina*	*ITS*, *trnT-L*, *waxy*	*waxy* most informative, *trnT-L* least informative
Mast and Givnish (2002)	*Banksia* & *Dryandra*	*trnT-L*, *trnL*, *trnL-F*, *rps16*, *psbA-trnH*	Not all data for markers given but *trnT-L* appears to be one of the more informative markers
Yang *et al.* (2002)	*Brassica* & *Raphanus*	*trnT-L*, *trnL*, *trnL-F*, *trnD-T*	*trnD-T* most informative
Patterson and Givnish (2003)	*Calochortus*	*trnT-L*, *trnL*, *trnL-F*, *rpl16*, *psbA-trnH*	Data for markers not given, combined analysis used to infer relationships

Table 3.1. continued

Study	**Genus studied**	**Makers used**	**Comments**
Valcárcel *et al.* (2003)	*Hedera*	*ITS*, *trnT-L*	*ITS* more informative, but *trnT-L* with enough resolution to serve as an independent source to infer ancestry
Bohs (2004)	*Solanum*	*ITS*, *trnT-L*, *trnL*, *trnL-F*	*trnT-L* with greatest resolving power
Gravendeel *et al.* (2004)	*Pleione*	*ITS*, *trnT-L*, *trnL*, *trnL-F*, *matK*	*ITS* most informative, *trnT-F* more variable than *matK*, *trnT-F* treated as a single unit
Nickrent *et al.* (2004)	*Arceuthobium*	*ITS*, *trnT-L*, *trnL*, *trnL-F*	*ITS* most informative, *trnT-F* treated as a single unit
Mast *et al.* (2004)	*Dodecatheon* & *Primula*	*matK*, *rpl16*, *rps16*, *trnT-L*, *trnL*, *trnL-F*	*matK* most informative, combined analysis used to infer relationships
Levin *et al.* (2005)	*Solanum*	*ITS*, *trnT-L*, *trnL*, *trnL-F*, *waxy*	*waxy* most informative, *trnT-F* treated as a single unit

The *trnT-L* spacer can be problematic in terms of amplification especially the 5' end (Lantz and Bremer, 2004). Renner and Chanderbali (2000) found that the 5' end is highly variable and had to be excluded because of ambiguity and alignment problems. It appears that this region (especially the 5' end of *trnT-L* spacer, viz. the priming site for Taberlet's primer 'a') is problematic in many different plant groups (Shaw *et al.*, 2005). Cronn *et al.* (2002) found it necessary to design a new primer. In several studies internal primers had to be designed to amplify and sequence this region (Razafimandimbison and Bremer, 2002; Fukuda *et al*., 2001; Valcárcel *et al.*, 2003).

The region is prone to large AT rich hotspots (Sauquet *et al.* 2003; Perret *et al.*, 2003; Mast and Givnish, 2002; Mummenhoff *et al.*, 2001), poly-T regions (Perret *et al.*, 2003) and poly-A chains (Liede *et al.*, 2002; Liede and Täuber, 2002). Stech (2004) found small indels of 1-4 bp within the *trnT-L* spacer. These short indels were mostly simple sequence repeats (A, T, AA, TT, AT, ATTT) situated in poly A/poly T stretches. Borsch *et al.* (2003) showed that high length sequence variability is confined to mutational hotspots in the *trnT-F* region, which were common. Most other microstructural changes present in the intergenic spacers were simple repeat motifs (4-6 bp).

These nucleotide repeats result in indels of dubious homology, length variation and ambiguous alignments. These segments have to be frequently excluded from analyses (Sauquet *et al.*, 2003; Perret *et al.*, 2003; Liede *et al.*, 2002; Liede and Täuber, 2002; Liede and Kunze, 2002; Mummenhoff *et al.*, 2001; Mast and Givnish, 2002). Frequent large indel events can result in loss of data and possibly increase noise (Neves *et al*., 2005). Mast and Givnish (2002) and Mummenhoff *et al.* (2001) have also reported that poly-AT tracks cause sequencing problems. These factors impact negatively on the *trnT-L* spacer's potential in phylogenetic reconstruction.

These regions of simple repetitive DNA (A, T, AT) are most likely the result of slipped-strand mispairing (Levinson and Gutman, 1987). Valcárcel *et al.* (2003) examined the sequence substitution and the secondary structure of the *trnT-L* foldings in *Hedera* (Araliaceae). Loops, stem-loops and nucleotide domains failed to reveal any hot spots for mutation or mutational triggers. These workers dismissed slipped-strand mispairing or intra-molecular recombination as factors accounting for these sequence repeats and concluded that secondary structure formation does not appear to significantly affect the evolution of this non-coding chloroplast spacer and that the indels were not homoplasious in nature.

Few studies have shown the limited use of the *trnT-L* spacer. Neves *et al.* (2005) found that although the *trnT-L* spacer was the most variable of the non-coding regions in their study (*trnT-F*), but most of the variation was autoapomorphic.

Nickrent *et al.* (2004) have reported that a single species (*Arceuthobium douglasii*) has a large deletion in the *trnT-L* spacer, which spanned into the *trnL* intron. This species lacked the *trnL* 5' exon but retained the 3' exon, which was considered to be a 'pseudogene'.

3.1.3.1.2. The *trnL* Intron

This is a Group I intron and ranges from c. 250 to 1 400 bp in plants (Shaw *et al*., 2005). The *trnL* intron shows sequence conservation in the regions flanking the *trnL* exons while the central part is variable (Bakker *et al*., 2000). Bakker *et al.* (2000) found that nucleotide substitutions in the *trnL* intron accumulated in a more uniform pattern than the *trnL-F* spacer in angiosperms.

The *trnL* intron contains several highly conserved motifs in Gnetales (Won and Renner, 2005). The conservative nature of this intron is attritubuted to the maintenance of secondary structure and sequence elements of the *trnL* gene which are critical for self-splicing from precursor RNAs (Simon *et al*., 2003).

The *trnL* intron is the oldest intron transmitted from cyanobacteria to the chloroplast. Its conserved nature and high AT content may explain why it evolves more slowly than other non-coding chloroplast sequences (Yang *et al.*, 2002). Yang *et al.* (2002) found the rate of nucleotide substitution in the *trnL* intron was less than the surrounding spacers. This was presumably due to the greater functional constraints imposed on the intron. Borsch *et al.* (2003) found that the *trnL* intron was less variable than the surrounding spacers due to the fewer length mutational changes in the intron. Length conservation of the intron may also relate to the role of the intron in splicing during mRNA processing. It also appears that the *trnL* intron and the *trnL-F* spacer evolve in concert. This may be because the tRNA genes of the intron and spacer are transcribed in the same direction (Borsch *et al.*, 2003 and references therein).

Sequences of this *trnL* intron are usually co-amplified with the *trnL-F* spacer (Shaw *et al.*, 2005) and together these two regions have become the most popular and widely used non-coding cpDNA markers (Shaw *et al.*, 2005; Kim and Lee, 2005). The *trnL-F* spacer is usually shorter than the intron ranging from less than 100 to 500 bp (Shaw *et al.*, 2005). The number of parsimony informative characters in the *trnL-F* spacer is usually greater than the *trnL* intron, despite the intron being usually larger (Shaw *et al.*, 2005).

In numerous studies the *trnL* intron has been used to complement, support and/or enhance the phylogenetic signal and potential of the *trnL-F* spacer (e.g. Udovicic and Ladiges, 2000; Reeves *et al.*, 2001; Morton *et al.*, 2003; Scheen *et al.*, 2004; Mols *et al.*, 2004; van der Niet *et al.*, 2005). In some studies the *trnL* intron has closely equalled or marginally out-performed the *trnL-F* spacer (e.g. Mummenhoff *et al.*, 2001; Bellstedt *et al.*, 2001; Razafimandimbson and Bremer, 2002; Oberlander *et al.*, 2004; van den Berg *et al*, 2005). This is due partly to greater length of the intron in these studies.

Based on these findings, the *trnL* intron was used in this study to determine if it would support and/or enhance the phylogenetic signal of the *trnT-L* spacer. In addition the amplification approach (see Materials and Methods) resulted in co-amplified PCR products for both the *trnT-L* spacer and *trnL* intron, thus facilitating sequencing.

3.1.3.2. The *psbA-trnH* intergenic spacer

Sang *et al*. (1997) were the first to use this region in phylogenetic studies in *Paeonia* (Paeoniaceae). It is a short region found between two highly conserved genes and is therefore, easily amplified. This spacer region lies in the inverted repeat region of the cp genome adjacent to the *trnK* gene. The two flanking genes are the *psbA* and *trnH* gene (Chandler *et al.*, 2001). Sang *et al*. (1997) found that the *psbA-trnH* sequences evolved slightly less rapidly than *ITS* sequences, but over three times faster than the *matK* coding region. However, *matK* sequences served as a better phylogenetic marker from the cp genome.

Although this region has a very high percentage of variable characters (Hamilton *et al*., 2003), it is usually coupled with other markers as it is too short and may not provide enough characters to build a well-resolved phylogeny (Shaw *et al*., 2005). Shaw *et al.* (2005) found the average length to be 465 bp and ranges from 198 to 1 077 bp. Although this spacer was the second most variable, it is relatively short and provides few overall characters (Shaw *et al*., 2005).

The region has proven to be useful in combined approaches at the species level (Udovicic and Ladiges, 2000; Chandler *et al*., 2001; Mast and Givnish, 2002; Patterson and Givnish, 2003; Scheen *et al.*, 2004; Butterworth and Wallace, 2004; Yamashiro *et al*., 2004). It has also been used with other markers at the infra-specific level (Holderegger and Abbott, 2003; Honjo *et al.* 2004; McKinnon *et al*., 2004; Howis *et al.*, in prep.).

In some studies at higher taxonomic levels larger parts of the spacer were difficult to align and were excluded from analyses (Renner, 1999; Renner and Chanderbali, 2000; Soltis *et al*., 2001). Schönenberger and Conti (2003) and Klak *et al.* (2003a) found this region to be of limited use. Initial screening of this region in *Kniphofia* found little sequence divergence and the option of exploring this marker was not pursued further.

3.1.3.3. The *rps16* intron

The plastid ribosomal protein 16 small subunit (*rps16*) gene has a group II intron that was first used by Oxelman *et al.* (1997) to construct relationships in the tribe Sileneae (Caryophyllaceae). The intron averages 846 bp in length and ranges from 784 to 946 bp (Shaw *et al*., 2005). Schönenberger and Conti (2003) found that *rps16* was one of the more informative markers for Penaeaceae, Oliniaceae, Rhynchocalyaceae and Alzateaceae. It has proven to be useful at the generic level (Asmussen *et al.*, 2000; Asmussen and Chase, 2001; Morton *et al.*, 2003).

This region cannot be used in certain groups as all or a portion of the *rps16* gene is absent in some angiosperm families (Doyle *et al.*, 1995). The *rps16* intron often does not provide enough characters to resolve relationships below generic levels (e.g. Ingram and Doyle, 2003; Wanntorp *et al*., 2001; Goldblatt *et al*., 2002; Muellner *et al.*, 2005). Initial screening of this region in *Kniphofia* found little sequence divergence and the option of exploring this marker was not pursued further.

3.1.3.4. Nuclear DNA: the 18S-5.8S-26S rDNA cistron

This region is part of a transcription unit of nDNA. The spacer sectors are not incorporated into mature ribosomes. *ITS 1* and *ITS 2* of the nDNA transcript appear to function at least in part of the maturation of nRNAs (Baldwin *et al.*, 1995). This region was used to obtain a data set independent from the cpDNA markers in *Kniphofia*, therefore, the use of this spacer in phylogenetic studies is reviewed.

The wide phylogenetic use of the 18S-5.8S-26S rDNA cistron is due to its structure and molecular evolution (Baldwin *et al.*, 1995; Álvarez and Wendel, 2003). It is structured in tandem arrays at one or more chromosomal loci. The basic structure of a transcribed single repeat unit of rDNA is as follows: an external transcribed spacer (*ETS*); the *18S* gene; an internal transcribed spacer (*ITS 1*); the *5.8 S* gene; a second internal transcribed spacer (*ITS 2*); the *26S* gene and an intergenic spacer (*IGS*). Each unit is repeated thousands of times in most plant genomes and separated from the next by the *IGS*. The tandem repeat structure and high copy number faciliates amplification and sequencing.

Other factors that make this region popular and advantageous according to Álvarez and Wendel (2003) are biparental inheritance, universality of primers for amplification, intragenomic uniformity, intergenomic variability and low functional constraints.

3.1.3.4.1. Use of *ITS* sequence data in lower level plant systematics studies

Preliminary studies indicated that *ITS* was conservative in length with high sequence variability, suggesting that the spacers would be easily alignable and variable enough to address lower level (various intra-familial levels) phylogenetic issues (Balwin *et al.*, 1995). The *18S* and *26S* genes are highly conserved and useful for higher taxonomic levels (family and above) of phylogeny reconstruction. The more rapidly evolving segments, *ITS1* and *ITS2* (commonly called the *ITS* region along with the *5.8S* gene) is the most utilised nuclear region for phylogenetic inference at lower levels (genus and below) (Álvarez and Wendel, 2003; Small *et al.*, 2004). In many studies *ITS* has out-performed cpDNA markers (e.g. Razafimandimbison and Bremer, 2002; Verboom *et al.*, 2003; Nickrent *et al*., 2004; van der Niet *et al*., 2005; Muellner *et al*., 2005; van den Berg *et al*., 2005; Chen *et al*., 2005).

The *ITS* region has proven useful at various infra-familial levels (generic, tribal and subtribal limits): Agavaceae (Bogler and Simpson, 1996), Rubiaceae (Razafimandimbison and Bremer, 2002; Lantz and Bremer, 2004) and Saxifragaceae (Soltis *et al*., 2001).

The *ITS* region has also proven useful in many species level studies, a few of which are summarised in Table 3.2. It has also proven in some instances to be variable at infra-specific level (e.g. McKinnon *et al*., 2004; Barker *et al*., 2005).

3.1.3.4.2. Problems with the *ITS* region

While the *ITS* region has contributed much to the field of plant phylogenetics, there are some major disadvantages (Álvarez and Wendel, 2003; Small *et al*. 2004; Mort and Crawford, 2004) which will be briefly reviewed below.

A fundamental pre-requisite and frequent assumption for historical inference is that the genes compared are orthologous as opposed to paralogous. Genes are considered orthologous if their relationships originated from organismal cladogenesis. This a misleading view as diploid individuals can contain two different orthologues. Their history may reflect divergence events among species. However, if there has been a history of gene/sequence duplication then the duplicated sequences are considered paralogous. When paralogous sequences are included in phylogenetic reconstruction the resulting phylogeny will confound divergence events by tracking the history of duplication. Incorrect assessment of orthology and paralogy leads to phylogenetic incongruence. This is also the consequence if sampling includes a mixture of orthologous and paralogous sequences (Álvarez and Wendel, 2003).

Table 3.2. Examples of phylogenetic studies that have utilised the *ITS* region at the species level.

Study	**Genus studied**	**Makers used**	**Comments**
Adams *et al.* (2000)	*Aloe*	*ITS* only	Limited sampling, no other study for comparison
Baumel *et al.* (2002)	*Spartina*	*ITS*, *trnT-L*, *waxy*	*waxy* most informative, followed by *ITS*, *trnT-L* least informative
Samuel *et al.* (2003)	*Hypochaeris*	*ITS*, *trnL*, *trnL-F*, *matK*	*ITS* most informative
Verboom *et al*. (2003)	*Ehrharta*	*ITS*, *trnL-F*	*ITS* more informative than *trnL-F*
Barker *et al.* (2004)	*Leucadendron*	*ITS* only	No other marker for comparison
Gravendeel *et al.* (2004)	*Pleione*	*ITS*, *trnT-L*, *trnL*, *trnL-F*, *matK*	*ITS* most informative
Nickrent *et al.* (2004)	*Arceuthobium*	*ITS*, *trnT-L*, *trnL*, *trnL-F*	*ITS* most informative
Muellner *et al*. (2005)	*Aglaia*	*ITS*, *rpl16*	*ITS* more informative
van der Niet *et al*. (2005)	*Satyrium*	*ITS*, *matK*, *trnL*, *trnL-F*	*ITS* most informative
Archibald *et al.* (2005)	*Zaluzianskya*	*ITS*, *rpl16*, *trnL*, *trnL-F*	*ITS* most informative

Nuclear genes have the ability to evolve in unison. Instead of each gene copy accumulating unique sequence variation via accumulation of mutations all repeat copies in the array may jointly share the same set of mutations resulting in intergenic sequence homogenisation i.e. concerted evolution (Álvarez and Wendel, 2003; Small *et al.*, 2004). Mechanisms such as high frequency crossing over or gene conversion are implicated in this process (Baldwin *et al.*, 1995). Concerted evolution was initially considered to be advantageous, as it would eliminate paralogous sequences and facilitate the inference of true homology in phylogenetic reconstruction (Álvarez and Wendel, 2003). However, the presence or absence of both or multiple copies per array and multiple arrays per genome and the presence, absence or variable extent of concerted evolution may homogenise sequences within and sometimes between arrays. Sequence variants can arise and be maintained within and between arrays resulting in distantly related nDNA types within individuals. Such erratic variation may be the norm rather than the exception but is often ignored, underreported or undetected. Thus, when concerted evolution is incomplete it results in a mixture of multiple divergent copies, which constitute paralogues and orthologues.

This complicates phylogenetic reconstruction. Even when sampling measures are taken, one or more repeat types may be lost in one or more descendant taxa thus resulting in a loss of possible historical evidence (see Álvarez and Wendel, 2003 for review). Evidence of *ITS* paralogues has been reported in several studies (Mayol and Rosselló, 2001; van den Berg *et al.*, 2005; Neves *et al.*, 2005). Multiple copies of *ITS* have been reported by some workers (Goldblatt *et al.*, 2002; Liede and Täuber, 2002; Okuyama *et al.*, 2005). Paralogues could lead to spurious phylogenetic estimates, thus *ITS* data need to be treated with caution and compared with other sources of data (Barker *et al*., 2004; Neves *et al.*, 2005).

Multiple nDNA arrays may arise from hybridisation, polyploidisation, gene/chromosome duplication and various forms of recombination. It cannot be assumed that strict orthology has been maintained for sequences amplified among a set of taxa. Direct sequencing may not detect paralogues and may require an extensive cloning approach (Rauscher *et al*., 2002). Reticulation, introgression or polyploidisation may give rise to the co-existence of divergent *ITS* repeat types and the direction of sequence homogenisation may be different for the different lineages. This becomes an important factor and consideration in groups with hybridisation and polyploidisation (Álvarez and Wendel, 2003). This could lead to incorrect estimates of relationships in studies using *ITS* sequences at lower taxonomic levels (Soltis and Soltis, 1998).

In the evolution of polyploids concerted evolution plays an important role in the maintenance of sequence homogeneity of multigene families (Zhang and Sang, 1999). The mode and rate of concerted evolution in rDNA varies in different groups (Li and Zhang, 2002). The degree to which concerted evolution may cause homogenisation depends on the extent to which the initial parents have diverged and the time of polyploidisation. Polyploids may exhibit additivity of parental rDNA sequences e.g. *Paeonia* (Sang *et al*., 1995). Concerted evolution may homogenise rDNA towards one parent in a hybrid genome while the other parental rDNA type is eliminated. In *Aegilops* concerted evolution of rDNA in allopolyploid species is uni-directional (Wang *et al.*, 2000). Li and Zhang (2002) found that in *Thinopyrum ponticum* (a decaploid) rDNA has experienced uni-directional concerted evolution towards diploid relatives. In some cases concerted evolution of rDNA may be bi-directional e.g. *Gossypium* (Wendel *et al*., 1995).

An alternate explanation for sequence homogenisation is the loss of rDNA loci of one or more genomes following the polyploidisation (Li and Zhang, 2002). Concerted evolution may fail to homogenise sequences in certain case e.g. recent hybridisation, development of pseudogenes, large number of rDNA repeats and asexual reproduction (Li and Zhang, 2002).

Several studies have used *ITS* sequences with other markers and/or morphological evidence to gain insights into evolutionary processes e.g. hybridisation and lineage sorting (e.g. Sang *et al.*, 1995; Sang *et al.*, 1997; Aguilar *et al*., 1999; Comes and Abbott, 2001; Goldman *et al.*, 2004; Howarth and Baum, 2005).

Not all 18S-5.8S-26S repeats remain functional and some may degenerate into pseudogenes (Álvarez and Wendel, 2003; Small *et al.*, 2004). Non-functional variants of *ITS* (pseudogenes) have been reported (Neves *et al*., 2005). Putative *ITS* pseudogenes have been found to be useful for phylogenetic inference in three species of Rubiaceae (Razafimandimbison *et al*., 2004).

Bell (2004) reported that *ITS* sequence data does not provide support for relationships within Valerianaceae. This was because the region appeared to be evolving too fast and suffers from alignment problems. Plana *et al.* (2004) found that large segments of *ITS* had high sequence divergences and were difficult to align in *Begonia*. In many studies *ITS* sequence data showed low divergence and has been implicated in recent rapid radiation (Baldwin and Sanderson, 1998; Harris *et al*., 2000; Malcomber, 2002; Klak *et al*.; 2003b; Richardson *et al.*, 2001; Warwick *et al.*, 2004; Howarth and Baum, 2005).

Based of the usefulness of the markers screened the *trnT-L* spacer, *trnL* intron and *ITS* region were used to examine phylogenetic relationships in *Kniphofia*. Initial *ITS* results showed little sequence divergence (below). Despite this, further investigations were done as this marker as it was the only independent nuclear marker that could be easily amplified and sequenced routinely.

3.2. Materials and Methods

3.2.1. Sampling strategy, Collection and Preservation

Whitehouse (2002b) has suggested that at the species level, an understanding of the taxonomy of the genus and variation within species needs to be developed prior to selection of exemplar collections to reliably represent a species. He also recommended that more than one collection should be chosen to cover the range of morphological and geographic diversity found within the species. If knowledge of the genus is superficial, an arbitrary choice of a specimen could result in one that lies at the boundary between two species or represents a case where introgression has occurred with a sympatric species (Whitehouse, 2002b). This is of particular importance, as species of *Kniphofia* can hybridise and are sometimes sympatric. However, *Kniphofia* has c. 71 species, a complex taxonomy and a wide distribution extending from southern to eastern Africa, Yemen and Madagascar. Understanding of species concepts and collecting material required a substantial amount of field work and time. Due to the limitations imposed by the number of taxa in *Kniphofia*, flowering times and resources, samples were sequenced as and when material became available. As many southern African species were sampled as possible to obtain species coverage and geographical coverage (at the quarter degree scale).

Moreover, based on a pilot study (Ramdhani *et al*., 2006) it became apparent that multiple samples per species had to be sequenced because many taxa appeared to be non-monophyletic. Thus a multiple exemplar approach was advocated. Every attempt has been made to include as many samples representing as many morphological species *sensu* Codd (1968, 2005) as possible. Four southern African species were not included in this study. *K. flammula* is a highly restricted species only known from the Glencoe region of KwaZulu-Natal. It was last collected in 1968. Attempts were made over two flowering seasons to locate living material but to no avail. *K. evansii* is also a restricted species found only in the Bergville District in high montane grasslands. I have tried to locate this species three times in the Catheral Peak area but have failed. *K. tabularis* is restricted to the Cape fold mountains. This species was not encountered in the limited time spent sampling in the Western Cape. *K. crassifolia* is only known form the type collection made by the Austrian botanist A. Rehmann. It was collected in 1880 from the Houtbosch region in Limpopo Province. No attempt was made to find this species as the original locality probably has been transformed by timber plantations (Pieter Winter, pers. comm.).

Material from other parts of Africa proved more difficult to obtain. Field work was done in the Bale Mountains in Ethiopia and the area around Addis Ababa (Tatek) in September 2003. Limited material was obtained from Kenya, Tanzania, Malawi and Madagascar from collecting done by colleagues. DNA was obtained from a single sample of herbarium origin (*K. splendida*, Chapman & Chapman 9061) from Mt Mulanje (Malawi). Table 3.3. lists the details of the samples used in this study.

Most leaf samples were dried with silica gel (Chase and Hills, 1991). In some cases plants collected in the field were cultivated and fresh material was used to extract DNA. Most samples collected have an accompanying herbarium voucher, which is housed at the Selmar Schonland Herbarium (GRA). Specimens collected in Ethiopia are housed at the National Herbarium of Ethiopia (ETH, Addis Ababa). In some instances DNA material was collected with no accompanying herbarium voucher, as the sites were visited when plants were not flowering. In these instances specific DNA collections were only included if the species in question were known to occur at the site from previous collections and/or field observations by other botanists. These were not assigned collection numbers and tagged as *sine numero* (*sn*). Likewise material collected by other collectors with no herbarium voucher were tagged *sine numero*. Subspecies, variant and forms were specified only when confidently known by the author.

Specimens obtained from botanical gardens were tagged with the reference number of the particular garden. In the case of *K. leucocephala* the only material available was from the Natal National Botanical Garden’s living collection in Pietermaritzberg. These plants were clones (via tissue culture) of specimens collected at the type locality due to its restricted distribution and critically endangered conservation status (Scott-Shaw, 1999).

Table 3.3. List of specimens used in phylogenetic reconstruction with locality details. Notes to abbreviations: Collectors initials, HB= H. Baijnath, NPB= N. P. Barker, JB= J. Burrows, TD= T. Dold, JMG= J.M. Grimshaw, CK= C. Kayombo, RAL= R.A. Lubke, RJM= R.J. McKenzie, AMM= A.M. Muasya, AN= A. Nicholas, CP= C. Peter, PBP= P.B. Phillipson, JP= J. Pote; SR= S. Ramdhani, AR= A. Rennie, BT= B. Tarr; Botanical garden material: NNBG= Natal National Botanical Garden (Pietermaritzburg); *sn*= unnumbered collections with no herbarium voucher. Herbarium abbreviations follow Holmgren *et al*. (1994).

Taxon	**Voucher (Herbarium)**	**Locality**	***trnT-L* spacer**	***trnL* intron**	***ITS***
K. acraea	TD 4626 (GRA)	Mountain Zebra National Park	X	X	X
K. albescens	SR & JB 314 (GRA)	Dirkiesdorp	X	X	X
K. albomontana	SR & AN 149 (GRA)	Greytown	X		X
K. angustifolia	SR 542 (GRA)	Cathedral Peak Nature Reserve	X		X
K. angustifolia	SR 453 (GRA)	Cathedral Peak Nature Reserve	X		X
K. ankaratrensis	PBP 5676 (P)	Madagascar	X		X
K. baurii	SR 174 (GRA)	Humansdorp	X		
K. baurii	SR 202 (GRA)	Kareedouw	X		

Table 3.3. continued

Taxon	**Voucher (Herbarium)**	**Locality**	***trnT-L* spacer**	***trnL* intron**	***ITS***
K. baurii	SR 275 (GRA)	Elands Heights	X		X
K. baurii	SR 285 (GRA)	Naudes Nek	X	X	X
K. baurii	SR 360 (GRA)	Port Elizabeth	X		X
K. baurii	SR 382 (GRA)	Kenton-on-Sea	X		X
K. baurii	SR 398 (GRA)	Mooi River	X		
K. baurii	RJM 1026 (GRA)	Natures Valley	X		
K. baurii	NPB 1923 (GRA)	Alicedale	X		X
K. brachystachya	SR *sn* (GRA)	Estcourt	X		X
K. breviflora	SR 452 (GRA)	Oliviershoek Pass	X	X	X
K. bruceae	SR & NPB 171 (GRA)	Komga	X	X	X
K. buchananii	SR & BT 305 (GRA)	Greytown	X		
K. buchananii	SR & BT 307 (GRA)	Greytown	X		X
K. buchananii	SR 458 (GRA)	Howick	X		
K. caulescens	SR 270 (GRA)	Elands Heights	X		X

Table 3.3. continued

Taxon	**Voucher (Herbarium)**	**Locality**	***trnT-L* spacer**	***trnL* intron**	***ITS***
K. caulescens	SR 278 (GRA)	Naudes Nek	X	X	X
K. caulescens	NPB 1821 (GRA)	Sani Pass	X		X
K. caulescens	RJM 974 (GRA)	Carlisles Hoek	X		
K. citrina	SR 176 (GRA)	Humansdorp	X		X
K. coddiana	SR *sn*	Umtamvuna Nature Reserve	X		X
K. coralligemma	SR 549 (GRA)	Iron Crown (Wolkberg)	X	X	X
K. drepanophylla	RAL 4816 (GRA)	Mkambati	X		X
K. drepanophylla	RJM 1100 (GRA)	Mkambati	X		
K. ensifolia subsp. *ensifolia*	JB *sn*	Witbank	X		X
K. ensifolia subsp. *autumnalis*	SR 448 (GRA)	Harrismith	X		X
K. fibrosa	SR & AR 297 (GRA)	Pervensey	X		X
K. fibrosa	PBP 5579 (GRA)	Dohne Hill	X		

Table 3.3. continued

Taxon	**Voucher (Herbarium)**	**Locality**	***trnT-L* spacer**	***trnL* intron**	***ITS***
K. fluviatilis	SR *sn*	Verloren Vallei			X
K. foliosa	SR 383 (ETH)	Gafesar Dam, Ethiopia	X		X
K. foliosa	SR 387 (ETH)	Bale, Ethiopia	X		X
K. foliosa	SR 389 (ETH)	Goba, Ethiopia	X		X
K. foliosa	SR 390 (ETH)	Bale, Ethiopia	X		X
K. foliosa	JMG 034 (ETH	Sebese Washi, Ethiopia	X	X	X
K. foliosa	JMG 038 (ETH)	Bale, Ethiopia	X		X
K. galpinii	SR 312 (GRA)	Long Toms Pass, Lydenberg	X		X
K. gracilis	SR & HB 321 (GRA)	Durban	X		X
K. gracilis	SR 561 (GRA)	Park Rynie	X		
K. gracilis	NNBG 77/99	Draycott	X		X
K. grantii	CP 4154 (GRA)	Nyika Plateau, Malawi	X		X
K. hirsuta	SR 282 (GRA)	Naudes Nek	X		X

Table 3.3. continued

Taxon	**Voucher (Herbarium)**	**Locality**	***trnT-L* spacer**	***trnL* intron**	***ITS***
K. ichopensis var. *ichopensis*	SR 242 (GRA)	Nottingham Road	X		X
K. ichopensis var. *ichopensis*	SR 286 (GRA)	Giants Castle Nature Reserve	X		X
K. ichopensis var. *ichopensis*	SR 289 (GRA)	Cathedral Peak Nature Reserve	X		X
K. ichopensis var. *ichopensis*	SR 409 (GRA)	Balgowan	X		
K. insignis	SR *sn*	Tatek, Ethiopia	X	X	X
K. isoetifolia	SR 386 (ETH)	Bale Mountains, Ethiopia	X		X
K. isoetifolia	SR 388 (ETH)	Goba, Ethiopia	X	X	X
K. isoetifolia	SR 393 (ETH)	Kofele, Ethiopia	X		X
K. latifolia	RSS *sn*	Greytown	X		X
K. laxiflora form B	SR 295 (GRA)	Kamberg Nature Reserve	X		X
K. laxiflora form B	NPB 1810 (GRA)	Bushmans Nek	X		X

Table 3.3. continued

Taxon	**Voucher (Herbarium)**	**Locality**	***trnT-L* spacer**	***trnL* intron**	***ITS***
K. laxiflora form B	SR 441 (GRA)	Nottingham Road	X		
K. laxiflora form B	SR 442 (GRA)	Michaelhouse	X		
K. laxiflora form B	SR 467 (GRA)	Weza	X	X	X
K. laxiflora form B	SR 468 (GRA)	Weza	X	X	X
K. laxiflora form C	SR *sn* (GRA)	Wakkerstroom	X		X
Kniphofia sp. cf. laxiflora	SR 283 (GRA)	Naudes Nek	X		X
K. leucocephala	NNBG	Richards Bay (clone of type)	X		X
K. linearifolia	SR & NPB 170 (GRA)	Komga			X
K. linearifolia	SR 269 (GRA)	Hogsback (Seymour)	X		X
K. linearifolia	SR 287 (GRA)	Loskop	X		
K. linearifolia	SR 290 (GRA)	Rosetta	X		X
K. linearifolia	SR 291 (GRA)	Kamberg Nature Reserve	X		X
K. linearifolia	SR & JB 311 (GRA)	Lydenberg	X	X	X

Table 3.3. continued

Taxon	**Voucher (Herbarium)**	**Locality**	***trnT-L* spacer**	***trnL* intron**	***ITS***
K. linearifolia	SR 313 (GRA)	Sabie			X
K. linearifolia	SR 328 (GRA)	Mt. Currie Nature Reserve	X		X
K. linearifolia	SR 343 (GRA)	Hogsback (Seymour)	X		X
K. linearifolia	SR 558 (GRA)	Underberg	X		
K. linearifolia	JP *sn* (GRA)	Stutterheim	X		
K. linearifolia	TD 4638 (GRA)	Satans Nek	X		
K. linearifolia	SR 400 (GRA)	Mooi River	X		
K. littoralis	SR & HB 200 (GRA)	Silverglen Nature Reserve	X		X
K. multiflora	SR & JB 310 (GRA)	Lydenberg	X	X	X
K. multiflora	SR & JB 315 (GRA)	Dirkiesdorp			X
K. northiae	SR 263 (GRA)	Hogsback (Seymour)	X		X
K. northiae	SR 274 (GRA)	Naudes Nek	X		
K. northiae	SR 446 (GRA)	Katberg	X	X	X
K. parviflora	SR 268 (GRA)	Hogsback (Seymour)	X	X	X

Table 3.3. continued

Taxon	**Voucher (Herbarium)**	**Locality**	***trnT-L* spacer**	***trnL* intron**	***ITS***
K. parviflora	SR 330 (GRA)	Mt. Currie Nature Reserve	X	X	X
K. pauciflora	HB *sn* (GRA)	Durban	X		X
K. porphyantha	SR *sn*	Verloren Vallei	X		X
K. praecox	SR 529 (GRA)	Jefferys Bay	X		X
K. praecox	SR 530 (GRA)	Elandsbos River	X		
K. praecox	SR 532 (GRA)	Haroldsbaai	X		
K. rigidifolia	SR *sn*	Lydenberg	X		X
K. ritualis	SR 300 (GRA)	Pervensey	X	X	X
K. rooperi	SR 237 (GRA)	East London	X		X
K. rooperi	TD 4559 (GRA)	Mkambati	X		
K. rooperi	SR 485 (GRA)	Riet River	X		X
K. rooperi	RAL 4229 (GRA)	Morgans Bay	X		
K. rooperi	SR 528 (GRA)	Van Stadens River	X		
K. sarmentosa	SR 207 (GRA)	Hex River Pass	X		X

Table 3.3. continued

Taxon	**Voucher (Herbarium)**	**Locality**	***trnT-L* spacer**	***trnL* intron**	***ITS***
K. schimperi	SR 391(ETH)	Sebsebe Washe, Ethiopia	X		X
K. schimperi	JMG 036 (ETH)	Sebsebe Washe, Ethiopia	X	X	X
K. stricta	SR 548 (GRA)	Haenertsberg	X		X
K. splendida	EG Chapman & JD Chapman 9061 (FHO)	Mt. Mulanje, Malawi	X		
K. stricta	SR 279 (GRA)	Rhodes	X	X	X
K. thodei	SR 407 (GRA)	Kamberg Nature Reserve	X		X
K. thomsonii	JMG 031 (ETH)	Senatti Plateau, Ethiopia	X	X	X
K. thomsonii	AAM 2647 (EA)	Mt. Elgon, Kenya	X		X
K. thomsonii	CK 4821 (GRA)	Mt. Kilimanjaro, Tanzania	X		X
K. triangularis subsp. *triangularis*	SR 264 (GRA)	Hogsback (Seymour)	X		X

Table 3.3. continued

Taxon	**Voucher (Herbarium)**	**Locality**	***trnT-L* spacer**	***trnL* intron**	***ITS***
K. triangularis subsp. *triangularis*	SR 266 (GRA)	Hogsback (Seymour)	X		X
K. triangularis subsp. *triangularis*	SR 299 (GRA)	Pervensey	X	X	X
K. triangularis subsp. *obtusiloba*	SR *sn*	Kemps Heights	X		X
K. typhoides	NNBG 139/99	Vryheid	X	X	X
K. typhoides	JB 8084 (GRA)	Witbank			X
K. tysonii subsp. *tysonii*	SR 302 (GRA)	Creighton	X	X	X
K. tysonii subsp. *tysonii*	SR 460 (GRA)	Balito	X		
K. umbrina	R Gama *sn*	Forbes Reef, Swaziland	X	X	X
K. uvaria	SR & NPB 166 (GRA)	Port Elizabeth	X		

Table 3.3. continued

Taxon	**Voucher (Herbarium)**	**Locality**	***trnT-L* spacer**	***trnL* intron**	***ITS***
K. uvaria	SR & NPB 172 (GRA)	Post Wellington	X		
K. uvaria	SR 186 (GRA)	Kurlandsdorp	X	X	X
K. uvaria	SR 201 (GRA)	Cape St. Francis	X		X
K. uvaria	SR 203 (GRA)	Elim	X		X
K. uvaria	SR 211 (GRA)	Clarkson	X	X	X
K. uvaria	SR 337 (GRA)	Hogsback (Seymour)	X		
K. uvaria	SR 342 (GRA)	Hogsback (Seymour)	X		X
K. uvaria	SR 344 (GRA)	Grahamstown	X		X
K. uvaria	SR 471 (GRA)	Dimbaza	X		
K. uvaria	SR 477 (GRA)	Grahamstown	X		X
K. uvaria	TD 4477	Port Elizabeth	X		

3.2.2. DNA Extraction, Amplification and Sequencing

Total genomic DNA was extracted using a modified hot CTAB method of Doyle and Doyle (1987). Polymerase Chain Reaction (PCR) amplifications were conducted either on a ThermoHybaid PCR Sprint Temperature Cycling System or a Corbett Research PC-960G Microplate Gradient Thermal Cycler using the following conditions: 95˚C for 45 seconds, 52-55˚C for 45 seconds and 72˚C for three minutes repeated between 30-35 cycles (depending on the necessary number of cycles needed for suitable amplification). Annealing temperature was also manipulated to obtain optimal PCR product. A 10 minute 72˚C extension was included at the end of the PCR program. The PCR reagents and volumes are shown in Appendix 3.

3.2.2.1. The *trnT*-*trnL* region

The *trnT-L* spacer was initially amplified by means of the PCR using primers ‘a’ and ‘b’ (Taberlet *et al*., 1991). The forward primer ‘a’ proved to be problematic in amplification. As mentioned in the introduction, this region is noted for being troublesome (e.g. Lantz and Bremer, 2004; Renner and Chanderbali, 2000). It appears that this region (especially the 5’ end of *trnT-L* spacer, viz. the priming site for ‘a’) is problematic in many different plant groups (Shaw *et al*., 2005). To circumvent this problem, an alternative internal primer, ‘Knip1’ was designed (Ramdhani *et al*., 2006). Subsequently, the Knip1-d primer combination proved to be more efficient for amplification. Primers Knip1-b and c-d were used to sequence the spacer and inton respectively (refer to Figure 3.1. and Table 3.4. for details).

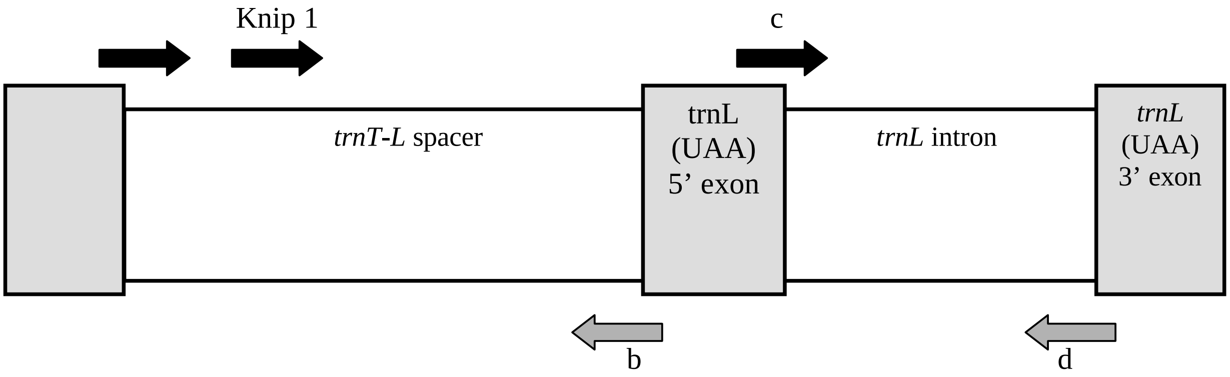


Figure 3.1. Schematic representation of the *trnT-L* region (spacer and intron) with primers (after Taberlet *et al*., 1991). Arrows indicate approximate starting points and directions of primers.

3.2.2.2. The *ITS* region

The *ITS* region (*ITS1*, *5.8S* and *ITS2*) was amplified using the primers 'ITS 18' and 'ITS 26' (Käss and Wink, 1997; modified by Lavin). These were used as flanking primers for amplification. Internal primers (both forward and reverse) were used for sequencing. These were primers 'ITS 1' and 'ITS 4' of White *et al.* (1990), as well as primers 'Chrys 5.8F' (Barker *et al*., unpublished) and 'Chromo5.8R' (Barker *et al*., 2005). Primers ITS 1-Chromo5.8R were used to sequence *ITS1* and part of the *5.8S* gene, while primers Chrys5.8F-ITS 4 were used to sequence the *5.8S* gene and *ITS2* (refer to Figure 3.2. and Table 3.4. for details).

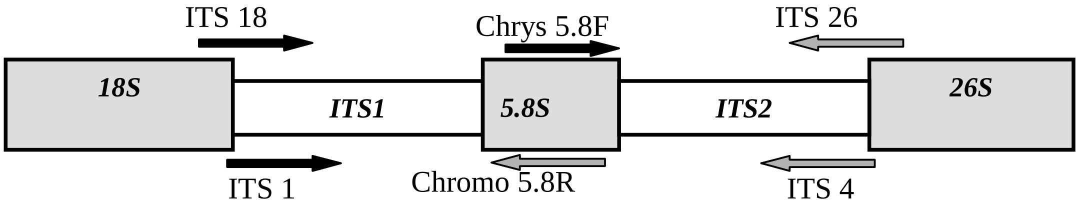


Figure 3.2. Schematic representation of the *ITS* region with primers used. Arrows indicate approximate starting points and directions of primer.

Table 3.4. Details of chloroplast and nuclear primers used in PCR* and sequencing# (F= forward, R= reverse).

Primer	**Direction**	**Reference**	**Length (bp)**	**Sequence**
a	F	Taberlet *et al*. (1991)	21	5’CATTACAAATGCGATTGCTCT3’
Knip1*&#	F	Ramdhani *et al*. (2006)	18	5’CTACCGGATCTTAGGTAT3’
b*&#	R	Taberlet *et al*. (1991)	20	5’TCTACCGATTTCGCCATATC3’
c *&#	F	Taberlet *et al*. (1991)	20	5’CGAAATCGGTAGACGCTACG3’
d *&#	R	Taberlet *et al*. (1991)	20	5’GGGGATAGAGGGACTTGAAC3’
ITS 18*	F	Käss and Wink (1997), modified by Lavin (pers. comm.)	26	5’GTCCACTGAACCTTATCATTTAGAGG3’
ITS 26*	R	Käss and Wink (1997), modified by Lavin (pers. comm.)	26	5’GCCGTTACTAAGGGAATCCTTGTTAG3’
ITS 1#	F	White *et al.* (1990)	19	5’TCCGTAGGTGAACCTGCGG3’
Chromo 5.8R#	R	Barker *et al.* (2005)	15	5’GATTCTGCAATTCAC3’
Chrys 5.8R#	F	Barker *et al.* (unpublished)	20	5’GACTCTCGGCAACGGATATC3’
ITS 4 #	R	White *et al.* (1990)	20	5’TCCTCCGCTTATTGATATGC 3’

3.2.2.3. Visualisation of PCR products

The PCR products were run on 1% agarose gels, which consisted of 0.5g agarose in 50ml TBE buffer [10.8g Tris (hydroxymethyl) aminomethane, 5.5g Boric Acid and 0.93g EDTA (ethylene diamine tetra-acetic acid di-sodium) made up to one litre with distilled water]. Five to seven microlitres of ethidium bromide was added to the molten solution and then left for 15 minutes to set. Ten microlitres of PCR product were mixed with five microlitres of loading buffer (bromophenol blue and xylene cyanol in glycerol). Samples were loaded onto a gel and left to run in a gel rig to run for c. ten minutes at 150 volts. PCR products were visualised with a UV transilluminator.

A clean bright band was taken as a positive result. Smearing indicated an unsatisfactory (negative) result. In these cases PCR conditions were manipulated (changing the number of cycles, annealing temperature or amount of DNA template) to obtain satisfactory bands.

3.2.2.4. PCR product purification

PCR products were purified with Promega Magic PCR Preps^{TM}, QIAGEN© QIAquick^{TM} or Promega Wizard ® kits following the manufacturers instructions. The purified PCR product was finally eluted with 25µl nuclease free water. Two microlitres of eluted purified product was then checked on a 1% agarose gel (see above).

3.2.2.5. DNA Sequencing

Purified PCR product was sequenced using an ABI Prism BigDye Terminator v3.0 or v3.1 Ready Reaction Cycle Sequencing Kit (Applied Biosystems) according to manufacturers instructions with primers for the respective marker (see above). Sequencing reactions usually contained: 2µl sequence mix, 3µl sequence buffer, 0.5µl primer, 2.5µl purified DNA template and 12µl nuclease free water to make a total reaction volume of 20µl. The amounts of template and water were adjusted depending on the quality of the template with the final reaction volume remaining 20µl.

Sequencing reactions were conducted on a ThermoHybaid PCR Sprint Temperature Cycling System using the following conditions: 95˚C for 45 seconds, 50˚C for 45 seconds and 60˚C for three minutes repeated for 30-35 cycles. The annealing temperature was also manipulated (50-52˚C) in some instances to obtain optimal product.

Cycle sequencing products were then precipitated as follows: 20µl of sequence product was added to 50µl 100% ethanol, 2µl 125mM EDTA solution and 2µl 3M sodium acetate solution. The mixture was shaken and left to stand for at least 15 minutes before centrifuging at 10 000 rpm for 15 minutes. The liquid was discarded leaving the pellet undisturbed. One hundred and fifty microlitres of 70% ethanol was added and samples were centrifuged for a further ten minutes. The supernatent was discarded leaving the pellet undisturbed and left to air-dry, and resuspended in Hi-Dye formamide. Sequencing was done on a ABI 3100 Genetic Analyzer at Rhodes University's Sequencing Unit.

3.2.3. Sequence Editing and Alignment

Sequences (forward and reverse) were assembled, checked and edited using Sequencher^{TM} version 3.1.1 and version 4.2.2. (Gene Codes Corporation). Consensus sequences were exported from Sequencher into MacClade version 4.06 (Maddison and Maddison, 2000).

Phylogenetic analyses based on DNA sequences are dependent on sequence alignment, and it is therefore important that the evolutionary events, which cause length variation, are recognised and used during the alignment of length-variable sequences (Asmussen and Chase, 2001). Non-coding regions such as those used here are known to have a higher substitution rate than coding sequences and also accumulate insertions/deletions (indels) at a faster rate. Non-coding DNA experiences a high frequency of indel mutations of varying lengths making sequence alignment problematic (Small *et al*., 1998). Additional confounding factors are:

i. homology of short repeats or individual nucleotides runs via slipped-strand mispairing.
ii. homoplasy resulting from the reduction in character states caused by high AT content.
iii. the multiple origin of small inversions that are localised in the loop of the stem-loop secondary structures.
iv. bias nucleotide substitutions in AT rich regions.

All alignments were done manually using MacClade. Gaps corresponding to indels were positioned to minimise the number of nucleotide differences among sequences.

Sequences were not submitted to GenBank and will be submitted at a later date when data will be published in full. The full alignment of the *trnT-L* spacer, *trnL* intron and *ITS* sequences are provided in Appendix 4, 5 and 6 respectively.

3.2.4. Phylogenetic Analyses

Several analytical approaches were used in phylogenetic reconstruction viz. distance, parsimony and bayesian methods. Out-groups varied slightly for each data set as outlined below.

Coding of indels should be awarded on the merits of the indel, when it has been established (with some degree of confidence) that the indel is homologous (sequences identical in length and sequence; Nickrent *et al*., 2004). A conservative approach was taken and indels were not coded and scored. Single base pair substitutions/mutations and indels associated with mononucleotide runs and repeat regions were re-checked against the original sequence chromatograms for verification after alignment.

3.2.4.1. Neighbor Joining (NJ)

The neighbor joining method (Saitou and Nei, 1987) was used to construct distance trees. Coding regions, exons, introns and intergenic spacers do not have the same molecular evolutionary constraints and these regions need to be portioned in model based approaches. The most appropriate model of sequence evolution for a given partition was determined using the Akaike Information Criterion (AIC) as implemented in the program MODELTEST version 3.06 (Posada and Crandall, 1998). The chloroplast genome of *Zea mays* L. from GenBank (accession X86563) was used as a guide to determine limits of the *trnT-L* spacer and *trnL* intron to partition these markers prior to NJ and Bayesian Inference analyses (see below). The model was incorporated into reconstructions performed using PAUP* version 4.0b10 (Swofford, 2002) for NJ analyses. Uncombined and combined partitions were treated as a single unit and a single model was implemented. The same approach was applied to all the data sets viz.: the *trnT-L* spacer, the *trnL* intron, combined *trnT-L* spacer and *trnL* intron, a subset of *trnT-L* sequences that had matching sequences to the *trnL* intron, the *ITS* region, and combined *ITS* and *trnT-L* spacer sequences. A subset of *trnT-L* sequences that had complementary sequences to the *trnL* intron matrix was analysed to establish if the phylogenies recovered for the *trnL* intron was a result of sample selection and if the *trnT-L* spacer subset matrix reflected the same topology as the larger (entire) *trnT-L* spacer matrix.

Nodal support was evaluated by generating 1 000 neighbor joining bootstrap replicates. *Bulbine latifolia* (SR 61) was used as the out-group with the exception of the *trnL* intron analysis. Four additional *trnL* intron sequences of *Bulbine* and *Bulbinella* retrieved from GenBank were included [*Bulbine semibarbata* (AJ290259), *Bulbine succulenta* (AJ290260), *Bulbine weisei* (AJ290261) and *Bulbinella cauda-felis* (AJ290262)]. All *Bulbine* samples mentioned above and *Bulbine latifolia* (SR 61) were used as the out-group.

3.2.4.2. Maximum Parsimony (MP)

Maximum parsimony analysis was conducted using PAUP* 4.0b10 (Swofford, 2002) for all data sets. Uninformative characters were excluded and all nucleotide characters were equally weighted and unordered. Gaps were treated as missing data. A random input analysis was performed to determine if there were multiple islands of equally most parsimonious trees

(Maddison, 1991) with 1 000 replicates with one tree kept at each replicate. A full heuristic search was conducted on the trees found by this method with TBR branch swapping and MAXTREES set at 10 000. A strict consensus tree was constructed from all the most parsimonious trees. Bootstraps values were obtained from 1 000 heuristic bootstrap replicates with MAXTREES set at 100. *Bulbine latifolia* (SR 61) was used as the out-group.

The same approach was applied to all the data sets with the exception of the *trnL* intron analysis. Four additional *trnL* out-groups sequences were included and all *Bulbine* samples were used as the out-group.

3.2.4.3. Bayesian Inference (BI)

The chloroplast genome of *Zea mays* from GenBank (accession X86563) was used as a guide to determine limits of the *trnT-L* spacer and *trnL* intron to partition these markers. The *ITS* partitions were determined using the *ITS* sequence of *Bulbine weisii* (GenBank accession AF234350). The matrix was partitioned into three regions (*ITS1*, *5.8S* and *ITS2*). MrModel version 2.2. (Nylander, Uppsala University, Sweden) was used to obtain the best model for the data sets and these models were incorporated into the BI analyses.

Bayesian inference was performed using MrBayes version 3.1.1 (Huelsenbeck and Ronquist, 2001). The analysis was conducted with four Monte Carlo Markov Chains (three heated and one cold). Chains were run for 3 000 000 generations and sampled every 100th generation. An *a proiri* burn in was not specified. Upon completion of analysis, the output files were examined to determine when log likelihood values stablised and determine the burn in. These burn in generations were excluded when constructing the Bayesian Inference trees. Posterior probabilities (PP) were estimated by constructing a 50% majority rule consensus tree in PAUP* 4.0b10 (Swofford, 2002). BI trees were retrieved using TREEVIEW (Page, 1996).

Bulbine latifolia (SR 61) was used as the out-group. The same approach was applied to all the data sets with the exception of the *trnL* intron analysis. Four additional *trnL* out-groups sequences were included. All *Bulbine* samples were used as the out-groups.

3.2.4.5. Partition homogeneity (or ILD) test for combined data sets

In this study a subset of *trnT-L* spacer and *trnL* intron sequences were combined. Due to the differences in lineages recovered a partition homogeneity (or ILD) test (Farris *et al*., 1994) which tests congruence in the phylogenetic signal of the two separate partitions was implemented. The ILD test addresses whether two data sets are arbitrary subdivisions of what should be a single larger data set. Tree comparisons and the ILD tests are useful initial comparisons. The ILD test was implemented in PAUP* 4.0b10 (Swofford, 2002) with 1 000 replicates, maximum trees set at 1 000 and TBR branch swapping.

The *trnT-L* spacer and *ITS* sequences were also combined. The ILD test was implemented as described above. This proved to be computationally prohibitive and the test was implemented with 100 replicates and maximum trees set at 100.

In both the above cases visual examination of nodes that are not well supported (bootstrap values of <70%) are considered non-conflicting and warranted merger of data sets (Mason-Gamer and Kellogg, 1996).

3.2.4.5.2. Sequencing to assess intra-population cpDNA polymorphisms

The *trnT-L* spacer was sequenced to check for intra-population polymorphisms in two taxa representing two populations [*K. northiae* (SR 274) from Naudes Nek and *K. rooperi* (SR 237) from East London]. Multiple individuals of each assession were sampled. Five and four samples were sequenced for *K. northiae* and *K. rooperi* respectively.

3.3. Results

3.3.1. Sampling

DNA samples of 51 of the 71 *Kniphofia* species (72% species coverage) were obtained during the course of the study. A total of 50 species were sequenced for the *trnT-L* spacer and 51 species were sequenced for the *ITS* region. Four of the 48 southern Africa taxa were not included (i.e. 92% species coverage for southern Africa). Specimens of *K. evansii, K. tabularis, K. crassifolia* and *K. flammula* were not obtained.

Samples of seven of the 23 Malagasy, Tropical and East African species were obtained (30% species coverage). Only the Bale Mountains (Ethiopia) received sufficient sampling attention. Uncollected species were difficult to obtain because of limited budgets and time constraints. Limited attempts were made to use herbarium material for DNA extractions. Herbarium material often go brown and do not appear to retain usable DNA. Herbarium material was only requested from one foreign herbarium (ETH). DNA material for most Ethiopian taxa were collected while doing field work in Ethiopia and these were used instead of herbarium material for DNA studies.

3.3.2. Phylogenetic analysis of *trnT-L* spacer data (Fig. 3.3.-3.5.)

trnT-L sequences were obtained for 125 samples of *Kniphofia* representing 50 species (Table 3.3.). A single *Bulbine* and *Bulbinella* sequence were also generated for this marker.

As discussed in the materials and methods section, Taberlet's primer 'a' was problematic and an internal primer, 'Knip1' was used. The priming site for 'Knip1' is approximately 945 bp upstream from the priming site of primer 'b'. Following alignment it was found that the initial part of this matrix was rich in $(AT)_n$ and $(T)_n$ repeats, which proved difficult to align in certain regions. In order to avoid alignment related homology assessment problems associated with these repeats the first 317 bp were excluded from analyses i.e. most of the problematic regions in terms of alignment were omitted. Effectively this meant that the *trnT-*

L spacer matrix started 628 bp upstream from the priming site of ‘b’. Thus only the 3’ region of the *trnT-L* spacer was used (hereafter referred to the *trnT-L* spacer).

The final aligned matrix with *Bulbine* and *Bulbinella* included was 609 bp in length (Appendix 4). Eighty eight (14.4%) characters were variable and 31 (5.1%) were parsimony informative with the out-groups included. When the out-groups were excluded these values reduced to 39 (6.4%) variable and 20 (3.3%) parsimony informative characters (Table 3.5.). Additional data (RI, CI and tree lengths values) are given in Table 3.6.

The *trnT-L* spacer supports the recognisition of five lineages for the NJ, MP and BI analyses (Fig. 3.3-3.6). These lineages are hereafter termed Groups 1-5 and labelled as such in the figures. In a preliminary investigation using the *trnT-L* spacer (Ramdhani *et al*., 2006), three lineages were recovered. Two of these were characterised by insertions. With a more thorough sampling and a trimmed data set used here, one of these lineages (Group 5) is still characterised by a nine bp insertion (position 544-552). The other group (Group 4) was characterised by a six bp insertion (position 87-92) except for a single sample (SR 453, *K. angustifolia*) for which the insertion is not present.

Of the five clades, Group 1 is the smallest with two species (*K. splendida* and *K. coralligemma*) and is not retrieved in the NJ and MP analyses (Fig. 3.3. & 3.4.). However, in the BI analysis this group is poorly supported with a posterior probability (PP)= 0.78 (Fig. 3.5.).

Group 2 has 17 samples representing eight species (*K. typhoides*, *K. brachystachya*, *K. uvaria*, *K. praecox*, *K. rooperi*, *K. citrina*, *K. sarmentosa*, *K. baurii* and *K. grantii*). This group is not well supported by the NJ [BS (bootstrap)= 54%)] (Fig. 3.3.) and BI analyses (PP= 0.87) (Fig. 3.5.). It was better supported by the MP analysis (BS= 71%) (Fig. 3.4.).

Table 3.5. Nucleotide sequence characteristics of the *trnT-L* spacer and *trnL* intron.

Region	**No. of Base pairs (bp)**	**No. of Variable bp (%)**	**Parsimony informative bp (%)**	**No. of samples (no. of taxa)**
trnT-L spacer including out-groups	609	88 (14.4%)	31 (5.1%)	127 (*Kniphofia*-50, *Bulbinella*-1, *Bulbine*-1)
trnT-L spacer excluding out-groups		39 (6.4%)	20 (3.3%)	125 (50)
trnL intron including out-groups	571	72 (12.6%)	39 (6.8%)	33 (*Kniphofia*-27, *Bulbinella*-2, *Bulbine*-4)
trnL intron excluding out-groups		36 (6.3%)	25 (4.4%)	27 (24)
trnT-L spacer subset of *trnL* intron including out-groups	598	74 (12.4%)	27 (4.5%)	29 (*Kniphofia*-27, *Bulbinella*-1, *Bulbine*-1)
trnT-L spacer subset of *trnL* intron excluding out-groups		20 (3.3%)	16 (2.7%)	27 (24)
Combined *trnT-L* spacer and *trnL* intron including out-groups	1159 (598 + 561)	113 (9.8%) (74 + 59)	54 (4.7%) (27 + 27)	29 (*Kniphofia*-27, *Bulbinella*-1, *Bulbine*-1)
Combined *trnT-L* spacer and *trnL* intron excluding out-groups		56 (4.8%) (20 + 36)	41 (3.5%) (16 + 25)	27 (24)

Table 3.6. Summary statistics of data sets analysed using MP and the resulting tree statistics.

DNA marker	**No. of trees**	**CI**	**RI**	**Tree length**
trnT-L spacer	10 000	0.630	0.949	54
trnL intron	10 000	0.596	0.777	77
trnT-L subset of *trnL* intron	10 000	0.829	0.933	35
Combined *trnT-L* and *trnL* intron	228	0.626	0.803	99
ITS	36	0.947	0.880	100
Combined trnT-L *and* ITS	10 000	0.750	0.921	160

Group 3 has 17 samples representing seven species from Madagascar, Tropical and East Africa (*K. foliosa*, *K. isoetifolia*, *K. schimperi*, *K. thomsonii*, *K. splendida*, *K. insignis* and *K. ankaratrenesis*). The group is weakly supported by the NJ analysis (BS= 56%)(Fig. 3.3.) and MP analysis (BS= 63%) (Fig. 3.4.). However, for the BI analyses it is well supported with a PP= 1.00 (Fig. 3.5.).

Group 4 is the largest lineage with 70 samples representing 33 species. The species included: *K. albescens*, *K. baurii*, *K. drepanophylla*, *K. rooperi*, *K. linearifolia*, *K. coddiana*, *K. hirsuta*, *K. laxiflora*, *K. ichopensis*, *K. parviflora*, *K. littoralis*, *K. fibrosa*, *K. stricta*, *K. latifolia*, *K. buchananii*, *K. ensifolia*, *K. triangularis*, *K. leucocephala*, *K. bruceae*, *K. tysonii*, *K. galpinii*, *K. multiflora*, *K. porphyrantha*, *K. breviflora*, *K. thodei*, *K. angustifolia*, *K. ritualis*, *K. pauciflora*, *K. albomontana*, *K. gracilis*, *K. uvaria*, *K. rigidifolia* and *K. umbrina*. Group 4 is weakly supported by the NJ analysis (BS= 63%) (Fig. 3.3.) and MP analysis (BS= 62%)(Fig. 3.4.). The BI analysis supported this group with a PP= 0.95 (Fig. 3.5.).

Group 5 has 19 samples representing nine species (*K. acraea*, *K. northiae*, *K. linearifolia*, *K. triangularis*, *K. parviflora*, *K. fibrosa*, *K. uvaria*, *K. rooperi* and *K. caulescens*). Group 5 was well supported for the NJ (BS= 74%) (Fig. 3.3.) and BI (PP= 0.96) (Fig. 3.5.) analyses, but not for the MP analysis (BS= 51%) (Fig. 3.4.).

It is interesting to note that species with multiple samples in Group 2 (*K. uvaria*, *K. praecox* and *K. baurii*), Group 3 (*K. foliosa, K. isoetifolia, K. schimperi*, *K. thomsonii*), Group 4 (*K. baurii*, *K. drepanophylla*, *K. rooperi*, *K. linearifolia*, *K. laxiflora*, *K. ichopensis*, *K. buchananii*, *K. ensifolia*, *K. triangularis*, *K. tysonii*, *K. angustifolia*, *K. gracilis* and *K. uvaria*) and Group 5 (*K. northiae*, *K. linearifolia*, *K. triangularis*, *K. uvaria* and *K. caulescens*) do not cluster to form monophyletic species lineages. In addition eight species were placed in more than one group (*K. baurii, K. fibrosa*, *K. linearifolia, K. parviflora, K. rooperi*, *K. splendida*, *K. triangularis* and *K. uvaria*). The implications of this will be discussed in detail later.

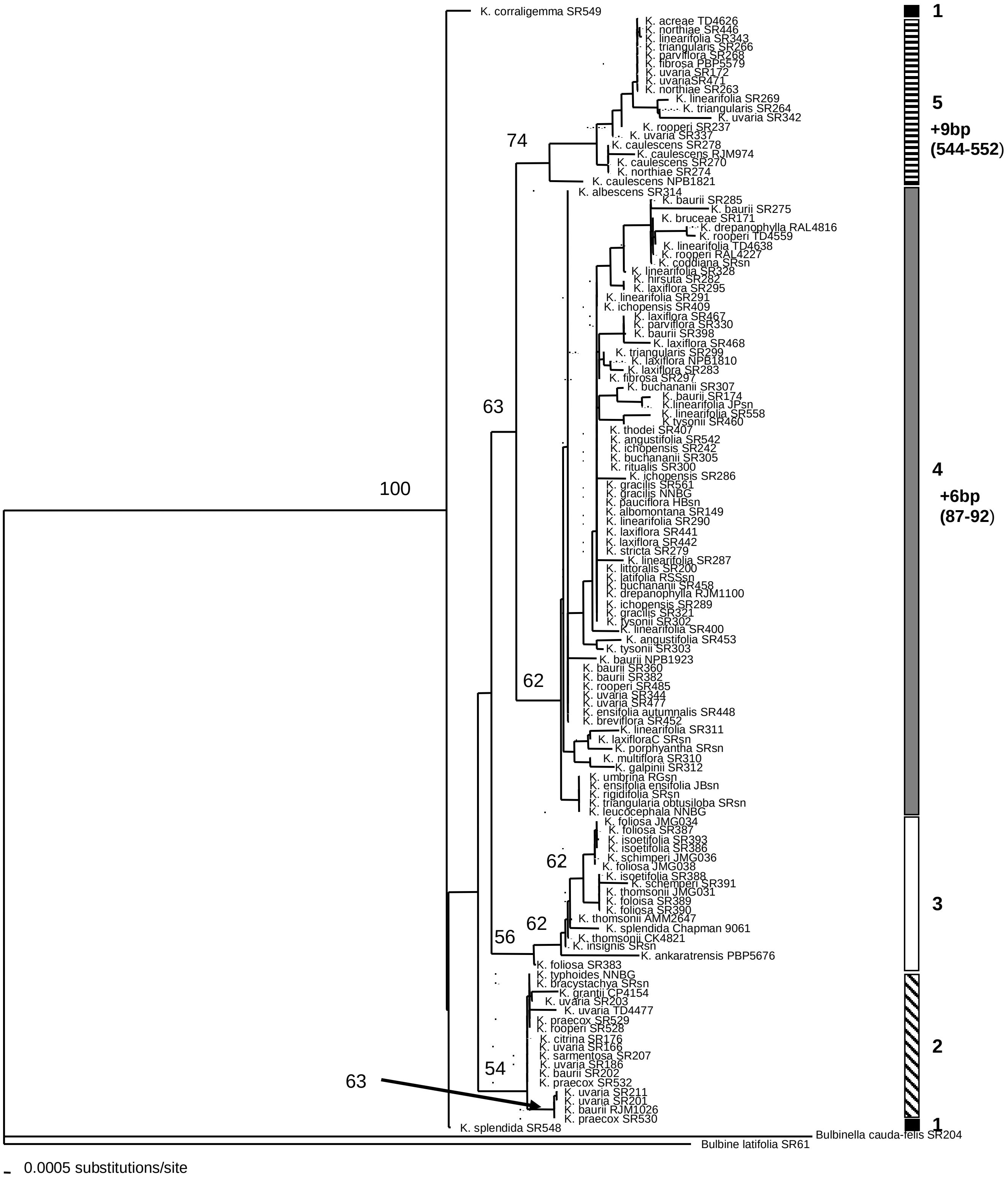


Fig. 3.3. Neighbor joining tree based on *trnT-L* spacer sequences, obtained using the K81uf + G model (determined by the Akaike Information Criterion). Major groups are denoted by bars to the right (discussed in text) and numbers below the group labels show position of insertions with bp size in parentheses. Bootstrap values (1 000 replicates) of >50% are indicated above the relevant nodes.

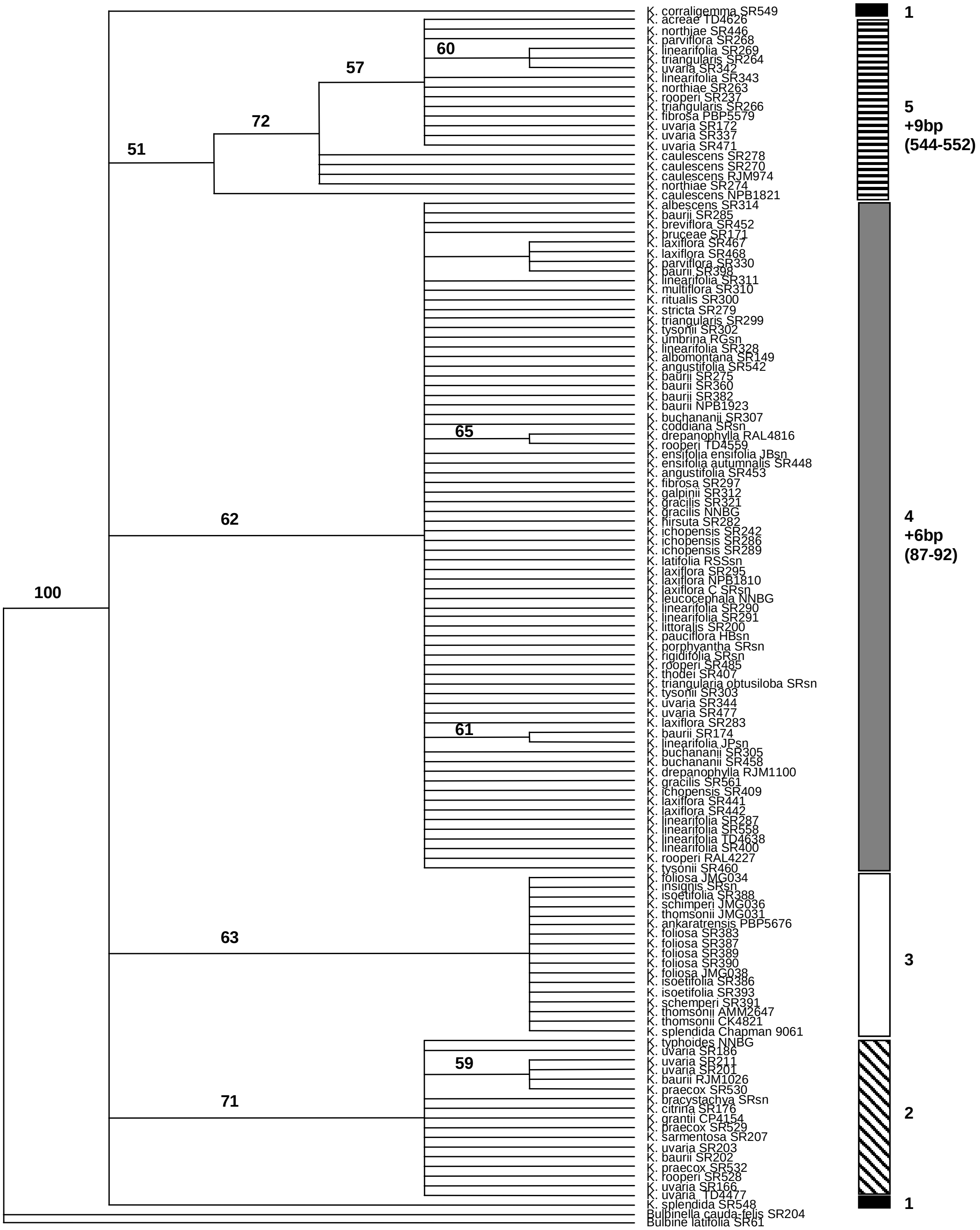


Fig. 3.4. Strict consensus tree of 10 000 most parsimonious trees based on *trnT-L* spacer sequences obtained from the maximum parsimony analysis. Length= 54; CI= 0.630; RI= 0.949. Major groups are denoted by bars to the right (discussed in text) and numbers below the group labels show position of insertions with bp size in parentheses. Bootstrap values (1 000 replicates) of >50% are indicated above the relevant nodes.

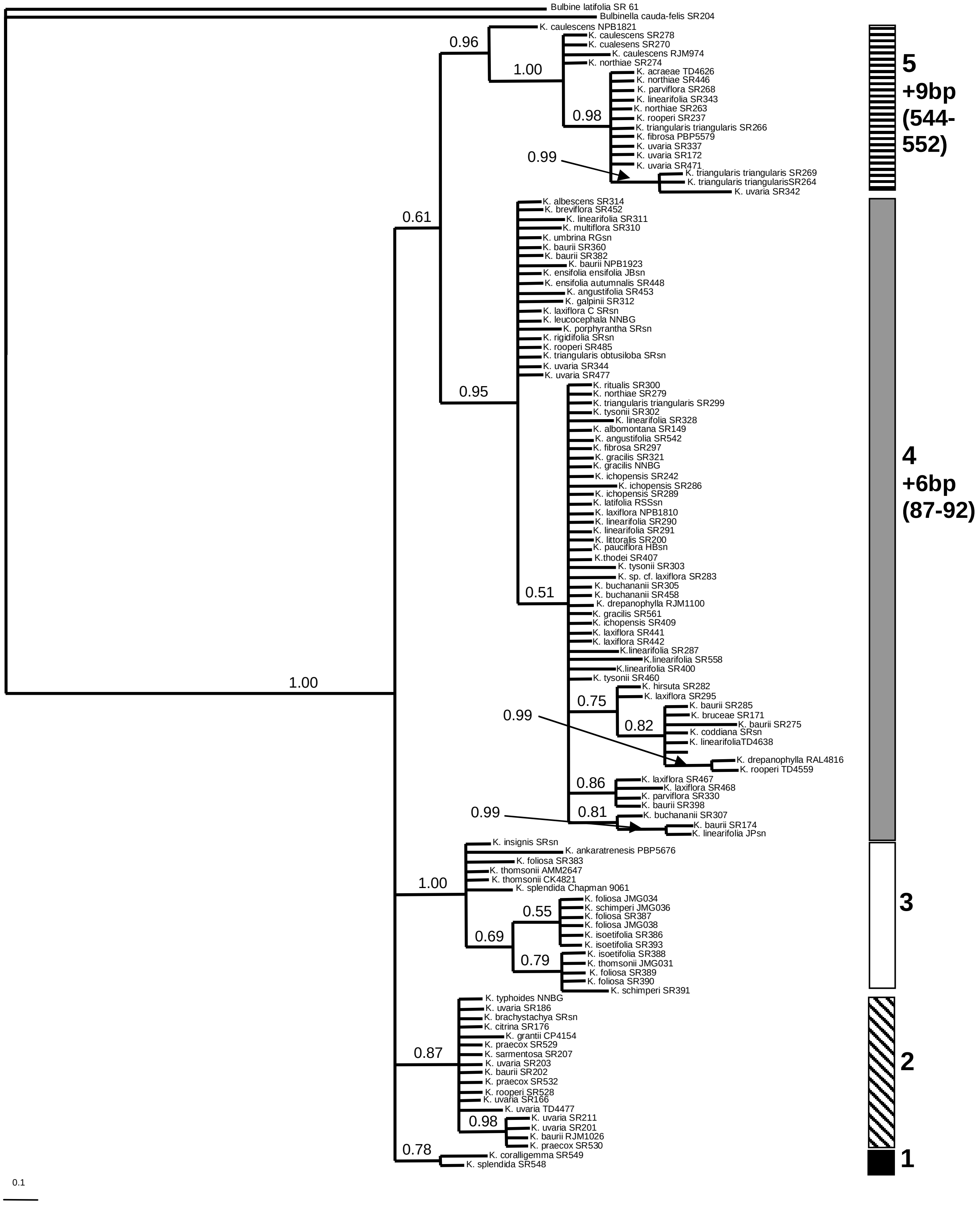


Fig. 3.5. Bayesian tree of the *trnT-L* spacer sequences estimated using the GTR + G model (determined by the Akaike Information Criterion). Major groups are denoted by bars to the right (discussed in text) and numbers below the group labels show position of insertions with bp size in parentheses. Numbers above the branches represent posterior probability values.

3.3.3. Phylogenetic analysis of *trnL* intron data (Fig. 3.6.-3.8.)

Sequences of the *trnL* intron were obtained for 27 samples of *Kniphofia* representing 24 species (Table 3.3.). A single *Bulbine* and *Bulbinella* sequence was also generated for this marker. A restrictive budget and time did not allow for all the *trnT-L* spacer samples to be sequenced for the *trnL* intron. Samples chosen had complementary sequences for the *trnT-L* spacer and were representative of the main lineages recovered by the *trnT-L* spacer. Four sequences of *Bulbine* and *Bulbinella* retrieved from GenBank provided additional out-groups.

The final aligned matrix with *Bulbine* and *Bulbinella* included was 571 bp in length (Appendix 5). Messy 3' ends were trimmed and the 5' *trnL* exon excluded. This region corresponds to positions 671 to 1 231 in the full alignment. Seventy-two (12.6%) characters were variable and 39 (6.8%) were parsimony informative with out-groups included. When the out-groups were excluded these values reduced to 36 (6.3%) variable and 25 (4.4%) parsimony informative characters (Table 3.5.). Additional data (RI, CI and tree lengths values) are given in Table 3.6.

The *trnL* intron had no indels that characterised lineages retrieved by the *trnT-L* spacer. A single sample had a unique 82 bp deletion (*K. ritualis*, SR 300). Large deletions are often problematic as they remove large amount of potentially informative sites (Asmussen and Chase, 2001). This sample was placed as sister to all the other *Kniphofia* samples in the NJ analysis (Fig. 3.6.). The deletion may account for this placement but in the MP and BI analyses this sample was nested in Group 4 (Fig. 3.7. & 3.8.).

The *trnL* intron data failed to recover the same groups of taxa that were found in the *trnT-L* spacer analyses. Group 1 had only a single sample (*K. coralligemma*) for the intron. Several attempts to sequence the intron for the other sample (*K. splendida*, SR 548) that was placed into Group 1 failed. Group 2 has three samples representing two species (*K. typhoides* and *K. uvaria*). Group 2 collapsed with one sample (*K. uvaria*, SR 211) not clustering with the two other samples in the NJ analysis (Fig. 3.6.). Group 2 also collapsed in the MP (Fig. 3.7.) and BI analyses (Fig. 3.8.), and was resolved as a polytomy with other groups.

Group 3 has five samples representing five species (*K. foliosa*, *K. thomsonii*, *K. insignis*, *K. schimperi* and *K. isoetifolia*). The group is well supported for both the NJ (BS= 74%) (Fig. 3.6.) and BI (PP= 1.00) (Fig. 3.8.) analyses, while the support for the MP analysis was weaker (BS= 69%) (Fig. 3.7.).

Group 4 had 13 samples representing 12 species (*K. albescens*, *K. baurii*, *K. stricta, K. bruceae, K. tysonii*, *K. breviflora*, *K. laxiflora*, *K. triangularis, K. parviflora*, *K. linearifolia*, *K. multiflora* and *K. ritualis*). This group forms a separate lineage with the exception of two samples [SR 300 (*K. ritualis*) and RG *sn* (*K. umbrina*)] in the NJ analysis (Fig. 3.6.), but with no support. In the MP analysis (Fig. 3.7.) Group 4 collapsed and was resolved as a polytomy with other groups. All samples that characterise this group clustered together in the BI analysis with weak support (PP= 0.53) (Fig. 3.8.).

Group 5 has four samples representing four species (*K. acraea*, *K. parviflora*, *K. northiae* and *K. caulescens*). This group collapsed in all the analytical approaches with no support (Fig. 3.6.-3.8).

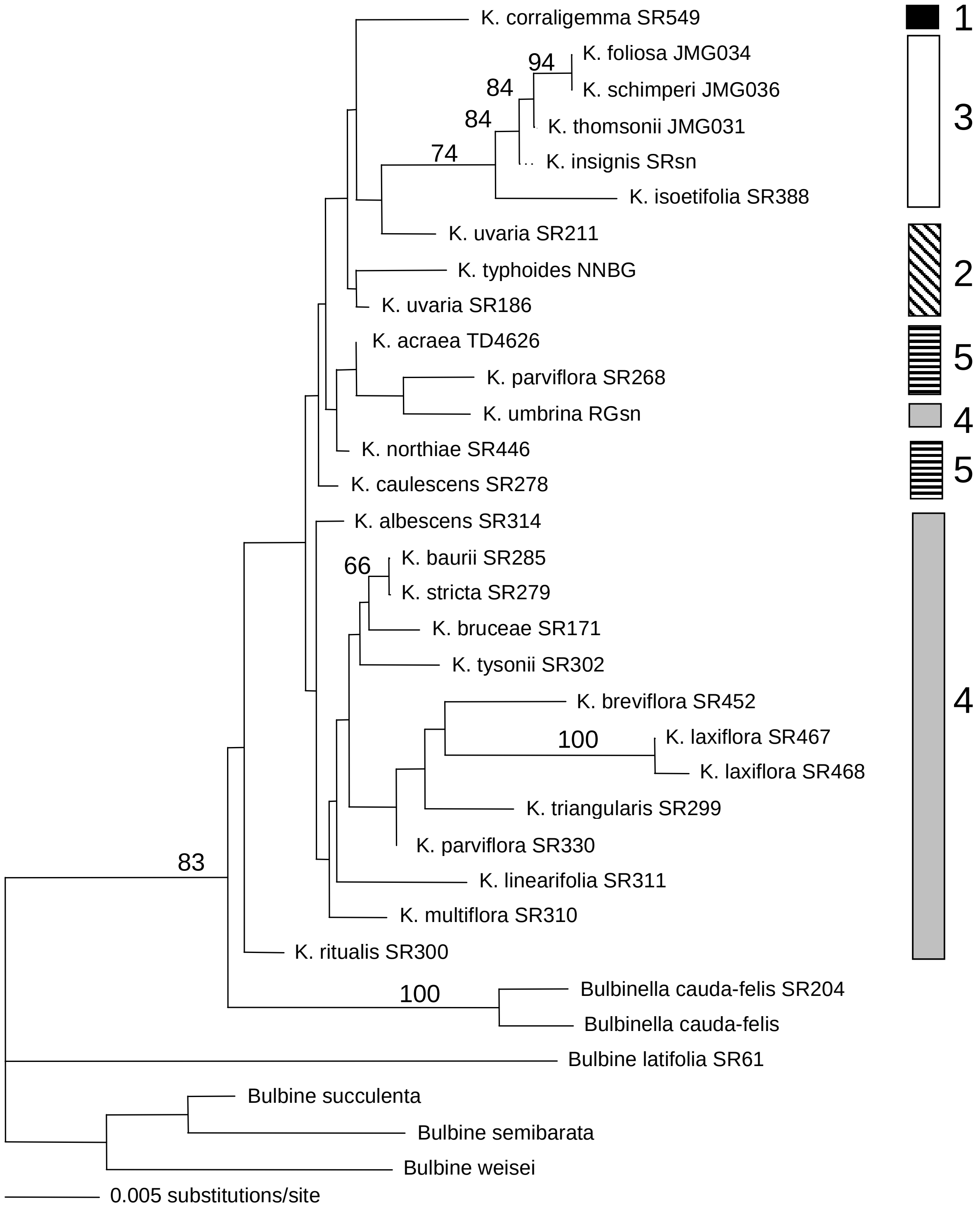


Fig. 3.6. Neighbor joining tree based on *trnL* intron sequences, obtained using the TVM + I + G model (determined by the Akaike Information Criterion). Major groups are denoted by bars to the right (discussed in text). Bootstrap values (1 000 replicates) of >50% are indicated above the relevant nodes.

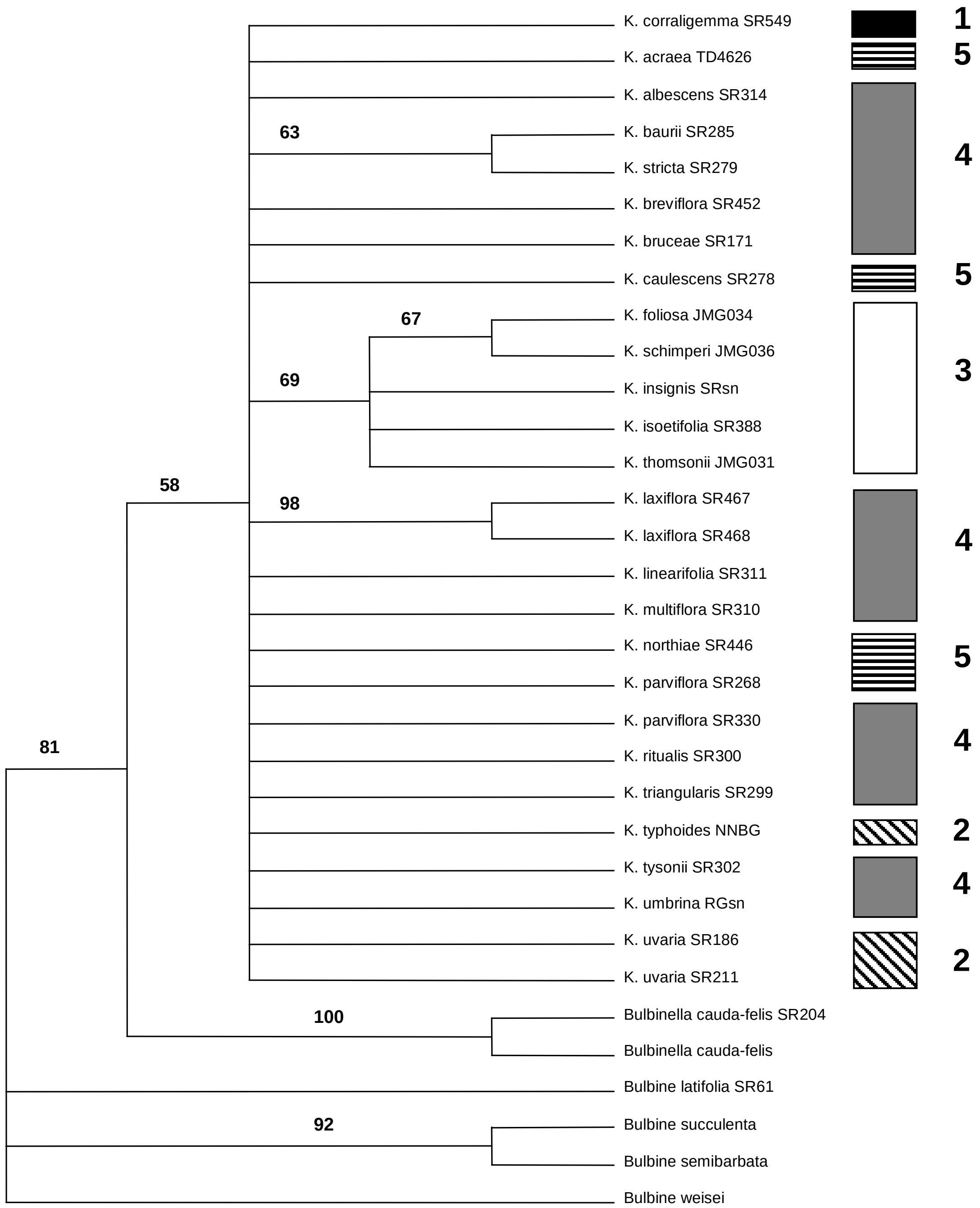


Fig. 3.7. Strict consensus tree of 10 000 most parsimonious trees based on *trnL* intron sequences obtained from the maximum parsimony analysis. Length= 77; CI= 0.597; RI= 0.777. Major groups are denoted by bars to the right (discussed in text). Bootstrap values (1 000 replicates) of >50% are indicated above the relevant nodes.

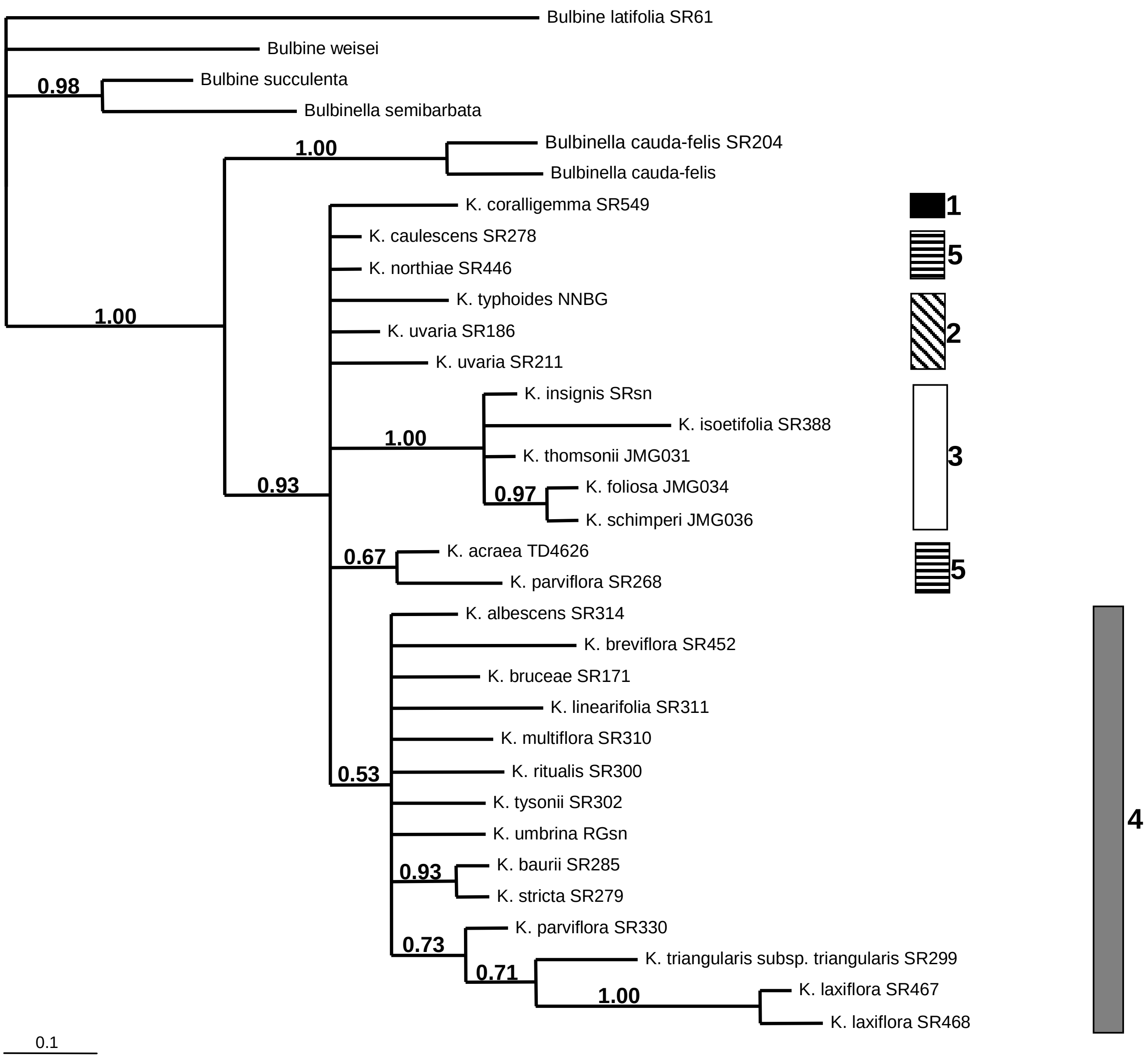


Fig. 3.8. Bayesian tree of the *trnL* intron sequences estimated using the GTR + I + G model (determined by the Akaike Information Criterion). Major groups are denoted by bars to the right (discussed in text). Numbers above the branches represent posterior probability values.

3.3.4. Phylogenetic analysis of *trnT-L* spacer subset of *trnL* intron data (Fig. 3.9.-3.11.)

A subset of only *trnT-L* sequences that matched sequences to the *trnL* intron matrix were analysed separately. This was done to establish if the phylogenies recovered for the *trnL* intron was a result of sample selection and if the *trnT-L* spacer subset matrix reflected the same topology as the larger (entire) *trnT-L* spacer matrix.

A total of 27 samples representing 24 species of *Kniphofia* were obtained. A single *Bulbine* and *Bulbinella* sequence was also generated. The final aligned matrix with *Bulbine* and *Bulbinella* included was 598 bp in length. Seventy-four (12.4%) characters were variable and 27 (4.5%) were parsimony informative. When the out-groups were excluded these values reduced to 20 (3.3%) variable and 16 (2.7%) parsimony informative characters (Table 3.5.). Additional data (RI, CI and tree lengths values) are given in Table 3.6.

The same five lineages found by the *trnT-L* spacer analyses (entire matrix) were also found. Group 4 and 5 are characterised by the same insertions found in the spacer (discussed above).

Group 1 has only a single sample (*K. coralligemma*) (Fig. 3.9.-3.11.). Group 2 were recovered as a single lineage, with good support in the NJ (BS= 73%) (Fig. 3.9.) and MP (BS= 75%) (Fig. 3.10.) analyses, while in the BI analysis this group also had fairly good support (PP= 0.94) (Fig. 3.11.). Group 3 had good support in the NJ (BS= 90%) (Fig. 3.9.), MP (BS= 89%) (Fig. 3.10.) and BI (PP= 1.00) (Fig. 3.11.) analyses. Group 4 was recovered as a single lineage with poor support in the NJ (BS= 66%) (Fig. 3.9.) and MP (BS= 63%) (Fig. 3.10.) analyses. However, in the BI analysis it was well supported (PP= 0.97) (Fig. 3.11.). Group 5 had good support for the NJ (BS= 96%) (Fig. 3.9.), MP (BS= 95%) (Fig. 3.10.) and BI (PP= 1.00) (Fig. 3.11.) analyses.

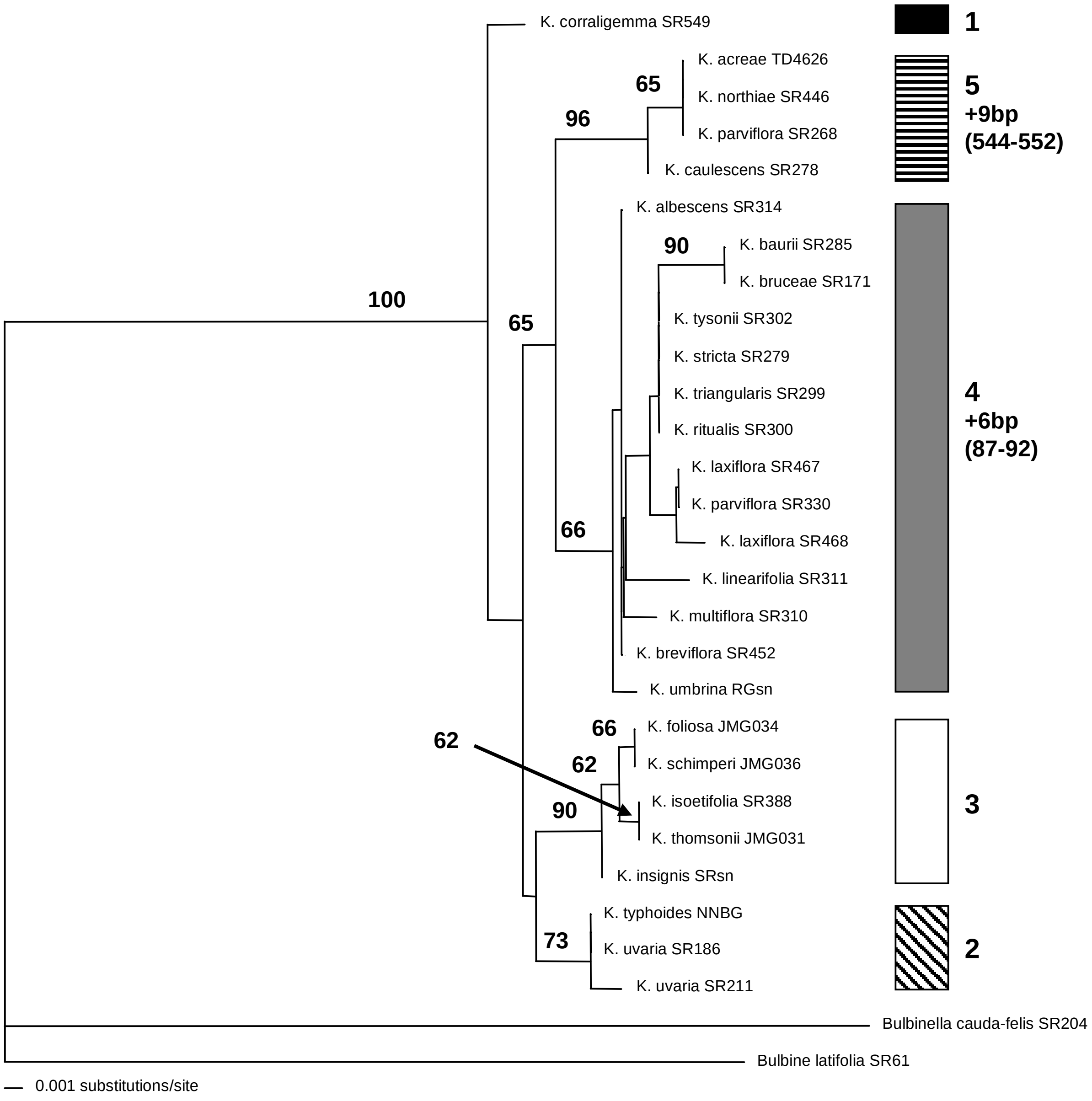


Fig. 3.9. Neighbor joining tree based on *trnT-L* spacer (subset of *trnL* intron) sequences, obtained using the K81uf + I model (determined by the Akaike Information Criterion) for the entire matrix. Major groups are denoted by bars to the right (discussed in text) and numbers below the group labels show position of insertions with bp size in parentheses. Bootstrap values (1 000 replicates) of >50% are indicated above the relevant nodes.

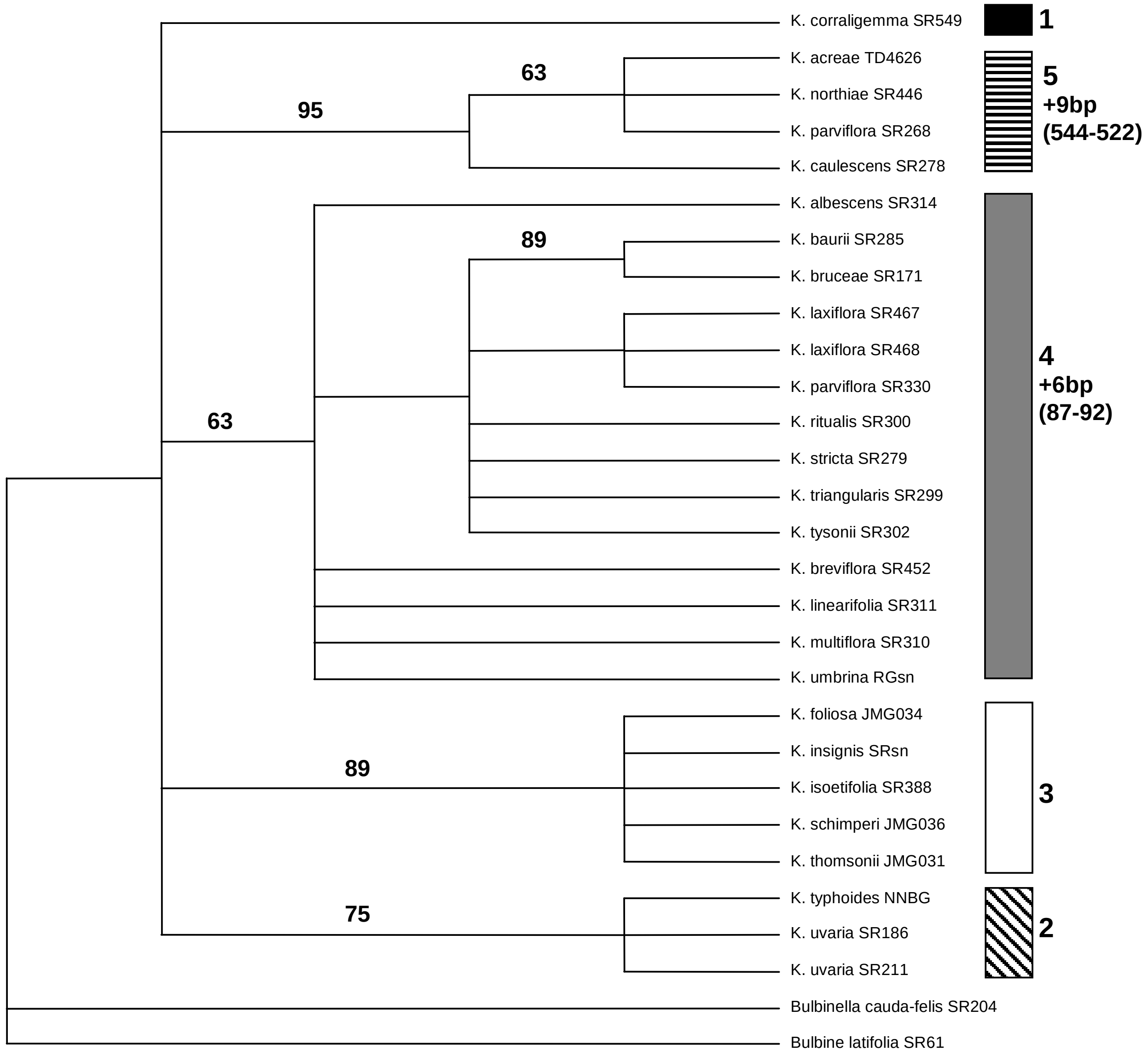


Fig. 3.10. Strict consensus tree of 10 000 most parsimonious trees based on on *trnT-L* spacer (subset of *trnL* intron) sequences obtained from the maximum parsimony analysis. Length= 35; CI= 0.892; RI= 0.933. Major groups are denoted by bars to the right (discussed in text) and numbers below the group labels show position of insertions with bp size in parentheses. Bootstrap values (1 000 replicates) of >50% are indicated above the relevant nodes.

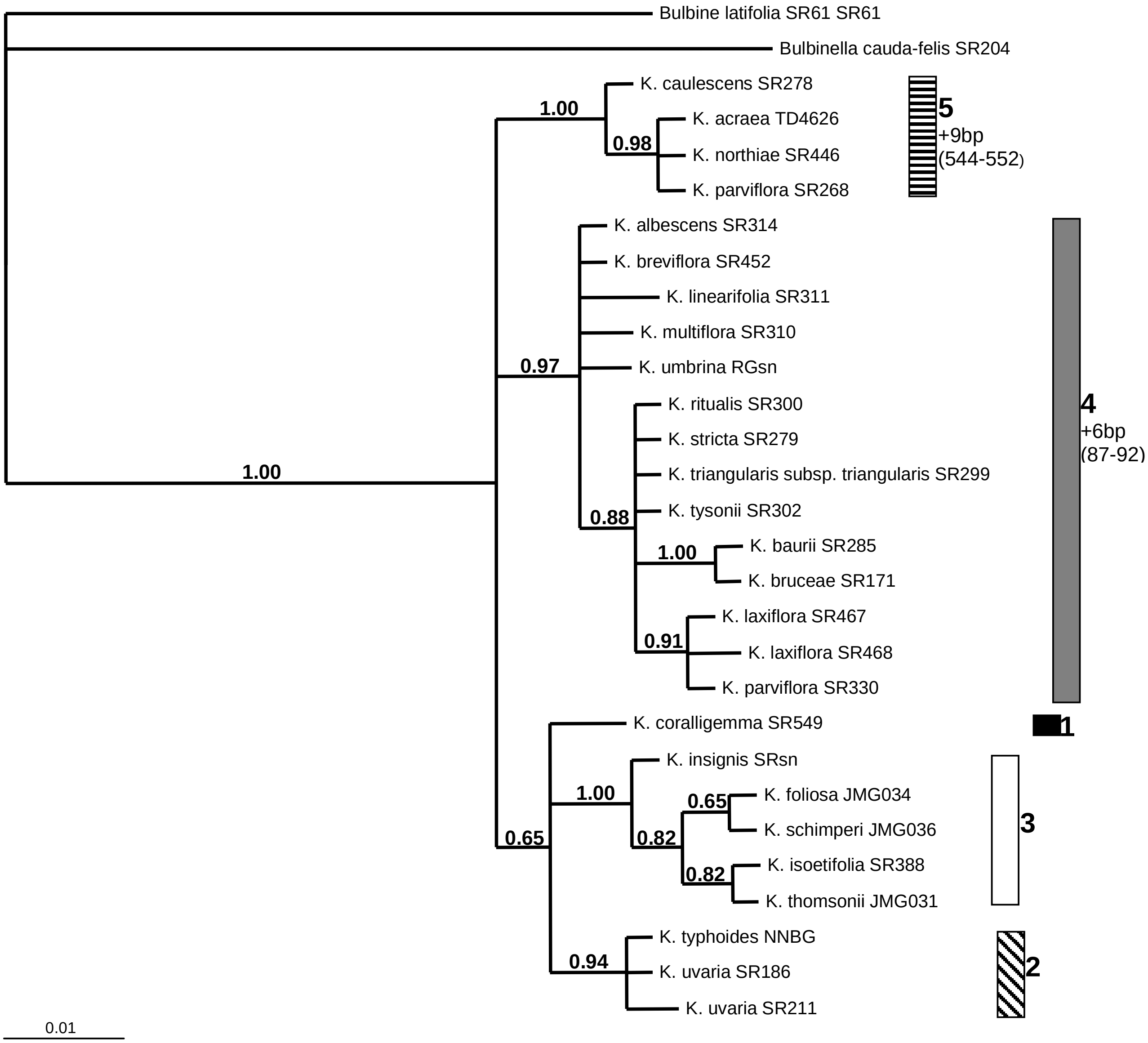


Fig. 3.11. Bayesian tree of the *trnT-L* spacer (subset of *trnL* intron) sequences estimated using the GTR + I model (determined by the Akaike Information Criterion). Major groups are denoted by bars to the right (discussed in text) and numbers below the group labels show position of insertions with bp size in parentheses. Numbers above the branches represent posterior probability values.

3.3.5. Phylogenetic analysis of combined *trnT-L* spacer and *trnL* intron data (Fig. 3.12.-3.14.)

Visual examination of the bootstrap values for the *trnL* intron NJ and MP phylogenies showed that none of the clades had bootstrap values >70%, with the exception of Group 3 in the NJ analysis (Fig. 3.6.). This group was not a source of conflict with the *trnT-L* spacer. The ILD test gave a value of 0.1650 with no significant incongruence in tree length between the data sets. Thus, the *trnL* intron and *trnT-L* spacer data sets were combined.

Combined sequences were obtained for 27 samples representing 24 species of *Kniphofia* (Table 3.3.). A single *Bulbine* and *Bulbinella* sequence was also generated. The final aligned matrix with *Bulbine* and *Bulbinella* included was 1 159 bp in length. One hundred and thirteen (9.8%) characters were variable and 54 (4.7%) were parsimony informative. When the out-groups were excluded these values reduced to 56 (4.8%) variable and 41 (3.5%) parsimony informative characters (Table 3.5.). Additional data (RI, CI and tree lengths values) are given in Table 3.6.

Group 5 and 4 are characterised by the same insertions found in the spacer (discussed above). The sample with the unique 82 bp deletion in the intron (*K. ritualis*, SR 300) did not affect the outcome of the analyses and was placed in Group 4. The analyses retrieved the same five lineages as the *trnT-L* data above, irrespective of the reconstruction approach.

Group 1 has only a single sample (*K. coralligemma*). Group 2 has no support in the NJ analysis (Fig. 3.12.) and weak support in the MP analysis (BS= 66%) (Fig. 3.13.), while in the BI analysis this group had good support (PP= 0.99) (Fig. 3.14.). Group 3 has good support in the NJ (BS= 97%) (Fig. 3.12.), MP (BS= 97%) (Fig. 3.13.) and BI (PP= 0.99) (Fig. 3.14.) analyses. Group 4 has poor support in the NJ analysis (BS= 67%) (Fig. 3.12.). However, in the MP analysis and BI analysis it was well supported with BS= 82% (Fig. 3.13.) and PP= 1.00 (Fig. 3.14.) respectively. Group 5 has good support for the NJ (BS= 86%) (Fig. 3.12.), MP (BS= 89%) (Fig. 3.13.) and BI (PP= 1.00) (Fig. 3.14.) analyses.

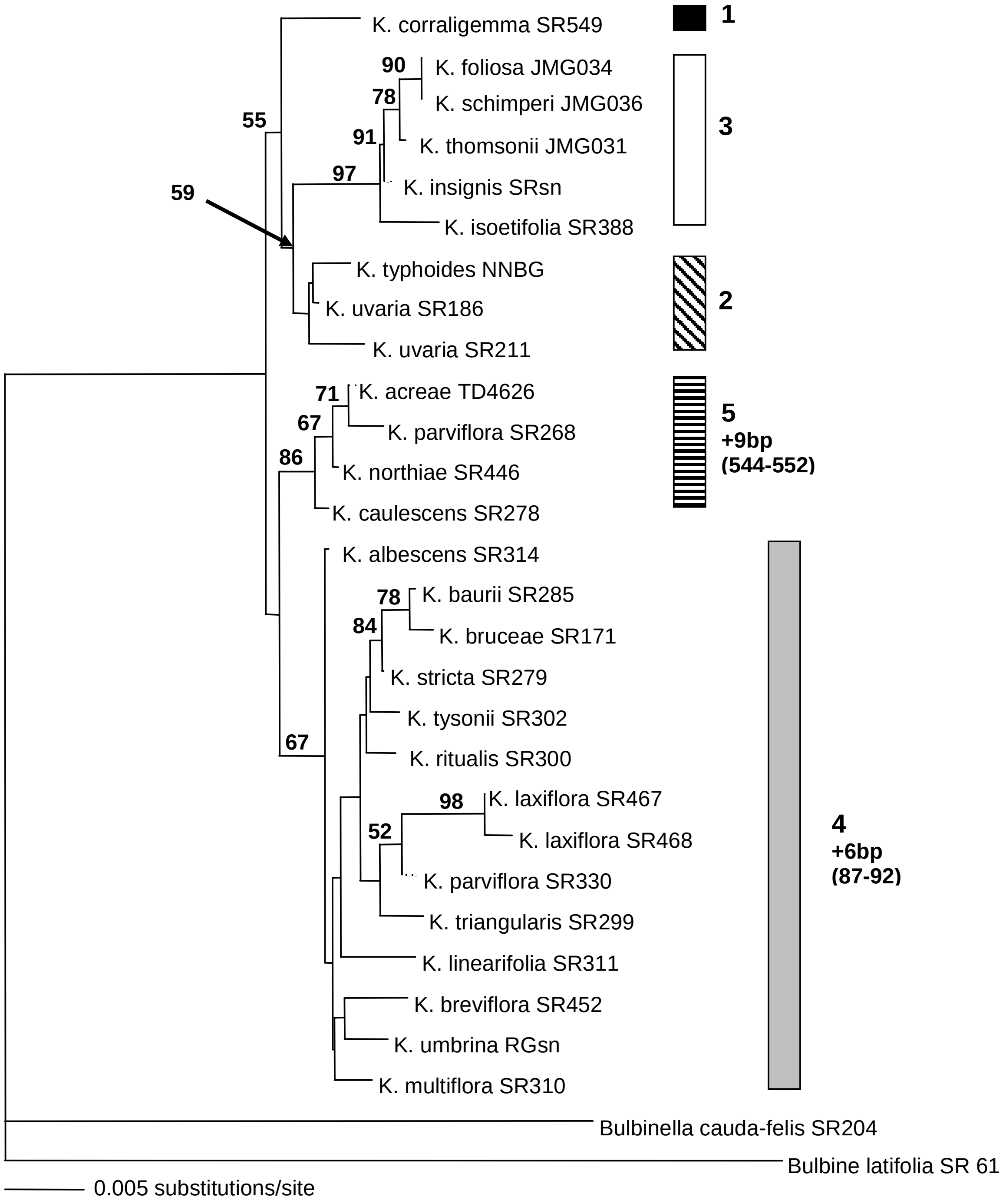


Fig. 3.12. Neighbor joining tree based on combined *trnT-L* spacer and *trnL* intron sequences, obtained using the GTR + I + G model (determined by the Akaike Information Criterion) for the entire matrix. Major groups are denoted by bars to the right (discussed in text) and numbers below the group labels show position of insertions with bp size in parentheses. Bootstrap values (1 000 replicates) of >50% are indicated above the relevant nodes.

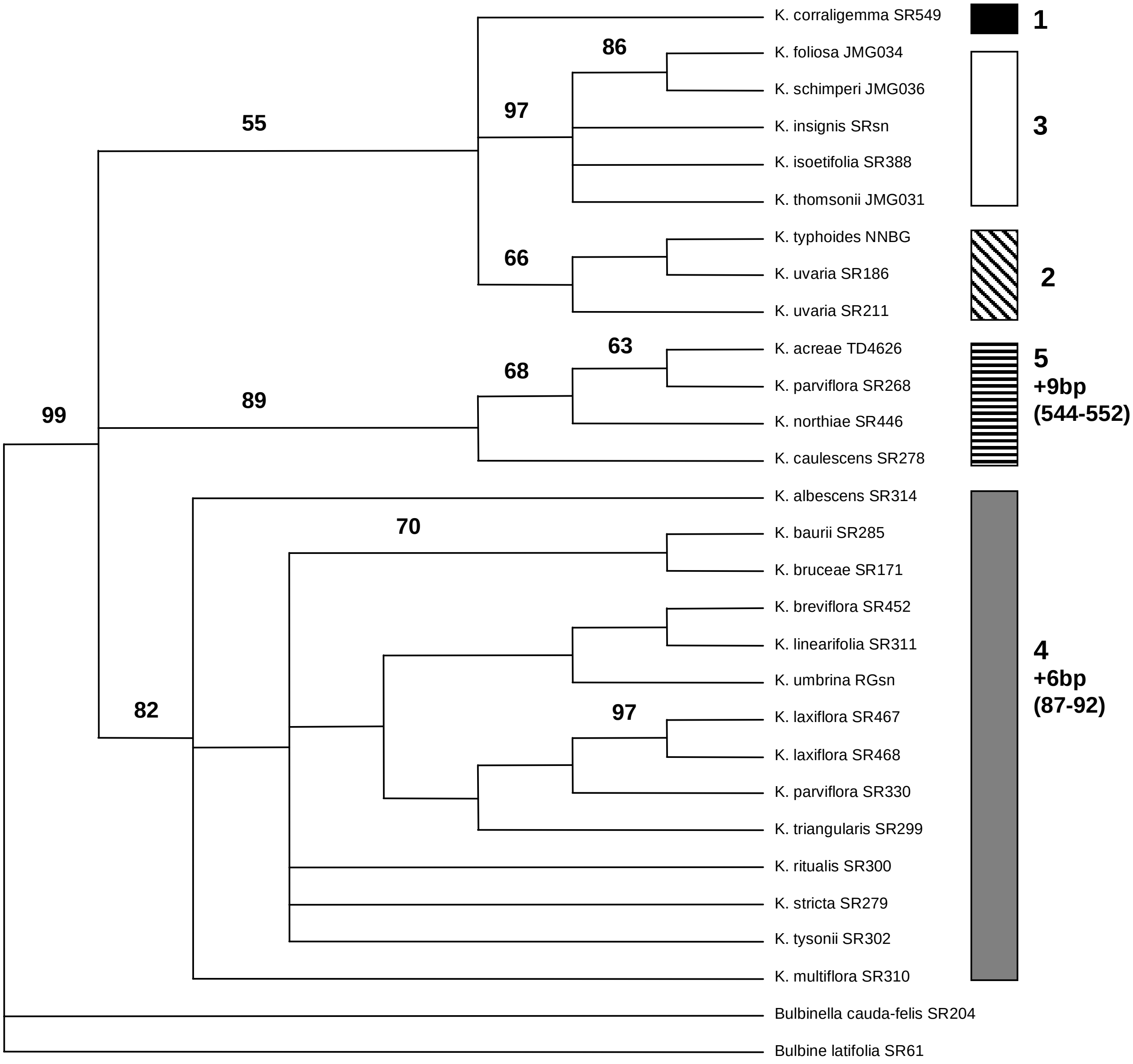


Fig. 3.13. Strict consensus tree of 228 most parsimonious trees based on combined *trnT-L* spacer and *trnL* intron sequences obtained from the maximum parsimony analysis. Length= 99; CI= 0.626; RI= 0.803. Major groups are denoted by bars to the right (discussed in text) and numbers below the group labels show position of insertions with bp size in parentheses. Bootstrap values (1 000 replicates) of >50% are indicated above the relevant nodes.

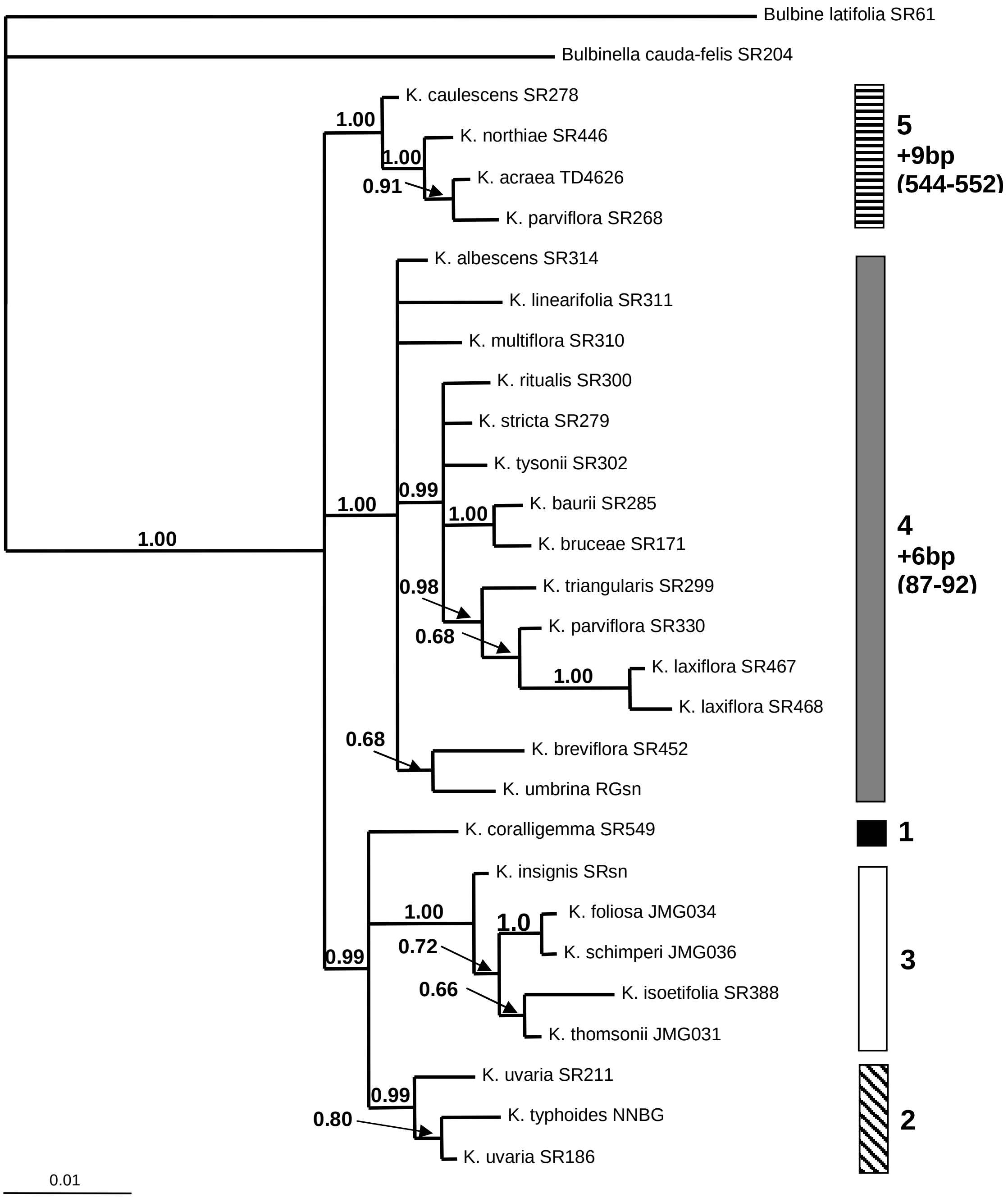


Fig. 3.14. Bayesian tree of the combined *trnT-L* spacer and *trnL* intron sequences estimated using the following models: GTR + G (*trnT-L* spacer) and GTR + I + G (*trnL* intron) (determined by the Akaike Information Criterion). Major groups are denoted by bars to the right (discussed in text) and numbers below the group labels show position of insertions with bp size in parentheses. Numbers above the branches represent posterior probability values.

3.3.6. Phylogenetic analysis of *ITS* data (Fig. 3.15.-3.17.)

The only nuclear marker screened for this study was the *ITS* region. Initial results showed little sequence divergence. Despite this, further investigations were done as this marker provided an independent and unlinked source of DNA sequence data and it was the only independent nuclear marker available that could be easily amplified and sequenced routinely.

ITS sequences were obtained for 99 samples representing 51 species of *Kniphofia* (Table 3.3.). A single *Bulbine* and *Bulbinella* sequence was also generated.

PCR products generated for the *ITS* region were resolved as single bands with no size difference. In addition no double peaks or ambiguous base calls were found in electrophenograms/trace files of *ITS* sequences, suggesting that there is no evidence of paralogues. No attempts at cloning were pursued as this is expensive and time consuming especially in studies with a large amount of samples or taxa.

The final aligned matrix with *Bulbine* and *Bulbinella* included was 830 bp (Appendix 6). Position 1-395 represents the *ITS1* spacer, positions 396-566 the *5.8S* gene and positions 567-830 the *ITS2* spacer. One hundred and seventy-six (21.1%) characters were variable and 72 (8.7%) were parsimony informative. When the out-groups were excluded these values reduced to 63 (7.6%) variable and 28 (3.4%) parsimony informative characters (Table 3.7.). Additional data (RI, CI and tree lengths values) are given in Table 3.6.

The *ITS* region had no indels that characterised lineages. The *ITS* data was of limited use as many sequences were identical. The analyses recovered a large polytomy of samples from Groups 1-5 with little structure and resolution (Fig. 3.15.- Fig. 3.17.). Most samples of Group 3 (representatives from Ethiopia), denoted as Clade A in the cladograms, formed a well supported lineage in the NJ (BS= 99%) (Fig. 3.15.), MP (BS= 100%) (Fig. 3.16.) and BI (PP= 0.99) (Fig. 3.17.) analyses.

Table 3.7. Nucleotide sequence characteristics of the *ITS* region, and the combined *trnT-L* spacer and *ITS* region.

Region	**No. of Base pairs (bp)**	**No. of Variable bp (%)**	**No. of Parsimony informative bp (%)**	**No. of samples (No. of taxa)**
ITS1 spacer	395	89 (10.7%)	41 (5.0%)	
5.8S gene	170	36 (4.3%)	14 (1.7%)	
ITS2 spacer	264	51 (6.1%)	17 (2.0%)	
ITS: Total including out-groups	**830**	**176 (21.1%)**	**72 (8.7%)**	**101** (*Kniphofia*- 51, *Bulbinella*- 1, *Bulbine*- 1)
ITS: Total excluding out-groups		**63 (7.6%)**	**28 (3.4%)**	**99 (51)**
Combined *trnT-L* spacer and *ITS* including out-groups	**1434** (604 + 830)	**260 (18.1%)** (84 + 176)	**101 (7.0%)** (29 + 72)	**96** (*Kniphofia*- 50, *Bulbinella*- 1, *Bulbine*- 1)
Combined *trnT-L* spacer and *ITS* excluding out-groups		**95 (6.6%)** (32 + 63)	**47 (3.2%)** (19 + 28)	**94 (50)**

Two *K. thomsonii* samples from Group 3, denoted as Clade B in cladograms, formed a well supported lineage the NJ (BS= 96%) (Fig. 3.15.), MP (BS= 95%) (Fig. 3.16.) and BI (PP= 0.98) (Fig. 3.17.) analyses. Samples of *K. caulescens* and *K. stricta* from Group 5, denoted as Clade C in cladograms, had good support in the NJ (BS= 88%) (Fig. 3.15.) and MP (BS= 96%) (Fig. 3.16.) analyses. In the BI analysis this lineage was recovered with some support (PP= 0.94) (Fig. 3.17.). Some samples (*K. galpinii*, *K. triangularis*, *K. fluviatalis*, *K. multiflora*, *K. umbrina*) from Group 4 (notably from Mpumalanga and Swaziland), denoted as Clade D in figures, formed a weakly supported lineage in the NJ (BS= 57%) (Fig. 3.15.), MP (BS= 62%) (Fig. 3.16.) and BI (PP= 0.73) (Fig. 3.17.) analyses.

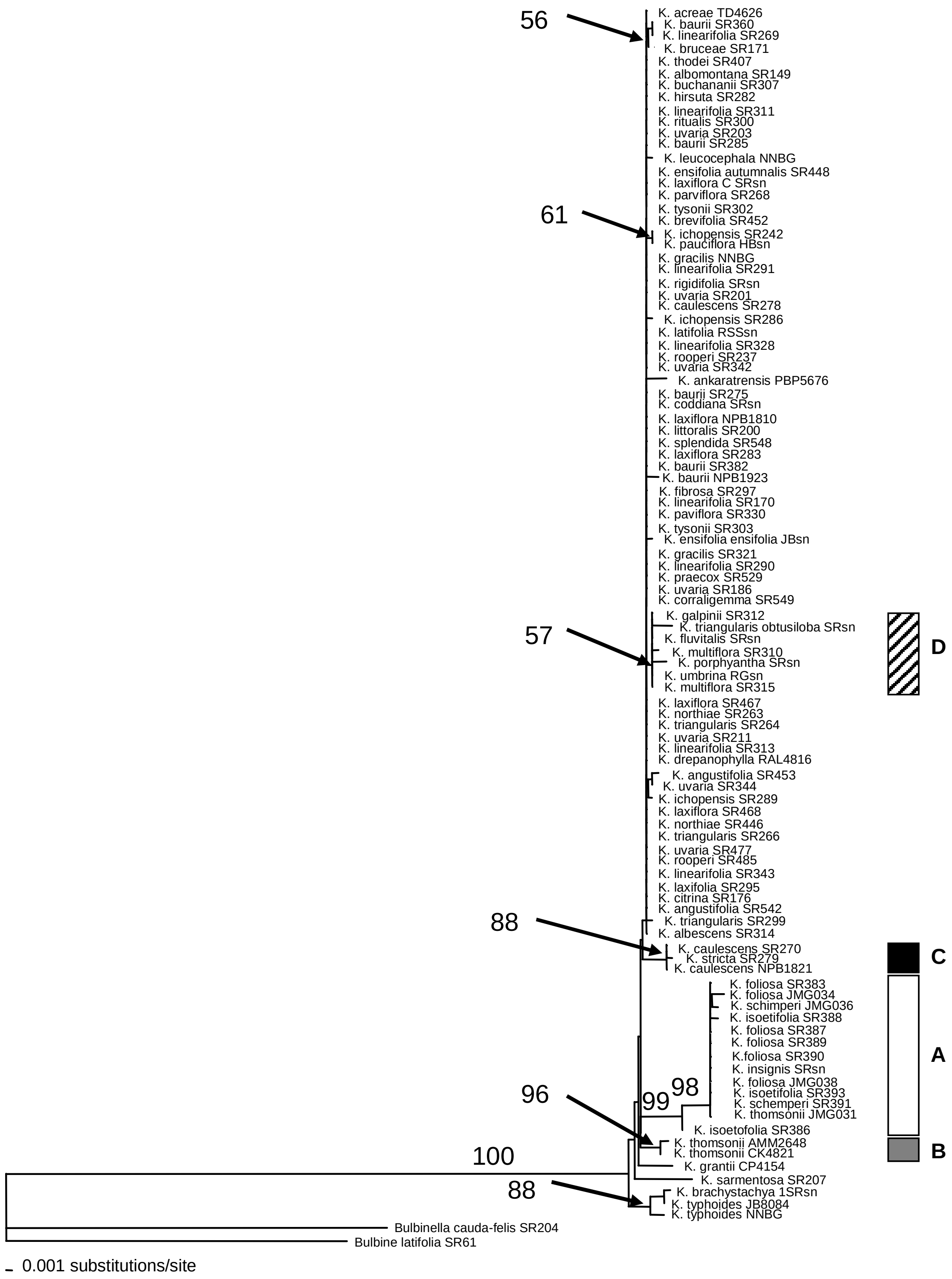


Fig. 3.15. Neighbor joining tree based on *ITS* sequences, obtained using GTR + G model for the entire matrix (determined by the Akaike Information Criterion). Groups denoted by bars to the right are discussed in the text. Bootstrap values (1 000 replicates) of >50% are indicated above the relevant nodes.

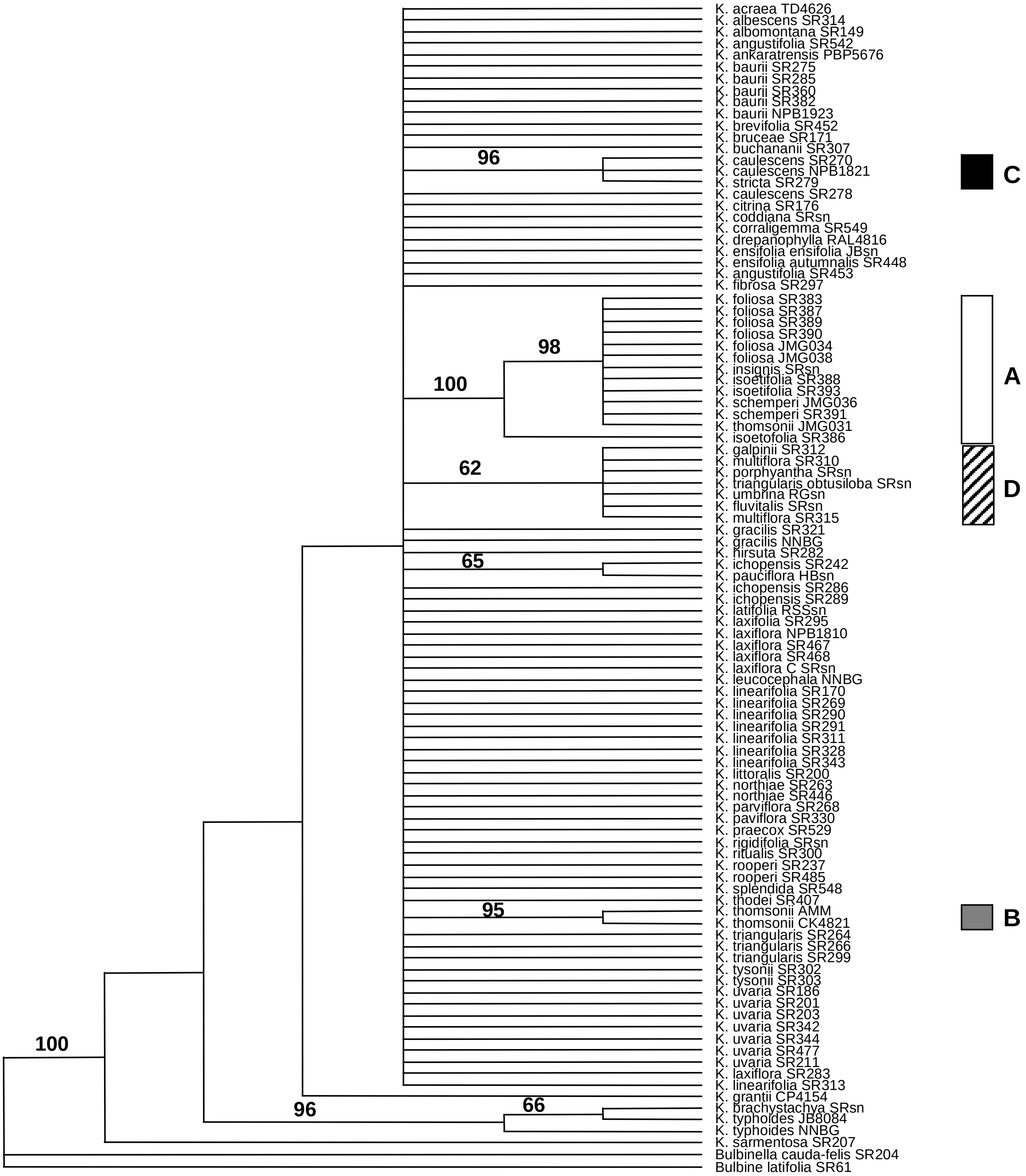


Fig. 3.16. Strict consensus tree of 36 most parsimonious trees based on *ITS* sequences obtained from the maximum parsimony analysis. Length= 100; CI= 0.880; RI= 0.947. Groups denoted by bars to the right are discussed in the text. Bootstrap values (1 000 replicates) of >50% are indicated above the relevant nodes.

Fig. 3.17. Bayesian tree for *ITS* sequences estimated using the following models: GTR + G (*ITS1*), HKY + I (*5.8S*) and GTR (*ITS2*) (determined by the Akaike Information Criterion). Groups denoted by bars to the right are discussed in the text. Numbers above the branches represent posterior probability values.

3.3.7. Phylogenetic analysis of combined *trnT-L* spacer and *ITS* data (Fig. 3.18.-3.20.)

Visual examination of the *ITS* phylogeny shows a large polytomy with no bootstrap values for the nodes defining the *trnT-L* groups. The ILD test for the combined *trnT-L* spacer and *ITS* gave a value of 0.100 indicating no significant incongruence in tree length between the data sets. Based on the above findings, the two markers were joined despite the limited potential of the *ITS* region to provide phylogenetic signal. Ninety-four combined sequences representing 50 species of *Kniphofia* were obtained (Table 3.3.). A single *Bulbine* and *Bulbinella* sequence were also included.

The final aligned matrix with *Bulbine* and *Bulbinella* included was 1 434 bp in length. Two hundred and sixty (18.1%) characters were variable and 101 (7.0%) were parsimony informative. When the out-groups were excluded these values reduced to 95 (6.6%) variable and 47 (3.2%) parsimony informative characters (Table 3.7.). Additional data (RI, CI and tree lengths values) are given in Table 3.6.

The large number of identical *ITS* sequences effectively meant that the *trnT-L* spacer signal dominated the low signal in the *ITS* data in the combined analyses and the resultant topology in most respects reflects the same lineages retrived by the *trnT-L* spacer alone, with exceptions noted below.

Group 1 is weakly supported in the NJ (BS= 66%) (Fig. 3.18.), MP (BS= 61%) (Fig. 3.19.) and BI (PP= 0.91) (Fig. 3.20.) analyses. Group 2 was not supported for the NJ (Fig. 3.18.) and MP (Fig. 3.19.) analyses as it forms a grade at the base of these topologies. However, the BI analysis recovered the group as a single lineage with PP= 0.62 (Fig. 3.20.). Group 3 was poorly supported in the NJ (BS= 60%) (Fig. 3.18.) and MP (BS= 59%) (Fig. 3.19.) analyses, while this group was well supported in the BI (PP= 0.98) (Fig. 3.20.) analysis. Group 4 was recovered as a single lineage but with no support in the NJ analysis (Fig. 3.18.). In the MP analysis (Fig. 3.19.), Group 4 formed a polytomy with some samples of *K. caulescens* from Group 5. Group 4 was recovered as a single lineage with fairly poor support in the BI analysis (PP= 0.74) (Fig. 3.20.). Group 5 was recovered as a single lineage but with no support in the NJ analysis (Fig. 3.18.), while this group was weakly supported in the BI (PP= 0.81) (Fig. 3.20.) analysis. As mentioned above, in the MP analysis (Fig. 3.19.) some samples of *K. caulescens* from Group 5 formed a polytomy with Group 4. The remaining samples representative of Group 5 formed a weakly supported lineage (BS= 53%).

All species with multiple samples in Group 2 (*K. uvaria*), Group 3 (*K. foliosa*, *K. isoetifolia*, *K. schimperi*, *K. thomsonii*), Group 4 (*K. baurii*, *K. linearifolia*, *K. triangularis, K. uvaria*, *K. angustifolia*, *K. ensifolia, K. gracilis, K. ichopensis, K. laxiflora* and *K. tysonii*) and Group 5 (*K. linearifolia*, *K. triangularis, K. northiae* and *K. caulescens*) failed to be resolved as monophyletic species lineages.

3.3.8. Sequencing of the *trnT-L* spacer to assess for intra-population cpDNA polymorphisms

Five samples from the population of *K. northiae* represented by SR 274 had identical sequences. This was also the case for *K. rooperi* (SR 237) with four samples sequenced. These two populations showed no evidence of intra-population cpDNA polymorphisms. The significance of these findings are dicussed later.

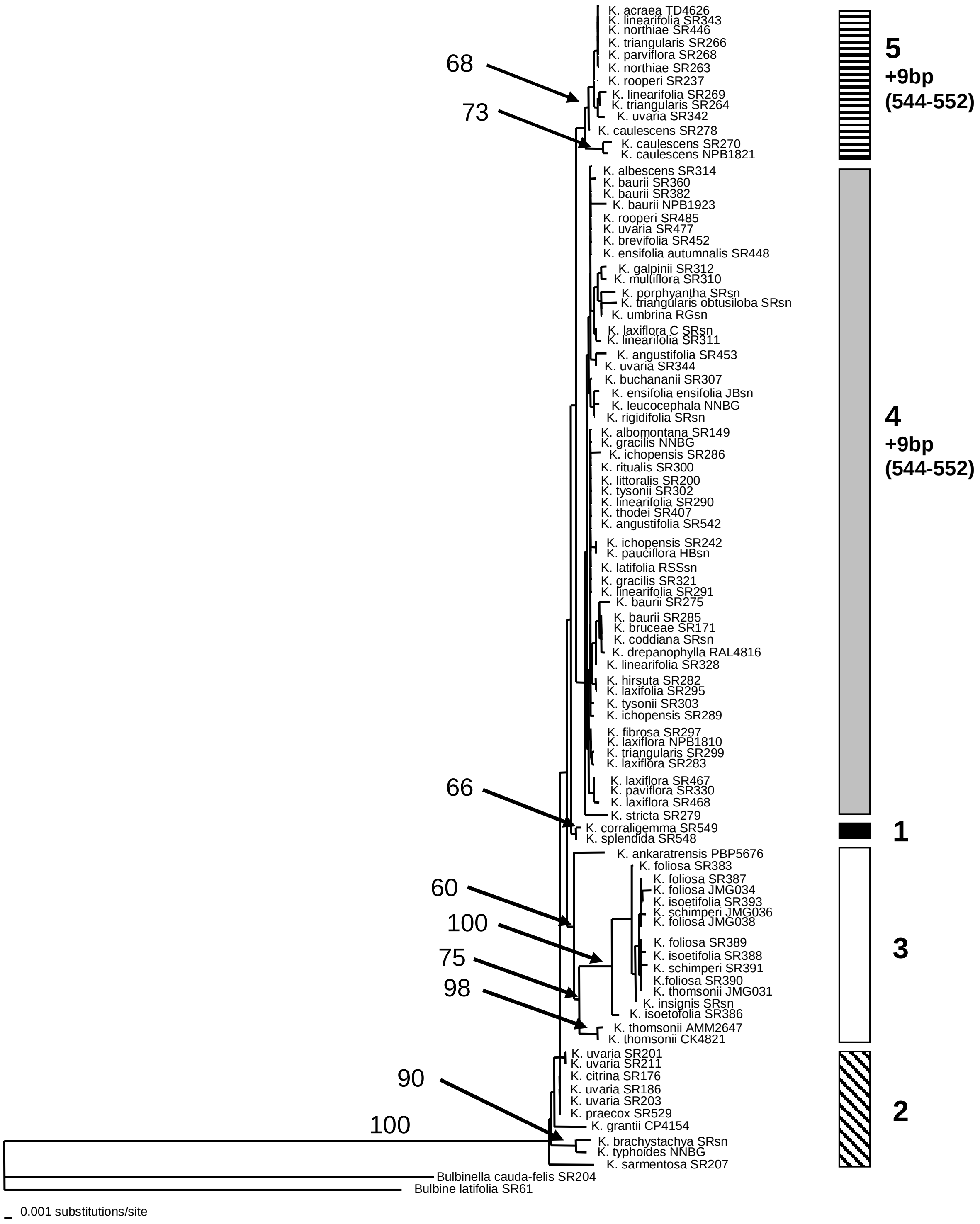


Fig. 3.18. Neighbor joining tree based on combined *trnT-L* spacer and *ITS* sequences, obtained using the TIM + I + G model for the entire matrix (determined by the Akaike Information Criterion). Major groups are denoted by bars to the right (discussed in text) and numbers below the group labels show position of insertions with bp size in parentheses. Bootstrap values (1 000 replicates) of >50% are indicated above the relevant nodes.

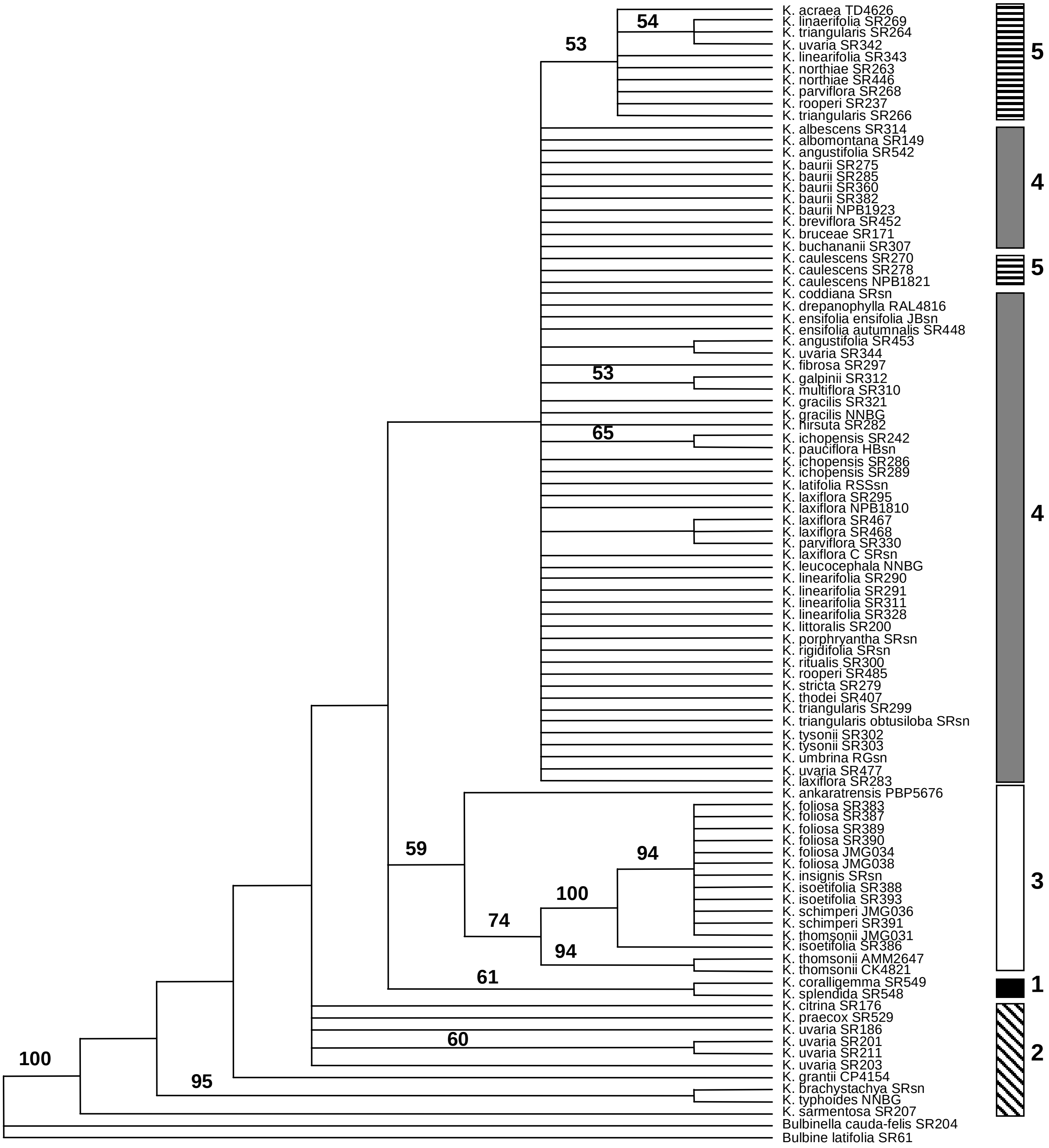


Fig. 3.19. Strict consensus tree of 10 000 most parsimonious trees based on of combined *trnT-L* spacer and *ITS* sequences obtained from the maximum parsimony analysis. Length= 160; CI= 0.750; RI= 0.921. Major groups are denoted by bars to the right (discussed in text). Bootstrap values (1 000 replicates) of >50% are indicated above the relevant nodes.

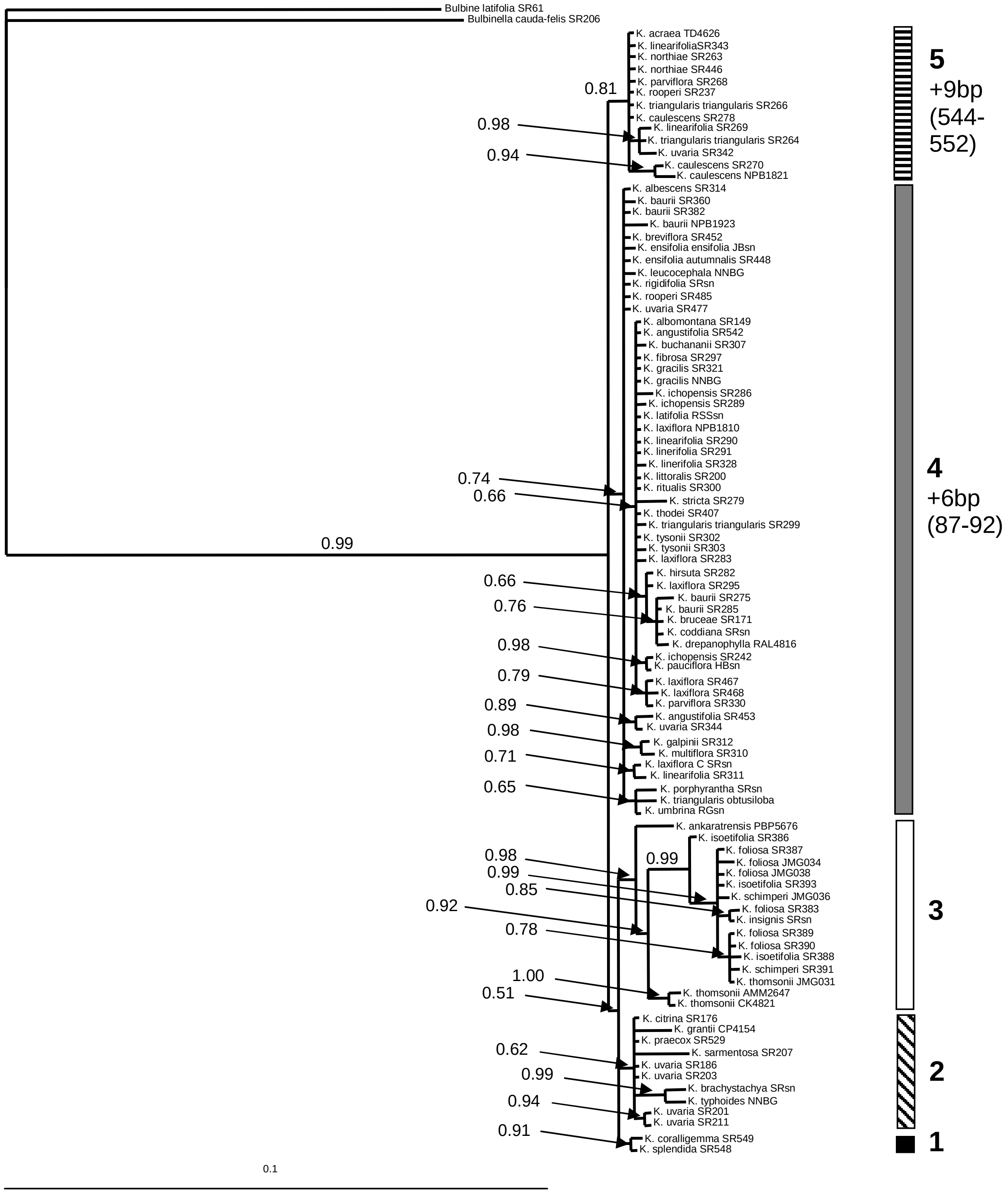


Fig. 3.20. Bayesian tree for the combined *trnT-L* spacer and *ITS* sequences estimated using the following models: GTR + G (*trnT-L* spacer), GTR + G (*ITS1*), HKY + I (*5.8S*) and GTR (*ITS2*) (determined by the Akaike Information Criterion). Major groups are denoted by bars to the right (discussed in text) and numbers below the group labels show position of insertions with bp size in parentheses. Numbers above and below the branches represent posterior probability values.

3.4. Discussion

3.4.1. Comparisons of chloroplast and nuclear markers

Of the regions used in this study, the *trnT-L* spacer was the most informative, providing more resolution than the other markers sequenced. As already stated, five lineages were recovered using the spacer. The *trnL* intron failed to recover the same topology as the *trnT-L* spacer with the exception of Group 3. A possible reason why the *trnL* intron did not recover a similar topology may be due to a lack of characters that define key nodes.

The *ITS* data were of limited use as many sequences were identical. The three analytical approaches failed to recover the same lineages as the *trnT-L* spacer and only parts of some groups were supported. Low sequence divergence of *ITS* has been reported in several studies especially in cases were a recent rapid radiation has been implicated (Baldwin and Sanderson, 1998; Harris *et al*., 2000; Richardson *et al*., 2001; Malcomber, 2002; Klak *et al*.; 2003b; Howarth and Baum, 2005). Other reasons for the lack of sequence divergence could be uni-directional homogenisation towards one type of sequence type via concerted evolution. Extensive gene flow via hybridisation (akin to a panmixis scenario) may also explain the predominance of only one sequence type. These aspects will be discussed in more detail later.

It is commonly assumed that combined analyses will reduce the differences between individual data sets thus providing a better approximation of organismal phylogeny (Borsch *et al*., 2005). Combining data sets is not always recommended as they may reflect different histories (Smith and Sytsma, 1990) and combining them results in the loss of this data. In some situations it is difficult to judge which data set performed better and a combined approach is favoured (Roalson *et al*., 2001). The combined chloroplast data sets (spacer and intron) generally recovered the same five lineages found by the *trnT-L* analyses, in all reconstruction approaches. In the combined *trnT-L* spacer and *ITS* data set Groups 1, 3, 4 and 5 were recovered with Group 2 not supported in the NJ and MP analyses. In the MP analysis, Group 4 formed a polytomy with some samples from Group 5 (viz. *K. caulescens*). However, in the BI analysis all five groups were recovered. This indicates that the *trnT-L* spacer data contributes most of the phylogenetic signal.

Due to the limited applicability of the *trnL* intron and the *ITS* region, the discussion below will be based primarily on the results of the *trnT-L* spacer (viz. the five groups recovered by this marker).

3.4.2. Non-monophyly of species

Despite a general lack of robust support, the most intriguing result in the phylogenetic reconstruction of *Kniphofia* is that all of the species with multiple samples were resolved as non-monophyletic. Some species had samples placed in more than one of the major lineages. In addition, several species with multiple samples, within a single major lineage failed to form monophyletic species clades (Table 3.8.). It should be emphasised that six species (*K. fibrosa, K. linearifolia, K. parviflora, K. rooperi, K. triangularis* and *K. uvaria*; Table 3.8.) are in different lineages characterised by major deletions (Groups and 5) i.e. their sequences are very different. In order to test the extent of species non-monophyly at the local scale one population of each of two species were examined for intra-population polymorphisms. Multiple samples of populations of *K. northiae* (represented by SR 274) and *K. rooperi* (represented by SR 237) revealed no polymorphisms within each population. The samples sizes (*K. northiae*: n= 5 and *K. rooperi*: n= 4) for this exercise were small. The possibility of intra-population polymorphisms cannot be excluded but these results suggest that populations are monomorphic.

What explanations are there for this unusual result (i.e. non-monophyly of species)? Three (not mutually exclusive) explanations are:

1. the alpha taxonomy is not correct and species are not adequately delimited.
2. the evolutionary history of the DNA regions used here are not reflecting the history of the morphological entities.
3. sequence divergence in chloroplast and nuclear markers are to too low to detect monophyly in morphological species.

Table 3.8. Species of *Kniphofia* with multiple samples which were placed in more than one major group delimited using the *trnT-L* spacer, also included are species with multiple samples, which are placed within a major single group but not clustering together to form monophyletic species clades.

Taxon	**Group/s**	**Samples**
1. *K. baurii*	**2** **4**	SR 202, RJM 1026 SR 174, SR 398, SR 275, SR 285, SR 360, 382, NPB 1923
2. *K. fibrosa*	**4** **5**	SR 297 PBP 5579
3. *K. linearifolia*	**5** **4**	SR 269, SR 343 SR 287, SR 290, SR 291, SR 558, JP *sn*, SR 400, SR328, TD 4638, SR 311
4. *K. parviflora*	**5** **4**	SR 268 SR 330
5. *K. rooperi*	**5** **4** **2**	SR 237 TD 4559, RAL 4227, SR 485 SR 528
6. *K. splendida*	**1** **3**	SR 548 Chapman 9061
7. *K. triangularis*	**5** **4**	SR 264, SR 266 SR 299, SR *sn K. triangularis* subsp. *obtusifolia*
8. *K. uvaria*	**2** **5** **4**	SR 166, SR 186, SR 201, SR 203, SR 211, TD 4477 SR 337, SR 342, SR 471, SR 172 SR 477, SR 344
9. *K. angustifolia*	**4**	SR 542, SR 453
10. *K. buchananii*	**4**	SR 305, SR 307, SR 458
11. *K. caulescens*	**5**	SR 270, SR 278, RJM 974, NPB 1821
12. *K. drepanophylla*	**4**	RAL 4816, RJM 1100
13. *K. ensifolia*	**4**	JB *sn*, SR 448
14. *K. foliosa*	**3**	JMG 034, SR 387, JMG 038, SR 398, SR 390, SR 383
15. *K. gracilis*	**4**	SR 321, SR 561, NNBG
16. *K. ichopensis*	**4**	SR 242, SR 289, SR 286, SR 407
17. *K. isoetofolia*	**3**	SR 388, SR 393, SR 386
18. *K. laxiflora*	**4**	SR *sn K. laxiflora* form C, SR 295, SR 441, SR 442, SR 468, SR 467, SR 283, NPB 1820
19. *K. northiae*	**5**	SR 274, SR 446, SR 263
20. *K. praecox*	**2**	SR 529, SR 530, SR 532
21. *K. schimperi*	**3**	JMG 036, SR 391
22. *K. thomsonii*	**3**	AMM 2647, JMG 031, CK 4821
23. *K. tysonii*	**4**	SR 302, SR 303, SR 460

As noted in the introduction of this study, the alpha taxonomy and species delimitations in this genus are difficult in many instances. Hybridisation has been invoked by taxonomists that have worked on the genus (Codd, 1968, 2005; Marais, 1973). However, in at least some instances non-monophyly is also found in readily identifiable species e.g. *K. northiae* and *K. parviflora* suggesting that possible mis-identification of species alone cannot be used to explain this result. Hybridisation and lineage sorting could be playing a role in the evolution of species in *Kniphofia*.

In some plant groups that have undergone recent radiation it may be difficult to generate sufficient phylogenetic signal due to low sequence divergence even for rapidly evolving regions (Small *et al.*, 1998). In many studies low sequence divergence and has been implicated in recent rapid radiations (Baldwin and Sanderson, 1998; Harris *et al.*, 2000; Malcomber, 2002; Klak *et al.*; 2003b; Richardson *et al.*, 2001; Warwick *et al.*, 2004; Howarth and Baum, 2005). This could result in non-monophyletic species (e.g. Harris *et al.*, 2000; Malcomber, 2002; Warwick *et al.*, 2004; Howarth and Baum, 2005). Additionallly, fixation and rapid concerted evolution following hybridisation may account for the predominance of a single *ITS* type (Álverez and Wendel, 2003). However, lack of sequence divergence is unlikely to exclusively explain the extensive non-monophyly in *Kniphofia* especially for the *trnT-L* cpDNA marker.

3.4.3. Hybridisation

Hybridisation is an important phenomenon in angiosperm evolution and speciation (Vriesendorp and Bakker, 2005; Church and Taylor, 2005; Okuyama *et al.*, 2005). Comparative molecular phylogenetics studies are showing that hybridisation is more prominent than previously thought. For example, Cronn *et al.* (2003) reported the role of hybridisation in the evolutionary history of *Gossypium gossypioides*. This study showed introgression in two stages in this species. Ainouche *et al.* (2003) studied hybridisation in *Spartina*, a genus with well documented cases of hybridisation involving small species groups.

Kniphofia is noted for hybridisation in horticulture, contributing to its horticultural appeal and numerous artificial hybrids are in cultivation (Taylor, 1985). Hybridisation (past and/or present) could be more extensive in wild populations and could account for the observed results as hybridisation can yield complex patterns of relationships and processes that are difficult to infer and explain.

The following species from southern Africa that were found to be non-monophyletic in this study have all been implicated in hybridisation events: *K. uvaria*, *K. rooperi*, *K. tysonii, K. linearifolia, K. praecox, K. baurii, K. drepanophylla, K. triangularis, K. fibrosa*, *K. angustifolia*, *K. buchananii, K. ensifolia, K. laxiflora*, *K. gracilis* and *K. ichopensis* (Codd, 1968, 2005). Taxonomic problems associated with these taxa were reviewed in detail earlier (Chapter 1). Two of the four Tropical African species (*K. schimperi* and *K. thomsonii*) that were found to be non-monophyletic in this study have also been implicated in hybridisation (Marais, 1973).

It is well documented that natural hybridisation leads to intermediate morphology, and this may explain the numerous cases of intermediate and integrading morphology, and species complexes with extensive variation reported by Codd (1968, 2005). A recent radiation suggests that not enough time has passed for currently delimited morphological species to differentiate fully and develop reproductive barriers, thus promoting hybridisation and mixing of haplotypes. Incomplete or weak reproductive barriers in taxa of complexes may promote hybridisation. Back-crossing could further complicate the issue. A highly reticulate evolution may explain why variation patterns in morphology become blurred (Mummenhoff *et al.*, 2004). Many problematic *Kniphofia* taxa appear to be either incipient species or populations *sensu* Lu (2001) that are in the process of diverging to the point of speciation but still have the potential to interbreed.

Hybridising species are often sympatric, share pollinators and/or flowering phenology (Chruch and Taylor, 2005). This description applies to many problematic species of *Kniphofia* from southern Africa, which are often wide-ranging species, display sympatry and flower contemporaneously. However, there is no robust support and conflict in the results to test hybridisation issues.

3.4.3.1. *ITS* and Hybridisation

Relying solely upon *ITS* to reveal phylogenetic patterns in complex genera is insufficient and is likely to be misleading in some respects of evolutionary history (Chase *et al*., 2003). Lack of phylogenetic signal has important consequences (Comes and Abbott, 2001). As found in *Kniphofia*, McKinnon *et al*. (2001) found *ITS* sequence data in *Eucalyptus* to be homogeneous, suggesting a low rate of sequence evolution, recent speciation and hybridisation between species resulting in homogenisation of sequences.

Gene flow can potentially disrupt the divergence of nuclear sequences (see Barker *et al*., 2005). Divergent rDNA copies may experience a variety of fates following merger in a single genome after reticulation. One possible outcome following hybridisation is that one paralogue becomes fixed within a genome as a consequence of concerted evolution (Álverez and Wendel, 2003). Rampant/extensive hybridisation (i.e. panmixis) could have promoted gene flow and rapid concerted evolution, and may account for the results i.e. the predominance of a single *ITS* type in *Kniphofia*.

Wang *et al.* (2000) showed that rDNA is homogenised uni-directionally after hybridisation and polyploidisation. The process of concerted evolution can be rapid and can occur in one generation after the combination of parental *ITS* types (Aguilar *et al*., 1999). Concerted evolution of *ITS* has also been reported to be rapid in the silversword alliance, which is of hybrid ancestry (Barrier *et al*., 1999).

Presently we have very little understanding on the features that may affect crossing over and gene conversion, but presumably the genomic location and number of arrays play an important role. Generation times and time since reticulation may also be important factors to consider (Álverez and Wendel, 2003).

As noted previously there was a lack of multiple peaks and ambiquous calls in the *ITS* electrophenograms/trace files, which would indicate the possibility of different paternal and maternal copies from hybridisation events. However, the lack of *ITS* variability makes this test difficult to apply in the case of *Kniphofia*, as hybridising individuals may contribute identical *ITS* sequences to the hybrid progeny.

3.4.4. Lineage sorting

The evolutionary history of cpDNA represents one particular ‘gene genealogy’ (matriarchal phylogeny) within an organismal pedigree. Stochastic matriarchal lineage sorting from a polymorphic ancestral gene pool can account for the discordance between species affiliations (conventional morphological taxon boundaries) and cpDNA genotype (Avise *et al.*, 1990). The persistence and sorting of ancestral polymorphisms may predate the divergence of the taxonomic lineages (Olsen and Schaal, 1999). It is biologically plausible that some individuals may be more closely related to a member of another species than to their conspecifics, solely due to patterns of maternal lineage survival and extinction accompanying the speciation process (Avise *et al.*, 1987). A consequence of lineage sorting is that species will not cluster on a phylogeny and appear non-monophyletic. Recent speciation could result in morphologically different species possessing undifferentiated cytotypes i.e. a species may have more than one cytotype (McKinnon *et al.*, 1999).

Thus reticulation and/or incomplete lineage sorting can explain the non-monophyly of *Kniphofia* species. Reticulation and incomplete lineage sorting may not be mutually exclusive and difficult to disentangle (Comes and Abbott, 2001; Goldman *et al.*, 2004; Church and Taylor, 2005).

Lineage sorting (instead of hybridisation) requires the maintenance of ancestral cpDNA polymorphisms through one or more speciation events (Comes and Abbott, 2001). Random sorting will have to occur with several losses of the polymorphic state. Determining the influence of lineage sorting requires the estimation of the age of species. This will show if haplotype divergence pre- or post dates speciation. If divergence predated speciation, then lineage sorting could account for haplotype sharing from a polymorphic ancestor. However, if speciation pre-dates haplotype divergence, interspecific hybridisation and introgression must be considered (McKinnon *et al*., 2001).

An indication of lineage sorting is the presence of polymorphisms within a population. Once this is established more detailed studies at the population level are required (e.g. Chiang *et al*., 2004). Multiple samples of populations of *K. northiae* and *K. rooperi* revealed no intra-population polymorphisms. These findings do not negate the possibility of incomplete lineage sorting and the results in this study may also be attributed to incomplete lineage sorting. However, it is impossible to determine whether haplotype divergence pre- or post-dated speciation. Determining age estimates in a phylogeny on a continental scale can be difficult (Plana *et al*., 2004). This is challenging when there is no fossil evidence or geological events cannot confidently be used to calibrate the phylogeny. Tree caliberation can be achieved by using sequence divergence rates from other groups with similar life histories, or closely related lineages. However, such results have to be considered as tentative. Different lineages may evolve at diffent rates depending on intrinsic and extrinsic factors. Caution must also be exercised in groups where hybridisation has been implicated. The age/s of speciations anatomises in the reticulations and only heterogenous assemblages can be dated, reflecting time of hybridisation rather than speciation. Moreover, this approach is not applicable when phylogenies are not robust with poorly supported nodes.

Lineage sorting and hybridisation are not mutually exclusive. The results obtained may be due to a combination of both phenomena. The extent of lineage sorting is usually determined by genetic heterogeneity within populations and migratory modes, which is associated with gene flow and natural hybridisation as well the geological time that the species have evolved through (Chiang *et al*., 2004). With the existing information it is impossible to distinguish the relative impact of hybridisation versus lineage sorting in *Kniphofia*.

Thus, the results of this study may reflect the combinational effects of a recent radiation, hybridisation, concerted evolution and/or incomplete lineage sorting.

3.4.5. Molecular phylogenies versus existing classification

Berger (1908) upheld *Notosceptrum* and divided *Kniphofia* into 14 formal sections. Codd (1968) grouped taxa into ten informal sections and did not support *Notosceptrum*. Marais (1973) and Codd (2005) did not apply any infra-generic groupings. Species included in this study are from all of Codd's (1968) informal sections. None of the sections delimited by Codd (1968) correspond to the lineages recovered from the nuclear and chloroplast markers for southern African material.

K. typhoides, *K. umbrina* and *K. brachystachya* of the segregate genus *Notosceptrum* where included in this study and results obtained here do not support the monophyly of this genus. *K. typhoides* and *K. brachystachya* are nested in Group 2, while *K. umbrina* is nested in Group 4. These results support Codd's (1967) inclusion of *Notosceptrum* in *Kniphofia*.

3.4.6. Geographical interpretation of phylogeny

If there has been gene flow and/or lineage sorting then conspecific individuals may be scattered in different lineages, but geographically localised genotypes should be shared between the different species (Whittemore and Schaal, 1991). Mapping samples of the five groups (Fig. 3.21.A.) revealed several geographic patterns. Composition of the five groups showed some congruence with geographic origin rather than the systematic arrangement based on morphology. Additionally these groups show some correspondence to the centres of diversity recovered by the numerical analysis (Chapter 2) that appears to suggest a historic link between the DNA signature and distribution patterns.

Group 1 contained samples from the Northern Province. Geographically most of the samples from Group 2 are from the Cape Region with outliers in KwaZulu-Natal (*K. typhoides*, *K. brachystachya*) and Malawi (*K. grantii*). A northern South Africa and Cape area of diversity were also recovered in the numerical analysis (Chapter 2). Group 3 is represented by material from Tropical and East Africa [with the exception of *K grantii* (Group 2) from Malawi], and

Madagascar. Species from Ethiopia (*K. foliosa*, *K. isoetifolia*, *K. schimperi*, *K. thomsonii* and *K. insignis*), Kenya (*K. thomsonii*), Tanzania (*K. thomsonii*), Malawi (*K. splendida*) and Madagascar (*K. ankaratrenesis*) are in this group. Group 4 includes samples predominantly from KwaZulu-Natal and the Eastern Cape, with some samples from Mpumalanga and Swaziland. Group 5 is represented by samples mostly from the Eastern Cape and KwaZulu-Natal. Groups 4 and 5 appears to reflect the distribution of the Cluster B (numerical analysis, Chapter 2), an area of diversity that covers much of northern, eastern and partly central SA. However, the boundaries of the three areas of diversity (from South Africa) mentioned above are not exactly the same as the distribution of the cpDNA groups because the distributional data has much wider geographical coverage.

Figure 3.21.B. shows a more detailed map of samples of the different groups from southern Africa. The above results viz. non-monophyly of species, the correlation of the five clades to geographic regions and the correlation of some of the clades to areas of diversity suggest that the results and data should be analysed from a phylogeographic perpective, rather than a phylogenetic one. These aspects are explored in the next chapter.

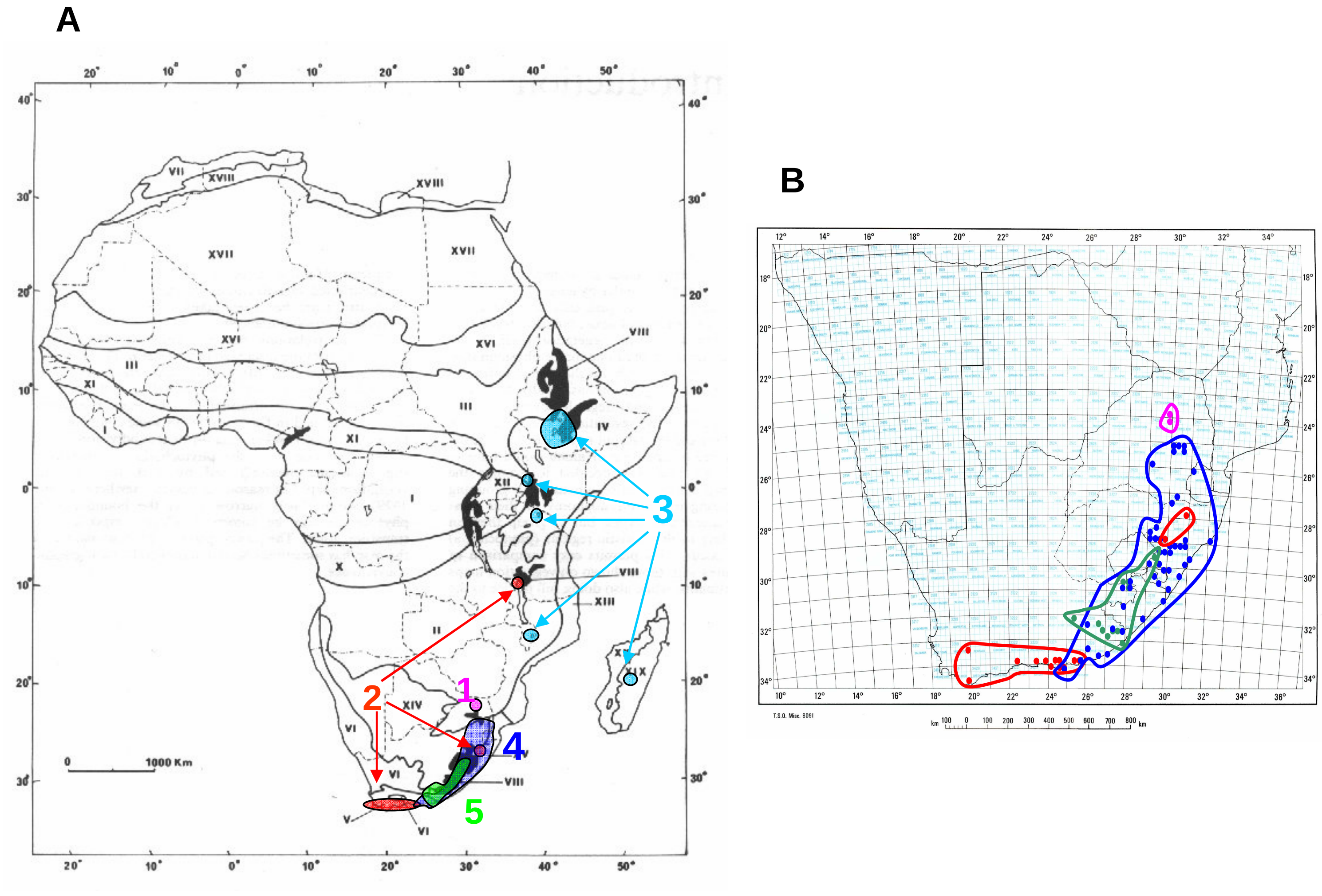


Fig. 3.21. A. Map showing distribution of cpDNA groups in Africa overlaid on the vegetation map of Africa (White, 1983), B. detail map of cpDNA groups in southern Africa (pink= Group 1, red= Group 2, blue= Group 4 and green= Group 5).

Chapter 4: Phylogeography

4.1. Introduction

Phylogeography is the study of the principles and processes governing the geographical distributions of genealogical lineages, especially at the intra-specific level (Avise *et al.*, 1987, 1998). However, this approach has been used at the inter-specific level especially when species show close relationships (Larena *et al.*, 2002; Dobeś *et al.*, 2004; Hughes *et al.*, 2005). It is an integrative discipline in evolutionary biology usually requiring input from molecular genetics, population genetics, phylogenetics, demography and historical biogeography (Avise, 1998, 2000).

In recent years there has been an increase in the number of studies using phylogeograhical approaches in plants, with investigations concentrated on the floras of the Northern Hemisphere (Hewitt, 2001). Several studies have, however, been done in the American tropics (Schaal and Olsen, 2000; Collevatti *et al.*, 2003; Lorenz-Lemke *et al.*, 2005) and the Southern Hemisphere (McKinnon *et al.*, 2004; Gardner *et al.*, 2004). A few phylogeographic studies exist for the African flora (Médail *et al.*, 2001; Hughes *et al.*, 2005; Barker *et al.*, 2005; Howis *et al.*, in prep.).

Of the African studies, Médail *et al.* (2001) examined the phylogeography of subspecies of *Olea europaea* to gain clarity on the systematics, ecology and biogeography of *Olea europaea* subsp. *maroccana*. It was found that *O. europaea* subsp. *maroccana* is a well differentiated relictual taxon that possibily originated from an ancestral unit within Tropical Africa. The results also indicated that *O. europaea* subsp. *maroccana* is not an intermediate between *O. europaea* subsp. *europaea* and *O. europaea* subsp. *laperrinei* as previously suggested. Barker *et al.* (2005) examined the phylogeography of two asteraceous species, *Chromolaena odorata* (a invasive species in South Africa) and *Chrysanthemoides monilifera* (a natural species to South Africa) and demonstrated that *ITS* sequence data can be a useful marker for phylogeographic studies. *Chromolaena odorata* showed little geographic or morphological correlation with genetic diversity, while considerable genetic structure was correlated to morphology and geography in *Chrysanthemoides monilifera*. Hughes *et al.* (2005) examined the phylogeography of *Streptocarpus primulifolius* and *Streptocarpus rexii* in relation to forest fragmentation in the eastern parts of South Africa. *S. primulifolius* was found to have high nDNA and cpDNA diversity which supported the hypothesis that this species is a coastal Pleistocene relict. *S. rexii*, which extends from high to low altitudes, has no or little nuclear diversity and most populations of *S. rexii* share a common chloroplast haplotype. Low genetic diversity and homogeneity indicated that *S. rexii* attained its current distribution during the Holocene. Hughes *et al.* (2005) considered this to be a consequence of forest habitat fragmentation.

A major difficulty in the phylogeographic study of plants is finding suitable genealogical markers. Most plant studies are phylogeographic in a broad sense, detecting patterns of genetic variation and geography and do not incorporate a genealogical perspective (Schaal and Olsen, 2000). Both nuclear and chloroplast markers have been used in plant phylogeographic studies. Nuclear *ITS* has proven useful in several studies (Barker *et al.*, 2005; Hughes *et al.*, 2005; Lorenz-Lemke *et al*., 2005). Schaal and Olsen (2000) have used the low copy gene *G3pdh* to study the phylogeography of *Manihot esculenta* and close relatives. Chloroplast markers have also proven to be useful (e.g. Noguchi *et al*., 2004; Dobeś *et al*., 2004; McKinnon *et al*., 2004; Gardner *et al*., 2004; DeChaine and Martin, 2005).

It is important to mention some of the differences in approach between phylogenetics and phylogeography. Phylogeography is a broad field with many methodologies (Avise, 2000), and the comparisons will concentrate on network methods as this was used in the present study (below). Phylogenetic methodologies are usually designed to determine evolutionary relationships above the species level. Species in this context are regarded as products of reproductive isolation and population fission during which mutations combined with population divergence leads to fixation of different alleles and eventually to non-overlapping gene pools. In a broad sense relationships are considered to be hierarchical (Posada and Crandall, 2001).

Phylogeographic approaches are targeted at the intra-specific level. Relationships are not considered hierarchical, as they are the result of sexual reproduction among individuals with a smaller number of recent mutations and frequent recombination. At the intra-specific level, the more traditional approaches used to infer inter-species relationship estimates (such as maximum likelihood and maximum parsimony) are not applicable as some of their underlying assumptions are violated. Evolutionary processes at the population level such as recombination and hybridisation of lineages generate reticulate relationships. Traditional phylogenetic methods are bifurcating, and make no allowance for such reticulations (Posada and Crandall, 2001). Additionally in natural populations haplotypes exist as sets of multiple identical copies. When one copy mutates it is unlikely that other copies of the ancestral haplotype mutates or that all copies of the ancestral haplotypes becomes extinct. This situation results in sampling of ancestral haplotypes persisting with descendants in a population characterised by multifurcations (Posada and Crandall, 2001).

Alternate approaches need to be followed to take into account the phenomena experienced at the population level or intra-specific level (Posada and Crandall, 2001). One solution is to apply network-based approaches. Networks can account for the processes acting at the species level and might be able to incorporate predictions from population genetics theory. Most network based approaches are distance methods with a common theme of minimising the distance (number of mutations) among haplotypes (Posada and Crandall, 2001). The network algorithm employed in this study is statistical parsimony as implemented in the program TCS (Clements *et al.*, 2000). It estimates the maximum number of differences among the haplotypes as a result of single substitutions (i.e. those that are not multiple substitutions at a single site) with 95% statistical confidence. This number is called the parsimony limit. Haplotypes differing by one change are then connected, and then those differing by two and so on until all the haplotypes are connected into a single network or when the parsimony limit is reached. This method emphasises what is shared among haplotypes that differ minimally rather than the differences among haplotypes and provides an empirical assessment of deviations from parsimony (Posada and Crandall, 2001).

Nested clade analyses (NCA) aim to assess the historic causes of geographic variation. In the NCA a haplotype tree is used to define a nested series of branches (clades). This allows for an evolutionary nested analysis of the spatial distribution of genetic variation. NCA can discriminate between phylogeographic associations due to recurrent but restricted gene flow versus historical events operating at the population level (Templeton, 1998). Nesting starts with the tips of the network and moves one mutational step into the interior uniting all haplotypes that are connected by this prodecure into ‘1-step clades’ or first level clades. Thereafter these ‘1-step clades’ are pruned off. The prodecure is repeated on the more interior portions of the network if needed until all haplotypes are placed in ‘1-step clades’. The next level (second level) uses 1-step clades as base units rather than haplotypes applying the rules above to determine 2-step clades. This process is repeated until the original network falls into a single category (Templeton, 1998).

Several phylogeographic studies have found the *trnT-L* spacer (used in this study) to be useful at the intra-specific level (Huang *et al.*, 2002; Saltonstall, 2002; Honjo *et al.*, 2004; Zhang *et al.*, 2005). Huang *et al.* (2002) examined the phylogeography of *Cyclobalanopsis glauca* (Fagaceae) incorporating 32 populations with 140 samples. A combined analysis was used with the *trnT-L* spacer being the most variable and informative. Huang *et al.* (2002) did not use TCS or phylogenies but concentrated on a genetic diversity approach.

Saltonstall (2002) studied *Phragmites australis* (Poaceae) world wide using 345 populations represented by 345 samples. A combined analysis was used with *trnT-L* spacer and *rbcL-psaI* sequence data. Not all the data for these markers were provided. Saltonstall (2002) used TCS to determine haplotypes but no NCA or phylogenies were presented. Twenty-seven haplotypes were recovered with a single haplotype (M) currently being the most common in North America, Europe and Asia. It is closely related to haplotypes from Europe, Asia and Africa, and is also predicted to be the ancestral haplotype. Haplotpye M is the most common and widely distributed in North America but is not closely related to other North American haplotypes. Saltonstall (2002) results indicate a cryptic invasion is occurring in North American *Phragmites australis* by a non-native genotype (viz. haplotype M), which is highly competitive with broad ecological tolerances. It has spread throughout North America displacing native types and has spread to regions not previously occupied by *Phragmites australis*.

Honjo *et al.* (2004) examined 66 populations (n= 275) of *Primula sieboldii* (Primulaceae) using several markers (the *trnT-L* spacer, the *trnL* intron, the *trnL-F* spacer, the *trnD-T* spacer and the *trnH-psbA* spacer). A combined analysis was presented and not all the data for these markers were given. Honjo *et al.* (2004) used TCS to determine the cpDNA haplotypes (n= 22), but a NCA was not done. In order to infer relationships among the haplotypes MP and NJ were used, with only the MP phylogeny presented. Most haplotypes were geographically confined but one was widely distributed throughout northern Japan, while several others were found in geographically distant regions. Three major phylogenetic clades were recovered and none of the haplotypes recovered were placed in more than one clade. Clade I was distributed in Kyushu and central Honshu, Clade II in western Honshu and Hokkaido and Clade III in central Honshu and Hokkaido.

Zhang *et al.* (2005) examined the phylogeography of *Juniperus przewalskii* (Cupressaceae) on the Qinghai-Tibetan Plateau. Twenty populations represented by 392 samples were studied using the *trnT-L* spacer, the *trnL* intron, the *trnL-F* spacer and the *trnS-G* region. A combined analysis was used with the *trnS-G* region being the most variable and informative. TCS was used to determine the haplotypes and a NCA was performed. Phylogenetic relationships among the haplotypes were determined using NJ, MP and Maximum-Likelihood, which resulted in the same topologies. Six haplotypes (A-F) were found which nested into three first level clades. Clade 1-1 contained haplotypes C, D and E, Clade 1-2 contained haplotypes E and B while Clade 1-3 contained only haplotype F. The nested clades corresponded to the main lineages recovered by the phylogenetic analyses and none of the haplotypes recovered were placed in more than one clade. The most widely distributed haplotype (A) was hypothesised not to be the ancestral haplotype. Zhang *et al.* (2005) findings indicate that the Qinghai-Tibetan Plateau was recolonised by *J. przewalskii* during the most recent post-glacial period by a post-glacial range expansion from the edge of the Qinghai-Tibetan Plateau. This was followed by recent fragmentation which was proposed to explain the current distribution of cpDNA haplotypes.

Based on the results presented in Chapter 3 it was deemed necessary to explore the *trnT-L* sequence data from a phylogeographic perspective rather than a strict phylogenetic context in an effort to understand and explain the geographical and phylogenetic patterns recovered. The *ITS* data was not analyses in this manner because of the low sequence divergence and recombination.

4.2. Materials and Methods

4.2.1. Data Sets

Two analyses were conducted. The first (Analysis I) was done on the entire *trnT-L* matrix with the following modifications: the out-groups (*Bulbine* and *Bulbinella*) and three *Kniphofia* sequences (SR 342= *K. uvaria*, J. Pote *sn*= *K. linearifolia*, TD 4559= *K. rooperi*), which had substantial regions of missing data, were excluded from the analysis. Messy ends were trimmed at the 3’ end of the spacer. Once the out-groups and incomplete sequences were removed, the matrix was re-checked and redundant gaps were removed to minimise internal node haplotypes. This approach was done primarily to compare results of the phylogenetic and phylogeographic approaches. In the second analysis (Analysis II) only South African (SA) samples were included. The matrix was then trimmed and edited as described above. This data set was subjected to a nested clade analysis. It is important to note that samples in the matrices analysed are not population samples but are treated in this study as such.

4.2.2. Nested Clade Analysis (NCA)

Haplotype networks were constructed using TCS version 1.13 (Clements *et al.*, 2000). Gaps were treated as missing data. Haplotypes were nested into hierarchically interlocking groups i.e. nested clades for both data sets.

A quantitative analysis of geographical data (i.e. NCA), as described by Templeton (1998) was performed using GeoDis version 2 (Posada *et al.*, 2000). GeoDis is a program that allows to test a null hypothesis of no association between geography and the inferred gene tree (Avise, 2000). Acceptance of the null hypothesis may be due to biological factors viz. high contemporary gene flow or recent historical association. The null hypothesis may also be accepted due to insufficient power of the test because of small samples sizes or poor sampling. When the null hypothesis is rejected the program can be used to gain insights on causes of associations between the phylogeny and geography (Avise, 2000). Statistically significant large and small D_c values (a measure of the geographical range of a particular clade), D_n values (the geographical range of a particular clade relative to its closest sister clades), $(I\text{-}T)_{Dc}$ (the D_c of the interior minus the tip clades) or $(I\text{-}T)_{Dn}$ ($D_{n\ interior} - D_{n\ tip}$) were interpreted using the inference key (available from http://inbio.byu.edu/Faculty /kac/crandal_lab/geodis.htm; Templeton, 1998).

This analysis was only done for SA samples, as the large spatial separation of Tropical and East African samples and the lack of sampling over the entire distributional range were deemed unsuitable for further analysis. The output files and the GeoDis inference key were used to determine possible biogeographic scenarios.

The TCS and GeoDis software is used mainly for population level studies with typically more than one sample per population. Throughout this study only one sample per population was analysed as it was initially anticipated that species would cluster along morphological lines and not geographically. Thus the original sampling approach was to collect as many morphological species as possible and to cover geographic distribution for SA and strictly speaking the sampling above is not suitable for a NCA. However, it was pursued to test if there was any association between DNA sequence data and geography, and determine the nature of the association. These aspects were done in an effort to better understand the biogeography and evolutionary history of *Kniphofia*.

An approach using a single sample per population recovered a haplotype network but problems were encountered using GeoDis. Initial attempts which treated each sample (and locality) as a separate population failed to recover statistical values to use the GeoDis inference key. Populations were then grouped at the quarter dergree grid (QDG) scale i.e. samples within a given QDG were treated as a single population. This also did not recover statistically usable values. Samples were then grouped at the half degree grid (HDG) scale. Single samples in QDG that were the only representative for a HDG were grouped with adjacent and immediate HDGs. This was done to minimise the number of populations and group samples that would otherwise cluster if a strict HDG clustering approach was not implemented. In several cases single samples (populations) for a QDG were not immediately adjacent to a designated HDG and prevented incorporation. These were treated as independent (‘lone’) HDGs. A similar approach was used for full degree grids to explore and compare the outcome at a different spatial scale.

4.3. Results

4.3.1. Analysis I: southern, East and Tropical African samples

The matrix consisted of 122 sequences representing 50 *Kniphofia* species and was 545 bp in length. The network recovered (Fig. 4.1.) had a total of 56 haplotypes of which 15 were internal nodes (i.e. unsampled haplotypes).

The remaining 41 haplotypes are listed in Appendix 7. Twenty-three first level clades were recovered of which four were internal node clades i.e. clades with no representative samples. Ten second level clades and three third level clades were recovered (Fig. 4.1.). Nesting at the fourth level incorporated the entire network. The loops are no described in both analyses as these contained internal node clades. Additionally loops can be broken down depending on what haplotype is basal in equally parsimonious solutions.

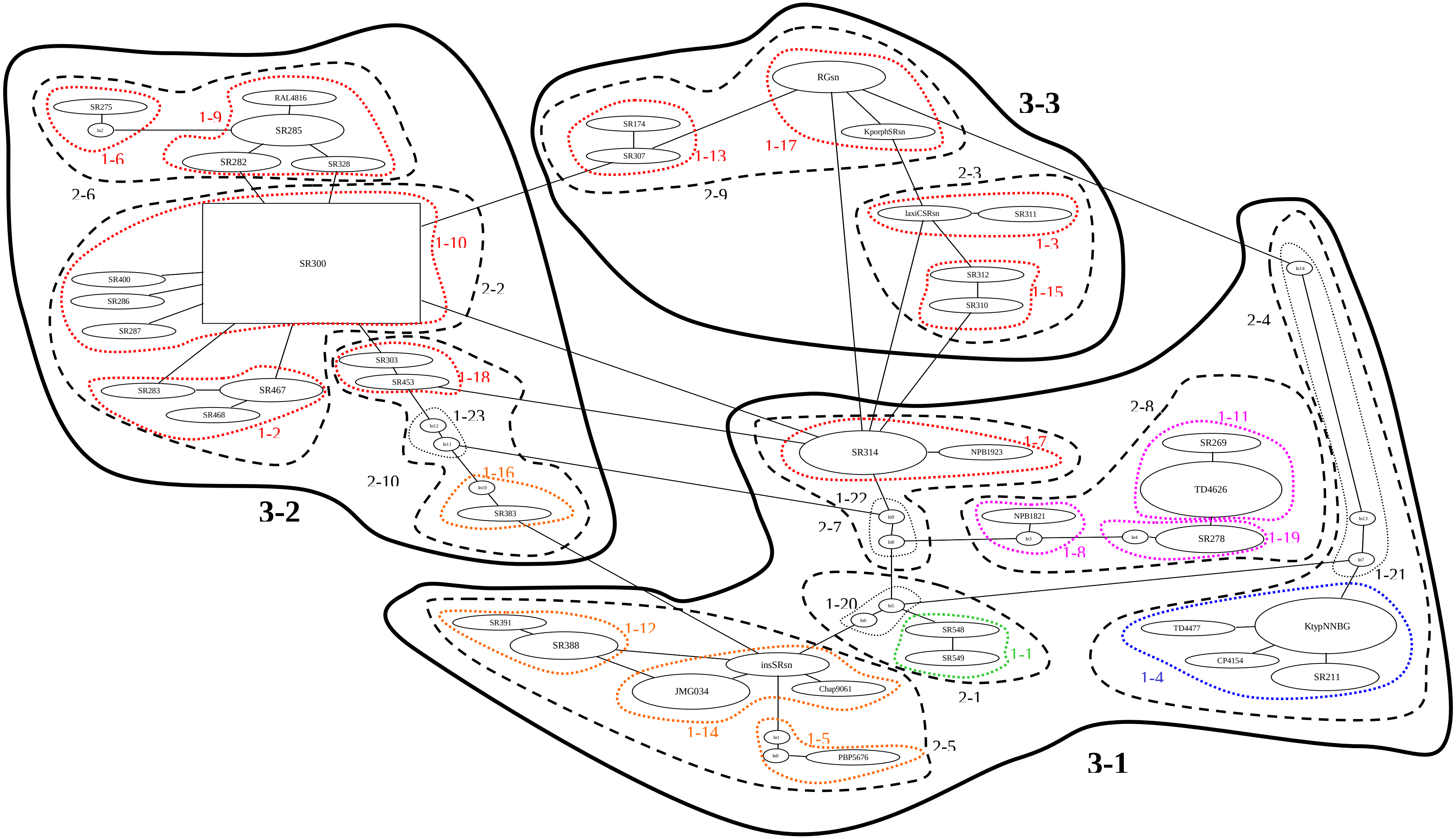


Fig. 4.1. Haplotype network with nested clades based on the *trnT-L* spacer of *Kniphofia*. Colors represent groups obtained from the phylogenetic analyses (Chapter 3) (Green= Group 1, Blue= Group 2, Orange= Group 3, Red= Group 4 and Pink= Group 5; refer to text for details).

4.3.1.1. Comparison of haplotype network and the lineages recovered by phylogenetic approaches

It is useful to compare nested clades with the phylogenetic groups recovered as most studies find that there is a correspondence (e.g. Zhang *et al.*, 2005). The bayesian inference tree which generally had good support for the five major groups (Chapter 3) is used below to compare nested clades and groups recovered in this study. The first level clades are too numerous to make any detail comparisons. All the first level nested clades (excluding internal node clades) were group specific (Fig. 4.1.) i.e. all first level clades contained samples from only one group as resolved by the phylogenetic methods (Chapter 3). All the second level nested clades were also group specific except Clade 2-10 which is composed of two first level clades, Clades 1-16 and 1-18 (Fig. 4.1.). Clade 1-16 has two samples from Group 4 while Clade 1-18 has one sample from Group 3 (SR 383= *K. foliosa* from Ethiopia).

The third level nested clades do not strictly reflect the same lineages recovered by the phylogenetic analyses (Fig. 4.2.). Clade 3-1 (n= 62) is composed of five second level clades and has samples from all five lineages recovered in the phylogenetic analyses (Fig. 4.1., 4.2. and 4.3.). Clade 2-1 is composed of all samples from Group 1 (n= 2). Clade 2-4 is composed of all samples from Group 2 (n= 17). Clade 2-5 is composed of all samples from Group 3 (n= 16), except SR 383 (*K. foliosa*) which is placed in Clade 3-2. Clade 2-8 is composed of all samples from Group 5 (n= 18). Clade 2-7 is composed of some samples from Group 4 (n= 9).

Clade 3-2 (n= 48) is composed of three second level clades and has samples from two lineages recovered in the phylogenetic analyses (Fig. 4.1., 4.2. and 4.4.). Clade 2-2 (n= 35) and Clade 2-6 (n= 10) are composed of samples from Group 4. However, Clade 2-10 is composed of samples from two phylogenetically delimited groups, Group 4 (n= 2) and Group 3 (n= 1). Clade 3-3 (n= 12) has two second level clades (Fig. 4.1., 4.2. and 4.5.) and contained only representatives from Group 4: Clade 2-3 (n= 4) and Clade 2-9 (n= 8).

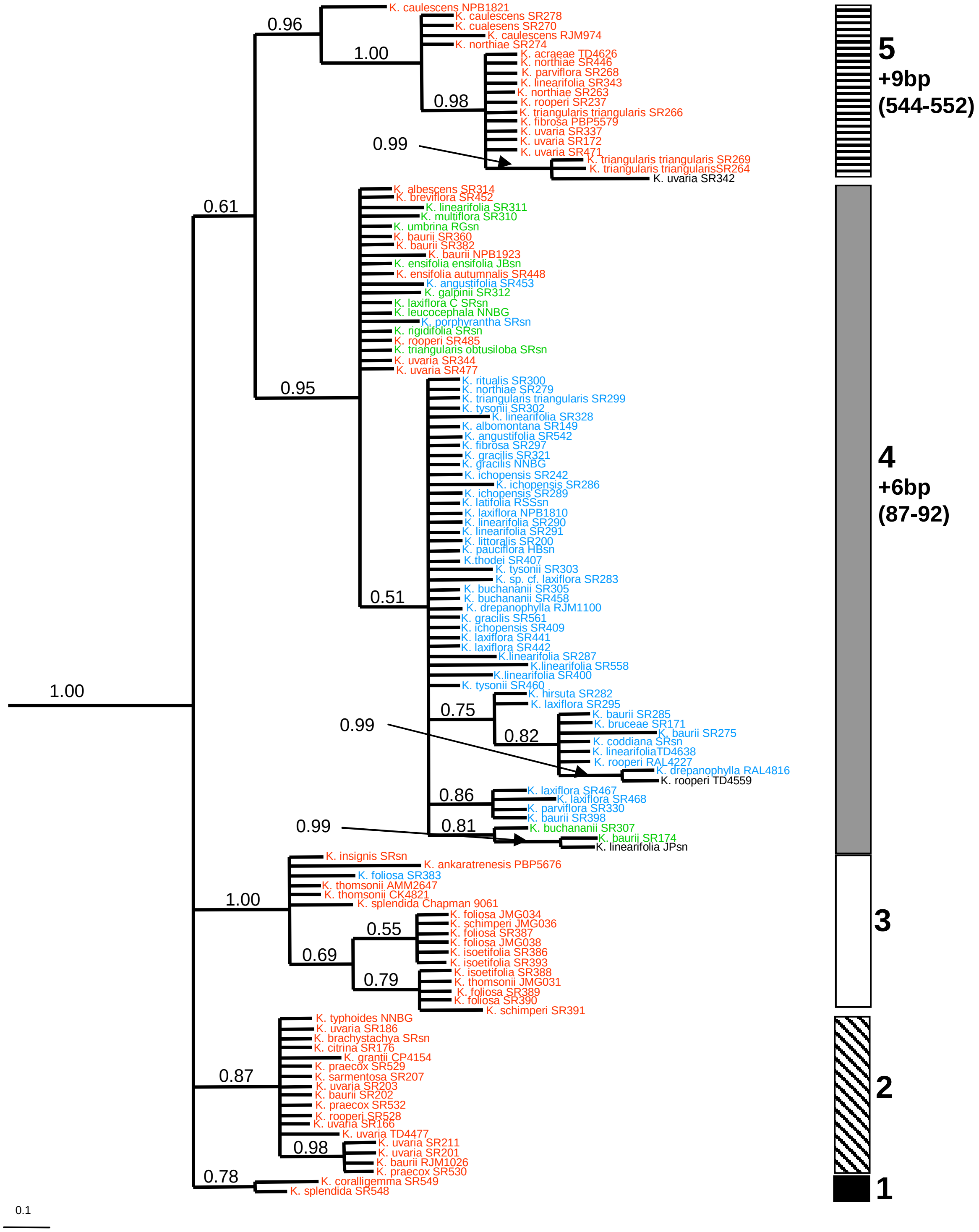


Fig. 4.2. Third level clades plotted on bayesian tree of the *trnT-L* spacer. Major cpDNA groups are denoted by bars to the right and numbers below the group labels show indel positions and size (out-groups not shown). Clade 3-1= red, Clade 3-2= blue and Clade 3-3= green.

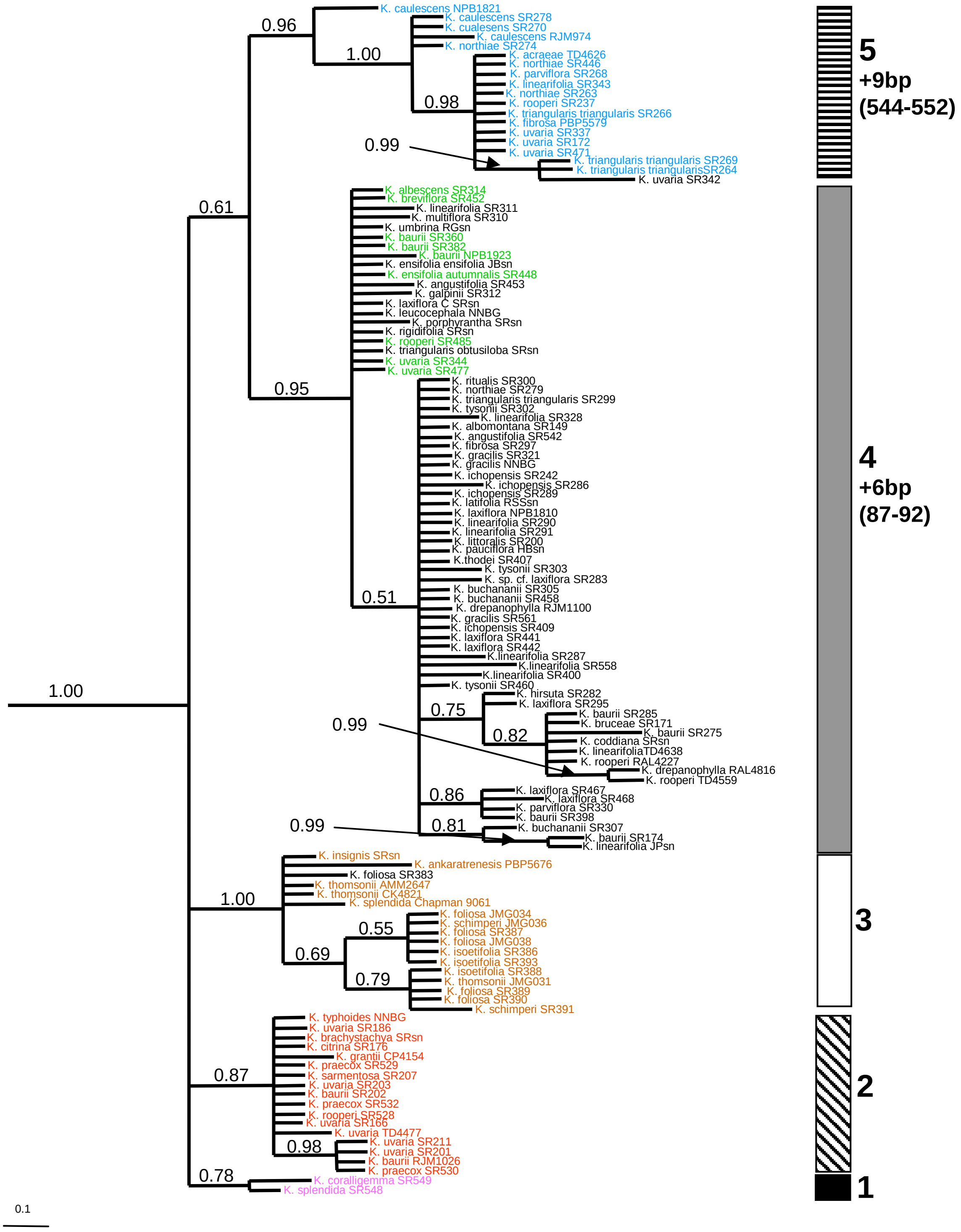


Fig. 4.3. Second level clades of Clade 3-1 plotted on bayesian tree of the *trnT-L* spacer. Major cpDNA groups are denoted by bars to the right and numbers below the group labels show indel positions and size (out-groups not shown). Clade 2-1= pink, Clade 2-4= red, Clade 2-5= brown, Clade 2-7= green and Clade 2-8= blue.

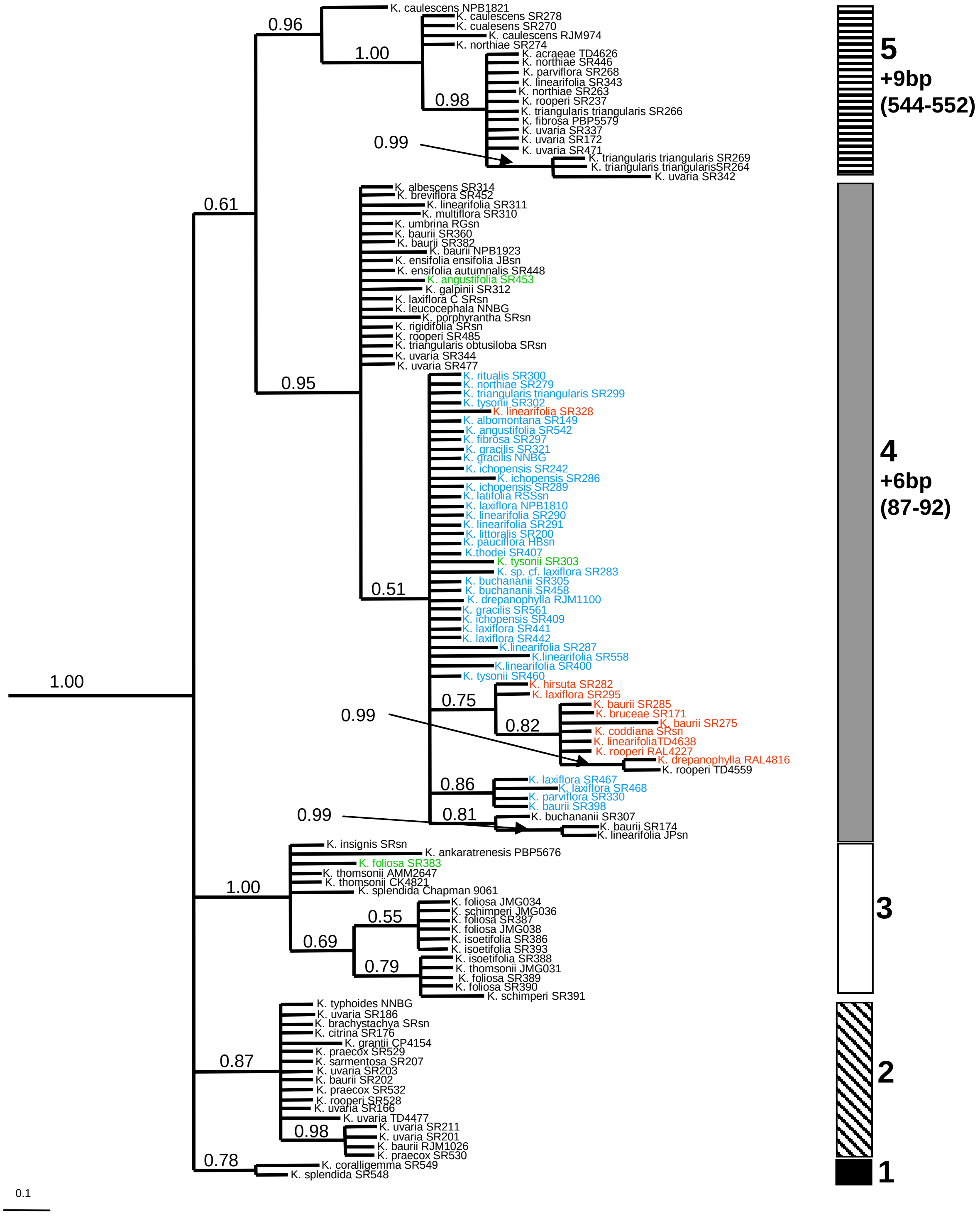


Fig. 4.4. Second level clades of Clade 3-2 plotted on bayesian tree of the *trnT-L* spacer. Major cpDNA groups are denoted by bars to the right and numbers below the group labels show indel positions and size (out-groups not shown). Clade 2-2= blue, Clade 2-6= red and Clade 2-10= green.

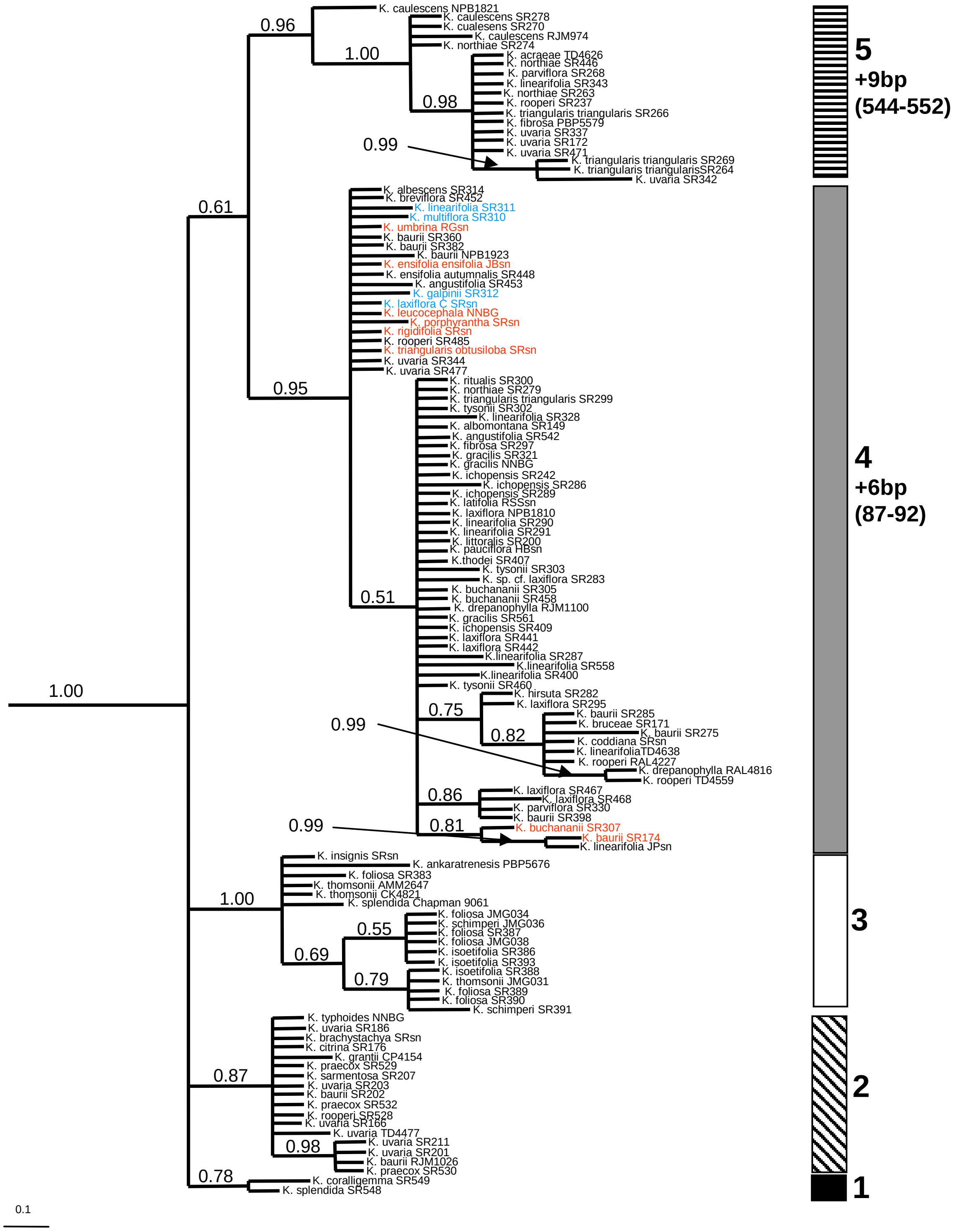


Fig. 4.5. Second level clades of Clade 3-3 plotted on bayesian tree of the *trnT-L* spacer. Major cpDNA groups are denoted by bars to the right and number below the group labels show indel positions and size (out-groups not shown). Clade 2-3= blue and Clade 2-9= red.

4.3.2. Analysis II: NCA of South African samples

The second matrix (only SA samples) consisted of 104 sequences representing 44 *Kniphofia* species and was 539 bp in length. The network recovered (Fig. 4.6.) had 42 haplotypes were recovered of which nine were internal node haplotypes. The remaining 33 haplotypes are characterised in Appendix 8. Eighteen first level clades recovered of which three were internal node clades i.e. clades with no representative samples. Seven second level clades and three third level clades were recovered. Nesting at the forth level incorporated the entire network.

It is not possible to directly compare the nested clades with the lineages recovered using phylogenetic approaches as no phylogenetic reconstructions were done exclusively on SA samples.

For the GeoDis analysis a total of 39 HDGs were delimited. Details of samples grouped into HDGs are given in Appendix 9. A total of 25 full degree grids were delimited (Appendix 10). The GoeDis output files are given in Appendix 11 and 12 for the half and full degree grid analyses respectively. The results discussed here focused only on the third level nested clades as these allowed for meaningful comparisons (see above). The inference key results are presented below for the half and full degree grid analyses. Statistically significant large and small D_c, D_n, (I-T) $_{Dc}$ and (I-T) $_{Dn}$ values from the GeoDis output file were used with the inference key in a stepwise manner to determine possible biogeographic scenarios. The numbers in the inference chain below represent the steps in the key.

Half degree grid inference chain:

Clade 3-1: 1→19→NO: **Allopatric fragmentation**

Clade 3-2: 1→2→11→17→4→NO: **Restricted gene flow with isolation by distance**

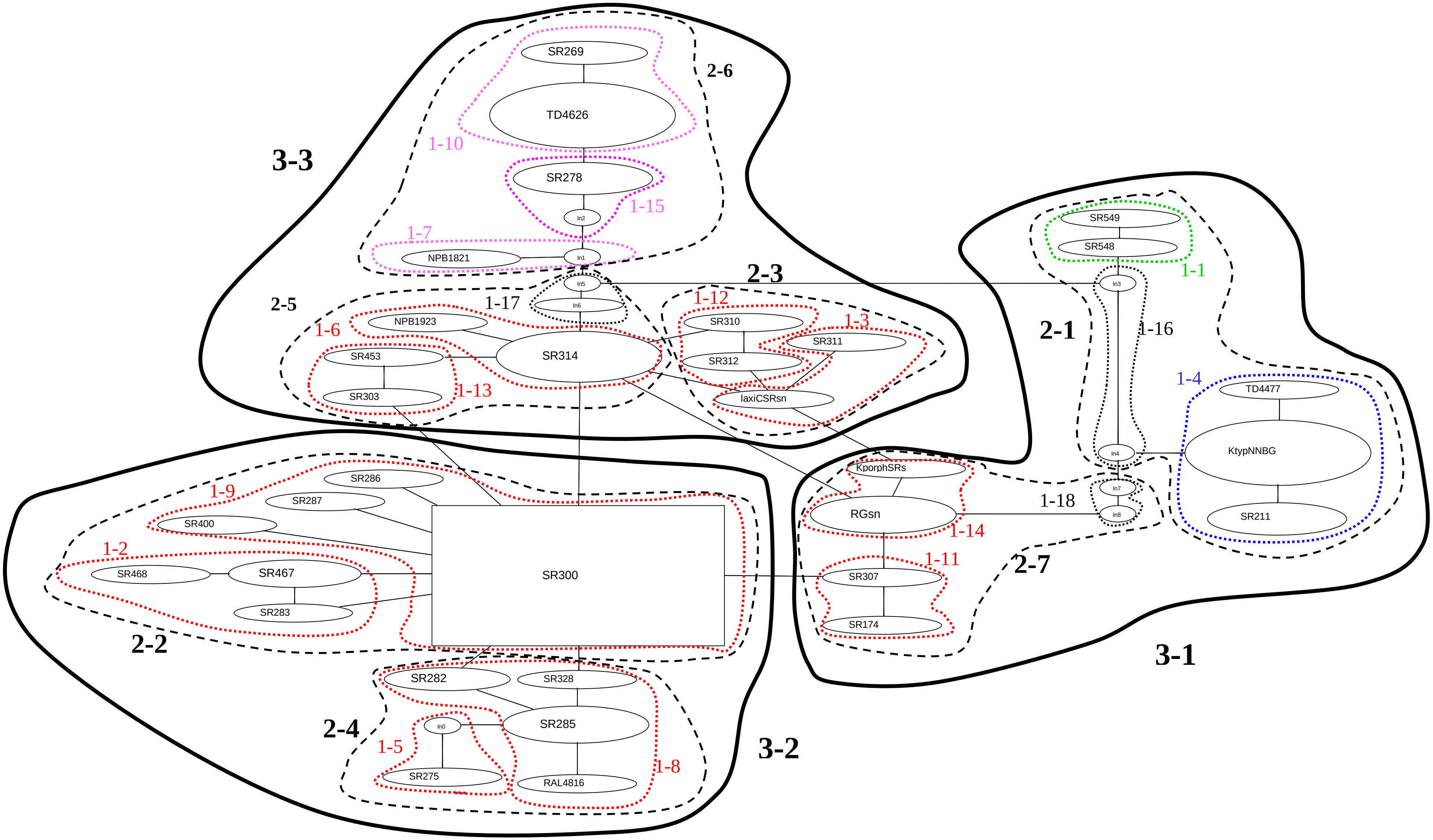


Fig. 4.6. Haplotype network with nested clades based on the *trnT-L* spacer for South Africa samples of *Kniphofia* (Green= Group 1, Blue= Group 2, Red= Group 4 and Pink= Group 5; refer to text for details).

Clade 3-3: 1→2→3→5→6→13→14→YES: **Sampling design inadequate to discriminate between contiguous range expansion, long distance colonisation and past fragmentation**

Full-degree inference chain:

Clade 3-1: 1→19→NO: **Allopatric fragmentation**

Clade 3-2: 1→2→11→YES (Range expansion)→12→NO: **Contiguous range expansion**

Clade 3-3: 1→2→3→5→6→7→YES: **Restricted gene flow/ Dispersal with some long distance dispersal**

4.4. Discussion

It must be emphasised that the results of the TCS and GeoDis analysis should not be over interpreted because of the sampling approaches (see Materials and Methods) and limited sampling done between SA and Ethiopia. Phylogeographical analyses are only meaningful if appropriate sampling is done across the entire distributional range. Small samples sizes or poor sampling may not recover an association between geography and the inferred gene tree (Avise, 2000). More sampling is required from the gaps between SA and Ethiopia to gain better insights. Moreover, not enough is known about how these methods are effected by phenomena such as the hybridisation and incomplete lineage sorting. Thus the interpretation of the results should be regarded as preliminary. Despite these limitations some interesting patterns were found.

Neighbor joining, maximum parsimony and bayesian inference recovered more or less similar groups (Chapter 3). The third level nested clades do not strictly reflect the same lineages recovered by the phylogenetic analyses (Chapter 3). The differences in the results may be due to the different methodological approaches. Phylogeographic approaches take into account the phenomena experienced at the population level and are not considered hierarchical. Evolutionary processes at the population level such as recombination and hybridisation of lineages generate reticulate relationships (Posada and Crandall, 2001). Traditional phylogenetic methods are bifurcating, and make no allowance for such reticulations. In a broad sense relationships are considered to be hierarchical (Posada and Crandall, 2001). However, the nesting process in TCS (Clements *et al*., 2000) appears to be hierarchical.

Parsimony is a character based method using only synapomorphic characters to find the tree or set of trees that have a minimum number of steps. Bayesian inference is a model based method that takes into account priors and is also character based. Neighbor joining is a distance based method. It takes into account gaps and missing data and is therefore sensitive to indels and missing data. In the TCS analysis employed, gaps were treated as missing data. It is interesting to note that the only nested clade which matches a phylogenetically delimited group characterised by an indel is Clade 2-8 which corresponds to Group 5. Group 4 which is also characterised by a six bp insertion in the phylogenetic approaches was not recovered as a single unit in the haplotype network irrespective of the level of nesting.

Setting the TCS software parameters to treat the gaps as 5th state characters did not recover a network in both analyses. It is possible that treating gaps as 5th state characters results in numerous sub-networks that do not reach the parsimony limit and are not able to connect and recover a usable network. The other possibility is that 5th state characters resulted in too many haplotypes that were beyond the computational capacity of the program.

4.4.1. Distribution of nested clades from haplotype network (Analysis I)

In the anaylsis of the full data set all the third level clades are linked i.e. none are placed at terminal positions in the network. This suggests that the clades may have once formed a single cohesive unit that has fragmented. This becomes more apparent when the samples from the third level nested clades are mapped (Fig. 4.7.-4.9.).

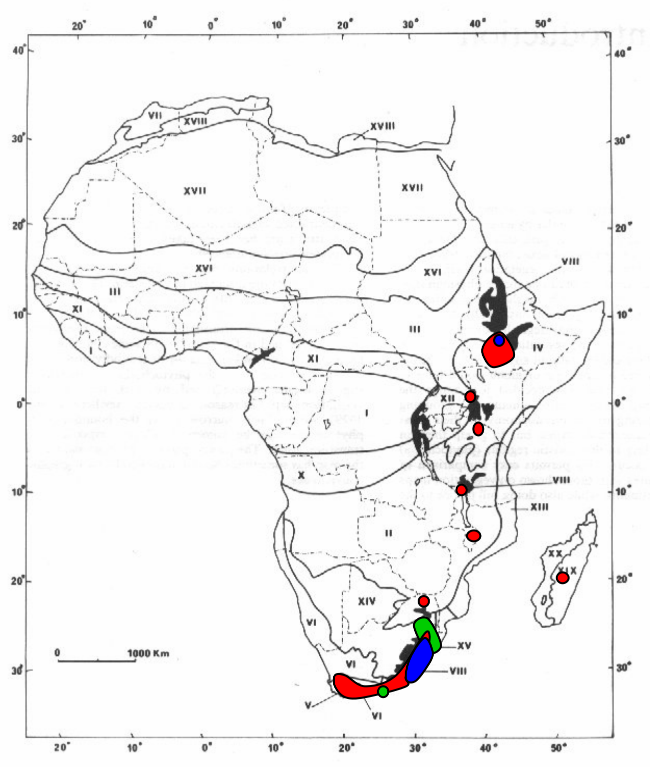


Fig. 4.7. Vegetation map of Africa (after White, 1983) showing distribution of third level nested clades (based on *trnT-L* spacer). Clade 3-1= red, Clade 3-2= blue and Clade 3-3= green.

Clade 3-1 is distributed from the Cape Region to the northern limits of southern Africa and the genetic signature is maintained at Afromontane disjuctions in Tropical and East Africa that were sampled in this study. The signature was also recovered for material from Madagascar (Fig. 4.7.). This suggested that the Cape Region and parts of Africa once formed a continuum in the past and this has been broken, with the haplotypes maintaining the genetic signature. All samples that were not southern African are from Afromontane regions. South African samples from Clade 3-1 are from a wide variety of habitats and altitudes (Fig. 4.8. and Fig. 4.9.A.). It is interesting to note that in the phylogenetic analyses (Chapter 3) a sample from Malawi also fell into the Cape clade (Group 2). This sample (*K. grantii*) was re-extracted and sequenced to rule out the possibility of mistaken origin. Another sample from Malawi (*K. splendida*, Chapman 9061) fell into the Tropical Africa clade (Group 3). *K. grantii* (Group 2) is placed within Clade 2-4, while *K. splendida* (Chapman 9061) is placed within Clade 2-5. Both Clade 2-4 and Clade 2-5 are nested in Clade 3-1 (Fig. 4.1.). The Cape-Malawi link also suggested that this haplotype extends more northwards than this study has detected.

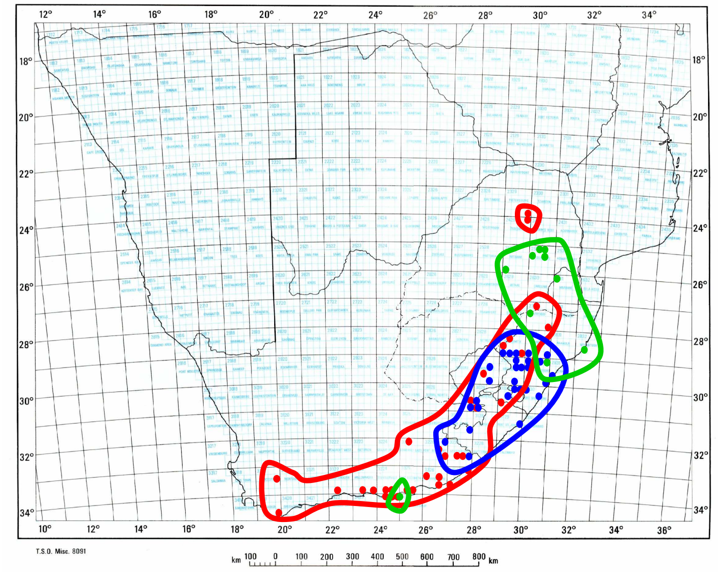


Fig. 4.8. A detailed map showing distribution of third level clades (based on *trnT-L* spacer) within South Africa. Clade 3-1= red, Clade 3-2= blue and Clade 3-3= green.

Numerous workers have noted the relationships between the Cape Region and the Afromontane Region (Levyns, 1964; Hedberg, 1965; Cowling, 1983a; Hilliard and Burtt, 1987; Linder, 1990; Linder, 2003, Galley and Linder, 2006). These links mostly concern Cape floral elements which are frequently found in most Afroalpine centres. Galley and Linder (2006) have suggested that Afromontane taxa with southern connections are derived in part from Cape clades either from one or several migrations northwards from the Cape Region. However, *Kniphofia* is not regarded as a Cape element and this study does not conclusively show that the Tropical and East African clade is derived from Cape clade (Chapter 3).

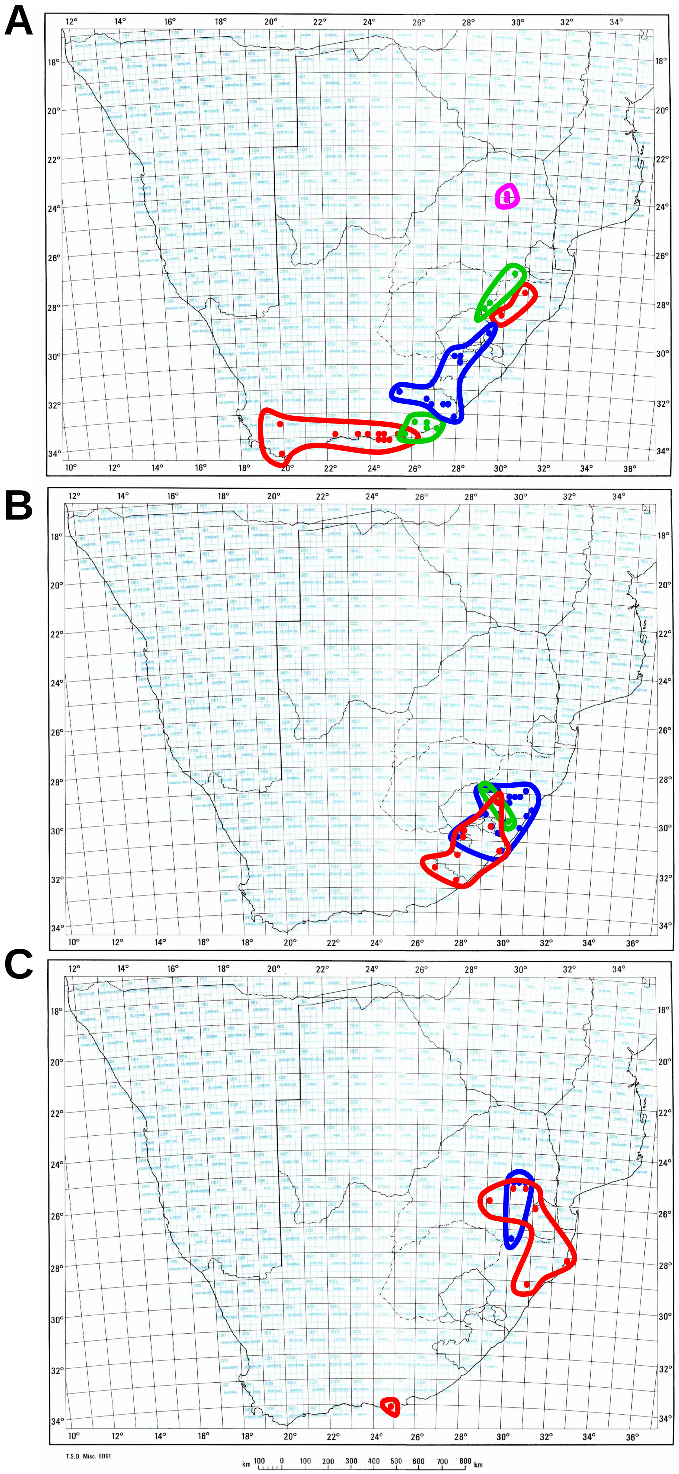


Fig. 4.9. Map showing distribution of second level clades that form units of third level nested clades (based on *trnT-L* spacer) for South African samples. A. Clade 3-1: Clade 2-1= pink, Clade 2-4= red, Clade 2-7= green and Clade 2-8= blue. B. Clade 3-2: Clade 2-2= blue, Clade 2-6= red and Clade 2-10= green. C. Clade 3-3: Clade 2-3= blue and Clade 2-9= red.

As mentioned above limited sampling was done in the Afromontane regions between SA and Ethiopia. Additional sampling is required for the gaps between SA and Ethiopia. It will be interesting to see the placement of additional material from regions not sampled, especially Tropical and East Africa.

In Clade 3-2, *K. foliosa* (SR 383) from Ethiopia grouped with material from SA (Fig. 4.7., 4.8., 4.9.B.). This also suggests that some SA material is more closely related to East African material rather than other SA samples. This genetic link between southern and East Africa may be more common but was not detected because of poor sampling. It also suggests that more than one genetic signature occurs between southern and East Africa. But more sampling is required to confirm this.

All samples in Clade 3-2 (except *K. foliosa* SR 383) and Clade 3-3 (Fig. 4.7., 4.8., 4.9.C.) are from the Afromontane Region (viz. Drakensberg), the adjacent Drakensberg-Maputoland-Pondoland transition and the Maputoland-Pondoland Region (within southern Africa). Samples occur from high altitudes in the Drakensberg to the coastal regions in habitats with a grassland affinity. It is generally assumed in phylogeographic studies that the most common haplotype is the also the most ancestral. Haplotype SR 300 (n= 27; Clade 3-2) is the most common haplotype but does not appear to be the most ancestral as it is not centrally placed within the network (Fig. 4.1.). Samples of this haplotype are also not basally placed in the phylogenies, which would support this haplotype being ancestral. It seems plausible to hypothesise that this haplotype is recently derived and has managed to spread in a relatively short period of time. Most of the samples of haplotype SR 300 are from KwaZulu-Natal (n= 25) covering a wide range of altitudes (coastal to high montane habitats). In southern Africa there ia a compensation of latitude for altitude. This compensation of latitude for altitude and the results above seem to indicate a range expansion for *Kniphofia* (see below).

It is also worth noting that *K. typhoides*, *K. umbrina* and *K. brachystachya* that were placed in the segregate genus *Notosceptrum* did not form a separate cluster in the haplotype network.

4.4.2. NCA of South African samples

The discussion below focuses only on the third level nested clades analysed at the full degree grid scale as this gave more meaningful results. This may be due to inadequacies in the half degree grid sampling approach, small samples sizes or poor sampling. At the full degree scale cpDNA haplotypes divided into threee major nested clades that showed some geographical patterns. The distribution of the three nested clades are mapped in Fig. 4.10. Biogeographic scenarios recovered by the GeoDis analysis at the full degree scale become more apparent when samples within the nested clades are mapped out Fig. 4.11.

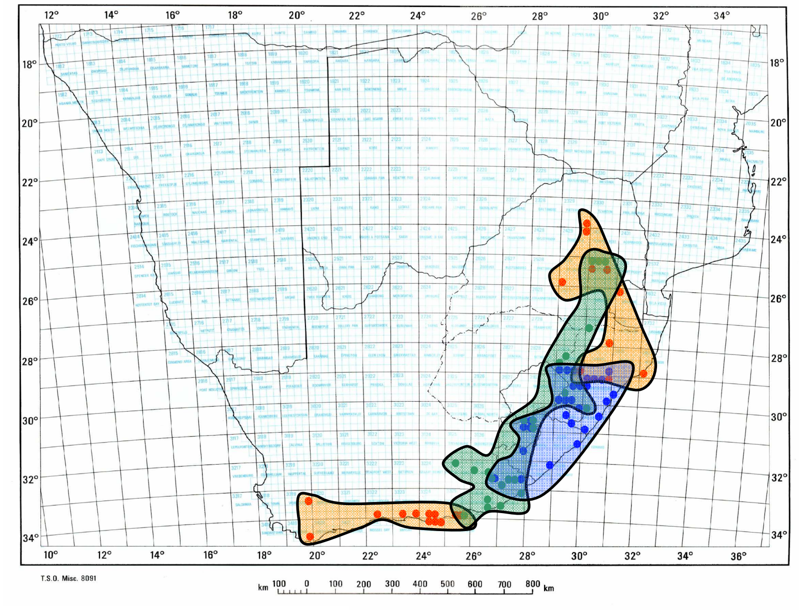


Fig. 4.10. Map showing distribution of third level nested clades based on the *trnT-L* spacer for southern Africa representatives of *Kniphofia* (Orange= Clade 3-1; Blue= Clade 3-2 and Green= Clade 3-3).

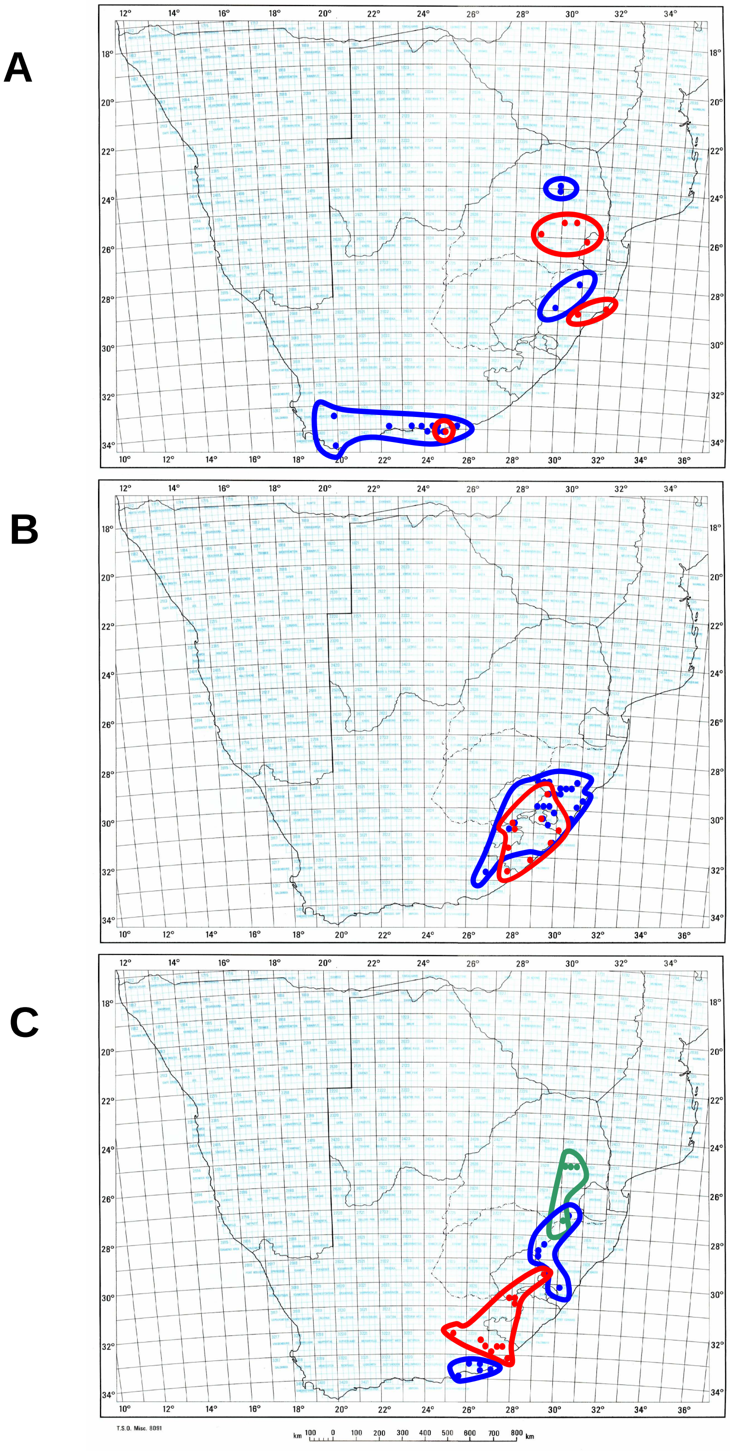


Fig. 4.11. Map showing distribution of second level clades that form components of third level nested clades based on the *trnT-L* spacer for southern Africa representatives of *Kniphofia*. A. Clade 3-1= 2-1 (blue) + 2-7 (red); B. Clade 3-2= 2-2 (blue) + 2-4 (red); C. Clade 3-3= 2-3 (green) + 2-5 (blue) + 2-6 (red).

Clade 3-1 showed allopatric fragmentation. This suggested that the Cape Region and parts of KZN and Mpumalanga formed a continuum at some stage in the past and these have been broken with the haplotypes maintaining the genetic signature. This does not rule out the possibility that a continuum does exist, and the sampling of this study did not recover it. Most of the samples from the KwaZulu-Natal and Mpumalanga are from the Afromontane Region with the exception of a single sample (*K. leucocephala* from Richards Bay).

Clade 3-2, showed a range expansion. Samples from this clade are from the Afromontane (Drakensberg) Region, the adjacent Drakensberg-Maputoland-Pondoland transition and the Maputoland-Pondoland Region. *Kniphofia* has been shown to be a strong Afromontane grassland affinity north of southern Africa. However, in southern Africa, *Kniphofia* occurs from high altitudes to the coastal regions. The compensation of latitude for altitude may explain a range expansion. *Kniphofia* may have expanded ranges to lower altitudes especially in the eastern parts of SA in the recent past possibly the last glacial cycle. This range expansion may have been accompanied by a radiation which may account for the high diversity in the eastern part of southern Africa viz. the Afromontane (Drakensberg) Region, the Drakensberg-Maputoland-Pondoland transition and the Maputoland-Pondoland Region (Chapter 2; also discussed in detail later).

Clade 3-3, showed restricted gene flow and some long distance dispersal. The distribution of this clade extends along the Drakensberg Range with limited samples in the low-lying Drakensberg-Maputoland-Pondoland transition. This pattern is not clear and is unlikely to support the extensive hybridisation suggested previously (Chapter 1 and 3).

4.5. Conclusion

The findings presented here should be regarded as preliminary because of the limited sampling. Also the current programs routinely used in phylogeographical studies cater for a single species or a small number of closely related species. A phylogeographic approach as advocated in this study may not be appropriate due to poor sampling, large spatial gaps between samples, the heterogeneity of morphological entities and the non-monophyly displayed by several species. Coalescent approaches may help in interpreting the data further. However, these were not attempted in this study because of the limiting nature of the data and the problems associated with finding suitable calibration points.

Despite these limitations some interesting patterns were detected. The comparitive study of the nested clades (recovered in the haplotype network of the entire *trnT-L* matrix) and the phylogenetic reconstruction approaches revealed that the nested clades did not strictly reflect the phylogenetically recovered lineages. Additionally Clade 3-1 appears to show fragmentation between Cape Region, northern parts of SA and the rest of Africa including Madagsacar. Clade 3-2 also indicates a SA-Ethiopia link. The other interesting pattern recovered was in Clades 3-2 and 3-3, which suggests a range expansion.

In the NCA of SA samples one of the nested clades, Clade 3-1, showed allopatric fragmentation between Cape Region and parts of KZN and Mpumalanga. A pattern that point to fragmentation was also detected in the comparitive analysis of the nest clades of the haplotype network and the phylogenetic lineages (above). The other interesting pattern recovered was in Clade 3-2, which points to a range expansion in the Afromontane (Drakensberg) Region, the adjacent Drakensberg-Maputoland-Pondoland transition and the Maputoland-Pondoland Region. *Kniphofia* may have expanded its range in the recent past possibly the last glacial cycle. This range expansion may have been accompanied by a radiation which may account for the high diversity in the eastern part of SA. The above findings provide valuable insights towards a better understanding of the biogeography and evolutionary history of *Kniphofia*.

Chapter 5: Anatomy

5.1. Introduction

Anatomical evidence can play an important role in the elucidation of phylogenetic relationships (Ellis, 1983a, 1989; Linder, 2000). Leaf anatomy has been used widely in taxonomically difficult groups to solve problems of relationship and classification (Davis and Heywood, 1973; Ellis, 1974, 1982, 1983b, 1985a, 1985b, 1986a, 1986b, 1987, 1988). Light and scanning electron microscopy have proven to be useful tools for the study of leaf anatomy in *Kniphofia* (Baijnath, 1980) and other asphodelaceous genera such as *Bulbine* (Baijnath, 1977; Baijnath, 1992b; Baijnath and Cutler, 1993; Ramdhani, 2002), *Aloe* (Brandham and Cutler, 1978; Carter *et al*., 1984; Smith and van Wyk, 1992), *Haworthia* (Cutler, 1978; Smith *et al*., 1996), *Poellnitzia* (Smith and van Wyk, 1992) and *Chortolirion* (Smith and van Wyk, 1992; Smith *et al*., 1996).

The above studies have shown that leaf anatomy can be used in conjunction with other sources of evidence to understand relationships. Baijnath (1980) examined the leaf anatomy of 18 species of *Kniphofia* and two natural hybrids (*K. citrina* X *K. uvaria* and *K. evansii* X *K. porphyrantha*). It was found that hybrids inherit some leaf surface characters from both parents (Baijnath, 1980). Vascular bundles and crystals were of particular interest. Anatomical data did not support the segregate genus *Notosceptrum* (Baijnath, 1980). Baijnath's (1980) study also provided additional support for the creation of a separate species status for the V-shaped leaf form of *K. northiae*, which was later described as *K. albomontana* (Baijnath, 1987). However, juveniles of *K. northiae* have a V-shaped leaf (personal observation).

In the development and execution of this study the focus was to determine phylogenetic relationships using DNA sequence data. At the initial stages of this project it was suggested that leaf anatomical studies may also be useful in understanding relationships. Consequently, anatomical studies were initiated to find characters from both the leaf surface and transverse sectional anatomy that will be informative in determining phylogenetic relationships. Initial attempts to analyse leaf surface characters phylogenetically was of limited use as there was intra-specific variation and specimens did not group into morphologically based species, a result also obtained for the cpDNA study (Ramdhani *et al.*, 2006). It was decided to attempt a phenetic approach to establish if anatomical characters can define species-specific clusters. Anatomical studies were thus done to determine variation between populations of the same species as well as between species. Anatomical findings were then contextualised in terms of the phylogenetic and phylogeographic frameworks based on DNA sequence data and builds upon on the initial work by Baijnath (1980). A detailed descriptive anatomical account is not provided due to the limitations imposed by time and the confusing results.

5.2. Materials and Methods

5.2.1. Sampling

Most of the leaf samples used for anatomical studies were collected from the field. A list of samples used is provided in Table 5.1. Leaf portions were selected at a standard level, midway between the base and apex of mature leaves [following Baijnath (1980)]. Fresh material was fixed in FAA (Formalin-Acetic-Alcohol; 85 parts 70% alcohol: 10 parts 40% formaldehyde: 5 parts acetic acid) for at least 24 hours. Leaves were also fixed in 50% ethanol depending on availability of fixative. In some instances herbarium material was used (see below).

Table 5.1. List of specimens used for anatomical studies. Locality and data pertaining to groups based on DNA sequence data from the *trnT-L* spacer are included. Additional details for collectors, localities, herbaria and additional abbreviations are given in Table 3.3. (Chapter 3).

Taxon	**Voucher (abbreviation)**	**Locality**	***trnT-L* spacer group**	**Leaf Surface: SEM**	**Leaf TS: LM**
K. acraea	TD 4626	Mountain Zebra National Park	5	X	X
K. albescens	SR & JB 314	Dirkiesdorp	4	X	X
K. angustifolia	SR 542	Cathedral Peak Nature Reserve	4	X	-
K. angustifolia	SR 453	Cathedral Peak Nature Reserve	4	X	X
K. ankaratrensis	PBP 5676	Madagascar	3	X	-
K. baurii	SR 174	Humansdorp	4	X	X
K. baurii	SR 275	Elands Heights	4	X	-
K. baurii	SR 285	Naudes Nek	4	X	X
K. baurii	SR 360	Port Elizabeth	4	-	X
K. baurii	NPB 1923	Alicedale	4	-	X
K. brachystachya	SR *sn*	Estcourt	2	X	X

Table 5.1. continued

Taxon	**Voucher (abbreviation)**	**Locality**	***trnT-L* spacer group**	**Leaf Surface: SEM**	**Leaf TS: LM**
K. breviflora	SR 452	Oliviershoek Pass	4	X	X
K. breviflora	SR *sn*	Greytown	-	X	-
K. bruceae	SR & NPB 171	Komga	4	X	X
K. buchananii	SR & BT 305	Greytown	4	-	X
K. buchananii	SR & BT 307	Greytown	4	X	X
K. buchananii	SR 458	Howick	4	-	X
K. caulescens	SR 270	Elands Heights	5	X	X
K. caulescens	SR 278	Naudes Nek	5	-	X
K. citrina	SR 176	Humansdorp	2	X	X
K. coddiana	SR *sn*	Umtamvuna Nature Reserve	4	X	X
K. coddiana	RAL 4820	Mkambati	-	-	X
K. coralligemma	SR 549	Iron Crown (Wolkberg)	1	X	X
K. drepanophylla	RJM 1100	Mkambati	4	X	X

Table 5.1. continued

Taxon	**Voucher (abbreviation)**	**Locality**	***trnT-L* spacer group**	**Leaf Surface: SEM**	**Leaf TS: LM**
K. ensifolia subsp. *ensifolia*	JB *sn*	Witbank	4	X	X
K. ensifolia subsp. *autumnalis*	SR 448	Harrismith	4	X	X
K. fibrosa	SR & AR 297	Pervensey	4	-	X
K. fibrosa	PBP 5579	Dohne Hill	5	X	X
K. fluviatilis	SR *sn*	Verloren Vallei	-	X	X
K. foliosa	JMG 034	Sebese Washi, Ethiopia	3	X	-
K. galpinii	SR 312	Long Toms Pass, Lydenberg	4	X	X
K. gracilis	SR & HB 321	Durban	4	X	X
K. gracilis	SR 308	Arhens	-	X	X
K. grantii	CP 4154	Nyika Plateau, Malawi	2	X	-
K. hirsuta	SR 282	Naudes Nek	4	X	X
K. ichopensis var. *ichopensis*	SR 242	Nottingham Road	4	X	X

Table 5.1. continued

Taxon	**Voucher (abbreviation)**	**Locality**	***trnT-L* spacer group**	**Leaf Surface: SEM**	**Leaf TS: LM**
K. ichopensis var. *ichopensis*	SR 241	Rosetta	-	-	X
K. ichopensis var. *ichopensis*	SR 409	Michaelhouse	4	-	X
K. insignis	SR *sn*	Tatek, Ethiopia	3	X	-
K. insignis	Teklehymanot 30 (= TT30) (ETH)	Lege Shekole, Ethiopia	-	X	-
K. isoetifolia	JMG 033	Bale Mountains, Ethiopia	-	X	-
K. latifolia	RSS *sn*	Greytown	4	X	X
K. laxiflora form B	SR 295	Kamberg Nature Reserve	4	X	X
K. laxiflora form B	SR 253	Himeville	-	X	X
K. laxiflora form B	SR 441	Nottingham Road	4	-	X
K. laxiflora form B	SR 442	Michaelhouse	4	-	X
K. laxiflora form B	SR 468	Weza	4	-	X
K. laxiflora form C	SR *sn*	Wakkerstroom	4	-	X

Table 5.1. continued

Taxon	**Voucher (abbreviation)**	**Locality**	***trnT-L*** **spacer group**	**Leaf Surface: SEM**	**Leaf TS: LM**
K. sp. cf. laxiflora	*SR 283*	Naudes Nek	4	-	X
K. leucocephala	NNBG	Richards Bay	4	X	X
K. linearifolia	SR 182	Knysna	-	X	X
K. linearifolia	SR 151	Michaelhouse	-	X	X
K. linearifolia	SR 170	Komga	-	X	X
K. linearifolia	SR 269	Hogsback (Seymour)	5	X	X
K. linearifolia	SR 287	Loskop	4	X	X
K. linearifolia	SR 290	Rosetta	4	X	X
K. linearifolia	SR 291	Kamberg Nature Reserve	4	X	X
K. linearifolia	SR & JB 311	Lydenberg	4	X	X
K. linearifolia	SR 328	Mt. Currie Nature Reserve	4	X	X
K. linearifolia	SR 343	Hogsback (Seymour)	5	X	X
K. linearifolia	SR 400	Mooi River	4	X	X
K. linearifolia	J Pote *sn*	Stutterheim	4	X	X
K. littoralis	SR & HB 200	Silverglen Nature Reserve	4	X	X

Table 5.1. continued

Taxon	**Voucher (abbreviation)**	**Locality**	***trnT-L* spacer group**	**Leaf Surface: SEM**	**Leaf TS: LM**
K. multiflora	SR & JB 310	Lydenberg	4	X	X
K. northiae	SR 263	Hogsback (Seymour)	5	X	X
K. northiae	SR 274	Naudes Nek	5	-	X
K. parviflora	SR 268	Hogsback (Seymour)	5	X	X
K. parviflora	SR 330	Mt. Currie Nature Reserve	4	-	X
K. pauciflora	HB *sn*	Durban	4	X	X
K. porphyantha	SR *sn*	Verloren Vallei	4	X	X
K. praecox	SR 529	Jefferys Bay	2	X	X
K. praecox	TD 4461	Katberg	-	X	X
K. pumila	Friss *et al.* 1079 (ETH)	Kebre Mengist, Ethiopia	-	X	-
K. rigidifolia	SR *sn*	Lydenberg	4	X	X
K. ritualis	SR 300	Pervensey	4	X	X
K. rooperi	SR 237	East London	5	X	X
K. rooperi	SR *sn*	Cape Recife	-	X	-

Table 5.1. continued

Taxon	**Voucher (abbreviation)**	**Locality**	***trnT-L* spacer group**	**Leaf Surface: SEM**	**Leaf TS: LM**
K. sarmentosa	SR 207	Hex River Pass	2	X	X
K. schimperi	JMG 036	Sebsebe Washe, Ethiopia	3	X	-
K. splendida	SR 548	Haenertsberg	1	X	X
K. stricta	SR 279	Rhodes	4	X	X
K. thodei	SR 407	Kamberg Nature Reserve	4	X	X
K. thomsonii	JMG 031	Senatti Plateau, Ethiopia	3	X	-
K. thomsonii	AAM 2647	Mt. Elgon, Kenya	3	X	-
K. thomsonii	CK 4821	Mt. Kilimanjaro, Tanzania	3	X	-
K. triangularis subsp. *triangularis*	SR 264	Hogsback (Seymour)	5	X	X
K. triangularis subsp. *triangularis*	SR 266	Hogsback (Seymour)	5	X	X
K. triangularis subsp. *triangularis*	SR 299	Pervensey	4	X	X
K. triangularis subsp. *triangularis*	SR 267	Hogsback (Seymour)	-	X	X

Table 5.1. continued

Taxon	**Voucher (abbreviation)**	**Locality**	***trnT-L* spacer group**	**Leaf Surface: SEM**	**Leaf TS: LM**
K. triangularis subsp. *triangularis*	SR 304	Hogsback (Seymour)	-	X	X
K. triangularis subsp. *obtusiloba*	SR *sn*	Kemps Heights	4	X	X
K. typhoides	JB 8084	Witbank	-	X	X
K. tysonii subsp. *tysonii*	SR 302	Creighton	4	-	X
K. tysonii subsp. *tysonii*	SR 199	Leisure Bay	-	X	X
K. tysonii subsp. *tysonii*	SR 303	Highflats	4	X	X
K. tysonii subsp. *tysonii*	SR 460	Balito	4	-	X
K. umbrina	R Gama *sn*	Forbes Reef, Swaziland	4	X	X
K. uvaria	SR 165	Glen Rosa	-	X	
K. uvaria	SR 166	Port Elizabeth	2	-	X

Table 5.1. continued

Taxon	**Voucher (abbreviation)**	**Locality**	***trnT-L* spacer group**	**Leaf Surface: SEM**	**Leaf TS: LM**
K. uvaria	SR & NPB 172	Post Wellington	5	X	X
K. uvaria	SR 186	Kurlandsdorp	2	X	X
K. uvaria	SR 201	Cape St. Francis	2	X	X
K. uvaria	SR 203	Elim	2	X	X
K. uvaria	SR 211	Clarkson	2	X	X
K. uvaria	SR 337	Hogsback (Seymour)	5	X	X
K. uvaria	SR 342	Hogsback (Seymour)	5	X	X
K. uvaria	SR 344	Grahamstown	4	X	X
K. uvaria	SR 471	Dimbaza	5	X	X
K. uvaria	SR 477	Grahamstown	4	X	X
K. uvaria	TD 4477	Port Elizabeth	2	X	X

The anatomical studies concentrated on southern African material as this area is the most speciose and most of the field work was done in this area. Every attempt was made to use the same samples as those of the DNA studies for both leaf transverse sectional (TS) and scanning electron microscopy (SEM) studies to build complementary data sets. This approach allows for the detection of genetic and anatomical similarity. Due to time constraints it was not possible to process all of the DNA samples anatomically. Consequently three well sampled species (*K. linearifolia*, *K. uvaria* and *K. triangularis*) which displayed non-monophyly based on the *trnT-L* spacer (Chapter 3) were chosen for extensive anatomical sampling.

Some herbarium samples from regions other than southern Africa were also included for scanning electron microscopy. Transverse sectional studies were not possible for these herbarium samples, as these did not re-hydrate satisfactorily.

5.2.2. Preparation of transverse sections for light microscopy (LM)

Samples were placed in 50% alcohol for 12 hours irrespective of prior fixation. Samples were then dehydrated through a series of tertiary butanol: 10%, 25%, 35%, 55% and 75% (12 hours each), and 100% (twice for 12 hours each), after which they were treated with a liquid parafin:tertiary butanol (1:1) mix and 100% liquid parafin (12 hours each). Samples were kept on a hot plate at c. 40°C from the 55% tertiary butanol to the 100% liquid parafin stage. Final infiltration was achieved with a liquid parafin:paraplast wax (1:1) mix (12 hours) and pure paraplast wax (thrice for 12 hours each). The liquid parafin:paraplast wax (1:1) mix and pure paraplast wax treatments were done in an oven at 60ºC.

Wax blocks were made with the samples embedded within. These blocks were trimmed and mounted for sectioning. Transverse sections were cut at 15µm using a steel blade on a Minot rotary microtome (Leitz Wetzlar). Sections were collected and carefully placed into bath of warm water and mounted onto a glass slide with Haupt's Adhesive and left in an oven to dry overnight. Sections were then conventionally stained with Safranin and Fast Green. Mounted sections were treated with xylol (twice for five minutes each) and a mixture of xylol:absolute ethanol (1:1) for three minutes. Thereafter slides were placed in a decreasing series of ethanol: 100%, 95% and 70% (three minutes each). Slides were left in Safranin for 12 hours to stain. Slides were placed in 70% and 90% ethanol (one minute each), dipped for five seconds in ammoniacal alcohol and placed in 100% ethanol (twice for two minutes each). Slides were stained with Fast Green for 10-15 seconds, rinsed in clove oil for 30 seconds and dipped in mixture of clove oil, absolute ethanol and xylol for five seconds. Slides were then treated with xylol (thrice, two minutes each). Permanent slides were made using Canada Balsam mountant. Slides were labeled and dried in an oven at 50ºC for five to seven days. Measurements for light microscopy (LM) were done with a graticule.

5.2.3. Preparation of leaf surface samples for SEM

Leaf portions were selected at standard levels (see above) and cut into manageable pieces. Samples were then dehydrated through a gradually increasing series of ethanol. Samples were finally dehydrated in dry alcohol (twice for 15 minutes each), and then critical point dried.

Leaves samples were mounted on brass stubs with conductive tape and sputter coated with gold. Gold coated samples were examined using a JOEL JSM840 Scanning Electron Microscope and photographed. To aid in interpretation, photographs were taken with the longitudinal axis of the leaf parallel to that of the screen. In an effort to maintain consistency and comparability leaves were photographed in the same region i.e. the central regions between the margin and keel in keeled samples. In triangular samples with no distinct keel, photographs were taken in the central region between one of the adaxial margins and the lower abaxial margin. In samples that were U-shape in outline, photographs were taken in the central region between the margin and the medial axis of the leaf. Care was taken to photograph regions between veins for standardised comparisons. Magnifications of SEM micrographs were recorded as a scale bar by the instrument.

Baijnath (1977), Baijnath and Cutler (1993) and Ramdhani (2002) found that the leaf surfaces were usually similar on both surfaces in *Bulbine*. However, Baijnath (1980) found that in *Kniphofia* this was the exception rather than the norm. It was therefore deemed necessary to examine both surfaces for variation. Differences in adaxial and abaxial surfaces increases the range of possible characters. Smith and van Wyk (1992) reported different infra-specific patterning on adaxial and abaxial surfaces especially in the *Chortolirion* and *Aloe bowiea*. Based of the above findings it is recommended that both leaf surfaces should be examined in Asphodelaceae.

5.2.4. Phenetic analysis

Anatomical characters (both TS and SEM) were selected and coded for phenetic analysis. The systematic anatomical work of Baijnath (1980) for *Kniphofia* was very detailed despite the small number of taxa examined, and his anatomical terminology well defined. There was no need to re-define the terminology used by Baijnath (1980), which is followed in this study to assist in interpretation and for standardised comparisons. A few additional comments are discussed below.

Characters pertaining to vascular bundles (VBs), especially medial VBs, were selected and coded from mature well developed bundles for standardised comparisons. Two characters that were apparent in the SEM micrographs were not included in the SEM data set: the position of the stomata on both the adaxial and abaxial surfaces, which were better interpreted from TS slides.

Sixty-five characters from leaf TS studies were selected and coded. The characters and coding scheme is given in Table 5.2., while the data matrix is given in Appendix 13.

Table 5.2. Transverse sectional (TS) leaf anatomical characters and characters states for *Kniphofia.*

	CHARACTER: character state
1	Leaf outline: 0= U-shaped, 1=V-shaped, 2= triangular
2	V-shaped leaf angle: 0= <90°, 1= 90°, 2= >90°
3	V-shaped leaf flange: 0= absent, 1= present
4	Mid-axial groove: 0= absent, 1= present
5	Adaxial stomata position: 0= superficially sunken, 1= sunken
6	Central mesophyll strip pronounced: 0= no, 1= yes
7	Vascular bundles distributed equi-distance from leaf surface: 0= no, 1=yes
8	Vascular bundles distributed between chlorenchyma & central mesophyll: 0= no, 1= yes
9	Vascular bundles distributed in alternate pattern: 0= no, 1= yes
10	Keel vascular bundle pronounced: 0= no, 1= yes
11	Marginal vascular bundle pronounced: 0= no, 1= yes
12	Transverse bridging vascular bundles: 0= absent, 1= present
13	Mid-adaxial vascular bundle: 0= absent, 1= present
14	Keel vascular bundle xylem more or less with T-shaped outline: 0= no, 1= yes
15	Keel vascular bundle xylem with stem of T pointing inwards: 0= no, 1= yes
16	Marginal vascular bundle xylem more or less with T-shaped outline: 0= no, 1= yes
17	Marginal vascular bundle xylem with stem of T pointing inwards: 0= no, 1= yes
18	Medial vascular bundle xylem more or less with T-shaped outline: 0= no, 1= yes
19	Medial vascular bundle xylem with stem of T pointing inwards: 0= no, 1= yes
20	Keel vascular bundle phloem outline: 0= T-shaped, 1= triangular, 2= rectangular
21	Keel vascular bundle phloem with stem of T away from xylem: 0= no, 1= yes
22	Keel vascular bundle phloem with stem of T reduced: 0= no, 1= yes
23	Marginal vascular bundle phloem outline: 0= T-shaped, 1= triangular, 2= rectangular
24	Marginal vascular bundle phloem with stem of T away from xylem: 0= no, 1= yes
25	Marginal vascular bundle phloem with stem of T reduced: 0= no, 1= yes
26	Medial vascular bundle phloem outline: 0= T-shaped, 1= triangular, 2= rectangular
27	Medial vascular bundle phloem with stem of T away from xylem: 0= no, 1= yes
28	Medial vascular bundle phloem with stem of T reduced: 0= no, 1= yes
29	Keel vascular bundle outer bundle sheath: 0= absent, 1= present
30	Keel vascular bundle outer bundle sheath composed of one layer of parenchyma cells: 0= no, 1=yes
31	Marginal vascular bundle outer bundle sheath: 0= absent, 1= present
32	Marginal vascular bundle outer bundle sheath composed of one layer of parenchyma cells: 0= no, 1=yes
33	Medial vascular bundle outer bundle sheath: 0= absent, 1= present
34	Medial vascular bundle outer bundle sheath composed of one layer of parenchyma cells: 0= no, 1= yes
35	Keel vascular bundle inner bundle sheath: 0= absent, 1= present
36	Keel vascular bundle inner bundle sheath complete: 0= no, 1= yes
37	Keel vascular bundle inner bundle sheath with inner and outer (2) sclerenchyma caps: 0= no, 1=yes
38	Keel vascular bundle inner bundle sheath with inner sclerenchyma caps having more cell layers than outer cap: 0= no, 1= yes

Table 5.2. continued

	CHARACTER: character state
39	Marginal vascular bundle inner bundle sheath: 0= absent, 1= present
40	Marginal vascular bundle inner bundle sheath complete: 0= no, 1= yes
41	Marginal vascular bundle inner bundle sheath with inner and outer (2) sclerenchyma caps: 0= no, 1= yes
42	Marginal vascular bundle inner bundle sheath with inner sclerenchyma caps having more cell layers than outer cap: 0= no, 1= yes
43	Medial vascular bundle inner bundle sheath: 0= absent, 1= present
44	Medial vascular bundle inner bundle sheath complete: 0= no, 1= yes
45	Medial vascular bundle inner bundle sheath with inner and outer (2) sclerenchyma caps: 0= no, 1= yes
46	Medial vascular bundle inner bundle sheath with inner sclerenchyma caps with more cell layers than outer cap: 0= no, 1= yes
47	Keel vascular bundle with parenchyma cells at xylem pole thickened: 0= no, 1= yes
48	Marginal vascular bundle with parenchyma cells at xylem pole thickened: 0= no, 1= yes
49	Medial vascular bundle with parenchyma cells at xylem pole thickened: 0= no, 1= yes
50	Raphide crystals present in chlorenchyma: 0= absent, 1= present
51	Keel vascular bundle with tannin cells present at xylem poles: 0= no, 1= yes
52	Keel vascular bundle with tannin cells present at phloem poles: 0= no, 1= yes
53	Marginal vascular bundle with tannin cells present at xylem poles: 0= no, 1= yes
54	Marginal vascular bundle with tannin cells present at phloem poles: 0= no, 1= yes
55	Medial vascular bundle with tannin cells present at xylem poles: 0= no, 1= yes
56	Medial vascular bundle with tannin cells present at phloem poles: 0= no, 1= yes
57	Adaxial stomata position: 0= superficially sunken, 1= sunken
58	Epidermal cells of keel apex thickened: 0= no, 1= yes
59	Epidermal cells of margin apex thickened: 0= no, 1= yes
60	Keel vascular bundle with tannin cells pronounced: 0= no, 1= yes
61	Margin vascular bundle with tannin cells pronounced: 0= no, 1= yes
62	Epidermal cells above mid-adaxial vascular bundle thickened: 0= no, 1= yes
63	Leaf folded upwards in marginal region: 0= no, 1= yes
64	Two marginal bundles present: 0= no, 1= yes
65	Abaxial medial vascular bundles usually larger than adaxial medial vascular bundles: 0= no, 1= yes

Seventeen characters were selected and coded from leaf SEM micrographs for phenetic analysis. The characters and coding scheme is given in Table 5.3., while the data matrix is given in Appendix 14. The individual data sets were combined which resulted in a total of 82 characters.

The TS and SEM data sets were analysed individually using NT-SYS version 2.0. (Rohlf, 1998). A similarity matrix was generated using the Simple Matching (SM) co-efficient and clustering was performed using the UPGMA (Unweighted Pair Group Method, Arithmetic Average) clustering method. Third character states were analysed with the default setting of NT-SYS version 2.0. The SM co-efficient and UPGMA clustering was used as this is a basic approach to determine if further analysis is required and to gain insights into the data. A principle component analysis was done on data sets using NT-SYS. These did not show conflict with the tree plots (phenograms). Thus data were not analysed further by using variable co-efficients and different clustering methods due to the limiting nature of the data. Matching samples for both leaf TS and SEM data sets were used to construct a combined data set, which was analysed as above. The topology of phenograms (separate and combined analyses) were reconstructed using MacClade version 4.06 (Maddison and Maddison, 2000) to trace the distribution of characters.

Table 5.3. Scanning electron microscopy (SEM) leaf anatomical characters and characters states for *Kniphofia.*

	CHARACTER: character states
1	Leaf surface dimorphism: 0= no, 1= yes
2	Adaxial epidermal cell shape: 0= rectangular, 1= polygonal
3	Abaxial epidermal cell shape: 0= rectangular, 1= polygonal
4	Adaxial longitudinal striae: 0= absent, 1= present
5	Adaxial transverse striae: 0= absent, 1= present
6	Abaxial longitudinal striae: 0= absent, 1= present
7	Abaxial transverse striae: 0= absent, 1= present
8	Adaxial papillae: 0= absent, 1= present
9	Abaxial papillae: 0= absent, 1= present
10	Adaxial stomatal rim: 0= absent, 1= present
11	Abaxial stomatal rim: 0= absent, 1= present
12	Adaxial trichomes: 0= absent, 1= present
13	Abaxial trichomes: 0= absent, 1= present
14	Adaxial wax: 0= absent, 1= sparse, 2= pronounced
15	Abaxial wax: 0= absent, 1= sparse, 2= pronounced
16	Adaxial papillae fused: 0= no, 1= yes
17	Abaxial papillae fused: 0= no, 1= yes

5.3. Results

5.3.1. Sampling

A total of 94 leaf samples representing 43 species for *Kniphofia* from southern Africa were sectioned. Five South African (SA) species were not sectioned due to lack of material. These were *K. albomontana*, *K. evansii, K. tabularis, K. flammula* and *K. crassifolia*. The sample of *K. albomontana* (SR 149) used in the DNA studies was collected prior to the commencement of this study so anatomical material was not collected for this species at that time. It was also decided not to use herbarium material of *K. evansii, K. tabularis, K. flammula* and *K. crassifolia* for the SEM studies as they were not included in the genetic studies.

A total of 91 leaf samples were processed for SEM studies representing a total of 51 species of *Kniphofia* (43 species for *Kniphofia* from southern Africa and eight from other parts of Africa and Madagascar). Herbarium material was used for: *K. ankaratrensis* (PBP 5676), *K. foliosa*, (JMG034), *K. grantii* (CP 4154), *K. insignis* (TT 30, SR *sn*), *K. isoetifolia* (JMG 033), *K. pumila* (Friss *et al*. 1079), *K. schimperi* (JMG 036) and *K. thomsonii* (JMG 031, CK 4821, AMM 2647). Most of these specimens had DNA sequence data available except for *K. insignis* (TT 30), *K. isoetifolia* (JMG 033) and *K. pumila* (Friss *et al*. 1079).

It was possible to obtain both TS and SEM data for a total of 75 complementary samples representing 43 species from southern Africa. Sixty-four of these samples also had DNA sequence data for the *trnT-L* spacer. Forty-one species (from SA) had complementary samples for the two anatomical and the cpDNA data sets. These samples represented all four of the *trnT-L* spacer lineages from southern Africa.

5.3.2. Characters

Several leaf anatomical characters (from both TS and SEM) warrant additional comments when compared with the study of Baijnath (1980). These may be an additional source of leaf anatomical characters.

5.3.2.1. Leaf TS anatomy

Leaf margin prickles were not considered in this study. Only a small number of sections were made per sample in this study. This meant that even when present the likelihood of detection was minimised. These were also not always apparent in the SEM study as the larger leaves had to be trimmed to fit mounting stubs. However, leaf surface macro-hairs were included.

Raphide crystals (Fig. 5.1.A.) were not given detailed attention here. Baijnath (1980) found that both fine and large raphides were present in the genus *Kniphofia* in contrast to other asphodelaceous genera and considered them to be of particular interest. These crystals are probably composed of calcium oxalate. Only large raphides were present in the related genus *Bulbinella* (Baijnath, 1980) while only fine raphides occur in the genus *Bulbine* (Baijnath, 1977; Baijnath and Cutler, 1993). Raphides occur as idioblasts in the chlorenchyma of *Chortolirion*, but in *Poellnitzia* and *Aloe* they are scattered in the chlorenchyma (Smith and van Wyk, 1992). The occurrence of different types of raphides may be more significant for delimitations at the generic level. In the present study crystals were fairly common in chlorenchyma as prismatic/rectangular and needle forms and were recorded as present or absent. The fine needle like crystals are probably raphides while the larger prismatic/rectangular forms are styloids (Prychid and Rudall, 1999). This requires further investigation as they may be useful systematic markers in *Kniphofia* and/or other related genera. No crystals were observed in the outer bundle sheath as reported by Baijnath (1980) and consequently these were not considered in this study.

Furthermore only a small number of sections were made per sample, this meant that even when present the likelihood of detecting these crystals were minimised. However, raphides require further investigation (Baijnath, 1980).

The order of VBs were not examined in this study. However, for comparative purposes, characters of medial bundles were selected and coded from large, mature and well developed bundles (Fig. 5.1.D. & E.). Botha *et al.* (1982) noted that in grasses so-called bundle orders and sizes intergrade with intermediate forms existing. Little is known about the development and functioning of VBs of different sizes and this aspect that requires further investigation in *Kniphofia*. Transverse bridging vascular bundles are not always apparent. Only a small number of sections were made per sample, this meant that even when present the likelihood of detecting these were minimised. The outline of phloem poles in mature VBs were not observed as a strictly inverted ‘T-shape’ (Baijnath, 1980), but either as a triangular or rectangular in outline (Fig. 5.1.E.).

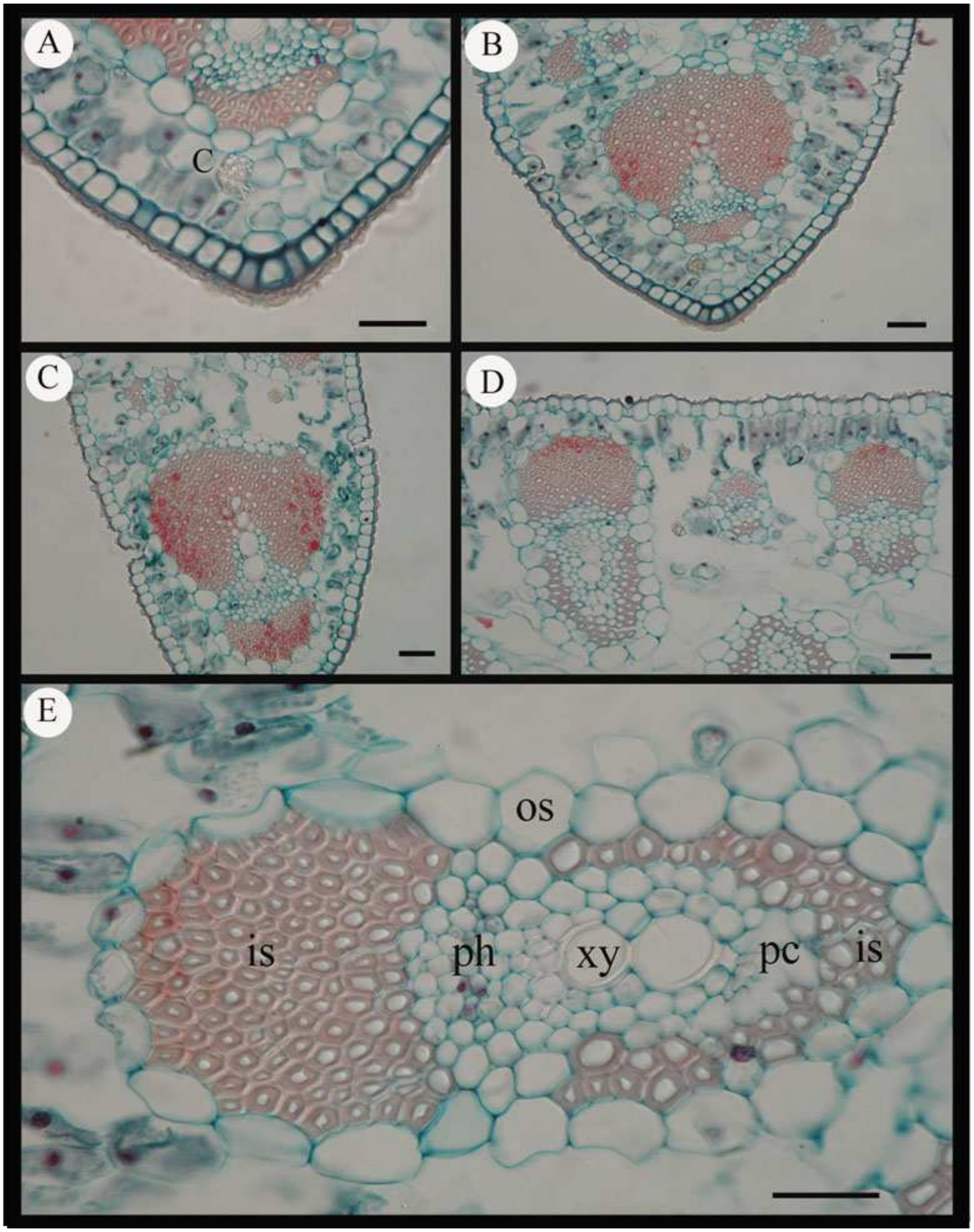


Fig. 5.1. Leaf transverse section of *K. laxiflora* (SR 295). A. raphide crystal (C). B. keel vascular bundle. C. marginal vascular bundle. D. medial vascular bundles. E. mature medial vascular bundle in detail (is= parts of inner sclerenchyma bundle sheath, os= outer parenchyma bundle sheath, pc= parenchyma cells, ph= phloem, xy= xylem) (all scale bars= 100µm).

5.3.2.2. Leaf SEM anatomy

Light microscopy studies on leaf surfaces were not done due to time limits. This was unfortunate as this method does have some merits as it allows for a more detailed examination of leaf surface structures and features less precisely inferred by SEM such as epidermal cell shape and outline. Also the sample size is much reduced as SEM images only cover a small area of the leaf surface depending on the magnification at which the image was captured. All images were taken at the lowest magnification of 300X with only a limited number of cells in full view in some cases. Longitudinal and transverse anticlinal walls cannot be examined in detail from SEM micrographs and the stomata type and position are difficult to determine accurately from SEM imagery. The above mentioned details are more suitable to interpret if SEM is used in conjunction with LM (Fig. 5.2.A & B).

Despite the limitations of SEM noted above it is an important and useful tool for inferring characters not visualised by LM. Some features may be too small to be detected by light microscopy or do not show up well in transmitted light. On the other hand there are other features more suited to examination and measurement by SEM (Arora *et al*., 1982) e.g. wax distribution and striations in *Kniphofia*. In *Kniphofia* wax crystals occur as distinct or irregular particles or flakes (Baijnath, 1980). Leaf surface wax (using SEM) was not examined in great detail in this study. Wax was coded as absent, sparse (Fig. 5.2.C.) or pronounced (Fig. 5.2.D.). This is a problematic character as not all samples were fixed in the same manner. Samples were either fixed in FAA or 50% ethanol depending on availability of fixative. Ideally for such comparisons material should be preserved and processed in exactly the same manner to make standardised comparisons. Additionally differences in wax distribution and amount could be due to developmental difference (e.g. leaf age) or it could be affected by environmental factors. Wax features may be of diagnostic significance but this aspect will require further investigation.

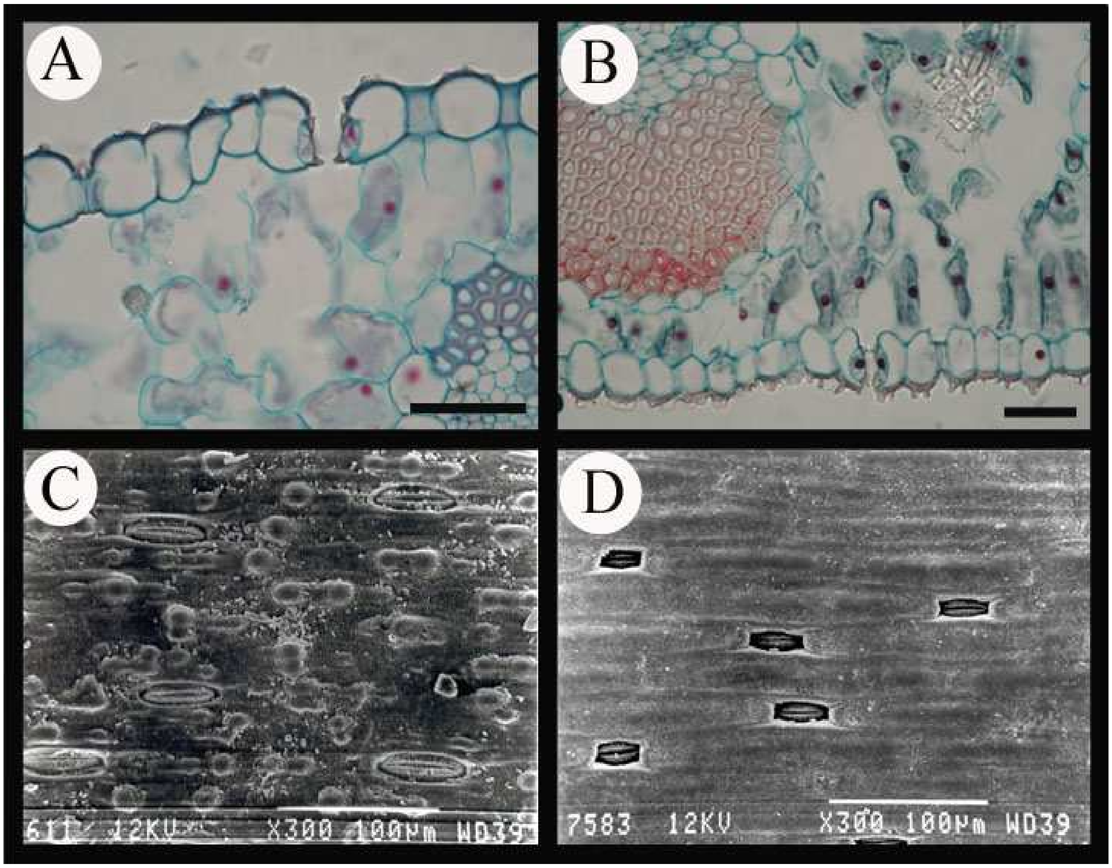


Fig. 5.2. A. leaf transverse section of *K. linearifolia* (SR 287) showing adaxial sunken stomata. B. leaf transverse section of *K. laxiflora* (SR 295) showing abaxial superficially sunken stomata. C. SEM micrograph of adaxial leaf surface of *K. linearifolia* (SR 269) showing wax crystals. D. SEM micrograph of adaxial leaf surface of *K. galpinii* (SR 312) showing lack of wax crystals (all scale bars= 100µm).

The leaf surface permutations regarding striae and papillae mentioned by Baijnath (1980) were not considered. These permutations were not coded and analysed as they would result in numerous combinations that are difficult to code and interpret. It would also entail the replication of individual characters that would require re-coding depending on the combined nature of the permutation and may be a source of conflict. Instead individual characters that contribute to the permutations were coded separately.

5.3.3. Leaf TS phenetic analysis

The phenogram derived for the leaf TS data is shown in Fig. 5.3. The analysis and discussion below will concentrate on species with multiple samples, as these would be expected to cluster together in groups.

Sixteen species had multiple samples for the TS study. These where *K. linearifolia* (n= 12), *K. uvaria* (n= 12), *K. triangularis* (n= 6), *K. tysonii* subsp. *tysonii* (n= 3), *K. laxiflora* (n= 7), *K. praecox* (n= 2), *K. fibrosa* (n= 2), *K. gracilis* (n= 2), *K. ichopensis* var. *ichopensis* (n= 3), *K. northiae* (n= 2), *K. parviflora* (n= 2), *K. buchananii* (n= 3), *K. caulescens* (n= 2), *K. baurii* (n= 2), *K. ensifolia* (n= 2) and *K. coddiana* (n= 2). Details of these samples are given in Table 5.1.

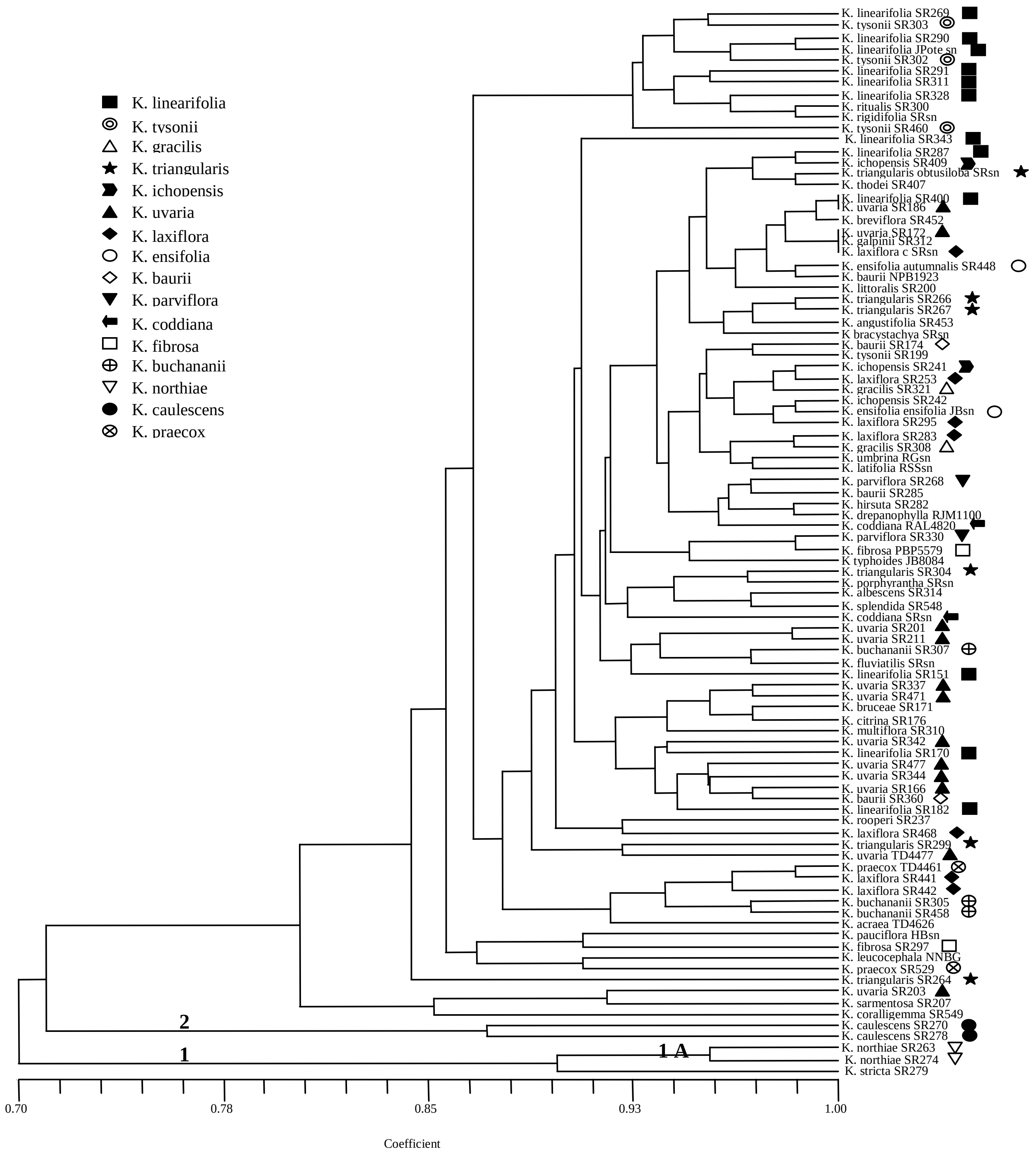


Fig. 5.3. UPGMA phenogram based on leaf TS characters. Clusters of significance are shown numerical on the phenogram (discussed in text). Symbols indicate morphological species of *Kniphofia*.

The phenogram shows structure but anatomical characters failed to recover species-specific groups. Specimens of only two species, *K. northiae* [Cluster 1A (SR 263 and SR 274)] and *K. caulescens* [Cluster 2 (SR 270 and SR 278)] clustered (Fig. 5.3.). There was also no correspondence to the four lineages recovered by the *trnT-L* spacer from southern Africa. Additionally the clusters did not show any geographic structure, except for *K. northiae* and *K. caulescens* (discussed later). Similarly, none of the nested clades (Chapter 4) correspond to the leaf TS based clusters irrespective of the level of nesting.

5.3.4. Leaf SEM phenetic analysis

The phenogram for the leaf SEM analysis is shown in Fig. 5.4. Thirteen species had multiple samples for this study. These where *K. linearifolia* (n= 12), *K. uvaria* (n= 12), *K. triangularis* (n= 6), *K. gracilis* (n= 2), *K. tysonii* subsp. *tysonii* (n= 2), *K. baurii* (n= 3), *K. angustifolia* (n= 2), *K. breviflora* (n= 2), *K. laxiflora* (n= 2), *K. ensifolia* (n= 2), *K. rooperi* (n= 2), *K. praecox* (n= 2) and *K. thomsonii* (n= 3).

Structure was observed in the phenogram but no species-specific clusters were recovered. The major clusters based on the phenetic analysis of SEM characters do not correspond to the five lineages recovered by the *trnT-L* spacer and did not show any geographic structure. Furthermore, none of the nested clades (Chapter 4) correspond to the leaf SEM based clusters irrespective of the level of nesting.

5.3.5. Combined leaf TS and SEM phenetic analysis

The phenogram for the combined analysis is shown in Fig. 5.5. Nine species had multiple samples for the combined analysis. These were *K. linearifolia* (n= 12), *K. uvaria* (n= 11), *K. triangularis* (n= 6), *K. tysonii* subsp. *tysonii* (n= 2), *K. gracilis* (n= 2), *K. praecox* (n= 2), *K. ensifolia* (n= 2), *K. laxiflora* (n= 2) and *K. baurii* (n= 2).

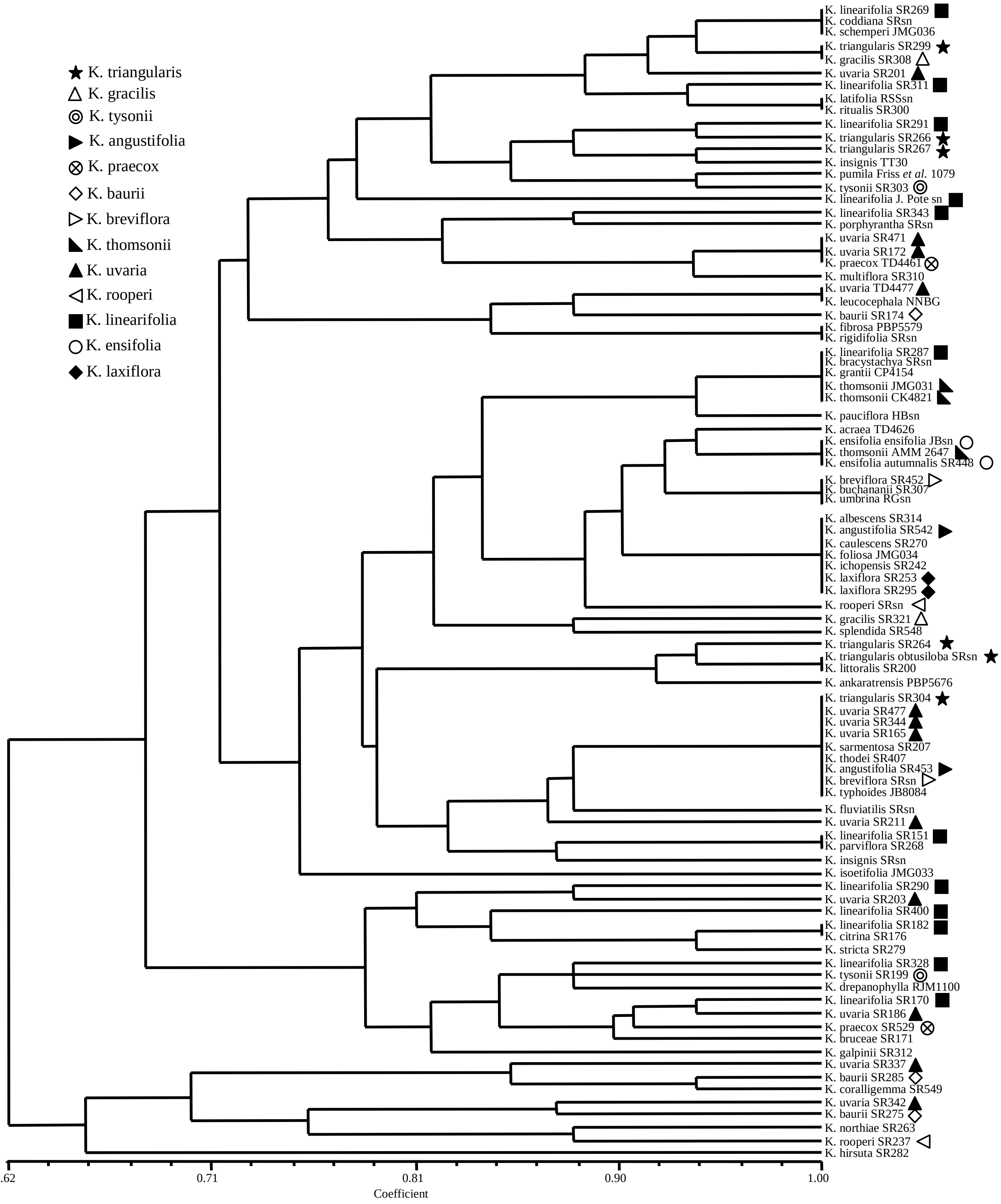


Fig. 5.4. UPGMA phenogram based on leaf SEM characters. Symbols indicate morphological species of *Kniphofia*.

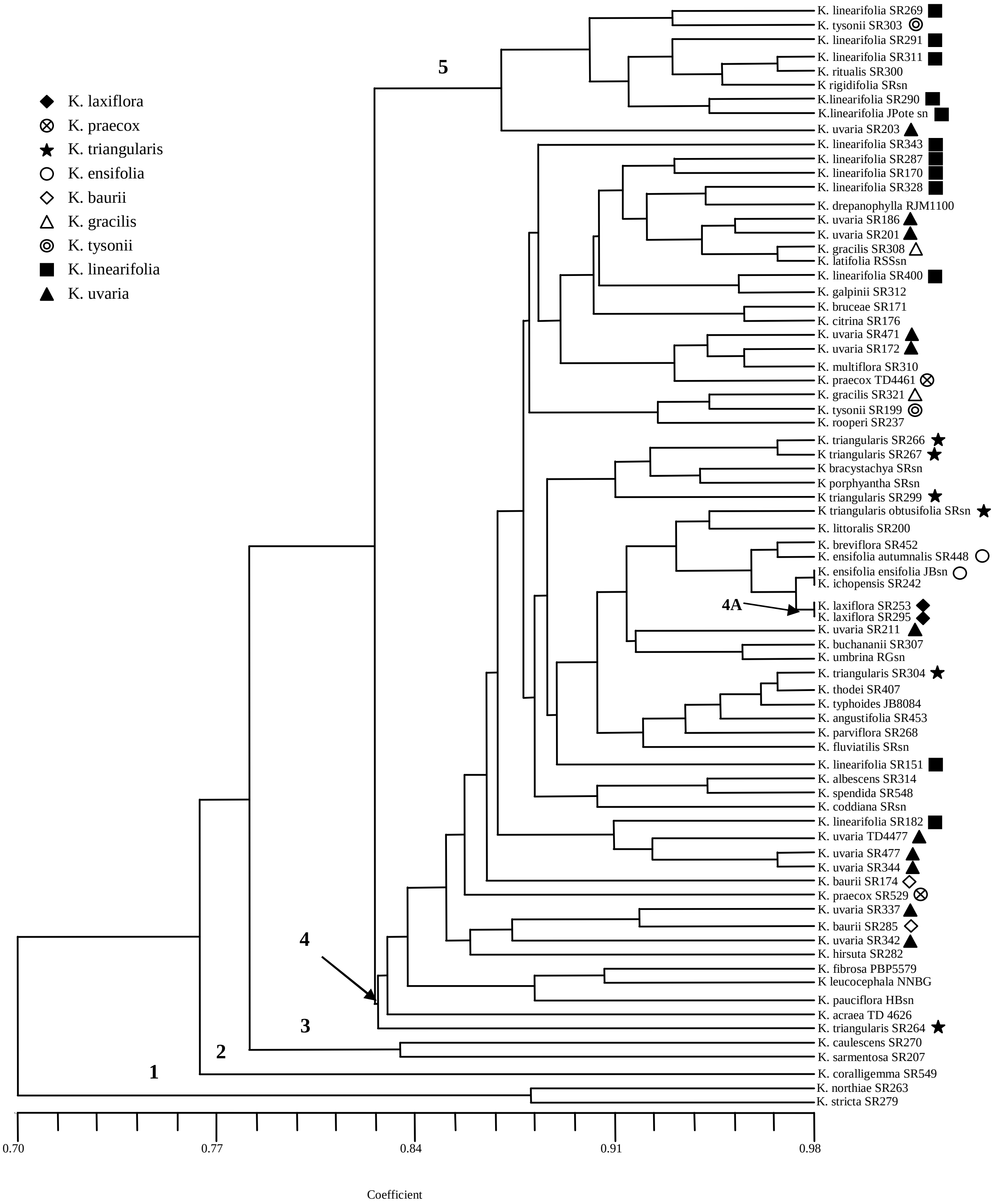


Fig. 5.5. UPGMA phenogram based on combined leaf TS and SEM characters. Clusters are shown numerical on the phenogram (discussed in text). Symbols indicate morphological species of *Kniphofia*.

Once again there was much structure in the phenogram but no species-specific clusters were recovered. *K. laxiflora* was the only species where multiple samples clustered into a group (Fig. 5.5., Cluster 4A). It is also worth noting that five of the nine samples in Cluster 5 (Fig. 5.5.) are *K. linearifolia*.

The major clusters of the combined analysis did not correspond to the four southern African lineages recovered by the *trnT-L* spacer and no geographic structure was apparent. Also none of the nested clades (Chapter 4) correspond to the leaf TS and SEM based clusters irrespective of the level of nesting.

5.3.6. Characters that define clusters

Despite the overall inability of the leaf anatomical characters used in this study to cluster morphological species, it is worth mentioning the characters that define major clusters and/or morphological species.

5.3.6.1. Leaf TS anatomy

No leaf TS anatomical characters exclusively defined the main clusters except the clusters designated as Cluster 1 and Cluster 2 (Fig. 5.3.). Cluster 2 [*K. caulescens* (SR 270 and SR 278)] was exclusively defined by a single character viz. the absence of the marginal vascular bundle inner bundle sheath (Fig. 5.6.A.).

Cluster 1 [*K. stricta* (SR 279) and *K. northiae* (SR 263 and SR 274)] was exclusively defined by one character, a U-shaped transectional outline (Fig. 5.6.B.). None of the leaf TS anatomical characters exclusively defined the *K. northiae* cluster (Fig. 5.3., Cluster 1A).

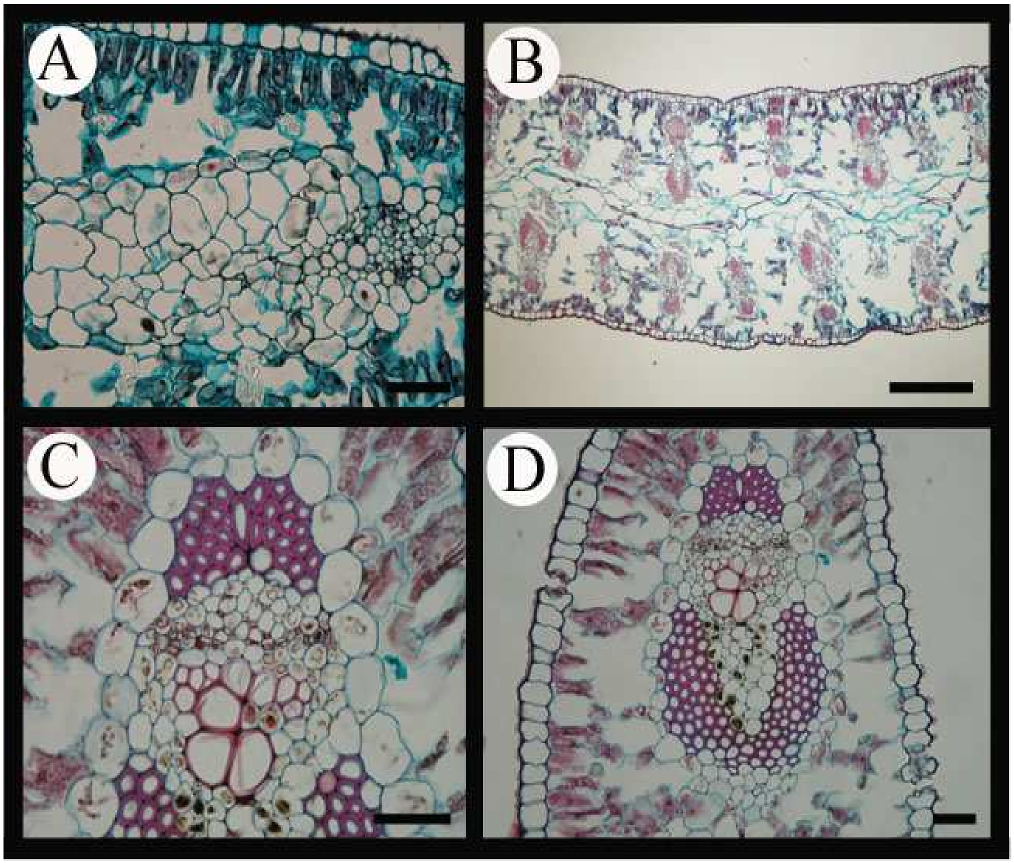


Fig. 5.6.A. leaf transverse section of *K. caulescens* (SR 270) showing the absence of the marginal vascular bundle inner bundle sheath. B. leaf transverse section of *K. northiae* (SR 263) in central region with no keel i.e. a U-shaped transectional outline. C. leaf transverse section of marginal vascular bundle of *K. coralligemma* (SR 549) with tannin cells present at the phloem pole. D. leaf transverse section of marginal vascular bundle of *K. coralligemma* (SR 549) with tannin cells present at the phloem and xylem pole (all scale bars= 100µm, except 5.5.B. scale bar= 1mm).

5.3.6.2. Leaf SEM anatomy

No leaf surface anatomical characters defined any of the main clusters.

5.3.6.3. Combined TS and SEM anatomy

No characters exclusively defined the main clusters designated as Cluster 5, Cluster 4 and Cluster 3 in the combined analysis (Fig. 5.5.). Cluster 2 was composed only of the single sample of *K. coralligemma* (SR 549) i.e. is not a strict cluster. It was exclusively defined by three characters: tannin cells present at the phloem pole of keel, margin and medial vascular bundles (Fig 5.6.C.). The importance of tannin cells at the phloem pole is uncertain. Baijnath (1980) found difficulty in interpreting the bundle sheaths in *Kniphofia*. An exact designation for larger parenchyma cells at the xylem poles is not clear. In *Bulbine* these cells are not filled with tannin as displayed by some species of *Kniphofia* (Baijnath, 1977; Baijnath and Cutler, 1993). Baijnath (1980) recorded that in *Kniphofia* tannins are found mostly in the parenchyma of vascular bundles towards the xylem poles and occasionally at the phloem poles (Fig 5.6.D.). He suggested that these tannin containing cells at the xylem pole might be a third bundle sheath or represent the inwards development of xylem parenchyma. He favored the latter explanation because phloem parenchyma cells between the tracheids and the conductive phloem also contain tannins and secondly the parenchyma cap cells towards the xylem poles in the bundles are heavily thickened and continuous with the inner sclerenchyma bundle sheath (Baijnath, 1980).

Cluster 1 (Fig. 5.5.) was composed of *K. stricta* (SR 279) and *K. northiae* (SR 263). It was exclusively defined by one character, a U-shaped transectional outline. The only taxa with more than one sample that clustered as a single species based on combined TS and SEM anatomy was *K. laxiflora* (Cluster 4A, n= 2), but no characters exclusively defined this grouping.

The results above indicate extensive anatomical variation within *Kniphofia* species. To further illustrate this, *K. uvaria*, which was well sampled is used below. Leaf surface SEM micrographs are shown as these are the easiest graphical means of depicting extensive variation (Fig. 5.7. & Fig. 5.8.). Only the abaxial surfaces are shown, as Baijnath (1980) found that the abaxial surface in *Kniphofia* is much more useful than the adaxial surface (discussed below).

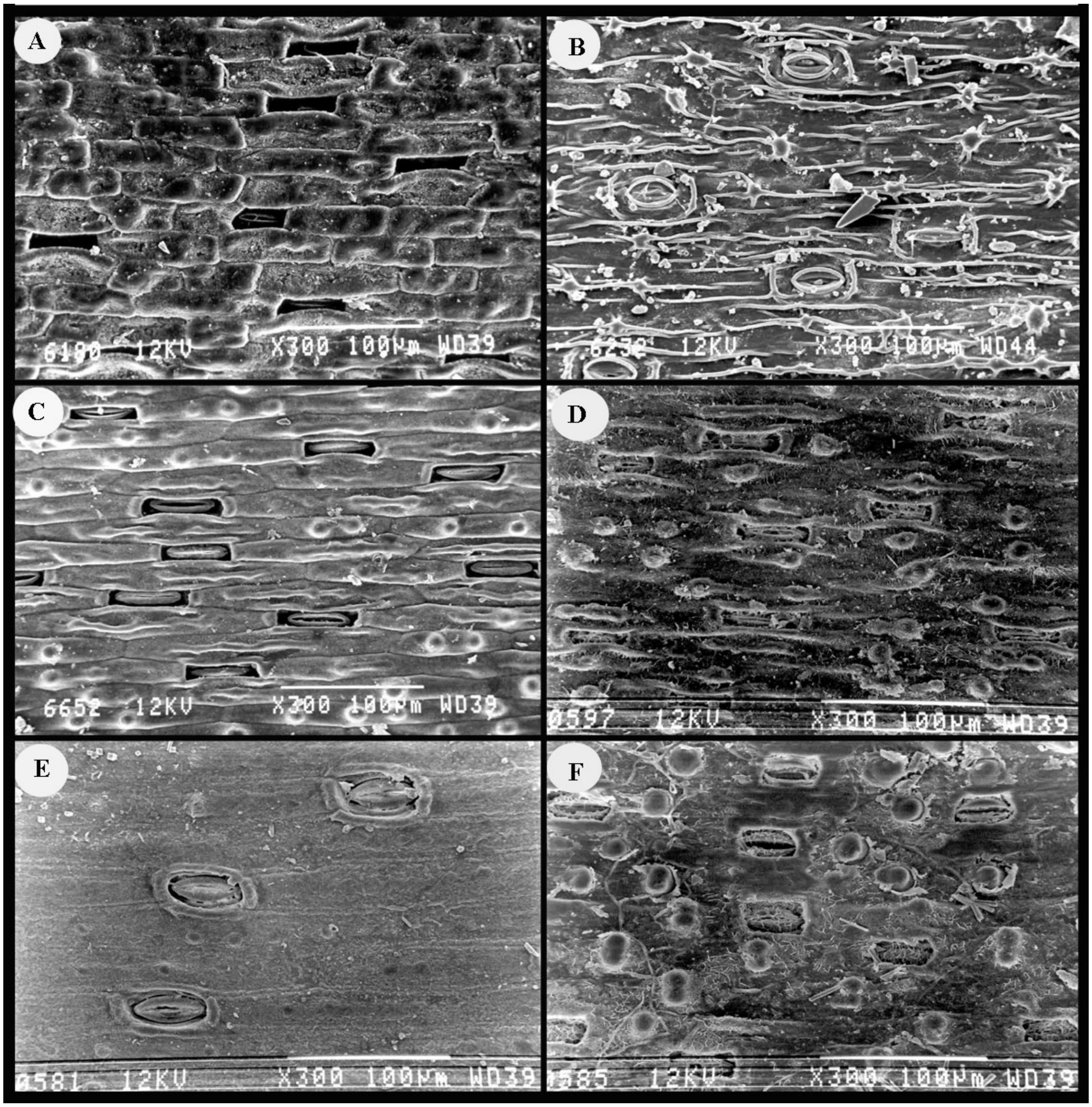


Fig. 5.7. SEM micrographs showing abaxial leaf surface variation in *K. uvaria.* A. SR 165. B. SR 172. C. SR 186. D. SR 201. E. SR 203. F. SR 211.

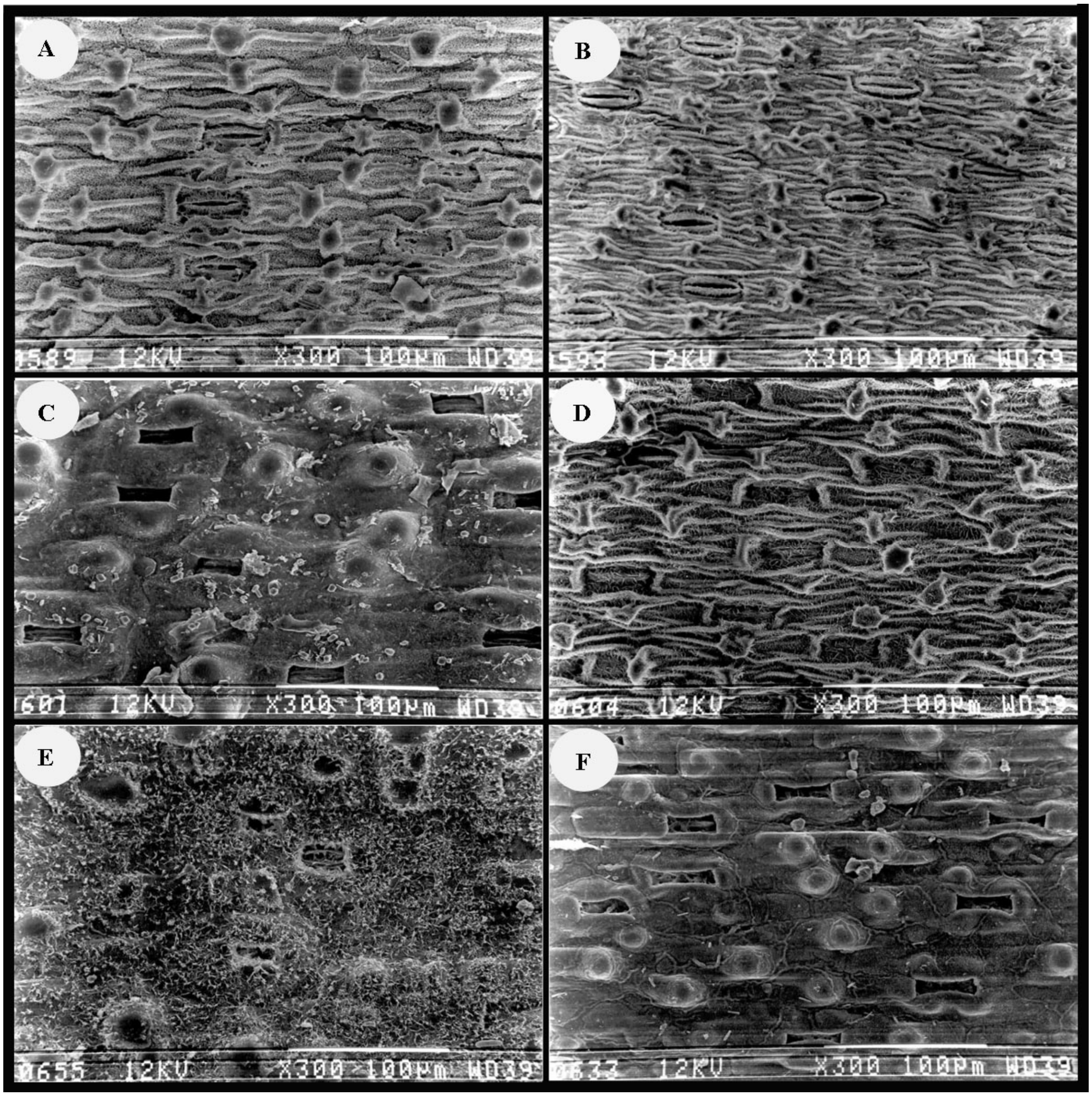


Fig. 5.8. SEM micrographs showing abaxial leaf surface variation in *K. uvaria*. A. SR 337. B. SR 342. C. SR 344. D. SR 471. E. SR 477. F. TD 4477.

The SEM micrographs show that the abaxial surfaces of *K. uvaria* represented by SR 337, SR 342 and SR 471 (Fig. 5.8.A., B. and D. respectively) compare favorably. SR 471 is from Dimbiza while SR 337 and SR 342 are from Hogsback (separate populations). Dimbiza and

Hogsback are in close geographic proximity and this may be reflected anatomically. Also, the abaxial surfaces of *K. uvaria* represented by SR 344 and TD 4477 (Fig. 5.8.C. and F. respectively) compare favorably. SR 344 is from Grahamstown while TD 4477 is from Port Elizabeth. Grahamstown and Port Elizabeth are in reasonably close geographical proximity and this may be reflected anatomically. The similarities discussed above are not reflected in clusters of the phenetic analysis (Fig. 5.4.). This is because adaxial characters, which are not considered above, were included in the phenetic analysis.

5.3.7. Comparison with Baijnath's (1980) results

Baijnath (1980) found that the abaxial surface in *Kniphofia* exhibits much more richness and complexity in ornamentation than the adaxial surface and emphasised the need for a routine examination of both surfaces. In this study it was found that in seven species (specimen sample size= 7 i.e. one sample per species) the adaxial surface was more complex in ornamentation than the abaxial surface. In 26 species (specimen sample size= 37) the adaxial surface and abaxial surface were more or less similar. In 25 species (specimen sample size= 47) the abaxial surface exhibited more complexity. These results are difficult to consolidate as there is much variation in the leaf surface within a morphological species and several species are found in more than one of the three delimited categories above. However, when the results are compared on a sample basis, free of taxonomic structure, the abaxial surface is generally more complex.

Baijnath (1980) in most cases did not use multiple samples for most *Kniphofia* species examined. However, he did examine three accessions of *K. linearifolia* and *K. uvaria*, and reported intra-specific leaf surface patterning variation. Baijnath (1980) did not provide detailed descriptive anatomical treatments for the species he examined, but his results were presented as a generalised anatomical account. He did provide several SEM plates of leaf surfaces, mostly of abaxial surfaces that make comparisons possible.

Some of the samples (five) examined by Baijnath (1980) were from herbarium material. In reconstructing herbarium material, wall dehydration and shrinkage and subsequent hydration may introduce artifacts making comparisons difficult. Furthermore tilt angles differ which gives a different topological impressions of the leaf surface sculpturing. However, comparisons with Baijnath's (1980) results and the result for this study were possible. *K. tysonii* subsp. *lebomboensis*, *K. albomontana*, *K. flammula* and *K. evansii* could not be compared because of lack of material. Baijnath (1980) did not supply SEM micrographs of *K. ensifolia* subsp. *ensifolia* and *K. parviflora,* and the images of *K. hirsuta* are of low magnification and unsuitable for comparisons.

The following taxa below examined by Baijnath (1980) do not compare favorably with the results of this study for abaxial leaf surface anatomy (SEM). Comparisons and comments on locality data, when possible to trace, are also included.

1. *K. northiae*. Codd *sn* [examined by Baijnath (1980)] has papillae absent, with no superficially sunken stomata. SR 263 (this study) has papillae present with superficially sunken stomata. *K. northiae* is a wide ranging species and the locality data for Codd *sn* could not be traced. Thus it is not possible to comment on geographic proximity in relation to anatomy.
2. *K. praecox*. Codd 9965 [examined by Baijnath (1980)] has papillae present, longitudinal striae are absent and the stomata have a distinct rim. TD 4461 (this study) has papillae present, numerous longitudinal striae present and no stomatal rim. SR 529 (this study) has papillae present, longitudinal striae are present and no stomatal rim. *K. praecox* is a wide ranging species with a complex and confusing taxonomy (Chapter 1). Codd 9965 was collected in Pretoria and is presumed to be a garden escape as it collected out of its natural range i.e. the locality data is dubious. Thus it is not possible to comment on geographic proximity in relation to anatomy. However, TD 4461 and SR 529 (this study) do not compare favorably. TD 4461 originates from Port Elizabeth and SR 529 from Jefferys Bay.

3. *K. sarmentosa*. Oliver 4420 [examined by Baijnath (1980)] has papillae present and longitudinal striae are present. SR 207 (this study) has papillae present and longitudinal striae are absent. *K. sarmentosa* has a fairly restricted distribution in the Cape Region, however, the locality data for Oliver 4420 could not be traced. Thus it is not possible to comment on geographic proximity in relation to anatomy.
4. *K splendida*. Admiraal 2227 [examined by Baijnath (1980)] has papillae present, longitudinal striae are present and the stomata have no distinct rim. SR 548 (this study) has papillae present, longitudinal striae are present and the stomata have a distinct rim. *K splendida* is a wide ranging species and the locality data for Admiraal 2227 could not be traced. Thus it is not possible to comment on geographic proximity in relation to anatomy.
5. *K. tysonii* subsp. *tysonii*. Codd 9364 [examined by Baijnath (1980)] has papillae present, longitudinal striae are present and the stomata are not superficially sunken. SR 303 (this study) has papillae absent, longitudinal striae are present and the stomata are not superficially sunken. SR 199 (this study) has papillae present, longitudinal striae are present and the stomata appear superficially sunken. *K. tysonii* subsp. *tysonii* is a wide ranging species. Codd 9364 was collected from Port Shepstone, SR 303 from Highflats and SR 199 from Leisure Bay. These regions are fairly close proximity, however, this is not reflected anatomically.
6. *K. baurii*. Codd 6797 [examined by Baijnath (1980)] has papillae present and longitudinal striae are present. SR 174 (this study) has indistinct papillae and longitudinal striae are absent. SR 275 and SR 285 (this study) have papillae present and longitudinal striae are present. SR 275 and SR 285 (this study) compare favorably but the micrograph for Codd 6797 [examined by Baijnath (1980)] covers a small area and is difficult to compare with SR 275 and SR 285 in detail. *K. baurii* is a wide ranging species. Codd 6797 was collected from Nqutu, SR 174 from Jefferys Bay, while SR 275 and SR 285 originate from the Naudes Nek region. SR 275 and SR 285 appear to reflect geographic proximity anatomically.

7. *K. gracilis*. Baijnath *sn* [examined by Baijnath (1980)] has papillae present, no longitudinal striae observed and stomata with a distinct rim. SR 308 and SR 321 (this study) has papillae present, longitudinal striae are present and no distinct stomatal rim, but in SR 308 the papillae are more dense. *K. gracilis* is a fairly restricted species but the locality data for Baijnath *sn* could not be traced. Thus it is not possible to comment on geographic proximity in relation to anatomy. However, SR 308 and SR 321 are from Arhens and Durban respectively which are fairly close geographically but this is not reflected anatomically.
8. *K. brachystachya.* Killick and Vahrmeijer 3630 [examined by Baijnath (1980)] has papillae present, no longitudinal striae were observed and stomata have a rim-like structure (indistinct rim). *K. brachystachya* SR *sn* (this study) has papillae present, no longitudinal striae and no distinct stomatal rim. *K. brachystachya* is a fairly restricted species. Killick and Vahrmeijer 3630 originates from Highmoor while *K. brachystachya* SR *sn* was collected near Escourt. These areas are fairly close geographically but this is not reflected anatomically.
9. *K. citrina*. Strey *sn* [examined by Baijnath (1980)] has papillae present, longitudinal striae are absent and the stomata appear superficially sunken. SR 176 (this study) has papillae present which appear to be fused, longitudinal striae are absent and the stomata appear superficially sunken. *K. citrina* is a fairly restricted species but the locality data for Strey *sn* could not be traced. Thus it is not possible to comment on geographic proximity in relation to anatomy.

The following taxa below examined by Baijnath (1980) compare favorably with the leaf surface anatomy results of this study.

1. *K. pauciflora*. Samples were similar abaxially in both studies. The plants of both studies were obtained from the same population at the Clairwood Race Course (Durban), which is the only known living wild population.

2. *K. linearifolia.* The abaxial surface of Marias 1021 [examined by Baijnath (1980)] does not match any of the samples of this study. Codd *sn* [examined by Baijnath (1980)] resembles SR 290 (this study) for the adaxial surface but not other *K. linearifolia* samples of this study. Furthermore, the abaxial surface of Codd *sn* [examined by Baijnath (1980)] does not resemble *K. linearifolia* samples used in this study. Locality data for Codd *sn* could not be traced. Thus it is not possible to comment on geographic proximity in relation to anatomy. Bruce 553 [examined by Baijnath (1980)]) has a similar adaxial surface to the adaxial surface of SR 269 and SR 287 (this study). Additionally the abaxial surface of Bruce 553 [examined by Baijnath (1980)] is similar to SR 269, SR 287 and SR 343 (all *K. linearifolia,* this study). Bruce 553 is from Keiskammahoek, SR 269 and SR 343 are from Hogsback while SR 287 is from Loskop (KwaZulu-Natal). Keiskammahoek and Hogsback are in close proximity which Bruce 553, SR 269 and SR 343 appears to reflect anatomically.
3. *K. uvaria.* SEM micrographs were not provided by Baijnath (1980) for Admiraal 1001 and Hanekom 2175. Bruce 232 [examined by Baijnath (1980)] is abaxially similar to SR 201 (this study). Bruce 232 originated from Atherstone (Albany District) while SR 201 was from Cape St Francis. These regions are in relatively close proximity which appears to be reflected anatomically.
4. *K. porphyrantha*. Baijnath *sn* [examined by Baijnath (1980)] is abaxially similar *to K. porphyrantha* (SR *sn,* this study). *K. porphyrantha* is a wide ranging species and the locality data for Baijnath *sn* could not be traced. Thus it is not possible to comment on geographic proximity in relation to anatomy.
5. *K. ensifolia* subsp. *autumnalis.* Van der Haasse *sn* [examined by Baijnath (1980)] compares well with SR 448 (this study) except that SR 448 has numerous wax crystals. *K. ensifolia* subsp. *autumnalis* is a restricted but locality data for Van der Haasse *sn* could not be traced. It appears that the close proximity of these samples are reflected anatomically except for wax crystals.

5.4. Discussion

The comparative exercise with Baijnath's (1980) results and results of this study indicate that leaf surface anatomical variation within morphological defined species of *Kniphofia* is much greater than has been detected by either study.

Studies on several monocot groups in which multiple samples have been used, show that leaf anatomy is conservative at the species level. Botha *et al.* (1982) found that internal anatomy in *Themeda triandra* (Poaceae) from three different climatic zones were similar. Ellis (1983a) found that in *Lintonia nutans* (Poaceae) leaf anatomy was conservative. Baijnath (1988) reported that the leaf anatomy of *Gloriosa superba*, *Sandersonia auranica* and *Littonia modesta* (Colchicaceae) did not show intra-population differences. Newton (1972) examined the relief markings on the abaxial surface of some *Aloe spp*. from West Africa and found that clones of *A. buettneri* and *A. macrocarpa* var. *major* were similar in their patterns. In *A. schweinfurthii* a basic pattern could be discerned but there was some variation in leaf surface ornamentation. Whilst intra-specific variation is evident, general patterns were recognised with multiple sampling (Newton, 1972). Baijnath and Cutler (1993) found that in *Bulbine*, leaf surface characters were diagnostic mainly at the species level. Ramdhani (2002) demonstrated that in most taxa of the closely related broad-leaved *Bulbine* complex (*Bulbine alooides, B. brunsvigiaefolia, B. latifolia* and *B. natalensis*) little or no intra-specific anatomical variation was apparent using multiple samples.

However, some workers have found intra-specific leaf surface variation in asphodelaceous genera. Cutler (1978) showed that there are slight differences in leaf surface sculpturing in *Haworthia reinwardtii* var. *chalumnensis*. Triploids and tetraploid plants were distinguishable by means of leaf surface characters. These findings suggested that epidermal surface features were under genetic control. Cutler (1978) also found that glass-house grown plants of *Haworthia* *reinwardtii* var. *chalumnensis* retained their epidermal features when compared to field collected material. Leaf epidermal patterns have been found to be under genetic control in the some members of the Alooideae and environmental factors have little influence (Cutler and Brandham, 1977; Cutler, 1978; Brandham and Cutler, 1978). Carter *et al.* (1984) used a multidisciplinary approach to revise the *Aloe somaliensis* complex [*A. hemmingi*, *A. jucunda*, *A. peckii* and *A. somaliensis* with two varieties (*somaliensis* and *marmorata*)]. *A. jucunda* displayed leaf surface variation. Anatomical and biochemical evidence showed no difference between *A. somaliensis* var. *somaliensis* and *marmorata*, and the latter was not upheld. The anatomical and biochemical differences between *A. hemmingi* and *A. somaliensis* were considered to be minor, resulting in *A. hemmingi* being reduced to a synonym of *A. somaliensis*. Smith and van Wyk (1992) reported intra-specific variation in the abaxial leaf surface of *A. bowiea* from different localities.

In this study it was found that in *Kniphofia* morphologically delimited species exhibited substantial anatomical variation. The phenetic study of anatomical characters for individual and combined data sets showed that anatomical characters do not cluster specimens based on the morphological species classification. Furthermore, the results for the most part do not fit any geographic pattern nor do they reflect the cpDNA groups recovered by the *trnT-L* spacer (Chapter 3) or the nested clades (Chapter 4).

Two possible factors may account for these results: environmental conditions and hybridisation.

5.4.1. Environmental conditions

Anatomical variation and plasticity may be due to environmental conditions. Newton (1972) and Carter *et al.* (1984) did not discuss the possibility of environmental influences on their results (above). Smith and van Wyk (1992) reported intra-specific variation in the abaxial leaf surface of *A. bowiea* from different localities, but noted that stomatal elevation (sunken vs superficial) is not a reliable indication of xeromorphy, habitat or climate. This species is restricted to the Coega area (Eastern Cape) and the habitat and environmental factors for these populations are presumed to be very similar due to the restricted distribution range (Tony Dold, pers. comm.). Cutler (1978) showed that leaf surface sculpturing in *Haworthia reinwardtii* var. *chalumnensis* was under genetic control and environmental factors have little influence. This was also found to be the situation in the some members of the Alooideae (Cutler and Brandham, 1977; Cutler, 1978; Brandham and Cutler, 1978).

Baijnath (1980) did not discuss the reasons for intra-specific variation in *K. linearifolia* and *K. uvaria.* Many species of *Kniphofia* occur in marshy habitats. Baijnath (1980) found that *K. gracilis* and *K. citrina* from dry grasslands areas have deeply sunken stomata, while the other species he examined has superficially or slightly depressed stomata. According to Baijnath (1980) the depth of stomata may be a plastic character and could be influenced by habitat.

If environmental factors have a major influence on variation in the leaf anatomy of *Kniphofia*, it would be expected that samples (and species) in similar habitats and/or close proximity would experience similar environmental conditions and would cluster to some extent. It is reasonable to presume that such clustering would also show geographic or environmental patterns and structure. However, this was not observed in this study, apart from the few exceptions noted above when the results of this study was compared with that of Baijnath's (1980). Additionally a few more exceptions are noted below.

In the leaf TS study (Fig. 5.3.) only two clusters showed geographic and environmental structure: Cluster 3 [*K. caulescens* (SR 270 and SR 278)] and Cluster 4 [*K. stricta* (SR 279) and *K. northiae* (SR 263 and SR 274)]. Both the specimens of *K. caulescens* (SR 270 and SR 278) are from Naudes Nek and are exposed to similar environmental conditions in Afromontane grasslands. In Cluster 4, *K. stricta* (SR 279) and *K. northiae* (SR 274) were also from Naudes Nek, while *K. northiae* (SR 263) originated from Hogsback. These samples are exposed to similar environmental conditions of Afromontane grasslands.

In the leaf SEM study there was no geographic or environmental structure apparent. While in the combined analysis (Fig. 5.5.) *K. stricta* (SR 279, Naudes Nek) and *K. northiae* (SR 263, Hogsback) clustered together which may indicate the effect of environmental adaptation.

Despite the few possible exceptions, leaf anatomical variation does not seem to be influenced by geographical or environmental factors. Variation observed here may thus be under genetic control as reported for other members of the Asphodelaceae (e.g. Cutler and Brandham, 1977; Cutler, 1978; Brandham and Cutler, 1978).

5.4.2. Hybridisation

Hybridisation may result in intermediate morphology (Arora *et al.*, 1982; Coetzee *et al.*, 1994) although this is not always the case (Rieseberg, 1995). As already discussed (Chapter 3) in *Kniphofia*, hybridisation may explain the numerous cases of intermediate and intergrading morphology, and species complexes with extensive variation reported by Codd (1968, 2005) making certain species difficult to delimit morphologically. Incomplete or weak reproductive barriers in taxa of these complexes may promote hybridisation. Sympatry, shared pollinators and/or flowering phenology provides circumstantial evidence supporting hybridisation. Back-crossing could further complicate the issue.

In some studies, intermediate anatomy of leaf surfaces of both parents have been reported in hybrid progeny. These intermediate forms resulting from hybridisation are a potential source of variation. Hybrid material of *Heracleum amntegazzianum* (Apiaceae) and *H. sphondylium* had a leaf surface anatomy intermediate between both parents (Arora *et al.*, 1982). Coetzee *et al.* (1994) also used anatomical data along with other evidence to identify a natural hybrid between *Pelargonium tomentosum* (Geraniaceae) and *P. patulum* var. *patulum* which was intermediate between the two putative parents.

Cutler and Brandham (1977) showed that leaf surface characters were under genetic control in bigeneric hybrids combinations of *Aloe*, *Gasteria* and *Haworthia* (Alooideae). Normally the hybrid plants showed intermediate leaf surface sculpturing between the parents for a number of features. Sometimes new character states were apparent. Genetic control of papillae was also reported (Cutler and Brandham, 1977). Cutler (1978) suggested that in *Haworthia reinwardtii* var. *chalumnensis* epidermal surface features were under genetic control (discussed above). Brandham and Cutler (1978) found that hybrids between *Aloe rauhii* and *A. dawei* contained either numerical or structural chromosome aberrations. *A. rauhii* is diploid ($2n= 14$) while *A. dawei* is tetraploid ($2n= 28$). Majority of the crosses were triploids but the chromosomes of some hybrids plants differed with either numerical or structural chromosome mutations. Some of these mutations were shown to have a direct effect on leaf surface characteristics, while others had different effects or none. The results suggested that leaf surface features were under genetic control.

Baijnath (1980) examined two natural hybrids viz. *K. citrina* X *K. uvaria* and *K. evansii* X *K. porphyrantha.* He found that natural hybrids inherited some leaf anatomical characters from both parents. It must be stressed that these were not controlled crosses. Comparisons made by Baijnath (1980) were not made with the exact populations of putative parental species but rather with different accessions of putative parental species. Furthermore, as these were not controlled crosses, Baijnath (1980) was uncertain if the putative hybrids were plants of the F_1 generation or products of back-crossing. More detailed studies are required with controlled crossings. Thus, based on the variation found in this study, inferring anatomical patterns of inheritance is not recommended.

As noted above leaf epidermal patterns have been found to be under genetic control in some members of the closely related subfamily Alooideae and that environmental factors have little influence (Cutler and Brandham, 1977; Cutler, 1978; Brandham and Cutler, 1978). Similar studies which include a cyto-nuclear component are required to show this in *Kniphofia* (Baijnath, 1980). It will also be interesting to examine population/s of representative taxa to assess inter- and intra-population variation.

The DNA sequence data results may reflect the same phenomena influencing anatomical variation, viz. hybridisation. Hybridisation has been invoked by taxonomists that have worked on the genus (Codd, 1968, 2005; Marais, 1973). Several species that are non-monophyletic in the DNA study have all been implicated in hybridisation events and hybridisation has been used to explain the extensive non-monophyly in *Kniphofia* (discussed in Chapter 3). Additionally several of the same species do not cluster in phenetic studies based on leaf anatomy.

Only two species with multiple samples (*K. northiae* and *K. caulescens*) clustered based on leaf TS anatomy. Of the remaining taxa (with multiple samples) in this study, *K. linearifolia*, *K. uvaria*, *K. triangularis*, *K. tysonii*, *K. laxiflora*, *K. praecox*, *K. fibrosa*, *K. gracilis*, *K. ichopensis* var. *ichopensis*, *K. buchananii*, *K. baurii* and *K. ensifolia* have all been implicated in hybridisation events (discussed in Chapter 1). It is also worth noting that two species with multiple samples, *K. parviflora* and *K. coddiana*, that did not cluster have no major taxonomic problems or history of hybridisation.

In the leaf SEM phenetic analysis *K. linearifolia*, *K. uvaria*. *K. triangularis*, *K. gracilis*, *K. tysonii*, *K. baurii*, *K. angustifolia*, *K. ensifolia*, *K. breviflora*, *K. laxiflora*, *K. rooperi*, *K. praecox* and *K. thomsonii* did not cluster based on morphological delimitations. All of the above species, with the exception of *K. breviflora* have been implicated in hybridisation events (discussed in Chapter 1). *K. breviflora* does have some taxonomic problems. It shares a close relationship with *K. buchananii* and *K. albescens*, and at times specimens of *K. breviflora* are difficult to separate from *K. albescens* (discussed in detail in Chapter 1). Both *K. buchananii* and *K. albescens* were included in this study, but these three taxa did not cluster together (Fig.5.4.) and thus there are no indications of close affinities based on leaf surface characters.

In the combined TS and SEM phenetic study *K. linearifolia*, *K. uvaria*, *K. triangularis, K. tysonii* subsp. *tysonii*, *K. gracilis*, *K. praecox*, *K. ensifolia* and *K. baurii* did not group into morphological units. *K. laxiflora* was the only species that clustered based on leaf TS and SEM anatomy. All of the above species have been implicated in hybridisation events (discussed in Chapter 1).

5.5. Conclusion

Studies which have used multiple complementary exemplars of species for both DNA and anatomical data could not be found and so it is difficult to draw parallels. This study has shown that in southern African *Kniphofia* species leaf anatomy is highly variable for morphologically delimited species and leaf anatomy does not recover species specific-groups. Linder (1986) noted that anatomical evidence from a small number of samples should be treated with caution. Smith and van Wyk (1992) cautioned that taxonomic changes on the basis of leaf anatomy alone should be based on a representative range of samples. The findings of this study supports the cautionary statements of Linder (1986) and Smith and van Wyk (1992).

The anatomical variation does not seem to be influenced by environmental or habitat factors. Hybridisation seems to be a more likely explanation for the substantial anatomical variation in southern African *Kniphofia* species. Baijnath (1980) noted the need for detailed investigations of the species complexes within *Kniphofia* based on the anatomical differences in species such as *K. linearifolia* and the morphological variation reported by Codd (1968, 2005). Such studies will require extensive sampling over the entire distribution range to assess variation. Also because of hybridisation it may not be possible to explain all the variation by examining isolated complexes but will require a much broader approach.

Chapter 6: Discussion and Conclusion

6.1. Summary of Findings

The taxonomic literature on *Kniphofia* revealed that it has a complicated alpha taxonomy. There are numerous cases of intermediate and intergrading morphology, and species complexes with extensive variation.

Biogeographical and chorological analyses indicate that *Kniphofia* has six centres of diversity, five of these are regarded as centres of endemism. The South Africa Centre is the most species rich and also the largest centre of endemism. *Kniphofia* shows a strong Afromontane Grassland affinity in Tropical and East Africa but is occasionally found beyond the boundaries of the Afromontane vegetation. In South Africa it is found from high altitudes to coastal habitats but the most speciose regions for *Kniphofia* are Afromontane grasslands. It is thus not considered to be an Afromontane element, but rather an Afromontane associate.

Five major lineages were identified using cpDNA, four of which are southern African. The fifth lineage is represented by material from Madagascar, East and Tropical Africa. The nuclear marker failed to provide resolution as many sequences were identical. An intriguing result is that all of the species with multiple samples were resolved as non-monophyletic. This could be due to low sequence divergence, hybridisation and/or incomplete lineage sorting. The five lineages showed some congruence with geographic origin rather than the systematic arrangement based on morphology.

The phylogeographic study did not recover the same lineages as the phylogenetic analyses and should be regarded as preliminary. However, some interesting patterns were detected. In the NCA of SA samples one of the nested clades, Clade 3-1, showed allopatric fragmentation between Cape Region and parts of KZN and Mpumalanga. A pattern that points to fragmentation was also detected in the comparative analysis of the nest clades of the haplotype network (SA, East and Tropical African material) and the phylogenetic lineages. The other interesting pattern recovered was in Clade 3-2, which points to a range expansion in the Afromontane (Drakensberg) Region, the adjacent Drakensberg-Maputoland-Pondoland transition and the Maputoland-Pondoland Region. *Kniphofia* may have expanded its range in the recent past possibly the last glacial cycle. This range expansion may have been accompanied by a radiation.

Morphologically delimited species of *Kniphofia* also exhibited substantial leaf anatomical variation. Phenetic analyses showed that anatomical characters do not cluster species when represented by multiple samples. Furthermore, the anatomical results do not fit any geographic pattern nor do they reflect the cpDNA groups recovered by the *trnT-L* spacer or the nested clades of the phylogeographic study. With notably few exceptions, it appears that leaf anatomical variation is not influenced by geographical or environmental factors. Hybridisation may, however, play a role.

The findings above are unusual when compared to most systematic studies which generally find good correspondence with alpha taxonomy and other lines of evidence. In the case of *Kniphofia*, neither DNA sequence data nor leaf anatomy reflect the alpha taxonomy. Thus, the explanation for the results requires detailed consideration. How can these result be interpreted? It is suggested that the key to understanding and explaining these results lies in the past. Tectonic and climate changes can be invoked as the cause of the biogeographic patterns observed in the molecular data.

6.2. Tectonic Events

Generation of a biogeographical hypothesis requires an understanding of the nature, amplitude and timing of palaeo-environmental changes (Cowling, 1983a). The five groups recovered by the *trnT-L* spacer phylogeny shows some geographic structure. This seems to indicates that vicariance events fragmented *Kniphofia* into the five present lineages. The branch lengths and topology of the *trnT-L* spacer (cpDNA) phylogeny appear to indicate that the five groups have been isolated for a substantial amount of time and the events that resulted in these nodes are old. However, branch lengths, percentages of divergence and dating of such divergence are not available for the *trnT-L* spacer in the literature. Dating the phylogenies for *Kniphofia* is not possible as there is no fossil evidence for *Kniphofia*. Additionally, geological events cannot confidently be used to calibrate the phylogenies as the ages of the different Afromontane islands vary (White, 1983) and the phylogenies are not robust with some poorly supported nodes.

The interplay between landscape development and changing climates since the Cretaceous has had a major influence on the present soil and vegetation distribution in southern Africa. Planation of the African surface was complete by the end of the Cretaceous. After the planation, landscape development in southern Africa was characterised by fragmentation of habitats with successive pulses of uplift and dissection followed by successive cycles of erosion (Partridge, 1997). South Africa has experienced two major uplifts (Partridge and Maud, 1987). The first was at the end of the early Moicene (c. 18 MYA). The magnitude of the uplift was moderate (between 150-300 m) and resulted in a slight westward tilting of the African surface with limited monoclinal warping. The second uplift c. 2.5 MYA was major (up to 900 m) in the eastern marginal areas. This asymmetrical uplift of the subcontinent resulted in major westward tilting of the interior land surfaces. There was also monoclinal warping along the southern and eastern coast margins (Partridge and Maud, 1987). Over the same period climate changed dramatically culminating in major aridification c. 2.8 MYA. This was followed by the recurrent glacial-interglacial cycles of the Pleistocene. It is postulated that this latter period has had the most effect on *Kniphofia*.

According to Axelrod and Raven (1978) there were two episodes of rapid speciation in South Africa. The first commenced in the Miocene with the uplift of Africa. The inter-montane valley basins favoured open savanna grasslands at the expense of forest. The open systems expanded with aridity and many taxa originated in these areas (Axelrod and Raven, 1978). The massive post-Miocene diversification within a large number of lineages has produced a flock of closely related and ecologically uniform species and infra-specific taxa, which is unrivaled in the world (Cowling and Hilton-Taylor, 1997; Linder, 2005). The second burst of speciation resulted from Pliocene-Pleistocene deformation with accompanying fluctuation of climate. As the rim of southern Africa was elevated and the basins enveloped in the interior, the low areas became drier while the mountains wetter. Climate alternated between wetter and drier phases which shifted populations continuously (Axelrod and Raven, 1978). The tectonic events and/or the consequences of them may have fragmented an ancestral *Kniphofia* into the four southern Africa lineages and the Tropical and East Africa lineage, followed by a burst of speciation as suggested by Axelrod and Raven (1978).

The five lineages show evidence for fairly recent differentiation as the branch length within lineages are small and there is evidence for the non-monophyly of several species. The *ITS* results for *Kniphofia* show low sequence divergence which also supports a recent radiation (discussed in detail later) possibly due to more recent glacial-interglacial cycles.

6.3. Quaternary Climate Change

Apart from the Miocene and Pleistocene uplift events, Quaternary climate change had a major effect on the African vegetation and flora (Hedberg, 1970; Brenan, 1978; Goldblatt, 1978). Glacial cycles and climate changes have had a great influence on vegetation resulting in shifts in biome composition and boundaries. These shifts were due to fluctuations in temperature, precipitation and seasonal distribution of moisture (Scott *et al*., 1997).

The glacial-interglacial cycles are largely due to changes in solar oscillations i.e. Milankovitch cycles. These include eccentricity (variations of the Earth’s orbit around the Sun), obliquity (variations in the Earth’s tilt) and the precession of the equinoxes (Olago *et al*., 2000). These glacial-interglacial cycles have resulted in 100 000 year ice age cycles which define Quaternary climate change (Wunsch, 2004). These variations effect the Earth's surface temperature by altering latitudinal radiation reception with strong cyclic signals at periods of c. 95 800 years (eccentricity), 41 000 years (obliquity), and 23 000 and 19 000 years (precession). Solar radiation reception at low latitudes is mainly affected by variations in eccentricity and precession of the equinoxes, whereas higher latitudes are mainly affected by variations in obliquity (Olago *et al.*, 2000). These orbital parameters are not sufficient to account for the strength of the observed climatic signal. Intrinsic feedback mechanisms amplify extrinsic forcing. These include factors such as the extent of polar sheets, CO_2 concentration, changes in atmospheric circulation, displacement of wind belts and changes of moisture flux to continents (Olago *et al.*, 2000). Wunsch (2004) argued that stochastic behavior should also not be discounted in driving glacial-interglacial cycles. Despite these factors, Milankovitch cycle driven climate change has attracted much attention and support in explaining evolutionary history and distribution of species (Dynesius and Jansson, 2000; Jansson and Dynesius, 2002). It is important to note that glacial periods are generally long with shorter interglacials i.e. cold conditions persists for a longer time (Fig. 6.1.).

Also evident are millennial-scale high amplitude flickers during the late Pleistocene termed Dangaard-Oeschger (D-O) cycle oscillations (Roy *et al*., 1996). These are sudden rapid warming events (by 6-10 ºC) lasting a few decades followed by millennia of slow cooling periods to form a saw-tooth shaped time series. There is still no explanation for this occurrence (Rial, 2004). These cycles must have repeatedly de-stablised species interactions in communities. However, there is surprisingly little evidence for accelerated extinctions or speciation associated with extreme climate changes (for examples see Roy *et al*., 1996). The D-O cycles may have profound impacts on plants. Depending on the magnitude and nature of the climatic shifts, species that have not lived together previously may come into contact, conversely co-occurring species may become separated. These individual adjustments of species distributions are common in the Pleistocene record (Roy *et al*., 1996).

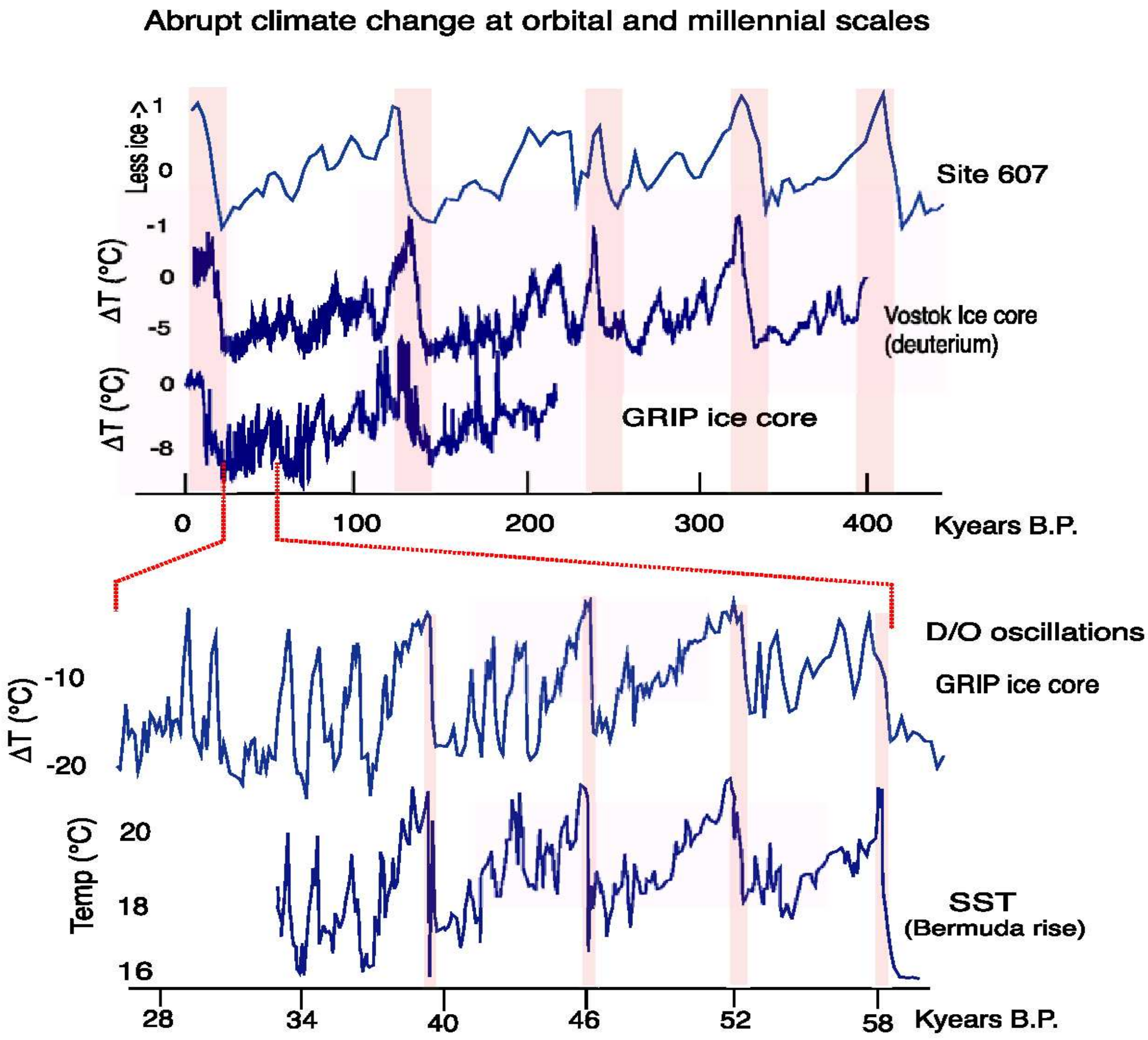


Fig. 6.1. An example of climate change across different time scales and proxy records. Note the extended cool periods and the more brief warm periods [taken from Rial (2004)].

Herbaceous plants will react more readily and have the potential migration speeds to track D-O scale events, but trees exhibit a lag to geographical response. Another paradox is that speciation and extinction rates fail to increase in the face of climatic instability. One interpretation is that species evolutionary stability is a consequence of environmental and ecological instability. As species track the shifting environment, populations break up and regroup thereby circumventing long-term isolation and genetic differentiation (Roy *et al*., 1996). In a phylogeographic scenario this will be detected as a fragmentation followed by a coalescent genetic signal if the marker is sensitive enough.

6.3.1. Refugia

African biodiversity hotspots have arisen from the persistence of refugia throughout the Quaternary glacial cycles (McClean *et al*., 2005). The climatic fluctuations during the Quaternary were pronounced but not catastrophic in southern Africa. The persistence of refugia may have contributed to South Africa's species richness and endemism.

Areas of topodiversity are likely to be important climate change refugia (McClean *et al*., 2005). Mountain systems are frequently viewed as areas of refugia. Linder (1983) suggested that for Disinae, southern African (Cape and Drakensberg) habitats were not lost in the Pleistocene. Carbutt and Edwards (2001) regard the Drakensberg as a historic high-altitude refugium for Cape elements. According to Linder (1983), in East Africa most habitats were lost with the exception of the high Rift Valley mountains. When the climate ameliorated c. 10 000 BP these refugia acted as source areas from where Disinae spread.

Other African mountains are also hypothesised to act as refugia (Linder, 1998). Lovett and Friis (1996) considered the Eastern Arc Mountains of Tanzania to be a refuge and have proposed that regions rich in restricted taxa have been climatically and geologically stable. Their explanation requires Pleistocene climatic change fluctuations to explain endemism. The East Usambara Mountains harbor many species which are separated from their closest relatives by wide intervals, suggesting that they have served as refugia for a formerly widespread flora which has become extinct over much of its former area (White, 1983).

The Afromontane vegetation that is now restricted to the isolated, temperate, moist, high altitude refugia (‘sky islands’) may have been much more widespread over the continent during cooler moist periods. Burgoyne *et al.* (2005) have suggested that the Afromontane phytochorion may be the largest assemblage of ancient persistent floristic elements in Africa with the grassland as a possible relictual type. Meadows and Linder (1993) have also suggested that Afromontane grasslands may represent ‘relict’ communities rather than forests in the southern Afromontane Region. Floristically, Afromontane forests and grasslands have nothing in common and do not appear to be interdependent. In some areas Afromontane Forest (with the same species component as in grasslands) occur successfully in a matrix that is floristically very different e.g. Fynbos (Burgoyne *et al.*, 2005). Burgoyne *et al.* (2005) have suggested that the forests and grasslands are very distinct and unrelated phytochoria that coincidentally happen to occupy the same climate refuge.

It is proposed that the evolutionary and biogeographic history of *Kniphofia* is strongly linked to climatic cycles and vegetation changes. It seems reasonable to hypothesise that the ancestral area for *Kniphofia* was much more geographically widespread when high altitude Afromontane grasslands were more extensive during cooler and drier, glacial episodes. During cooler and drier conditions grasslands expanded in Tropical and East Africa and shifted to lower altitudes (Scott, 2002). *Kniphofia* on the high mountains of Tropical and East Africa would have tracked the Afromontane grasslands and expanded their ranges. This would suggest that *Kniphofia* had a widespread distribution that covered most of the current disjunctions for the genus.

During wetter and warmer interglacials periods it is proposed that *Kniphofia* retreated into refugia on the mountains of Tropical and East Africa. In South Africa where latitude compensates for altitude, *Kniphofia* may have maintained a distribution that extended into the lowlands even during interglacials.

6.3.2. Climate and vegetation changes on the African Mountains

The climatic and vegetation diversity of the African mountains renders the interpretation of the palaeo-record extremely difficult (White, 1981). Additionally there is no fossil record for *Kniphofia*. Since it is not possible to accurately trace cyclic climate change beyond 30 000 years (van Zinderen Bakker, 1983), climate change during the Last Glacial Cycle (LGC) and its influence on the Afromontane vegetation is examined in order to gain insights that may assist in explaining the results obtained for *Kniphofia*. It must be noted that the present glacial-interglacial cycle is one of many that have preceded it, through which *Kniphofia* has survived. The current *in situ* diversity and distribution, and molecular data for *Kniphofia* are used here to demonstrate how a single cycle of climate change could influence the evolutionary and biogeograpical history of *Kniphofia*. This can be used to gain insights to how *Kniphofia* would have responded, survived and evolved through preceding cycles depending on the intensity and timing of climate change.

The climatic and vegetation changes for the three most speciose centres of diversity [South Africa, South-central Africa and Rift Valley (including the Ethiopia Subcentre)] are examined below. Each centre covers large spatial areas and it is expected that the climate and vegetation signals would at times be conflicting within a given centre. It is also difficult to untangle the effects of moisture, temperature and CO_2 in certain areas. More palaeo-botanical research is required to refine the late Pleistocene and Holocene vegetation history of southern Africa (Scott *et al*., 1997) and other African regions. Consequently, only broad patterns are taken into account.

The discussion below concentrates on Afromontane vegetation of the Forest Belt because *Kniphofia* displays a strong Afromontane grassland affinity. The Afromontane Forest Belt is a dynamic mosaic of forest and grassland (Meadows and Linder, 1993). It is not possible to directly infer past distributions of *Kniphofia* because of the lack of fossil material. Thus in this study the distribution of the Forest Belt during past prevailing conditions is used as a proxy to gain insights on the past distribution of *Kniphofia*.

6.3.3. The Rift Valley Centre

This region corresponds to the following regional mountain systems as defined by White (1978): the Ethiopian, the Imatongs-Usambara and part of the Kivu-Ruwenzori regional mountain systems. The Rift Valley Centre broadly corresponds mostly to Linder's (1983) East Africa Centre for Disinae. In this study the Ethiopia Subcentre of diversity is treated as a subunit of the Rift Valley Centre. It is also a subcentre of endemism (Chapter 2). Thus the Ethiopia Subcentre was examined in greater detail to determine if there are any features that may explain endemism. Fig. 6.2. summarises the discussion below.

At Lake Sacred (Kenya), Street-Perrot *et al.* (1997) have recorded dry montane forest (*Podocarpus*) between 24 000 BP (years before present) and 34 000 BP. Bonnefille and Chaliė (2000) have evidence for a well developed forest belt in the central East African Mountains for this time period. Before 30 000 BP the cooling was consistent with the occurrence of montane conifer forest in the Burundi Highlands (>2 200 m) which is now occupied by tropical rainforest (Bonnefille *et al.*, 1990). Bonnefille *et al.* (1990) have suggested a 4 ± 2ºC temperature decrease during 30 000-13 000 BP in several Rift Valley sites. The lowest temperature was recorded between 25 000-15 000 BP (Bonnefille *et al.*, 1990).

According to Street-Perrot *et al.* (1997) the Last Glacial phase extended from 24 000-13 000 BP, with a decrease in temperature by 5-9ºC. The Last Glacial Maximum (LGM) is recorded at c. 18 200 BP (Street-Perrot *et al.*, 1997). Bonnefille *et al.* (1990) have suggested that the optimal time for glacial advance in East Africa was c. 21 500 BP when the climate was cold but moist.

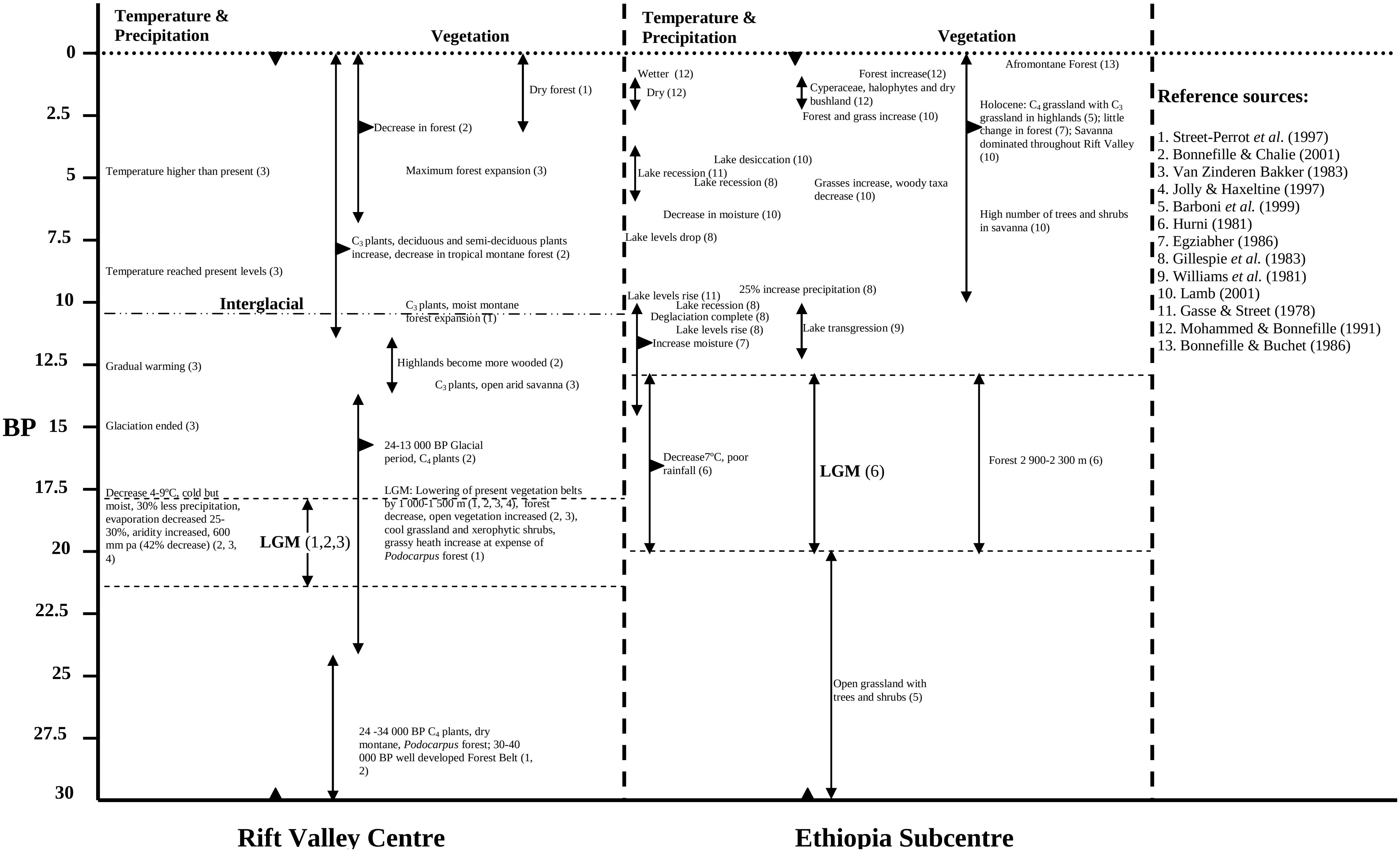


Fig. 6.2. Summary of climatic and vegetation changes in the Rift Valley Centre and Ethiopia Subcentre of diversity for *Kniphofia* during the past 30 000 years (details in text). Numbers in parentheses are reference sources which are listed (**BP** on the time axis= 1 000 years before present).

However, van Zinderen Bakker (1983) recorded the LGM at c. 18 000 BP and noted that the climate in East Africa was dry with a 6ºC lower temperature then present (van Zinderen Bakker, 1983). There was a decrease in evaporation (25-30%), aridity increased and conditions were dry (van Zinderen Bakker, 1983). Jolly and Haxeltine (1997) found that there was a 6ºC decrease in temperature, with 30% less precipitation (Kashivu, Burundi). Some areas received high rainfall. The area around Lake Kivu received 1 364 mm of rainfall per year during the LGM suggesting that it may have served as a refuge for montane forests. During the glacial period 30 000-15 000 BP there was a general 32% decrease in rainfall relative to present values. In African equatorial regions 'precipitation decrease' is a more appropriate term than 'glacial aridity' (Bonnefille and Chaliė, 2000).

In Tropical Africa, displacement of vegetation belts, although difficult to evaluate, depends not only on cooling but also involves precipitation (Bonnefille *et al.*, 1990). According to van Zinderen Bakker (1983), during the LGM the present vegetation belts shifted 1 000-1 100 m downwards. Jolly and Haxeltine (1997) noted that the tree line dropped by 1 000 m during the LGM. Street-Perrot *et al.* (1997) found that the vegetation descended by 1 000-1 100 m between 24 000-13 000 BP.

The lowland forests being the most sensitive probably survived in limited areas. The three vegetation belts above the moist montane forest viz. the dry montane forests, the Ericaceous Belt and the Afroalpine Belt persisted at a much lower altitude during the hypothermal times. However, according to van Zinderen Bakker (1983) the Afroalpine Belt and the Afromontane Forest Belt could not make contact with the lowlands.

There was a general decrease in forest with open vegetation becoming more prevalent during the Last Glacial. This could have served as a migration route for plant and animals adapted to dry conditions (van Zinderen Bakker, 1983). Cool grassland and xerophytic shrubs increased at the expense of *Podocarpus* forest (Jolly and Haxeltine, 1997). During the Last Glacial (24 000-13

000 BP) grassy heathlands composed of C_4 grasses and ericaceous shrubs with limited trees have been recorded by Street-Perrot *et al.* (1997).

Bonnefille and Chaliė (2000) found that during the Last Glacial between 16 000-18 000 BP there was a decrease in montane forest trees which were replaced by open-type vegetation in which there was a spread of Ericaceous Belt elements. The grassland was dominated by C_4 grasses. Low CO_2 levels promoted grassland development and retarded C_3 tree cover (Bonnefille and Chaliė, 2000).

The glaciations on the East African mountains ended c. 15 000 BP. Between 14 500-12 000 BP open arid savanna was recorded at sites presently occupied by lowland forests (van Zinderen Bakker, 1983). The gradual warming had a marked effect c. 12 600 BP. Forest elements spread from refuges along the western Rift Valley in an eastern direction probably mostly by long distance dispersal (van Zinderen Bakker, 1983). Bonnefille and Chaliė (2000) found an increase in arboreal pollen at c. 13 500 BP, and by c. 12 000 BP the highland vegetation became more wooded.

At about 10 500 BP the temperature on the mountains reached its present level (van Zinderen Bakker, 1983). Street-Perrot *et al.* (1997) noted that c. 10 300 BP there was a dominance of C_3 plants (moist montane forest) during the interglacial. Between 9 000-8 000 BP maximum forest cover was attained, reaching an altitude of 1 820-2 240 m (Bonnefille and Chaliė, 2000).

During 6 000-7 000 BP there was a decrease in tropical mountain forests with replacement by deciduous or semi-deciduous plants. In the last 6 000 years there has been a progressive decrease in arboreal pollen with notable declines at c. 5 800 BP and 3 000 BP (Bonnefille and Chaliė, 2000). At c. 4 000-4 600 BP the temperature on the mountains was higher than at present and forest expansion reached its maximum (van Zinderen Bakker, 1983). Around 3 200 BP, Street-

Perrot *et al.* (1997) noted a dry forest vegetation (*Podocapus* and *Olea*) increase at Sacred Lake (Kenya).

During the LGM the abundance of C_4 grasslands increased in areas that are currently wooded in equatorial Africa. As CO_2 concentration decreased, it gave C_4 vegetation the advantage to expand to ranges above the tree line (Scott, 2002). During the LGM, tropical areas that are currently clothed by montane forests, probably resembled subtropical regions (where grasses flourish today) but without the extreme seasonality of the subtropics. Although C_4 expansion occurred in the tropics during the LGM, its spread was curbed in the southern direction by subtropical latitudes, regions of high altitude and especially regions with pronounced winter seasonality (Scott, 2002).

6.3.3.1. The Ethiopia Subcentre (summary presented in Fig. 6.2.)

This region corresponds to the Ethiopian regional mountain systems as defined by White (1978). Many studies done in Ethiopia for the LGC (Last Glacial Cycle) have concentrated on Rift Valley lake levels and lake sedimentation to reconstruct climatic changes because of the important hominoid sites in the area. Lake levels and evolution is complex. In additional to climatic factors, lake levels and evolution involves episodic eruptions, faulting, reactivation of faults and pyroclastic accumulation (Williams *et al.*, 1981). These factors may mask climatic variables, so palaeo-data from lakes in the geologically unstable African Rift Valley should be treated with caution.

Barboni *et al.* (1999) examined phytoliths as palaeo-environmental indicators in the Middle Awash Valley. The Pleistocene was dominated high amounts of Poaceae morphotypes (75%) and 13% of dicotyledon morphotypes. The results indicate open grassland with more trees and shrubs which developed under humid conditions or conditions more humid than present. Hurni (1981) found that in the Simien Mountains the temperature was 7ºC lower than present during the Last Glacial period which extended between 20 000-12 000 BP. This was a time of poor run off and rainfall. Hurni (1981) postulated that montane forests were at altitudes between 2 900-2 200 m. Egziabher (1986) noted that between 10 000-14 500 BP there was an increase in moisture following a long arid phase.

Gillespie *et al*. (1983) examined lake level sequence in the Ziway-Shala basin during the past 14 000 years. Deglaciation of the mountains was completed before 11 500 BP. The lake rose c. 12 000 BP but a major recession was recorded c. 10 400 BP. Williams *et al.* (1981) recorded two major lake level transgressions at Lake Besaka viz. c. 11 000-12 000 BP and c. 10 000 BP. Gasse and Street (1978) found at least two distinct lacustral phases during the late Pleistocene in the lakes of the northern Rift Valley and Afar. This was followed by a very arid period during which the lakes examined recessed to their present levels or less (Gasse and Street, 1978).

The Holocene is characterised by low content in woody dicotyledons (<2%) but high Poaceae phytoliths (93%) (Barboni *et al.,* 1999). Chloridoideae grasslands (C_4 affinity) resembling modern subdesertic shrub steppe and C_3 Pooideae grasses would have covered the highlands (Barboni *et al.,* 1999). The climatic shifts during the past 10 000 years were considered by Egziabher (1986) to be small with minimal impact to the overall picture with regard to forests. Lamb (2001) found evidence for a savanna dominated vegetation in the Rift Valley (at Lake Tilo) throughout the Holocene despite evidence for strong variations in the moisture regime. The Holocene climate of this area has always been characterised by a wet and dry season (Lamb, 2001).

Gasse and Street (1978) recorded high lake levels c. 10 000 BP and a regression between 6 000-4 000 BP. However, no discussion on how this affected vegetation was provided. At Ziway-Shala c. 9 000 BP precipitation is estimated to have been at least 25% greater than today. Around 8 500 BP the lake levels began to fall. The lowest level was recorded c. 7 800-7 200 BP (Gillespie *et* *al.*, 1983). Lamb (2001) recorded a higher number of trees and shrubs in the savanna c. 7 000 BP at Lake Tilo. After 7 000 BP there was a decrease in moisture (Lamb, 2001).

Around 5 000 BP there was a major recession at Ziway-Shala. Since then dry conditions have prevailed (Gillespie *et al.*, 1983). Grasses increased and the diversity of woody species declined c. 5 500 BP. Lake Tilo began to desiccate c. 4 500 BP (Lamb, 2001). However, the pollen record shows no marked vegetation response to this climate change. Lamb (2001) recorded distinct vegetation changes c. 2 400 BP. *Podocarpus*, *Juniperus* and *Hagenia* increased on the uplands on either side of the Rift Valley. This was interpreted to be a response to a drier climate. Grasses also become more abundant and may reflect the climate changes at Lake Tilo (Lamb, 2001).

Mohammed and Bonnefille (1991) examined the vegetation and climate around Lake Langeno from c. 2 500-800 BP. During 2 500-2 100 BP there were humid conditions and high precipitation with maximum development of *Podocarpus* forests. The humid phase ended c. 2 100 ± 220 BP with drier climatic conditions prevailing. Shoreline vegetation included Cyperaceae, halophytes (Chenopodiaceae and Amaranthaceae) as well as dry evergreen bushland (*Olea-Euclea-Dodonaea viscosa*). This phase ended c. 1 060 ± 200 BP. Between 1 060-800 BP conditions became wetter which is indicated by an increase in *Podocarpus* and *Juniperus* vegetation. Afromontane forests have been at Wenchi for the last 800 years (Bonnefille and Buchet, 1986).

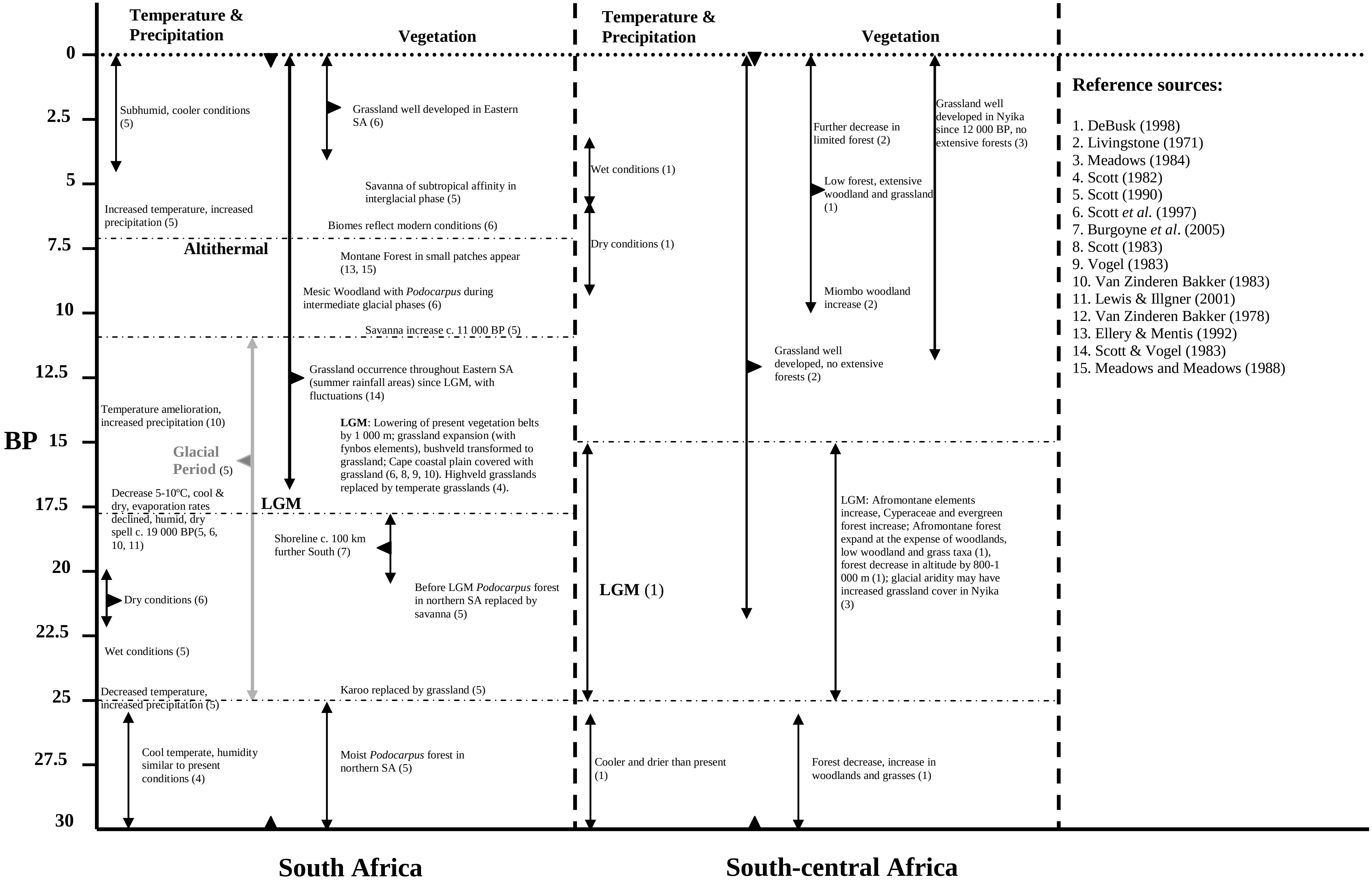
The palaeo-vegetation data for the Ethiopia Subcentre is rather fragmentary and incomplete. Many of the studies above do not include data on vegetation changes. Thus it is more useful to discuss the implications of past climate and vegetation changes in the broader context of the Rift Valley Centre (of which the Ethiopia Subcentre is a part) until more detailed studies are forthcoming for Ethiopia.

The review of climatic and vegetation changes for the Rift Valley Centre aids in interpreting the situation for *Kniphofia* during this time frame. *Kniphofia* on the high mountains of Tropical and East Africa would have tracked Afromontane grasslands and expanded their ranges during cooler and drier conditions. During the LGM in equatorial Africa C_4 grasslands increased in abundance and distribution (Bonnefille and Chaliė, 2000; Scott, 2002) and shifted to lower altitudes due to the displacement of vegetation belts. This would suggest that *Kniphofia* had a widespread distribution that covered most of the present disjunctions. The warmer and wet conditions of the interglacial probably did not favor Afromontane grasslands (Meadows and Linder, 1993) and it is most likely that during interglacial times in Tropical and East African forests would have been favored at the expense of grasslands (van Zinderen Bakker, 1983). Afromontane grasslands (including *Kniphofia*) would have retracted to high altitudes as now seen on the highlands of Tropical and East Africa and would have become limited to high altitude refugia in Tropical and East Africa. This explains the current restricted distribution of *Kniphofia* to the Afromontane vegetation in these areas as isolated and disjunct populations.

6.3.4. The South-central Centre (summary presented in Fig. 6.3.)

This region corresponds to the Uluguru-Mulanje and part of the Kivu-Ruwenzori regional mountain systems as defined by White (1978) and broadly corresponds to Linder's (1983) South-central Centre for Disinae.

DeBusk (1998) examined the pollen record for Lake Malawi which spanned over the past 37 000 years. The period 37 500-35 900 BP is represented by dry conditions with low lake levels and open vegetation (*Hyphaene* woodlands, lakeshore marshes and dry wooded grasslands). Between 35 900-34 000 BP montane forests were widespread with woodland reduction but still present indicating a cold moist climate. From 34 000-26 400 BP dry conditions that are slightly cooler than present are evident and forests decreased (DeBusk, 1998).



Subhumid, cooler conditions (5)

Increased temperature, increased precipitation (5)

Temperature amelioration, increased precipitation (10)

Decrease 5-10ºC, cool & dry, evaporation rates declined, humid, dry spell c. 19 000 BP(5, 6, 10, 11)

Dry conditions (6)

Wet conditions (5)

Decreased temperature, increased precipitation (5)

Cool temperate, humidity similar to present conditions (4)

Grassland well developed in Eastern SA (6)

Savanna of subtropical affinity in interglacial phase (5)

Biomes reflect modern conditions (6)

Montane Forest in small patches appear (13, 15)

Mesic Woodland with *Podocarpus* during intermediate glacial phases (6)

Savanna increase c. 11 000 BP (5)

Grassland occurrence throughout Eastern SA (summer rainfall areas) since LGM, with fluctuations (14)

LGM: Lowering of present vegetation belts by 1 000 m; grassland expansion (with fynbos elements), bushveld transformed to grassland; Cape coastal plain covered with grassland (6, 8, 9, 10). Highveld grasslands replaced by temperate grasslands (4).

Shoreline c. 100 km further South (7)

Before LGM *Podocarpus* forest in northern SA replaced by savanna (5)

Karoo replaced by grassland (5)

Moist *Podocarpus* forest in northern SA (5)

Wet conditions (1)

Dry conditions (1)

Cooler and drier than present (1)

Further decrease in limited forest (2)

Low forest, extensive woodland and grassland (1)

Miombo woodland increase (2)

Grassland well developed in Nyika since 12 000 BP, no extensive forests (3)

Grassland well developed, no extensive forests (2)

LGM: Afromontane elements increase, Cyperaceae and evergreen forest increase; Afromontane forest expand at the expense of woodlands, low woodland and grass taxa (1), forest decrease in altitude by 800-1 000 m (1); glacial aridity may have increased grassland cover in Nyika (3)

Forest decrease, increase in woodlands and grasses (1)

Reference sources:

1. DeBusk (1998)
2. Livingstone (1971)
3. Meadows (1984)
4. Scott (1982)
5. Scott (1990)
6. Scott *et al.* (1997)
7. Burgoyne *et al*. (2005)
8. Scott (1983)
9. Vogel (1983)
10. Van Zinderen Bakker (1983)
11. Lewis & Illgner (2001)
12. Van Zinderen Bakker (1978)
13. Ellery & Mentis (1992)
14. Scott & Vogel (1983)
15. Meadows and Meadows (1988)

Fig. 6.3. Summary of climatic and vegetation changes in the South Africa and South-central Centre of diversity for *Kniphofia* during the past 30 000 years (details in text). Numbers in parentheses are reference sources which are listed (**BP** on the time axis= 1 000 years before present).

An increase in Poaceae is recorded with a fairly high percentage of woodland. Montane forests continued to exist in the catchment areas of the lake possibly at high altitudes. The prevailing conditions appear to be intermediate between modern and glacial periods (DeBusk, 1998). Livingstone (1971) examined the pollen record for Lake Young (Ishiba Nganda) in northern Zambia. Neither montane nor moist forest of low or intermediate altitudes appear to have extensive distributions in this part of Zambia during the last 22 000 years. Grasses dominate the entire pollen spectra.

The end of the Pleistocene spanning the LGM is characterised by a high percentage of Afromontane elements accompanied by low percentages of woodland and grass taxa, and relatively high percentage of Cyperaceae and evergreen forests at Lake Malawi (DeBusk, 1998). There was an expansion of Afromontane Forest at the expense of woodlands.

Woodlands managed to maintain large coverage in the catchment of the lake. The expansion of the montane forest is accounted for by the depression of altitude belts with the cooling climate. The lowering of the montane forest’s altitude by 800-1 000 m implies that most of the catchment of Lake Malawi was within reach of Afromontane Forest (DeBusk, 1998). However, DeBusk (1998) noted that this lowering was not enough to account for the very high percentage of montane forest taxa. It is likely that there were extensive areas of closed montane forests in the catchment of Lake Malawi.

The Holocene reflects a similar climate and vegetation to current conditions. There is evidence for Miombo woodland increase c. 9 000 BP (Livingstone, 1971). At c. 3 000 BP there was a further decline in the limited evergreen forests (Livingstone, 1971). There are indications for slightly drier conditions between 8 000-6 150 BP at Lake Malawi. Conditions are recorded as slightly wetter between 6 150-3 000 BP. Throughout the Holocene there is evidence for low percentages of forest elements but more extensive woodlands and grasslands (DeBusk, 1998).

Meadows (1984) examined the environmental changes on the Nyika Plateau during the last 12 000 years. This period is characterised by a dominance of grasslands over forests. During some periods the forests did expand but not more than 10% (present cover of forest is estimated at 5%). Palaeontological evidence for the South-central centre fails to recover large scale vegetation fluctuations during the LGC and the vegetation on the Nyika Plateau has not altered much during the past 12 000 years (Meadows, 1984). Much of the area currently occupied by grasslands on the Nyika Plateau could be above the tree line i.e. in areas that may be too cold and dry for extensive tree growth at present. This situation was probably intensified during the Last Glacial when conditions in most parts of Tropical Africa were cooler and drier than at present. Fire would also have played a role in the maintenance of grasslands (Meadows, 1984).

It is also interesting that the vegetation of the Inyanga Highlands (Zimbabwe Centre) is characterized by grassland from the early Holocene with *Brachystegia* woodland developing c. 4 600 BP (Tomlinson, 1974).

Kniphofia in the South-central Centre is also associated with Afromontane grasslands. A similar situation as hypothesised for the Rift Valley may be applicable to the South-central Centre (discussed above). However, there is a surprising lack of grassland expansion and a notable forest expansion at Lake Malawi during the LGM. According to DeBusk (1998) the Late Pleistocene expansion of the forest patches would corroborate with recent fragmentation of the montane forests by grasslands without conflicting with evidence for the existence of montane grasslands throughout the Holocene (e.g. Meadows, 1984; Meadows and Linder, 1993).

There is a general lack of endemism in plants on the highlands of Malawi. The similarity among areas of montane vegetation in Malawi suggests that there was continuity between the now separate patches of montane vegetation in the recent past (DeBusk, 1998). This centre shows a chorological relationship with the South Africa and Zimbabwe Centres, but has a stronger relationship with the Rift Valley Centre for *Kniphofia* (Chapter 2). This centre may be associated with an overlap function to the north (Rift Valley Centre), south (Zimbabwe and South Africa Centres) and west (Cameroon Centre) (discussed later).

6.3.5. The South Africa Centre (summary presented in Fig. 6.3.)

The Drakensberg regional mountain system as defined by White (1978) and Linder's (1983) Cape and Natal-Transvaal Centres for Disinae fall within the South Africa Centre. In this study the South Africa Centre for *Kniphofia* was divided into three subcentres of diversity, of which only the Extended Drakensberg Subcentre is a subcentre of endemism. The Extended Drakensberg Subcentre or other areas of diversity recovered in Chapter 2 have not been treated independently in the discussion below as was done for the Ethiopia Subcentre. There is considerable intermingling in the southern Africa flora which partly diminishes the value of treating subcentres independently. The treatment of subcentres may have merits when examining southern Africa in isolation (Chapter 2). However, in the broader African context the South Africa Centre is best treated as a single unit for *Kniphofia*.

In southern Africa marked cycles of vegetation changes resulted in shifts in biome composition and boundaries in response to glacial cycles. These shifts were caused by fluctuations in temperature, precipitation and seasonal distribution of moisture (Scott *et al.*, 1997). The effects of orbital changes prevailed for a much longer period causing numerous and regular cycles of change in vegetation through the Pleistocene and Tertiary. Both recurring glacials and interglacials must have influenced evolutionary processes in plant communities and contributed to defining the modern vegetation. Vegetation patterns during the LGC which are a reflection of these complex changes can therefore be expected to include a relatively wide diversity of community types (Scott *et al.*, 1997). Climatic oscillations have also caused large scale migrations of vegetation types (as suggested by pollen data). It seems likely that at certain times when new conditions arose, new combinations of species were present (Scott, 1983).

Modern biomes were well established by the Quaternary (Scott *et al.*, 1997). African grasslands have become adapted to Late Tertiary glacial cycles (Scott, 2002). Grasslands in South Africa were well established by the Miocene and have been present consistently throughout the last c. 300 000 years in the interior of South Africa. Southern African grasslands are a transition between tropical and temperate (Afroalpine and Afromontane affinity) grasslands and their compositions must have fluctuated markedly in the past (Scott, 2002). Only broad trends can be identified for the Late Pleistocene. Pollen data from c. 40 000-75 000 BP indicate that forests were more widespread under moist conditions (Scott *et al.*, 1997). Highveld grass types (of tropical affinity) expanded regularly during the Quaternary at the expense of woody vegetation. Pleistocene pollen records for woodlands outside the present Grassland Biome suggests that grassy vegetation occupied a much greater area to the north during past cooler episodes (Scott *et al.*, 1997).

In southern Africa between 30 000-26 000 BP the climate was most likely cool-temperate and the humidity did not vary much from present semi-arid to sub-humid conditions (Scott, 1982). Wonderkrater and Zoutpan show cool moist *Podocarpus* forest prior to 25 000 BP. Before the onset of the LGM, forests near Wonderkrater were replaced by drier, slightly warmer savanna (Scott, 1990). At c. 25 000 BP a drastic change occurred which resulted in the Karoo being replaced by grassland (affinity not specified). Higher precipitation and a decrease in temperature were responsible for the ecological change during this period (van Zinderen Bakker, 1978).

During the Last Glacial phase (25 000-11 000 BP) there was an estimated 5-6ºC lowering of temperature. This coincides with relatively humid climates, except for the coldest time when it was dry. At Clarens, more Fynbos and swamps are recorded in the wet conditions c. 23 000 BP (Scott, 1990). This was followed by slightly drier times (22 600-20 000 BP), and a considerably drier and cooler climate c. 20 000-18 000 BP. From the end of the Pleistocene to 10 000 BP precipitation fluctuated considerably reaching low levels c. 18 000 BP during the LGM. Evaporation rates declined with cooler conditions (Scott *et al.*, 1997). During 21 000-18 000 BP the southern coast of South Africa was significantly exposed with the shoreline extending c. 100 km further south of the present coast line (Burgoyne *et al.*, 2005). Burgoyne *et al.* (2005) have suggested that grasslands (tropical affinity) along the south-eastern coast were more extensive. The remnants of these grasslands are now found in the sublittoral grasslands of the Maputoland-Pondoland Region, which are edaphically controlled and probably more extensive today because of frequent fire (Burgoyne *et al.*, 2005).

During the LGM vegetation belts were lowered by c. 1 000 m in altitude responding to c. 5ºC drop in temperature (Scott *et al.*, 1997; Scott, 1983; Vogel, 1983; van Zinderen Bakker, 1983). In some regions this drop in temperature was as much as 10ºC (van Zinderen Bakker, 1983; Lewis and Illgner, 2001). Cooler and moist conditions prevailed during this time, similar to the lower parts of the present Afroalpine Belt in Lesotho (van Zinderen Bakker, 1983). Upland grasslands (probably of temperate affinity) and shrublands were present in areas presently occupied by tropical savanna during the glacial phase. This phase was generally humid with a dry spell c. 19 000 BP (Scott, 1990). Grasses (presumably of tropical affinity) become more prominent after 18 000 BP when wetter conditions gradually returned (Scott, 1990). Climatic changes have generally influenced the long-term history of grasslands. Lower temperatures and less marked seasonal rainfall patterns allowed the downward spread of Afromontane Fynbos and grasses of C_3 temperate affinity (Scott *et al.*, 1997).

Mountain Fynbos was restricted to the upper reaches of the higher mountains during cooler and drier glacial conditions in the South-eastern Cape. The lowlands of the South-eastern Cape, which currently supports grassy-fynbos, would have been a mixture of Fynbos, karooid and C_3 temperate grassland elements (Cowling, 1983a). Cooler and drier conditions would have promoted fire, favoring Afromontane grasslands rather than Afromontane forests (Meadows and Linder, 1993). Highveld grasslands of tropical affinity were replaced by high altitude grasslands of temperate affinity (Scott, 1982). There is general consensus that temperate grasslands were more extensive during the LGM (Scott *et al.*, 1997) and have dominated most of the summer rainfall montane areas throughout the Holocene (Meadows and Linder, 1993).

During the glacial periods temperate grasslands of the interior were replaced by Alpine grasslands. The coastal plains of the Cape Region were devoid of forest and covered with grassland (not specified but presumably of temperate affinity) (van Zinderen-Bakker, 1978). Alpine vegetation was unable to survive at the highest altitudes. This vegetation only reached current altitudes c. 8 000 BP during the Holocene warm up (van Zinderen-Bakker, 1978).

Temperature has ameliorated since c. 13 000-14 000 BP while precipitation increased (van Zinderen Bakker, 1983). Vegetation alternated markedly ranging from woodland savanna during the warm interglacial phases to cool open grasslands including Fynbos elements during the glacial maxima and to mesic woodland with *Podocarpus* forests during intermediate phases (Scott *et al.*, 1997). Grasslands occupied roughly the same area during the Holocene as it does today with shifts in boundaries. During the climate optimum (i.e. the altithermal) in the middle Holocene c. 7 000 BP, on the northern boundary of the main highveld region, bushveld spread southwards over the edge of the plateau (Scott and Vogel, 1983).

In the former Transvaal, tropical savanna elements increased since 11 000 BP suggesting a gradual warming until c. 6 500 BP. This phase started with moist climates (c. 11 000 BP), indicated by *Olea* and *Podocarpus* pollen which was replaced by relatively dry Kalahari thornveld types by c. 8 000 BP. Broad leaved savanna elements including Combretaceae became prominent c. 6 500 BP indicating wetter conditions (Scott, 1990). Montane forest elements appeared c. 8 000 BP when the xeric elements declined and forests have been existing since this time in small patches, similar to the mosaic that exists in the region today (Ellery and Mentis, 1992). Rainfall declined markedly at the start of the Holocene, but by c. 7 000 BP the biomes began to reflect modern conditions although smaller fluctuations continued until recently (Scott *et al.*, 1997).

Meadows and Meadows (1988) have shown that in the Winterberg there are notable signs of drier and cooler conditions with a more xeric element, which indicates a cool grassy-fynbos transitional to Fynbos during the late Pleistocene (c. 12 500 BP to the early Holocene). Montane forests first appeared c. 8 000 BP during the warmer early Holocene when conditions were probably warmer and moister than present. Forests were not extensive and did not extend beyond localised patches that are reflected in the region today (Meadows and Meadows, 1988). In the South-eastern Cape during the altithermal, Fynbos would have expanded into the lowlands. Subtropical C_4 grasses and Afromontane elements would have penetrated into lowland communities on more fertile soils resulting in the present day grassy-fynbos (Cowling, 1983a).

Eeley *et al.* (1999) suggested a significant forest expansion in KwaZulu-Natal during the last altithermal. Some studies in the Maputoland area show extensive *Podocarpus* forest after the LGM. At c. 5 000 BP forests reached maximum extent and retreated from Maputoland in a northerly direction. The forests occupying the upper Mkuze River retreated towards the Drakensberg and the Natal mist belt (Mazus, 2000). Indications are that by the middle Holocene, *Podocarpus* spread in the interior and has never reached the same proportions as during the phases of the Late and Middle Pleistocene or even the LGM (Scott *et al*., 1997).

Sites from the former northern Transvaal and the Kalahari show dense woodland and relatively warm conditions by 6 500 BP while more open slightly cooler vegetation developed sometime afterwards c. 4 000-2 000 BP. Deposits from Deelpan (Free State) indicate grassland with karooid elements after 4 000 BP (Scott, 1990).

In general the past 6 500 years started with relatively dense vegetation under warmer, moist conditions in most parts of South Africa. Later in the Holocene there was more open vegetation related to slight cooling and good moisture availability but possible minor dry spells (Scott, 1990). During the late Holocene c. 4 000-1 000 BP the grasslands were very well-developed in the transitional areas suggesting that the grassland boundaries must have been further west (Scott *et al*., 1997).

Prior to the LGC *Kniphofia* was probably confined to high altitude Afromontane grassland. During the LGM these grasslands (with *Kniphofia*) descended and expanded to the lowlands in southern Africa. This may partly explain the present distribution patterns observed for *Kniphofia* in southern Africa (discussed in Chapter 2). Consequently, the lowering of altitude thresholds has resulted in the wider distribution of *Kniphofia* in vegetation that is not strictly Afromontane, especially in the Drakensberg-Maputoland-Pondoland transition. As *Kniphofia* expanded its range into the lowlands of southern Africa, populations may have been trapped in refugial pockets of grassland which possibly promoted morphological divergence. There are 13 *Kniphofia* species that have a highly restricted grassland distribution. This may have resulted in an array of recent morpho-species that are too young to have undergone complete lineage sorting and which can potentially still hybridise.

In the South-eastern Cape during the altithermal, Fynbos would have expanded to the lowlands with subtropical C_4 grasses and Afromontane elements also penetrating into lowland communities (Cowling, 1983a). *Kniphofia* could have used these opportunities to spread into the Cape and Karoo regions. It seems likely that *Kniphofia* tracked the subtropical C_4 grasses and Afromontane elements as they penetrated into the south-eastern Cape lowlands and tracked the C_4 grasses as they moved further westwards deeper into the Fynbos and Karoo. However, the details of the range expansion without a major morphological divergence into the Cape Region is difficult to interpret but it is interesting to note that tropical C_4 elements (Panicoideae and Chloridoideae) can to some extent successfully penetrate the Cape Region but also fail to speciate (Linder, 1989).

Radio isotope examination of 20 *Kniphofia* samples (representing 19 species) from all five cpDNA lineages by the Stable Light Isotope Unit (Archaeology Department, University of Cape Town) revealed that all samples had a C_3 isotope signature. Southern Africa samples represented material collected from coastal to high altitude montane habitats. The samples from Madagascar, Tropical and East Africa were from high altitude montane habitats.

Plants with a C_3 metabolism are advantaged in cool conditions, while plants with a C_4 metabolism are advantaged in warm conditions (e.g. Cowling, 1983b). Thus, it seems reasonable to postulate that during glacial periods (temperate situations) the C_3 condition is advantageous while the C_4 condition is advantageous during interglacials (tropical conditions). However, in southern African the situation is complex as grasslands are a transition between tropical and temperate grasslands and their compositions must have fluctuated markedly in the past (Scott, 2002). Currently the most extensive vegetation of the Afromontane Forest Belt in southern Africa is *Themeda triandra* [a C_4 species (Cowling, 1983b)] grassland (White, 1978). In South Africa patterns are obscured because ‘temperate’ grasses descend much lower and the most abundant tropical grass (*Tremeda triandra*) ascends relatively high (White, 1983) i.e. Afromontane grasslands in southern Africa are composed of both temperate and tropical elements with C_4 and C_3 conditions. More research is required on the (present and past) composition, abundance, affinities and distribution of the temperate and tropical elements of Afromontane grasslands in southern Africa.

Despite these obscurities it appears that in southern Africa *Kniphofia* was able to compete with C_4 grassland elements as they penetrated the Fynbos and Karoo during the Holocene. *Kniphofia* is also postulated to be able to compete with C_4 grassland elements of tropical affinity in the lowlands of eastern South Africa under warm conditions as it expanded its range and radiated.

It is important to note that Afromontane grasslands as a unit may not have existed during the glacials in its present configuration. The LGM was not only colder but also drier with environments different from the present situation. More research is required on the rainfall, temperature and soil requirements for *Kniphofia* to understand how it survived glacial periods and how this may have effected its evolutionary history.

6.4. How can tectonics, climate cycles, genetic and geographic patterns explain the evolutionary history of *Kniphofia*?

Within the five lineages there is evidence for recent differentiation as the branch length are small and there is evidence for the non-monophyly of several species. Short branch lengths, non-monophyly, and numerous identical haplotypes (both cpDNA and *ITS*) collectively appear to indicate that a rapid radiation has taken place in southern Africa.

Climate change can create vacant and new niches for evolution of remaining species (Goldblatt, 1978). Knox and Palmer (1995) have reported a radiation for *Dendrosenecio* from the East African Mountains within the past few million years. *D. meruensis* is hypothesised to be derived within the past 200 000 years (Knox and Palmer, 1995). No dating was provided for giant lobelias radiation/s by Knox and Palmer (1998) but the split of *L. sancta*/*L. ritabeaniana* from a *L. lukwangulensis*-like ancestor is speculated to be 7 MYA (million years ago). These dates are far older than the present study is suggesting for divergence and morphological speciation in *Kniphofia* but could easily be the age of the ancestor of the genus as a whole.

The low sequence divergence of *ITS* has been reported for several taxa in cases where a recent rapid radiation has been implicated (Baldwin and Sanderson, 1998; Harris *et al*., 2000; Richardson *et al*., 2001; Malcomber, 2002; Klak *et al*., 2003b; Howarth and Baum, 2005). The *ITS* results for *Kniphofia* show low sequence divergence which supports a hypothesis of recent radiation. While it is not possible to date the *Kniphofia* radiation, it seems unlikely that all the results obtained for *Kniphofia* are the consequence of a single glacial cycle (i.e. the LGC), as this will represent an unprecedented fast rate of molecular and morphological evolution. However, the possibility of rapid concerted evolution of *ITS* sequences cannot be ruled out.

According to Jansson and Dynesius (2002) high orbital forced dynamics (ORD) caused by Milankovitch oscillations are manifested by the following traits: low β clades (at least 100 000 years old) with generally high α clades (products of recent cladogenesis nested within β clades), low level of spatial genetic divergence in β clades, little geographic subdivision and large ranges, high vagility, low specialization, polyploidy and little β-anagenesis. *Kniphofia* appears to display most of these traits except that there is geographic structure in the main clades and there is no reported polyploidy in *Kniphofia* (Webber, 1932; de Wet, 1960; Nayak and Sen, 1992).

The phylogenetic studies of cpDNA showed evidence of non-monophyly for many species suggestive of a history of hybridisation and/or incomplete lineage sorting. If there has been gene flow and/or incomplete lineage sorting then conspecific individuals may be scattered in different lineages, but geographically localised genotypes should be shared between the different species (Whittemore and Schaal, 1991). This appears to be the situation in *Kniphofia*. Composition of the four southern African groups (and the Tropical and East African group) show more congruence with geographic origin rather than the taxonomic arrangement based on morphology. A recent radiation also suggests that not enough time has passed for currently delimited morphological species to differentiate fully and develop reproductive barriers, thus promoting hybridisation and mixing of haplotypes. Hybridisation and incomplete lineage sorting may not be mutually exclusive and both these factors may explain the non-monophyly in geographically based cpDNA lineages. Hybridisation may have also promoted concerted evolution of *ITS* sequences. This may also account for the low sequence divergence of *ITS*. Thus, the results of this study may reflect the combinational effects of a recent radiation, hybridisation, concerted evolution and incomplete lineage sorting.

If cyclic climatic changes have influenced the evolutionary history of *Kniphofia* it implies that populations would have (at different phases of the climatic cycle) fragmented and possibly coalesced. Fragmentation and isolation can explain the high number of restricted grassland species in southern Africa.

6.4.1. Altitudinal Shifts

Climate changes in mountainous regions can account for altitudinal contractions and expansions resulting in species ascending and descending mountain systems (Knox and Palmer, 1995; Larena *et al*., 2002). Knox and Palmer (1995) examined diversification of *Dendrosenecio* in East Africa, which involved repeated altitudinal radiations with Pleistocene climate fluctuations playing a role in altitudinal vegetation distribution. Larena *et al*. (2002) demonstrated that Pleistocene glacial induced altitudinal migrations in *Armeria* may have resulted in gene flow and hybrid taxa. Knox and Palmer (1998) also found that in the genus *Lobelia* (viz. the Giant Lobelias) there is a combination of geographic and repeated altitudinal speciation with hybridisation potentially playing an important role. Knox and Palmer (1998) made no inferences on the influence of past climatic changes.

Altitudinal contractions and expansions result in isolation and secondary contact but also allows for intermediate transient situations. Alternation between long isolations and intermittent establishment in transient habitat would add new species to the same mountain slopes (Fjeldså and Lovett, 1997). A reticulate history may be associated with altitudinal distributional changes in southern Africa for *Kniphofia*. Repeated expansion and contractions along altitudinal belts could result in the accumulation of a mixture of genetic signatures (haplotypes) as isolated populations in *Kniphofia* could have made secondary contact promoting gene flow and possible hybridisation. Altitudinal shifting of the vegetation belts associated with climatic changes in the Pleistocene may account for introgression events that have resulted in the non-monophyly of *Kniphofia* species.

Altitudinal shifting may have caused instability and disturbance as vegetation transgressed across altitudes. Grimshaw (1998) considered the climatic consequences of global glaciations as a disturbance in the Afromontane Region. The Afromontane vegetation (especially trees) are tolerant of the effects of altitude and regimes of repeated disturbance (Grimshaw, 1998). This implies that many elements of the Afromontane flora are well adapted to overcoming the effects of disturbance and may in fact use it to their advantage. Once these elements become established they may facilitate the introduction and colonisation of other less flexible ecological Afromontane elements.

Steep and complex landscapes are often used to explain gradient, parapatric speciation or microgeographic speciation (Fjeldså and Lovett, 1997). For example new species could be polyploids resulting from hybridisation between different species inhabiting different vegetation/biomes at ecotones or the result of past hybridisations with parents absent from present day floras (Fjeldså and Lovett, 1997). This is proposed to be the case for some African montane taxa. The species flock of *Impatiens* from the Uluguru Mountains indicate microgeographic as well as reticulate speciation. A similar species flock exists in *Saintpaulia* where ten of the 19 species inhabit the Usambara Mountains (Fjeldså and Lovett, 1997). This above scenario may also apply to *Kniphofia* in the Drakensberg.

6.4.2. Forest Encroachment

Grassland pockets surrounded by a matrix of forest in some regions may have been a minor contributing factor to fragmentation of grasslands and possibly populations of *Kniphofia* during the altithermal when forests were more widespread. Forests are a more recent vegetation than grasslands in eastern KwaZulu-Natal (West *et al.*, 2000). Forests have been existing in small patches during the past 8 000 years, similar to the mosaic that exists in the region today (Ellery and Mentis, 1992; Meadows and Meadows, 1988). There is general consensus that forests did not reach the levels suggested by Eeley *et al.* (1999) and forests have been expanding and are more abundant now than they have been in the recent past (William Bond, pers. comm.). This negates to possibility of forests becoming extensive to a degree that resulted in isolation of grassland pockets. Thus forest encroachment resulting in long-term grassland isolation is unlikely to explain the patterns recovered for *Kniphofia* in southern Africa.

6.4.3. Wetlands Patches

Many *Kniphofia* species have a strong affinity to moist areas (marshy areas, swamps, vleis and wetlands). Meadows (1988) noted the importance of wetland sediments as tools for reconstruction of palaeo-environments in southern Africa. Rogers (1997) reviewed freshwater wetlands for southern Africa. Unfortunately, no data on palaeo-distributions in relation to climatic cycles were reported in either study. There is a paucity of knowledge of how wetland distribution changed in response to past climate change, but work in this field is currently being initiated (William Ellery, pers. comm.). It is an unfortunate paradox that wetland sediments have contributed much to our understanding of past vegetation in southern Africa but not on wetlands themselves.

Wetlands expand and shrink with variation in water supply, and many may disappear and reappear depending upon the hydrogeomorphic setting. Some wetlands will be more vulnerable to this pattern than others. Wetlands in headwater settings are likely to be vulnerable. These may become geographically isolated during drying, since their integration into the drainage networks are broken. Wetlands that are integrated into the middle and lower reaches of drainage networks are likely to expand and shrink, but unlikely to become insularised (William Ellery, pers. comm.).

According to Grimshaw (1998) swamps could have served as stepping stones for Afromontane vegetation and may explain the crossing of the lowlands gaps between East and

West Africa. During pluvial periods swamps may have been more extensive facilitating dispersal by reducing the distances involved (Grimshaw, 1998). Further work on wetland palaeo-distributions will determine the extent to which wetlands have contracted and expanded under prevailing climatic cycles. This will shed light on their role in isolating plant assemblages or constituent taxa and whether they would have allowed subsequent contacts.

6.5. Disjunctions and Migrations

The events responsible for the establishment of the Afromontane Region (and related disjunctions) are complex with a long history, spanning beyond the past 25 000 years, and a single model is unlikely to account for the entire Afromontane diversity (White, 1981). Present distribution patterns do not provide all the data to untangle distributions for the Afromontane Region (Grimshaw, 1998). However, it does provide valuable clues and a foundation to build upon.

Disjunctions in the Afromontane flora have been referred to as vicariance events, indicating changes in the distribution patterns of the floras (Friis, 1983; Linder, 1998). Others have alluded to a dispersal explanation. The Drakensberg has been treated as a migration route for both southern (Cape) and tropical elements (van der Schijff and Schoonraad, 1971; Carbutt and Edwards, 2001). Dispersal may be facilitated by stepping stones during cooler periods when habitats on lower peaks were suitable for Afromontane species (Clayton, 1983).

The lowering of vegetation zones during the LGM could have allowed open vegetation to extend from South Africa to Zambia in the present Miombo woodland at 1 400 m (Scott, 1983). Hedberg (1969) expressed reservations on the extent of direct migrations between mountains during the Pleistocene and favored independent long distance dispersal events to explain the disjunct Afroalpine floras. He agreed that a shift of vegetation belts must have occurred with direct migrations possible only for some of the forest species between some mountains and not for Afroalpine species. Grimshaw (1998) found that the distances for inter-mountain dispersal were not great considering that the widest gap separating individual islands in the Afromontane archipelago between the Imatong Mountains (Sudan) and

Mulanje (Malawi) is only 140 km. Grimshaw (1998) noted the importance of smaller peaks acting as stepping stones and facilitating dispersal. These would have been clothed with Afromontane vegetation viz. forest in wet periods in the recent past.

It is hypothesised that *Kniphofia* was more widespread when grasslands were more extensive (glacial times). During wetter and warmer periods (interglacials) *Kniphofia* retreated into refugia on the mountains of Tropical and East Africa. Vicariance and dispersal seem to accompany the contraction (interglacials) and expansion (glacial) of ranges that are more or less in synchrony with the cyclic climate changes. Under the 'pulse-turnover' hypothesis evolutionary change is expected to be synchronised with climatic change (Lahr and Foley, 2003). When climates change so does habitat distributions. Accordingly populations will either contract or disperse (expand distributions). This provides conditions for selection to act upon and may bring about evolutionary change or extinction (Lahr and Foley, 2003). This has been suggested as a phenomenon experienced by the entire flora of the Afromontane Region (Burgoyne *et al.*, 2005). However, different elements of the flora would have had different responses depending on life history traits, climatic tolerances, vegetation preferences and associations.

According to Axelrod and Raven (1978) southern African genera that have extended their ranges northward along the mountains of East Africa include *Kniphofia.* It is not possible to judge the centre of origin and the direction of migrations for *Kniphofia* from this study. The directions moved by Afromontane genera with subsequent radiations and divergence is a matter to be considered for each genus independently.

The disjunction of many Afromontane elements in West Africa warrants additional attention as it also applies to *Kniphofia*. A single species (*K. reflexa*) is found in the Cameroon Centre. *K. dubia* and *K. benguellensis* from the highlands of Angola are placed in the South-central Centre (Chapter 2). White (1978, 1981) postulated that a southern migratory track of montane forests along the highlands of the divide between the Zaire and Zambezi basins by which the Afromontane flora of East Africa reached the isolated West African mountains. Establishment of aridity in the north of the basin precludes a northern exchange route

(DeBusk, 1998). There appears to be a gradient of increasing moisture availability between Equatorial Africa and Lake Malawi during the LGM (DeBusk, 1998). Moist conditions during the LGM in South-central Africa supports the presence of a southern migratory track of montane forest along the highlands of the divide between the Zaire and Zambezi basins supporting the suggestion by White (1978, 1981). Distances separating modern satellite populations are as little as 300 km. During past cooler climatic situations these now disjunct populations could have been continuous. This continuous belt would have allowed migration between Malawi and Angola (DeBusk, 1998) and possibly further north into West Africa. This allowed the Afromontane flora of East Africa to reach the isolated West African mountains.

However, Livingstone (1971) found that in northern Zambia during the last 22 000 years, grasslands have dominated. Dupont *et al.* (1996) examined *Podocarpus* distribution in West Africa during the Pleistocene, and showed widespread distributions of *Podocarpus* forest in the highlands of Guinea, Nigeria, Cameroon, Congo (Democratic Republic of Congo) and Angola. These workers found that the direction of spread was from south to north (Angola to Gabon). At c. 24 000 BP forests had limited distribution and were centred around Cameroon and Congo probably due to aridity as the LGM approached. After the LGM *Podocarpus* forests spread northwards to Nigeria and southwards into Angola during the first half of the Holocene. Lowland forest occupied most of the mountains of Cameroon, Gabon and Congo during this time. The dry conditions may account for the decline in *Podocarpus* forest distribution except in these equatorial highlands. In this area *Podocarpus* forests may have benefited from the cold climate of the LGM. Expansion of the lowland rain forest would have also pushed mountain forest to higher altitudes (Dupont *et al.*, 1996).

According to DeBusk (1998) the Afromontane expansion occurred under cooler but not drier conditions than present. The interchange would also not have occurred as a continuous belt of forest but rather as stepping stones formed by montane populations. However, data to test this hypothesis would require vegetation and climatic reconstruction of areas such as western Zambia and Angola (Dupont *et al.*, 1996). The paucity of data for this region is unfortunate and additional data is needed to confirm the existence of the southern migratory route.

Many of the disjunctions of Afromontane elements in the Zaire and Zambezi basins are in habitats that are nutrient deficient, either on oligotrophic substrates or in swamps (Grimshaw, 1998). According to Grimshaw (1998) this supports the hypothesis that Afromontane trees are adapted to nutrient poor conditions. Swamps and mountains could have served as stepping stones and may explain the crossing of the lowlands gaps between East and West Africa. During pluvial periods swamps may have promoted dispersal by reducing the distances involved (Grimshaw, 1998). This is particularly relevant to *Kniphofia* as it has an affinity for wet conditions.

The distance and altitude of major gaps regions were examined for the centers of diversity for *Kniphofia*. Within the Rift Valley centre the gap between the Ethiopia and Ruwenzori subcentres is c. 200 km. The lowest altitudes are between 200-500 m while the highest peak in the gap is Mt Kanta (2 518 m). Between the Rift Valley and South-central Africa centres the gap at the shortest distance is c. 200 km. The lowest altitudes are between 500-1 000 m, while the highest peak in the gap is Mt Manzanza (2 575 m). Within the South-central Africa centre the gap between the Angolan Highlands is c. 800 km. The altitude ranges between 1 000-2 000 m for this entire region, while the highest region in the gap is South East of Balombo (2 620 m). Angola is poorly explored botanically and *Kniphofia* may occur in this gap region. Between the South-central Africa and Zimbabwe centres the gap is c. 300 km. The lowest altitude is c. 200 m, while the highest peak in the gap is Mt Gorongosa (1 862 m). The Zimbabwe and South Africa centre are separated by c. 300 km. The lowest altitude is c. 200 m, while the highest region is the Matobo Hills (1 543 m). If vegetation belts descended by 1 000 m during the last or previous glacials then most of the gaps would have easily bridged by Afromontane grasslands, with the high points between gaps as acting as stepping stones.

The exception is the Cameroon Centre on continental Africa. The nearest centre to the Cameroon Centre is the Rift Valley Centre. The Rift Valley and Cameroon Centre gap is c. 2 000 km. The lowest altitudes are between 500-1 000 m, with several peaks that range from 1 000-1 400 m in between [highest peak in the gap is Mt Nqaoui (1 400 m) on the Cameroon border with the Central African Republic). The Cameroon Centre is also c. 2 200 km from the nearest highlands in Angola with *Kniphofia*. The distances from the Rift Valley Centre and Angolan highlands (South-central Africa Centre) are great (2 000 km and 2 200 km respectively).

Establishment of aridity in the north most likely precludes a northern exchange route (DeBusk, 1998) for *Kniphofia* i.e. a Rift Valley-Cameroon linking route. A continuous belt of Afromontane vegetation (Afromontane Grassland) during glacials would have allowed *Kniphofia* to bridge the present disjunctions with the high points between gaps as acting as stepping stones in southern and East Africa. The Cameroon Centre was most probably reached from the south via the Angolan highlands as a component of the Afromontane vegetation (DeBusk, 1998). It is possible that *Kniphofia* migrated between Malawi, Zambia and Angola and possibly further north into Cameroon using peaks and swampy regions in between as stepping stones when Afromontane vegetation was more continuous (i.e. glacial periods) or during pluvial periods. No *Kniphofia* samples were obtained from Angola, Zambia and Cameroon. It will be interesting to see where these samples would be placed in the phylogeny.

Two other disjunctions, Madagascar and Yemen, also merit additional consideration as they are presently linked but not confined to continental Africa.

6.5.1. Madagascar

The Africa-Madagascar separation began c. 165 MYA (Jurassic) and ended c. 121 MYA (Rabinowitz *et al.*, 1983). Most African-Madagascan disjunct plant genera are likely to have achieved these distributions by recent long distance dispersal (Goldblatt, 1978; Axelrod and Raven, 1978). The Malagasy disjunction appears to be a result of dispersal from Tropical Africa. Attachment of seeds in mud to the feet of birds was considered to be a mode of long distance dispersal, particularly in plants growing in moist habitats (marshes, mud-flats and streambanks) with small seeds (Carlquist, 1967). This may also apply to *Kniphofia* as it is frequently found in marshy areas and have relatively small seeds.

6.5.2. Yemen

The Afar Plume links Ethiopia, Eritrea, Djibouti and Yemen. This area was covered by Tertiary flood basalts, which were once contiguous from Ethiopia to Yemen (Mohr *et al*., 1983; Bosworth *et al*., 2005). Data suggests that rifting was established in the central and eastern parts of the Gulf of Aden c. 30 MYA. Girdler and Styles (1978) have proposed a two stage seafloor spreading for the Gulf of Aden. The first stage was between 30-15 MYA. The second stage started c. 4.9 MYA to the present time. The separation of Arabia from Africa to form the Red Sea and the Gulf of Aden is estimated at 15 MYA (White, 1983). It is possible that the distribution of *K. sumarae* (Yemen) is not a result of dispersal but rather vicariance that separated Ethiopia and Yemen. This would mean that *Kniphofia* is old and northern taxa may be relictual. However, samples from Ethiopia were not resolved as basal and are not regarded as old. *K. sumarae* was not included in this study. It will be interesting to see where this sample will be placed in the phylogeny.

6.6. Reconciling anatomical data with biogeography

In *Kniphofia* morphologically delimited species exhibited substantial anatomical variation. The results for the most part do not fit any geographic pattern nor do they reflect the cpDNA groups recovered by the *trnT-L* spacer. A reticulate history caused by repeated altitudinal shifting of the vegetation belts associated with climatic changes in the Pleistocene may also account for the substantial anatomical variation in southern African *Kniphofia* species.

Cutler *et al.* (1980) examined a group of shrubby *Aloe* species in the East African (termed the East Africa shrubby species). Leaf surface anatomy alone was not sufficient to understand this group. In summary a form very close to *A. morejensis* was postulated to have undergone chromosome doubling somewhere in the southern Rift Valley of Kenya to produce a tetraploid which is now evolving in several directions into the other species of this group. Habitat details were not given, but several taxa appear to be from the lower reaches of the

Afromontane Region. Cutler *et al.* (1980) also did not discuss the influence of climate cycles on the evolutionary history of this group.

The anatomical work of Ellis (1980a, 1980b, 1981a, 1981b) on the grass genus *Merxmuellera* (*M. disticha, M. stricta, M. drakensbergensis, M. stereophylla, M. macowanii, M. davyi, M. aureocephala*) in the Drakensberg of southern Africa is very interesting as it shares some common themes with the proposed evolutionary history of *Kniphofia*. The details of these studies are not given here but the broad conclusions are of significance to this study. He has shown evidence which supports an adaptive radiation associated with alternating environmental conditions particularly altitudinal effects in the Drakensberg Range for *Merxmuellera* (Ellis, 1980a). The adaptive radiation is still actively continuing (Ellis, 1980b). He was also able to provide evidence for species of hybrid origin (Ellis, 1981b).

However, there are some notable differences between *Mermuellera* and *Kniphofia*. The monophyly of *Kniphofia* as a whole has not been disputed. Barker *et al.* (1999, 2003) showed that *Merxmuellera* is polyphyletic. The number of species of *Kniphofia* are much greater than *Merxmuellera*, and thus morphological diversity is greater. Ellis' (1980b) work indicates that an adaptive radiation is occurring at high altitudes i.e. an 'upward' radiation for *Merxmuellera*. The opposite situation seems to apply to *Kniphofia* where the radiation has been at lower altitudes i.e. a 'downward' radiation.

Additionally *Merxmuellera* species seem to have a more conservative morphology while displaying much variation in anatomy. *Kniphofia* on the other hand displays both variable morphology and anatomy. The *Merxmuellera* adaptive radiation in response to similar environment conditions has resulted in similar phenotypic expression by the ecotypic forms of each species (Ellis, 1981b). The higher altitude Alpine anatomical 'forms' of *Merxmuellera* species may be experiencing morphological convergent evolution in response to similar environmental conditions (Ellis, 1980b) but retaining distinctive (or ancestral) anatomical types. This may explain the lack of morphological diversity in the adaptive radiation proposed for some *Merxmuellera* species.

Anatomical data for other Afromontane genera are needed to assess, compare and correlate patterns. Such patterns may reveal how different Afromontane elements have had different responses depending on life history traits, climatic tolerances, vegetation preferences and associations.

6.7. Species concepts

What are species, how do they come to be, and how do we discover them? These remain the most elusive and intractable challenges to natural historians (Brower *et al.*, 1996). In groups with reticulate ancestry species concepts with an underlying monophyletic basis are of little use. In a genus where gene flow occurs, the biological species concept is inadequate. The Hennigian species concept applies to reproductively isolated natural populations. Gene flow and possible hybridisation eliminates this application to *Kniphofia*. The phylogenetic species concept is based on monophyly. This is also not applicable in the case of *Kniphofia* as species display non-monophyly.

Kniphofia may be regarded as a mixture of more or less discrete morphological units that are inter-fertile. Many taxa appear to be either incipient species or populations that are in the process of diverging to the point of speciation but retaining the potential to interbreed. Early stages of reproductive isolation and genetic differentiation may be taking place among various populations and species complexes. Over time, geographical and phenological discontinuities may arise that reinforce genetic differentiation, thus producing evolutionary entities that can be considered species (Nickrent *et al*., 2004). In *Kniphofia* incipient speciation may be occurring and adopting a strict species definition is thus elusive.

6.8. Classification

Both the nuclear and chloroplast trees are inconsistent with the sectional classification proposed by Berger (1908) and Codd (1968) and both phylogenies also do not support the segregate genus *Notosceptrum*.

Reducing the entire genus to a single taxonomic species or five clades/lineages is not considered appropriate, as there is evidence of morphological structure reflected by the alpha taxonomy of many, although not all, taxa. Some species are clearly morphologically definable e.g. *K. parviflora* but are non-monophyletic according to DNA sequence data. Reduction to a single species may reflect a more accurate evolutionary history but will create a morphologically heterogeneous assemblage, which is considered impractical at this point in time. Recognising five clades/lineages as possible species or subspecies units is also unpragmatic, as all the clades/lineages recovered in this study will be composed of morphologically heterogeneous assemblages. Identification, description and communication of these clades will be problematic. If either of the above steps are advocated it will result in instability in classification. This is of particular importance as not all currently recognised morphological species were sampled so their final placement is uncertain and future research may find different and/or additional lineages. Furthermore, classification based on only one marker especially a cpDNA marker that is maternally inherited in a group that apparently readily hybridises is undesirable and not recommended.

The existing classification may not reflect the evolutionary history and phylogeny of the genus accurately, but does provides a framework for identification, communication and interpretation of additional evidence. Thus, a conservative approach is taken and the existing morphological based classification is upheld and no changes are proposed.

6.9. Conclusion

The cpDNA and nuclear phylogenies for *Kniphofia* do not provide complete resolution and are not robust. Despite these limitations, a phylogenetic hypothesis for *Kniphofia* using molecular plastid and nuclear DNA sequence data was obtained. The DNA sequence data (especially the cpDNA data) when interpreted in a broader context that encapsulates tectonic, climate change, distributional, phylogenetic, phylogeographic and anatomical patterns does provide evidence to give insights on the evolution, biogeography and complicated alpha taxonomy of *Kniphofia*.

The present study on the phylogenetic relationships, evolutionary history and biogeographic patterns of *Kniphofia* has made a significant and much needed contribution to the better understanding of this very popular but little-studied genus of petaloid monocotyledons. This study has provided insights into the potential factors and processes driving evolution in this genus. It has also detected previously unknown phylogenetic and biogeographic patterns and is the first to invoke and incorporate past climatic change across the entire African continent as a mechanism driving diversification and speciation in an angiosperm group. However, many issues need further investigation and attention, and this study provides a framework for additional systematic research. The patterns detected and the explanation of these patterns may need reassessment as information from additional markers and/or samples become available. Thus there is much scope for the improvement, refinement and further development of the hypotheses presented here.

The distribution patterns of *Kniphofia* in southern Africa and the Afromontane Region is very similar to several other genera (e.g. *Alepidia*, *Freesia*, *Dierama*, *Dietes* and *Knowltonia*). It is presumed that they are under the same evolutionary and environmental (both present and past) forces and may have been influenced in a similar manner as *Kniphofia*. Many of the factors that have influenced the evolutionary history and biogeography of *Kniphofia* are probably also applicable to these genera. However, no studies with a phylogenetic or phylogeographic framework are currently available for these genera. Such studies may either confirm and strengthen the findings of this study, find different patterns or may provide insights to alternate hypotheses to explain the results obtained for *Kniphofia.*

According to White (1981), events responsible for the establishment of the Afromontane Region (and related disjunctions) are complex with a long history, spanning beyond the past 25 000 years, and a single model is unlikely to account for the entire diversity of Afromontane chorology. Further research may contribute to phytogeographic hypotheses explaining migration routes due to climate change and expansions/contractions. Carbutt and Edwards (2001) noted the importance of species level cladograms in determining and understanding the Afromontane flora and its historic origins. Phylogeographic studies on selected species or groups of closely related species that have an Afromontane distribution may also be invaluable in understanding the history of the Afromontane Region, directions of migrations and refugial areas for specific taxa.

In the past, work on the Afromontane Region has focused on studies that documented the diversity, vegetation and relationships with other vegetation. Factors driving speciation and evolution in the Afromontane flora have received very little attention. A major challenge is to shift focus from documenting patterns to explaining processes driving speciation and evolution.

Data from tectonics, past climate changes, present distribution patterns, genetic studies, vegetation history, ecology, anatomy and systematics have to be integrated effectively to gain an understanding of origins, evolution and speciation in plant groups of the Afromontane Region. Additionally data from such multidisciplinary research will ultimately contribute to a better understanding of factors that have in the past and are presently shaping the flora of Africa as a whole.

This will also assist zoologists who are studying Afromontane fauna that are restricted to specific Afromontane vegetation types. Research on the fauna of the African mountains has already been initiated. Bowie *et al.* (2004) showed that how forest expansion driven by climate change in the mid-Pleistocene (1.1-0.7 MYA) have influenced the evolution and biogeography of the olive sunbird (*Nectarina olivacea/obscura*). Bowie *et al.* (2006) demonstrated using the starred robin (*Pogonocichla stella*) how aridification in response to glaciation during the Pleistocene had a major influence on speciation in the mountains of East and Central Africa. Quérouil *et al.* (2003) examined the phylogeography of two shrew species (*Sylvisorex johnstoni* and *S. ollula*) in western central Africa. Both species are tropical forest dwellers. This study suggests that both species originated in the Plio-Pleistocene and their haplotype distribution reflect forest fragmentation and expansion associated with climatic change in the Pleistocene (Quérouil *et al.*, 2003). These studies do not have a direct bearing on this study (i.e. *Kniphofia*), but they demonstrate how specific palaeo-climate and vegetation changes can trigger profound effects on evolutionary and biogeographic history depending on the organism examined. Furthermore, they contribute to a better understanding of how the African biota has survived in space and time.

6.10. Future work

In concluding the present study several avenues of investigation are recommended in order to further unravel the threads in the *Kniphofia* puzzle. Some of the research avenues mentioned below might also contribute to a better understanding of the Afromontane Region and other Afromontane groups that have a similar distribution pattern as *Kniphofia*.

6.10.1. Species complexes

Baijnath (1980) noted the need for detailed investigations of species complexes based on the anatomical differences in species such as *K. linearifolia* and the morphological variation reported by Codd (1968, 2005). Such studies will require extensive sampling over the entire distribution range to assess variation. Also because of the possible prevalence of hybridisation it may not be feasible to explain all the variation by examining isolated complexes but will require a much broader approach.

Morphometric studies of species complexes are needed to identify morphological characters important for identification of difficult species. A phenetic analysis should also be done on floral characters which not only accounts for morphological variation and influences hybridization. Widespread species should be examined for clinal variation in morphology and factors associated with this variation.

6.10.2. Ecological studies

More research is required on the ecology of *Kniphofia*. This should include rainfall, temperature, soil and substrate requirements for *Kniphofia* species. Pollination studies are also needed (see below). This will help to better understand how *Kniphofia* survived changing environmental conditions of glacial periods and how this may have effected its evolutionary and biogeographic history.

6.10.3. Reproductive biology and breeding studies

Cronn and Wendel (2003) noted the important contribution that reproductive biology may have in understanding hybridisation. Artificial hybridisation attests to the potential for natural hybridisation between species (Cronn *et al*., 2003). No studies could be found that have studied the pollination and/or floral biology of *Kniphofia*. Kniphofias are known to be visited by sunbirds in southern Africa. These may be the likely pollinators. There is ample evidence from horticulture that *Kniphofia* species hybridise easily. Baijnath (1992a) managed to cross *K. leucocephala* and *K. pauciflora* as flowering times overlapped. Both species were predominately self-incompatible. However, hybrid plants were not studied in detail. In the present study no artificial hybridisation experiments where done. More detailed studies are required with controlled crossings. Crossing experiments and comparison (morphological, anatomical, cytological and molecular) of progeny and parents should be done to test hybrid hypotheses and to determine the nature and extent of hybridisation. These studies should also include aspects of floral and pollination biology.

6.10.4. Cytology and Polyploidy

Hybridisation and polyploidy are frequent modes of evolution in plants (Baumel, *et al.* 2002; Soltis *et al.* 2003; Doyle *et al.* 2003; Linder and Rieseberg, 2004). There is a well established link between hybridisation and polyploidy in the literature (McDade, 1990; Sang *et al*., 1995; Church and Taylor, 2005; Ainouche *et al*., 2003; Guo *et al*., 2004).

Very few lineages of angiosperms have been unaffected by polyploid events (Valcárcel *et al*., 2003). Polyploidy is common in plants with estimates ranging from 30-80% in angiosperms (Hegarty and Hiscock, 2005). Polyploidisation can have major effects on genome structure and function (Soltis *et al*., 2003; Adams and Wendel, 2005). It can also have major effects on evolution and ecology of taxa involved (Soltis *et al*., 2003). Hence results from nuclear markers may be more complex than those of chloroplast markers in cases of polyploidy as nuclear markers can reflect multiple origins in a polyploid taxon (Mason-Gramer, 2004).

Polyploids are also known to hybridise more than their diploid counterparts (Church and Taylor, 2005). Most polyploid plants species that have been examined with molecular markers are polyphyletic, having arisen multiple times from the same diploid species (Soltis and Soltis, 2000b). The success of polyploids is attributed to their genetic variability (Doyle *et al*., 1999).

Chromosome counts for *Kniphofia* are few. Webber (1932) examined the karyology of *K. aloides* (i.e. *K. uvaria*) in detail. He found that there were six pairs of chromosomes (*2n= 12*). De Wet (1960) noted the somatic chromosome number of *2n= 12* in 17 species of *Kniphofia* (viz. South African representatives, including *K. typhoides* which was previously placed in *Notosceptrum*). Chromosome morphologies showed little difference and there was no polyploidy. Nayak and Sen (1992) examined the karyology of *K. nelsonii* (i.e. *K. triangularis*) and *K. uvaria* clones. Most of the cells examined were diploid (*2n= 12*), however, these workers found that some cells were aneuploid or tetraploid.

Diploid hybrid speciation has been shown in a number of plant groups (e.g. Wolfe *et al*., 1998) and cannot be excluded as a possibility for *Kniphofia*. Future cytotaxonomical investigations are highly recommended to establish if polyploidy exists in this genus and infer primitive versus derived chromosome numbers and morphologies.

Leaf epidermal patterns have been found to be under genetic control as in some members of the Alooideae (Cutler and Brandham, 1977; Cutler, 1978; Brandham and Cutler, 1978). Similar studies which include a cyto-nuclear component are required to show this in *Kniphofia* (Baijnath, 1980).

6.10.5. Multiple sampling

The results of this study emphasise the importance of using multiple exemplars in molecular studies of problematic groups. Sample acquisition is a major problem especially when working on groups with very wide distributions. However, attempts should be made to include as many samples as possible. Sampling only one sample per species may lead to erroneous conclusions and shallow insights of patterns at the species level and below (Soltis *et al*., 1992). Single exemplar studies may not recover underlying patterns. Insights into reticulation and lineage sorting can only emerge from multiple exemplar sampling approaches. More comprehensive coverage of species and distributional ranges of *Kniphofia* are needed especially for Tropical and East Africa.

6.10.6. Population studies

A component of increased sampling entails studies at the population level. In order to understand evolutionary processes and relationships, examination of population within species or closely related species are needed (Wolfe *et al*., 1998; Schaal and Olsen, 2000; Ferguson and Jansen, 2002). Increased sampling at the population level is needed to gain a more comprehensive understanding of morphological, anatomical and genetic variation and patterns. Population level studies are needed to confirm putative hybrids and their parental taxa or populations.

6.10.7. Application of additional markers and methodologies

Use of more sensitive molecular markers such as amplified fragment length polymorphisms (AFLPs), microsatellites and inter simple sequence repeats (ISSRs) may prove to be useful (Wolfe *et al*., 1998; Gravendeel *et al*., 2004; Vriesendorp and Bakker, 2005). Single or low copy nuclear genes appear to be better markers for the parental polymorphisms in hybrids than *ITS* because of the effects of concerted evolution (Sang and Zhang, 1999). Additional studies with alternative markers may provide scope for determining age of nodes. This data will assist in assessing the role of lineage sorting in *Kniphofia*. Alternative markers may also contribute to a better understanding of the evolutionary and the biogeographic history of *Kniphofia.*

Modern molecular cytogenetic techniques such as genomic *in situ* hybridisation (GISH) (e.g. Chase *et al*., 2003) and fluorescent *in situ* hybridisation (FISH) (e.g. Taketa *et al*., 2005) has opened new avenues to study hybridisation. Linkage disequilibrium studies may also be useful. This involves the search of genetically linked markers. Tightly linked markers in hybrids are more likely to come from the same parent and therefore display linkage disequilibrium (Linder and Rieseberg, 2004). Coalescent approaches may help in interpreting the data further. However, these were not attempted in this study because of the limiting nature of the data and the problems associated with finding suitable calibration points.

The Afromontane Region is under extreme anthropogenic pressure (Burgoyne *et al.*, 2005). Data obtained from multidisciplinary research as outlined above will serve to highlight the importance of conserving the Afromontane Region and to curb the loss of this unique vegetation, its flora and fauna.

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Appendices

Appendix 1: Data matrix with *Kniphofia* species as characters and QDGs as terminal units

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3421AD	0000000000	0000000000	0000000000	0000000000	00000001
3421AC	0000000000	0000000000	0000000000	0000000000	00000001
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3420AB	0000000000	0000000000	0000000000	0000000000	00000001
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3419AB	0000000000	0000000000	0000000000	0000000000	00000001
3419AA	0000000000	0000000000	0000000000	0000000000	01000001
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3228AB	0000000000	0000000000	0000000100	0000000000	00000000
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3227DC	0000000000	0000000000	0000000100	0000000100	00000001
3227DB	0000000100	0000000000	0000000000	0000000100	00000000

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2930AD   0000000010 0000000000 0000100000 0000000000 00000000
2930AC   0000000010 0000000001 0001010100 0000000000 00000100
2930AB   0000000000 0000000000 0000010000 0000000000 00000100
2930AA   0000000000 0000000000 0000010000 0000000000 00000000
2929DD   0001000000 0000000100 0000010100 0100000000 00010000
2929DC   0000000000 0000000101 0000010000 0100000000 00010000
2929DB   0000000000 0000000000 0000010100 0000000000 00000000
2929DA   0000000000 0000000000 0000000100 0000000000 00000000
2929CD   0000000000 0000000101 0000010100 0000000000 00010000
2929CC   0000010001 0000000100 0001010100 1001001000 00110000
2929CB   0010011001 0000000100 0000010100 0000001000 00010000
2929BD   0001001000 0000000001 0001010100 1000000000 00000000
2929BC   0001011001 0000000000 0001000000 0000001000 00100000
2929BB   0001010000 0000000000 0001010100 1001000000 00100000
2929BA   0011001000 0000000001 0001010100 0001000000 00100000
2929AD   0001000000 0000000000 0000010100 0000000000 00100000
2929AC   0000000001 0000000000 0000000000 0000001000 00010000
2929AB   0011010001 0000001100 0001010100 1101001000 00000000
2929AA   0001000001 0000000000 0000000000 1000001000 00000000
2928DC   0000000001 0000000000 0000000000 0000000000 00000000
```

2928CA	0000000000	0000000000	0000000000	0000001000	00000000
2928AD	0000000001	0000000000	0000000000	0000000000	00000000
2928AC	0000000001	0000000000	0010000000	0001001000	00100000
2928AB	0000000001	0000000000	0000000000	0000000000	00000000
2928AA	0000000000	0000000000	0000000000	0000001000	00110000
2927DC	0000000000	0000000000	0000000000	0000001000	00000000
2927BD	0000000001	0000000000	0010000000	1000001000	00010000
2927BC	0000000001	0000000000	0000000000	0000000000	00110000
2927BB	0000000001	0000000000	0000000000	0000001000	00000000
2927AD	0000000000	0000000000	0000000000	0000001000	00000000
2927AC	0000000000	0000000000	0000000000	0000001000	00000000
2927AB	0000000000	0000000000	0000000000	0000001000	00000000
2926BB	0000000000	0000000000	0000000000	0000001000	00000000
2925CD	0000000000	0000010000	0000000000	0000000000	00000000
2925CC	0000000000	0000010000	0000000000	0000000000	00000000
2925CB	0000000000	0000010000	0000000000	0000000000	00000000
2925AB	0000000000	0000010000	0000000000	0000000000	00000000
2832CC	0000000000	0000000000	0000001010	0000000000	00000000
2832AD	0000100000	0000000000	0000010010	0000000000	00000000
2832AC	0000000000	0000000000	0000010010	0000000000	00000000
2832AB	0000000000	0000000000	0000010000	0000000000	00000000
2832AA	0000000000	0000000000	0100010000	0000000000	00000100
2831DD	0000000000	0000000000	0000010010	0000000000	00000000
2831DC	0000000000	0000000000	0000010010	0000000000	00000000
2831CD	0000000000	0000000000	0000000110	0000000000	00000000
2831CC	0000000000	0000000000	0100000000	0000000000	00000000
2831CB	0000000000	0000000000	0000000000	0000000000	00000100
2831CA	0000000010	0000000000	0000100100	0000000000	00000100
2831BB	0000000000	0000000000	0000000000	0000000000	00000100
2830DD	0000000010	0000000000	0000000100	0000000000	00010010
2830DB	0000000000	0000000000	0100010000	0000000000	00000100
2830BA	0000100000	0000000000	0000000000	0000000000	00000100
2830AD	0000000000	0000000000	1000000000	0000000000	00000000
2830AB	0000100000	0000000000	0000000000	0000000000	00000000
2830AA	0000000000	0000000010	0000000000	0000000000	00000000
2829DD	0000010000	0000000000	0000000000	0000000000	00000000
2829DC	0000000000	0000000000	0100000000	0000000000	00000000
2829CC	0011000000	0000001000	0001010100	0001001000	00000000
2829CB	0000000001	0000000000	0000000000	0100000000	00000000
2829CA	0000001000	0000000000	0000000101	0001000000	00010000
2829BD	0000000000	0000000000	0000000000	0000000000	00010000
2829BB	0100000000	0000000000	0000000000	0000000000	00000000
2829BA	0000000000	0000000000	0000000100	0000000000	00000000
2829AD	0010001001	0000010001	0000000101	0001000000	00011000
2829AC	0010000001	0000000000	0000000100	0001000000	00010000
2828DD	0000001001	0000000000	0000000000	0001001000	00000000
2828DC	0000000001	0000000000	0000000000	0000000000	00100000
2828DB	0010001001	0000000000	0000000100	1001001000	00110000
2828DA	0000000000	0000000000	0000000000	0001001000	00010000
2828CD	0000000001	0000000000	0000000000	0000000000	00000000
2828CC	0000000001	0000000000	0000000000	0000001000	00110000
2828CB	0000000001	0000000000	0000000000	0000001000	00010000
2828CA	0000000000	0000000000	0000000000	0000001000	00010000
2828BD	0000000000	0000000000	0000000000	0000000000	00010000
2828BC	0000000001	0000000000	0000000000	0000000000	00010000
2828AD	0000000000	0000000000	0000000000	0000000000	00010000
2828AC	0000000000	0000000000	0000000000	0000000000	00010000
2828AB	0000000000	0000000000	0000000000	0000001000	00010000
2827DC	0000000000	0000000000	0000000000	0000001000	00000000
2827DA	0000000000	0000000000	0000000000	0000001000	00000000
2827CD	0000000000	0000000000	0000000000	0000001000	00000000
2827BC	0000000000	0000000000	0000000000	0000001000	00000000
2826DD	0000000000	0000010000	0000000000	0000000000	00000000
2826DC	0000000000	0000010000	0000000000	0000000000	00000000
2824AA	0000000000	0000010000	0000000000	0000000000	00000000
2731DD	0000000000	0000000000	0000000000	0000000000	00000100
2731CD	0000000000	0000000100	0000010100	0000000000	00010100
2731CB	0000000000	0000000000	0000000000	0000000000	00010000
2731AA	0000000000	0000000000	0000000100	0000000000	00000000
2730DB	0000000000	0000000000	0000000101	0001000000	00001000
2730DA	0000000000	0000000000	1000000101	0000000000	00000000
2730CD	0000000000	0000000000	0000000000	0000000000	00001000
2730CB	0100000000	0000000000	0000010100	0000000000	00000000
2730CA	0000000000	0000000000	0000000000	0001000000	00000000
2730BC	0100000000	0000000000	0000010000	0000000000	00000000
2730BB	0100000000	0000000000	0000000000	0001000000	00000000
2730AD	0100000000	0000000001	0000000101	0001000000	00000000
2730AC	0100100000	0000000001	0000000101	0001000000	00000000
2730AB	0100000000	0000000000	0000010100	0000000000	00000000

2730AA	0100000000	0000000000	0000000100	0000000000	00000000
2729DD	0000100000	0000000000	0000000000	0000000000	00000000
2729DC	0000000000	0000000000	0000000000	0001000000	00000000
2729DA	0000000001	0000000000	0000000000	0000000000	00000000
2729CC	0000000000	0000000000	0000000100	0000000000	00000000
2729BD	0000000000	0000000000	0000000000	0001000000	00000000
2729BB	0100000000	0000000000	0000000000	0000000000	00000000
2728DA	0000000000	0000010000	0000000000	0000000000	00000000
2728CD	0000000001	0000000000	0000000000	0000000000	00000000
2631DB	0000000000	0000000000	0000000000	0000000000	00000100
2631CD	0000000000	0000000000	0000000000	0000000001	00000000
2631BD	0000000000	0000000000	0000000000	0001000000	00000100
2631AC	0000000000	0000000000	0000000100	0000000000	00000000
2631AA	0000000000	0000000000	0000000100	0001000001	00000010
2630DC	0100000000	0000000001	0000000100	0001000000	00000000
2630CB	0100000000	0000000000	1000000100	0000000000	00000000
2630BC	0000000000	0000000000	0000000000	0001000000	00000000
2630BB	0000000000	0000000000	0000000100	0001000001	00000000
2630BA	0000000000	0000000000	1000000000	0001000000	00000000
2630AB	0000000000	0000000000	0000000000	0001000000	00000000
2630AA	0000000000	0000000000	0000000001	0001000000	00000000
2629DD	0100000000	0000000000	0000000000	0000000000	00000000
2629DB	0100000000	0000000000	0000000000	0001000000	00000000
2629CC	0100000000	0000000000	0000000000	0000000000	00001000
2629BD	0100000000	0000000000	0000000000	0001000000	00000000
2629AD	0000000000	0000000000	0000000000	0000000000	00001000
2629AC	0000000000	0000000000	0000000000	0000000000	00001000
2629DC	0000000000	0000000000	0000000000	0000000000	00001000
2628CA	0000000000	0000000000	0000000000	0001000000	00000000
2628BA	0000000000	0000000000	0000000000	0000000000	00001000
2628AD	0000000000	0000000000	0000000000	0001000000	00000000
2628AB	0000000000	0000000000	0000000000	0001000000	00001000
2628AA	0000000000	0000010000	0000000000	0000000000	00000000
2627DD	0000000000	0000000000	0000000000	0000000000	00001000
2627DC	0000000000	0000000000	0000000000	0000000000	00001000
2627CD	0000000000	0000000000	0000000000	0000000000	00001000
2627CC	0000000000	0000010000	0000000000	0000000000	00001000
2627CA	0000000000	0000010000	0000000000	0000000000	00001000
2627BD	0000000000	0000010000	0000000000	0000000000	00000000
2627BC	0000000000	0000000000	0000000000	0001000000	00000000
2627BB	0000000000	0000000000	0000000000	0001000000	00000000
2626DC	0000000000	0000010000	0000000000	0000000000	00000000
2626BD	0000000000	0000010000	0000000000	0000000000	00000000
2531DD	0000000000	0000000000	0000000000	0000000000	00000100
2531CD	0000000000	0000000000	1000000000	0000000000	00000000
2531CC	0000000000	0000000000	1000000100	0001000000	00000000
2531CA	0000000000	0000000000	1000000001	0000000000	00000000
2531AC	0000000000	0000000001	0000000000	0000000000	00000000
2531AA	0000000000	0000000000	0000000101	0000000000	00000000
2530DD	0000000000	0000000000	1000000101	0000000001	00010000
2530DC	0000000000	0000000000	0000000100	0000000000	00000000
2530DB	0000000000	0000000000	1000000100	0000000000	00000000
2530DA	0000000000	0000000000	1000000100	0000000000	00010000
2530CC	0000000000	0000000000	0000000000	0001010000	00000000
2530CB	0000000000	0000000000	1000000101	0000010000	00011000
2530CA	0000000000	0000000001	0000000000	0001010000	00000000
2530BD	0000000000	0000000000	1000000101	0000000000	00000000
2530BC	0000000000	0000000000	1000000100	0000000000	00010000
2530BB	0000000000	0000000000	0000000101	0001000001	00000000
2530BA	0000000000	0000000001	1000000100	0000000001	00010000
2530AD	0000000000	0000000000	0000000100	0000010000	00000000
2530AC	0000000000	0000000001	0000000100	0001010000	00010000
2530AB	0000000000	0000000000	1000000100	0000010000	00010000
2530AA	0000000000	0000010000	0000000000	0000010000	00000000
2529CD	0000000000	0000010000	0000000000	0001000000	00000000
2529CC	0000000000	0000010000	0000000000	0001000000	00000000
2529CB	0000000000	0000010000	0000000000	0000000000	00000000
2529CA	0000000000	0000010000	0000000000	0000000000	00000000
2529BD	0000000000	0000010000	0000000000	0000000000	00000000
2529BC	0000000000	0000010000	0000000000	0000000000	00000000
2529BB	0000000000	0000000000	0000000100	0000000000	00000000
2529AD	0000000000	0000010000	0000000000	0000000000	00000000
2529AB	0000000000	0000010000	0000000000	0000000000	00000000
2528DD	0000000000	0000010000	0000000000	0000000000	00000000
2528DC	0000000000	0000010000	0000000000	0001000000	00000000
2528CD	0000000000	0000010000	0000000000	0001000000	00000000
2528CC	0000000000	0000010000	0000000000	0001000000	00000000
2528CB	0000000000	0000010000	0000000000	0001000000	00000000
2528CA	0000000000	0000010000	0000000000	0001000000	00000000

2527CD	0000000000 0000010000 0000000000 0000000000 00000000
2527CB	0000000000 0000010000 0000000000 0000000000 00000000
2527CA	0000000000 0000010000 0000000000 0000000000 00000000
2526DD	0000000000 0000010000 0000000000 0000000000 00000000
2526DA	0000000000 0000010000 0000000000 0000000000 00001000
2526CA	0000000000 0000010000 0000000000 0000000000 00000000
2526AD	0000000000 0000010000 0000000000 0000000000 00000000
2525BD	0000000000 0000010000 0000000000 0000000000 00000000
2431CC	0000000000 0000000000 0000000100 0000000000 00000000
2431CA	0000000000 0000000000 0000000001 0000000000 00000000
2430DD	0000000000 0000000000 1000000101 0000010000 00000000
2430DC	0000000000 0000000000 1000000100 0000000000 00001000
2430DB	0000000000 0000000000 1000000100 0001000000 00010000
2430CD	0000000000 0000000000 0000000000 0000000000 00001000
2430CA	0000000000 0000010000 0000000000 0000000000 00000000
2430AB	0000000000 0010000000 0000000000 0000000000 00000000
2430AA	0000000000 0010000000 0000000000 0000000001 00000000
2429BB	0000000000 0010000000 0000000000 0000000000 00000000
2429AA	0000000000 0000010000 0000000000 0000000000 00000000
2428CD	0000000000 0000010000 0000000000 0000000000 00000000
2428CB	0000000000 0000010000 0000000000 0000000000 00000000
2428BC	0000000000 0000010000 0000000000 0000000000 00000000
2428AC	0000000000 0000010000 0000000000 0000000000 00000000
2427BC	0000000000 0010010000 0000000000 0000000000 00000000
2330CC	0000000000 0010000000 0000000001 0000000001 00000000
2330CA	0000000000 0000000000 0000000001 0000000001 00000000
2329DD	0000000000 0011000000 0000000001 0000000001 00000000
2329BB	0000000000 0010000000 0000000000 0000000001 00000000
2329AA	0000000000 0010000000 0000000000 0000000000 00000000
2328CB	0000000000 0000010000 0000000000 0000000000 00000000
2328BB	0000000000 0010000000 0000000000 0000000000 00000000
2230CD	0000000000 0010000000 0000000001 0000000001 00000000
2230CC	0000000000 0010000000 0000000000 0000000000 00000000
2229DD	0000000000 0010000000 0000000001 0000000000 00000000

Appendix 2: Data matrix with *Kniphofia* species as characters and HDGs as terminal units (with singleton HDGs removed)

```
3424BX    0000100000 1000000000 0000000000 0000000000 00000001
3423AX    0000000000 0000000000 0000000100 0000100000 00000001
3421BX    0000000000 0000000000 0000000000 0000000000 00000001
3419AX    0000000000 0000000000 0000000000 0000000000 01000001
3418BX    0000000000 0000000000 0000000000 0000000000 01000001
3326DX    0000100000 1000000000 0000000000 0000000000 00000000
3326BX    0000100000 1000000000 0000000000 0000000000 00000000
3326AX    0000000000 1000000000 0000000000 0000000000 00000001
3325DX    0000100000 1000000000 0000000000 0000000000 00000001
3325CX    0000000000 1000000000 0000000000 0000000000 00000001
3324CX    0000100000 0000000000 0000000000 0000000000 00000001
3323DX    0000100000 0000000000 0000000000 0000100000 00000001
3323CX    0000100000 0000000000 0000000000 0000000000 00000001
3322DX    0000000000 0000000000 0000000000 0000100000 00000001
3319CX    0000000000 0000000000 0000000100 0000000000 00000001
3319BX    0000000000 0000000000 0000000100 0000000010 00000000
3318DX    0000000000 0000000000 0000000000 0000000000 01000001
3228CX    0000000000 0000000000 0000000000 0100000100 00000000
3228AX    0000100000 0000000000 0000000100 0000000000 00000000
3227DC    0000000100 1000000000 0000000100 0000000100 00000001
3227CX    0000100000 1000000100 0000000100 0100000100 00010001
3227AX    0000000000 0000000000 0000000100 0100000000 00010001
3226DX    0000000000 0000000000 0000000100 1100000000 00010001
3226CX    0000000000 0000000000 0000000100 0000000000 00010001
3226BX    0000100000 0000000000 0000000100 1000000000 00010001
3226AX    0000000001 0000000000 0000000100 0000000000 00010001
3225DX    0000000000 0000000000 0000000100 0000000000 00010000
3225AX    1000000000 0000000000 0000000000 0000000000 00000001
3224BX    0000000000 0000000000 0000000100 0000000000 00000001
3222AX    0000000000 0000000000 0000000000 0000100000 00000001
3130AX    0000000000 0100000000 0000010000 0100000100 00000000
3129DX    0000000000 0000000000 0000010100 0000000000 00000000
3129CX    0000100000 0000000000 0000000100 0000000000 00000000
3129BX    0000000000 0100100000 0100010100 0100000100 00000000
3128DX    0000100000 0000000000 0100000100 1000000000 00000100
3128CX    0000100000 0000000000 0000000100 0100000000 00000001
3128AX    0000100000 0000000000 0000000100 1100000000 00010001
3127DX    0000100000 0000000000 0000000000 0100000000 00000000
3127BX    0000100000 0000000000 0000000100 0100000000 10010001
3126DX    0000000001 0000000000 0000000100 1000000000 10010001
3126BX    0000000000 0000000000 0000000100 0000000000 10000000
3030DX    0000000000 0000000000 0100000000 0000000100 00000000
3030CX    0000100000 0100000000 0100000100 0000000100 00000100
3030BX    0000000000 0000000000 0100010010 0000000100 00010100
3030AX    0000000000 0000000000 0101010110 0000000000 00000100
3029DX    0100110000 0000100000 0100010100 0100000000 00000100
3029CX    0000100000 0000000000 0000010100 1101000000 00000000
3029BX    0000010000 0000000000 0000010100 0100000000 00000100
3029AX    0000100000 0000000000 0000010100 0100000000 00010000
3028CX    0000100000 0000000000 0010000100 1100001000 10010000
3028BX    0000100001 0000000001 0000000100 0000000000 10010000
3027DX    0010000001 0000000000 0010000000 1000000000 10010000
3027CX    0000000001 0000000000 0000000000 0000000000 10010000
2931CX    0000000000 0000000000 0100010010 0010000000 00000000
2931AX    0000000000 0000000000 0000000010 0000000100 00000000
2930DX    0000000010 0000000000 0100010110 0010000000 00000100
2930CX    0000100010 0000000000 0001010100 0000000000 00010100
2930BX    0010000010 0000000000 0101100000 0000000000 00000100
2930AX    0000000010 0000000001 0001110100 0000000000 00000100
2929DX    0001000000 0000000101 0000010100 0100000000 00010000
2929CX    0010011001 0000000101 0001010100 1001001000 00110000
2929BX    0011011001 0000000001 0001010100 1001001000 00100000
2929AX    0011010001 0000001100 0001010100 1101001000 00110000
2928AX    0000000001 0000000000 0010000000 0001001000 00110000
2927BX    0000000001 0000000000 0010000000 1000001000 00110000
2832CX    0000000000 0000000000 0000001010 0000000000 00000000
2832AX    0000100000 0000000000 0100010010 0000000000 00000100
2831DX    0000000000 0000000000 0000010010 0000000000 00000000
2831CX    0000000010 0000000000 0100100110 0000000000 00000100
2830DX    0000000010 0000000000 0100010100 0000000000 00010110
2830BX    0000100000 0000000000 0000000000 0000000000 00000100
2830AX    0000100000 0000000010 1000000000 0000000000 00000000
2829DX    0000010000 0000000000 0100000000 0000000000 00000000
```

```
2829CX    0011001001 0000001000 0001010101 0101001000 00010000
2829BX    0100000000 0000000000 0000000100 0000000000 00010000
2829AX    0010001001 0000010001 0000000101 0001000000 00011000
2828DX    0010001001 0000000000 0000000100 1001001000 00110000
2828CX    0000000001 0000000000 0000000000 0000001000 00110000
2828BX    0000000001 0000000000 0000000000 0000000000 00010000
2828AX    0000000000 0000000000 0000000000 0000001000 00010000
2731CX    0000000000 0000000100 0000010100 0000000000 00010100
2730DX    0000000000 0000000000 1000000101 0001000000 00001000
2730CX    0100000000 0000000000 0000010100 0001000000 00001000
2730BX    0100000000 0000000000 0000010000 0001000000 00000000
2730AX    0100100000 0000000001 0000010101 0001000000 00000000
2729DX    0000100001 0000000000 0000000000 0001000000 00000000
2729BX    0100000000 0000000000 0000000000 0001000000 00000000
2728DX    0000000001 0000010000 0000000000 0000000000 00000000
2631BX    0000000000 0000000000 0000000000 0001000000 00000100
2631AX    0000000000 0000000000 0000000100 0001000001 00000010
2630DX    0100000000 0000000001 0000000100 0001000000 00000000
2630CX    0100000000 0000000000 1000000100 0000000000 00000000
2630BX    0000000000 0000000000 1000000100 0001000001 00000000
2630AX    0000000000 0000000000 0000000001 0001000000 00000000
2629DX    0100000000 0000000000 0000000000 0001000000 00000000
2629CX    0100000000 0000000000 0000000000 0000000000 00001000
2629BX    0100000000 0000000000 0000000000 0001000000 00000000
2628AX    0000000000 0000010000 0000000000 0001000000 00001000
2627CX    0000000000 0000010000 0000000000 0000000000 00001000
2627BX    0000000000 0000010000 0000000000 0001000000 00000000
2531CX    0000000000 0000000000 1000000101 0001000000 00000000
2531AX    0000000000 0000000001 0000000101 0000000000 00000000
2530DX    0000000000 0000000000 1000000101 0000000001 00010000
2530CX    0000000000 0000000001 1000000101 0001010000 00011000
2530BX    0000000000 0000000001 1000000101 0001000001 00010000
2530AX    0000000000 0000010001 1000000100 0001010000 00010000
2529CX    0000000000 0000010000 0000000000 0001000000 00000000
2529BX    0000000000 0000010000 0000000100 0000000000 00000000
2528DX    0000000000 0000010000 0000000000 0001000000 00000000
2528CX    0000000000 0000010000 0000000000 0001000000 00000000
2526DX    0000000000 0000010000 0000000000 0000000000 00001000
2431CX    0000000000 0000000000 0000000101 0000000000 00000000
2430DX    0000000000 0000000000 1000000101 0001010000 00011000
2430CX    0000000000 0000010000 0000000000 0000000000 00001000
2430AX    0000000000 0010000000 0000000000 0000000001 00000000
2427BX    0000000000 0010010000 0000000000 0000000000 00000000
2330CX    0000000000 0010000000 0000000001 0000000001 00000000
2329DX    0000000000 0011000000 0000000001 0000000001 00000000
2329BX    0000000000 0010000000 0000000000 0000000001 00000000
2230CX    0000000000 0010000000 0000000001 0000000001 00000000
2229DX    0000000000 0010000000 0000000001 0000000000 00000000
```

Appendix 3: PCR reagents

Table 1. Table of PCR reagents and volumes (µl) used for PCR reactions

Mg concentration	H_2O	10X Buffer	dNTPs	Primer 1	Primer 2	BioTaq	DNA	$MgCl_2$
1]	35.5	5	2	2	2	0.1	2.5	1
2]	34.5	5	2	2	2	0.1	2.5	2
3]	33.5	5	2	2	2	0.1	2.5	3
4]	32.5	5	2	2	2	0.1	2.5	4
5]	31.5	5	2	2	2	0.1	2.5	5

Mg concentration= Magnesium concentration
H_2O= PCR quality water
10X Buffer= 10X Bioline NH_4 dilution buffer ($MgCl_2$ free)
BioTaq= Bioline Taq polymerase enzyme
DNA= DNA template
$MgCl_2$= 50mM solution of $MgCl_2$ provided with enzyme and enzyme and 10X Buffer

Appendix 4: Final sequence alignments of the *trnT-L* spacer

```
[                                            10          20          30          40          50         60]
[                                            .          .          .          .          .          .]

Bulbine latifolia SR61             ATTTTAAAAA ATAGATTTAT AAATAGAAAT TTTTATTAAT GAGAATTGAA T---TTAAGT   [57]
Bulbinella cauda-felis SR204       TATTTATAGA ATAGATTTCT AAATAGAAAT TTTGATTAAT GAAAAT---- ----TTAAGT   [52]
K. acreae TD4626                   AATTTCAAAA ATATATTTAT AAATAGAAAT TTTGATTAAT GATAAT---- ----TTAAGT   [52]
K. albescens SR314                 AATTTCAAAA ATATATTTAT AAATAGAAAT TTTGATTAAT GATAAT---- ----TTAAGT   [52]
K. albomontana SR149               AATTTCAAAA ATATATTTAT AAATAGAAAT TTTGATTAAT GATAAT---- ----TTAAGT   [52]
K. angustifolia SR453              AATTTCAAAA ATATATTTAT AAATAGAAAT TTGGATTAAT GATAAT---- ----TTAAGT   [52]
K. angustifolia SR542              AATTTCAAAA ATATATTTAT AAATAGAAAT TTTGATTAAT GATAAT---- ----TTAAGT   [52]
K. ankaratrensis PBP5676           AATTTCAAAA ATATATTTAT TAATAGAAAT TTAGATTAAT GATAAT---- ----TTAAGT   [52]
K. baurii SR174                    AATTTCAAAA ATATATTTAT AAATAGAAAT TTTGATTAAT GATAAT---- ----TTAAGT   [52]
K. baurii SR202                    AATTTCAAAA ATATATTTAT AAATAGAAAT TTTGATTAAT GATAAT---- ----TTAAGT   [52]
K. baurii SR275                    AATTTCAAAA ATATATTTAT AAATAGAAAT TTGGATTAAT GATAAT---- ----TTAAGT   [52]
K. baurii SR285                    AATTTCAAAA ATATATTTAT AAATAGAAAT TTTGATTAAT GATAAT---- ----TTAAGT   [52]
K. baurii SR360                    AATTTCAAAA ATATATTTAT AAATAGAAAT TTTGATTAAT GATAAT---- ----TTAAGT   [52]
K. baurii SR382                    AATTTCAAAA ATATATTTAT AAATAGAAAT TTTGATTAAT GATAAT---- ----TTAAGT   [52]
K. baurii SR398                    AATTTCAAAA ATATATTTAT AAATAGAAAT TTTGATTAAT GATAAT---- ----TTAAGT   [52]
K. baurii NPB1923                  AATTTTAAAA ATATATTTAT AAATAGAAAT TTTGATTAAT GATAAT---- ----TTAAGT   [52]
K. baurii RJM1026                  AATTTCAAAA ATATATTTAT AAATAGAAAT TTGGATTAAT GATAAT---- ----TTAAGT   [52]
K. bracystachya SRsn               AATTTCAAAA ATATATTTAT AAATAGAAAT TTTGATTAAT GATAAT---- ----TTAAGT   [52]
K. breviflora SR452                AATTTCAAAA ATATATTTAT AAATAGAAAT TTTGATTAAT GATAAT---- ----TTAAGT   [52]
K. bruceae SR171                   AATTTCAAAA ATATATTTAT AAATAGAAAT TTTGATTAAT GATAAT---- ----TTAAGT   [52]
K. buchananii SR305                AATTTCAAAA ATATATTTAT AAATAGAAAT TTTGATTAAT GATAAT---- ----TTAAGT   [52]
K. buchananii SR307                AATTTCAAAA ATATATTTAT AAATAGAAAT TTTGATTAAT GATAAT---- ----TTAAGT   [52]
K. buchananii SR458                AATTTCAAAA ATATATTTAT AAATAGAAAT TTTGATTAAT GATAAT---- ----TTAAGT   [52]
K. caulescens SR270                AATTTCAAAA ATATATTTAT AAATAGAAAT TTTGATTAAT GATAAT---- ----TTAAGT   [52]
K. caulescens SR278                AATTTCAAAA ATATATTTAT AAATAGAAAT TTTGATTAAT GATAAT---- ----TTAAGT   [52]
K. caulescens NPB1821              AATTTCAAAA ATATATTTAT AAATAGAAAT TTTGATTAAT GATAAT--AA TAATTTAAGT   [58]
K. caulescens RJM974               AATTTCAAAA ATATATTTAT AAATAGAAAT TTTGATTAAT GATAAT---- ----TTAAGT   [52]
K. citrina SR176                   AATTTCAAAA ATATATTTAT AAATAGAAAT TTTGATTAAT GATAAT---- ----TTAAGT   [52]
K. coddiana SRsn                   AATTTCAAAA ATATATTTAT AAATAGAAAT TTTGATTAAT GATAAT---- ----TTAAGT   [52]
K. corraligemma SR549              AATTTCAAAA ATATATTTAT AAATAGAAAT TTTGATTAAT GATAAT---- ----TTAAGT   [52]
K. drepanophylla RAL4816           AATTTCAAAA ATATATTTAT AAATAGAAAT TTTGATTAAT GATAAT---- ----TTAAGT   [52]
K. drepanophylla RJM1100           AATTTCAAAA ATATATTTAT AAATAGAAAT TTTGATTAAT GATAAT---- ----TTAAGT   [52]
K. ensifolia autumnalis SR448      AATTTCAAAA ATATATTTAT AAATAGAAAT TTTGATTAAT GATAAT---- ----TTAAGT   [52]
K. ensifolia ensifolia JBsn        AATTTCAAAA ATATATTTAT AAATAGAAAT TTTGATTAAT GATAAT---- ----TTAAGT   [52]
K. fibrosa SR297                   AATTTCAAAA ATATATTTAT AAATAGAAAT TTTGATTAAT GATAAT---- ----TTAAGT   [52]
K. fibrosa PBP5579                 AATTTCAAAA ATATATTTAT AAATAGAAAT TTTGATTAAT GATAAT---- ----TTAAGT   [52]
K. foliosa SR383                   AATTTCAAAA ATATATTTAT TAATAGAAAT TTAGATTAAT GATAAT---- ----TTAAGT   [52]
K. foliosa SR387                   AATTTCAAAA ATATATTTAT TAATAGAAAT TTAGATTAAT GATAAT---- ----TTAAGT   [52]
K. foloisa SR389                   AATTTCAAAA ATATATTTAT TAATAGAAAT TTAGATTAAT GATAAT---- ----TTAAGT   [52]
K. foliosa SR390                   AATTTCAAAA ATATATTTAT TAATAGAAAT TTAGATTAAT GATAAT---- ----TTAAGT   [52]
K. foliosa JMG034                  AATTTCAAAA ATATATTTAT TAATAGAAAT TTAGATTAAT GATAAT---- ----TTAAGT   [52]
K. foliosa JMG038                  AATTTCAAAA ATATATTTAT TAATAGAAAT TTAGATTAAT GATAAT---- ----TTAAGT   [52]
K. galpinii SR312                  AATTTCAAAA ATATATTTAT AAATAGAAAT TTTGATTAAT GATAAT---- ----TTAAGT   [52]
K. gracilis SR321                  AATTTCAAAA ATATATTTAT AAATAGAAAT TTTGATTAAT GATAAT---- ----TTAAGT   [52]
K. gracilis SR561                  AATTTCAAAA ATATATTTAT AAATAGAAAT TTTGATTAAT GATAAT---- ----TTAAGT   [52]
K. gracilis NNBG                   AATTTCAAAA ATATATTTAT AAATAGAAAT TTTGATTAAT GATAAT---- ----TTAAGT   [52]
K. grantii CP4154                  AATTTCAAAA ATATATTTAT AAATAGAAAT TTTGATTAAT GATAAT---- ----TAAAGT   [52]
K. hirsuta SR282                   AATTTCAAAA ATATATTTAT AAATAGAAAT TTTGATTAAT GATAAT---- ----TTAAGT   [52]
K. ichopensis SR242                AATTTCAAAA ATATATTTAT AAATAGAAAT TTTGATTAAT GATAAT---- ----TTAAGT   [52]
K. ichopensis SR286                AATTTCAAAA ATATATTTAT AAATAGAAAT TTTGATTAAT GATAAT---- ----TTAAGT   [52]
K. ichopensis SR289                AATTTCAAAA ATATATTTAT AAATAGAAAT TTTGATTAAT GATAAT---- ----TTAAGT   [52]
K. ichopensis SR409                AATTTCAAAA ATATATTTAT AAATAGAAAT TTTGATTAAT GATAAT---- ----TTAAGT   [52]
K. insignis SRsn                   AATTTCAAAA ATATATTTAT TAATAGAAAT TTAGATTAAT GATAAT---- ----TTAAGT   [52]
K. isoetifolia SR386               AATTTCAAAA ATATATTTAT TAATAGAAAT TTAGATTAAT GATAAT---- ----TTAAGT   [52]
K. isoetifolia SR388               AATTTCAAAA ATATATTTAT TAATAGAAAT TTAGATTAAT GATAAT---- ----TTAAGT   [52]
K. isoetifolia SR393               AATTTCAAAA ATATATTTAT TAATAGAAAT TTAGATTAAT GATAAT---- ----TTAAGT   [52]
K. latifolia RSSsn                 AATTTCAAAA ATATATTTAT AAATAGAAAT TTTGATTAAT GATAAT---- ----TTAAGT   [52]
K. laxiflora SR283                 AATTTCAAAA ATATATTTAT AAATAGAAAT TTTGATTAAT GATAAT---- ----TTAAGT   [52]
K. laxiflora SR295                 AATTTCAAAA ATATATTTAT AAATAGAAAT TTTGATTAAT GATAAT---- ----TTAAGT   [52]
K. laxiflora SR441                 AATTTCAAAA A----TTTAT AAATAGAAAT TTTGATTAAT GATAAT---- ----TTAAGT   [48]
K. laxiflora SR442                 AATTTCAAAA ATATATTTAT AAATAGAAAT TTTGATTAAT GATAAT---- ----TTAAGT   [52]
K. laxiflora SR467                 AATTTCAAAA ATATATTTAT AAATAGAAAT TTTGATTAAT GATAAT---- ----TTAAGT   [52]
K. laxiflora SR468                 AATTTCAAAA ATATATTTAT AAATAGAAAT TTTGATTAAT GATAAT---- ----TTAAGT   [52]
K. laxifloraC SRsn                 AATTTCAAAA ATATATTTAT AAATAGAAAT TTTGATTAAT GATAAT---- ----TTAAGT   [52]
K. laxiflora NPB1810               AATTTCAAAA A----TTTAT AAATAGAAAT TTTGATTAAT GATAAT---- ----TTAAGT   [48]
K. leucocephala NNBG               AATTTCAAAA ATATATTTAT AAATAGAAAT TTTGATTAAT GATAAT---- ----TTAAGT   [52]
K. linearifolia SR269              AATTTCAAAA ATATATTTAT AAATAGAAAT TTTGATTAAT GATAAT---- ----TTAAGT   [52]
K. linearifolia SR287              AATTTCAAAA ATATATTTAT AAATATAAAT TTTGATTAAT GATAAT---- ----TTAAGT   [52]
K. linearifolia SR290              AATTTCAAAA ATATATTTAT AAATAGAAAT TTTGATTAAT GATAAT---- ----TTAAGT   [52]
K. linearifolia SR291              AATTTCAAAA ATATATTTAT AAATAGAAAT TTTGATTAAT GATAAT---- ----TTAAGT   [52]
K. linearifolia SR311              AATTTCAAAA ATATATTTAT AAATAGAAAT TTTGATTAAT GATAAT---- ----TTAAGT   [52]
K. linearifolia SR328              AATTTCAAAA ATATATTTAT AAATAGAAAT TTTGATTAAT GATAAT---- ----TTAAGT   [52]
K. linearifolia SR343              AATTTCAAAA ATATATTTAT AAATAGAAAT TTTGATTAAT GATAAT---- ----TTAAGT   [52]
K. linearifolia SR400              AATTTAAAAA ATATATTTAT AAATAGAAAT TTTGATTAAT GATAAT---- ----TTAAGT   [52]
K. linearifolia SR558              AATTTCAAAA ATATATTTAT AAATAGAAAT TTTGATTAAT GATAAT---- ----TTAAGT   [52]
K. linearifolia JPsn               AATTTCAAAA ATATATTTAT AAATAGAAAT TTTGATTAAT GATAAT---- ----TTAAGT   [52]
K. linearifolia TD4638             AATTTCAAAA ATATATTTAT AAATAGAAAT TTTGATTAAT GATAAT---- ----TTAAGT   [52]
K. littoralis SR200                AATTTCAAAA ATATATTTAT AAATAGAAAT TTTGATTAAT GATAAT---- ----TTAAGT   [52]
K. multiflora SR310                AATTTCAAAA ATATATTTAT AAATAGAAAT TTTGATTAAT GATAAT---- ----TTAAGT   [52]
K. northiae SR263                  AATTTCAAAA ATATATTTAT AAATAGAAAT TTTGATTAAT GATAAT---- ----TTAAGT   [52]
K. northiae SR274                  AATTTCAAAA ATATATTTAT AAATAGAAAT TTTGATTAAT GATAAT---- ----TTAAGT   [52]
K. northiae SR446                  AATTTCAAAA ATATATTTAT AAATAGAAAT TTTGATTAAT GATAAT---- ----TTAAGT   [52]
K. pauciflora HBsn                 AATTTCAAAA ATATATTTAT AAATAGAAAT TTTGATTAAT GATAAT---- ----TTAAGT   [52]
K. parviflora SR268                AATTTCAAAA ATATATTTAT AAATAGAAAT TTTGATTAAT GATAAT---- ----TTAAGT   [52]
K. parviflora SR330                AATTTCAAAA ATATATTTAT AAATAGAAAT TTTGATTAAT GATAAT---- ----TTAAGT   [52]
K. porphyantha SRsn                AATTTCAAAA ATATATTTAT AAATAGAAAT TTTGATTAAT GATAAT---- ----TTAAGT   [52]
K. praecox SR529                   AATTTCAAAA A----TTTAT AAATAGAAAT TTTGATTAAT GATAAT---- ----TTAAGT   [48]
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K. praecox SR530                   AATTTCAAAA ATATATTTAT AAATAGAAAT TTGGATTAAT GATAAT---- ----TTAAGT   [52]
K. praecox SR532                   AATTTCAAAA ATATATTTAT AAATAGAAAT TTTGATTAAT GATAAT---- ----TTAAGT   [52]
K. rigidifolia SRsn                AATTTCAAAA ATATATTTAT AAATAGAAAT TTTGATTAAT GATAAT---- ----TTAAGT   [52]
K. ritualis SR300                  AATTTCAAAA ATATATTTAT AAATAGAAAT TTTGATTAAT GATAAT---- ----TTAAGT   [52]
K. rooperi SR237                   AATTTCAAAA ATATATTTAT AAATAGAAAT TTTGATTAAT GATAAT---- ----TTAAGT   [52]
K. rooperi SR485                   AATTTCAAAA ATATATTTAT AAATAGAAAT TTTGATTAAT GATAAT---- ----TTAAGT   [52]
K. rooperi SR528                   AATTTCAAAA ATATATTTAT AAATAGAAAT TTTGATTAAT GATAAT---- ----TTAAGT   [52]
K. rooperi RAL4227                 AATTTCAAAA ATATATTTAT AAATAGAAAT TTTGATTAAT GATAAT---- ----TTAAGT   [52]
K. rooperi TD4559                  AATTTCAAAA ATATATTTAT AAATAGAAAT TTTGATTAAT GATAAT---- ----TTAAGT   [52]
K. sarmentosa SR207                AATTTCAAAA ATATATTTAT AAATAGAAAT TTTGATTAAT GATAAT---- ----TTAAGT   [52]
K. schemperi SR391                 AATTTCAAAA ATATATTTAT TAATAGAAAT TTAGATTAAT GATAAT---- ----TTAAGT   [52]
K. schimperi JMG036                AATTTCAAAA ATATATTTAT TAATAGAAAT TTAGATTAAT GATAAT---- ----TTAAGT   [52]
K. splendida SR548                 AATTTCAAAA ATATATTTAT AAATAGAAAT TTTGATTAAT GATAAT---- ----TTAAGT   [52]
K. splendida Chapman 9061          AATTTCAAAA ATATATTTAT TAATAGAAAT TTAGATTAAT GATAAT---- ----TTAAGT   [52]
K. stricta SR279                   AATTTCAAAA ATATATTTAT AAATAGAAAT TTTGATTAAT GATAAT---- ----TTAAGT   [52]
K. thodei SR407                    AATTTCAAAA ATATATTTAT AAATAGAAAT TTTGATTAAT GATAAT---- ----TTAAGT   [52]
K. thomsonii JMG031                AATTTCAAAA ATATATTTAT TAATAGAAAT TTAGATTAAT GATAAT---- ----TTAAGT   [52]
K. thomsonii AMM2647               AATTTCAAAA ATATATTTAT TAATAGAAAT TTAGATTAAT GATAAT---- ----TTAAGT   [52]
K. thomsonii CK4821                AATTTCAAAA ATATATTTAT TAATAGAAAT TTAGATTAAT GATAAT---- ----TTAAGT   [52]
K. triangularis SR264              AATTTCAAAA ATATATTTAT AAATAGAAAT TTTGATTAAT GATAAT---- ----TTAAGT   [52]
K. triangularis SR266              AATTTCAAAA ATATATTTAT AAATAGAAAT TTTGATTAAT GATAAT---- ----TTAAGT   [52]
K. triangularis SR299              AATTTCAAAA ATATATTTAT AAATAGAAAT TTTGATTAAT GATAAT---- ----TTAAGT   [52]
K. triangularia obtusiloba SRsn    AATTTCAAAA ATATATTTAT AAATAGAAAT TTTGATTAAT GATAAT---- ----TTAAGT   [52]
K. typhoides NNBG                  AATTTCAAAA ATATATTTAT AAATAGAAAT TTTGATTAAT GATAAT---- ----TTAAGT   [52]
K. tysonii SR302                   AATTTCAAAA ATATATTTAT AAATAGAAAT TTTGATTAAT GATAAT---- ----TTAAGT   [52]
K. tysonii SR303                   AATTTCAAAA ATATATTTAT AAATAGAAAT TTGGATTAAT GATAAT---- ----TTAAGT   [52]
K. tysonii SR460                   AATTTCAAAA ATATATTTAT AAATAGAAAT TTTGATTAAT GATAAT---- ----TTAAGT   [52]
K. umbrina RGsn                    AATTTCAAAA ATATATTTAT AAATAGAAAT TTTGATTAAT GATAAT---- ----TTAAGT   [52]
K. uvaria SR166                    AATTTCAAAA ATATATTTAT AAATAGAAAT TTTGATTAAT GATAAT---- ----TTAAGT   [52]
K. uvaria SR186                    AATTTCAAAA ATATATTTAT AAATAGAAAT TTTGATTAAT GATAAT---- ----TTAAGT   [52]
K. uvaria SR172                    AATTTCAAAA ATATATTTAT AAATAGAAAT TTTGATTAAT GATAAT---- ----TTAAGT   [52]
K. uvaria SR201                    AATTTCAAAA ATATATTTAT AAATAGAAAT TTGGATTAAT GATAAT---- ----TTAAGT   [52]
K. uvaria SR203                    AATTTCAAAA ATATATTTAT AAATAGAAAT TTTGATTAAT GATAAT---- ----TTAAGT   [52]
K. uvaria SR211                    AATTTCAAAA ATATATTTAT AAATAGAAAT TTGGATTAAT GATAAT---- ----TTAAGT   [52]
K. uvaria SR337                    AATTTCAAAA ATATATTTAT AAATAGAAAT TTTGATTAAT GATAAT---- ----TTAAGT   [52]
K. uvaria SR342                    AATTTCAAAA ATATATTTAT AAATAGAAAT TTTGATTAAT GATAAT---- ----TTAAGT   [52]
K. uvaria SR344                    AATTTCAAAA ATATATTTAT AAATAGAAAT TTTGATTAAT GATAAT---- ----TTAAGT   [52]
K. uvaria SR471                    AATTTCAAAA ATATATTTAT AAATAGAAAT TTTGATTAAT GATAAT---- ----TTAAGT   [52]
K. uvaria SR477                    AATTTCAAAA ATATATTTAT AAATAGAAAT TTTGATTAAT GATAAT---- ----TTAAGT   [52]
K. uvaria TD4477                   AATTTCAAAA ATATATTTAT AAATAGAAAT TTTGATTAAT GATAAT---- ----TTAAGT   [52]

[                                            70          80          90          100         110        120]
[                                            .          .          .          .          .         .]

Bulbine latifolia SR61             AATCAGATTT TTGATAATAT CAAATT-TGA TATT---ATG ATTAAAAAAA AAAAAATGGA   [113]
Bulbinella cauda-felis SR204       AATCCTATTT TTGATAATAT CAAATT-TGA TATTATTATG ATTC----AA AAAAAATGGA   [107]
K. acreae TD4626                   AATCAAATTT --GATATTAT GA--TT---- ---------- --------TT AAAAAATGGA   [86]
K. albescens SR314                 AATCAAATTT --GATATTAT GA--TT---- ---------- --------TA AAAAAATGGA   [86]
K. albomontana SR149               AATCAAATTT --GATATTAT GA--TTATGA TT-------- --------TA AAAAAATAGA   [92]
K. angustifolia SR453              AATCAAATTT --GATATTAT GA--TT---- ---------- --------TA AAAAAATGGA   [86]
K. angustifolia SR542              AATCAAATTT --GATATTAT GA--TTATGA TT-------- --------TA AAAAAATAGA   [92]
K. ankaratrensis PBP5676           AATCAAATTT --GATATTAT GA--TT---- ---------- --------TA AAAAAACGGA   [86]
K. baurii SR174                    AATCAAATTT --GATATTAT GA--TTATGA TT-------- --------TT AAAAAATAGA   [92]
K. baurii SR202                    AATCAAATTT --GATATTAT GA--TT---- ---------- --------TA AAAAAATGGA   [86]
K. baurii SR275                    AATCCAATTT --GATATTAT GA--TTATGA TT-------- --------TA AAAAAATAGA   [92]
K. baurii SR285                    AATCCAATTT --GATATTAT GA--TTATGA TT-------- --------TA AAAAAATAGA   [92]
K. baurii SR360                    AATCAAATTT --GATATTAT GA--TT---- ---------- --------TA AAAAAATGGA   [86]
K. baurii SR382                    AATCAAATTT --GATATTAT GA--TT---- ---------- --------TA AAAAAATGGA   [86]
K. baurii SR398                    AATCAAATTT --GATATTAT GA--TTATGA TT-------- --------TA AAAAAATAGA   [92]
K. baurii NPB1923                  AATCAAATTT --GATATTAT GA--TT---- ---------- --------TA AAAAAATGGA   [86]
K. baurii RJM1026                  AATCAAATTT --GATATTAT GA--TT---- ---------- --------TA AAAAAATGGA   [86]
K. bracystachya SRsn               AATCAAATTT --GATATTAT GA--TT---- ---------- --------TA AAAAAATGGA   [86]
K. breviflora SR452                AATCAAATTT --GATATTAT GA--TT---- ---------- --------TA AAAAAATGGA   [86]
K. bruceae SR171                   AATCCAATTT --GATATTAT GA--TTATGA TT-------- --------TA AAAAAATAGA   [92]
K. buchananii SR305                AATCAAATTT --GATATTAT GA--TTATGA TT-------- --------TA AAAAAATAGA   [92]
K. buchananii SR307                AATCAAATTT --GATATTAT GA--TTATGA TT-------- --------TA AAAAAATAGA   [92]
K. buchananii SR458                AATCAAATTT --GATATTAT GA--TTATGA TT-------- --------TA AAAAAATAGA   [92]
K. caulescens SR270                AATCAAATTT --GATATTAT GA--TT---- ---------- --------TA AAAAAATGGA   [86]
K. caulescens SR278                AATCAAATTT --GATATTAT GA--TT---- ---------- --------TA AAAAAATGGA   [86]
K. caulescens NPB1821              AATCAAATTT --GATATTAT GA--TT---- ---------- --------TA AAAAAATGGA   [92]
K. caulescens RJM974               AATCAAATTT --GATATTAT GA--TT---- ---------- --------TA AAAAAATGGA   [86]
K. citrina SR176                   AATCAAATTT --GATATTAT GA--TT---- ---------- --------TA AAAAAATGGA   [86]
K. coddiana SRsn                   AATCCAATTT --GATATTAT GA--TTATGA TT-------- --------TA AAAAAATAGA   [92]
K. corraligemma SR549              AATCAAATTT --GATATTAT GA--TT---- ---------- --------AA AAAAAATGGA   [86]
K. drepanophylla RAL4816           AATCCAATTT --GATATTAT GA--TTATGA TT-------- --------TA AAAAAATAGA   [92]
K. drepanophylla RJM1100           AATCAAATTT --GATATTAT GA--TTATGA TT-------- --------TA AAAAAATAGA   [92]
K. ensifolia autumnalis SR448      AATCAAATTT --GATATTAT GA--TT---- ---------- --------TA AAAAAATGGA   [86]
K. ensifolia ensifolia JBsn        AATCAAATTT --GATATTAT GA--TT---- ---------- --------TA AAAAAATGGA   [86]
K. fibrosa SR297                   AATCAAATTT --GATATTAT GA--TTATGA TT-------- --------TA AAAAAATAGA   [92]
K. fibrosa PBP5579                 AATCAAATTT --GATATTAT GA--TT---- ---------- --------TT AAAAAATGGA   [86]
K. foliosa SR383                   AATCAAATTT --GATATTAT GA--TT---- ---------- --------TA AAAAAATGGA   [86]
K. foliosa SR387                   AATCAAATTT --GATATTAT GA--TT---- ---------- --------TA AAAAAATGGA   [86]
K. foloisa SR389                   AATCAAATTT --GATATTAT GA--TT---- ---------- --------TA AAAAAATGGA   [86]
K. foliosa SR390                   AATCAAATTT --GATATTAT GA--TT---- ---------- --------TA AAAAAATGGA   [86]
K. foliosa JMG034                  AATCAAATTT --GATATTAT GA--TT---- ---------- --------TA AAAAAATGGA   [86]
K. foliosa JMG038                  AATCAAATTT --GATATTAT GA--TT---- ---------- --------TA AAAAAATGGA   [86]
K. galpinii SR312                  AATCAAATTT --GATATTAT GA--TT---- ---------- --------TA AAAAAATGGA   [86]
K. gracilis SR321                  AATCAAATTT --GATATTAT GA--TTATGA TT-------- --------TA AAAAAATAGA   [92]
K. gracilis SR561                  AATCAAATTT --GATATTAT GA--TTATGA TT-------- --------TA AAAAAATAGA   [92]
K. gracilis NNBG                   AATCAAATTT --GATATTAT GA--TTATGA TT-------- --------TA AAAAAATAGA   [92]
K. grantii CP4154                  AATCAAATTT --GATATTAT GA--TT---- ---------- --------TA AAAAAATGGA   [86]
K. hirsuta SR282                   AATCCAATTT --GATATTAT GA--TTATGA TT-------- --------TA AAAAAATAGA   [92]
K. ichopensis SR242                AATCAAATTT --GATATTAT GA--TTATGA TT-------- --------TA AAAAAATAGA   [92]
K. ichopensis SR286                AATCAAATTT --GATATTAT GA--TTATGA TT-------- --------TA AAAAAATAGA   [92]
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K. ichopensis SR289                AATCAAATTT --GATATTAT GA--TTATGA TT-------- --------TA AAAAAATAGA   [92]
K. ichopensis SR409                AATCAAATTT --GATATTAT GA--TTATGA TT-------- --------TA AAAAAATAGA   [92]
K. insignis SRsn                   AATCAAATTT --GATATTAT GA--TT---- ---------- --------TA AAAAAATGGA   [86]
K. isoetifolia SR386               AATCAAATTT --GATATTAT GA--TT---- ---------- --------TA AAAAAATGGA   [86]
K. isoetifolia SR388               AATCAAATTT --GATATTAT GA--TT---- ---------- --------TA AAAAAATGGA   [86]
K. isoetifolia SR393               AATCAAATTT --GATATTAT GA--TT---- ---------- --------TA AAAAAATGGA   [86]
K. latifolia RSSsn                 AATCAAATTT --GATATTAT GA--TTATGA TT-------- --------TA AAAAAATAGA   [92]
K. laxiflora SR283                 AATCAAATTT --GATATTAT GA--TTATGA TT-------- --------TA AAAAAATAGA   [92]
K. laxiflora SR295                 AATCCAATTT --GATATTAT GA--TTATGA TT-------- --------TA AAAAAATAGA   [92]
K. laxiflora SR441                 AATCAAATTT --GATATTAT GA--TTATGA TT-------- --------TA AAAAAATAGA   [88]
K. laxiflora SR442                 AATCAAATTT --GATATTAT GA--TTATGA TT-------- --------TA AAAAAATAGA   [92]
K. laxiflora SR467                 AATCAAATTT --GATATTAT GA--TTATGA TT-------- --------TA AAAAAATAGA   [92]
K. laxiflora SR468                 AATCAAATTT --GATATTAT GA--TTATGA TT-------- --------TA AAAAAATAGA   [92]
K. laxifloraC SRsn                 AATCAAATTT --GATATTAT GA--TT---- ---------- --------TA AAAAAATGGA   [86]
K. laxiflora NPB1810               AATCAAATTT --GATATTAT GA--TTATGA TT-------- --------TA AAAAAATAGA   [88]
K. leucocephala NNBG               AATCAAATTT --GATATTAT GA--TT---- ---------- --------TA AAAAAATGGA   [86]
K. linearifolia SR269              AATCAAATTT --GATATTAT GA--TT---- ---------- --------TT TAAAAATGGA   [86]
K. linearifolia SR287              AATCAAATTT --GATATTAT GA--TTATGA TT-------- --------TA AAAAAATAGA   [92]
K. linearifolia SR290              AATCAAATTT --GATATTAT GA--TTATGA TT-------- --------TA AAAAAATAGA   [92]
K. linearifolia SR291              AATCAAATTT --GATATTAT GA--TTATGA TT-------- --------TA AAAAAATAGA   [92]
K. linearifolia SR311              AATCAAATTT --GATATTAT GA--TT---- ---------- --------TA AAAAAATGGA   [86]
K. linearifolia SR328              AATCAAATTT --GATATTAT GA--TTATGA TT-------- --------TA AAAAAATAGA   [92]
K. linearifolia SR343              AATCAAATTT --GATATTAT GA--TT---- ---------- --------TT AAAAAATGGA   [86]
K. linearifolia SR400              AATCAAATTT --GATATTAT GA--TTATGA TT-------- --------TA AAAAAATAGA   [92]
K. linearifolia SR558              AATCAAATTT --GATATTAT GA--TTATGA TT-------- --------TA AAAAAATAGA   [92]
K. linearifolia JPsn               AATCAAATTT --GATATTAT GA--TTATGA TT-------- --------TT AAAAAATAGA   [92]
K. linearifolia TD4638             AATCCAATTT --GATATTAT GA--TTATGA TT-------- --------TA AAAAAATAGA   [92]
K. littoralis SR200                AATCAAATTT --GATATTAT GA--TTATGA TT-------- --------TA AAAAAATAGA   [92]
K. multiflora SR310                AATCAAATTT --GATATTAT GA--TT---- ---------- --------TA AAAAAATGGA   [86]
K. northiae SR263                  AATCAAATTT --GATATTAT GA--TT---- ---------- --------TT AAAAAATGGA   [86]
K. northiae SR274                  AATCAAATTT --GATATTAT GA--TT---- ---------- --------TA AAAAAATGGA   [86]
K. northiae SR446                  AATCAAATTT --GATATTAT GA--TT---- ---------- --------TT AAAAAATGGA   [86]
K. pauciflora HBsn                 AATCAAATTT --GATATTAT GA--TTATGA TT-------- --------TA AAAAAATAGA   [92]
K. parviflora SR268                AATCAAATTT --GATATTAT GA--TT---- ---------- --------TT AAAAAATGGA   [86]
K. parviflora SR330                AATCAAATTT --GATATTAT GA--TTATGA TT-------- --------TA AAAAAATAGA   [92]
K. porphyantha SRsn                AATCAAATTT --GATATTAT GA--TT---- ---------- --------TA AAAAAATGGA   [86]
K. praecox SR529                   AATCAAATTT --GATATTAT GA--TT---- ---------- --------TA AAAAAATGGA   [82]
K. praecox SR530                   AATCAAATTT --GATATTAT GA--TT---- ---------- --------TA AAAAAATGGA   [86]
K. praecox SR532                   AATCAAATTT --GATATTAT GA--TT---- ---------- --------TA AAAAAATGGA   [86]
K. rigidifolia SRsn                AATCAAATTT --GATATTAT GA--TT---- ---------- --------TA AAAAAATGGA   [86]
K. ritualis SR300                  AATCAAATTT --GATATTAT GA--TTATGA TT-------- --------TA AAAAAATAGA   [92]
K. rooperi SR237                   AATCAAATTT --GATATTAT GA--TT---- ---------- --------TT AAAAAATGGA   [86]
K. rooperi SR485                   AATCAAATTT --GATATTAT GA--TT---- ---------- --------TA AAAAAATGGA   [86]
K. rooperi SR528                   AATCAAATTT --GATATTAT GA--TT---- ---------- --------TA AAAAAATGGA   [86]
K. rooperi RAL4227                 AATCCAATTT --GATATTAT GA--TTATGA TT-------- --------TA AAAAAATAGA   [92]
K. rooperi TD4559                  AATCCAATTT --GATATTAT GA--TTATGA TT-------- --------TA AAAAAATAGA   [92]
K. sarmentosa SR207                AATCAAATTT --GATATTAT GA--TT---- ---------- --------TA AAAAAATGGA   [86]
K. schemperi SR391                 AATCAAATTT --GATATTAT GA--TT---- ---------- --------TA AAAAAATGGA   [86]
K. schimperi JMG036                AATCAAATTT --GATATTAT GA--TT---- ---------- --------TA AAAAAATGGA   [86]
K. splendida SR548                 AATCAAATTT --GATATTAT GA--TT---- ---------- --------AA AAAAAATGGA   [86]
K. splendida Chapman 9061          AATCAAATTT --GATATTAT GA--TT---- ---------- --------TA AAAAAATGGA   [86]
K. stricta SR279                   AATCAAATTT --GATATTAT GA--TTATGA TT-------- --------TA AAAAAATAGA   [92]
K. thodei SR407                    AATCAAATTT --GATATTAT GA--TTATGA TT-------- --------TA AAAAAATAGA   [92]
K. thomsonii JMG031                AATCAAATTT --GATATTAT GA--TT---- ---------- --------TA AAAAAATGGA   [86]
K. thomsonii AMM2647               AATCAAATTT --GATATTAT GA--TT---- ---------- --------TA AAAAAATGGA   [86]
K. thomsonii CK4821                AATCAAATTT --GATATTAT GA--TT---- ---------- --------TA AAAAAATGGA   [86]
K. triangularis SR264              AATCAAATTT --GATATTAT GA--TT---- ---------- --------TT TAAAAATGGA   [86]
K. triangularis SR266              AATCAAATTT --GATATTAT GA--TT---- ---------- --------TT AAAAAATGGA   [86]
K. triangularis SR299              AATCAAATTT --GATATTAT GA--TTATGA TT-------- --------TA AAAAAATAGA   [92]
K. triangularia obtusiloba SRsn    AATCAAATTT --GATATTAT GA--TT---- ---------- --------TA AAAAAATGGA   [86]
K. typhoides NNBG                  AATCAAATTT --GATATTAT GA--TT---- ---------- --------TA AAAAAATGGA   [86]
K. tysonii SR302                   AATCAAATTT --GATATTAT GA--TTATGA TT-------- --------TA AAAAAATAGA   [92]
K. tysonii SR303                   AATCAAATTT --GATATTAT GA--TTATGA TT-------- --------TA AAAAAATAGA   [92]
K tysonii SR460                    AATCAAATTT --GATATTAT GA--TTATGA TT-------- --------TA AAAAAATAGA   [92]
K. umbrina RGsn                    AATCAAATTT --GATATTAT GA--TT---- ---------- --------TA AAAAAATGGA   [86]
K. uvaria SR166                    AATCAAATTT --GATATTAT GA--TT---- ---------- --------TA AAAAAATGGA   [86]
K. uvaria SR186                    AATCAAATTT --GATATTAT GA--TT---- ---------- --------TA AAAAAATGGA   [86]
K. uvaria SR172                    AATCAAATTT --GATATTAT GA--TT---- ---------- --------TT AAAAAATGGA   [86]
K. uvaria SR201                    AATCAAATTT --GATATTAT GA--TT---- ---------- --------TA AAAAAATGGA   [86]
K. uvaria SR203                    AATCAAATTT --GATATTAT GA--TT---- ---------- --------TA AAAAAATGGA   [86]
K. uvaria SR211                    AATCAAATTT --GATATTAT GA--TT---- ---------- --------TA AAAAAATGGA   [86]
K. uvaria SR337                    AATCAAATTT --GATATTAT GA--TT---- ---------- --------TT AAAAAATGGA   [86]
K. uvaria SR342                    AATCAAATTT --GATATTAT GA--TT---- ---------- --------TT TAAAAATGGA   [86]
K. uvaria SR344                    AATCAAATTT --GATATTAT GA--TT---- ---------- --------TA AAAAAATGGA   [86]
K. uvaria SR471                    AATCAAATTT --GATATTAT GA--TT---- ---------- --------TT AAAAAATGGA   [86]
K. uvaria SR477                    AATCAAATTT --GATATTAT GA--TT---- ---------- --------TA AAAAAATGGA   [86]
K. uvaria TD4477                   AATCAAATTT --GATATTAT GA--TT---- ---------- --------TA AAAAAATGGA   [86]

[                                            130         140         150         160         170        180]
[                                            .          .          .          .          .         .]

Bulbine latifolia SR61             ATGATTTCTC AGAATAT--- --TTATAAAA AATTTTGTTA A-----TTAT ATTATAGGGG   [163]
Bulbinella cauda-felis SR204       ATTATTTCTC AGAAAAGAAA AGTTATAACA AATTTTGCTA A-----TTAT ATTATAGGGG   [162]
K. acreae TD4626                   ATTATTTCTC AGAATAG--- --TTATAACA AATTTTGCTA A-----TTAT ATTATAGGGG   [136]
K. albescens SR314                 ATTATTTCTC AGAATAG--- --TTATAACA AATTTTGCTA A-----TTAT ATTATAGGGG   [136]
K. albomontana SR149               ATTATTTCTC AGAATAG--- --TTATAACA AATTTTGCTA A-----TTAT ATTATAGGGG   [142]
K. angustifolia SR453              ATTATTTCTC AGAATAG--- --TTATAACA AATTTTGCTA A-----TTAT ATTATAGGGG   [136]
K. angustifolia SR542              ATTATTTCTC AGAATAG--- --TTATAACA AATTTTGCTA A-----TTAT ATTATAGGGG   [142]
K. ankaratrensis PBP5676           ATTATTTCTC AGAATAG--- --TTATAACA AATTTTGCTA A-----TTAT ATTATAGGGG   [136]
K. baurii SR174                    ATTATTTCTC AGAATAG--- --TTATAACA AATTTTGCTA A-----TTAT ATTATAGGGG   [142]
K. baurii SR202                    ATTATTTCTC AGAATAG--- --TTATAACA AATTTTGCTA A-----TTAT ATTATAGGGG   [136]
K. baurii SR275                    ATTATTTCTC AGAATAG--- --TTATAACA AATTTTGCTA A-----TTAT ATTATAGGGG   [142]
K. baurii SR285                    ATTATTTCTC AGAATAG--- --TTATAACA AATTTTGCTA A-----TTAT ATTATAGGGG   [142]
K. baurii SR360                    ATTATTTCTC AGAATAG--- --TTATAACA AATTTTGCTA A-----TTAT ATTATAGGGG   [136]
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K. baurii SR382                    ATTATTTCTC AGAATAG--- --TTATAACA AATTTTGCTA A-----TTAT ATTATAGGGG   [136]
K. baurii SR398                    ATTATTTCTC AGAATAG--- --TTATAACA AATTTTGCTA A-----TTAT ATTATAGGGG   [142]
K. baurii NPB1923                  ATTATTTCTC AGAATAG--- --TTATAACA AATTTTGCTA A-----TTAT ATTATAGGGG   [136]
K. baurii RJM1026                  ATTATTTCTC AGAATAG--- --TTATAACA AATTTTGCTA A-----TTAT ATTATAGGGG   [136]
K. bracystachya SRsn               ATTATTTCTC AGAATAG--- --TTATAACA AATTTTGCTA A-----TTAT ATTATAGGGG   [136]
K. breviflora SR452                ATTATTTCTC AGAATAG--- --TTATAACA AATTTTGCTA A-----TTAT ATTATAGGGG   [136]
K. bruceae SR171                   ATTATTTCTC AGAATAG--- --TTATAACA AATTTTGCTA A-----TTAT ATTATAGGGG   [142]
K. buchananii SR305                ATTATTTCTC AGAATAG--- --TTATAACA AATTTTGCTA A-----TTAT ATTATAGGGG   [142]
K. buchananii SR307                ATTATTTCTC AGAATAG--- --TTATAACA AATTTTGCTA A-----TTAT ATTATAGGGG   [142]
K. buchananii SR458                ATTATTTCTC AGAATAG--- --TTATAACA AATTTTGCTA A-----TTAT ATTATAGGGG   [142]
K. caulescens SR270                ATTATTTCTC AGAATAG--- --TTATAACA AATTTTGCTA A-----TTAT ATTATAGGGG   [136]
K. caulescens SR278                ATTATTTCTC AGAATAG--- --TTATAACA AATTTTGCTA A-----TTAT ATTATAGGGG   [136]
K. caulescens NPB1821              ATTATTTCTC AGAATAG--- --TTATAACA AATTTTGCTA A-----TTAT ATTATAGGGG   [142]
K. caulescens RJM974               ATTATTTCTC AGAATAG--- --TTATAACA AATTTTGCTA ATTATATTAT ATTATAGGGG   [141]
K. citrina SR176                   ATTATTTCTC AGAATAG--- --TTATAACA AATTTTGCTA A-----TTAT ATTATAGGGG   [136]
K. coddiana SRsn                   ATTATTTCTC AGAATAG--- --TTATAACA AATTTTGCTA A-----TTAT ATTATAGGGG   [142]
K. corraligemma SR549              ATTATTTCTC AGAATAG--- --TTATAACA AATTTTGCTA A-----TTAT ATTATAGGGG   [136]
K. drepanophylla RAL4816           ATTATTTCTC AGAATAG--- --TTATAACA AATTTTGCTA A-----TTAT ATTATAGGGG   [142]
K. drepanophylla RJM1100           ATTATTTCTC AGAATAG--- --TTATAACA AATTTTGCTA A-----TTAT ATTATAGGGG   [142]
K. ensifolia autumnalis SR448      ATTATTTCTC AGAATAG--- --TTATAACA AATTTTGCTA A-----TTAT ATTATAGGGG   [136]
K. ensifolia ensifolia JBsn        ATTATTTCTC AGAATAG--- --TTATAACA AATTTTGCTA A-----TTAT ATTATAGGGG   [136]
K. fibrosa SR297                   ATTATTTCTC AGAATAG--- --TTATAACA AATTTTGCTA A-----TTAT ATTATAGGGG   [142]
K. fibrosa PBP5579                 ATTATTTCTC AGAATAG--- --TTATAACA AATTTTGCTA A-----TTAT ATTATAGGGG   [136]
K. foliosa SR383                   ATTATTTCTC AGAATAG--- --TTATAACA AATTTTGCTA A-----TTAT ATTATAGGGG   [136]
K. foliosa SR387                   ATTATTTCTC AGAATAG--- --TTATAACA AATTTTGCTA A-----TTAT ATTATAGGGG   [136]
K. foloisa SR389                   ATTATTTCTC AGAATAG--- --TTATAACA AATTTTGCTA A-----TTAT ATTATAGGGG   [136]
K. foliosa SR390                   ATTATTTCTC AGAATAG--- --TTATAACA AATTTTGCTA A-----TTAT ATTATAGGGG   [136]
K. foliosa JMG034                  ATTATTTCTC AGAATAG--- --TTATAACA AATTTTGCTA A-----TTAT ATTATAGGGG   [136]
K. foliosa JMG038                  ATTATTTCTC AGAATAG--- --TTATAACA AATTTTGCTA A-----TTAT ATTATAGGGG   [136]
K. galpinii SR312                  ATTATTTCTC AGAATAG--- --TTATAACA AATTTTGCTA A-----TTAT ATTATAGGGG   [136]
K. gracilis SR321                  ATTATTTCTC AGAATAG--- --TTATAACA AATTTTGCTA A-----TTAT ATTATAGGGG   [142]
K. gracilis SR561                  ATTATTTCTC AGAATAG--- --TTATAACA AATTTTGCTA A-----TTAT ATTATAGGGG   [142]
K. gracilis NNBG                   ATTATTTCTC AGAATAG--- --TTATAACA AATTTTGCTA A-----TTAT ATTATAGGGG   [142]
K. grantii CP4154                  ATTATTTCTC AGAATAG--- --TTATAACA AATTTTGCTA A-----TTAT ATTATAGGGG   [136]
K. hirsuta SR282                   ATTATTTCTC AGAATAG--- --TTATAACA AATTTTGCTA A-----TTAT ATTATAGGGG   [142]
K. ichopensis SR242                ATTATTTCTC AGAATAG--- --TTATAACA AATTTTGCTA A-----TTAT ATTATAGGGG   [142]
K. ichopensis SR286                ATTATTTCTC AGAATAG--- --TTATAACA AATTTTGCTA A-----TTAT ATTATAGGGG   [142]
K. ichopensis SR289                ATTATTTCTC AGAATAG--- --TTATAACA AATTTTGCTA A-----TTAT ATTATAGGGG   [142]
K. ichopensis SR409                ATTATTTCTC AGAATAG--- --TTATAACA AATTTTGCTA A-----TTAT ATTATAGGGG   [142]
K. insignis SRsn                   ATTATTTCTC AGAATAG--- --TTATAACA AATTTTGCTA A-----TTAT ATTATAGGGG   [136]
K. isoetifolia SR386               ATTATTTCTC AGAATAG--- --TTATAACA AATTTTGCTA A-----TTAT ATTATAGGGG   [136]
K. isoetifolia SR388               ATTATTTCTC AGAATAG--- --TTATAACA AATTTTGCTA A-----TTAT ATTATAGGGG   [136]
K. isoetifolia SR393               ATTATTTCTC AGAATAG--- --TTATAACA AATTTTGCTA A-----TTAT ATTATAGGGG   [136]
K. latifolia RSSsn                 ATTATTTCTC AGAATAG--- --TTATAACA AATTTTGCTA A-----TTAT ATTATAGGGG   [142]
K. laxiflora SR283                 ATTATTTCTC AGAATAG--- --TTATAACA AATTTTGCTA A-----TTAT ATTATAGGGG   [142]
K. laxiflora SR295                 ATTATTTCTC AGAATAG--- --TTATAACA AATTTTGCTA A-----TTAT ATTATAGGGG   [142]
K. laxiflora SR441                 ATTATTTCTC AGAATAG--- --TTATAACA AATTTTGCTA A-----TTAT ATTATAGGGG   [138]
K. laxiflora SR442                 ATTATTTCTC AGAATAG--- --TTATAACA AATTTTGCTA A-----TTAT ATTATAGGGG   [142]
K. laxiflora SR467                 ATTATTTCTC AGAATAG--- --TTATAACA AATTTTGCTA A-----TTAT ATTATAGGGG   [142]
K. laxiflora SR468                 ATTATTTCTC AGAATAG--- --TTATAACA AATTTTGCTA A-----TTAT ATTATAGGGG   [142]
K. laxifloraC SRsn                 ATTATTTCTC AGAATAG--- --TTATAACA AATTTTGCTA A-----TTAT ATTATAGGGG   [136]
K. laxiflora NPB1810               ATTATTTCTC AGAATAG--- --TTATAACA AATTTTGCTA A-----TTAT ATTATAGGGG   [138]
K. leucocephala NNBG               ATTATTTCTC AGAATAG--- --TTATAACA AATTTTGCTA A-----TTAT ATTATAGGGG   [136]
K. linearifolia SR269              ATTATTTCTC AGAATAG--- --TTATAACA AATTTTGCTA A-----TTAT ATTATAGGGG   [136]
K. linearifolia SR287              ATTATTTCTC AGAATAG--- --TTATAACA AATTTTGCTA A-----TTAT ATTATAGGGG   [142]
K. linearifolia SR290              ATTATTTCTC AGAATAG--- --TTATAACA AATTTTGCTA A-----TTAT ATTATAGGGG   [142]
K. linearifolia SR291              ATTATTTCTC AGAATAG--- --TTATAACA AATTTTGCTA A-----TTAT ATTATAGGGG   [142]
K. linearifolia SR311              ATTATTTCTC AGAATAG--- --TTATAACA AATTTTGCTA A-----TTAT ATTATAGGGG   [136]
K. linearifolia SR328              ATTATTTCTC AGAATAG--- --TTATAACA AATTTTGCTA A-----TTAT ATTATAGGGG   [142]
K. linearifolia SR343              ATTATTTCTC AGAATAG--- --TTATAACA AATTTTGCTA A-----TTAT ATTATAGGGG   [136]
K. linearifolia SR400              ATTATTTCTC AGAATAG--- --TTATAACA AATTTTGCTA A-----TTAT ATTATAGGGG   [142]
K. linearifolia SR558              ATTATTTCTC AGAATAG--- --TTATAACA AATTTTGCTA A-----TTAT ATTATAGGGG   [142]
K. linearifolia JPsn               ATTATTTCTC AGAATAG--- --TTATAACA AATTTTGCTA A-----TTAT ATTATAGGGG   [142]
K. linearifolia TD4638             ATTATTTCTC AGAATAG--- --TTATAACA AATTTTGCTA A-----TTAT ATTATAGGGG   [142]
K. littoralis SR200                ATTATTTCTC AGAATAG--- --TTATAACA AATTTTGCTA A-----TTAT ATTATAGGGG   [142]
K. multiflora SR310                ATTATTTCTC AGAATAG--- --TTATAACA AATTTTGCTA A-----TTAT ATTATAGGGG   [136]
K. northiae SR263                  ATTATTTCTC AGAATAG--- --TTATAACA AATTTTGCTA A-----TTAT ATTATAGGGG   [136]
K. northiae SR274                  ATTATTTCTC AGAATAG--- --TTATAACA AATTTTGCTA A-----TTAT ATTATAGGGG   [136]
K. northiae SR446                  ATTATTTCTC AGAATAG--- --TTATAACA AATTTTGCTA A-----TTAT ATTATAGGGG   [136]
K. pauciflora HBsn                 ATTATTTCTC AGAATAG--- --TTATAACA AATTTTGCTA A-----TTAT ATTATAGGGG   [142]
K. parviflora SR268                ATTATTTCTC AGAATAG--- --TTATAACA AATTTTGCTA A-----TTAT ATTATAGGGG   [136]
K. parviflora SR330                ATTATTTCTC AGAATAG--- --TTATAACA AATTTTGCTA A-----TTAT ATTATAGGGG   [142]
K. porphyantha SRsn                ATTATTTCTC AGAATAG--- --TTATAACA AATTTTGCTA A-----TTAT ATTATAGGGG   [136]
K. praecox SR529                   ATTATTTCTC AGAATAG--- --TTATAACA AATTTTGCTA A-----TTAT ATTATAGGGG   [132]
K. praecox SR530                   ATTATTTCTC AGAATAG--- --TTATAACA AATTTTGCTA A-----TTAT ATTATAGGGG   [136]
K. praecox SR532                   ATTATTTCTC AGAATAG--- --TTATAACA AATTTTGCTA A-----TTAT ATTATAGGGG   [136]
K. rigidifolia SRsn                ATTATTTCTC AGAATAG--- --TTATAACA AATTTTGCTA A-----TTAT ATTATAGGGG   [136]
K. ritualis SR300                  ATTATTTCTC AGAATAG--- --TTATAACA AATTTTGCTA A-----TTAT ATTATAGGGG   [142]
K. rooperi SR237                   ATTATTTCTC AGAATAG--- --TTATAACA AATTTTGCTA A-----TTAT ATTATAGGGG   [136]
K. rooperi SR485                   ATTATTTCTC AGAATAG--- --TTATAACA AATTTTGCTA A-----TTAT ATTATAGGGG   [136]
K. rooperi SR528                   ATTATTTCTC AGAATAG--- --TTATAACA AATTTTGCTA A-----TTAT ATTATAGGGG   [136]
K. rooperi RAL4227                 ATTATTTCTC AGAATAG--- --TTATAACA AATTTTGCTA A-----TTAT ATTATAGGGG   [142]
K. rooperi TD4559                  ATTATTTCTC AGAATAG--- --TTATAACA AATTTTGCTA A-----TTAT ATTATAGGGG   [142]
K. sarmentosa SR207                ATTATTTCTC AGAATAG--- --TTATAACA AATTTTGCTA A-----TTAT ATTATAGGGG   [136]
K. schemperi SR391                 ATTATTTCTC AGAATAG--- --TTATAACA AATTTTGCTA A-----TTAT ATTATAGGGG   [136]
K. schimperi JMG036                ATTATTTCTC AGAATAG--- --TTATAACA AATTTTGCTA A-----TTAT ATTATAGGGG   [136]
K. splendida SR548                 ATTATTTCTC AGAATAG--- --TTATAACA AATTTTGCTA A-----TTAT ATTATAGGGG   [136]
K. splendida Chapman 9061          ATTATTTCTC AGAATAG--- --TTATAACA AATTTTGCTA A-----TTAT ATTATAGGGG   [136]
K. stricta SR279                   ATTATTTCTC AGAATAG--- --TTATAACA AATTTTGCTA A-----TTAT ATTATAGGGG   [142]
K. thodei SR407                    ATTATTTCTC AGAATAG--- --TTATAACA AATTTTGCTA A-----TTAT ATTATAGGGG   [142]
K. thomsonii JMG031                ATTATTTCTC AGAATAG--- --TTATAACA AATTTTGCTA A-----TTAT ATTATAGGGG   [136]
K. thomsonii AMM2647               ATTATTTCTC AGAATAG--- --TTATAACA AATTTTGCTA A-----TTAT ATTATAGGGG   [136]
K. thomsonii CK4821                ATTATTTCTC AGAATAG--- --TTATAACA AATTTTGCTA A-----TTAT ATTATAGGGG   [136]
K. triangularis SR264              ATTATTTCTC AGAATAG--- --TTATAACA AATTTTGCTA A-----TTAT ATTATAGGGG   [136]
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K. triangularis SR266              ATTATTTCTC AGAATAG--- --TTATAACA AATTTTGCTA A-----TTAT ATTATAGGGG   [136]
K. triangularis SR299              ATTATTTCTC AGAATAG--- --TTATAACA AATTTTGCTA A-----TTAT ATTATAGGGG   [142]
K. triangularia obtusiloba SRsn    ATTATTTCTC AGAATAG--- --TTATAACA AATTTTGCTA A-----TTAT ATTATAGGGG   [136]
K. typhoides NNBG                  ATTATTTCTC AGAATAG--- --TTATAACA AATTTTGCTA A-----TTAT ATTATAGGGG   [136]
K. tysonii SR302                   ATTATTTCTC AGAATAG--- --TTATAACA AATTTTGCTA A-----TTAT ATTATAGGGG   [142]
K. tysonii SR303                   ATTATTTCTC AGAATAG--- --TTATAACA AATTTTGCTA A-----TTAT ATTATAGGGG   [142]
K. tysonii SR460                   ATTATTTCTC AGAATAG--- --TTATAACA AATTTTGCTA A-----TTAT ATTATAGGGG   [142]
K. umbrina RGsn                    ATTATTTCTC AGAATAG--- --TTATAACA AATTTTGCTA A-----TTAT ATTATAGGGG   [136]
K. uvaria SR166                    ATTATTTCTC AGAATAG--- --TTATAACA AATTTTGCTA A-----TTAT ATTATAGGGG   [136]
K. uvaria SR186                    ATTATTTCTC AGAATAG--- --TTATAACA AATTTTGCTA A-----TTAT ATTATAGGGG   [136]
K. uvaria SR172                    ATTATTTCTC AGAATAG--- --TTATAACA AATTTTGCTA A-----TTAT ATTATAGGGG   [136]
K. uvaria SR201                    ATTATTTCTC AGAATAG--- --TTATAACA AATTTTGCTA A-----TTAT ATTATAGGGG   [136]
K. uvaria SR203                    ATTATTTCTC AGAATAG--- --TTATAACA AATTTTGCTA A-----TTAT ATTATAGGGG   [136]
K. uvaria SR211                    ATTATTTCTC AGAATAG--- --TTATAACA AATTTTGCTA A-----TTAT ATTATAGGGG   [136]
K. uvaria SR337                    ATTATTTCTC AGAATAG--- --TTATAACA AATTTTGCTA A-----TTAT ATTATAGGGG   [136]
K. uvaria SR342                    ATTATTTCTC AGAATAG--- --TTATAACA AATTTTGCTA A-----TTAT ATTATAGGGG   [136]
K. uvaria SR344                    ATTATTTCTC AGAATAG--- --TTATAACA AATTTTGCTA A-----TTAT ATTATAGGGG   [136]
K. uvaria SR471                    ATTATTTCTC AGAATAG--- --TTATAACA AATTTTGCTA A-----TTAT ATTATAGGGG   [136]
K. uvaria SR477                    ATTATTTCTC AGAATAG--- --TTATAACA AATTTTGCTA A-----TTAT ATTATAGGGG   [136]
K. uvaria TD4477                   ATTATTTCTC AGAATAG--- --TTATAACA AATTTTGCTA A-----TTAT ATTATAGGGG   [136]

[                                            190         200         210         220         230        240]
[                                            .          .          .          .          .         .]

Bulbine latifolia SR61             ATCGGCCCTA AGAAAAGTAT AAGATAAGGA -TAAAGATAC AATCAAAATT CTAATGCGAC   [222]
Bulbinella cauda-felis SR204       ATAGAGCCTA CGAAAAGTAT AAGATAAGGA TTAAAGATAC AATCAAAATT CTAATGCAAC   [222]
K. acreae TD4626                   ATCGGTCCTA AGAAAAGTAT AAGATAAGGA -TAAAGATAC AATCAAAATT CTAATGCGAC   [195]
K. albescens SR314                 ATCGGTCCTA AGAAAAGTAT AAGATAAGGA -TAAAGATAC AATCAAAATT CTAATGCGAC   [195]
K. albomontana SR149               ATCGGTCCTA AGAAAAGTAT AAGATAAGGA -TAAAGATAC AATCAAAATT CTAATGCGAC   [201]
K. angustifolia SR453              ATCGGTCCTA AGAAAAGTAT AAGATAAGGA -TAAAGATAC AATCAAAATT CTAATGCGAC   [195]
K. angustifolia SR542              ATCGGTCCTA AGAAAAGTAT AAGATAAGGA -TAAAGATAC AATCAAAATT CTAATGCGAC   [201]
K. ankaratrensis PBP5676           ATCGGTCCTA AGAAAAGTAT AAGATAAGGA -TAAAGATAC AATCAAAATT CTAATGCGAC   [195]
K. baurii SR174                    ATCGGTCCTA AGAAAAGTAT AAGATAAGGA -TAAAGATAC AATCAAAATT CTAATGCGAC   [201]
K. baurii SR202                    ATCGGTCCTA AGAAAAGTAT AAGATAAGGA -TAAAGATAC AATCAAAATT CTAATGCGAC   [195]
K. baurii SR275                    ATCGGTCCTA AGAAAAGTAT AAGATAAGGA -TAAAGATTC AATCAAAATT CTAATGCGAC   [201]
K. baurii SR285                    ATCGGTCCTA AGAAAAGTAT AAGATAAGGA -TAAAGATAC AATCAAAATT CTAATGCGAC   [201]
K. baurii SR360                    ATCGGTCCTA AGAAAAGTAT AAGATAAGGA -TAAAGATAC AATCAAAATT CTAATGCGAC   [195]
K. baurii SR382                    ATCGGTCCTA AGAAAAGTAT AAGATAAGGA -TAAAGATAC AATCAAAATT CTAATGCGAC   [195]
K. baurii SR398                    ATCGGTCCTA AGAAAAGTAT AAGATAAGGA -TAAAGATAC AATCAAAATT CTAATGCGAC   [201]
K. baurii NPB1923                  ATCGGTCCTA AGAAAAGTAT AAGATAAGGA -TAAAGATAC AATCAAAATT CTAATGCGAC   [195]
K. baurii RJM1026                  ATCGGTCCTA AGAAAAGTAT AAGATAAGGA -TAAAGATAC AATCAAAATT CTAATGCGAC   [195]
K. bracystachya SRsn               ATCGGTCCTA AGAAAAGTAT AAGATAAGGA -TAAAGATAC AATCAAAATT CTAATGCGAC   [195]
K. breviflora SR452                ATCGGTCCTA AGAAAAGTAT AAGATAAGGA -TAAAGATAC AATCAAAATT CTAATGCGAC   [195]
K. bruceae SR171                   ATCGGTCCTA AGAAAAGTAT AAGATAAGGA -TAAAGATAC AATCAAAATT CTAATGCGAC   [201]
K. buchananii SR305                ATCGGTCCTA AGAAAAGTAT AAGATAAGGA -TAAAGATAC AATCAAAATT CTAATGCGAC   [201]
K. buchananii SR307                ATCGGTCCTA AGAAAAGTAT AAGATAAGGA -TAAAGATAC AATCAAAATT CTAATGCGAC   [201]
K. buchananii SR458                ATCGGTCCTA AGAAAAGTAT AAGATAAGGA -TAAAGATAC AATCAAAATT CTAATGCGAC   [201]
K. caulescens SR270                ATCGGTCCTA AGAAAAGTAT AAGATAAGGA -TAAAGATAC AATCAAAATT CTAATGCGAC   [195]
K. caulescens SR278                ATCGGTCCTA AGAAAAGTAT AAGATAAGGA -TAAAGATAC AATCAAAATT CTAATGCGAC   [195]
K. caulescens NPB1821              ATCGGTCCTA AGAAAAGTAT AAGATAAGGA -TAAAGATAC AATCAAAATT CTAATGCGAC   [201]
K. caulescens RJM974               ATCGGTCCTA AGAAAAGTAT AAGATAAGGA -TAAAGATAC AATCAAAATT CTAATGCGAC   [200]
K. citrina SR176                   ATCGGTCCTA AGAAAAGTAT AAGATAAGGA -TAAAGATAC AATCAAAATT CTAATGCGAC   [195]
K. coddiana SRsn                   ATCGGTCCTA AGAAAAGTAT AAGATAAGGA -TAAAGATAC AATCAAAATT CTAATGCGAC   [201]
K. corraligemma SR549              ATCGGTCCTA AGAAAAGTAT AAGATAAGGA -TAAAGATAC AATCAAAATT CTAATGCGAC   [195]
K. drepanophylla RAL4816           ATCGGTCCTA AGAAAAGTAT AAGATAAGGA -TAAAGATAC AATCAAAATT CTAATGCGAT   [201]
K. drepanophylla RJM1100           ATCGGTCCTA AGAAAAGTAT AAGATAAGGA -TAAAGATAC AATCAAAATT CTAATGCGAC   [201]
K. ensifolia autumnalis SR448      ATCGGTCCTA AGAAAAGTAT AAGATAAGGA -TAAAGATAC AATCAAAATT CTAATGCGAC   [195]
K. ensifolia ensifolia JBsn        ATCGGTCCTA AGAAAAGTAT AAGATAAGGA -TAAAGATAC AATCAAAATT CTAATGCGAC   [195]
K. fibrosa SR297                   ATCGGTCCTA AGAAAAGTAT AAGATAAGGA -TAAAGATAC AATCAAAATT CTAATGCGAC   [201]
K. fibrosa PBP5579                 ATCGGTCCTA AGAAAAGTAT AAGATAAGGA -TAAAGATAC AATCAAAATT CTAATGCGAC   [195]
K. foliosa SR383                   ATCGGTCCTA AGAAAAGTAT AAGATAAGGA -TAAAGATAC AATCAAAATT CTAATGCGAC   [195]
K. foliosa SR387                   ATCGGTCCTA AGAAAAGTAT AAGATAAGGA -TAAAGATAC AATTAAAATT CTAATGCGAC   [195]
K. foloisa SR389                   ATCGGTCCTA AGAAAAGTAT AAGATAAGGA -TAAAGATAC AATGAAAATT CTAATGCGAC   [195]
K. foliosa SR390                   ATCGGTCCTA AGAAAAGTAT AAGATAAGGA -TAAAGATAC AATGAAAATT CTAATGCGAC   [195]
K. foliosa JMG034                  ATCGGTCCTA AGAAAAGTAT AAGATAAGGA -TAAAGATAC AATTAAAATT CTAATGCGAC   [195]
K. foliosa JMG038                  ATCGGTCCTA AGAAAAGTAT AAGATAAGGA -TAAAGATAC AATTAAAATT CTAATGCGAC   [195]
K. galpinii SR312                  GTCGGTCCTA AGAAAAGTAT AAGATAAGGA -TAAAGATAC AATCAAAATT CTAATGCGAC   [195]
K. gracilis SR321                  ATCGGTCCTA AGAAAAGTAT AAGATAAGGA -TAAAGATAC AATCAAAATT CTAATGCGAC   [201]
K. gracilis SR561                  ATCGGTCCTA AGAAAAGTAT AAGATAAGGA -TAAAGATAC AATCAAAATT CTAATGCGAC   [201]
K. gracilis NNBG                   ATCGGTCCTA AGAAAAGTAT AAGATAAGGA -TAAAGATAC AATCAAAATT CTAATGCGAC   [201]
K. grantii CP4154                  ATCGGTCCTA AGAAAAGTAT AAGATAAGGA -TAAAGATAC AATCAAAATT CTAATGCGAC   [195]
K. hirsuta SR282                   ATCGGTCCTA AGAAAAGTAT AAGATAAGGA -TAAAGATAC AATCAAAATT CTAATGCGAC   [201]
K. ichopensis SR242                ATCGGTCCTA AGAAAAGTAT AAGATAAGGA -TAAAGATAC AATCAAAATT CTAATGCGAC   [201]
K. ichopensis SR286                ATCGGTCCTA AGAAAAGTAT AAGATAAGGA -TAAAGATAC AATCAAAATT CTAATGCGAC   [201]
K. ichopensis SR289                ATCGGTCCTA AGAAAAGTAT AAGATAAGGA -TAAAGATAC AATCAAAATT CTAATGCGAC   [201]
K. ichopensis SR409                ATCGGTCCTA AGAAAAGTAT AAGATAAGGA -TAAAGATAC AATCAAAATT CTAATGCGAC   [201]
K. insignis SRsn                   ATCGGTCCTA AGAAAAGTAT AAGATAAGGA -TAAAGATAC AATCAAAATT CTAATGCGAC   [195]
K. isoetifolia SR386               ATCGGTCCTA AGAAAAGTAT AAGATAAGGA -TAAAGATAC AATTAAAATT CTAATGCGAC   [195]
K. isoetifolia SR388               ATCGGTCCTA AGAAAAGTAT AAGATAAGGA -TAAAGATAC AATGAAAATT CTAATGCGAC   [195]
K. isoetifolia SR393               ATCGGTCCTA AGAAAAGTAT AAGATAAGGA -TAAAGATAC AATTAAAATT CTAATGCGAC   [195]
K. latifolia RSSsn                 ATCGGTCCTA AGAAAAGTAT AAGATAAGGA -TAAAGATAC AATCAAAATT CTAATGCGAC   [201]
K. laxiflora SR283                 ATCGGTCCTA AGAAAAGTAT AAGATAAGGA -TAAAGATAC AATCAAAATT CTAATGCGAC   [201]
K. laxiflora SR295                 ATCGGTCCTA AGAAAAGTAT AAGATAAGGA -TAAAGATAC AATCAAAATT CTAATGCGAC   [201]
K. laxiflora SR441                 ATCGGTCCTA AGAAAAGTAT AAGATAAGGA -TAAAGATAC AATCAAAATT CTAATGCGAC   [197]
K. laxiflora SR442                 ATCGGTCCTA AGAAAAGTAT AAGATAAGGA -TAAAGATAC AATCAAAATT CTAATGCGAC   [201]
K. laxiflora SR467                 ATCGGTCCTA AGAAAAGTAT AAGATAAGGA -TAAAGATAC AATCAAAATT CTAATGCGAC   [201]
K. laxiflora SR468                 ATCGGTCCTA AGAAAAGTAT AAGATAAGGA -TAAAGATAC AATCAAAATT CTAATGCGAC   [201]
K. laxifloraC SRsn                 ATCGGTCCTA AGAAAAGTAT AAGATAAGGA -TAAAGATAC AATCAAAATT CTAATGCGAC   [195]
K. laxiflora NPB1810               ATCGGTCCTA AGAAAAGTAT AAGATAAGGA -TAAAGATAC AATCAAAATT CTAATGCGAC   [197]
K. leucocephala NNBG               ATCGGTCCTA AGAAAAGTAT AAGATAAGGA -TAAAGATAC AATCAAAATT CTAATGCGAC   [195]
K. linearifolia SR269              ATCGGTCCTA AGAAAAGTAT AAGATAAGGA -TAAAGATAC AATCAAAATT CTAATGCGAC   [195]
K. linearifolia SR287              ATCGGTCCTA AGAAAAGTAT AAGATAAGGA -TAAAGATAC AATCAAAATT CTAATGCGAC   [201]
K. linearifolia SR290              ATCGGTCCTA AGAAAAGTAT AAGATAAGGA -TAAAGATAC AATCAAAATT CTAATGCGAC   [201]
K. linearifolia SR291              ATCGGTCCTA AGAAAAGTAT AAGATAAGGA -TAAAGATAC AATCAAAATT CTAATGCGAC   [201]
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K. linearifolia SR311              ATCGGTCCTA AGAAAAGTAT AAGATAAGGA -TAAAGATAC AATCAAAATT CTAATGCGAC   [195]
K. linearifolia SR328              ATCGGTCCTA AGAAAAGTAT AAGATAAGGA -TAAAGATAC AATCAAAATT CTAATGCGAC   [201]
K. linearifolia SR343              ATCGGTCCTA AGAAAAGTAT AAGATAAGGA -TAAAGATAC AATCAAAATT CTAATGCGAC   [195]
K. linearifolia SR400              ATCGGTCCTA AGAAAAGTAT AAGATAAGGA -TAAAGATAC AATCAAAATT CTAATGCGAC   [201]
K. linearifolia SR558              ATCGGTCCTA AGAAAAGTAT AAGATAAGGA -TAAAGATAC AATCAAAATT CTAATGCGAC   [201]
K. linearifolia JPsn               ATCGGTCCTA AGAAAAGTAT AAGATAAGGA -TAAAGATAC AATCAAAATT CTAATGCGAC   [201]
K. linearifolia TD4638             ATCGGTCCTA AGAAAAGTAT AAGATAAGGA -TAAAGATAC AATCAAAATT CTAATGCGAC   [201]
K. littoralis SR200                ATCGGTCCTA AGAAAAGTAT AAGATAAGGA -TAAAGATAC AATCAAAATT CTAATGCGAC   [201]
K. multiflora SR310                GTCGGTCCTA AGAAAAGTAT AAGATAAGGA -TAAAGATAC AATCAAAATT CTAATGCGAC   [195]
K. northiae SR263                  ATCGGTCCTA AGAAAAGTAT AAGATAAGGA -TAAAGATAC AATCAAAATT CTAATGCGAC   [195]
K. northiae SR274                  ATCGGTCCTA AGAAAAGTAT AAGATAAGGA -TAAAGATAC AATCAAAATT CTAATGCGAC   [195]
K. northiae SR446                  ATCGGTCCTA AGAAAAGTAT AAGATAAGGA -TAAAGATAC AATCAAAATT CTAATGCGAC   [195]
K. pauciflora HBsn                 ATCGGTCCTA AGAAAAGTAT AAGATAAGGA -TAAAGATAC AATCAAAATT CTAATGCGAC   [201]
K. parviflora SR268                ATCGGTCCTA AGAAAAGTAT AAGATAAGGA -TAAAGATAC AATCAAAATT CTAATGCGAC   [195]
K. parviflora SR330                ATCGGTCCTA AGAAAAGTAT AAGATAAGGA -TAAAGATAC AATCAAAATT CTAATGCGAC   [201]
K. porphyantha SRsn                ATCGGTCCTA AGAAAAGTAT AAGATAAGGA -TAAAGATAC AATCAAAATT CTAATGCGAC   [195]
K. praecox SR529                   ATCGGTCCTA AGAAAAGTAT AAGATAAGGA -TAAAGATAC AATCAAAATT CTAATGCGAC   [191]
K. praecox SR530                   ATCGGTCCTA AGAAAAGTAT AAGATAAGGA -TAAAGATAC AATCAAAATT CTAATGCGAC   [195]
K. praecox SR532                   ATCGGTCCTA AGAAAAGTAT AAGATAAGGA -TAAAGATAC AATCAAAATT CTAATGCGAC   [195]
K. rigidifolia SRsn                ATCGGTCCTA AGAAAAGTAT AAGATAAGGA -TAAAGATAC AATCAAAATT CTAATGCGAC   [195]
K. ritualis SR300                  ATCGGTCCTA AGAAAAGTAT AAGATAAGGA -TAAAGATAC AATCAAAATT CTAATGCGAC   [201]
K. rooperi SR237                   ATCGGTCCTA AGAAAAGTAT AAGATAAGGA -TAAAGATAC AATCAAAATT CTAATGCGAC   [195]
K. rooperi SR485                   ATCGGTCCTA AGAAAAGTAT AAGATAAGGA -TAAAGATAC AATCAAAATT CTAATGCGAC   [195]
K. rooperi SR528                   ATCGGTCCTA AGAAAAGTAT AAGATAAGGA -T-AAGATAC AATCAAAATT CTAATGCGAC   [194]
K. rooperi RAL4227                 ATCGGTCCTA AGAAAAGTAT AAGATAAGGA -TAAAGATAC AATCAAAATT CTAATGCGAC   [201]
K. rooperi TD4559                  ATCGGTCCTA AGAAAAGTAT AAGATAAGGA -TAAAGATAC AATCAAAATT CTAATGCGAT   [201]
K. sarmentosa SR207                ATCGGTCCTA AGAAAAGTAT AAGATAAGGA -TAAAGATAC AATCAAAATT CTAATGCGAC   [195]
K. schemperi SR391                 ATCGGTCCTA AGAAAAGTAT AAGATAAGGA -TAAAGATAC AATGAAAATT CTAATGCGAC   [195]
K. schimperi JMG036                ATCGGTCCTA AGAAAAGTAT AAGATAAGGA -TAAAGATAC AATTAAAATT CTAATGCGAC   [195]
K. splendida SR548                 ATCGGTCCTA AGAAAAGTAT AAGATAAGGA -TAAAGATAC AATCAAAATT CTAATGCGAC   [195]
K. splendida Chapman 9061          ATCGGTCCTA AGAAAAGTAT AAGATAAGGA -TAAAGATAC AATCAAAATT CTAATGCGAC   [195]
K. stricta SR279                   ATCGGTCCTA AGAAAAGTAT AAGATAAGGA -TAAAGATAC AATCAAAATT CTAATGCGAC   [201]
K. thodei SR407                    ATCGGTCCTA AGAAAAGTAT AAGATAAGGA -TAAAGATAC AATCAAAATT CTAATGCGAC   [201]
K. thomsonii JMG031                ATCGGTCCTA AGAAAAGTAT AAGATAAGGA -TAAAGATAC AATGAAAATT CTAATGCGAC   [195]
K. thomsonii AMM2647               ATCGGTCCTA AGAAAAGTAT AAGATAAGGA -TAAAGATAC AATCAAAATT CTAATGCGAC   [195]
K. thomsonii CK4821                ATCGGTCCTA AGAAAAGTAT AAGATAAGGA -TAAAGATAC AATCAAAATT CTAATGCGAC   [195]
K. triangularis SR264              ATCGGTCCTA AGAAAAGTAT AAGATAAGGA -TAAAGATAC AATCAAAATT CTAATGCGAC   [195]
K. triangularis SR266              ATCGGTCCTA AGAAAAGTAT AAGATAAGGA -TAAAGATAC AATCAAAATT CTAATGCGAC   [195]
K. triangularis SR299              ATCGGTCCTA AGAAAAGTAT AAGATAAGGA -TAAAGATAC AATCAAAATT CTAATGCGAC   [201]
K. triangularia obtusiloba SRsn    ATCGGTCCTA AGAAAAGTAT AAGATAAGGA -TAAAGATAC AATCAAAATT CTAATGCGAC   [195]
K. typhoides NNBG                  ATCGGTCCTA AGAAAAGTAT AAGATAAGGA -TAAAGATAC AATCAAAATT CTAATGCGAC   [195]
K. tysonii SR302                   ATCGGTCCTA AGAAAAGTAT AAGATAAGGA -TAAAGATAC AATCAAAATT CTAATGCGAC   [201]
K. tysonii SR303                   ATCGGTCCTA AGAAAAGTAT AAGATAAGGA -TAAAGATAC AATCAAAATT CTAATGCGAC   [201]
K. tysonii SR460                   ATCGGTCCTA AGAAAAGTAT AAGATAAGGA -TAAAGATAC AATCAAAATT CTAATGCGAC   [201]
K. umbrina RGsn                    ATCGGTCCTA AGAAAAGTAT AAGATAAGGA -TAAAGATAC AATCAAAATT CTAATGCGAC   [195]
K. uvaria SR166                    ATCGGTCCTA AGAAAAGTAT AAGATAAGGA -TAAAGATAC AATCAAAATT CTAATGCGAC   [195]
K. uvaria SR186                    ATCGGTCCTA AGAAAAGTAT AAGATAAGGA -TAAAGATAC AATCAAAATT CTAATGCGAC   [195]
K. uvaria SR172                    ATCGGTCCTA AGAAAAGTAT AAGATAAGGA -TAAAGATAC AATCAAAATT CTAATGCGAC   [195]
K. uvaria SR201                    ATCGGTCCTA AGAAAAGTAT AAGATAAGGA -TAAAGATAC AATCAAAATT CTAATGCGAC   [195]
K. uvaria SR203                    ATCGGTCCTA AGAAAAGTAT AAGATAAGGA -TAAAGATAC AATCAAAATT CTAATGCGAC   [195]
K. uvaria SR211                    ATCGGTCCTA AGAAAAGTAT AAGATAAGGA -TAAAGATAC AATCAAAATT CTAATGCGAC   [195]
K. uvaria SR337                    ATCGGTCCTA AGAAAAGTAT AAGATAAGGA -TAAAGATAC AATCAAAATT CTAATGCGAC   [195]
K. uvaria SR342                    ATCGGTCCTA AGAAAAGTAT AAGATAAGGA -TAAAGATAC AATCCAAATT CTAATGCGAC   [195]
K. uvaria SR344                    ATCGGTCCTA AGAAAAGTAT AAGATAAGGA -TAAAGATAC AATCAAAATT CTAATGCGAC   [195]
K. uvaria SR471                    ATCGGTCCTA AGAAAAGTAT AAGATAAGGA -TAAAGATAC AATCAAAATT CTAATGCGAC   [195]
K. uvaria SR477                    ATCGGTCCTA AGAAAAGTAT AAGATAAGGA -TAAAGATAC AATCAAAATT CTAATGCGAC   [195]
K. uvaria TD4477                   ATCGGTCCTA AGAAAAGTAT AAGATAAGGA -T-AAGATAC AATCAAAATT CTAATGCGAC   [194]

[                                            250        260        270        280        290            300]
[                                            .          .          .          .          .         .]

Bulbine latifolia SR61             ATTCCTCTGA TTTCCTTGGA AAAAGAAGAA AATAGAGTG- ---AAAAAAA AAGAAGAAAG   [278]
Bulbinella cauda-felis SR204       ATTCCTTTGA TTTCCTTGGA AAAAGAAGGA AATGGGGC-- -AAAAAAAAA AAGAAGAAAT   [279]
K. acreae TD4626                   ATTCCTCTGA TTTCCTTAGA AAAAGAAGGA AATAGGGCG- --AAAAAAAA AATAAGAAAG   [252]
K. albescens SR314                 ATTCCTCTTA TTTCCTTAGA AAAAGAAGGA AATAGGGCG- ---AAAAAAA AATAAGAAAG   [251]
K. albomontana SR149               ATTCCTCTTA TTTCCTTAGA AAAAGAAGGA AATAGGGCG- -AAAAAAAAA AATAAGAAAG   [259]
K. angustifolia SR453              ATTCCTCTTA TTTCCTTAGA AAAAGAAGGA AATAGGGCG- ---AAAAAAA AATAAGAAAG   [251]
K. angustifolia SR542              ATTCCTCTTA TTTCCTTAGA AAAAGAAGGA AATAGGGCG- -AAAAAAAAA AATAAGAAAG   [259]
K. ankaratrensis PBP5676           ATTCCTCTGA TTTCCTTAGA AAAAGAAGGA AATAGGGCG- -AAAAAAAAA AATAAGAAAG   [253]
K. baurii SR174                    ATTCCTCTTA TTTCCTTAGA AAAAGAAGGA AATAGGGCG- AAAAAAAAAA AATAAGAAAG   [260]
K. baurii SR202                    ATTCCTCTGA TTTCCTTAGA AAAAGAAGGA AATAGGGCG- --AAAAAAAA AATAAGAAAG   [252]
K. baurii SR275                    ATTCCTCTTA TTTCCTTAGA AAAAGAAGGA AATAGGGCG- -AAAAAAAAA AATAAGAAAG   [259]
K. baurii SR285                    ATTCCTCTTA TTTCCTTAGA AAAAGAAGGA AATAGGGCG- -AAAAAAAAA AATAAGAAAG   [259]
K. baurii SR360                    ATTCCTCTTA TTTCCTTAGA AAAAGAAGGA AATAGGGCG- ---AAAAAAA AATAAGAAAG   [251]
K. baurii SR382                    ATTCCTCTTA TTTCCTTAGA AAAAGAAGGA AATAGGGCG- ---AAAAAAA AATAAGAAAG   [251]
K. baurii SR398                    ATTCCTCTTA TTTCCTTAGA AAAAGAAGGA AATAGGGCG- -AAAAAAAAA AATAAGAAAG   [259]
K. baurii NPB1923                  ATTCCTCTTA TTTCCTTAGA AAAAGAAGGA AATAGGGCG- ---AAAAAAA AATAAGAAAG   [251]
K. baurii RJM1026                  ATTCCTCTGA TTTCCTTAGA AAAAGAAGGA AATAGGGCG- --AAAAAAAA AATAAGAAAG   [252]
K. bracystachya SRsn               ATTCCTCTGA TTTCCTTAGA AAAAGAAGGA AATAGGGCG- -AAAAAAAAA AATAAGAAAG   [253]
K. breviflora SR452                ATTCCTCTTA TTTCCTTAGA AAAAGAAGGA AATAGGGCG- ---AAAAAAA AATAAGAAAG   [251]
K. bruceae SR171                   ATTCCTCTTA TTTCCTTAGA AAAAGAAGGA AATAGGGCG- --AAAAAAAA AATAAGAAAG   [258]
K. buchananii SR305                ATTCCTCTTA TTTCCTTAGA AAAAGAAGGA AATAGGGCG- -AAAAAAAAA AATAAGAAAG   [259]
K. buchananii SR307                ATTCCTCTTA TTTCCTTAGA AAAAGAAGGA AATAGGGCG- -AAAAAAAAA AATAAGAAAG   [259]
K. buchananii SR458                ATTCCTCTTA TTTCCTTAGA AAAAGAAGGA AATAGGGCG- -AAAAAAAAA AATAAGAAAG   [259]
K. caulescens SR270                ATTCCTCTGA TTTCCTTAGA AAAAGAAGGA AATAGGGCG- --AAAAAAAA AATAAGAAAG   [252]
K. caulescens SR278                ATTCCTCTGA TTTCCTTAGA AAAAGAAGGA AATAGGGCG- --AAAAAAAA AATAAGAAAG   [252]
K. caulescens NPB1821              ATTCCTCTGA TTTCCTTAGA AAAAGAAGGA AATAGGGCG- ---AAAAAAA AATAAGAAAG   [257]
K. caulescens RJM974               ATTCCTCTGA TTTCCTTAGA AAAAGAAGGA AATAGGGCG- -AAAAAAAAA AATAAGAAAG   [258]
K. citrina SR176                   ATTCCTCTGA TTTCCTTAGA AAAAGAAGGA AATAGGGCG- -AAAAAAAAA AATAAGAAAG   [253]
K. coddiana SRsn                   ATTCCTCTTA TTTCCTTAGA AAAAGAAGGA AATAGGGCG- --AAAAAAAA AATAAGAAAG   [258]
K. corraligemma SR549              ATTCCTCTGA TTTCCTTAGA AAAAGAAGGA AATAGGGCG- --AAAAAAAA AATAAGAAAG   [252]
K. drepanophylla RAL4816           ATTCCTCTTA TTTCCTTAGA AAAAGAAGGA AATAGGGCG- --AAAAAAAA AATAAGAAAG   [258]
K. drepanophylla RJM1100           ATTCCTCTTA TTTCCTTAGA AAAAGAAGGA AATAGGGCG- -AAAAAAAAA AATAAGAAAG   [259]
K. ensifolia autumnalis SR448      ATTCCTCTTA TTTCCTTAGA AAAAGAAGGA AATAGGGCG- ---AAAAAAA AATAAGAAAG   [251]
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K. ensifolia ensifolia JBsn	ATTCCTCTTA TTTCCTTAGA AAAAGAAGGA AATAGGGCG- ---AAAAAAA AATAAGAAAG	[251]
K. fibrosa SR297	ATTCCTCTTA TTTCCTTAGA AAAAGAAGGA AATAGGGCG- -AAAAAAAAA AATAAGAAAG	[259]
K. fibrosa PBP5579	ATTCCTCTGA TTTCCTTAGA AAAAGAAGGA AATAGGGCG- --AAAAAAAA AATAAGAAAG	[252]
K. foliosa SR383	ATTCCTCTGA TTTCCTTAGA AAAAGAAGGA AATAGGGCG- --AAAAAAAA AATAAGAAAG	[252]
K. foliosa SR387	ATTCCTCTGA TTTCCTTAGA AAAAGAAGGA AATAGGGCG- --AAAAAAAA AATAAGAAAG	[252]
K. foloisa SR389	ATTCCTCTGA TTTCCTTAGA AAAAGAAGGA AATAGGGCG- AAAAAAAAAA AATAAGAAAG	[254]
K. foliosa SR390	ATTCCTCTGA TTTCCTTAGA AAAAGAAGGA AATAGGGCG- AAAAAAAAAA AATAAGAAAG	[254]
K. foliosa JMG034	ATTCCTCTGA TTTCCTTAGA AAAAGAAGGA AATAGGGCG- -AAAAAAAAA AATAAGAAAG	[253]
K. foliosa JMG038	ATTCCTCTGA TTTCCTTAGA AAAAGAAGGA AATAGGGCG- -AAAAAAAAA AATAAGAAAG	[253]
K. galpinii SR312	ATTCCTCTTA TTTCCTTAGA AAAAGAAGGA AATAGGGCG- ----AAAAAA AATAAGAAAG	[250]
K. gracilis SR321	ATTCCTCTTA TTTCCTTAGA AAAAGAAGGA AATAGGGCG- -AAAAAAAAA AATAAGAAAG	[259]
K. gracilis SR561	ATTCCTCTTA TTTCCTTAGA AAAAGAAGGA AATAGGGCG- --AAAAAAAA AATAAGAAAG	[258]
K. gracilis NNBG	ATTCCTCTTA TTTCCTTAGA AAAAGAAGGA AATAGGGCG- AAAAAAAAAA AATAAGAAAG	[260]
K. grantii CP4154	ATTCCTCTGA TTTCCTTAGA AAAAGAAGGA AATAGGGCG- --AAAAAAAA AATAAGAAAG	[252]
K. hirsuta SR282	ATTCCTCTTA TTTCCTTAGA AAAAGAAGGA AATAGGGCGA AAAAAAAAAA AATAAGAAAG	[261]
K. ichopensis SR242	ATTCCTCTTA TTTCCTTAGA AAAAGAAGGA AATAGGGCG- -AAAAAAAAA AATAAGAAAG	[259]
K. ichopensis SR286	ATTCCTCTTA TTTCCTTAGA AAAAGAAGGA AATAGGGCG- --AAAAAAAA AATAAGAAAG	[258]
K. ichopensis SR289	ATTCCTCTTA TTTCCTTAGA AAAAGAAGGA AATAGGGCG- -AAAAAAAAA AATAAGAAAG	[259]
K. ichopensis SR409	ATTCCTCTTA TTTCCTTAGA AAAAGAAGGA AATAGGGCG- AAAAAAAAAA AATAAGAAAG	[260]
K. insignis SRsn	ATTCCTCTGA TTTCCTTAGA AAAAGAAGGA AATAGGGCG- --AAAAAAAA AATAAGAAAG	[252]
K. isoetifolia SR386	ATTCCTCTGA TTTCCTTAGA AAAAGAAGGA AATAGGGCG- --AAAAAAAA AATAAGAAAG	[252]
K. isoetifolia SR388	ATTCCTCTGA TTTCCTTAGA AAAAGAAGGA AATAGGGCG- AAAAAAAAAA AATAAGAAAG	[254]
K. isoetifolia SR393	ATTCCTCTGA TTTCCTTAGA AAAAGAAGGA AATAGGGCG- --AAAAAAAA AATAAGAAAG	[252]
K. latifolia RSSsn	ATTCCTCTTA TTTCCTTAGA AAAAGAAGGA AATAGGGCG- -AAAAAAAAA AATAAGAAAG	[259]
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K. laxiflora SR295	ATTCCTCTTA TTTCCTTAGA AAAAGAAGGA AATAGGGCG- --AAAAAAAA AATAAGAAAG	[258]
K. laxiflora SR441	ATTCCTCTTA TTTCCTTAGA AAAAGAAGGA AATAGGGCG- -AAAAAAAAA AATAAGAAAG	[255]
K. laxiflora SR442	ATTCCTCTTA TTTCCTTAGA AAAAGAAGGA AATAGGGCG- -AAAAAAAAA AATAAGAAAG	[259]
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K. laxifloraC SRsn	ATTCCTCTTA TTTCCTTAGA AAAAGAAGGA AATAGGGCG- ---AAAAAAA AATAAGAAAG	[251]
K. laxiflora NPB1810	ATTCCTCTTA TTTCCTTAGA AAAAGAAGGA AATAGGGCG- AAAAAAAAAA AATAAGAAAG	[256]
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K. linearifolia SR269	ATTCCTCTGA TTTCCTTAGA AAAAGAAGGA AATAGGGCG- --AAAAAAAA AATAAGAAAG	[252]
K. linearifolia SR287	ATTCCTCTTA TTTCCTTAGA AAAAGAAGGA AATAGGGCG- --AAAAAAAA AATAAGAAAG	[258]
K. linearifolia SR290	ATTCCTCTTA TTTCCTTAGA AAAAGAAGGA AATAGGGCG- --AAAAAAAA AATAAGAAAG	[258]
K. linearifolia SR291	ATTCCTCTTA TTTCCTTAGA AAAAGAAGGA AATAGGGCG- AAAAAAAAAA AATAAGAAAG	[260]
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K. linearifolia SR343	ATTCCTCTGA TTTCCTTAGA AAAAGAAGGA AATAGGGCG- --AAAAAAAA AATAAGAAAG	[252]
K. linearifolia SR400	ATTCCTCTTA TTTCCTTAGA AAAAGAAGGA AATAGGGCG- ---AAAAAAA AATAAGAAAG	[257]
K. linearifolia SR558	ATTCCTCTTA TTTCCTTAGA AAAAGAAGGA AATAGGGCG- --AAAAAAAA AATAAGAAAG	[258]
K. linearifolia JPsn	ATTCCTCTTA TTTCCTTAGA AAAAGAAGGA AATAGGGCG- AAAAAAAAAA AATAAGAAAG	[260]
K. linearifolia TD4638	ATTCCTCTTA TTTCCTTAGA AAAAGAAGGA AATAGGGCG- ---AAAAAAA AATAAGAAAG	[257]
K. littoralis SR200	ATTCCTCTTA TTTCCTTAGA AAAAGAAGGA AATAGGGCG- --AAAAAAAA AATAAGAAAG	[258]
K. multiflora SR310	ATTCCTCTTA TTTCCTTAGA AAAAGAAGGA AATAGGGCG- ---AAAAAAA AATAAGAAAG	[251]
K. northiae SR263	ATTCCTCTGA TTTCCTTAGA AAAAGAAGGA AATAGGGCG- -AAAAAAAAA AATAAGAAAG	[253]
K. northiae SR274	ATTCCTCTGA TTTCCTTAGA AAAAGAAGGA AATAGGGCG- --AAAAAAAA AATAAGAAAG	[252]
K. northiae SR446	ATTCCTCTGA TTTCCTTAGA AAAAGAAGGA AATAGGGCG- --AAAAAAAA AATAAGAAAG	[252]
K. pauciflora HBsn	ATTCCTCTTA TTTCCTTAGA AAAAGAAGGA AATAGGGCG- -AAAAAAAAA AATAAGAAAG	[259]
K. parviflora SR268	ATTCCTCTGA TTTCCTTAGA AAAAGAAGGA AATAGGGCG- --AAAAAAAA AATAAGAAAG	[252]
K. parviflora SR330	ATTCCTCTTA TTTCCTTAGA AAAAGAAGGA AATAGGGCG- --AAAAAAAA AATAAGAAAG	[258]
K. porphyantha SRsn	ATTCCTCTTA TTTCCTTAGA AAAAGAAGGA AATAGGGCG- ---AAAAAAA AATAAGAAAG	[251]
K. praecox SR529	ATTCCTCTGA TTTCCTTAGA AAAAGAAGGA AATAGGGCG- --AAAAAAAA AATAAGAAAG	[248]
K. praecox SR530	ATTCCTCTGA TTTCCTTAGA AAAAGAAGGA AATAGGGCG- --AAAAAAAA AATAAGAAAG	[252]
K. praecox SR532	ATTCCTCTGA TTTCCTTAGA AAAAGAAGGA AATAGGGCG- --AAAAAAAA AATAAGAAAG	[252]
K. rigidifolia SRsn	ATTCCTCTTA TTTCCTTAGA AAAAGAAGGA AATAGGGCG- ---AAAAAAA AATAAGAAAG	[251]
K. ritualis SR300	ATTCCTCTTA TTTCCTTAGA AAAAGAAGGA AATAGGGCG- --AAAAAAAA AATAAGAAAG	[258]
K. rooperi SR237	ATTCCTCTGA TTTCCTTAGA AAAAGAAGGA AATAGGGCG- -AAAAAAAAA AATAAGAAAG	[253]
K. rooperi SR485	ATTCCTCTTA TTTCCTTAGA AAAAGAAGGA AATAGGGCG- ---AAAAAAA AATAAGAAAG	[251]
K. rooperi SR528	ATTCCTCTGA TTTCCTTAGA AAAAGAAGGA AATAGGGCG- --AAAAAAAA AATAAGAAAG	[251]
K. rooperi RAL4227	ATTCCTCTTA TTTCCTTAGA AAAAGAAGGA AATAGGGCG- --AAAAAAAA AATAAGAAAG	[258]
K. rooperi TD4559	ATTCCTCTTA TTTCCTTAGA AAAAGAAGGA AATAGGGCG- --AAAAAAAA AATAAGAAAG	[258]
K. sarmentosa SR207	ATTCCTCTGA TTTCCTTAGA AAAAGAAGGA AATAGGGCG- AAAAAAAAAA AATAAGAAAG	[254]
K. schemperi SR391	ATTCCTCTGA TTTCCTTAGA AAAAGAAGGA AATAGGGCG- -AAAAAAAAA AATAAGAAAG	[253]
K. schimperi JMG036	ATTCCTCTGA TTTCCTTAGA AAAAGAAGGA AATAGGGCG- -AAAAAAAAA AATAAGAAAG	[253]
K. splendida SR548	ATTCCTCTGA TTTCCTTAGA AAAAGAAGGA AATAGGGCG- --AAAAAAAA AATAAGAAAG	[252]
K. splendida Chapman 9061	ATTCCTCTGA TTTCCTTAGA AAAAGAAGGA AATAGGGCG- -AAAAAAAAA AATAAGAAAG	[253]
K. stricta SR279	ATTCCTCTTA TTTCCTTAGA AAAAGAAGGA AATAGGGCGA AAAAAAAAAA AATAAGAAAG	[261]
K. thodei SR407	ATTCCTCTTA TTTCCTTAGA AAAAGAAGGA AATAGGGCG- AAAAAAAAAA AATAAGAAAG	[260]
K. thomsonii JMG031	ATTCCTCTGA TTTCCTTAGA AAAAGAAGGA AATAGGGCG- AAAAAAAAAA AATAAGAAAG	[254]
K. thomsonii AMM2647	ATTCCTCTGA TTTCCTTAGA AAAAGAAGGA AATAGGGCG- ----AAAAAA AATAAGAAAG	[250]
K. thomsonii CK4821	ATTCCTCTGA TTTCCTTAGA AAAAGAAGGA AATAGGGCG- ---AAAAAAA AATAAGAAAG	[251]
K. triangularis SR264	ATTCCTCTGA TTTCCTTAGA AAAAGAAGGA AATAGGGCG- --AAAAAAAA AATAAGAAAG	[252]
K. triangularis SR266	ATTCCTCTGA TTTCCTTAGA AAAAGAAGGA AATAGGGCG- --AAAAAAAA AATAAGAAAG	[252]
K. triangularis SR299	ATTCCTCTTA TTTCCTTAGA AAAAGAAGGA AATAGGGCG- -AAAAAAAAA AATAAGAAAG	[259]
K. triangularia obtusiloba SRsn	ATTCCTCTTA TTTCCTTAGA AAAAGAAGGA AATAGGGCG- ---AAAAAAA AATAAGAAAG	[251]
K. typhoides NNBG	ATTCCTCTGA TTTCCTTAGA AAAAGAAGGA AATAGGGCG- --AAAAAAAA AATAAGAAAG	[252]
K. tysonii SR302	ATTCCTCTTA TTTCCTTAGA AAAAGAAGGA AATAGGGCG- --AAAAAAAA AATAAGAAAG	[258]
K. tysonii SR303	ATTCCTCTTA TTTCCTTAGA AAAAGAAGGA AATAGGGCG- --AAAAAAAA AATAAGAAAG	[258]
K tysonii SR460	ATTCCTCTTA TTTCCTTAGA AAAAGAAGGA AATAGGGCG- -AAAAAAAAA AATAAGAAAG	[259]
K. umbrina RGsn	ATTCCTCTTA TTTCCTTAGA AAAAGAAGGA AATAGGGCG- ---AAAAAAA AATAAGAAAG	[251]
K. uvaria SR166	ATTCCTCTGA TTTCCTTAGA AAAAGAAGGA AATAGGGCG- --AAAAAAAA AATAAGAAAG	[252]
K. uvaria SR186	ATTCCTCTGA TTTCCTTAGA AAAAGAAGGA AATAGGGCG- --AAAAAAAA AATAAGAAAG	[252]
K. uvaria SR172	ATTCCTCTGA TTTCCTTAGA AAAAGAAGGA AATAGGGCG- --AAAAAAAA AATAAGAAAG	[252]
K. uvaria SR201	ATTCCTCTGA TTTCCTTAGA AAAAGAAGGA AATAGGGCG- --AAAAAAAA AATAAGAAAG	[252]
K. uvaria SR203	ATTCCTCTGA TTTCCTTAGA AAAAGAAGGA AATAGGGCG- --AAAAAAAA AATAAGAAAG	[252]
K. uvaria SR211	ATTCCTCTGA TTTCCTTAGA AAAAGAAGGA AATAGGGCG- --AAAAAAAA AATAAGAAAG	[252]
K. uvaria SR337	ATTCCTCTGA TTTCCTTAGA AAAAGAAGGA AATAGGGCG- --AAAAAAAA AATAAGAAAG	[252]
K. uvaria SR342	ATTCCTCTGA TTTCCTTAGA AAAAGAAGGA AATAGGGCG- --AAAAAAAA AATAAGAAAG	[252]
K. uvaria SR344	ATTCCTCTTA TTTCCTTAGA AAAAGAAGGA AATAGGGCG- ---AAAAAAA AATAAGAAAG	[251]
K. uvaria SR471	ATTCCTCTGA TTTCCTTAGA AAAAGAAGGA AATAGGGCG- --AAAAAAAA AATAAGAAAG	[252]
K. uvaria SR477	ATTCCTCTTA TTTCCTTAGA AAAAGAAGGA AATAGGGCG- ---AAAAAAA AATAAGAAAG	[251]
K. uvaria TD4477	ATTCCTCTGA TTTCCTTAGA AAAAGAAGGA AATAGGGCG- --AAAAAAAA AATAAGAAAG	[251]

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[                                            310        320        330        340        350            360]
[                                            .          .          .          .          .          .]

Bulbine latifolia SR61             AATATCGCCC TTTTCAGTAT TCCAAATCGC GATGTAAAAA CGAAAAAAAA AAGGGGGGGG   [338]
Bulbinella cauda-felis SR204       AATATCGACC CTTTCAGTAT TGCAAATTGC GATGTAAAA- --AAAAA--- ---GAGGGGG   [330]
K. acreae TD4626                   AATATCGATC CTTTCAGTAT TCCAAATCGC GATGTGAAAC CGAAAAA--- --GGGGGGGG   [307]
K. albescens SR314                 AATATCGATC CTTTCAGTAT TCCAAATCGC GATGTAAAAC CGAAA----- --GGGGGGGG   [304]
K. albomontana SR149               AATATCGATC CTTTCAGTAT TCCAAATCGC GATGTAAAAC CGAAAA---- ---GGGGGGG   [312]
K. angustifolia SR453              AATATCGATC CTTTCAGTAT TCCAAATCGC GATGTAAAAC CGAAA----- --GGGGGGGG   [304]
K. angustifolia SR542              AATATCGATC CTTTCAGTAT TCCAAATCGC GATGTAAAAC CGAAAA---- ---GGGGGGG   [312]
K. ankaratrensis PBP5676           AATATTGATC CTTTCAGTAT TCCAAATCGC GATGTAAAAC CGAAAAA--- -GGGGGGGGG   [309]
K. baurii SR174                    AATATCGATC CTTTCAGTAT TCCAAATCGC GATGTAAAAC CGAAAA---- ---GGGGGGG   [313]
K. baurii SR202                    AGTATTGATC CTTTCAGTAT TCCAAATCGC GATGTAAAAC CGAAAAAA-- --GGGGGGGG   [308]
K. baurii SR275                    AATATCGATC CTTTCAGTAT TCCAAATCGC AATGTAAAAC CGAAA----- ---GGGGGGG   [311]
K. baurii SR285                    AATATCGATC CTTTCAGTAT TCCAAATCGC AATGTAAAAC CGAAA----- ---GGGGGGG   [311]
K. baurii SR360                    AATATCGATC CTTTCAGTAT TCCAAATCGC GATGTAAAAC CGAAA----- ---GGGGGGG   [303]
K. baurii SR382                    AATATCGATC CTTTCAGTAT TCCAAATCGC GATGTAAAAC CGAAA----- ---GGGGGGG   [303]
K. baurii SR398                    AATATCGATC CTTTCAGTAT TCCAAATCGC GATGTAAAAC CGAAAA---- ---GGGGGGG   [312]
K. baurii NPB1923                  AATATCGATC CTTTCAGTAT TCCAAATCGC GATGTAAAAC CGAAA----- ---GGGGGGG   [303]
K. baurii RJM1026                  AGTATTGATC CTTTCAGTAT TCCAAATCGC GATGTAAAAC CGAAAAAA-- --GGGGGGGG   [308]
K. bracystachya SRsn               AGTATTGATC CTTTCAGTAT TCCAAATCGC GATGTAAAAC CGAAAAAAA- --GGGGGGGG   [310]
K. breviflora SR452                AATATCGATC CTTTCAGTAT TCCAAATCGC GATGTAAAAC CGAAA----- --GGGGGGGG   [304]
K. bruceae SR171                   AATATCGATC CTTTCAGTAT TCCAAATCGC AATGTAAAAC CGAAA----- ---GGGGGGG   [310]
K. buchananii SR305                AATATCGATC CTTTCAGTAT TCCAAATCGC GATGTAAAAC CGAAAA---- ---GGGGGGG   [312]
K. buchananii SR307                AATATCGATC CTTTCAGTAT TCCAAATCGC GATGTAAAAC CGAAAA---- ---GGGGGGG   [312]
K. buchananii SR458                AATATCGATC CTTTCAGTAT TCCAAATCGC GATGTAAAAC CGAAAA---- ---GGGGGGG   [312]
K. caulescens SR270                AATATCGATC CTTTCAGTAT TCCAAATCGC GATGTGAAAC CGAAAA---- --GGGGGGGG   [306]
K. caulescens SR278                AATATCGATC CTTTCAGTAT TCCAAATCGC GATGTGAAAC CGAAAA---- --GGGGGGGG   [306]
K. caulescens NPB1821              AATATCGATC CTTTCAGTAT TCCAAATCGC GATGTAAAAC CGAAAA---- ---GGGGGGG   [310]
K. caulescens RJM974               AATATCGATC CTTTCAGTAT TCCAAATCGC GATGTGAAAC CGAAAA---- --GGGGGGGG   [312]
K. citrina SR176                   AGTATTGATC CTTTCAGTAT TCCAAATCGC GATGTAAAAC CGAAAAAA-- -GGGGGGGGG   [310]
K. coddiana SRsn                   AATATCGATC CTTTCAGTAT TCCAAATCGC AATGTAAAAC CGAAA----- ---GGGGGGG   [310]
K. corraligemma SR549              AATATTGATC CTTTCAGTAT TCCAAATCGC GATGTAAAAC CGAAAAAA-- --GGGGGGGG   [308]
K. drepanophylla RAL4816           AATATCGATC CTTTCAGTAT TCCAAATCGC AATGTAAAAC CGAAA----- ---GGGGGGG   [310]
K. drepanophylla RJM1100           AATATCGATC CTTTCAGTAT TCCAAATCGC GATGTAAAAC CGAAAA---- ---GGGGGGG   [312]
K. ensifolia autumnalis SR448      AATATCGATC CTTTCAGTAT TCCAAATCGC GATGTAAAAC CGAAA----- --GGGGGGGG   [304]
K. ensifolia ensifolia JBsn        AATATCGATC CTTTCAGTAT TCCAAATCGC GATGTAAAAC CGAAA----- --GGGGGGGG   [304]
K. fibrosa SR297                   AATATCGATC CTTTCAGTAT TCCAAATCGC GATGTAAAAC CGAAA----- -GGGGGGGGG   [313]
K. fibrosa PBP5579                 AATATCGATC CTTTCAGTAT TCCAAATCGC GATGTGAAAC CGAAAAA--- --GGGGGGGG   [307]
K. foliosa SR383                   AATATTGATC CTTTCAGTAT TCCAAATCGC GATGTAAAAC CGAAAAAA-- --GGGGGGGG   [308]
K. foliosa SR387                   AATATTGATC CTTTCAGTAT TCCAAATCGC GATGTAAAAC CGAAAAAA-- --GGGGGGGG   [308]
K. foloisa SR389                   AATATTGATC CTTTCAGTAT TCCAAATCGC GATGTAAAAC CGAAAAAA-- --GGGGGGGG   [310]
K. foliosa SR390                   AATATTGATC CTTTCAGTAT TCCAAATCGC GATGTAAAAC CGAAAAAA-- --GGGGGGGG   [310]
K. foliosa JMG034                  AATATTGATC CTTTCAGTAT TCCAAATCGC GATGTAAAAC CGAAAAAA-- --GGGGGGGG   [309]
K. foliosa JMG038                  AATATTGATC CTTTCAGTAT TCCAAATCGC GATGTAAAAC CGAAAAAA-- --GGGGGGGG   [309]
K. galpinii SR312                  AATATCGATC CTTTCAGTAT TCCAAATCGC GATGTAAAAC CGAAA----- --GGGGGGGG   [303]
K. gracilis SR321                  AATATCGATC CTTTCAGTAT TCCAAATCGC GATGTAAAAC CGAAAA---- ---GGGGGGG   [312]
K. gracilis SR561                  AATATCGATC CTTTCAGTAT TCCAAATCGC GATGTAAAAC CGAAA----- -GGGGGGGGG   [312]
K. gracilis NNBG                   AATATCGATC CTTTCAGTAT TCCAAATCGC GATGTAAAAC CGAAAA---- ---GGGGGGG   [313]
K. grantii CP4154                  AGTATTGATC CTTTCAGTAT TCCAAATCGC GATGTAAAAC CGAAAAAAA- ---GGGGGGG   [308]
K. hirsuta SR282                   AATATCGATC CTTTCAGTAT TCCAAATCGC GATGTAAAAC CGAAA----- --GGGGGGGG   [314]
K. ichopensis SR242                AATATCGATC CTTTCAGTAT TCCAAATCGC GATGTAAAAC CGAAAA---- ---GGGGGGG   [312]
K. ichopensis SR286                AATATCGACC CTTTCAGTAT TCCAAATCGC GATGTAAAAC CGAAA----- -GGGGGGGGG   [312]
K. ichopensis SR289                AATATCGATC CTTTCAGTAT TCCAAATCGC GATGTAAAAC CGAAAA---- ---GGGGGGG   [312]
K. ichopensis SR409                AATATCGATC CTTTCAGTAT TCCAAATCGC GATGTAAAAC CGAAAA---- ---GGGGGGG   [313]
K. insignis SRsn                   AATATTGATC CTTTCAGTAT TCCAAATCGC GATGTAAAAC CGAAAAAA-- --GGGGGGGG   [308]
K. isoetifolia SR386               AATATTGATC CTTTCAGTAT TCCAAATCGC GATGTAAAAC CGAAAAAA-- --GGGGGGGG   [308]
K. isoetifolia SR388               AATATTGATC CTTTCAGTAT TCCAAATCGC GATGTAAAAC CGAAAAAA-- --GGGGGGGG   [310]
K. isoetifolia SR393               AATATTGATC CTTTCAGTAT TCCAAATCGC GATGTAAAAC CGAAAAAA-- --GGGGGGGG   [308]
K. latifolia RSSsn                 AATATCGATC CTTTCAGTAT TCCAAATCGC GATGTAAAAC CGAAAA---- ---GGGGGGG   [312]
K. laxiflora SR283                 AATATCGATC CTTTCAGTAT TCCAAATCGC GATGTAAAAC CGAAA----- --GGGGGGGG   [311]
K. laxiflora SR295                 AATATCGATC CTTTCAGTAT TCCAAATCGC GATGTAAAAC CGAAAA---- ---GGGGGGG   [311]
K. laxiflora SR441                 AATATCGATC CTTTCAGTAT TCCAAATCGC GATGTAAAAC CGAAAA---- ---GGGGGGG   [308]
K. laxiflora SR442                 AATATCGATC CTTTCAGTAT TCCAAATCGC GATGTAAAAC CGAAAA---- ---GGGGGGG   [312]
K. laxiflora SR467                 AATATCGATC CTTTCAGTAT TCCAAATCGC GATGTAAAAC CGAAAA---- GGGGGGGGGG   [315]
K. laxiflora SR468                 AATATCGATC CTTTCAGTAT TCCAAATCGC GATGTAAAAC CGAAAA---- GGGGGGGGGG   [315]
K. laxifloraC SRsn                 AATATCGATC CTTTCAGTAT TCCAAATCGC GATGTAAAAC CGAAA----- --GGGGGGGG   [304]
K. laxiflora NPB1810               AATATCGATC CTTTCAGTAT TCCAAATCGC GATGTAAAAC CGAAA----- -GGGGGGGGG   [310]
K. leucocephala NNBG               AATATCGATC CTTTCAGTAT TCCAAATCGC GATGTAAAAC CGAAA----- --GGGGGGGG   [305]
K. linearifolia SR269              AATATCGATC CTTTCAGTAT TCCAAATCGC GATGTGAAAC CGAAAAA--- --GGGGGGGG   [307]
K. linearifolia SR287              AATATCGATC CTTTCAGTAT TCCAAATCGC GATGTAAAAC CGAAA----- --GGGGGGGG   [311]
K. linearifolia SR290              AATATCGATC CTTTCAGTAT TCCAAATCGC GATGTAAAAC CGAAAAA--- ----GGGGGG   [311]
K. linearifolia SR291              AATATCGATC CTTTCAGTAT TCCAAATCGC GATGTAAAAC CGAAAA---- ---GGGGGGG   [313]
K. linearifolia SR311              AATATCGATC CTTTCAGTAT TCCAAATCGC GATGTAAAAC CGAAA----- --GGGGGGGG   [304]
K. linearifolia SR328              AATATCGATC CTTTCAGTAT TCCAAATCGC AATGTAAAAC CGAAA----- ---GGGGGGG   [310]
K. linearifolia SR343              AATATCGATC CTTTCAGTAT TCCAAATCGC GATGTGAAAC CGAAAAA--- --GGGGGGGG   [307]
K. linearifolia SR400              AATATCGATC CTTTCAGTAT TCCAAATCGC GATGTAAAAC CGAAAA---- ---GGGGGGG   [310]
K. linearifolia SR558              AATATCGATC CTTTCAGTAT TCCAAATCGC GATGTAAAAC CGAAA----- -GGGGGGGGG   [312]
K. linearifolia JPsn               AATATCGATC CTTTCAGTAT TCCAAATCGC GATGTAAAAC CGAAAA---- ---GGGGGGG   [313]
K. linearifolia TD4638             AATATCGATC CTTTCAGTAT TCCAAATCGC AATGTAAAAC CGAAA----- ---GGGGGGG   [309]
K. littoralis SR200                AATATCGATC CTTTCAGTAT TCCAAATCGC GATGTAAAAC CGAAAA---- ---GGGGGGG   [311]
K. multiflora SR310                AATATCGATC CTTTCAGTAT TCCAAATCGC GATGTAAAAC CGAAA----- --GGGGGGGG   [304]
K. northiae SR263                  AATATCGATC CTTTCAGTAT TCCAAATCGC GATGTGAAAC CGAAAAA--- -GGGGGGGGG   [309]
K. northiae SR274                  AATATCGATC CTTTCAGTAT TCCAAATCGC GATGTGAAAC CGAAAA---- --GGGGGGGG   [306]
K. northiae SR446                  AATATCGATC CTTTCAGTAT TCCAAATCGC GATGTGAAAC CGAAAA---- ---GGGGGGG   [305]
K. pauciflora HBsn                 AATATCGATC CTTTCAGTAT TCCAAATCGC GATGTAAAAC CGAAAA---- ---GGGGGGG   [312]
K. parviflora SR268                AATATCGATC CTTTCAGTAT TCCAAATCGC GATGTGAAAC CGAAAAA--- --GGGGGGGG   [307]
K. parviflora SR330                AATATCGATC CTTTCAGTAT TCCAAATCGC GATGTAAAAC CGAAA----- -GGGGGGGGG   [312]
K. porphyantha SRsn                AATATCGATC CTTTCAGTAT TCCAAATCGC GATGTAAAAC CGAAA----- --GGGGGGGG   [304]
K. praecox SR529                   AGTATTGATC CTTTCAGTAT TCCAAATCGC GATGTAAAAC CGAAAAAA-- --GGGGGGGG   [304]
K. praecox SR530                   AGTATTGATC CTTTCAGTAT TCCAAATCGC GATGTAAAAC CGAAAAAA-- --GGGGGGGG   [308]
K. praecox SR532                   AGTATTGATC CTTTCAGTAT TCCAAATCGC GATGTAAAAC CGAAAAAA-- --GGGGGGGG   [308]
K. rigidifolia SRsn                AATATCGATC CTTTCAGTAT TCCAAATCGC GATGTAAAAC CGAAA----- --GGGGGGGG   [304]
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K. ritualis SR300                  AATATCGATC CTTTCAGTAT TCCAAATCGC GATGTAAAAC CGAAA----- -GGGGGGGGG   [312]
K. rooperi SR237                   AATATCGATC CTTTCAGTAT TCCAAATCGC GATGTGAAAC CGAAAAA--- ---GGGGGGG   [307]
K. rooperi SR485                   AATATCGATC CTTTCAGTAT TCCAAATCGC GATGTAAAAC CGAAA----- ---GGGGGGG   [303]
K. rooperi SR528                   AGTATTGATC CTTTCAGTAT TCCAAATCGC GATGTAAAAC CGAAAAAA-- -GGGGGGGGG   [308]
K. rooperi RAL4227                 AATATCGATC CTTTCAGTAT TCCAAATCGC AATGTAAAAC CGAAA----- ---GGGGGGG   [310]
K. rooperi TD4559                  AATATCGATC CTTTCAGTAT TCCAAATCGC AATGTAAAAC CGAAA----- ---GGGGGGG   [310]
K. sarmentosa SR207                AGTATTGATC CTTTCAGTAT TCCAAATCGC GATGTAAAAC CGAAAAAAA- --GGGGGGGG   [311]
K. schemperi SR391                 AATATTGATC CTTTCAGTAT TCCAAATCGC GATGTAAAAC CGAAAAAA-- --GGGGGGGG   [309]
K. schimperi JMG036                AATATTGATC CTTTCAGTAT TCCAAATCGC GATGTAAAAC CGAAAAAA-- --GGGGGGGG   [309]
K. splendida SR548                 AATATTGATC CTTTCAGTAT TCCAAATCGC GATGTAAAAC CGAAAAAA-- --GGGGGGGG   [308]
K. splendida Chapman 9061          AATATTGATC CTTTCAGTAT TCCAAATCGC GATGTAAAAC CGAAAA---- GGGGGGGGGG   [309]
K. stricta SR279                   AATATCGATC CTTTCAGTAT TCCAAATCGC GATGTAAAAC CGAAA----- --GGGGGGGG   [314]
K. thodei SR407                    AATATCGATC CTTTCAGTAT TCCAAATCGC GATGTAAAAC CGAAAA---- ---GGGGGGG   [313]
K. thomsonii JMG031                AATATTGATC CTTTCAGTAT TCCAAATCGC GATGTAAAAC CGAAAAAA-- --GGGGGGGG   [310]
K. thomsonii AMM2647               AATATTGATC CTTTCAGTAT TCCAAATCGC GATGTAAAAC CGAAAAAA-- -GGGGGGGGG   [307]
K. thomsonii CK4821                AATATTGATC CTTTCAGTAT TCCAAATCGC GATGTAAAAC CGAAAA---- GGGGGGGGGG   [307]
K. triangularis SR264              AATATCGATC CTTTCAGTAT TCCAAATCGC GATGTGAAAC CGAAAAA--- --GGGGGGGG   [307]
K. triangularis SR266              AATATCGATC CTTTCAGTAT TCCAAATCGC GATGTGAAAC CGAAAAA--- --GGGGGGGG   [307]
K. triangularis SR299              AATATCGATC CTTTCAGTAT TCCAAATCGC GATGTAAAAC CGAAA----- -GGGGGGGGG   [313]
K. triangularia obtusiloba SRsn    AATATCGATC CTTTCAGTAT TCCAAATCGC GATGTAAAAC CGAAA----- --GGGGGGGG   [304]
K. typhoides NNBG                  AGTATTGATC CTTTCAGTAT TCCAAATCGC GATGTAAAAC CGAAAAAAA- -GGGGGGGGG   [310]
K. tysonii SR302                   AATATCGATC CTTTCAGTAT TCCAAATCGC GATGTAAAAC CGAAAA---- ---GGGGGGG   [311]
K. tysonii SR303                   AATATCGATC CTTTCAGTAT TCCAAATCGC GATGTAAAAC CGAAAA---- ---GGGGGGG   [311]
K. tysonii SR460                   AATATCGATC CTTTCAGTAT TCCAAATCGC GATGTAAAAC CGAAAA---- ---GGGGGGG   [312]
K. umbrina RGsn                    AATATCGATC CTTTCAGTAT TCCAAATCGC GATGTAAAAC CGAAA----- --GGGGGGGG   [304]
K. uvaria SR166                    AGTATTGATC CTTTCAGTAT TCCAAATCGC GATGTAAAAC CGAAAAAA-- --GGGGGGGG   [308]
K. uvaria SR186                    AGTATTGATC CTTTCAGTAT TCCAAATCGC GATGTAAAAC CGAAAAAA-- --GGGGGGGG   [308]
K. uvaria SR172                    AATATCGATC CTTTCAGTAT TCCAAATCGC GATGTGAAAC CGAAAAA--- --GGGGGGGG   [307]
K. uvaria SR201                    AGTATTGATC CTTTCAGTAT TCCAAATCGC GATGTAAAAC CGAAAAAA-- --GGGGGGGG   [308]
K. uvaria SR203                    AGTATTGATC CTTTCAGTAT TCCAAATCGC GATGTAAAAC CGAAAAAAAA -GGGGGGGGG   [311]
K. uvaria SR211                    AGTATTGATC CTTTCAGTAT TCCAAATCGC GATGTAAAAC CGAAAAAA-- --GGGGGGGG   [308]
K. uvaria SR337                    AATATCGATC CTTTCAGTAT TCCAAATCGC GATGTGAAAC CGAAAAA--- --GGGGGGGG   [307]
K. uvaria SR342                    AATATCGATC CTTTCAGTAT TCCAAATCGC GATGTGAAAC CGAAAAA--- --GGGGGGGG   [307]
K. uvaria SR344                    AATATCGATC CTTTCAGTAT TCCAAATCGC GATGTAAAAC CGAAA----- ---GGGGGGG   [303]
K. uvaria SR471                    AATATCGATC CTTTCAGTAT TCCAAATCGC GATGTGAAAC CGAAAAA--- --GGGGGGGG   [307]
K. uvaria SR477                    AATATCGATC CTTTCAGTAT TCCAAATCGC GATGTAAAAC CGAAA----- ---GGGGGGG   [303]
K. uvaria TD4477                   AGTATTGATC CTTTCAGTAT TCCAAATCGC GATGTAAAAC CGAAAAAA-- -GGGGGGGGG   [308]

[                                            370         380         390         400         410        420]
[                                            .          .          .          .          .         .]

Bulbine latifolia SR61             GTAAACCACA TATATAT--- -GTGGGATAT ATCTATCTAT ATTGAATTGC GGATACATCA   [394]
Bulbinella cauda-felis SR204       -----CCGCA TATATAT--- -GTAGGATAT ATATATCTAT ATTGAATTGC GGATACATCA   [381]
K. acreae TD4626                   -----CCACA TATATATATA TGTGGGATAT ATCTATCTAT ATTGAATTGC GGATACATCA   [362]
K. albescens SR314                 ----ACCACA TATATAT--- -GTGGGATAT ATCTATCTAT ATTGAATTGC GGATACATCA   [356]
K. albomontana SR149               ----ACCACA TATATAT--- -GTGGGATAT ATCTATCTAT ATTGAATTGC GGATACATCA   [364]
K. angustifolia SR453              ----ACCACA TATATAT--- -GTGGGATAT ATCTATCTAT ATTGAATTGC GGATACATCA   [356]
K. angustifolia SR542              ----ACCACA TATATAT--- -GTGGGATAT ATCTATCTAT ATTGAATTGC GGATACATCA   [364]
K. ankaratrensis PBP5676           ----ACCACA TATATATAT- -GTGGGATAT ATCTATCTAT ATTGAATTGC GGATACATCA   [363]
K. baurii SR174                    ----ACCACA TATATAT--- -GTGGGATAT ATCTATCTAT ATTGAATTGC GGATACATCA   [365]
K. baurii SR202                    -----CCACA TATATATAT- -GTGGGATAT ATCTATCTAT ATTGAATTGC GGATACATCA   [361]
K. baurii SR275                    ----ACCACA TATATAT--- -GTGGGATAT ATCTATCTAT ATTGAATTGC GGATACATCA   [363]
K. baurii SR285                    ----ACCACA TATATAT--- -GTGGGATAT ATCTATCTAT ATTGAATTGC GGATACATCA   [363]
K. baurii SR360                    ----ACCACA TATATAT--- -GTGGGATAT ATCTATCTAT ATTGAATTGC GGATACATCA   [355]
K. baurii SR382                    ----ACCACA TATATAT--- -GTGGGATAT ATCTATCTAT ATTGAATTGC GGATACATCA   [355]
K. baurii SR398                    ----ACCACA TATATAT--- -GTGGGATAT ATCTATCTAT ATTGAATTGC GGATACATCA   [364]
K. baurii NPB1923                  ----ACCACA TATATAT--- -GTGGGATAT ATCTATCTAT ATTGAATTGC GGATACATCA   [355]
K. baurii RJM1026                  -----CCACA TATATATAT- -GTGGGATAT ATCTATCTAT ATTGAATTGC GGATACATCA   [361]
K. bracystachya SRsn               -----CCACA TATATATAT- -GTGGGATAT ATCTATCTAT ATTGAATTGC GGATACATCA   [363]
K. breviflora SR452                ----ACCACA TATATAT--- -GTGGGATAT ATCTATCTAT ATTGAATTGC GGATACATCA   [356]
K. bruceae SR171                   ----ACCACA TATATAT--- -GTGGGATAT ATCTATCTAT ATTGAATTGC GGATACATCA   [362]
K. buchananii SR305                ----ACCACA TATATAT--- -GTGGGATAT ATCTATCTAT ATTGAATTGC GGATACATCA   [364]
K. buchananii SR307                ----ACCACA TATATAT--- -GTGGGATAT ATCTATCTAT ATTGAATTGC GGATACATCA   [364]
K. buchananii SR458                ----ACCACA TATATAT--- -GTGGGATAT ATCTATCTAT ATTGAATTGC GGATACATCA   [364]
K. caulescens SR270                -----CCACA TATATATAT- -GTGGGATAT ATCTATCTAT ATTGAATTGC GGATACATCA   [359]
K. caulescens SR278                -----CCACA TATATATAT- -GTGGGATAT ATCTATCTAT ATTGAATTGC GGATACATCA   [359]
K. caulescens NPB1821              -----CCACA TATATATATA TGTGGGATAT ATCTATCTAT ATTGAATTGC GGATACATCA   [365]
K. caulescens RJM974               -----CCACA TATATATAT- -GTGGGATAT ATCTATCTAT ATTGAATTGC GGATACATCA   [365]
K. citrina SR176                   -----CCACA TATATATAT- -GTGGGATAT ATCTATCTAT ATTGAATTGC GGATACATCA   [363]
K. coddiana SRsn                   ----ACCACA TATATAT--- -GTGGGATAT ATCTATCTAT ATTGAATTGC GGATACATCA   [362]
K. corraligemma SR549              -----CCACA TATATATATA TGTGGGATAT ATCTATCTAT ATTGAATTGC GGATACATCA   [363]
K. drepanophylla RAL4816           ----ACCACA TATATAT--- -GTGGGATAT ATCTATCTAT ATTGAATTGC GGATACATCA   [362]
K. drepanophylla RJM1100           ----ACCACA TATATAT--- -GTGGGATAT ATCTATCTAT ATTGAATTGC GGATACATCA   [364]
K. ensifolia autumnalis SR448      ----ACCACA TATATAT--- -GTGGGATAT ATCTATCTAT ATTGAATTGC GGATACATCA   [356]
K. ensifolia ensifolia JBsn        ----ACCACA TATATAT--- -GTGGGATAT ATCTATCTAT ATTGAATTGC GGATACATCA   [356]
K. fibrosa SR297                   -----CCACA TATATAT--- -GTGGGATAT ATCTATCTAT ATTGAATTGC GGATACATCA   [364]
K. fibrosa PBP5579                 -----CCACA TATATATATA TGTGGGATAT ATCTATCTAT ATTGAATTGC GGATACATCA   [362]
K. foliosa SR383                   ----ACCACA TATATATAT- -GTGGGATAT ATCTATCTAT ATTGAATTGC GGATACATCA   [362]
K. foliosa SR387                   ----ACCACA TATATATAT- -GTGGGATAT ATCTATCTAT ATTGAATTGC GGATACATCA   [362]
K. foloisa SR389                   ----ACCACA TATATATAT- -GTGGGATAT ATCTATCTAT ATTGAATTGC GGATACATCA   [364]
K. foliosa SR390                   ----ACCACA TATATATAT- -GTGGGATAT ATCTATCTAT ATTGAATTGC GGATACATCA   [364]
K. foliosa JMG034                  ----ACCACA TATATATAT- -GTGGGATAT ATCTATCTAT ATTGAATTGC GGATACATCA   [363]
K. foliosa JMG038                  ----ACCACA TATATATAT- -GTGGGATAT ATCTATCTAT ATTGAATTGC GGATACATCA   [363]
K. galpinii SR312                  ----ACCACA TATATAT--- -GTGGGATAT ATCTATCTAT ATTGAATTGC GGATACATCA   [355]
K. gracilis SR321                  ----ACCACA TATATAT--- -GTGGGATAT ATCTATCTAT ATTGAATTGC GGATACATCA   [364]
K. gracilis SR561                  ----ACCACA TATATAT--- -GTGGGATAT ATCTATCTAT ATTGAATTGC GGATACATCA   [364]
K. gracilis NNBG                   ----ACCACA TATATAT--- -GTGGGATAT ATCTATCTAT ATTGAATTGC GGATACATCA   [365]
K. grantii CP4154                  -----CCACA TATATATAT- -GTGGGATAT ATCTATCTAT ATTGAATTGC GGATACATCA   [361]
K. hirsuta SR282                   ----ACCACA TATATAT--- -GTGGGATAT ATCTATCTAT ATTGAATTGC GGATACATCA   [366]
K. ichopensis SR242                ----ACCACA TATATAT--- -GTGGGATAT ATCTATCTAT ATTGAATTGC GGATACATCA   [364]
K. ichopensis SR286                ----ACCACA TATATAT--- -GTGGGATAT ATCTATCTAT ATTGAATTGC GGATACATCA   [364]
K. ichopensis SR289                ----ACCACA TATATAT--- -GTGGGATAT ATCTATCTAT ATTGAATTGC GGATACATCA   [364]
K. ichopensis SR409                ----ACCACA TATATAT--- -GTGGGATAT ATCTATCTAT ATTGAATTGC GGATACATCA   [365]
K. insignis SRsn                   ----ACCACA TATATATAT- -GTGGGATAT ATCTATCTAT ATTGAATTGC GGATACATCA   [362]
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K. isoetifolia SR386               ----ACCACA TATATATAT- -GTGGGATAT ATCTATCTAT ATTGAATTGC GGATACATCA   [362]
K. isoetifolia SR388               ----ACCACA TATATATAT- -GTGGGATAT ATCTATCTAT ATTGAATTGC GGATACATCA   [364]
K. isoetifolia SR393               ----ACCACA TATATATAT- -GTGGGATAT ATCTATCTAT ATTGAATTGC GGATACATCA   [362]
K. latifolia RSSsn                 ----ACCACA TATATAT--- -GTGGGATAT ATCTATCTAT ATTGAATTGC GGATACATCA   [364]
K. laxiflora SR283                 ----TCCACA TATATAT--- -GTGGGATAT ATCTATCTAT ATTGAATTGC GGATACATCA   [363]
K. laxiflora SR295                 ----ACCACA TATATAT--- -GTGGGATAT ATCTATCTAT ATTGAATTGC GGATACATCA   [363]
K. laxiflora SR441                 ----ACCACA TATATAT--- -GTGGGATAT ATCTATCTAT ATTGAATTGC GGATACATCA   [360]
K. laxiflora SR442                 ----ACCACA TATATAT--- -GTGGGATAT ATCTATCTAT ATTGAATTGC GGATACATCA   [364]
K. laxiflora SR467                 -----CCACA TATATAT--- -GTGGGATAT ATCTATCTAT ATTGAATTGC GGATACATCA   [366]
K. laxiflora SR468                 -----CCACA TATATAT--- -GTGGGATAT ATCTATCTAT ATTGAATTGC GGATACATCA   [366]
K. laxifloraC SRsn                 ----ACCACA TATATAT--- -GTGGGATAT ATCTATCTAT ATTGAATTGC GGATACATCA   [356]
K. laxiflora NPB1810               -----CCACA TATATATAT- -GTGGGATAT ATCTATCTAT ATTGAATTGC GGATACATCA   [363]
K. leucocephala NNBG               ----ACCACA TATATAT--- -GTGGGATAT ATCTATCTAT ATTGAATTGC GGATACATCA   [357]
K. linearifolia SR269              -----CCACA TATATATATA TGTGGGATAT ATCTATCTAT ATTGAATTGC GGATACATCA   [362]
K. linearifolia SR287              ----ACCACA TATATAT--- -GTGGGATAT ATCTATCTAT ATTGAATTGC GGATACATCA   [363]
K. linearifolia SR290              ----ACCACA TATATAT--- -GTGGGATAT ATCTATCTAT ATTGAATTGC GGATACATCA   [363]
K. linearifolia SR291              ----ACCACA TATATAT--- -GTGGGATAT ATCTATCTAT ATTGAATTGC GGATACATCA   [365]
K. linearifolia SR311              ----ACCACA TATATAT--- -GTGGGATAT ATCTATCTAT ATTGAATTGC GGATACATCA   [356]
K. linearifolia SR328              ----ACCACA TATATAT--- -GTGGGATAT ATCTATCTAT ATTGAATTGC GGATACATCA   [362]
K. linearifolia SR343              -----CCACA TATATATATA TGTGGGATAT ATCTATCTAT ATTGAATTGC GGATACATCA   [362]
K. linearifolia SR400              ----ACCACA TATATAT--- -GTGGGATAT ATCTATCTAT ATTGAATTGC GGATACATCA   [362]
K. linearifolia SR558              ----ACCACA TATATAT--- -GTGGGATAT ATCTATCTAT ATTGAATTGC GGATACATCA   [364]
K. linearifolia JPsn               ----ACCACA TATATAT--- -GTGGGATAT ATCTATCTAT ATTGAATTGC GGATACATCA   [365]
K. linearifolia TD4638             ----ACCACA TATATAT--- -GTGGGATAT ATCTATCTAT ATTGAATTGC GGATACATCA   [361]
K. littoralis SR200                ----ACCACA TATATAT--- -GTGGGATAT ATCTATCTAT ATTGAATTGC GGATACATCA   [363]
K. multiflora SR310                ----ACCACA TATATAT--- -GTGGGATAT ATCTATCTAT ATTGAATTGC GGATACATCA   [356]
K. northiae SR263                  -----CCACA TATATATATA TGTGGGATAT ATCTATCTAT ATTGAATTGC GGATACATCA   [364]
K. northiae SR274                  -----CCACA TATATATAT- -GTGGGATAT ATCTATCTAT ATTGAATTGC GGATACATCA   [359]
K. northiae SR446                  -----CCACA TATATATATA TGTGGGATAT ATCTATCTAT ATTGAATTGC GGATACATCA   [360]
K. pauciflora HBsn                 ----ACCACA TATATAT--- -GTGGGATAT ATCTATCTAT ATTGAATTGC GGATACATCA   [364]
K. parviflora SR268                -----CCACA TATATATATA TGTGGGATAT ATCTATCTAT ATTGAATTGC GGATACATCA   [362]
K. parviflora SR330                -----CCACA TATATAT--- -GTGGGATAT ATCTATCTAT ATTGAATTGC GGATACATCA   [363]
K. porphyantha SRsn                ----ACCACA TATATAT--- -GTGGGATAT ATCTATCTAT ATTGAATTGC GGATACATCA   [356]
K. praecox SR529                   -----CCACA TATATATAT- -GTGGGATAT ATCTATCTAT ATTGAATTGC GGATACATCA   [357]
K. praecox SR530                   -----CCACA TATATATAT- -GTGGGATAT ATCTATCTAT ATTGAATTGC GGATACATCA   [361]
K. praecox SR532                   -----CCACA TATATATAT- -GTGGGATAT ATCTATCTAT ATTGAATTGC GGATACATCA   [361]
K. rigidifolia SRsn                ----ACCACA TATATAT--- -GTGGGATAT ATCTATCTAT ATTGAATTGC GGATACATCA   [356]
K. ritualis SR300                  ----ACCACA TATATAT--- -GTGGGATAT ATCTATCTAT ATTGAATTGC GGATACATCA   [364]
K. rooperi SR237                   -----CCACA TATATATATA TGTGGGATAT ATCTATCTAT ATTGAATTGC GGATACATCA   [362]
K. rooperi SR485                   ----ACCACA TATATAT--- -GTGGGATAT ATCTATCTAT ATTGAATTGC GGATACATCA   [355]
K. rooperi SR528                   -----CCACA TATATATAT- -GTGGGATAT ATCTATCTAT ATTGAATTGC GGATACATCA   [361]
K. rooperi RAL4227                 ----ACCACA TATATAT--- -GTGGGATAT ATCTATCTAT ATTGAATTGC GGATACATCA   [362]
K. rooperi TD4559                  ----ACCACA TATATAT--- -GTGGGATAT ATCTATCTAT ATTGAATTGC GGATACATCA   [362]
K. sarmentosa SR207                ----ACCACA TATATATAT- -GTGGGATAT ATCTATCTAT ATTGAATTGC GGATACATCA   [365]
K. schemperi SR391                 ----ACCACA TATATATAT- -GTGGGATAT ATCTATCTAT ATTGAATTGC GGATACATCA   [363]
K. schimperi JMG036                ----ACCACA TATATATAT- -GTGGGATAT ATCTATCTAT ATTGAATTGC GGATACATCA   [363]
K. splendida SR548                 -----CCACA TATATATATA TGTGGGATAT ATCTATCTAT ATTGAATTGC GGATACATCA   [363]
K. splendida Chapman 9061          ----ACCACA TATATATAT- -GTCGGATAT ATCTATCTAT ATTGAATTGC GGATACATCA   [363]
K. stricta SR279                   ----ACCACA TATATAT--- -GTGGGATAT ATCTATCTAT ATTGAATTGC GGATACATCA   [366]
K. thodei SR407                    ----ACCACA TATATAT--- -GTGGGATAT ATCTATCTAT ATTGAATTGC GGATACATCA   [365]
K. thomsonii JMG031                ----ACCACA TATATATAT- -GTGGGATAT ATCTATCTAT ATTGAATTGC GGATACATCA   [364]
K. thomsonii AMM2647               ----ACCACA TATATATAT- -GTGGGATAT ATCTATCTAT ATTGAATTGC GGATACATCA   [361]
K. thomsonii CK4821                ----ACCACA TATATATAT- -GTGGGATAT ATCTATCTAT ATTGAATTGC GGATACATCA   [361]
K. triangularis SR264              -----CCACA TATATATATA TGTGGGATAT ATCTATCTAT ATTGAATTGC GGATACATCA   [362]
K. triangularis SR266              -----CCACA TATATATATA TGTGGGATAT ATCTATCTAT ATTGAATTGC GGATACATCA   [362]
K. triangularis SR299              -----CCACA TATATAT--- -GTGGGATAT ATCTATCTAT ATTGAATTGC GGATACATCA   [364]
K. triangularia obtusiloba SRsn    ----ACCACA TATATAT--- -GTGGGATAT ATCTATCTAT ATTGAATTGC GGATACATCA   [356]
K. typhoides NNBG                  ----ACCACA TATATATAT- -GTGGGATAT ATCTATCTAT ATTGAATTGC GGATACATCA   [364]
K. tysonii SR302                   ----ACCACA TATATAT--- -GTGGGATAT ATCTATCTAT ATTGAATTGC GGATACATCA   [363]
K. tysonii SR303                   ----ACCACA TATATAT--- -GTGGGATAT ATCTATCTAT ATTGAATTGC GGATACATCA   [363]
K. tysonii SR460                   ----ACCACA TATATAT--- -GTGGGATAT ATCTATCTAT ATTGAATTGC GGATACATCA   [364]
K. umbrina RGsn                    ----ACCACA TATATAT--- -GTGGGATAT ATCTATCTAT ATTGAATTGC GGATACATCA   [356]
K. uvaria SR166                    -----CCACA TATATATAT- -GTGGGATAT ATCTATCTAT ATTGAATTGC GGATACATCA   [361]
K. uvaria SR186                    -----CCACA TATATATAT- -GTGGGATAT ATCTATCTAT ATTGAATTGC GGATACATCA   [361]
K. uvaria SR172                    -----CCACA TATATATATA TGTGGGATAT ATCTATCTAT ATTGAATTGC GGATACATCA   [362]
K. uvaria SR201                    -----CCACA TATATATAT- -GTGGGATAT ATCTATCTAT ATTGAATTGC GGATACATCA   [361]
K. uvaria SR203                    ----ACCACA TATATATAT- -GTGGGATAT ATCTATCTAT ATTGAATTGC GGATACATCA   [365]
K. uvaria SR211                    -----CCACA TATATATAT- -GTGGGATAT ATCTATCTAT ATTGAATTGC GGATACATCA   [361]
K. uvaria SR337                    -----CCACA TATATATATA TGTGGGATAT ATCTATCTAT ATTGAATTGC GGATACATCA   [362]
K. uvaria SR342                    -----CCACA TATATATATA TGTGGGATAT ATCTATCTAT ATTGAATTGC GGATACATCA   [362]
K. uvaria SR344                    ----ACCACA TATATAT--- -GTGGGATAT ATCTATCTAT ATTGAATTGC GGATACATCA   [355]
K. uvaria SR471                    -----CCACA TATATATATA TGTGGGATAT ATCTATCTAT ATTGAATTGC GGATACATCA   [362]
K. uvaria SR477                    ----ACCACA TATATAT--- -GTGGGATAT ATCTATCTAT ATTGAATTGC GGATACATCA   [355]
K. uvaria TD4477                   -----CCACA TATATATAT- -GTGGGATAT ATCTATCTAT ATTGAATTGC GGATACATCA   [361]

[                                            430        440        450        460        470           480]
[                                            .          .          .          .          .         .]

Bulbine latifolia SR61             ATGATA-GAA TCATTTTTGA TTGAAACAAA TATGGTTCAG ACAATAGAGA TGAGATAAAA   [453]
Bulbinella cauda-felis SR204       ATGATA-GAA TCATTTTTGA TTGAAACAAA TATGGTTCAT ACAATAGAGA TGAAAT----   [436]
K. acreae TD4626                   ATGATA-GAA TCATTTTTGA TTGAAACAAA TAGGGTTCAT ACAATAGAGA TAAAAT----   [417]
K. albescens SR314                 ATGATA-GAA TCATTTTTGA TTGAAACAAA TGGGGTTCAT ACAATAGAGA TGAAAT----   [411]
K. albomontana SR149               ATGATA-GAA TCATTTTTGA TTGAAACAAA TGGGGTTCAT ACAATAGAGA TGAAAT----   [419]
K. angustifolia SR453              ATGATA-GAA TCATTTTTGA TTGAAACAAA TGGGGTTCAT ACAATAGAGA TGAAAT----   [411]
K. angustifolia SR542              ATGATA-GAA TCATTTTTGA TTGAAACAAA TGGGGTTCAT ACAATAGAGA TGAAAT----   [419]
K. ankaratrensis PBP5676           ATGATA-GAA TCATTTTTGA TTGAAACAAA TAGGGTTCAT ACAATAGATA TGAAAT----   [418]
K. baurii SR174                    ATGATA-GAA TCATTTTTGA TTGAAACAAA TGGGGTTCAT ACAATAGAGA TGAAAT----   [420]
K. baurii SR202                    ATGATA-GAA TCATTTTTGA TTGAAACAAA TAGGGTTCAT ACAATAGAGA TGAAAT----   [416]
K. baurii SR275                    ATGATA-GAA TCATTTTTGA TTGAAACAAA TGGGGTTCAT ACAATAGAGA TGAAAT----   [418]
K. baurii SR285                    ATGATA-GAA TCATTTTTGA TTGAAACAAA TGGGGTTCAT ACAATAGAGA TGAAAT----   [418]
K. baurii SR360                    ATGATA-GAA TCATTTTTGA TTGAAACAAA TGGGGTTCAT ACAATAGAGA TGAAAT----   [410]
K. baurii SR382                    ATGATA-GAA TCATTTTTGA TTGAAACAAA TGGGGTTCAT ACAATAGAGA TGAAAT----   [410]
K. baurii SR398                    ATGATA-GAA TCATTTTTGA TTGAAACAAA TGGGGTTCAT ACAATAGAGA TGAAAT----   [419]
K. baurii NPB1923                  ATGATA-GAA TCATTTTTGA TTGAAACAAA TGGGGTTCAT ACAATAGAGA TGAAAT----   [410]
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K. baurii RJM1026                   ATGATA-GAA TCATTTTTGA TTGAAACAAA TAGGGTTCAT ACAATAGAGA TGAAAT----   [416]
K. bracystachya SRsn                ATGATA-GAA TCATTTTTGA TTGAAACAAA TAGGGTTCAT ACAATAGAGA TGAAAT----   [418]
K. breviflora SR452                 ATGATA-GAA TCATTTTTGA TTGAAACAAA TGGGGTTCAT ACAATAGAGA TGAAAT----   [411]
K. bruceae SR171                    ATGATA-GAA TCATTTTTGA TTGAAACAAA TGGGGTTCAT ACAATAGAGA TGAAAT----   [417]
K. buchananii SR305                 ATGATA-GAA TCATTTTTGA TTGAAACAAA TGGGGTTCAT ACAATAGAGA TGAAAT----   [419]
K. buchananii SR307                 ATGATA-GAA TCATTTTTGA TTGAAACAAA TGGGGTTCAT ACAATAGAGA TGAAAT----   [419]
K. buchananii SR458                 ATGATA-GAA TCATTTTTGA TTGAAACAAA TGGGGTTCAT ACAATAGAGA TGAAAT----   [419]
K. caulescens SR270                 ATGATA-GAA TCATTTTTGA TTGAAACAAA TAGGGTTCAT ACAATAGAGA TAAAAT----   [414]
K. caulescens SR278                 ATGATA-GAA TCATTTTTGA TTGAAACAAA TAGGGTTCAT ACAATAGAGA TAAAAT----   [414]
K. caulescens NPB1821               ATGATATGA- TCATTTTTGA TTGAAACAAA TAGGGTTCAT ACTATAGAGA TAAAAT----   [420]
K. caulescens RJM974                ATGATA-GAA TCATTTTTGA TTGAAACAAA TAGGGTTCAT ACAATAGAGA TAAAAT----   [420]
K. citrina SR176                    ATGATA-GAA TCATTTTTGA TTGAAACAAA TAGGGTTCAT ACAATAGAGA TGAAAT----   [418]
K. coddiana SRsn                    ATGATA-GAA TCATTTTTGA TTGAAACAAA TGGGGTTCAT ACAATAGAGA TGAAAT----   [417]
K. corraligemma SR549               ATGATA-GAA TCATTTTTGA TTGAAACAAA TAGGGTTCAT ACAATAGAGA TGAAAT----   [418]
K. drepanophylla RAL4816            ATGATA-GAA TCATTTTTGA TTGAAACAAA TGGGGTTCAT ACAATAGAGA TGAAAT----   [417]
K. drepanophylla RJM1100            ATGATA-GAA TCATTTTTGA TTGAAACAAA TGGGGTTCAT ACAATAGAGA TGAAAT----   [419]
K. ensifolia autumnalis SR448       ATGATA-GAA TCATTTTTGA TTGAAACAAA TGGGGTTCAT ACAATAGAGA TGAAAT----   [411]
K. ensifolia ensifolia JBsn         ATGATA-GAA TCATTTTTGA TTGAAACAAA TGGGGTTCAT ACAATAGAGA TGAAAT----   [411]
K. fibrosa SR297                    ATGATA-GAA TCATTTTTGA TTGAAACAAA TGGGGTTCAT ACAATAGAGA TGAAAT----   [419]
K. fibrosa PBP5579                  ATGATA-GAA TCATTTTTGA TTGAAACAAA TAGGGTTCAT ACAATAGAGA TAAAAT----   [417]
K. foliosa SR383                    ATGATA-GAA TCATTTTTGA TTGAAACAAA TGGGGTTCAT ACAATAGAGA TGAAAT----   [417]
K. foliosa SR387                    ATGATA-GAA TCATTTTTGA TTGAAACAAA TAGGGTTCAT ACAATAGAGA TGAAAT----   [417]
K. foloisa SR389                    ATGATA-GAA TCATTTTTGA TTGAAACAAA TAGGGTTCAT ACAATAGAGA TGAAAT----   [419]
K. foliosa SR390                    ATGATA-GAA TCATTTTTGA TTGAAACAAA TAGGGTTCAT ACAATAGAGA TGAAAT----   [419]
K. foliosa JMG034                   ATGATA-GAA TCATTTTTGA TTGAAACAAA TAGGGTTCAT ACAATAGAGA TGAAAT----   [418]
K. foliosa JMG038                   ATGATA-GAA TCATTTTTGA TTGAAACAAA TAGGGTTCAT ACAATAGAGA TGAAAT----   [418]
K. galpinii SR312                   ATGATA-GAA TCATTTTTGA TTGAAACAAA TGGGGTTCAT CCAATAGAGA TGAAAT----   [410]
K. gracilis SR321                   ATGATA-GAA TCATTTTTGA TTGAAACAAA TGGGGTTCAT ACAATAGAGA TGAAAT----   [419]
K. gracilis SR561                   ATGATA-GAA TCATTTTTGA TTGAAACAAA TGGGGTTCAT ACAATAGAGA TGAAAT----   [419]
K. gracilis NNBG                    ATGATA-GAA TCATTTTTGA TTGAAACAAA TGGGGTTCAT ACAATAGAGA TGAAAT----   [420]
K. grantii CP4154                   ATGATA-GAA TCATTTTTGA TTGAAACAAA TAGGGTTCAT ACAATAGAGA TGAAAT----   [416]
K. hirsuta SR282                    ATGATA-GAA TCATTTTTGA TTGAAACAAA TGGGGTTCAT ACAATAGAGA TGAAAT----   [421]
K. ichopensis SR242                 ATGATA-GAA TCATTTTTGA TTGAAACAAA TGGGGTTCAT ACAATAGAGA TGAAAT----   [419]
K. ichopensis SR286                 ATGATA-GAA TCATTTTTGA TTGAAACAAA TGGGGTTCAT ACAATAGAGA TGAAAT----   [419]
K. ichopensis SR289                 ATGATA-GAA TCATTTTTGA TTGAAACAAA TGGGGTTCAT ACAATAGAGA TGAAAT----   [419]
K. ichopensis SR409                 ATGATA-GAA TCATTTTTGA TTGAAACAAA TGGGGTTCAT ACAATAGAGA TGAAAT----   [420]
K. insignis SRsn                    ATGATA-GAA TCATTTTTGA TTGAAACAAA TAGGGTTCAT ACAATAGAGA TGAAAT----   [417]
K. isoetifolia SR386                ATGATA-GAA TCATTTTTGA TTGAAACAAA TAGGGTTCAT ACAATAGAGA TGAAAT----   [417]
K. isoetifolia SR388                ATGATA-GAA TCATTTTTGA TTGAAACAAA TAGGGTTCAT ACAATAGAGA TGAAAT----   [419]
K. isoetifolia SR393                ATGATA-GAA TCATTTTTGA TTGAAACAAA TAGGGTTCAT ACAATAGAGA TGAAAT----   [417]
K. latifolia RSSsn                  ATGATA-GAA TCATTTTTGA TTGAAACAAA TGGGGTTCAT ACAATAGAGA TGAAAT----   [419]
K. laxiflora SR283                  ATGATA-GAA TCATTTTTGA TTGAAACAAA TGGGGTTCAT ACAATAGAGA TGAAAT----   [418]
K. laxiflora SR295                  ATGATA-GAA TCATTTTTGA TTGAAACAAA TGGGGTTCAT ACAATAGAGA TGAAAT----   [418]
K. laxiflora SR441                  ATGATA-GAA TCATTTTTGA TTGAAACAAA TGGGGTTCAT ACAATAGAGA TGAAAT----   [415]
K. laxiflora SR442                  ATGATA-GAA TCATTTTTGA TTGAAACAAA TGGGGTTCAT ACAATAGAGA TGAAAT----   [419]
K. laxiflora SR467                  ATGATA-GAA TCATTTTTGA TTGAAACAAA TGGGGTTCAT ACAATAGAGA TGAAAT----   [421]
K. laxiflora SR468                  ATGATA-GAA TCATTTTTGA TTGAAACAAA TGGGGTTCAT CCAATAGAGA TGAAAT----   [421]
K. laxifloraC SRsn                  ATGATA-GAA TCATTTTTGA TTGAAACAAA TGGGGTTCAT CCAATAGAGA TGAAAT----   [411]
K. laxiflora NPB1810                ATGATA-GAA TCATTTTTGA TTGAAACAAA TGGGGTTCAT ACAATAGAGA TGAAAT----   [418]
K. leucocephala NNBG                ATGATA-GAA TCATTTTTGA TTGAAACAAA TGGGGTTCAT ACAATAGAGA TGAAAT----   [412]
K. linearifolia SR269               ATGATA-GAA TCATTTTTGA TTGAAACAAA TAGGGTTCAT ACAATAGAGA TAAAAT----   [417]
K. linearifolia SR287               ATGATA-GAA TCATTTTTGA TTGAAACAAA TGGGGTTCAT ACAATAGAGA TGAAAT----   [418]
K. linearifolia SR290               ATGATA-GAA TCATTTTTGA TTGAAACAAA TGGGGTTCAT ACAATAGAGA TGAAAT----   [418]
K. linearifolia SR291               ATGATA-GAA TCATTTTTGA TTGAAACAAA TGGGGTTCAT ACAATAGAGA TGAAAT----   [420]
K. linearifolia SR311               ATGATA-GAA TCATTTTTGA TTGAAACAAA TGGGGTTCAT CCAATAGAGA TGAAAT----   [411]
K. linearifolia SR328               ATGATA-GAA TCATTTTTGA TTGAAACAAA TGGGGTTCAT ACAATAGAGA TGAAAT----   [417]
K. linearifolia SR343               ATGATA-GAA TCATTTTTGA TTGAAACAAA TAGGGTTCAT ACAATAGAGA TAAAAT----   [417]
K. linearifolia SR400               ATGATA-GAA TCATTTTTGA TTGAAACAAA TGGGGTTCAT ACAATAGAGA TGAAAT----   [417]
K. linearifolia SR558               ATGATA-GAA TCATTTTTGA TTGAAACAAA TGGGGTTCAT ACAATAGAGA TGAAAT----   [419]
K. linearifolia JPsn                ATGATA-GAA TCATTTTTGA TTGAAACAAA TGGGGTTCAT ACAATAGAGA TGAAAT----   [420]
K. linearifolia TD4638              ATGATA-GAA TCATTTTTGA TTGAAACAAA TGGGGTTCAT ACAATAGAGA TGAAAT----   [416]
K. littoralis SR200                 ATGATA-GAA TCATTTTTGA TTGAAACAAA TGGGGTTCAT ACAATAGAGA TGAAAT----   [418]
K. multiflora SR310                 ATGATA-GAA TCATTTTTGA TTGAAACAAA TGGGGTTCAT ACAATAGAGA TGAAAT----   [411]
K. northiae SR263                   ATGATA-GAA TCATTTTTGA TTGAAACAAA TAGGGTTCAT ACAATAGAGA TAAAAT----   [419]
K. northiae SR274                   ATGATA-GAA TCATTTTTGA TTGAAACAAA TAGGGTTCAT ACAATAGAGA TAAAAT----   [414]
K. northiae SR446                   ATGATA-GAA TCATTTTTGA TTGAAACAAA TAGGGTTCAT ACAATAGAGA TAAAAT----   [415]
K. pauciflora HBsn                  ATGATA-GAA TCATTTTTGA TTGAAACAAA TGGGGTTCAT ACAATAGAGA TGAAAT----   [419]
K. parviflora SR268                 ATGATA-GAA TCATTTTTGA TTGAAACAAA TAGGGTTCAT ACAATAGAGA TAAAAT----   [417]
K. parviflora SR330                 ATGATA-GAA TCATTTTTGA TTGAAACAAA TGGGGTTCAT ACAATAGAGA TGAAAT----   [418]
K. porphyantha SRsn                 ATGATA-GAA TCATTTTTGA TTGAAACAAA TGGGGTTCAT CCAATAGAGA TGAAAT----   [411]
K. praecox SR529                    ATGATA-GAA TCATTTTTGA TTGAAACAAA TAGGGTTCAT ACAATAGAGA TGAAAT----   [412]
K. praecox SR530                    ATGATA-GAA TCATTTTTGA TTGAAACAAA TAGGGTTCAT ACAATAGAGA TGAAAT----   [416]
K. praecox SR532                    ATGATA-GAA TCATTTTTGA TTGAAACAAA TAGGGTTCAT ACAATAGAGA TGAAAT----   [416]
K. rigidifolia SRsn                 ATGATA-GAA TCATTTTTGA TTGAAACAAA TGGGGTTCAT ACAATAGAGA TGAAAT----   [411]
K. ritualis SR300                   ATGATA-GAA TCATTTTTGA TTGAAACAAA TGGGGTTCAT ACAATAGAGA TGAAAT----   [419]
K. rooperi SR237                    ATGATA-GAA TCATTTTTGA TTGAAACAAA TAGGGTTCAT ACAATAGAGA T-AAAT----   [416]
K. rooperi SR485                    ATGATA-GAA TCATTTTTGA TTGAAACAAA TGGGGTTCAT ACAATAGAGA TGAAAT----   [410]
K. rooperi SR528                    ATGATA-GAA TCATTTTTGA TTGAAACAAA TAGGGTTCAT ACAATAGAGA TGAAAT----   [416]
K. rooperi RAL4227                  ATGATA-GAA TCATTTTTGA TTGAAACAAA TGGGGTTCAT ACAATAGAGA TGAAAT----   [417]
K. rooperi TD4559                   ATGATA-GAA TCATTTTTGA TTGAAACAAA TGGGGTTCAT ACAATAGAGA TGAAAT----   [417]
K. sarmentosa SR207                 ATGATA-GAA TCATTTTTGA TTGAAACAAA TAGGGTTCAT ACAATAGAGA TGAAAT----   [420]
K. schemperi SR391                  ATGATA-GAA TCATTTTTGA TTGAAACAAA TAGGGTTCAT ACAATAGAGA TGAAAT----   [418]
K. schimperi JMG036                 ATGATA-GAA TCATTTTTGA TTGAAACAAA TAGGGTTCAT ACAATAGAGA TGAAAT----   [418]
K. splendida SR548                  ATGATA-GAA TCATTTTTGA TTGAAACAAA TAGGGTTCAT ACAATAGAGA TGAAAT----   [418]
K. splendida Chapman 9061           ATGATA-GAA TCATTTTTGA TTGAAACAAA TAGGGTTCAT ACAATAGAGA TGAAAT----   [418]
K. stricta SR279                    ATGATA-GAA TCATTTTTGA TTGAAACAAA TGGGGTTCAT ACAATAGAGA TGAAAT----   [421]
K. thodei SR407                     ATGATA-GAA TCATTTTTGA TTGAAACAAA TGGGGTTCAT ACAATAGAGA TGAAAT----   [420]
K. thomsonii JMG031                 ATGATA-GAA TCATTTTTGA TTGAAACAAA TAGGGTTCAT ACAATAGAGA TGAAAT----   [419]
K. thomsonii AMM2647                ATGATA-GAA TCATTTTTGA TTGAAACAAA TAGGGTTCAT ACAATAGAGA TGAAAT----   [416]
K. thomsonii CK4821                 ATGATA-GAA TCATTTTTGA TTGAAACAAA TAGGGTTCAT ACAATAGAGA TGAAAT----   [416]
K. triangularis SR264               ATGATA-GAA TCATTTTTGA TTGAAACAAA TAGGGTTCAT ACAATAGAGA T-AAAT----   [416]
K. triangularis SR266               ATGATA-GAA TCATTTTTGA TTGAAACAAA TAGGGTTCAT ACAATAGAGA TAAAAT----   [417]
K. triangularis SR299               ATGATA-GAA TCATTTTTGA TTGAAACAAA TGGGGTTCAT ACAATAGAGA TGAAAT----   [419]
K. triangularia obtusiloba SRsn     ATGATA-GAA TCATTTTTGA TTGAAACAAA TGGGGTTCAT ACAATAGAGA TGAAAT----   [411]
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K. typhoides NNBG                  ATGATA-GAA TCATTTTTGA TTGAAACAAA TAGGGTTCAT ACAATAGAGA TGAAAT----   [419]
K. tysonii SR302                   ATGATA-GAA TCATTTTTGA TTGAAACAAA TGGGGTTCAT ACAATAGAGA TGAAAT----   [418]
K. tysonii SR303                   ATGATA-GAA TCATTTTTGA TTGAAACAAA TGGGGTTCAT ACAATAGAGA TGAAAT----   [418]
K. tysonii SR460                   ATGATA-GAA TCATTTTTGA TTGAAACAAA TGGGGTTCAT ACAATAGAGA TGAAAT----   [419]
K. umbrina RGsn                    ATGATA-GAA TCATTTTTGA TTGAAACAAA TGGGGTTCAT ACAATAGAGA TGAAAT----   [411]
K. uvaria SR166                    ATGATA-GAA TCATTTTTGA TTGAAACAAA TAGGGTTCAT ACAATAGAGA TGAAAT----   [416]
K. uvaria SR186                    ATGATA-GAA TCATTTTTGA TTGAAACAAA TAGGGTTCAT ACAATAGAGA TGAAAT----   [416]
K. uvaria SR172                    ATGATA-GAA TCATTTTTGA TTGAAACAAA TAGGGTTCAT ACAATAGAGA TAAAAT----   [417]
K. uvaria SR201                    ATGATA-GAA TCATTTTTGA TTGAAACAAA TAGGGTTCAT ACAATAGAGA TGAAAT----   [416]
K. uvaria SR203                    ATGATA-GAA TCATTTTTGA TTGAAACAAA TAGGGTTCAT ACAATAGAGA TGAAAT----   [420]
K. uvaria SR211                    ATGATA-GAA TCATTTTTGA TTGAAACAAA TAGGGTTCAT ACAATAGAGA TGAAAT----   [416]
K. uvaria SR337                    ATGATA-GAA TCATTTTTGA TTGAAACAAA TAGGGTTCAT ACAATAGAGA TAAAAT----   [417]
K. uvaria SR342                    ATGATA-GAA TCATTTTTGA TTGAAACAAA TAGGGTTCAT ACAATAGAGA TGAAAT----   [417]
K. uvaria SR344                    ATGATA-GAA TCATTTTTGA TTGAAACAAA TGGGGTTCAT ACAATAGAGA TGAAAT----   [410]
K. uvaria SR471                    ATGATA-GAA TCATTTTTGA TTGAAACAAA TAGGGTTCAT ACAATAGAGA TAAAAT----   [417]
K. uvaria SR477                    ATGATA-GAA TCATTTTTGA TTGAAACAAA TGGGGTTCAT ACAATAGAGA TGAAAT----   [410]
K. uvaria TD4477                   ATGATA-GAA TCATTTTTGA TTGAAACAAA TAGGGTTCAT ACAATAGAGA TGAAAT----   [416]

[                                            490         500         510         520         530        540]
[                                            .          .          .          .          .         .]

Bulbine latifolia SR61             TGAGAGAGGA TATCCGAAAA AGAAAATAGG AA-CATCCAC TTTTTCAATA TAGGAATCCT   [512]
Bulbinella cauda-felis SR204       -GAGAGAGGA TATCCGAAAA AGAAAATAGG AA-CATACAC TTTTTCAATA TGGGAATCAT   [494]
K. acreae TD4626                   -GAGAGAAGA TATCCGAAAA AGAAAAT-AA AAGCATACAC TTTTTCAATA TGGGAATCAT   [475]
K. albescens SR314                 -GAGAGAAGA TATCCGAAAA AGAAAAT-AG AAGCATACAC TTTTTCAATA TGGGAATCAT   [469]
K. albomontana SR149               -GAGAGAAGA TATCCGAAAA AGAAAAT-AG AAGCATACAC TTTTTCAATA TGGGAATCAT   [477]
K. angustifolia SR453              -GAGAGAAGA TATCCGAAAA AGAAAAT-AG AAGCATACAC TTTTTCAATA TGGGAATCAT   [469]
K. angustifolia SR542              -GAGAGAAGA TATCCGAAAA AGAAAAT-AG AAGCATACAC TTTTTCAATA TGGGAATCAT   [477]
K. ankaratrensis PBP5676           -GAGAGAAGA TATCCGAAAA AGAAAAT-GG AAGCATACAC TTTTTCAATA TGGGAATCAT   [476]
K. baurii SR174                    -GAGAGAAGA TATCCGAAAA AGAAAAT-GG AAGCATACAC TTTTTCAATA TGGGAATCAT   [478]
K. baurii SR202                    -GAGAGAAGA TATCCGAAAA AGAAAAT-GG AAGCATACAC TTTTTCAATA TGGGAATCAT   [474]
K. baurii SR275                    -GAGAGAAGA TATCCGAAAA AGAAAAT-AG AAGCATACAC TTTTTCAATA TGGGAATCAT   [476]
K. baurii SR285                    -GAGAGAAGA TATCCGAAAA AGAAAAT-AG AAGCATACAC TTTTTCAATA TGGGAATCAT   [476]
K. baurii SR360                    -GAGAGAAGA TATCCGAAAA AGAAAAT-AG AAGCATACAC TTTTTCAATA TGGGAATCAT   [468]
K. baurii SR382                    -GAGAGAAGA TATCCGAAAA AGAAAAT-AG AAGCATACAC TTTTTCAATA TGGGAATCAT   [468]
K. baurii SR398                    -GAGAGAAGA TATCCGAAAA AGAAAAT-AA AAGCATACAC TTTTTCAATA TGGGAATCAT   [477]
K. baurii NPB1923                  -GAGAGAAGA TATCCGAAAA AGAAAAT-AG AAGCATACAC TTTTTCAATA TGGGAATCAT   [468]
K. baurii RJM1026                  -GAGAGAAGA TATCCGAAAA AGAAAAT-GG AAGCATACAC TTTTTCAATA TGGGAATCAT   [474]
K. bracystachya SRsn               -GAGAGAAGA TATCCGAAAA AGAAAAT-GG AAGCATACAC TTTTTCAATA TGGGAATCAT   [476]
K. breviflora SR452                -GAGAGAAGA TATCCGAAAA AGAAAAT-AG AAGCATACAC TTTTTCAATA TGGGAATCAT   [469]
K. bruceae SR171                   -GAGAGAAGA TATCCGAAAA AGAAAAT-AG AAGCATACAC TTTTTCAATA TGGGAATCAT   [475]
K. buchananii SR305                -GAGAGAAGA TATCCGAAAA AGAAAAT-AG AAGCATACAC TTTTTCAATA TGGGAATCAT   [477]
K. buchananii SR307                -GAGAGAAGA TATCCGAAAA AGAAAAT-GG AAGCATACAC TTTTTCAATA TGGGAATCAT   [477]
K. buchananii SR458                -GAGAGAAGA TATCCGAAAA AGAAAAT-AG AAGCATACAC TTTTTCAATA TGGGAATCAT   [477]
K. caulescens SR270                -GAGAGAAGA TATCCGAAAA AGAAAAT-AA AAGCATACAC TTTTTCAATA TGGGAATCAT   [472]
K. caulescens SR278                -GAGAGAAGA TATCCGAAAA AGAAAAT-AA AAGCATACAC TTTTTCAATA TGGGAATCAT   [472]
K. caulescens NPB1821              -GAGAGAAGA TATCCGAAAA AGAAAAT-AG AAGCATACAC TTTTTCAATA TGGGAATCAT   [478]
K. caulescens RJM974               -GAGAGAAGA TATCCGAAAA AGAAAAT-AA AAGCATACAC TTTTTCAATA TGGGAATCAT   [478]
K. citrina SR176                   -GAGAGAAGA TATCCGAAAA AGAAAAT-GG AAGCATACAC TTTTTCAATA TGGGAATCAT   [476]
K. coddiana SRsn                   -GAGAGAAGA TATCCGAAAA AGAAAAT-AG AAGCATACAC TTTTTCAATA TGGGAATCAT   [475]
K. corraligemma SR549              -GAGAGAAGA TATCCGAAAA AGAAAAT-AG AAGCATACAC TTTTTCAATA TGGGAATCAT   [476]
K. drepanophylla RAL4816           -GAGAGAAGA TATCCGAAAA AGAAAAT-AG AAGCATACAC TTTTTCAATA TGGGAATCAT   [475]
K. drepanophylla RJM1100           -GAGAGAAGA TATCCGAAAA AGAAAAT-AG AAGCATACAC TTTTTCAATA TGGGAATCAT   [477]
K. ensifolia autumnalis SR448      -GAGAGAAGA TATCCGAAAA AGAAAAT-AG AAGCATACAC TTTTTCAATA TGGGAATCAT   [469]
K. ensifolia ensifolia JBsn        -GAGAGAAGA TATCCGAAAA AGAAAAT-GG AAGCATACAC TTTTTCAATA TGGGAATCAT   [469]
K. fibrosa SR297                   -GAGAGAAGA TATCCGAAAA AGAAAAT-AG AAGCATACAC TTTTTCAATA TGGGAATCAT   [477]
K. fibrosa PBP5579                 -GAGAGAAGA TATCCGAAAA AGAAAAT-AA AAGCATACAC TTTTTCAATA TGGGAATCAT   [475]
K. foliosa SR383                   -GAGAGAAGA TATCCGAAAA AGAAAAT-AG AAGCATACAC TTTTTCAATA TGGGAATCAT   [475]
K. foliosa SR387                   -GAGAGAAGA TATCCGAAAA AGAAAAT-AG AAGCATACAC TTTTTCAATA TGGGAATCAT   [475]
K. foloisa SR389                   -GAGAGAAGA TATCCGAAAA AGAAAAT-AG AAGCATACAC TTTTTCAATA TGGGAATCAT   [477]
K. foliosa SR390                   -GAGAGAAGA TATCCGAAAA AGAAAAT-AG AAGCATACAC TTTTTCAATA TGGGAATCAT   [477]
K. foliosa JMG034                  -GAGAGAAGA TATCCGAAAA AGAAAAT-AG AAGCATACAC TTTTTCAATA TGGGAATCAT   [476]
K. foliosa JMG038                  -GAGAGAAGA TATCCGAAAA AGAAAAT-AG AAGCATACAC TTTTTCAATA TGGGAATCAT   [476]
K. galpinii SR312                  -GAGAGAAGA TATCCGAAAA AGAAAAT-AG AAGCATACAC TTTTTCAATA TGGGAATCAT   [468]
K. gracilis SR321                  -GAGAGAAGA TATCCGAAAA AGAAAAT-AG AAGCATACAC TTTTTCAATA TGGGAATCAT   [477]
K. gracilis SR561                  -GAGAGAAGA TATCCGAAAA AGAAAAT-AG AAGCATACAC TTTTTCAATA TGGGAATCAT   [477]
K. gracilis NNBG                   -GAGAGAAGA TATCCGAAAA AGAAAAT-AG AAGCATACAC TTTTTCAATA TGGGAATCAT   [478]
K. grantii CP4154                  -GAGAGAAGA TATCCGAAAA AGAAAAT-GG AAGCATACAC TTTTTCAATA TGGGAATCAT   [474]
K. hirsuta SR282                   -GAGAGAAGA TATCCGAAAA AGAAAAT-AG AAGCATACAC TTTTTCAATA TGGGAATCAT   [479]
K. ichopensis SR242                -GAGAGAAGA TATCCGAAAA AGAAAAT-AG AAGCATACAC TTTTTCAATA TGGGAATCAT   [477]
K. ichopensis SR286                -GAGAGAAGA TATCCGAAAA AGAAAAT-AG AAGCATACAC TTTTTCAATA TGGGAATCAT   [477]
K. ichopensis SR289                -GAGAGAAGA TATCCGAAAA AGAAAAT-AG AAGCATACAC TTTTTCAATA TGGGAATCAT   [477]
K. ichopensis SR409                -GAGAGAAGA TATCCGAAAA AGAAAAT-AG AAGCATACAC TTTTTCAATA TGGGAATCAT   [478]
K. insignis SRsn                   -GAGAGAAGA TATCCGAAAA AGAAAAT-AG AAGCATACAC TTTTTCAATA TGGGAATCAT   [475]
K. isoetifolia SR386               -GAGAGAAGA TATCCGAAAA AGAAAAT-AG AAGCATACAC TTTTTCAATA TGGGAATCAT   [475]
K. isoetifolia SR388               -GAGAGAAGA TATCCGAAAA AGAAAAT-AG AAGCATACAC TTTTTCAATA TGGGAATCAT   [477]
K. isoetifolia SR393               -GAGAGAAGA TATCCGAAAA AGAAAAT-AG AAGCATACAC TTTTTCAATA TGGGAATCAT   [475]
K. latifolia RSSsn                 -GAGAGAAGA TATCCGAAAA AGAAAAT-AG AAGCATACAC TTTTTCAATA TGGGAATCAT   [477]
K. laxiflora SR283                 -GAGAGAAGA TATCCGAAAA AGAAAAT-AG AAGCATACAC TTTTTCAATA TGGGAATCAT   [476]
K. laxiflora SR295                 -GAGAGAAGA TATCCGAAAA AGAAAAT-AG AAGCATACAC TTTTTCAATA TGGGAATCAT   [476]
K. laxiflora SR441                 -GAGAGAAGA TATCCGAAAA AGAAAAT-AG AAGCATACAC TTTTTCAATA TGGGAATCAT   [473]
K. laxiflora SR442                 -GAGAGAAGA TATCCGAAAA AGAAAAT-AG AAGCATACAC TTTTTCAATA TGGGAATCAT   [477]
K. laxiflora SR467                 -GAGAGAAGA TATCCGAAAA AGAAAAT-AA AAGCATACAC TTTTTCAATA TGGGAATCAT   [479]
K. laxiflora SR468                 -GAGAGAAGA TATCCGAAAA AGAAAAT-AA AAGCATACAC TTTTTCAATA TGGGAATCAT   [479]
K. laxifloraC SRsn                 -GAGAGAAGA TATCCGAAAA AGAAAAT-AG AAGCATACAC TTTTTCAATA TGGGAATCAT   [469]
K. laxiflora NPB1810               -GAGAGAAGA TATCCGAAAA AGAAAAT-AG AAGCATACAC TTTTTCAATA TGGGAATCAT   [476]
K. leucocephala NNBG               -GAGAGAAGA TATCCGAAAA AGAAAAT-GG AAGCATACAC TTTTTCAATA TGGGAATCAT   [470]
K. linearifolia SR269              -GAGAGAAGA TATCCGAAAA AGAAAAT-AA AAGCATACAC TTTTTCAATA TGGGAATCAT   [475]
K. linearifolia SR287              -GAGAGAAGA TATCCGAAAA AGAAAAT-AG AAGCATACAC TTTTTCAATA TGGGAATCAT   [476]
K. linearifolia SR290              -GAGAGAAGA TATCCGAAAA AGAAAAT-AG AAGCATACAC TTTTTCAATA TGGGAATCAT   [476]
K. linearifolia SR291              -GAGAGAAGA TATCCGAAAA AGAAAAT-AG AAGCATACAC TTTTTCAATA TGGGAATCAT   [478]
K. linearifolia SR311              -GAGAGAAGA TATCCGAAAA AGAAAAT-AG AAGCATACAC TTTTTCAATA TGGGAATCAT   [469]
K. linearifolia SR328              -GAGAGAAGA TATCCGAAAA AGAAAAT-AG AAGCATACAC TTTTTCAATA TGGGAATCAT   [475]
K. linearifolia SR343              -GAGAGAAGA TATCCGAAAA AGAAAAT-AA AAGCATACAC TTTTTCAATA TGGGAATCAT   [475]
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K. linearifolia SR400              -GAGAGAAGA TATCCGAAAA AGAAAAT-AG AAGCATACAC TTTTTCAATA TGGGAATCAT   [475]
K. linearifolia SR558              -GAGAGAAGA TATCCGAAAA AGAAAAT-AG AAGCATACAC TTTTTCAATA TGGGAATCAT   [477]
K. linearifolia JPsn               -GAGAGAAGA TATCCGAAAA AGAAAAT??? ?????????? ?????????? ??????????   [479]
K. linearifolia TD4638             -GAGAGAAGA TATCCGAAAA AGAAAAT-AG AAGCATACAC TTTTTCAATA TGGGAATCAT   [474]
K. littoralis SR200                -GAGAGAAGA TATCCGAAAA AGAAAAT-AG AAGCATACAC TTTTTCAATA TGGGAATCAT   [476]
K. multiflora SR310                -GAGAGAAGA TATCCGAAAA AGAAAAT-AG AAGCATACAC TTTTTCAATA TGGGAATCAT   [469]
K. northiae SR263                  -GAGAGAAGA TATCCGAAAA AGAAAAT-AA AAGCATACAC TTTTTCAATA TGGGAATCAT   [477]
K. northiae SR274                  -GAGAGAAGA TATCCGAAAA AGAAAAT-AA AAGCATACAC TTTTTCAATA TGGGAATCAT   [472]
K. northiae SR446                  -GAGAGAAGA TATCCGAAAA AGAAAAT-AA AAGCATACAC TTTTTCAATA TGGGAATCAT   [473]
K. pauciflora HBsn                 -GAGAGAAGA TATCCGAAAA AGAAAAT-AG AAGCATACAC TTTTTCAATA TGGGAATCAT   [477]
K. parviflora SR268                -GAGAGAAGA TATCCGAAAA AGAAAAT-AA AAGCATACAC TTTTTCAATA TGGGAATCAT   [475]
K. parviflora SR330                -GAGAGAAGA TATCCGAAAA AGAAAAT-AA AAGCATACAC TTTTTCAATA TGGGAATCAT   [476]
K. porphyantha SRsn                -GAGAGAAGA TATCCGAAAA AGAAAAT-GG AAGCATACAC TTTTTCAATA TGGGAATCAT   [469]
K. praecox SR529                   -GAGAGAAGA TATCCGAAAA AGAAAAT-GG AAGCATACAC TTTTTCAATA TGGGAATCAT   [470]
K. praecox SR530                   -GAGAGAAGA TATCCGAAAA AGAAAAT-GG AAGCATACAC TTTTTCAATA TGGGAATCAT   [474]
K. praecox SR532                   -GAGAGAAGA TATCCGAAAA AGAAAAT-GG AAGCATACAC TTTTTCAATA TGGGAATCAT   [474]
K. rigidifolia SRsn                -GAGAGAAGA TATCCGAAAA AGAAAAT-GG AAGCATACAC TTTTTCAATA TGGGAATCAT   [469]
K. ritualis SR300                  -GAGAGAAGA TATCCGAAAA AGAAAAT-AG AAGCATACAC TTTTTCAATA TGGGAATCAT   [477]
K. rooperi SR237                   -GAGAGAAGA TATCCGAAAA AGAAAAT-AA AAGCATACAC TTTTTCAATA TGGGAATCAT   [474]
K. rooperi SR485                   -GAGAGAAGA TATCCGAAAA AGAAAAT-AG AAGCATACAC TTTTTCAATA TGGGAATCAT   [468]
K. rooperi SR528                   -GAGAGAAGA TATCCGAAAA AGAAAAT-GG AAGCATACAC TTTTTCAATA TGGGAATCAT   [474]
K. rooperi RAL4227                 -GAGAGAAGA TATCCGAAAA AGAAAAT-AG AAGCATACAC TTTTTCAATA TGGGAATCAT   [475]
K. rooperi TD4559                  -GAGAGAAGA TATCCGAAAA AGAAA????? ?????????? ?????????? ??????????   [476]
K. sarmentosa SR207                -GAGAGAAGA TATCCGAAAA AGAAAAT-GG AAGCATACAC TTTTTCAATA TGGGAATCAT   [478]
K. schemperi SR391                 -GAGAGAAGA TATCCGAAAA AGAAAAT-AG AAGCATACAC TTTTTCAATA TGGGAATCAT   [476]
K. schimperi JMG036                -GAGAGAAGA TATCCGAAAA AGAAAAT-AG AAGCATACAC TTTTTCAATA TGGGAATCAT   [476]
K. splendida SR548                 -GAGAGAAGA TATCCGAAAA AGAAAAT-AG AAGCATACAC TTTTTCAATA TGGGAATCAT   [476]
K. splendida Chapman 9061          -GAGAGAAGA TATCCGAAAA AGAAAAT-AG AAGCATACAC TTTTTCAATA TGGGAATCAT   [476]
K. stricta SR279                   -GAGAGAAGA TATCCGAAAA AGAAAAT-AG AAGCATACAC TTTTTCAATA TGGGAATCAT   [479]
K. thodei SR407                    -GAGAGAAGA TATCCGAAAA AGAAAAT-AG AAGCATACAC TTTTTCAATA TGGGAATCAT   [478]
K. thomsonii JMG031                -GAGAGAAGA TATCCGAAAA AGAAAAT-AG AAGCATACAC TTTTTCAATA TGGGAATCAT   [477]
K. thomsonii AMM2647               -GAGAGAAGA TATCCGAAAA AGAAAAT-AG AAGCATACAC TTTTTCAATA TGGGAATCAT   [474]
K. thomsonii CK4821                -GAGAGAAGA TATCCGAAAA AGAAAAT-AG AAGCATACAC TTTTTCAATA TGGGAATCAT   [474]
K. triangularis SR264              -GAGAGAAGA TATCCGAAAA AGAAAAT-AA AAGCATACAC TTTTTCAATA TGGGAATCAT   [474]
K. triangularis SR266              -GAGAGAAGA TATCCGAAAA AGAAAAT-AA AAGCATACAC TTTTTCAATA TGGGAATCAT   [475]
K. triangularis SR299              -GAGAGAAGA TATCCGAAAA AGAAAAT-AG AAGCATACAC TTTTTCAATA TGGGAATCAT   [477]
K. triangularia obtusiloba SRsn    -GAGAGAAGA TATCCGAAAA AGAAAAT-GG AAGCATACAC TTTTTCAATA TGGGAATCAT   [469]
K. typhoides NNBG                  -GAGAGAAGA TATCCGAAAA AGAAAAT-GG AAGCATACAC TTTTTCAATA TGGGAATCAT   [477]
K. tysonii SR302                   -GAGAGAAGA TATCCGAAAA AGAAAAT-AG AAGCATACAC TTTTTCAATA TGGGAATCAT   [476]
K. tysonii SR303                   -GAGAGAAGA TATCCGAAAA AGAAAAT-AG AAGCATACAC TTTTTCAATA TGGGAATCAT   [476]
K. tysonii SR460                   -GAGAGAAGA TATCCGAAAA AGAAAAT-AG AAGCATACAC TTTTTCAATA TGGGAATCAT   [477]
K. umbrina RGsn                    -GAGAGAAGA TATCCGAAAA AGAAAAT-GG AAGCATACAC TTTTTCAATA TGGGAATCAT   [469]
K. uvaria SR166                    -GAGAGAAGA TATCCGAAAA AGAAAAT-GG AAGCATACAC TTTTTCAATA TGGGAATCAT   [474]
K. uvaria SR186                    -GAGAGAAGA TATCCGAAAA AGAAAAT-GG AAGCATACAC TTTTTCAATA TGGGAATCAT   [474]
K. uvaria SR172                    -GAGAGAAGA TATCCGAAAA AGAAAAT-AA AAGCATACAC TTTTTCAATA TGGGAATCAT   [475]
K. uvaria SR201                    -GAGAGAAGA TATCCGAAAA AGAAAAT-GG AAGCATACAC TTTTTCAATA TGGGAATCAT   [474]
K. uvaria SR203                    -GAGAGAAGA TATCCGAAAA AGAAAAT-GG AAGCATACAC TTTTTCAATA TGGGAATCAT   [478]
K. uvaria SR211                    -GAGAGAAGA TATCCGAAAA AGAAAAT-GG AAGCATACAC TTTTTCAATA TGGGAATCAT   [474]
K. uvaria SR337                    -GAGAGAAGA TATCCGAAAA AGAAAAT--- --GC-TACAC TTTTTCAATA TGGGAATCAT   [470]
K. uvaria SR342                    -GAGAGAAGA TATCCGAAAA AGAAAAT-AA AAGCATACAC TTTTTCA-T? ??????????   [474]
K. uvaria SR344                    -GAGAGAAGA TATCCGAAAA AGAAAAT-AG AAGCATACAC TTTTTCAATA TGGGAATCAT   [468]
K. uvaria SR471                    -GAGAGAAGA TATCCGAAAA AGAAAAT-AA AAGCATACAC TTTTTCAATA TGGGAATCAT   [475]
K. uvaria SR477                    -GAGAGAAGA TATCCGAAAA AGAAAAT-AG AAGCATACAC TTTTTCAATA TGGGAATCAT   [468]
K. uvaria TD4477                   -GAGAGAAGA TATCCGAAAA AGAAAAT-GG AAGCATACAC TTTTTCAATA TGGGAATCAT   [474]

[                                            550         560         570         580         590        600]
[                                             .          .          .          .          .         .]

Bulbine latifolia SR61             TAT------- --ATAAA-AA ATT-CCACAG TTCCGAGATA AATGAAA-GA GGTGGGTAAA   [560]
Bulbinella cauda-felis SR204       TAT------- --ATAAA-AA ATT-CAACAG TTCCAAGATA AATGAA-GGA GGTGGATAAA   [542]
K. acreae TD4626                   TATAATCATT ATATAAA-AA ATT-CAACAG TTCCAAGATA AATGAAA-GA GGTGGGTAAA   [532]
K. albescens SR314                 TAT------- --ATAAA-AA ATT-CAACAG TTCCAAGATA AATGAAA-GA GGTGGGTAAA   [517]
K. albomontana SR149               TAT------- --ATAAA--A ATT-CAACAG TTCCAAGATA AATGAAA-GA GGTGGGTAAA   [524]
K. angustifolia SR453              TAT------- --ATAAA-AA ATT-CAACAG TTCCAAGATA AAT??????? ??????????   [518]
K. angustifolia SR542              TAT------- --ATAAA-AA ATT-CAACAG TTCCAAGATA AATGAAA-GA GGTGGGTAAA   [525]
K. ankaratrensis PBP5676           TAT------- --ATAAA-AA ATT-CaaCAG TTCCAAGATA AATGAAA-GA GGTGGGTAAA   [524]
K. baurii SR174                    TAT------- --ATAAA-AA ATT-CAACAG TTCCAAGATA AATGAAA-GA GGTGGGTAAA   [526]
K. baurii SR202                    TAT------- --ATAAA-AA ATT-CAACAG TTCCAAGATA AATGAAATGA GGTGGGTAAA   [523]
K. baurii SR275                    TAT------- --ATAAA-AA ATT-CAACAG TTCCAAGATA AATGAAA-GA GGTGGGTAAA   [524]
K. baurii SR285                    TAT------- --ATAAA-AA ATT-CAACAG TTCCAAGATA AATGAAA-GA GGTGGGTAAA   [524]
K. baurii SR360                    TAT------- --ATAAA-AA ATT-CAACAG TTCCAAGATA AATGAAA-GA GGTGGGTAAA   [516]
K. baurii SR382                    TAT------- --ATAAA-AA ATT-CAACAG TTCCAAGATA AATGAAA-GA GGTGGGTAAA   [516]
K. baurii SR398                    TAT------- --ATAAA-AA ATT-CAACAG TTCCAAGATA AATGAAA-GA GG-GGGTAAA   [524]
K. baurii NPB1923                  TAT------- --ATAAA-AA ATT-CAACAG TTCCAAGATA AATGAAA-GA GGTGGGTAAA   [516]
K. baurii RJM1026                  TAT------- --ATAAA-AA ATT-CAACAG TTCCAAGATA AATGAAATGA GGTGGGTAAA   [523]
K. bracystachya SRsn               TAT------- --ATAAA-AA ATT-CAACAG TTCCAAGATA AATGAAATGA GGTGGGTAAA   [525]
K. breviflora SR452                TAT------- --ATAAA-AA ATT-CAACAG TTCCAAGATA AATGAAA-GA GGTGGGTAAA   [517]
K. bruceae SR171                   TAT------- --ATAAA-AA ATT-CAACAG TTCCAAGATA AATGAAA-GA GGTGGGTAAA   [523]
K. buchananii SR305                TAT------- --ATAAA-AA ATT-CAACAG TTCCAAGATA AATGAAA-GA GGTGGGTAAA   [525]
K. buchananii SR307                TAT------- --ATAAA-AA ATT-CAACAG TTCCAAGATA AATGAAA-GA GGTGGGTAAA   [525]
K. buchananii SR458                TAT------- --ATAAA-AA ATT-CAACAG TTCCAAGATA AATGAAA-GA GGTGGGTAAA   [525]
K. caulescens SR270                TATAATCATT ATATAAA-AA ATT-CAACAG TTCCAAGATA AATGAAA-GA GGTGGGTAAA   [529]
K. caulescens SR278                TATAATCATT ATATAAA-AA ATT-CAACAG TTCCAAGATA AATGAAA-GA GGTGGGTAAA   [529]
K. caulescens NPB1821              TATAATCATT ATATAAA-AA ATT-CAACAG TTCCAAGATA AATGAAA-GA GGTGGGTAAA   [535]
K. caulescens RJM974               TATAATCATT ATATAAA-AA ATT-CAACAG TTCCAAGATA AATGAAA-GA GGTGGGTCAA   [535]
K. citrina SR176                   TAT------- --ATAAA-AA ATT-CAACAG TTCCAAGATA AATGAAATGA GGTGGGTAAA   [525]
K. coddiana SRsn                   TAT------- --ATAAA-AA ATT-CAACAG TTCCAAGATA AATGAAA-GA GGTGGGTAAA   [523]
K. corraligemma SR549              TAT------- --ATAAA-AA ATT-CACCAG TTCCAAGATA AATGAAA-GA GGTGGGTAAA   [524]
K. drepanophylla RAL4816           TAT------- --ATAAA-AA ATT-CAACAG TTCCAAGATA AATGAAA-GA GGTGGGTAAA   [523]
K. drepanophylla RJM1100           TAT------- --ATAAA-AA ATT-CAACAG TTCCAAGATA AATGAAA-GA GGTGGGTAAA   [525]
K. ensifolia autumnalis SR448      TAT------- --ATAAA-AA ATT-CAACAG TTCCAAGATA AATGAAA-GA GGTGGGTAAA   [517]
K. ensifolia ensifolia JBsn        TAT------- --ATAAA-AA ATT-CAACAG TTCCAAGATA AATGAAA-GA GGTGGGTAAA   [517]
K. fibrosa SR297                   TAT------- --ATAAA-AA ATT-CAACAG TTCCAAGATA AATGAAA-GA GGTGGGTAAA   [525]
K. fibrosa PBP5579                 TATAATCATT ATATAAA-AA ATT-CAACAG TTCCAAGATA AATGAAA-GA GGTGGGTAAA   [532]
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K. foliosa SR383                   TAT------- --ATAAA-AA ATT-CAACAG TTCCAAGATA AATGAAA-GA GGTGGGTAAA   [523]
K. foliosa SR387                   TAT------- --ATAAA-AA ATT-CAACAG TTCCAAGATA AATGAAA-GA GGTGGGTAAA   [523]
K. foloisa SR389                   TAT------- --ATAAA-AA ATT-CAACAG TTCCAAGATA AATGAAA-GA GGTGGGTAAA   [525]
K. foliosa SR390                   TAT------- --ATAAA-AA ATT-CAACAG TTCCAAGATA AATGAAA-GA GGTGGGTAAA   [525]
K. foliosa JMG034                  TAT------- --ATAAA-AA ATT-CAACAG TTCCAAGATA AATGAAA-GA GGTGGGTAAA   [524]
K. foliosa JMG038                  TAT------- --ATAAA-AA ATT-CAACAG TTCCAAGATA AATGAAA-GA GGTGGGTAAA   [524]
K. galpinii SR312                  TAT------- --ATAAA-AA ATT-CAACAG TTCCAAGATA AATGAAA-GA GGTGGGTAAA   [516]
K. gracilis SR321                  TAT------- --ATAAA-AA ATT-CAACAG TTCCAAGATA AATGAAA-GA GGTGGGTAAA   [525]
K. gracilis SR561                  TAT------- --ATAAA-AA ATT-CAACAG TTCCAAGATA AATGAAA-GA GGTGGGTAAA   [525]
K. gracilis NNBG                   TAT------- --ATAAA-AA ATT-CAACAG TTCCAAGATA AATGAAA-GA GGTGGG-AAA   [525]
K. grantii CP4154                  TAT------- --ATAAA-AA ATT-CAACAG TTCCAAGATA AATGAAATGA GGTGGGTAAA   [523]
K. hirsuta SR282                   TAT------- --ATAAA-AA ATT-CAACAG TTCCAAGATA AATGAAA-GA GGTGGG-AAA   [526]
K. ichopensis SR242                TAT------- --ATAAA-AA ATT-CAACAG TTCCAAGATA AATGAAA-GA GGTGGGTAAA   [525]
K. ichopensis SR286                TAT------- --ATAAA-AA ATT-CAACAG TTCCAAGATA AATGAAA-GA ??????????   [525]
K. ichopensis SR289                TAT------- --ATAAA-AA ATT-CAACAG TTCCAAGATA AATGAAA-GA GGTGGGTAAA   [525]
K. ichopensis SR409                TAT------- --ATAAA-AA ATT-CAACAG TTCCAAGATA AATGAAA-GA GGTGGGTAAA   [526]
K. insignis SRsn                   TAT------- --ATAAA-AA ATT-CAACAG TTCCAAGATA AATGAAA-GA GGTGGGTAAA   [523]
K. isoetifolia SR386               TAT------- --ATAAA-AA ATT-CAACAG TTCCAAGATA AATGAAA-GA GGTGGGTAAA   [523]
K. isoetifolia SR388               TAT------- --ATAAA-AA ATT-CAACAG TTCCAAGATA AATGAAA-GA GGTGGGTAAA   [525]
K. isoetifolia SR393               TAT------- --ATAAA-AA ATT-CAACAG TTCCAAGATA AATGAAA-GA GGTGGGTAA?   [523]
K. latifolia RSSsn                 TAT------- --ATAAA-AA ATT-CAACAG TTCCAAGATA AATGAAA-GA GGTGGGTAAA   [525]
K. laxiflora SR283                 TAT------- --ATAAA-AA ATT-CAACAG TTCCAAGATA AATGAAA-GA GGTGGGTAAA   [524]
K. laxiflora SR295                 TAT------- --ATAAA-AA ATT-CAACAG TTCCAAGATA AATGAAA-GA GGTGGGTAAA   [524]
K. laxiflora SR441                 TAT------- --ATAAA-AA ATT-CAACAG TTCCAAGATA AATGAAA-GA GGTGGGTAAA   [521]
K. laxiflora SR442                 TAT------- --ATAAA-AA ATT-CAACAG TTCCAAGATA AATGAAA-GA GGTGGGTAAA   [525]
K. laxiflora SR467                 TAT------- --ATAAA-AA ATT-CAACAG TTCCAAGATA AATGAAA-GA GGTGGGTAAA   [527]
K. laxiflora SR468                 TAT------- --ATAAA-AA ATT-CAACAG TTCCAAGATA AATGAAA-GA GGTGGGTAAA   [527]
K. laxifloraC SRsn                 TAT------- --ATAAA-AA ATT-CAACAG TTCCAAGATA AATGAAA-GA GGTGGGTAAA   [517]
K. laxiflora NPB1810               TAT------- --ATAAA-AA ATT-CAACAG TTCCAAGATA AATGAAA-GA GGTGGGTAAA   [524]
K. leucocephala NNBG               TAT------- --ATAAA-AA ATT-CAACAG TTCCAAGATA AATGAAA-GA GGTGGGTAAA   [518]
K. linearifolia SR269              TATAATCATT ATATAAA-AA ATT-CAACAG TTCCAAGATA AATGAAA-GA GGTGGGTAAA   [532]
K. linearifolia SR287              TAT------- --ATAAA-AA ATT-CAACAG TTCCAAGATA AATGAAA-GA GGTGGGTAAA   [524]
K. linearifolia SR290              TAT------- --ATAAA-AA ATT-CAACAG TTCCAAGATA AATGAAA-GA GGTGGGTAAA   [524]
K. linearifolia SR291              TAT------- --ATAAA-AA ATT-CAACAG TTCCAAGATA AATGAAA-GA GGTGGGTAAA   [526]
K. linearifolia SR311              TAT------- --ATAAA-AA ATT-CAACAG TTCCAAGATA AATGAAA-GA GGTGGGTAAA   [517]
K. linearifolia SR328              TAT------- --ATAAA-AA ATT-CAACAG TTCCAAGATA AATGAAA-GA GGTGGGTAAA   [523]
K. linearifolia SR343              TATAATCATT ATATAAA-AA ATT-CAACAG TTCCAAGATA AATGAAA-GA GGTGGG????   [532]
K. linearifolia SR400              TAT------- --ATAAA-AA ATT-CAACAG TTCCAAGATA AATGAAA-GA GGTGGGTAAA   [523]
K. linearifolia SR558              TAT------- --ATAAA-AA ATT-CAACAG TTCCAAGATA AATAAAAAAA GGTGGGTAAA   [526]
K. linearifolia JPsn               ?????????? ?????????? ?????????? ?????????? ?????????? ??????????   [539]
K. linearifolia TD4638             TAT------- --ATAAA-AA ATT-CAACAG TTCCAAGATA AATGAAA-GA GGTGGGTAAA   [522]
K. littoralis SR200                TAT------- --ATAAA-AA ATT-CAACAG TTCCAAGATA AATGAAA-GA GGTGGGTAAA   [524]
K. multiflora SR310                TAT------- --ATAAA-AA ATT-CAACAG TTCCAAGATA AATGAAA-GA GGTGGGTAAA   [517]
K. northiae SR263                  TATAATCATT ATATAAA-AA ATT-CAACAG TTCCAAGATA AATGAAA-GA GGTGGGTAAA   [534]
K. northiae SR274                  TATAATCATT ATATAAA-AA ATT-CAACAG TTCCAAGATA AATGAAA-GA GGTGGGTAAA   [529]
K. northiae SR446                  TATAATCATT ATATAAA-AA ATT-CAACAG TTCCAAGATA AATGAAA-GA GGTGGGTAAA   [530]
K. pauciflora HBsn                 TAT------- --ATAAA-AA ATT-CAACAG TTCCAAGATA AATGAAA-GA GGTGGGTAAA   [525]
K. parviflora SR268                TATAATCATT ATATAAA-AA ATT-CAACAG TTCCAAGATA AATGAAA-GA GGTGGGTAAA   [532]
K. parviflora SR330                TAT------- --ATAAA-AA ATT-CAACAG TTCCAAGATA AATGAAA-GA GGTGGGTAAA   [524]
K. porphyantha SRsn                TAT------- --ATAAA-AA ATT-CAACAG TTCCAAGATA AATGAAA-GA GGTGGGTAAA   [517]
K. praecox SR529                   TAT------- --ATAAA-AA ATT-CAACAG TTCCAAGATA AATGAAATGA GGTGGGTAAA   [519]
K. praecox SR530                   TAT------- --ATAAA-AA ATT-CAACAG TTCCAAGATA AATGAAATGA GGTGGGTAAA   [523]
K. praecox SR532                   TAT------- --ATAAA-AA ATT-CAACAG TTCCAAGATA AATGAAATGA GGTGGGTAAA   [523]
K. rigidifolia SRsn                TAT------- --ATAAA-AA ATT-CAACAG TTCCAAGATA AATGAAA-GA GGTGGGTAAA   [517]
K. ritualis SR300                  TAT------- --ATAAA-AA ATT-CAACAG TTCCAAGATA AATGAAA-GA GGTGGGTAAA   [525]
K. rooperi SR237                   TATAATCATT ATATAAA-AA ATT-CAACAG TTCCAAGATA AATGAAA-GA GGTGGGTAAA   [531]
K. rooperi SR485                   TAT------- --ATAAA-AA ATT-CAACAG TTCCAAGATA AATGAAA-GA GGTGGGTAAA   [516]
K. rooperi SR528                   TAT------- --ATAAA-AA ATT-CAACAG TTCCAAGATA AATGAAATGA GGTGGGTAAA   [523]
K. rooperi RAL4227                 TAT------- --ATAAA-AA ATT-CAACAG TTCCAAGATA AATGAAA-GA GGTGGGTAAA   [523]
K. rooperi TD4559                  ?????????? ?????????? ?????????? ?????????? ?????????? ??????????   [536]
K. sarmentosa SR207                TAT------- --ATAAA-AA ATT-CAACAG TTCCAAGATA AATGAAATGA GGTGGGTAAA   [527]
K. schemperi SR391                 TAT------- --ATAAA-AA ATT-CAACAT TTCCAAGATA AATGAAA-GA GGTGGGTAAA   [524]
K. schimperi JMG036                TAT------- --ATAAA-AA ATT-CAACAG TTCCAAGATA AATGAAA-GA GGTGGGTAAA   [524]
K. splendida SR548                 TAT------- --ATAAA-AA ATT-CAACAG TTCCAAGATA AATGAAA-GA GGTGGGTAAA   [524]
K. splendida Chapman 9061          TAT------- --ATAAA-AA ATT-CAACAG TTCCAAGATA AATGAAA-GA GGTGGGTAAA   [524]
K. stricta SR279                   TAT------- --ATAAA-AA ATT-CAACAG TTCCAAGATA AATGAAA-GA GGTGGGTAAA   [527]
K. thodei SR407                    TAT------- --ATAAA-AA ATT-CAACAG TTCCAAGATA AATGAAA-GA GGTGGGTAAA   [526]
K. thomsonii JMG031                TAT------- --ATAAA-AA ATT-CAACAG TTCCAAGATA AATGAAA-GA GGTGGGTAAA   [525]
K. thomsonii AMM2647               TAT------- --ATAAA-AA ATT-CAACAG TTCCAAGATA AATGAAAT-A GGTG??????   [522]
K. thomsonii CK4821                TAT------- --ATAAA-AA --TGCAACAG TTCCAAGATA AATGAAA-GA GGTGGGTAAA   [521]
K. triangularis SR264              TATAATCATT ATATAAA-AA ATT-CAACAG TTCCAAGATA AATGAAA-GA GGTGGGTAAA   [531]
K. triangularis SR266              TATAATCATT ATATAAAAAA ATT-CAACAG TTCCAAGATA AATGAAA-GA GGTGGGTAAA   [533]
K. triangularis SR299              TAT------- --ATAAA-AA ATT-CAACAG TTCCAAGATA AATGAAA-GA GGTGGGTAAA   [525]
K. triangularia obtusiloba SRsn    TAT------- --ATAAA-AA ATT-CAACAG TTCCAAGATA AATGAAA-GA GGTGGGTAAA   [517]
K. typhoides NNBG                  TAT------- --ATAAA-AA ATT-CAACAG TTCCAAGATA AATGAAATGA GGTGGGTAAA   [526]
K. tysonii SR302                   TAT------- --ATAAA-AA ATT-CAACAG TTCCAAGATA AATGAAA-GA GGTGGGTAAA   [524]
K. tysonii SR303                   TAT------- --ATAAA-AA ATT-CAACAG TTCCAAGATA AATGAAA-GA GGTGGGTAAA   [524]
K. tysonii SR460                   TAT------- --ATAAA-AA ATT-CAACAG TTCCAAGATA AAT-AAA--A GGTGGGTAAA   [523]
K. umbrina RGsn                    TAT------- --ATAAA-AA ATT-CAACAG TTCCAAGATA AATGAAA-GA GGTGGGTAAA   [517]
K. uvaria SR166                    TAT------- --ATAAA-AA ATT-CAACAG TTCC-AGATA AATGAAATGA GGTGGGTAAA   [522]
K. uvaria SR186                    TAT------- --ATAAA-AA ATT-CAACAG TTCCAAGATA AATGAAATGA GGTGGGTAAA   [523]
K. uvaria SR172                    TATAATCATT ATATAAA-AA ATT-CAACAG TTCCAAGATA AATGAAA-GA GGTGGGTAAA   [532]
K. uvaria SR201                    TAT------- --ATAAA-AA ATT-CAACAG TTCCAAGATA AATGAAATGA GGTGGGTAAA   [523]
K. uvaria SR203                    TAT------- --ATAAA-AA ATT-CAACAG TTCCAAGATA AATGAAA-GA GGTGGGTAAA   [526]
K. uvaria SR211                    TAT------- --ATAAA-AA ATT-CAACAG TTCCAAGATA AATGAAATGA GGTGGGTAAA   [523]
K. uvaria SR337                    TATAATCATT ATATAAA-AA ATT-CAACAG TTCCAAGATA AATGAAA--- GGTGGGTAAA   [525]
K. uvaria SR342                    ?????????? ?????????? ?????????? ?????????? ?????????? ??????????   [534]
K. uvaria SR344                    TAT------- --ATAAA-AA ATT-CAACAG TTCCAAGATA AATGAAA-GA GGTGGGTAAA   [516]
K. uvaria SR471                    TATAATCATT ATATAAA-AA ATT-CAACAG TTCCAAGATA AATGAAA-GA GGTGGGTAAA   [532]
K. uvaria SR477                    TAT------- --ATAAA-AA ATT-CAACAG TTCCAAGATA AATGAAA-GA GGTGGGTAAA   [516]
K. uvaria TD4477                   TAT------- --ATAAA-AA ATT-CCACAG TTCCAAGATA AATGAAATGA GGTGGGTAAA   [523]

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Bulbine latifolia SR61             ATTACAACT   [569]
Bulbinella cauda-felis SR204       ATTACAACT   [551]
K. acreae TD4626                   ATTACAACT   [541]
K. albescens SR314                 ATTACAACT   [526]
K. albomontana SR149               ATTACAACT   [533]
K. angustifolia SR453              ?????????   [527]
K. angustifolia SR542              ATTACAACT   [534]
K. ankaratrensis PBP5676           AtTACAACT   [533]
K. baurii SR174                    ATTACAACT   [535]
K. baurii SR202                    ATTACAACT   [532]
K. baurii SR275                    ATTACAACT   [533]
K. baurii SR285                    ATTACAACT   [533]
K. baurii SR360                    ATTACAACT   [525]
K. baurii SR382                    ATTACAACT   [525]
K. baurii SR398                    ATTACAACT   [533]
K. baurii NPB1923                  ATTACAACT   [525]
K. baurii RJM1026                  ATTACAACT   [532]
K. bracystachya SRsn               ATTACA???   [534]
K. breviflora SR452                ATTACAACT   [526]
K. bruceae SR171                   ATTACAACT   [532]
K. buchananii SR305                ATTACAACT   [534]
K. buchananii SR307                ATTACAACT   [534]
K. buchananii SR458                ATTACAACT   [534]
K. caulescens SR270                ATTACAACT   [538]
K. caulescens SR278                ATTACAACT   [538]
K. caulescens NPB1821              ATTACAACT   [544]
K. caulescens RJM974               ATTACAACT   [544]
K. citrina SR176                   ATTACAACT   [534]
K. coddiana SRsn                   ATTACAACT   [532]
K. corraligemma SR549              ATTACAACT   [533]
K. drepanophylla RAL4816           ATTACAACT   [532]
K. drepanophylla RJM1100           ATTACAACT   [534]
K. ensifolia autumnalis SR448      ATTACAACT   [526]
K. ensifolia ensifolia JBsn        ATTACAACT   [526]
K. fibrosa SR297                   ATTACAACT   [534]
K. fibrosa PBP5579                 ATTACAACT   [541]
K. foliosa SR383                   ATTACAACT   [532]
K. foliosa SR387                   ATTAC????   [532]
K. foloisa SR389                   ATTACAACT   [534]
K. foliosa SR390                   ATTACAACT   [534]
K. foliosa JMG034                  ATTACAACT   [533]
K. foliosa JMG038                  ATTACAACT   [533]
K. galpinii SR312                  ATTACAACT   [525]
K. gracilis SR321                  ATTACAACT   [534]
K. gracilis SR561                  ATTACAACT   [534]
K. gracilis NNBG                   ATTACAACT   [534]
K. grantii CP4154                  ATTACAACT   [532]
K. hirsuta SR282                   ATTACAACT   [535]
K. ichopensis SR242                ATTACAACT   [534]
K. ichopensis SR286                ?????????   [534]
K. ichopensis SR289                ATTACAACT   [534]
K. ichopensis SR409                ATTACAACT   [535]
K. insignis SRsn                   ATTACAACT   [532]
K. isoetifolia SR386               ATTACAACT   [532]
K. isoetifolia SR388               ATTACAACT   [534]
K. isoetifolia SR393               ?????????   [532]
K. latifolia RSSsn                 ATTACAACT   [534]
K. laxiflora SR283                 ATTACAACT   [533]
K. laxiflora SR295                 ATTACAACT   [533]
K. laxiflora SR441                 ATTACAACT   [530]
K. laxiflora SR442                 ATTACAACT   [534]
K. laxiflora SR467                 ATTACAACT   [536]
K. laxiflora SR468                 ATTACAACT   [536]
K. laxifloraC SRsn                 ATTACAACT   [526]
K. laxiflora NPB1810               ATTACAACT   [533]
K. leucocephala NNBG               ATTACAACT   [527]
K. linearifolia SR269              ATTACAACT   [541]
K. linearifolia SR287              ATTACAACT   [533]
K. linearifolia SR290              ATTACAACT   [533]
K. linearifolia SR291              ATTACAACT   [535]
K. linearifolia SR311              ATTACAACT   [526]
K. linearifolia SR328              ATTACAACT   [532]
K. linearifolia SR343              ?????????   [541]
K. linearifolia SR400              ATTACAACT   [532]
K. linearifolia SR558              ATTACAACT   [535]
K. linearifolia JPsn               ?????????   [548]
K. linearifolia TD4638             ATTACAACT   [531]
K. littoralis SR200                ATTACAACT   [533]
K. multiflora SR310                ATTACAACT   [526]
K. northiae SR263                  ATTACAACT   [543]
K. northiae SR274                  ATTACAACT   [538]
K. northiae SR446                  ATTACAACT   [539]
K. pauciflora HBsn                 ATTACAACT   [534]
K. parviflora SR268                ATTACAACT   [541]
K. parviflora SR330                ATTACAACT   [533]
K. porphyantha SRsn                ATTACAACT   [526]
K. praecox SR529                   ATTACAACT   [528]
K. praecox SR530                   ATTACAACT   [532]
K. praecox SR532                   ATTACAACT   [532]
K. rigidifolia SRsn                ATTACAACT   [526]
K. ritualis SR300                  ATTACAACT   [534]
K. rooperi SR237                   ATTACAACT   [540]
K. rooperi SR485                   ATTACAACT   [525]
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K. rooperi SR528                   ATTACAACT   [532]
K. rooperi RAL4227                 ATTACAACT   [532]
K. rooperi TD4559                  ?????????   [545]
K. sarmentosa SR207                ATTACAACT   [536]
K. schemperi SR391                 ATTACAACT   [533]
K. schimperi JMG036                ATTACAACT   [533]
K. splendida SR548                 AT???????   [533]
K. splendida Chapman 9061          ATTACAACT   [533]
K. stricta SR279                   ATTACAACT   [536]
K. thodei SR407                    ATTACAACT   [535]
K. thomsonii JMG031                ATTACAACT   [534]
K. thomsonii AMM2647               ?????????   [531]
K. thomsonii CK4821                ATTACAACT   [530]
K. triangularis SR264              ATTACAACT   [540]
K. triangularis SR266              ATTACAACT   [542]
K. triangularis SR299              ATTACAACT   [534]
K. triangularia obtusiloba SRsn    ATTACAACT   [526]
K. typhoides NNBG                  ATTACAACT   [535]
K. tysonii SR302                   ATTACAACT   [533]
K. tysonii SR303                   ATTACAACT   [533]
K. tysonii SR460                   ATTACAACT   [532]
K. umbrina RGsn                    ATTACAACT   [526]
K. uvaria SR166                    ATTACAACT   [531]
K. uvaria SR186                    ATTACAACT   [532]
K. uvaria SR172                    ATTACAACT   [541]
K. uvaria SR201                    ATTA?????   [532]
K. uvaria SR203                    ?????????   [535]
K. uvaria SR211                    ATTACAACT   [532]
K. uvaria SR337                    ATTACAACT   [534]
K. uvaria SR342                    ?????????   [543]
K. uvaria SR344                    ATTACAACT   [525]
K. uvaria SR471                    ATTACAACT   [541]
K. uvaria SR477                    ATTACAACT   [525]
K. uvaria TD4477                   ATTACAACT   [532]
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Appendix 5: Final sequence alignments of the *trnL* intron with additional out-groups from Genbank

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[                                              10          20          30          40          50          60]
[                                              .          .          .          .          .          .]

Bulbine latifolia SR61               GATTGGATTG AGCCTTATTA TGGAAACCTG CTAAGTGGTA ACTTCCAAAT TCAGAGAAAC   [60]
Bulbine semibarbata AJ290259         ????GGATTG AGAATTAGTA TGGAAACCTG CTAAGTGGTA ACTTCCAAAT TCAGAGAAAC   [60]
Bulbine succulenta AJ290260          GATTGGATTG AGCCTTAGTA TGGAAACCTG CTAAGTGGTA ACTTCCAAAT TCAGAGAAAC   [60]
Bulbine weisei AJ290261              ????GGATTG AGCCTTAGTA TGGAAACCTG CTAAGTGGTA ACTTCCAAAT TCAGAGAAAC   [60]
Bulbinella cuada-felis SR204         GATTGGATTG AGCCTTAGTA TGGAAACCTG CTAAGTGGTA ACTTCCAAAT TCAGAGAAAC   [60]
Bulbinella cauda-felis AJ290262      GAT?GGATTG AGC-TTAGTA TGGAA-CCTG CTAAGTGGTA ACTTCCAAAT TCAGAGAAAC   [58]
K. acreae TD4626                     GATTGGATTG -GCCTTAGTA TGGAAACCTG CTAAGTGGTA ACTTCCAAAT TCAGAGAAAC   [59]
K. albescens SR314                   GATTGGAGTG AGCCTTAGTA TGGAAACCTG CTAAGTGGTA ACTTCCAA-T TCAGAGAAAC   [59]
K. baurii SR285                      GATTGGATTG AGCCTTAGTA TGGAAACCTG CTAAGTGGTA ACTTCCAAAT TCAGAGAAAC   [60]
K. breviflora SR452                  GATTGGATTG AGCCTTAGTA TGGAAACCTG CTAAGTGGTA ACTTCCAAAT TCAGAGAAAC   [60]
K. bruceae SR171                     GGTTGGATTG AGCCTTAGTA TGGAAACCTG CTAAGTGGTA ACTTCCAAAT TCAGAGAAAC   [60]
K. caulescens SR278                  GATTGGATTG AGCCTTAGTA TGGAAACCTG CTAAGTGGTA ACTTCCAAAT TCAGAGAAAC   [60]
K. corraligemma SR549                GATTGGATTG AGCCTTAGTA TGGAAACCTG CTAAGTGGTA ACTTCCAAAT TCAGAGAAAC   [60]
K. foliosa JMG034                    AATTGGATTG AGCCTTAGTA TGGAAACCTG CTAAGTGGTA ACTTCCAAAT TCAGAGAAAC   [60]
K. insignis SRsn                     AATTGGATTG AGCCTTAGTA TGGAAACCTG CTAAGTGGTA ACTTCCAAAT TCAGAGAAAC   [60]
K. isoetifolia SR388                 AATTGGATTG AGCCTTAGTA TGGAAACCTG CTAAGTGGTA ACTTCCAAAT TCAGAGAAAC   [60]
K. laxiflora SR467                   GATTGGATTG AGCCTTAGTA TGGAAACCTG CTAAGTGGTA ACTTCCAAAT TCAGAGAAAC   [60]
K. laxiflora SR468                   GATTGGATTG AGCCTTAGTA TGGAAACCTG CTAAGTGGTA ACTTCCAAAT TCAGAGAAAC   [60]
K. linearifolia SR311                GATTGGATTG AGCCTTATTA TGGAAACCTG CTAAGTGGTA ACTTCCAAAT TCAGAGAAAC   [60]
K. multiflora SR310                  GATTGGATTG AGCCTTAGTA TGGAAACCTG CTCAGTGGTA ACTTCCAAAT TCAGAGAAAC   [60]
K. northiae SR446                    GATTGGATTG AGCCTTAGTA TGGAAACCTG CTAAGTGGTA ACTTCCAAAT TCAGAGAAAC   [60]
K. parviflora SR268                  GATTGGATTG AGCCTTAGTA TGGAAACCTG CTAAGTGGTA ACTTCCAAAT TCAGAGAAAC   [60]
K. parviflora SR330                  GATTGGATTG AGCCTTAGTA TGGAAACCTG CTAAGTGGTA ACTTCCAAAT TCAGAGAAAC   [60]
K. ritualis SR300                    GATTGGATTG AGCCTTAGTA TGGAAACCTG CTAAGTGGTA ACTTCCAAAT TCAGAGAAAC   [60]
K. schimperi JMG036                  AATTGGATTG AGCCTTAGTA TGGAAACCTG CTAAGTGGTA ACTTCCAAAT TCAGAGAAAC   [60]
K. stricta SR279                     GATTGGATTG AGCCTTAGTA TGGAAACCTG CTAAGTGGTA ACTTCCAAAT TCAGAGAAAC   [60]
K. thomsonii JMG031                  AATTGGATTG AGCCTTAGTA TGGAAACCTG CTAAGTGGTA ACTTCCAAAT TCAGAGAAAC   [60]
K. triangularis SR299                GATTGGATTG AGCCTTAATA TGGAAACCTG CTAAGTGGTA ACTTCCAA-T TCAGAGAAAC   [59]
K. typhoides NNBG                    GATTGTATTG AGCCTTAGTA TGGAAACCTG CTAAGTAGTA ACTTCCAAAT TCAGAGAAAC   [60]
K. tysonii SR302                     GATTGGATTG GGCCTTATTA TGGAA-CCTG CTAAGTGGTA ACTTCCAAAT TCAGAGAAAC   [59]
K. umbrina RGsn                      GATTGGATTG AGCCTTAGTA TGGAAACCTG CTAAGTGGTA ACTTCCAAAT TCAGAGAAAC   [60]
K. uvaria SR186                      GATTGGATTG AGCCTTAGTA TGGAAACCTG CTAAGTGGTA ACTTCCAAAT TCAGAGAAAC   [60]
K. uvaria SR211                      GATTGGATTG AGCCTTATTA TGGAAACCTG CTAAGTGGTA ACTTCCAAAT TCAGAGAAAC   [60]

[                                              70          80          90          100         110         120]
[                                              .          .          .          .          .          .]

Bulbine latifolia SR61               CCTGGAACTA AAAATGGGCA ATCCTGAGCC AAATCTTTTT TTTTT--AAG AAAAAA-TGA   [117]
Bulbine semibarbata AJ290259         CCTGGAACTA AAAATGGGCA ATCCTGAGCC AAATCTTTTT TTTTT---AG AAAAAA-TGA   [116]
Bulbine succulenta AJ290260          CCTGGAACTA AAAATGGGCA ATCCTGAGCC AAATCTTTTT TTTTTTT-AG AAAAAA-TGA   [118]
Bulbine weisei AJ290261              CCTGGAACTA AAAATGGGCA ATCCTGAGCC AAATCTTTTT TTTT----AG AAAAAA-TAA   [115]
Bulbinella cuada-felis SR204         CCTGGAACTA AAAATGGGCA ATCCTGAGCC AAATCTTTTT TTT-----AG AAAAAA-TGA   [114]
Bulbinella cauda-felis AJ290262      CCTGGAACTA AAAATGGGCA ATCCTGAGCC AAATCTTTTT TTT-----AG AAAAAA-TGA   [112]
K. acreae TD4626                     CCTGGAACTA AAAATGGGCA ATCCTGAGCC AAATCTTTTT TTTTT----G AAAAAA-TGA   [114]
K. albescens SR314                   CCTGGAACTA AAAATGGGCA ATCCTGAGCC AAATCTTTTT TTTT-----G AAAAAA-TGA   [113]
K. baurii SR285                      CCTGGAACTA AAAATGGGCA ATCCTGAGCC AAATCTTTTT TTTTTT---G AAAAAAATGA   [117]
K. breviflora SR452                  CCTGGAACTA AAAATGGGCA ATCCTGAGCC AAATCTTTTT TTTT-----G AAAAAA-TGA   [114]
K. bruceae SR171                     CCTGGAACTA AAAATGGGCA ATCCTGAGCC AAATCTTTTT TTTTTTT--G AAAAAAATGA   [118]
K. caulescens SR278                  CCTGGAACTA AAAATGGGCA ATCCTGAGCC AAATCTTTTT TTTTTT---G AAAAAA-TGA   [116]
K. corraligemma SR549                CCTGGAACTA AAAATGGGCA ATCCTGAGCC AAATCTTTTT TTTTTT---G AAAAAA-TGA   [116]
K. foliosa JMG034                    CCTGGAACTA AAAATGGGCA ATCCTGAGCC AAATCTTTTT TTTTT----G AAAAAA-TGA   [115]
K. insignis SRsn                     CCTGGAACTA AAAATGGGCA ATCCTGAGCC AAATCTTTTT TTTTT----G AAAAAA-TGA   [115]
K. isoetifolia SR388                 CCTGGAACTA AAAATGGGCA ATCCTGAGCC AAATCTTTTT TTTTTT---G AAAAAA-TGA   [116]
K. laxiflora SR467                   CCTGGAACTA AAAATGGGCA ATCCTGAGCC AAATCTTTTT TTTTTTT--C AAAAAAATGA   [118]
K. laxiflora SR468                   CCTGGAACTA AAAATGGGCA ATCCTGAGCC AAATCTTTTT TTTTTTT--C AAAAAAATGA   [118]
K. linearifolia SR311                CCTGGAACTA AAAATGGGCA ATCCTGAGCC AAATCTTTTT TTTT-----G AAAAAA-TGA   [114]
K. multiflora SR310                  CCTGGAACTA AAAATGGGCA ATCCTGAGCC AAATCTTTTT TTTTT----G AAAAAA-TGA   [115]
K. northiae SR446                    CCTGGAACTA AAAATGGGCA ATCCTGAGCC AAATCTTTTT TTTTT----G AAAAAA-TGA   [115]
K. parviflora SR268                  CCTGGAACTA AAAATGGGCA ATCCTGAGCC AAATCTTTTT TTTTT----G AAAAAA-TGA   [115]
K. parviflora SR330                  CCTGGAACTA AAAATGGGCA ATCCTGAGCC AAATCTTTTT TTTTTTT--C AAAAAAATGA   [118]
K. ritualis SR300                    CCTGGAACTA AAAATGGGCA ATCCTGAGCC AAATCTTTTT TTTTT----G AAAAAA-TGA   [115]
K. schimperi JMG036                  CCTGGAACTA AAAATGGGCA ATCCTGAGCC AAATCTTTTT TTTTT----G AAAAAA-TGA   [115]
K. stricta SR279                     CCTGGAACTA AAAATGGGCA ATCCTGAGCC AAATCTTTTT TTTTTT---G AAAAAA-TGA   [116]
K. thomsonii JMG031                  CCTGGAACTA AAAATGGGCA ATCCTGAGCC AAATCTTTTT TTTTTT---G AAAAAA-TGA   [116]
K. triangularis SR299                CCTGGAACTA AAAATGGGCA ATCCTGAGCC AAATCTTTTT TTTTTTT--C AAAAAAATGA   [117]
K. typhoides NNBG                    CCTGGAACTA AAAATGGGCA ATCCTGAGCC AAATCTTTTT TTTTTTT--G AAAAAA-TGA   [117]
K. tysonii SR302                     CCTGGAACTA AAAATGGGCA ATCCTGAGCC AAATCTTTTT TTTT-----G AAAAAA-TGA   [113]
K. umbrina RGsn                      CCTGGAACTA AAAATGGGCA ATCCTGAGCC AAATCTTTTT TTTT-----G AAAAAA-TGA   [114]
K. uvaria SR186                      CCTGGAACTA AAAATGGGCA ATCCTGAGCC AAATCTTTTT TTTTTT---G AAAAAA-TGA   [116]
K. uvaria SR211                      CCTGGAACTA AAAATGGGCA ATCCTGAGCC AAATCTTTTT TTTTTTT--G AAAAAA-TGA   [117]

[                                              130         140         150         160         170         180]
[                                              .          .          .          .          .          .]

Bulbine latifolia SR61               TTAATGGGAC AAGAATAAAA AAGGATAGGT GCAGAGACTC AATGGAAGCT GTTCTAACGA   [177]
Bulbine semibarbata AJ290259         TTAATGGGAC AATAATAAAA AAGGATAGGT GCAGAGACTC AATGGAAGCT GTTCTAACGA   [176]
Bulbine succulenta AJ290260          TTAATGGGAC AAGAATAAAA AAGGATAGGT GCAGAGACTC AATGGAAGCT GTTCTAACGA   [178]
Bulbine weisei AJ290261              TTAATG---- -AGAATAAAA AAGGATAGGT GCAGAGACTC AACGGAAGCT GTTCTAACGA   [170]
Bulbinella cuada-felis SR204         TTAATCGGAC AAGAATAAAA AAGGATAGGT GCAGAGACTC AATGGAAGCT GTTCTAACGA   [174]
Bulbinella cauda-felis AJ290262      TTAATCGGAC AAGAATAAAA AAGGATAGGT GCAGAGACTC AATGGAAGCT GTTCTAACGA   [172]
K. acreae TD4626                     TTAATCGGAC AAGAATAAAA AAGGATAGGT GCAGAGACTC AATGGAAGCT GTTCTAACGA   [174]
K. albescens SR314                   TTAATCGGAC AAGAATAAAA AAGGATAGGT GCAGAGACTC AATGGAAGCT GTTCTAACGA   [173]
K. baurii SR285                      TTAATCGAAC AAGAATAAAA AAGGATAGGT GCAGAGACTC AATGGAAGCT GTTCTAACGA   [177]
K. breviflora SR452                  TTAATCGGAC AAGAATAAAA AAGGATAGGT GCAGAGACTC AATGGAAGCT GTTCTAACGA   [174]
K. bruceae SR171                     TTAATCGAAC AAGAATAAAA AAGGATAGGT GCAGAGACTC AATGGAAGCT GTTCTAACGA   [178]
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K. caulescens SR278                  TTAATCGGAC AAGAATAAAA AAGGATAGGT GCAGAGACTC AATGGAAGCT GTTCTAACGA   [176]
K. corraligemma SR549                TTAATAGGAC AAGAATAAAA AAGGATAGGT GCAGAGACTC AATGGAAGCT GTTCTAACGA   [176]
K. foliosa JMG034                    TTAATTGGAC AAGAATAAAA AAGGATAGGT GCAGAGACTC AATGGAAGCT GTTCTAACGA   [175]
K. insignis SRsn                     TTAATCGGAC AAGAATAAAA AAGGATAGGT GCAGAGACTC AATGGAAGCT GTTCTAACGA   [175]
K. isoetifolia SR388                 TTAATCGGAC AAGAATAAAA AAGGATAGGT GCAGAGACTC AATGGAAGCT GTTCTAACGA   [176]
K. laxiflora SR467                   TTAATCGAAC AAGAATAAAA AAGGATAGGT GCAGAGACTC AATGGAAGCT GTTCTAACGA   [178]
K. laxiflora SR468                   TTAATCGAAC AAGAATAAAA AAGGATAGGT GCAGAGACTC AATGGAAGCT GTTCTAACGA   [178]
K. linearifolia SR311                TTAATCGGAC AAGAATAAAA AAGGATAGGT GCAGAGACTC AATGGAAGCT GTTCTAACGA   [174]
K. multiflora SR310                  TTAATCGGAC AAGAATAAAA AAGGATAGGT GCAGAGACTC AATGGAAGCT GTTCTAACGA   [175]
K. northiae SR446                    TTAATCGGAC AAGAATAAAA AAGGATAGGT GCAGAGACTC AATGGAAGCT GTTCTAACGA   [175]
K. parviflora SR268                  TTAATCGGAC AAGAATAAAA AAGGATAGGT GCAGAGACTC AATGGAAGCT GTTCTAACGA   [175]
K. parviflora SR330                  TTAATCGAAC AAGAATAAAA AAGGATAGGT GCAGAGACTC AATGGAAGCT GTTCTAACGA   [178]
K. ritualis SR300                    TTAATCGAAC AAGAATAAAA AAGGATAGGT GCAGAGACTC AATGGAAGCT GTTCTAACGA   [175]
K. schimperi JMG036                  TTAATTGGAC AAGAATAAAA AAGGATAGGT GCAGAGACTC AATGGAAGCT GTTCTAACGA   [175]
K. stricta SR279                     TTAATCGAAC AAGAATAAAA AAGGATAGGT GCAGAGACTC AATGGAAGCT GTTCTAACGA   [176]
K. thomsonii JMG031                  TTAATCGGAC AAGAATAAAA AAGGATAGGT GCAGAGACTC AATGGAAGCT GTTCTAACGA   [176]
K. triangularis SR299                TTAATCGAAC AAGAATAAAA AAGGATAGGT GCAGAGACTC AATGGAAGCT GTTCTAACGA   [177]
K. typhoides NNBG                    TTAATCGGAC AAGAATAAAA AAGGATAGGT GCAGAGACTC AATGGAAGCT GTTCTAACGA   [177]
K. tysonii SR302                     TTAATCGAAC AAGAATAAAA AAGGATAGGT GCAGAGACTC AATGGAAGCT GTTCTAACGA   [173]
K. umbrina RGsn                      TTAATCGGAC AAGAATAAAA AAGGATAGGT GCAGAGACTC AATGGAAGCT GTTCTAACGA   [174]
K. uvaria SR186                      TTAATCGGAC AAGAATAAAA AAGGATAGGT GCAGAGACTC AATGGAAGCT GTTCTAACGA   [176]
K. uvaria SR211                      TTAATCGGAC AAGAATAAAA AAGGATAGGT GCAGAGACTC AATGGAAGCT GTTCTAACGA   [177]

[                                              190         200         210         220         230        240]
[                                              .          .          .          .          .          .]

Bulbine latifolia SR61               ATGGAGTTGA TTACGTTGCG TTGGTAGCAG GGGAATCCTT CTTTCGAAA- -----AAAGG   [231]
Bulbine semibarbata AJ290259         ATGGAGTTGA TTACGTTGCG TTGGTAGCAG GGGAATCTTT CTTTCGAAA- -----AAGGG   [230]
Bulbine succulenta AJ290260          ATGGAGTTGA TTACGTTGCG TTGGTAGCAG AGGAATTCTT CTTTCGAAA- -----AAGGG   [232]
Bulbine weisei AJ290261              ATGGAGTTGA TTACGTTGCG TTGGTAGCAG GGGAATCCTT CTTTCGAAA- -----AAAGG   [224]
Bulbinella cuada-felis SR204         ATGGAGTTGA TTACGTTGCG TTGGTAGCTG G--AATCCTT CTTTCGAAAT TAAAGAAAGG   [232]
Bulbinella cauda-felis AJ290262      ATGGAGTTGA TTACGTTGCG TTGGTAGCTG G--AATCCTT CTTTCGAAAT TAAAGAAAGG   [230]
K. acreae TD4626                     ATGGAGTTGA TTACGTTGCG TTGGTAGCTG G--AATCCTT CTTTCGAAAT TAAAGAAAGG   [232]
K. albescens SR314                   ATGGAGTTGA TTACGTTGCG TTGGTAGCTG G--AATCCTT CTTTCGAAAT TAAAGAAAGG   [231]
K. baurii SR285                      ATGGAGTTGA TTACGTTGCG TTGGTAGCTG G--AATCCTT CTTTCAAAAT TAAAGAAAGG   [235]
K. breviflora SR452                  ATGGAGTTGA TTACGTTGCG TTGGTAGCTG G--AATCCTT CTTTCGAAAT TAAAGAAAGG   [232]
K. bruceae SR171                     ATGGAGTTGA TTACGTTGCG TTGGTAGCTG G--AATCCTT CTTTCGAAAT TAAAGAAAGG   [236]
K. caulescens SR278                  ATGGAGTTGA TTACGTTGCG TTGGTAGCTG G--AATCCTT CTTTCGAAAT TAAAGAAAGG   [234]
K. corraligemma SR549                ATGGAGTTGA TTACGTTGCG TTGGTAGCTG G--AATCCTT CTTTCGAAAT TAAAGAAAGG   [234]
K. foliosa JMG034                    ATGGAGTTGA TTACGTTGCG TTGGTAGCTG G--AATCCTT CTTTCGAAAT TAAAGAAAGG   [233]
K. insignis SRsn                     ATGGAGTTGA TTACGTTGCG TTGGTAGCTG G--AATCCTT CTTTCGAAAT TAAAGAAAGG   [233]
K. isoetifolia SR388                 ATGGAGTTGA TTACGTTGCG TTGGTAGCTG G--AATCCTT CTTTCGAAAT TAAAGAAAGG   [234]
K. laxiflora SR467                   AGGGAGTTGA TTACGTTGCG TTGGTAGCTG G--AATCCTT CTTTCGAAAT TAAAGAAAGG   [236]
K. laxiflora SR468                   AGGGAGTTGA TTACGTTGCG TTGGTAGCTG G--AATCCTT CTTTCGAAAT TAAAGAAAGG   [236]
K. linearifolia SR311                ATGGAGTTGA TTACGTTGCG TTGGTAGCTG G--AATCCTT CTTTCGAAAT TAAAGAAAGG   [232]
K. multiflora SR310                  ATGGAGTTGA TTACGTTGCG TTGGTAGCTG G--AATCCTT CTTTCGAAAT TAAAGAAAGG   [233]
K. northiae SR446                    ATGGAGTTGA TTACGTTGCG TTGGTAGCTG G--AATCCTT CTTTCGAAAT TAAAGAAAGG   [233]
K. parviflora SR268                  ATGGAGTTGA TTACGTTGCG TTGGTAGCTG G--AATCCTT CTTTCGAAAT TAAAGAAAGG   [233]
K. parviflora SR330                  ATGGAGTTGA TTACGTTGCG TTGGTAGCTG G--AATCCTT CTTTCGAAAT TAAAGAAAGG   [236]
K. ritualis SR300                    ATGGAGTTGA TTACGTTGCG TTGGTAGCTG G--AATCCTT CTTTCGAAAT TAAAGAAGGG   [233]
K. schimperi JMG036                  ATGGAGTTGA TTACGTTGCG TTGGTAGCTG G--AATCCTT CTTTCGAAAT TAAAGAAAGG   [233]
K. stricta SR279                     ATGGAGTTGA TTACGTTGCG TTGGTAGCTG G--AATCCTT CTTTCAAAAT TAAAGAAAGG   [234]
K. thomsonii JMG031                  ATGGAGTTGA TTACGTTGCG TTGGTAGCTG G--AATCCTT CTTTCGAAAT TAAAGAAAGG   [234]
K. triangularis SR299                ATGGAGTTGA TTACGTTGCG TTGGTAGCTG G--AATCCTT CTTTCGAAAT TAAAGAAAGG   [235]
K. typhoides NNBG                    ATGGAGTTGA TTACGTTGCG TTGGTAGCTG G--AATCCTT CTTTCGAAAT TAAAGAAAGG   [235]
K. tysonii SR302                     ATGGAGTTGA TTACGTTGCG TTGGTAGCTG G--AATCCTT CTTTCGAAAT TAAAGAAAGG   [231]
K. umbrina RGsn                      ATGGAGTTGA TTACGTTGCG TTGGTAGCTG G--AATCCTT CTTTCGAAAT TAAAGAAAGG   [232]
K. uvaria SR186                      ATGGAGTTGA TTACGTTGCG TTGGTAGCTG G--AATCCTT CTTTCGAAAT TAAAGAAAGG   [234]
K. uvaria SR211                      ATGGAGTTGA TTACGTTGCG TTGGTAGCTG G--AATCCTT CTTTCGAAAT TAAAGAAAGG   [235]

[                                              250         260         270         280         290        300]
[                                              .          .          .          .          .          .]

Bulbine latifolia SR61               ATAACCTCTA TATTTAATAC ATACGTATAC ATACTGACAT AGCAAACGAT TAATCCCGAA   [291]
Bulbine semibarbata AJ290259         ATAACCTCTA TATCTAATAC ATACGTATAC ATACTGACAT AGCAAACGAT TAATCACGAA   [290]
Bulbine succulenta AJ290260          ATAACCTCTA TATCTAATAC ATACGTATAC ATACTGACAT AGCAAACGAT TAATCACGAA   [292]
Bulbine weisei AJ290261              ATAACCTCTA TATCTAATAC ATACGTATAC ATACTGACAT AGCAAACGAT TAATCACGAA   [284]
Bulbinella cuada-felis SR204         ATGACCTGTA TATCTAATAC ATACGTATAC ATACTGACAT AGCAAACGAT TAATCACGAA   [292]
Bulbinella cauda-felis AJ290262      ATGACCTGTA TATCTAATAC ATACGTATAC ATACTGACAT AGCAAACGAT TAATCACGAA   [290]
K. acreae TD4626                     ATGACCCATA TATCTAATAC ATACGTATAC ATACTGACAT AGCAAACGAT TAATCACGAA   [292]
K. albescens SR314                   ATGACCCATA TATCTAATAC ATACGTATAC ATACTGACAT AGCAAACGAT TAATCACGAA   [291]
K. baurii SR285                      ATGACCCATA TATCTAATAC ATACGTATAC ATACTGACAT AGCAAACGAT TAATCACGAA   [295]
K. breviflora SR452                  ATGACCCATA TATCTAATAC ATACGTATAC ATACTGACAT AGCAAACGAT TAATCACGAA   [292]
K. bruceae SR171                     ATGACCCATA TATCTAATAC ATACGTATAC ATACTGACAT AGCAAACGAT TAATCACGAA   [296]
K. caulescens SR278                  ATGACCCATA TATCTAATAC ATACGTATAC ATACTGACAT AGCAAACGAT TAATCACGAA   [294]
K. corraligemma SR549                ATGACCCATA TATCTAATAC ATACGTATAC ATACTGACAT AGCAAACGAT TAATCACGAA   [294]
K. foliosa JMG034                    ATGACCCATA TATCTAATAC ATACGTATAC ATACTGACAT AGCAAACGAT TAATCACGAA   [293]
K. insignis SRsn                     ATGACCCATA TATCTAATAC ATACGTATAC ATACTGACAT AGCAAACGAT TAATCACGAA   [293]
K. isoetifolia SR388                 ATGACCCATA TATCTAATAC ATACGTATAC ATACTGACAT AGCAAACGAT TAATCACGAA   [294]
K. laxiflora SR467                   ATGACCCATA TATCTAATAC ATACGTATAC ATACTGACAT AGCAAACGAT TAATCACGAA   [296]
K. laxiflora SR468                   ATGACCCATA TATCTAATAC ATACGTATAC ATACTGACAT AGCAAACGAT TAATCACGAA   [296]
K. linearifolia SR311                ATGACCCATA TATCTAATAC ATACGTATAC ATACTGACAT AGCAAACGAT TAATCACGAA   [292]
K. multiflora SR310                  ATGACCCATA TATCTAATAC ATACGTATAC ATACTGACAT AGCAAACGAT TAATCACGAA   [293]
K. northiae SR446                    ATGACCCATA TATCTAATAC ATACGTATAC ATACTGACAT AGCAAACGAT TAATCACGAA   [293]
K. parviflora SR268                  ATGACCCATA TATCTAATAC ATACGTATAC ATACTGACAT AGCAAACGAT TAATCACGAA   [293]
K. parviflora SR330                  ATGACCCATA TATCTAATAC ATACGTATAC ATACTGACAT AGCAAACGAT TAATCACGAA   [296]
K. ritualis SR300                    ATGACCCATA TATCTAATAC ATACGTATAC ATACTGACAT AGCAAACGAT TAATCACGAA   [293]
K. schimperi JMG036                  ATGACCCATA TATCTAATAC ATACGTATAC ATACTGACAT AGCAAACGAT TAATCACGAA   [293]
K. stricta SR279                     ATGACCCATA TATCTAATAC ATACGTATAC ATACTGACAT AGCAAACGAT TAATCACGAA   [294]
K. thomsonii JMG031                  ATGACCCATA TATCTAATAC ATACGTATAC ATACTGACAT AGCAAACGAT TAATCACGAA   [294]
K. triangularis SR299                ATGACCCATA TATCTAATAC ATACGTATAC ATACTGACAT AGCAAACGAT TAATCACGAA   [295]
K. typhoides NNBG                    ATGACCCATA TATCTAATAC ATACGTATAC ATACTGACAT AGCAAACGAT TAATCACGAA   [295]
K. tysonii SR302                     ATGACCCATA TATCTAATAC ATACGTATAC ATACTGACAT AGCAAACGAT TAATCACGAA   [291]
K. umbrina RGsn                      ATGACCCATA TATCTAATAC ATACGTATAC ATACTGACAT AGCAAACGAT TAATCACGAA   [292]
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K. uvaria SR186                      ATGACCCATA TATCTAATAC ATACGTATAC ATACTGACAT AGCAAACGAT TAATCACGAA   [294]
K. uvaria SR211                      ATGACCCATA TATCTAATAC ATACGTATAC ATACTGACAT AGCAAACGAT TAATCACGAA   [295]


[                                              310         320         330         340         350        360]
[                                              .          .          .          .          .          .]

Bulbine latifolia SR61               CCGAATACAT TATATAT--- ---------- -----GTATA TGCAAAATTC AAAGTTATTG   [333]
Bulbine semibarbata AJ290259         CCGAATATAT TATATATATA TAT------- ---------- -GCAAAATTC AGAGTTATTG   [332]
Bulbine succulenta AJ290260          CCGAATACAT TATATATATA TAT------- -----GTATA TGCAAAATTC AGAGTTATTG   [340]
Bulbine weisei AJ290261              CCGAATACAT TATATAT--- ---------- -----GTATA TGCAAAATTC AGAGTTATTG   [326]
Bulbinella cuada-felis SR204         CCAAATACAT TATATAT--- ---------- -----GTATA TGCAAAATTC AGAGTTATTG   [334]
Bulbinella cauda-felis AJ290262      CTAAATACAT TATATAT--- ---------- -----GTATA TGCAAAATTC AGAGTTATTG   [332]
K. acreae TD4626                     CCGAATACAT TATATATATA TATATATATA TAT--GTATA TGCAAAATTC AGAGTTATTG   [350]
K. albescens SR314                   CCGAATACAT TATATATATA TATATATAT- -----GTATA TGCAAAATTC AAAGTTATTG   [345]
K. baurii SR285                      CCGAATACAT TATATATATA TATATATA-- ------TATA TGCAAAATTC AAAGTTATTG   [347]
K. breviflora SR452                  CCGAATACAT TATATATATA TATATAT--- -----GTATA TGCAAAATTC AAAGTTATTG   [344]
K. bruceae SR171                     CCGAATACAT TATATATATA TA-------- ------TATA TGCAAAATTC AAAGTTATTG   [342]
K. caulescens SR278                  CCGAATACAT TATATATATA TATATATATA T----GTATA TGCAAAATTC AGAGTTATTG   [350]
K. corraligemma SR549                CCGAATACAT TATATATATA TATAT----- -----GTATA TGCAAAATTC AGAATTATTG   [344]
K. foliosa JMG034                    CCGAATACAT TATATATATA TATAT----- -----GTATA TGCAAAATTC AGAATTATTG   [343]
K. insignis SRsn                     CCGAATACAT TATATATATA TATAT----- -----GTATA TGCAAAATTC AGAATTATTG   [343]
K. isoetifolia SR388                 CCGAATACAT TATATATATA TATATAT--- -----GTATA TGCAAAATTC AGAATTATTG   [346]
K. laxiflora SR467                   CCGAATACAT TATATATATA TATATATATA T----GTATA TGCAAAATTC AAAGTTATTG   [352]
K. laxiflora SR468                   CCGAATACAT TATATATATA TATATATATA T----GTATA TGCAAAATTC AAAGTTATTG   [352]
K. linearifolia SR311                CCGAATACAT TATATATATA TATATAT--- -----GTATA TGCAAAATTC AAAGTTATTG   [344]
K. multiflora SR310                  CCGAATACAT TATATATATA TATAT----- -----GTATA TGCAAAATTC AAAGTTATTG   [343]
K. northiae SR446                    CCGAATACAT TATATATATA TATATAT--- -----GTATA TGCAAAATTC AGAGTTATTG   [345]
K. parviflora SR268                  CCGAATACAT TATATATATA TATATATATA TATATGTATA TGCAAAATTC AGAGTTATTG   [353]
K. parviflora SR330                  CCGAATACAT TATATATATA TATATAT--- -----GTATA TGCAAAATTC AAAGTTATTG   [348]
K. ritualis SR300                    CCGAATACAT TATATATATA TATATATATA ---------- ---------- ----------   [323]
K. schimperi JMG036                  CCGAATACAT TATATATATA TATAT----- -----GTATA TGCAAAATTC AGAATTATTG   [343]
K. stricta SR279                     CCGAATACAT TATATATATA TATATA---- ------TATA TGCAAAATTC AAAGTTATTG   [344]
K. thomsonii JMG031                  CCGAATACAT TATATATATA TATATAT--- -----GTATA TGCAAAATTC AGAATTATTG   [346]
K. triangularis SR299                CCGAATACAT TATATATATA TATATATATA T----GTATA TGCAAAATTC AAAGTTATTG   [351]
K. typhoides NNBG                    CCGAATACAT TATATATATA TAT------- -----GTATA TGCAAAATTC AGAATTATTG   [343]
K. tysonii SR302                     CCGAATACAT TATATATATA TATATATA-- -----GTATA TGCAAAATTC AAAGTTATTG   [344]
K. umbrina RGsn                      CCGAATACAT TATATATATA TATATATATA TATATGTATA TGCAAAATTC AAAGTTATTG   [352]
K. uvaria SR186                      CCGAATACAT TATATATATA TATAT----- -----GTATA TGCAAAATTC AGAATTATTG   [344]
K. uvaria SR211                      CCGAATACAT TATATATATA TATATAT--- -----GTATA TGCAAAATTC AGAATTATTG   [347]

[                                              370         380         390         400         410        420]
[                                              .          .          .          .          .          .]

Bulbine latifolia SR61               GGGATCTATT CCAATCGAGG TTGAAGGAAG AATCGAATAT TCGAATATTC AGTCACTCAT   [393]
Bulbine semibarbata AJ290259         TGGATCTATT CCAATCGAGG TTGAAGGAAG AATCGAATAT TCAGTGATCC TATCACTCAT   [392]
Bulbine succulenta AJ290260          TGGATCTATT CCAATCGAGG TTGAAGGAAG AATCGAATAT TCAGTGATCC TATCACTCAT   [400]
Bulbine weisei AJ290261              TGGATCTATT CCAATCAAGG TTGAAGGAAG AATCGAATAT TCAGTGATCC TATCACTCAT   [386]
Bulbinella cuada-felis SR204         TGAATTTATT CCAATCGAGG TTGAAGTAAA AATGGAATAT TCAGTGATCA AATCACTTAT   [394]
Bulbinella cauda-felis AJ290262      TGGATTTATT CCAATCGAGG TTGAAGGAAA AATGGAATAT TCAGTGATCA AATCACTTAT   [392]
K. acreae TD4626                     TGGATCTATT CCAATCGAGG TTGAAGGAAG AATCGAATAT TCAGTGATCA AATCACTCAT   [410]
K. albescens SR314                   TGGATCTATT CCAATCGAGG TTGAAGGAAG AATCGAATAT TCAGTGATCA AATCACTCAT   [405]
K. baurii SR285                      TGGATCTATT CCAATCGAGG TTGAAGGAAG AATCGAATAT TCAGTGATCA AATCACTCAT   [407]
K. breviflora SR452                  TGGATCTATT CCAATCGAGG TTGAAGGAAG AATCGAATAT TCAGTGATCA AATCACTCAT   [404]
K. bruceae SR171                     TGGATCTATT CCAATCGAGG TTGAAGGAAG AATCGAATAT TCAGTGATCA AATCACTCAT   [402]
K. caulescens SR278                  TGGATCTATT CCAATCGAGG TTGAAGGAAG AATCGAATAT TCAGTGATCA AATCACTCAT   [410]
K. corraligemma SR549                TGGATCTATT CCAATCGAGG TTGAAGGAAG AATCGAATAT TCAGTGATCA AATCACTCAT   [404]
K. foliosa JMG034                    TGGATCTATT CCAATCGAGG TTGAAGGAAG AATCGAATAT TCAGTGATCA AATCACTTAT   [403]
K. insignis SRsn                     TGGATCTATT CCAATCGAGG TTGAAGGAAG AATCGAATAT TCAGTGATCA AATCACTTAT   [403]
K. isoetifolia SR388                 TGGATCTATT CCAATCGAGG TTGAAGGAAG AATCGAATAT TCAGTGATCA AATCACTTAT   [406]
K. laxiflora SR467                   GGGATCTATT CCAATCGAGG TTGAAGGAAG AATCGAATAT TCAGTGATCA AATCACTCAT   [412]
K. laxiflora SR468                   GGGATCTATT CCAATCGAGG TTGAAGGAAG AATCGAATAT TCAGTGATCA AATCACTCAT   [412]
K. linearifolia SR311                GGGATCTATT CCAATCGAGG TTGAAGGAAG AATCGAATAT TCAGTGATCA AATCACTCAT   [404]
K. multiflora SR310                  TGGATCTATT CCAATCGAGG TTGAAGGAAG AATCGAATAT TCAGTGATCA AATCACTCAT   [403]
K. northiae SR446                    TGGATCTATT CCAATCGAGG TTGAAGGAAG AATCGAATAT TCAGTGATCA AATCACTCAT   [405]
K. parviflora SR268                  TGGATCTATT CCAATCGAGG TTGAAGGAAG AATCGAATAT TCAGTGATCA AATCACTCAT   [413]
K. parviflora SR330                  TGGATCTATT CCAATCGAGG TTGAAGGAAG AATCGAATAT TCAGTGATCA AATCACTCAT   [408]
K. ritualis SR300                    ---------- ---------- ---------- ---------- ---------- ---------T   [324]
K. schimperi JMG036                  TGGATCTATT CCAATCGAGG TTGAAGGAAG AATCGAATAT TCAGTGATCA AATCACTTAT   [403]
K. stricta SR279                     TGGATCTATT CCAATCGAGG TTGAAGGAAG AATCGAATAT TCAGTGATCA AATCACTCAT   [404]
K. thomsonii JMG031                  TGGATCTATT CCAATCGAGG TTGAAGGAAG AATCGAATAT TCAGTGATCA AATCACTTAT   [406]
K. triangularis SR299                TGGATCTATT CCAATCGAGG TTGAAGGAAG AATCGAATAT TCAGTGATCA AATCACTCAT   [411]
K. typhoides NNBG                    TGGATCTATT CCAATCGAGG TTGAAGGAAG AATCGAATAT TCAGTGATCA AATCACTCAT   [403]
K. tysonii SR302                     TGGATCTATT CCAATCGAGG TTGAAGGAAG AATCGAATAT TCAGTGATCA AATCACTCAT   [404]
K. umbrina RGsn                      TGGATCTATT CCAATCGAGG TTGAAGGAAG AATCGAATAT TCAGTGATCA AATCACTCAT   [412]
K. uvaria SR186                      TGGATCTATT CCAATCGAGG TTGAAGGAAG AATCGAATAT TCAGTGATCA AATCACTCAT   [404]
K. uvaria SR211                      TGGATCTATT CCAATCGAGG TTGAAGGAAG AATCGAATAT TCAGTGATCA AATCACTCAT   [407]


[                                              430         440         450         460         470        480]
[                                              .          .          .          .          .          .]

Bulbine latifolia SR61               TCC-----AT AGTTTGATAG GCCTTTTTTT TTT---AA-- ---CTGATTA ATCGGACGAG   [440]
Bulbine semibarbata AJ290259         TCCAGACCAG AGTTTGATAG GCCTTTTTTT TT----AA-- ---CTGATTA ATCGGACGAG   [443]
Bulbine succulenta AJ290260          TCC-----AG AGTTTGATAG GCCTTTTTTT TTT---AA-- ---CTGATTA ATCGGACGAG   [447]
Bulbine weisei AJ290261              TCT-----AT AGTTTGATAG GACTTTTTTT TTTTT-AA-- ---CTGATTA ATTGGACGAG   [435]
Bulbinella cuada-felis SR204         TCC-----AG AGTTTGATAG GCCTTTTTTT TT---GAAAA A--CTGATTA ATCGGACGAG   [444]
Bulbinella cauda-felis AJ290262      TCC-----AG AGTTTGATAG GCCTTTTTTT TTT--GAAAA A--CTGATTA ATCGTACGAG   [443]
K. acreae TD4626                     TCC-----AG AGTTTGATAG ACCTTTTTTT TT---GAAAA AA--TGATTA ATCGGACGAG   [460]
K. albescens SR314                   TCC-----AG AGTTTGATAG ACCTTTTTTT TTT--GAAAA AA--TGATTA ATCGGACGAG   [456]
K. baurii SR285                      TCC-----AG AGTTTGATAG ACCTTTTTTT TTT--GAAAA AA--TGATTA ATCGGACGAG   [458]
K. breviflora SR452                  TCC-----AG AGTTTGATAG ACCTTTTTTT TTT--GAAAA AA--TGATTA ATCGGACAAA   [455]
K. bruceae SR171                     TCC-----AG AGTTTGATAG ACCTTTTTTT TTT--GAAAA AA--TGATTA ATCGGACGAG   [453]
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K. caulescens SR278                  TCC-----AG AGTTTGATAG ACCTTTTTTT T----GAAAA AA--TGATTA ATCGGACGAG   [459]
K. corraligemma SR549                TCC-----AG AGTTTGATAG ACCTTTTTTT TT---GAAAA AA--TGATTA ATCGGACGAG   [454]
K. foliosa JMG034                    TCC-----AG AGTTTGATAA TCCTTTTTTT -----GAAAA AA--TGATTA ATCGGACGAG   [451]
K. insignis SRsn                     TCC-----AG AGTTTGATAA TCCTTTTTTT -----GAAAA AA--TGATTA ATCGGACGAG   [451]
K. isoetifolia SR388                 TCC-----AG AGTTTGATAA TCCTTTTTTT -----GAAAA AA--TGATTA ATCGGACGAA   [454]
K. laxiflora SR467                   TCC-----AG AGTTTGATAG ACCTTTTTTT TTT--GAAAA AA--TGATTA ATCGGACGAA   [463]
K. laxiflora SR468                   TCC-----AG AGTTTGATAG ACCTTTTTTT TTT--GAAAA AA--TGATTA ATCGGACGAA   [463]
K. linearifolia SR311                TCC-----AG AGTTTGATAG ACCTTTTTTT TTT--GAAAA AA--TGATTA ATCGGACGAA   [455]
K. multiflora SR310                  TCC-----AG AGTTTGATAG ACCTTTTTTT TT---GAAAA AA--TGATTA ATCGGACGAG   [453]
K. northiae SR446                    TCC-----AG AGTTTGATAG ACCTTTTTTT TTT--GAAAA AA--TGATTA ATCGGACGAG   [456]
K. parviflora SR268                  TCC-----AG AGTTTGATAG ACCTTTTTTT TT---GAAAA AA--TGATTA TTCGGACGAG   [463]
K. parviflora SR330                  TCC-----AG AGTTTGATAG ACCTTTTTTT TT---GAAAA AA--TGATTA ATCGGACGAG   [458]
K. ritualis SR300                    TCC-----AG AGTTTGATAG ACCTTTTTTT TTT--GAAAA AA--TGATTA ATCGGACGAG   [375]
K. schimperi JMG036                  TCC-----AG AGTTTGATAA TCCTTTTTTT -----GAAAA AA--TGATTA ATCGGACGAG   [451]
K. stricta SR279                     TCC-----AG AGTTTGATAG ACCTTTTTTT TT---GAAAA AA--TGATTA ATCGGACGAG   [454]
K. thomsonii JMG031                  TCC-----AG AGTTTGATAA TCCTTTTTTT -----GAAAA AA--TGATTA ATCGGACGAG   [454]
K. triangularis SR299                TCC-----AG AGTTTGATAG ACCTTTTTTT TT---GAAAA AA--TGATTA ATCGGACAAG   [461]
K. typhoides NNBG                    TCC-----AG AGTTTGATAG ACCTTTTTTT TTT--GAAAA AAA-TGATTA ATCGGACGAG   [455]
K. tysonii SR302                     TCC-----AG AGTTTGATAG ACCTTTTTTT TT---GAAAA AA--TGATTA ATCGGACGAG   [454]
K. umbrina RGsn                      TCC-----AG AGTTTGATAG ACCTTTTTTT TTT--GAAAA AA--TGATTA TTCGGACGAG   [463]
K. uvaria SR186                      TCC-----AG AGTTTGATAG ACCTTTTTTT T----GAAAA AA--TGATTA ATCGGACGAG   [453]
K. uvaria SR211                      TCC-----AG AGTTTG---- --CTTTTTTT T----GAAAA AA--TGATTA ATCGTACGAG   [450]

[                                              490        500        510        520        530        540]
[                                              .          .          .          .          .         .]

Bulbine latifolia SR61               AATAAAGAGA GAGTCCCATT CTACATGTCA ATACCGACAA CAATGAAATT TATAGTAAGA   [500]
Bulbine semibarbata AJ290259         AATAAAGAGA GAGTCCCATT CTACATGTCA ATACCGACAA CAAGGAAATT TATAGTAAGA   [503]
Bulbine succulenta AJ290260          AATAAAGAGA GAGTCCCATT CTACATGTCA ATACCGACAA CAAGGAAATT TATAGTAAGA   [507]
Bulbine weisei AJ290261              AATAAAGAGA GAGTCCCATT CTACATGTCA ATACCGACAA CAATGAAATT TATAGTAAGA   [495]
Bulbinella cuada-felis SR204         AATAAAGAGA GAGTCCCATT CTACATGTCA ATACCGACAA CAATGAAATT TATAGTAAGA   [504]
Bulbinella cauda-felis AJ290262      AATAAAGAGA GAGTCCCATT CTACATGTCA ATACCGACAA CAATGAAATT TATAGTAAGA   [503]
K. acreae TD4626                     AATAAAGAGA GAGTCCCATT CTACATGTCA ATACCGACAG CAATGAAATT TATAGTAAGA   [520]
K. albescens SR314                   AATAAAGAGA GAGTCCCATT CTACATGTCA ATACCGACAA CAATGAAA-T TATAGTAAGA   [515]
K. baurii SR285                      AATAAAGAGA GAGTCCCATT CTACATGTCA ATACCGACAA CAATGAAATT TATAGTAAGA   [518]
K. breviflora SR452                  AATAAAGAGA GAGTCCCTTT CTACATGTCA ATACCGACAA CAATGAATTT TATAGTAAGA   [515]
K. bruceae SR171                     AATAAAGAGA GAGTCCCATT CTACATGTCA ATACCGACAA CAATGAAATT TATAGTAAGA   [513]
K. caulescens SR278                  AATAAAGAGA GAGTCCCATT CTACATGTCA ATACCGACAA CAATGAAATT TATAGTAAGA   [519]
K. corraligemma SR549                AATAAAGAGA GAGTCCCATT CAACATGTCA ATACCGACAA CAATGAAATT TATAGTAAGA   [514]
K. foliosa JMG034                    AATAAAGAGA GAGTCCCATT CTACATGTCA ATACCGACAA CAATGAAATT TATAGTAAGA   [511]
K. insignis SRsn                     AATAAAGAGA GAGTCCCATT CTACATGTCA ATACCGACAA CAATGAAATT TATAGTAAGA   [511]
K. isoetifolia SR388                 AATAAAGAGA GAGTCCCATT CTACATGTCA ATACCGACAA CAATGAATTT TATAGTAAGA   [514]
K. laxiflora SR467                   AATAAAGAGA GAGTCCCTTT CTACGTGTCA ATACCGACAA CAATGAATTT TATAGTAAGA   [523]
K. laxiflora SR468                   AATAAAGAGA GAGTCCCTTT CTACGTGTCA ATACCGACAA CAATGAATTT TATAGTAAGA   [523]
K. linearifolia SR311                AATAAAGAGA GAGTCCCATT CTACATGTCA ATACCGACAA CAATGAAATT TATAGTAAGA   [515]
K. multiflora SR310                  AATAAAGAGA GAGTCCCATT CTACATGTCA ATACCGACAA CAATGAAATT TATAGGAAGA   [513]
K. northiae SR446                    AATAAAGAGA GAGTCCCATT CTACATGTCA ATACCGACAA CAATGAAATT TATAGTAAGA   [516]
K. parviflora SR268                  AATAAAGAGA GAGTCCCTTT CTACATGTCA ATACCGACAG CAATGAAATT TATAGTAAGA   [523]
K. parviflora SR330                  AATAAAGAGA GAGTCCCATT CTACA????? ?????????? ?????????? ??????????   [518]
K. ritualis SR300                    AATAAAGAGA GAGTCCCATT CTACATGTCA ATACCGACAA CAATGAAATT TATAGTAAGA   [435]
K. schimperi JMG036                  AATAAAGAGA GAGTCCCATT CTACATGTCA ATACCGACAA CAATGAAATT TATAGTAAGA   [511]
K. stricta SR279                     AATAAAGAGA GAGTCCCATT CTACATGTCA ATACCGACAA CAATGAAATT TATAGTAAGA   [514]
K. thomsonii JMG031                  AATAAAGAGA GAGTCCCATT CTACATGTCA ATACCGACAA CAATGAAATT TATAGTAAGA   [514]
K. triangularis SR299                AATAAAGAGA GAGTCCCTTT CTACATGTCA ATACCGACAA CAATGAAATT TATAGTAAGA   [521]
K. typhoides NNBG                    AATAAAGAGA GAGTCCCATT CTACATGTCA ATACCGACAA CAATGAAATT TATAGTAAGA   [515]
K. tysonii SR302                     AATAAAGAGA GAGTCCCATT CTACATGTCA ATACCGACAA CAATGAAATT TATAGTAAGA   [514]
K. umbrina RGsn                      AATAAAGAGA GAGTCCCTTT CTACATGTCA ATACCGACAA CAATGAAATT TATAGTAAGA   [523]
K. uvaria SR186                      AATAAAGAGA GAGTCCCATT CTACATGTCA ATACCGACAA CAATGAAATT TATAGTAAGA   [513]
K. uvaria SR211                      AATAAAGAGA GAGTCCCATT CTACATGTCA ATACCGACAA CAATGAAATT TATAGTAAGA   [510]

[                                              550        560        570]
[                                              .          .          . ]

Bulbine latifolia SR61               GGAAAATCCG CCGACTTT-A AAAATCGGGA G   [530]
Bulbine semibarbata AJ290259         GGAAAATCCG TCGACTTT-A GAAATCGTGA ?   [533]
Bulbine succulenta AJ290260          GGAAAATCCG TCGACTTT-A GAAATCGTGA ?   [537]
Bulbine weisei AJ290261              GGAAAATCCG TCGACTTT-A GAAATCGTGA G   [525]
Bulbinella cuada-felis SR204         GGAAAATCCG TCGACTTTTA GAAATCGTGA G   [535]
Bulbinella cauda-felis AJ290262      GGAAAATCCG TCGACTTT-A GAAATCGTGA ?   [533]
K. acreae TD4626                     GGAAAATCC? ?????????? ?????????? ?   [551]
K. albescens SR314                   GGAAAA???? ?????????? ?????????? ?   [546]
K. baurii SR285                      GGAAAATCCG TCGACT???? ?????????? ?   [549]
K. breviflora SR452                  GGAAAACCCG TCAACTTT-A AAAATCGGGA G   [545]
K. bruceae SR171                     GGAAAATCCG TCGACTTT-A GAAATCGTGA G   [543]
K. caulescens SR278                  GGAAAATCCG TCGACTTT-A GAAATCGTGA G   [549]
K. corraligemma SR549                GGAAAATCCG TCGACTTT-A GAAATCGAGA G   [544]
K. foliosa JMG034                    GGAAAATCCG TCGACTTT-A GAAATCGTGA G   [541]
K. insignis SRsn                     GGAAAATCCG TCGACTT??? ?????????? ?   [542]
K. isoetifolia SR388                 GGAAAATCCG TCAACTTT-A AAAATCGGGA G   [544]
K. laxiflora SR467                   GGAAAATCCG CCGACTTT-A AAAATCGGGA G   [553]
K. laxiflora SR468                   GGAAAATCCC CCGACTTT-A AAAATCGGGA G   [553]
K. linearifolia SR311                GGAAAATCCC TCGACTTT-A AAAATCGGGA G   [545]
K. multiflora SR310                  GGAAA????? ?????????? ?????????? ?   [544]
K. northiae SR446                    GGAAAATCCG TCGACTTT-A AAAATCGGGA G   [546]
K. parviflora SR268                  GGAAAATCCG TCGACTTT-A AAAATCGTGA G   [553]
K. parviflora SR330                  ?????????? ?????????? ?????????? ?   [549]
K. ritualis SR300                    GGAAAATCCC TCGACTTT-A GAAATCGGGA G   [465]
K. schimperi JMG036                  GGAAAATCCG TCGACTTT-A GAAATCGTGA G   [541]
K. stricta SR279                     GGAAAATCCG TCGAC????? ?????????? ?   [545]
K. thomsonii JMG031                  GGAAAATCCG TCGACTTT-A GAAATCGTGA G   [544]
K. triangularis SR299                GGAAAATCCG TCGACTTT-A AAAATCGGGA G   [551]
K. typhoides NNBG                    GGAAAATCCG TCGACTTT-A AAAATCGGGA G   [545]
K. tysonii SR302                     GGAAAATCCG TCGACTTT-A GAAATCGGGA G   [544]
K. umbrina RGsn                      GGAAAATCCG TCCACTTT-A AAAATCGGGA G   [553]
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K. uvaria SR186                      GGAAAATCCG TCGACTTT-A AAAATCGTGA G   [543]
K. uvaria SR211                      GGAAAATCCG TCGACTTT-A GAAATCGTGA G   [540]
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Appendix 6: Final sequence alignments of the *ITS* region

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[                                            10          20          30          40          50          60]
[                                            .          .          .          .          .         .]

Bulbine latifolia SR61             TATCATTTAG AGGAAGGAGA AGTCGTAACA AGGTTTCCGT AGGTGAACCT GCGGAAGGAT   [60]
Bulbinella cauda-felis SR204       ?????????? ?????????? ?????????? ?????????? ?????????? ??????????   [60]
K. acreae TD4626                   TATCATTTAG AGGAAGGAGA AGTCGTAACA AGGTTTCCGT AGGTGAACCT GCGGAAGGAT   [60]
K. albescens SR314                 TATCATTTAG AGGAAGGAGA AGTCGTAACA AGGTTTCCGT AGGTGAACCT GCGGAAGGAT   [60]
K. albomontana SR149               TATCATTTAG AGGAAGGAGA AGTCGTAACA AGGTTTCCGT AGGTGAACCT GCGGAAGGAT   [60]
K. angustifolia SR453              TATCATTTAG AGGAAGGAGA AGTCGTAACA AGGTTTCCGT AGGTGAACCT GCGGAAGGAT   [60]
K. angustifolia SR542              TATCATTTAG AGGAAGGAGA AGTCGTAACA AGGTTTCCGT AGGTGAACCT GCGGAAGGAT   [60]
K. ankaratrensis PBP5676           TATCATTTAG AGGAAGGAGA AGTCGTAACA AGGTTTCCGT AGGTGAACCT GCGGAAGGAT   [60]
K. baurii SR275                    TATCATTTAG AGGAAGGAGA AGTCGTAACA AGGTTTCCGT AGGTGAACCT GCGGAAGGAT   [60]
K. baurii SR285                    TATCATTTAG AGGAAGGAGA AGTCGTAACA AGGTTTCCGT AGGTGAACCT GCGGAAGGAT   [60]
K. baurii SR360                    TATCATTTAG AGGAAGGAGA AGTCGTAACA AGGTTTCCGT AGGTGAACCT GCGGAAGGAT   [60]
K. baurii SR382                    TATCATTTAG AGGAAGGAGA AGTCGTAACA AGGTTTCCGT AGGTGAACCT GCGGAAGGAT   [60]
K. baurii NPB1923                  TATCATTTAG AGGAAGGAGA AGTCGTAACA AGGTTTCCGT AGGTGAACCT GCGGAAGGAT   [60]
K. brachystachya SRsn              TATCATTTAG AGGAAGGAGA AGTCGTAACA AGGTTTCCGT AGGTGAACCT GCGGAAGGAT   [60]
K. brevifolia SR452                TATCATTTAG AGGAAGGAGA AGTCGTAACA AGGTTTCCGT AGGTGAACCT GCGGAAGGAT   [60]
K. bruceae SR171                   ?????????? ?????????? ?????????? ?????????? ?????????? ??????????   [60]
K. buchananii SR307                TATCATTTAG AGGAAGGAGA AGTCGTAACA AGGTTTCCGT AGGTGAACCT GCGGAAGGAT   [60]
K. caulescens SR270                TATCATTTAG AGGAAGGAGA AGTCGTAACA AGGTTTCCGT AGGTGAACCT GCGGAAGGAT   [60]
K. caulescens SR278                TATCATTTAG AGGAAGGAGA AGTCGTAACA AGGTTTCCGT AGGTGAACCT GCGGAAGGAT   [60]
K. caulescens NPB1821              TATCATTTAG AGGAAGGAGA AGTCGTAACA AGGTTTCCGT AGGTGAACCT GCGGAAGGAT   [60]
K. citrina SR176                   TATCATTTAG AGGAAGGAGA AGTCGTAACA AGGTTTCCGT AGGTGAACCT GCGGAAGGAT   [60]
K. coddiana SRsn                   TATCATTTAG AGGAAGGAGA AGTCGTAACA AGGTTTCCGT AGGTGAACCT GCGGAAGGAT   [60]
K. corraligemma SR549              TATCATTTAG AGGAAGGAGA AGTCGTAACA AGGTTTCCGT AGGTGAACCT GCGGAAGGAT   [60]
K. drepanophylla RAL4816           TATCATTTAG AGGAAGGAGA AGTCGTAACA AGGTTTCCGT AGGTGAACCT GCGGAAGGAT   [60]
K. ensifolia ensifolia JBsn        TATCATTTAG AGGAAGGAGA AGTCGTAACA AGGTTTCCGT AGGTGAACCT GCGGAAGGAT   [60]
K. ensifolia autumnalis SR448      TATCATTTAG AGGAAGGAGA AGTCGTAACA AGGTTTCCGT AGGTGAACCT GCGGAAGGAT   [60]
K. fibrosa SR297                   TATCATTTAG AGGAAGGAGA AGTCGTAACA AGGTTTCCGT AGGTGAACCT GCGGAAGGAT   [60]
K. fluvitalis SRsn                 TATCATTTAG AGGAAGGAGA AGTCGTAACA AGGTTTCCGT AGGTGAACCT GCGGAAGGAT   [60]
K. foliosa SR383                   TATCATTTAG AGGAAGGAGA AGTCGTAACA AGGTTTCCGT AGGTGAACCT GCGGAAGGAT   [60]
K. foliosa SR387                   TATCATTTAG AGGAAGGAGA AGTCGTAACA AGGTTTCCGT AGGTGAACCT GCGGAAGGAT   [60]
K. foliosa SR389                   TATCATTTAG AGGAAGGAGA AGTCGTAACA AGGTTTCCGT AGGTGAACCT GCGGAAGGAT   [60]
K. foliosa SR390                   TATCATTTAG AGGAAGGAGA AGTCGTAACA AGGTTTCCGT AGGTGAACCT GCGGAAGGAT   [60]
K. foliosa JMG034                  TATCATTTAG AGGAAGGAGA AGTCGTAACA AGGTTTCCGT AGGTGAACCT GCGGAAGGAT   [60]
K. foliosa JMG038                  TATCATTTAG AGGAAGGAGA AGTCGTAACA AGGTTTCCGT AGGTGAACCT GCGGAAGGAT   [60]
K. galpinii SR312                  TATCATTTAG AGGAAGGAGA AGTCGTAACA AGGTTTCCGT AGGTGAACCT GCGGAAGGAT   [60]
K. gracilis SR321                  TATCATTTAG AGGAAGGAGA AGTCGTAACA AGGTTTCCGT AGGTGAACCT GCGGAAGGAT   [60]
K. gracilis NNBG                   TATCATTTAG AGGAAGGAGA AGTCGTAACA AGGTTTCCGT AGGTGAACCT GCGGAAGGAT   [60]
K. grantii CP4154                  TATCATTTAG AGGAAGGAGA AGTCGTAACA AGGTTTCCGT AGGTGAACCT GCGGAAGGAT   [60]
K. hirsuta SR282                   TATCATTTAG AGGAAGGAGA AGTCGTAACA AGGTTTCCGT AGGTGAACCT GCGGAAGGAT   [60]
K. ichopensis SR242                TATCATTTAG AGGAAGGAGA AGTCGTAACA AGGTTTCCGT AGGTGAACCT GCGGAAGGAT   [60]
K. ichopensis SR286                TATCATTTAG AGGAAGGAGA AGTCGTAACA AGGTTTCCGT AGGTGAACCT GCGGAAGGAT   [60]
K. ichopensis SR289                TATCATTTAG AGGAAGGAGA AGTCGTAACA AGGTTTCCGT AGGTGAACCT GCGGAAGGAT   [60]
K. insignis SRsn                   TATCATTTAG AGGAAGGAGA AGTCGTAACA AGGTTTCCGT AGGTGAACCT GCGGAAGGAT   [60]
K. isoetofolia SR386               TATCATTTAG AGGAAGGAGA AGTCGTAACA AGGTTTCCGT AGGTGAACCT GCGGAAGGAT   [60]
K. isoetifolia SR388               TATCATTTAG AGGAAGGAGA AGTCGTAACA AGGTTTCCGT AGGTGAACCT GCGGAAGGAT   [60]
K. isoetifolia SR393               TATCATTTAG AGGAAGGAGA AGTCGTAACA AGGTTTCCGT AGGTGAACCT GCGGAAGGAT   [60]
K. latifolia RSSsn                 TATCATTTAG AGGAAGGAGA AGTCGTAACA AGGTTTCCGT AGGTGAACCT GCGGAAGGAT   [60]
K. laxiflora SR283                 TATCATTTAG AGGAAGGAGA AGTCGTAACA AGGTTTCCGT AGGTGAACCT GCGGAAGGAT   [60]
K. laxifolia SR295                 TATCATTTAG AGGAAGGAGA AGTCGTAACA AGGTTTCCGT AGGTGAACCT GCGGAAGGAT   [60]
K. laxiflora SR467                 TATCATTTAG AGGAAGGAGA AGTCGTAACA AGGTTTCCGT AGGTGAACCT GCGGAAGGAT   [60]
K. laxiflora SR468                 TATCATTTAG AGGAAGGAGA AGTCGTAACA AGGTTTCCGT AGGTGAACCT GCGGAAGGAT   [60]
K. laxifloraC SRsn                 TATCATTTAG AGGAAGGAGA AGTCGTAACA AGGTTTCCGT AGGTGAACCT GCGGAAGGAT   [60]
K. laxiflora NPB1810               TATCATTTAG AGGAAGGAGA AGTCGTAACA AGGTTTCCGT AGGTGAACCT GCGGAAGGAT   [60]
K. leucocephala NNBG               TATCATTTAG AGGAAGGAGA AGTCGTAACA AGGTTTCCGT AGGTGAACCT GCGGAAGGAT   [60]
K. linearifolia SR170              TATCATTTAG AGGAAGGAGA AGTCGTAACA AGGTTTCCGT AGGTGAACCT GCGGAAGGAT   [60]
K. linearifolia SR269              TATCATTTAG AGGAAGGAGA AGTCGTAACA AGGTTTCCGT AGGTGAACCT GCGGAAGGAT   [60]
K. linearifolia SR290              TATCATTTAG AGGAAGGAGA AGTCGTAACA AGGTTTCCGT AGGTGAACCT GCGGAAGGAT   [60]
K. linearifolia SR291              TATCATTTAG AGGAAGGAGA AGTCGTAACA AGGTTTCCGT AGGTGAACCT GCGGAAGGAT   [60]
K. linearifolia SR311              TATCATTTAG AGGAAGGAGA AGTCGTAACA AGGTTTCCGT AGGTGAACCT GCGGAAGGAT   [60]
K. linearifolia SR313              TATCATTTAG AGGAAGGAGA AGTCGTAACA AGGTTTCCGT AGGTGAACCT GCGGAAGGAT   [60]
K. linearifolia SR328              TATCATTTAG AGGAAGGAGA AGTCGTAACA AGGTTTCCGT AGGTGAACCT GCGGAAGGAT   [60]
K. linearifolia SR343              TATCATTTAG AGGAAGGAGA AGTCGTAACA AGGTTTCCGT AGGTGAACCT GCGGAAGGAT   [60]
K. littoralis SR200                TATCATTTAG AGGAAGGAGA AGTCGTAACA AGGTTTCCGT AGGTGAACCT GCGGAAGGAT   [60]
K. multiflora SR310                TATCATTTAG AGGAAGGAGA AGTCGTAACA AGGTTTCCGT AGGTGAACCT GCGGAAGGAT   [60]
K. multiflora SR315                TATCATTTAG AGGAAGGAGA AGTCGTAACA AGGTTTCCGT AGGTGAACCT GCGGAAGGAT   [60]
K. northiae SR263                  TATCATTTAG AGGAAGGAGA AGTCGTAACA AGGTTTCCGT AGGTGAACCT GCGGAAGGAT   [60]
K. northiae SR446                  TATCATTTAG AGGAAGGAGA AGTCGTAACA AGGTTTCCGT AGGTGAACCT GCGGAAGGAT   [60]
K. parviflora SR268                TATCATTTAG AGGAAGGAGA AGTCGTAACA AGGTTTCCGT AGGTGAACCT GCGGAAGGAT   [60]
K. paviflora SR330                 TATCATTTAG AGGAAGGAGA AGTCGTAACA AGGTTTCCGT AGGTGAACCT GCGGAAGGAT   [60]
K. pauciflora HBsn                 TATCATTTAG AGGAAGGAGA AGTCGTAACA AGGTTTCCGT AGGTGAACCT GCGGAAGGAT   [60]
K. porphyantha SRsn                TATCATTTAG AGGAAGGAGA AGTCGTAACA AGGTTTCCGT AGGTGAACCT GCGGAAGGAT   [60]
K. praecox SR529                   TATCATTTAG AGGAAGGAGA AGTCGTAACA AGGTTTCCGT AGGTGAACCT GCGGAAGGAT   [60]
K. rigidifolia SRsn                TATCATTTAG AGGAAGGAGA AGTCGTAACA AGGTTTCCGT AGGTGAACCT GCGGAAGGAT   [60]
K. ritualis SR300                  TATCATTTAG AGGAAGGAGA AGTCGTAACA AGGTTTCCGT AGGTGAACCT GCGGAAGGAT   [60]
K. rooperi SR237                   TATCATTTAG AGGAAGGAGA AGTCGTAACA AGGTTTCCGT AGGTGAACCT GCGGAAGGAT   [60]
K. rooperi SR485                   TATCATTTAG AGGAAGGAGA AGTCGTAACA AGGTTTCCGT AGGTGAACCT GCGGAAGGAT   [60]
K. sarmentosa SR207                TATCATTTAG AGGAAGGAGA AGTCGTAACA AGGTTTCCGT AGGTGAACCT GCGGAAGGAT   [60]
K. schemperi SR391                 TATCATTTAG AGGAAGGAGA AGTCGTAACA AGGTTTCCGT AGGTGAACCT GCGGAAGGAT   [60]
K. schemperi JMG036                TATCATTTAG AGGAAGGAGA AGTCGTAACA AGGTTTCCGT AGGTGACCCT GCGGAAGGAT   [60]
K. splendida SR548                 TATCATTTAG AGGAAGGAGA AGTCGTAACA AGGTTTCCGT AGGTGAACCT GCGGAAGGAT   [60]
K. stricta SR279                   TATCATTTAG AGGAAGGAGA AGTCGTAACA AGGTTTCCGT AGGTGAACCT GCGGAAGGAT   [60]
K. thodei SR407                    TATCATTTAG AGGAAGGAGA AGTCGTAACA AGGTTTCCGT AGGTGAACCT GCGGAAGGAT   [60]
K. thomsonii JMG031                TATCATTTAG AGGAAGGAGA AGTCGTAACA AGGTTTCCGT AGGTGAACCT GCGGAAGGAT   [60]
K. thomsonii AMM                   TATCATTTAG AGGAAGGAGA AGTCGTAACA AGGTTTCCGT AGGTGAACCT GCGGAAGGAT   [60]
K. thomsonii CK4821                TATCATTTAG AGGAAGGAGA AGTCGTAACA AGGTTTCCGT AGGTGAACCT GCGGAAGGAT   [60]
K. triangularis SR264              TATCATTTAG AGGAAGGAGA AGTCGTAACA AGGTTTCCGT AGGTGAACCT GCGGAAGGAT   [60]
K. triangularis SR266              TATCATTTAG AGGAAGGAGA AGTCGTAACA AGGTTTCCGT AGGTGAACCT GCGGAAGGAT   [60]
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K. triangularis SR299              TATCATTTAG AGGAAGGAGA AGTCGTAACA AGGTTTCCGT AGGTGAACCT GCGGAAGGAT   [60]
K. triangularis obtusiloba SRsn    TATCATTTAG AGGAAGGAGA AGTCGTAACA AGGTTTCCGT AGGTGAACCT GCGGAAGGAT   [60]
K. typhoides JB8084                TATCATTTAG AGGAAGGAGA AGTCGTAACA AGGTTTCCGT AGGTGAACCT GCGGAAGGAT   [60]
K. typhoides NNBG                  TATCATTTAG AGGAAGGAGA AGTCGTAACA AGGTTTCCGT AGGTGAACCT GCGGAAGGAT   [60]
K. tysonii SR302                   TATCATTTAG AGGAAGGAGA AGTCGTAACA AGGTTTCCGT AGGTGAACCT GCGGAAGGAT   [60]
K. tysonii SR303                   TATCATTTAG AGGAAGGAGA AGTCGTAACA AGGTTTCCGT AGGTGAACCT GCGGAAGGAT   [60]
K. umbrina RGsn                    TATCATTTAG AGGAAGGAGA AGTCGTAACA AGGTTTCCGT AGGTGAACCT GCGGAAGGAT   [60]
K. uvaria SR186                    TATCATTTAG AGGAAGGAGA AGTCGTAACA AGGTTTCCGT AGGTGAACCT GCGGAAGGAT   [60]
K. uvaria SR201                    TATCATTTAG AGGAAGGAGA AGTCGTAACA AGGTTTCCGT AGGTGAACCT GCGGAAGGAT   [60]
K. uvaria SR203                    TATCATTTAG AGGAAGGAGA AGTCGTAACA AGGTTTCCGT AGGTGAACCT GCGGAAGGAT   [60]
K. uvaria SR211                    TATCATTTAG AGGAAGGAGA AGTCGTAACA AGGTTTCCGT AGGTGAACCT GCGGAAGGAT   [60]
K. uvaria SR342                    TATCATTTAG AGGAAGGAGA AGTCGTAACA AGGTTTCCGT AGGTGAACCT GCGGAAGGAT   [60]
K. uvaria SR344                    TATCATTTAG AGGAAGGAGA AGTCGTAACA AGGTTTCCGT AGGTGAACCT GCGGAAGGAT   [60]
K. uvaria SR477                    TATCATTTAG AGGAAGGAGA AGTCGTAACA AGGTTTCCGT AGGTGAACCT GCGGAAGGAT   [60]

[                                            70          80          90          100         110        120]
[                                            .          .          .          .          .         .]

Bulbine latifolia SR61             CATTGTCGAG ACCCGAAA-G GACGACCGCG AACCGTTGAT CTCTTTCTAA CGGGCGCCGG   [119]
Bulbinella cauda-felis SR204       ?????????? ?????????? ?????????? ?????????? ?????????? CGGGGGCA--   [118]
K. acreae TD4626                   CATTGTCGTA ACTATAAACG GACGA-CGCG AACCAGTGAG CTCTCTC-AA TACTGGCGCC   [118]
K. albescens SR314                 CATTGTCGTA ACTATAAACG GACGA-CGCG AACCAGTGAG CTCTCTC-AA TACTGGCGCC   [118]
K. albomontana SR149               CATTGTCGTA ACTATAAACG GACGA-CGCG AACCAGTGAG CTCTCTC-AA TACTGGCGCC   [118]
K. angustifolia SR453              CATTGTCGTA ACTATAAACG GACGA-CGCG AACCAGTGAG CTCTCTC-AA TACTGGCGCC   [118]
K. angustifolia SR542              CATTGTCGTA ACTATAAACG GACGA-CGCG AACCAGTGAG CTCTCTC-AA TACTGGCGCC   [118]
K. ankaratrensis PBP5676           CATTGTCGTA ACTATAAACG GACGA-CGCG AACCAGTGAG CTCTCTC-AA TACTGGCGCC   [118]
K. baurii SR275                    CATTGTCGTA ACTATAAACG GACGA-CGCG AACCAGTGAG CTCTCTC-AA TACTGGCGCC   [118]
K. baurii SR285                    CATTGTCGTA ACTATAAACG GACGA-CGCG AACCAGTGAG CTCTCTC-AA TACTGGCGCC   [118]
K. baurii SR360                    CATTGCCGTA ACTATAAACG GACGA-CGCG AACCAGTGAG CTCTCTC-AA TACTGGCGCC   [118]
K. baurii SR382                    CATTGTCGTA ACTATAAACG GACGA-CGCG AACCAGTGAG CTCTCTC-AA TACTGGCGCC   [118]
K. baurii NPB1923                  CATTGTCGTA ACTATAAACG GACGA-CGCG AACCAGTGAG CTCTCTC-AA TACTGGCGCC   [118]
K. brachystachya SRsn              CATTGTCGTA ACTATAAACG GACGA-CGCG AACTAGTGAG CTCTCTC-AA AACTGGCGCC   [118]
K. brevifolia SR452                CATTGTCGTA ACTATAAACG GACGA-CGCG AACCAGTGAG CTCTCTC-AA TACTGGCGCC   [118]
K. bruceae SR171                   ?????????? ?????????? GACGA-CGCG AACCAGTGAG CTCTCTC-AA TACTGGCGCC   [118]
K. buchananii SR307                CATTGTCGTA ACTATAAACG GACGA-CGCG AACCAGTGAG CTCTCTC-AA TACTGGCGCC   [118]
K. caulescens SR270                CATTGTCGTA ACTATAAACG GACGA-CGCG AACCAGTGAG CTCTCTC-AA CACTGGCGCC   [118]
K. caulescens SR278                CATTGTCGTA ACTATAAACG GACGA-CGCG AACCAGTGAG CTCTCTC-AA TACTGGCGCC   [118]
K. caulescens NPB1821              CATTGTCGTA ACTATAAACG GACGA-CGCG AACCAGTGAG CTCTCTC-AA CACTGGCGCC   [118]
K. citrina SR176                   CATTGTCGTA ACTATAAACG GACGA-CGCG AACCAGTGAG CTCTCTC-AA TACTGGCGCC   [118]
K. coddiana SRsn                   CATTGTCGTA ACTATAAACG GACGA-CGCG AACCAGTGAG CTCTCTC-AA TACTGGCGCC   [118]
K. corraligemma SR549              CATTGTCGTA ACTATAAACG GACGA-CGCG AACCAGTGAG CTCTCTC-AA TACTGGCGCC   [118]
K. drepanophylla RAL4816           CATTGTCGTA ACTATAAACG GACGA-CGCG AACCAGTGAG CTCTCTC-AA TACTGGCGCC   [118]
K. ensifolia ensifolia JBsn        CATTGTCGTA ACTATAAACG GACGA-CGCG AACCAGTGAG CTCTCTC-AA TACTGGCGCC   [118]
K. ensifolia autumnalis SR448      CATTGTCGTA ACTATAAACG GACGA-CGCG AACCAGTGAG CTCTCTC-AA TACTGGCGCC   [118]
K. fibrosa SR297                   CATTGTCGTA ACTATAAACG GACGA-CGCG AACCAGTGAG CTCTCTC-AA TACTGGCGCC   [118]
K. fluvitalis SRsn                 CATTGTCGTA ACTATAAACG GACGA-CGCG AACCAGTGAG CTCTCTC-AA TACTGGCGCC   [118]
K. foliosa SR383                   CATTGTCGTA ACTATAAACG GACGA-CGCG AACCAGTGAG CTCTCTA-AA AAATGGCGCC   [118]
K. foliosa SR387                   CATTGTCGTA ACTATAAACG GACGA-CGCG AACCAGTGAG CTCTCTA-AA AAATGGCGCC   [118]
K. foliosa SR389                   CATTGTCGTA ACTATAAACG GACGA-CGCG AACCAGTGAG CTCTCTA-AA AAATGGCGCC   [118]
K. foliosa SR390                   CATTGTCGTA ACTATAAACG GACGA-CGCG AACCAGTGAG CTCTCTA-AA AAATGGCGCC   [118]
K. foliosa JMG034                  CATTGTCGTA ACTATAAACG GACGA-CGCG AACCAGTGAG CTCTCTA-AA AAATGGCGCC   [118]
K. foliosa JMG038                  CATTGTCGTA ACTATAAACG GACGA-CGCG AACCAGTGAG CTCTCTA-AA AAATGGCGCC   [118]
K. galpinii SR312                  CATTGTCGTA ACTATAAACG GACGA-CGCG AACCAGTGAG CTCTCTC-AA TACTGGCGCC   [118]
K. gracilis SR321                  CATTGTCGTA ACTATAAACG GACGA-CGCG AACCAGTGAG CTCTCTC-AA TACTGGCGCC   [118]
K. gracilis NNBG                   CATTGTCGTA ACTATAAACG GACGA-CGCG AACCAGTGAG CTCTCTC-AA TACTGGCGCC   [118]
K. grantii CP4154                  CATTGTCGTA ACTATAAACG GACGA-CGCG AACCAGTGAG CTCTCTC-AA AACCGGCGCC   [118]
K. hirsuta SR282                   CATTGTCGTA ACTATAAACG GACGA-CGCG AACCAGTGAG CTCTCTC-AA TACTGGCGCC   [118]
K. ichopensis SR242                CATTGTCGTA ACTATAAACG GACGA-CGCG AACCAGTGAG CTCTCTC-AA TACTGGCGCC   [118]
K. ichopensis SR286                CATTGTCGTA ACTATAAACG GACGA-CGCG AACCAGTGAG CTCTCTC-AA TACTGGCGCC   [118]
K. ichopensis SR289                CATTGTCGTA ACTATAAACG GACGA-CGCG AACCAGTGAG CTCTCTC-AA TACTGGCGCC   [118]
K. insignis SRsn                   CATTGTCGTA ACTATAAACG GACGA-CGCG AACCAGTGAG CTCTCTA-AA AAATGGCGCC   [118]
K. isoetofolia SR386               CATTGTCGTA ACTATAAACG GACGA-CGCG AACCAGTGAG CTCTCTC-AA AAATGGCGCC   [118]
K. isoetifolia SR388               CATTGTCGTA ACTATAAACG GACGA-CGCG AACCAGTGAG CTCTCTA-AA AAATGGCGCC   [118]
K. isoetifolia SR393               CATTGTCGTA ACTATAAACG GACGA-CGCG AACCAGTGAG CTCTCTA-AA AAATGGCGCC   [118]
K. latifolia RSSsn                 CATTGTCGTA ACTATAAACG GACGA-CGCG AACCAGTGAG CTCTCTC-AA TACTGGCGCC   [118]
K. laxiflora SR283                 CATTGTCGTA ACTATAAACG GACGA-CGCG AACCAGTGAG CTCTCTC-AA TACTGGCGCC   [118]
K. laxifolia SR295                 CATTGTCGTA ACTATAAACG GACGA-CGCG AACCAGTGAG CTCTCTC-AA TACTGGCGCC   [118]
K. laxiflora SR467                 CATTGTCGTA ACTATAAACG GACGA-CGCG AACCAGTGAG CTCTCTC-AA TACTGGCGCC   [118]
K. laxiflora SR468                 CATTGTCGTA ACTATAAACG GACGA-CGCG AACCAGTGAG CTCTCTC-AA TACTGGCGCC   [118]
K. laxifloraC SRsn                 CATTGTCGTA ACTATAAACG GACGA-CGCG AACCAGTGAG CTCTCTC-AA TACTGGCGCC   [118]
K. laxiflora NPB1810               CATTGTCGTA ACTATAAACG GACGA-CGCG AACCAGTGAG CTCTCTC-AA TACTGGCGCC   [118]
K. leucocephala NNBG               CATTGTCGTA ACTATAAACG GACGA-CGCG AACCAGTGAG CTCTCTC-AA TACTGGCGCC   [118]
K. linearifolia SR170              CATTGTCGTA ACTATAAACG GACGA-CGCG AACCAGTGAG CTCTCTC-AA TACTGGCGCC   [118]
K. linearifolia SR269              CATTGCCGTA ACTATAAACG GACGA-CGCG AACCAGTGAG CTCTCTC-AA TACTGGCGCC   [118]
K. linearifolia SR290              CATTGTCGTA ACTATAAACG GACGA-CGCG AACCAGTGAG CTCTCTC-AA TACTGGCGCC   [118]
K. linearifolia SR291              CATTGTCGTA ACTATAAACG GACGA-CGCG AACCAGTGAG CTCTCTC-AA TACTGGCGCC   [118]
K. linearifolia SR311              CATTGTCGTA ACTATAAACG GACGA-CGCG AACCAGTGAG CTCTCTC-AA TACTGGCGCC   [118]
K. linearifolia SR313              CATTGTCGTA ACTATAAACG GACGA-CGCG AACCAGTGAG CTCTCTC-AA TACTGGCGCC   [118]
K. linearifolia SR328              CATTGTCGTA ACTATAAACG GACGA-CGCG AACCAGTGAG CTCTCTC-AA TACTGGCGCC   [118]
K. linearifolia SR343              CATTGTCGTA ACTATAAACG GACGA-CGCG AACCAGTGAG CTCTCTC-AA TACTGGCGCC   [118]
K. littoralis SR200                CATTGTCGTA ACTATAAACG GACGA-CGCG AACCAGTGAG CTCTCTC-AA TACTGGCGCC   [118]
K. multiflora SR310                CATTGTCGTA ACTATAAACG GACGA-CGCG AACCGGTGAG CTCTCTC-AA TACTGGCGCC   [118]
K. multiflora SR315                CATTGTCGTA ACTATAAACG GACGA-CGCG AACCAGTGAG CTCTCTC-AA TACTGGCGCC   [118]
K. northiae SR263                  CATTGTCGTA ACTATAAACG GACGA-CGCG AACCAGTGAG CTCTCTC-AA TACTGGCGCC   [118]
K. northiae SR446                  CATTGTCGTA ACTATAAACG GACGA-CGCG AACCAGTGAG CTCTCTC-AA TACTGGCGCC   [118]
K. parviflora SR268                CATTGTCGTA ACTATAAACG GACGA-CGCG AACCAGTGAG CTCTCTC-AA TACTGGCGCC   [118]
K. paviflora SR330                 CATTGTCGTA ACTATAAACG GACGA-CGCG AACCAGTGAG CTCTCTC-AA TACTGGCGCC   [118]
K. pauciflora HBsn                 CATTGTCGTA ACTATAAACG GACGA-CGCG AACCAGTGAG CTCTCTC-AA TACTGGCGCC   [118]
K. porphyantha SRsn                CATTGTCGTA ACTATAAACG GACGA-CGCG AACCAGTGAG CTCTCTC-AA TACTGGCGCC   [118]
K. praecox SR529                   CATTGTCGTA ACTATAAACG GACGA-CGCG AACCAGTGAG CTCTCTC-AA TACTGGCGCC   [118]
K. rigidifolia SRsn                CATTGTCGTA ACTATAAACG GACGA-CGCG AACCAGTGAG CTCTCTC-AA TACTGGCGCC   [118]
K. ritualis SR300                  CATTGTCGTA ACTATAAACG GACGA-CGCG AACCAGTGAG CTCTCTC-AA TACTGGCGCC   [118]
K. rooperi SR237                   CATTGTCGTA ACTATAAACG GACGA-CGCG AACCAGTGAG CTCTCTC-AA TACTGGCGCC   [118]
K. rooperi SR485                   CATTGTCGTA ACTATAAACG GACGA-CGCG AACCAGTGAG CTCTCTC-AA TACTGGCGCC   [118]
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K. sarmentosa SR207                CATTGTCGTA ACTATAAACG GACGA-CGCG AACCAGTGAG CTCTCTC-AA AACTGGCGCC   [118]
K. schemperi SR391                 CATTGTCGTA ACTATAAACG GACGA-CGCG AACCAGTGAG CTCTCTA-AA AAATGGCGCC   [118]
K. schemperi JMG036                CATTGTCGTA ACTATAAACG GACGA-CGCG AACCAGTGAG CTCTCTA-AA AAATGGCGCC   [118]
K. splendida SR548                 CATTGTCGTA ACTATAAACG GACGA-CGCG AACCAGTGAG CTCTCTC-AA TACTGGCGCC   [118]
K. stricta SR279                   CATTGTCGTA ACTATAAACG GACGA-CGCG AACCAGTGAG CTCTCTC-AA CACTGGCGCC   [118]
K. thodei SR407                    CATTGTCGTA ACTATAAACG GACGA-CGCG AACCAGTGAG CTCTCTC-AA TACTGGCGCC   [118]
K. thomsonii JMG031                CATTGTCGTA ACTATAAACG GACGA-CGCG AACCAGTGAG CTCTCTA-AA AAATGGCGCC   [118]
K. thomsonii AMM                   CATTGTCGTA ACTATAAACG GACGA-CGCG AACAAGTGAG CTCTCTC-AA AACTGGCGCC   [118]
K. thomsonii CK4821                CATTGTCGTA ACTATAAACG GACGA-CGCG AACAAGTGAG CTCTCTC-AA AACTGGCGCC   [118]
K. triangularis SR264              CATTGTCGTA ACTATAAACG GACGA-CGCG AACCAGTGAG CTCTCTC-AA TACTGGCGCC   [118]
K. triangularis SR266              CATTGTCGTA ACTATAAACG GACGA-CGCG AACCAGTGAG CTCTCTC-AA TACTGGCGCC   [118]
K. triangularis SR299              CATTGTCGTA ACTATAAACG GACGA-CGCG AACCAGTGAG CTCTCTC-AA TACTGGCGCC   [118]
K. triangularis obtusiloba SRsn    CATTGTCGTA ACTATTAACG GACGA-CGCG AACCAGTGAG CTCTCTC-AA TACTGGCGCC   [118]
K. typhoides JB8084                CATTGTCGTA ACTATAAACG GACGA-CGCG AACTAGTGAG CTCTCTC-AA AACTGGCGCC   [118]
K. typhoides NNBG                  CATTGTCGTA ACTATAAACG GACGA-CGCG AACcAGTGAG CTCTCTC-AA TACTGGTGCC   [118]
K. tysonii SR302                   CATTGTCGTA ACTATAAACG GACGA-CGCG AACCAGTGAG CTCTCTC-AA TACTGGCGCC   [118]
K. tysonii SR303                   CATTGTCGTA ACTATAAACG GACGA-CGCG AACCAGTGAG CTCTCTC-AA TACTGGCGCC   [118]
K. umbrina RGsn                    CATTGTCGTA ACTATAAACG GACGA-CGCG AACCAGTGAG CTCTCTC-AA TACTGGCGCC   [118]
K. uvaria SR186                    CATTGTCGTA ACTATAAACG GACGA-CGCG AACCAGTGAG CTCTCTC-AA TACTGGCGCC   [118]
K. uvaria SR201                    CATTGTCGTA ACTATAAACG GACGA-CGCG AACCAGTGAG CTCTCTC-AA TACTGGCGCC   [118]
K. uvaria SR203                    CATTGTCGTA ACTATAAACG GACGA-CGCG AACCAGTGAG CTCTCTC-AA TACTGGCGCC   [118]
K. uvaria SR211                    CATTGTCGTA ACTATAAACG GACGA-CGCG AACCAGTGAG CTCTCTC-AA TACTGGCGCC   [118]
K. uvaria SR342                    CATTGTCGTA ACTATAAACG GACGA-CGCG AACCAGTGAG CTCTCTC-AA TACTGGCGCC   [118]
K. uvaria SR344                    CATTGTCGTA ACTATAAACG GACGA-CGCG AACCAGTGAG CTCTCTC-AA TACTGGCGCC   [118]
K. uvaria SR477                    CATTGTCGTA ACTATAAACG GACGA-CGCG AACCAGTGAG CTCTCTC-AA TACTGGCGCC   [118]

[                                           130         140         150         160         170        180]
[                                           .          .          .          .          .         .]

Bulbine latifolia SR61             TGCCTAGCTC CGACGCTCGC GCCCCGCTCC GGCGCCATGT CCTCC-GCG- ACGGGC--GT   [175]
Bulbinella cauda-felis SR204       T-----GCTC CGGCGTTGAC GCCCCGCCCC GCCGCTCCGT CCTC--ACGG ATGGAC--GT   [169]
K. acreae TD4626                   T-CCGGGCGC CGACGCCGAG ACCCCGGTGT GCCG-----T CCT--TGCGG ATGG-CATGT   [169]
K. albescens SR314                 T-CCGGGCGC CGACGCCGAG ACCCCGGTGT GCCG-----T CCT--TGCGG ATGG-CATGT   [169]
K. albomontana SR149               T-CCGGGCGC CGACGCCGAG ACCCCGGTGT GCCG-----T CCT--TGCGG ATGG-CATGT   [169]
K. angustifolia SR453              T-CCGGGCGC CGACGCCGAG ACCCCGGTGT GCCT-----T CCT--TGCGG ATGG-CATGT   [169]
K. angustifolia SR542              T-CCGGGCGC CGACGCCGAG ACCCCGGTGT GCCG-----T CCT--TGCGG ATGG-CATGT   [169]
K. ankaratrensis PBP5676           T-CCGGGCGC CGACGCCGAG ACCCCGGTGT GCCG-----T CCT--TGCGG ATGG-CATGT   [169]
K. baurii SR275                    T-CCGGGCGC CGACGCCGAG ACCCCGGTGT GCCG-----T CCT--TGCGG ATGG-CATGT   [169]
K. baurii SR285                    T-CCGGGCGC CGACGCCGAG ACCCCGGTGT GCCG-----T CCT--TGCGG ATGG-CATGT   [169]
K. baurii SR360                    T-CCGGGCGC CGACGCCGAG ACCCCGGTGT GCCG-----T CCT--TGCGG ATGG-CATGT   [169]
K. baurii SR382                    T-CCGGGCGC CGACGCCGAG ACCCCGGTGT GCCG-----T CCT--TGCGG ATGG-CATGT   [169]
K. baurii NPB1923                  T-CCGGGCGC CGACGCCGAG ACCCCGGTGT GCCG-----T CCT--TGCGG ATGG-CATGT   [169]
K. brachystachya SRsn              T-CCGGGCGC CTACGCTGAG ACCCCGGTGT GCCG-----T CCT--TGCGG ATGG-CATGT   [169]
K. brevifolia SR452                T-CCGGGCGC CGACGCCGAG ACCCCGGTGT GCCG-----T CCT--TGCGG ATGG-CATGT   [169]
K. bruceae SR171                   T-CCGGGCGC CGACGCCGAG ACCCCGGTGT GCCG-----T CCT--TGCGG ATGG-CATGT   [169]
K. buchananii SR307                T-CCGGGCGC CGACGCCGAG ACCCCGGTGT GCCG-----T CCT--TGCGG ATGG-CATGT   [169]
K. caulescens SR270                T-CCGGGCGC CGACGCCGAG ACCCCGGTGT GTCG-----T CCT--TGCGG ATGG-CATGT   [169]
K. caulescens SR278                T-CCGGGCGC CGACGCCGAG ACCCCGGTGT GCCG-----T CCT--TGCGG ATGG-CATGT   [169]
K. caulescens NPB1821              T-CCGGGCGC CGACGCCGAG ACCCCGGTGT GTCG-----T CCT--TGCGG ATGG-CATGT   [169]
K. citrina SR176                   T-CCGGGCGC CGACGCCGAG ACCCCGGTGT GCCG-----T CCT--TGCGG ATGG-CATGT   [169]
K. coddiana SRsn                   T-CCGGGCGC CGACGCCGAG ACCCCGGTGT GCCG-----T CCT--TGCGG ATGG-CATGT   [169]
K. corraligemma SR549              T-CCGGGCGC CGACGCCGAG ACCCCGGTGT GCCG-----T CCT--TGCGG ATGG-CATGT   [169]
K. drepanophylla RAL4816           T-CCGGGCGC CGACGCCGAG ACCCCGGTGT GCCG-----T CCT--TGCGG ATGG-CATGT   [169]
K. ensifolia ensifolia JBsn        T-CCGGGCGC CGACGCCGAG ACCCCGGTGT GCCG-----T CCT--TGCGG ATGG-CATGT   [169]
K. ensifolia autumnalis SR448      T-CCGGGCGC CGACGCCGAG ACCCCGGTGT GCCG-----T CCT--TGCGG ATGG-CATGT   [169]
K. fibrosa SR297                   T-CCGGGCGC CGACGCCGAG ACCCCGGTGT GCCG-----T CCT--TGCGG ATGG-CATGT   [169]
K. fluvitalis SRsn                 T-CCGGGCGC CGACGCCGAG ACCCCGGTGT GCCG-----T CCT--TGCGG ATGG-CATGT   [169]
K. foliosa SR383                   T-CCGGGCGC CGACGCCGAG AACCCGGTGT GCCG-----T CCT--TGCGG ATGG-CATGT   [169]
K. foliosa SR387                   T-CCGGGCGC CGACGCCGAG AACCCGGTGT GCCG-----T CCT--TGCGG ATGG-CATGT   [169]
K. foliosa SR389                   T-CCGGGCGC CGACGCCGAG AACCCGGTGT GCCG-----T CCT--TGCGG ATGG-CATGT   [169]
K. foliosa SR390                   T-CCGGGCGC CGACGCCGAG AACCCGGTGT GCCG-----T CCT--TGCGG ATGG-CATGT   [169]
K. foliosa JMG034                  T-CCGGGCGC CGACGCCGAG AACCCGGTGT GCCG-----T CCT--TGCGG ATGG-CATGT   [169]
K. foliosa JMG038                  T-CCGGGCGC CGACGCCGAG AACCCGGTGT GCCG-----T CCT--TGCGG ATGG-CATGT   [169]
K. galpinii SR312                  T-CCGGGCGC CGACGCCGAG ACCCCGGTGT GCCG-----T CCT--TGCGG ATGG-CATGT   [169]
K. gracilis SR321                  T-CCGGGCGC CGACGCCGAG ACCCCGGTGT GCCG-----T CCT--TGCGG ATGG-CATGT   [169]
K. gracilis NNBG                   T-CCGGGCGC CGACGCCGAG ACCCCGGTGT GCCG-----T CCT--TGCGG ATGG-CATGT   [169]
K. grantii CP4154                  T-CCGGGCGC CGACGCTGAG ACCCCGGTGT GCCG-----T CCT--TGCGG ATGG-CATGT   [169]
K. hirsuta SR282                   T-CCGGGCGC CGACGCCGAG ACCCCGGTGT GCCG-----T CCT--TGCGG ATGG-CATGT   [169]
K. ichopensis SR242                T-CCGGGCGC CGACGCCGAG ACCCCGGTGT GCCG-----T CCT--TGCGG ATGG-CATGT   [169]
K. ichopensis SR286                T-ACGGGCGC CGACGCCGAG ACCCCGGTGT GCCG-----T CCT--TGCGG ATGG-CATGT   [169]
K. ichopensis SR289                T-CCGGGCGC CGACGCCGAG ACCCCGGTGT GCCT-----T CCT--TGCGG ATGG-CATGT   [169]
K. insignis SRsn                   T-CCGGGCGC CGACGCCGAG AACCCGGTGT GCCG-----T CCT--TGCGG ATGG-CATGT   [169]
K. isoetofolia SR386               T-CCGGGCGC CGACGCCGAG ACCCCGGTGT GCCG-----T CCT--TGCGG ATGG-CATGT   [169]
K. isoetifolia SR388               T-CCGGGCGC CGACGTCGAG AACCCGGTGT GCCG-----T CCT--TGCGG ATGG-CATGT   [169]
K. isoetifolia SR393               T-CCGGGCGC CGACGCCGAG AACCCGGTGT GCCG-----T CCT--TGCGG ATGG-CATGT   [169]
K. latifolia RSSsn                 T-CCGGGCGC CGACGCCGAG ACCCCGGTGT GCCG-----T CCT--TGCGG ATGG-CATGT   [169]
K. laxiflora SR283                 T-CCGGGCGC CGACGCCGAG ACCCCGGTGT GCCG-----T CCT--TGCGG ATGG-CATGT   [169]
K. laxifolia SR295                 T-CCGGGCGC CGACGCCGAG ACCCCGGTGT GCCG-----T CCT--TGCGG ATGG-CATGT   [169]
K. laxiflora SR467                 T-CCGGGCGC CGACGCCGAG ACCCCGGTGT GCCG-----T CCT--TGCGG ATGG-CATGT   [169]
K. laxiflora SR468                 T-CCGGGCGC CGACGCCGAG ACCCCGGTGT GCCG-----T CCT--TGCGG ATGG-CATGT   [169]
K. laxifloraC SRsn                 T-CCGGGCGC CGACGCCGAG ACCCCGGTGT GCCG-----T CCT--TGCGG ATGG-CATGT   [169]
K. laxiflora NPB1810               T-CCGGGCGC CGACGCCGAG ACCCCGGTGT GCCG-----T CCT--TGCGG ATGG-CATGT   [169]
K. leucocephala NNBG               T-CCGGGCGC CGACGCCGAG ACCCCGGTGT GCCG-----T CCT--TGCGG ATGG-CATGT   [169]
K. linearifolia SR170              T-CCGGGCGC CGACGCCGAG ACCCCGGTGT GCCG-----T CCT--TGCGG ATGG-CATGT   [169]
K. linearifolia SR269              T-CCGGGCGC CGACGCCGAG ACCCCGGTGT GCCG-----T CCT--TGCGG ATGG-CATGT   [169]
K. linearifolia SR290              T-CCGGGCGC CGACGCCGAG ACCCCGGTGT GCCG-----T CCT--TGCGG ATGG-CATGT   [169]
K. linearifolia SR291              T-CCGGGCGC CGACGCCGAG ACCCCGGTGT GCCG-----T CCT--TGCGG ATGG-CATGT   [169]
K. linearifolia SR311              T-CCGGGCGC CGACGCCGAG ACCCCGGTGT GCCG-----T CCT--TGCGG ATGG-CATGT   [169]
K. linearifolia SR313              T-CCGGGCGC CGACGCCGAG ACCCCGGTGT GCCG-----T CCT--TGCGG ATGG-CATGT   [169]
K. linearifolia SR328              T-CCGGGCGC CGACGCCGAG ACCCCGGTGT GCCG-----T CCT--TGCGG ATGG-CATGT   [169]
K. linearifolia SR343              T-CCGGGCGC CGACGCCGAG ACCCCGGTGT GCCG-----T CCT--TGCGG ATGG-CATGT   [169]
K. littoralis SR200                T-CCGGGCGC CGACGCCGAG ACCCCGGTGT GCCG-----T CCT--TGCGG ATGG-CATGT   [169]
K. multiflora SR310                T-CCGGGCGC CGACGCCGAG ACCCCGGTGT GCCG-----T CCT--TGCGG ATGG-CATGT   [169]
K. multiflora SR315                T-CCGGGCGC CGACGCCGAG ACCCCGGTGT GCCG-----T CCT--TGCGG ATGG-CATGT   [169]
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K. northiae SR263                  T-CCGGGCGC CGACGCCGAG ACCCCGGTGT GCCG-----T CCT--TGCGG ATGG-CATGT   [169]
K. northiae SR446                  T-CCGGGCGC CGACGCCGAG ACCCCGGTGT GCCG-----T CCT--TGCGG ATGG-CATGT   [169]
K. parviflora SR268                T-CCGGGCGC CGACGCCGAG ACCCCGGTGT GCCG-----T CCT--TGCGG ATGG-CATGT   [169]
K. paviflora SR330                 T-CCGGGCGC CGACGCCGAG ACCCCGGTGT GCCG-----T CCT--TGCGG ATGG-CATGT   [169]
K. pauciflora HBsn                 T-CCGGGCGC CGACGCCGAG ACCCCGGTGT GCCG-----T CCT--TGCGG ATGG-CATGT   [169]
K. porphyantha SRsn                T-CCGGGCGC CGACGCCGAG ACCCCGGTGT GCCG-----T CCT--TGCGG ATGG-CATGT   [169]
K. praecox SR529                   T-CCGGGCGC CGACGCCGAG ACCCCGGTGT GCCG-----T CCT--TGCGG ATGG-CATGT   [169]
K. rigidifolia SRsn                T-CCGGGCGC CGACGCCGAG ACCCCGGTGT GCCG-----T CCT--TGCGG ATGG-CATGT   [169]
K. ritualis SR300                  T-CCGGGCGC CGACGCCGAG ACCCCGGTGT GCCG-----T CCT--TGCGG ATGG-CATGT   [169]
K. rooperi SR237                   T-CCGGGCGC CGACGCCGAG ACCCCGGTGT GCCG-----T CCT--TGCGG ATGG-CATGT   [169]
K. rooperi SR485                   T-CCGGGCGC CGACGCCGAG ACCCCGGTGT GCCG-----T CCT--TGCGG ATGG-CATGT   [169]
K. sarmentosa SR207                T-CCGGGCGC CGACGCCGAG ACCCCGGTGT GCCC-----T CCT--TGCGG ATGT-CATGT   [169]
K. schemperi SR391                 T-CCGGGCGC CGACGCCGAG AACCCGGTGT GCCG-----T CCT--TGCGG ATGG-CATGT   [169]
K. schemperi JMG036                T-CCGGGCGC CGACGCCGAG AACCCGGTGT GCCG-----T CCT--TGCGG ATGG-CATGT   [169]
K. splendida SR548                 T-CCGGGCGC CGACGCCGAG ACCCCGGTGT GCCG-----T CCT--TGCGG ATGG-CATGT   [169]
K. stricta SR279                   T-CCGGGCGC CGACGCCGAG ACCCCGGTGT GTCG-----T CCT--TGCGG ATGG-CATGT   [169]
K. thodei SR407                    T-CCGGGCGC CGACGCCGAG ACCCCGGTGT GCCG-----T CCT--TGCGG ATGG-CATGT   [169]
K. thomsonii JMG031                T-CCGGGCGC CGACGCCGAG AACCCGGTGT GCCG-----T CCT--TGCGG ATGG-CATGT   [169]
K. thomsonii AMM                   T-CCAGGCGC CGACGCCGAG ACCCCGGTGT GCCG-----T CCC--TGCGG ATGG-CATGT   [169]
K. thomsonii CK4821                T-CCAGGCGC CGACGCCGAG ACCCCGGTGT GCCG-----T CCT--TGCGG ATGG-CATGT   [169]
K. triangularis SR264              T-CCGGGCGC CGACGCCGAG ACCCCGGTGT GCCG-----T CCT--TGCGG ATGG-CATGT   [169]
K. triangularis SR266              T-CCGGGCGC CGACGCCGAG ACCCCGGTGT GCCG-----T CCT--TGCGG ATGG-CATGT   [169]
K. triangularis SR299              T-CCGTGCGC CGACGCCGAG ACCCCGGTGT GCCG-----T CCT--TGCGG ATGG-CATGT   [169]
K. triangularis obtusiloba SRsn    T-CCGGGCGC CGACGCCGAG ACCCTGGTGT GCCG-----T CCT--TGCGG ATGG-CATGT   [169]
K. typhoides JB8084                T-CCGGGCGC CTACGCTGAG ACCCCGGTGT GCCG-----T CCT--TGCGG ATGG-CATGT   [169]
K. typhoides NNBG                  T-CCGGGCGC CTACGCTGAG ACCCCGGTGT GCCG-----T CCT--TGCGG ATGG-CATGT   [169]
K. tysonii SR302                   T-CCGGGCGC CGACGCCGAG ACCCCGGTGT GCCG-----T CCT--TGCGG ATGG-CATGT   [169]
K. tysonii SR303                   T-CCGGGCGC CGACGCCGAG ACCCCGGTGT GCCG-----T CCT--TGCGG ATGG-CATGT   [169]
K. umbrina RGsn                    T-CCGGGCGC CGACGCCGAG ACCCCGGTGT GCCG-----T CCT--TGCGG ATGG-CATGT   [169]
K. uvaria SR186                    T-CCGGGCGC CGACGCCGAG ACCCCGGTGT GCCG-----T CCT--TGCGG ATGG-CATGT   [169]
K. uvaria SR201                    T-CCGGGCGC CGACGCCGAG ACCCCGGTGT GCCG-----T CCT--TGCGG ATGG-CATGT   [169]
K. uvaria SR203                    T-CCGGGCGC CGACGCCGAG ACCCCGGTGT GCCG-----T CCT--TGCGG ATGG-CATGT   [169]
K. uvaria SR211                    T-CCGGGCGC CGACGCCGAG ACCCCGGTGT GCCG-----T CCT--TGCGG ATGG-CATGT   [169]
K. uvaria SR342                    T-CCGGGCGC CGACGCCGAG ACCCCGGTGT GCCG-----T CCT--TGCGG ATGG-CATGT   [169]
K. uvaria SR344                    T-CCGGGCGC CGACGCCGAG ACCCCGGTGT GCCG-----T CCT--TGCGG ATGG-CATGT   [169]
K. uvaria SR477                    T-CCGGGCGC CGACGCCGAG ACCCCGGTGT GCCG-----T CCT--TGCGG ATGG-CATGT   [169]

[                                            190         200         210         220         230        240]
[                                           .          .          .          .          .          .]

Bulbine latifolia SR61             CTGGG-CGAG -CGGCGAAAC ATGACCCCCC -GGCGCGATT GGGCGCCAAG GAACACAT-C   [231]
Bulbinella cauda-felis SR204       C-GGGACGAG ACGGCGCAAC AAGACCCCCC CGGCGCGAT- GGGCGCCAAG GAACACAT-C   [226]
K. acreae TD4626                   CCGGGATCTC T--GCGGAAC AAGACCCCCC -GGCGCGAT- GGGCGCCAAG GAACACTTGC   [225]
K. albescens SR314                 CCGGGATCTC T--GCGGAAC AAGACCCCCC -GGCGCGAT- GGGCGCCAAG GAACACTTGC   [225]
K. albomontana SR149               CCGGGATCTC T--GCGGAAC AAGACCCCCC -GGCGCGAT- GGGCGCCAAG GAACACTTGC   [225]
K. angustifolia SR453              CCGGGATCTC T--GCGGAAC AAGACCCCCC -GGCGCGAT- GGGCGCCAAG GAACACTTGC   [225]
K. angustifolia SR542              CCGGGATCTC T--GCGGAAC AAGACCCCCC -GGCGCGAT- GGGCGCCAAG GAACACTTGC   [225]
K. ankaratrensis PBP5676           CTTGGATCTC T--GCGGAAC AAGACCCCCC -GGCGCGAT- GGGCGCCAAG GAACACTTGC   [225]
K. baurii SR275                    CCGGGATCTC T--GCGGAAC AAGACCCCCC -GGCGCGAT- GGGCGCCAAG GAACACTTGC   [225]
K. baurii SR285                    CCGGGATCTC T--GCGGAAC AAGACCCCCC -GGCGCGAT- GGGCGCCAAG GAACACTTGC   [225]
K. baurii SR360                    CCGGGATCTC T--GCGGAAC AAGACCCCCC -GGCGCGAT- GGGCGCCAAG GAACACTTGC   [225]
K. baurii SR382                    CCGGGATCTC T--GCGGAAC AAGACCCCCC -GGCGCGAT- GGGCGCCAAG GAACACTTGC   [225]
K. baurii NPB1923                  CCGGGATCTC T--GCGGAAC AAGACCCCCC -GGCGCGAT- GGGCGCCAAG GAACACTTGC   [225]
K. brachystachya SRsn              CCGGGATCTC T--GCGGAAC AAGACCCCCC -GGCGCGAT- GGGCGCCAAG GAACACTTGC   [225]
K. brevifolia SR452                CCGGGATCTC T--GCGGAAC AAGACCCCCC -GGCGCGAT- GGGCGCCAAG GAACACTTGC   [225]
K. bruceae SR171                   CCGGGATCTC T--GCGGAAC AAGACCCCCC -GGCGCGAT- GGGCGCCAAG GAACACTTGC   [225]
K. buchananii SR307                CCGGGATCTC T--GCGGAAC AAGACCCCCC -GGCGCGAT- GGGCGCCAAG GAACACTTGC   [225]
K. caulescens SR270                CCGGGATCTC T--GCGGAAC AAGACCCCCC -GGCGCGAT- GGGCGCCAAG GAACACTTGC   [225]
K. caulescens SR278                CCGGGATCTC T--GCGGAAC AAGACCCCCC -GGCGCGAT- GGGCGCCAAG GAACACTTGC   [225]
K. caulescens NPB1821              CCGGGATCTC T--GCGGAAC AAGACCCCCC -GGCGCGAT- GGGCGCCAAG GAACACTTGC   [225]
K. citrina SR176                   CCGGGATCTC T--GCGGAAC AAGACCCCCC -GGCGCGAT- GGGCGCCAAG GAACACTTGC   [225]
K. coddiana SRsn                   CCGGGATCTC T--GCGGAAC AAGACCCCCC -GGCGCGAT- GGGCGCCAAG GAACACTTGC   [225]
K. corraligemma SR549              CCGGGATCTC T--GCGGAAC AAGACCCCCC -GGCGCGAT- GGGCGCCAAG GAACACTTGC   [225]
K. drepanophylla RAL4816           CCGGGATCTC T--GCGGAAC AAGACCCCCC -GGCGCGAT- GGGCGCCAAG GAACACTTGC   [225]
K. ensifolia ensifolia JBsn        TCGGGATCTC T--GCGGAAC AAGACCCCCC -GGCGCGAT- GGGCGCCAAG GAACACTTGC   [225]
K. ensifolia autumnalis SR448      CCGGGATCTC T--GCGGAAC AAGACCCCCC -GGCGCGAT- GGGCGCCAAG GAACACTTGC   [225]
K. fibrosa SR297                   CCGGGATCTC T--GCGGAAC AAGACCCCCC -GGCGCGAT- GGGCGCCAAG GAACACTTGC   [225]
K. fluvitalis SRsn                 CCGGGATCTC T--GCGGAAC AAGACCCCCC -GGCGCGAT- GGGCGCCAAG GAACACTTGC   [225]
K. foliosa SR383                   CCGGGATCTC C--GCGGAAC AAGACCCCCC -GGCGCGAT- GGGCGCCAAG GAACACTTGC   [225]
K. foliosa SR387                   CCGGGATCTC C--GCGGAAC AAGACCCCCC -GGCGCGAT- GGGCGCCAAG GAACACTTGC   [225]
K. foliosa SR389                   CCGGGATCTC C--GCGGAAC AAGACCCCCC -GGCGCGAT- GGGCGCCAAG GAACACTTGC   [225]
K. foliosa SR390                   CCGGGATCTC C--GCGGAAC AAGACCCCCC -GGCGCGAT- GGGCGCCAAG GAACACTTGC   [225]
K. foliosa JMG034                  CCGGGATCTC C--GCGGAAC AAGACCCCCC -GGCGCGAT- GGGCGCCAAG GAACACTTGC   [225]
K. foliosa JMG038                  CCGGGATCTC C--GCGGAAC AAGACCCCCC -GGCGCGAT- GGGCGCCAAG GAACACTTGC   [225]
K. galpinii SR312                  CCGGGATCTC T--GCGGAAC AAGACCCCCC -GGCGCGAT- GGGCGCCAAG GAACACTTGC   [225]
K. gracilis SR321                  CCGGGATCTC T--GCGGAAC AAGACCCCCC -GGCGCGAT- GGGCGCCAAG GAACACTTGC   [225]
K. gracilis NNBG                   CCGGGATCTC T--GCGGAAC AAGACCCCCC -GGCGCGAT- GGGCGCCAAG GAACACTTGC   [225]
K. grantii CP4154                  CCGGGATCTC T--GCGGAAC AATACCCCCC -GGCGCGAT- GGGCGCCAAG GAACACTTGC   [225]
K. hirsuta SR282                   CCGGGATCTC T--GCGGAAC AAGACCCCCC -GGCGCGAT- GGGCGCCAAG GAACACTTGC   [225]
K. ichopensis SR242                CCGGGATCTC T--GCGGAAC AAGACCCCCC -GGCGCGAT- GGGCGCCAAG GAACACTTGC   [225]
K. ichopensis SR286                CCGGGATCTC T--GCGGAAC AAGACCCCCC -GGCGCGAT- GGGCGCCAAG GAACACTTGC   [225]
K. ichopensis SR289                CCGGGATCTC T--GCGGAAC AAGACCCCCC -GGCGCGAT- GGGCGCCAAG GAACACTTGC   [225]
K. insignis SRsn                   CCGGGATCTC C--GCGGAAC AAGACCCCCC -GGCGCGAT- GGGCGCCAAG GAACACTTGC   [225]
K. isoetofolia SR386               CCGGGATCTC C--GCGGAAC AAGACCCCCC -GGCGCGAT- GGGCGCCAAG GAACACTTGC   [225]
K. isoetifolia SR388               CCGGGATCTC C--GCGGAAC AAGACCCCCC -GGCGCGAT- GGGCGCCAAG GAACACTTGC   [225]
K. isoetifolia SR393               CCGGGATCTC C--GCGGAAC AAGACCCCCC -GGCGCGAT- GGGCGCCAAG GAACACTTGC   [225]
K. latifolia RSSsn                 CCGGGATCTC T--GCGGAAC AAGACCCCCC -GGCGCGAT- GGGCGCCAAG GAACACTTGC   [225]
K. laxiflora SR283                 CCGGGATCTC T--GCGGAAC AAGACCCCCC -GGCGCGAT- GGGCGCCAAG GAACACTTGC   [225]
K. laxifolia SR295                 CCGGGATCTC T--GCGGAAC AAGACCCCCC -GGCGCGAT- GGGCGCCAAG GAACACTTGC   [225]
K. laxiflora SR467                 CCGGGATCTC T--GCGGAAC AAGACCCCCC -GGCGCGAT- GGGCGCCAAG GAACACTTGC   [225]
K. laxiflora SR468                 CCGGGATCTC T--GCGGAAC AAGACCCCCC -GGCGCGAT- GGGCGCCAAG GAACACTTGC   [225]
K. laxifloraC SRsn                 CCGGGATCTC T--GCGGAAC AAGACCCCCC -GGCGCGAT- GGGCGCCAAG GAACACTTGC   [225]
K. laxiflora NPB1810               CCGGGATCTC T--GCGGAAC AAGACCCCCC -GGCGCGAT- GGGCGCCAAG GAACACTTGC   [225]
K. leucocephala NNBG               CCGGGATCTC T--GCGGAAC AAGACCCCCC -GGCGCGAT- GGGCGCCAAG GAACACTTGC   [225]
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K. linearifolia SR170              CCGGGATCTC T--GCGGAAC AAGACCCCCC -GGCGCGAT- GGGCGCCAAG GAACACTTGC   [225]
K. linearifolia SR269              CCGGGATCTC T--GCGGAAC AAGACCCCCC -GGCGCGAT- GGGCGCCAAG GAACACTTGC   [225]
K. linearifolia SR290              CCGGGATCTC T--GCGGAAC AAGACCCCCC -GGCGCGAT- GGGCGCCAAG GAACACTTGC   [225]
K. linearifolia SR291              CCGGGATCTC T--GCGGAAC AAGACCCCCC -GGCGCGAT- GGGCGCCAAG GAACACTTGC   [225]
K. linearifolia SR311              CCGGGATCTC T--GCGGAAC AAGACCCCCC -GGCGCGAT- GGGCGCCAAG GAACACTTGC   [225]
K. linearifolia SR313              CCGGGATCTC T--GCGGAAC AAGACCCCCC -GGCGCGAT- GGGCGCCAAG GAACACTTGC   [225]
K. linearifolia SR328              CCGGGATCTC T--GCGGAAC AAGACCCCCC -GGCGCGAT- GGGCGCCAAG GAACACTTGC   [225]
K. linearifolia SR343              CCGGGATCTC T--GCGGAAC AAGACCCCCC -GGCGCGAT- GGGCGCCAAG GAACACTTGC   [225]
K. littoralis SR200                CCGGGATCTC T--GCGGAAC AAGACCCCCC -GGCGCGAT- GGGCGCCAAG GAACACTTGC   [225]
K. multiflora SR310                CCGGGATCTC T--GCGGAAC AAGACCCCCC -GGCGCGAT- GGGCGCCAAG GAACACTTGC   [225]
K. multiflora SR315                CCGGGATCTC T--GCGGAAC AAGACCCCCC -GGCGCGAT- GGGCGCCAAG GAACACTTGC   [225]
K. northiae SR263                  CCGGGATCTC T--GCGGAAC AAGACCCCCC -GGCGCGAT- GGGCGCCAAG GAACACTTGC   [225]
K. northiae SR446                  CCGGGATCTC T--GCGGAAC AAGACCCCCC -GGCGCGAT- GGGCGCCAAG GAACACTTGC   [225]
K. parviflora SR268                CCGGGATCTC T--GCGGAAC AAGACCCCCC -GGCGCGAT- GGGCGCCAAG GAACACTTGC   [225]
K. paviflora SR330                 CCGGGATCTC T--GCGGAAC AAGACCCCCC -GGCGCGAT- GGGCGCCAAG GAACACTTGC   [225]
K. pauciflora HBsn                 CCGGGATCTC T--GCGGAAC AAGACCCCCC -GGCGCGAT- GGGCGCCAAG GAACACTTGC   [225]
K. porphyantha SRsn                CCGGGATCTC T--GCGGAAC AAGACCCCCC -GGCGCGAT- GGGCGCCAAG GAACACTTGC   [225]
K. praecox SR529                   CCGGGATCTC T--GCGGAAC AAGACCCCCC -GGCGCGAT- GGGCGCCAAG GAACACTTGC   [225]
K. rigidifolia SRsn                CCGGGATCTC T--GCGGAAC AAGACCCCCC -GGCGCGAT- GGGCGCCAAG GAACACTTGC   [225]
K. ritualis SR300                  CCGGGATCTC T--GCGGAAC AAGACCCCCC -GGCGCGAT- GGGCGCCAAG GAACACTTGC   [225]
K. rooperi SR237                   CCGGGATCTC T--GCGGAAC AAGACCCCCC -GGCGCGAT- GGGCGCCAAG GAACACTTGC   [225]
K. rooperi SR485                   CCGGGATCTC T--GCGGAAC AAGACCCCCC -GGCGCGAT- GGGCGCCAAG GAACACTTGC   [225]
K. sarmentosa SR207                CCGGGATCTC T--GCGGAAC AAGACCCCCC -GGCGCGAT- GGGCGCCAAG GAACACTTGC   [225]
K. schemperi SR391                 CCGGGATCTC C--GCGGAAC AAGACCCCCC -GGCGCGAT- GGGCGCCAAG GAACACTTGC   [225]
K. schemperi JMG036                CCGGGATCTC C--GCGGAAC AAGACCCCCC -GGCGCGAT- GGGCGCCAAG GAACACTTGC   [225]
K. splendida SR548                 CCGGGATCTC T--GCGGAAC AAGACCCCCC -GGCGCGAT- GGGCGCCAAG GAACACTTGC   [225]
K. stricta SR279                   CCGGGATCTC T--GCGGAAC AAGACCCCCC -GGCGCGAT- GGGCGCCAAG GAACACTTGC   [225]
K. thodei SR407                    CCGGGATCTC T--GCGGAAC AAGACCCCCC -GGCGCGAT- GGGCGCCAAG GAACACTTGC   [225]
K. thomsonii JMG031                CCGGGATCTC C--GCGGAAC AAGACCCCCC -GGCGCGAT- GGGCGCCAAG GAACACTTGC   [225]
K. thomsonii AMM                   CCGGGATCTC T--GCGGAAC AAGACCCCCC -GGCGCGAT- GGGCGCCAAG GAACACTTGC   [225]
K. thomsonii CK4821                CCGGGATCTC T--GCGGAAC AAGACCCCCC -GGCGCGAT- GGGCGCCAAG GAACACTTGC   [225]
K. triangularis SR264              CCGGGATCTC T--GCGGAAC AAGACCCCCC -GGCGCGAT- GGGCGCCAAG GAACACTTGC   [225]
K. triangularis SR266              CCGGGATCTC T--GCGGAAC AAGACCCCCC -GGCGCGAT- GGGCGCCAAG GAACACTTGC   [225]
K. triangularis SR299              CCGGGATCTC T--GCGGAAC AAGACCCCCC -GGCGCGAT- GGGCGCCAAG GAACACTTGC   [225]
K. triangularis obtusiloba SRsn    CCGGGATCTC T--GCGGAAC AAGACCCCCC -GGCGCGAT- GGGCGCCAAG GAACACTTGC   [225]
K. typhoides JB8084                CCGGGATCTC T--GCGGAAC AAGACCCCCC -GGCGCGAT- GGGCGCCAAG GAACACTTGC   [225]
K. typhoides NNBG                  CCGGGATCTC T--GCGGAAC AAGACCCCCC -GGCGCGAT- GGGCGCCAAG GAACACTTGC   [225]
K. tysonii SR302                   CCGGGATCTC T--GCGGAAC AAGACCCCCC -GGCGCGAT- GGGCGCCAAG GAACACTTGC   [225]
K. tysonii SR303                   CCGGGATCTC T--GCGGAAC AAGACCCCCC -GGCGCGAT- GGGCGCCAAG GAACACTTGC   [225]
K. umbrina RGsn                    CCGGGATCTC T--GCGGAAC AAGACCCCCC -GGCGCGAT- GGGCGCCAAG GAACACTTGC   [225]
K. uvaria SR186                    CCGGGATCTC T--GCGGAAC AAGACCCCCC -GGCGCGAT- GGGCGCCAAG GAACACTTGC   [225]
K. uvaria SR201                    CCGGGATCTC T--GCGGAAC AAGACCCCCC -GGCGCGAT- GGGCGCCAAG GAACACTTGC   [225]
K. uvaria SR203                    CCGGGATCTC T--GCGGAAC AAGACCCCCC -GGCGCGAT- GGGCGCCAAG GAACACTTGC   [225]
K. uvaria SR211                    CCGGGATCTC T--GCGGAAC AAGACCCCCC -GGCGCGAT- GGGCGCCAAG GAACACTTGC   [225]
K. uvaria SR342                    CCGGGATCTC T--GCGGAAC AAGACCCCCC -GGCGCGAT- GGGCGCCAAG GAACACTTGC   [225]
K. uvaria SR344                    CCGGGATCTC T--GCGGAAC AAGACCCCCC -GGCGCGAT- GGGCGCCAAG GAACACTTGC   [225]
K. uvaria SR477                    CCGGGATCTC T--GCGGAAC AAGACCCCCC -GGCGCGAT- GGGCGCCAAG GAACACTTGC   [225]

[                                            250         260         270         280         290        300]
[                                            .          .          .          .          .         .]

Bulbine latifolia SR61             GGAAGGAGGG AGACGGCGAC GCT------- --------CC T---GGAGCG CTCGCCCCGA   [273]
Bulbinella cauda-felis SR204       GGTCGGAGGG AGACGGCGAC GCTTCCGGAT A-TATACGCC TC-CGGAGTT TTCCCCCCGC   [284]
K. acreae TD4626                   GGCCGGAGGG AGACGGCGTG CCT-CCGGGG GCTTTAAGCC TC-CGGACCG TTCGCCCCGA   [283]
K. albescens SR314                 GGCCGGAGGG AGACGGCGTG CCT-CCGGGG GCTTTAAGCC TC-CGGACCG TTCGCCCCGA   [283]
K. albomontana SR149               GGCCGGAGGG AGACGGCGTG CCT-CCGGGG GCTTTAAGCC TC-CGGACCG TTCGCCCCGA   [283]
K. angustifolia SR453              GGCCGGAGGG AGACGGCGTG CCT-CCGGGG GCTTTAAGCC TC-CGGACCG TTCGCCCCGA   [283]
K. angustifolia SR542              GGCCGGAGGG AGACGGCGTG CCT-CCGGGG GCTTTAAGCC TC-CGGACCG TTCGCCCCGA   [283]
K. ankaratrensis PBP5676           GGCCGGAGGG AGACGGCGTG CCT-CCGGGG GCTTTAAGCC TC-CGGACCG TTCGCCCCGA   [283]
K. baurii SR275                    GGCCGGAGGG AGACGGCGTG CCT-CCGGGG GCTTTAAGCC TC-CGGACCG TTCGCCCCGA   [283]
K. baurii SR285                    GGCCGGAGGG AGACGGCGTG CCT-CCGGGG GCTTTAAGCC TC-CGGACCG TTCGCCCCGA   [283]
K. baurii SR360                    GGCCGGAGGG AGACGGCGTG CCT-CCGGGG GCTTTAAGCC TC-CGGACCG TTCGCCCCGA   [283]
K. baurii SR382                    GGCCGGAGGG AGACGGCGTG CCT-CCGGGG GCTTTAAGCC TC-CGGACCG TTCGCCCCGA   [283]
K. baurii NPB1923                  GGCCGGAGGG AGACGGCGTG CCT-CCGGGG GCTTTAAGCC TC-CGGACCG TTCGCCCCGA   [283]
K. brachystachya SRsn              GGCCGGAGGG AGACGGCGTG CCT-CCGGGG GCTTTAAGCC TC-CGGACCG TTCGCCCCGA   [283]
K. brevifolia SR452                GGCCGGAGGG AGACGGCGTG CCT-CCGGGG GCTTTAAGCC TC-CGGACCG TTCGCCCCGA   [283]
K. bruceae SR171                   GGCCGGAGGG AGACGGCGTG CCT-CCGGGG GCTTTAAGCC TC-CGGACCG TTCGCCCCGA   [283]
K. buchananii SR307                GGCCGGAGGG AGACGGCGTG CCT-CCGGGG GCTTTAAGCC TC-CGGACCG TTCGCCCCGA   [283]
K. caulescens SR270                GGCCGGAGGG AGACGGCGTG CCT-CCGGGG GCTTTAAGCC TC-CGGACCG TTCGCCTCGA   [283]
K. caulescens SR278                GGCCGGAGGG AGACGGCGTG CCT-CCGGGG GCTTTAAGCC TC-CGGACCG TTCGCCCCGA   [283]
K. caulescens NPB1821              GGCCGGAGGG AGACGGCGTG CCT-CCGGGG GCTTTAAGCC TC-CGGACCG TTCGCCTCGA   [283]
K. citrina SR176                   GGCCGGAGGG AGACGGCGTG CCT-CCGGGG GCTTTAAGCC TC-CGGACCG TTCGCCCCGA   [283]
K. coddiana SRsn                   GGCCGGAGGG AGACGGCGTG CCT-CCGGGG GCTTTAAGCC TC-CGGACCG TTCGCCCCGA   [283]
K. corraligemma SR549              GGCCGGAGGG AGACGGCGTG CCT-CCGGGG GCTTTAAGCC TC-CGGACCG TTCGCCCCGA   [283]
K. drepanophylla RAL4816           GGCCGGAGGG AGACGGCGTG CCT-CCGGGG GCTTTAAGCC TC-CGGACCG TTCGCCCCGA   [283]
K. ensifolia ensifolia JBsn        GGCCGGAGGG AGACGGCGTG CCT-CCGGGG GCTTTAAGCC TC-CGGACCG TTCGCCCCGA   [283]
K. ensifolia autumnalis SR448      GGCCGGAGGG AGACGGCGTG CCT-CCGGGG GCTTTAAGCC TC-CGGACCG TTCGCCCCGA   [283]
K. fibrosa SR297                   GGCCGGAGGG AGACGGCGTG CCT-CCGGGG GCTTTAAGCC TC-CGGACCG TTCGCCCCGA   [283]
K. fluvitalis SRsn                 GGCCGGAGGG AGACGGCGTG CCT-CCGGGG GCTTTAAGCC TC-CGGACCG TTCGCCCCGA   [283]
K. foliosa SR383                   GGTCGGAGGG AGACGGCGTG CCT-ACGGGG GCTTTAAGCC TC-CGGACCG TTCGCCCCGA   [283]
K. foliosa SR387                   GGTCGGAGGG AGACGGCGTG CCT-ACGGGG GCTTTAAGCC TC-CGGACCG TTCGCCCCGA   [283]
K. foliosa SR389                   GGTCGGAGGG AGACGGCGTG CCT-ACGGGG GCTTTAAGCC TC-CGGACCG TTCGCCCCGA   [283]
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K. foliosa JMG034                  GGTCGGAGGG AGACGGCGTG CCT-ACGGGG GCTTTAAGCC TC-CGGACCG TTCGCCCCGA   [283]
K. foliosa JMG038                  GGTCGGAGGG AGACGGCGTG CCT-ACGGGG GCTTTAAGCC TC-CGGACCG TTCGCCCCGA   [283]
K. galpinii SR312                  GGCCGGAGGG AGACGGCGTG CCT-CCGGGG GCTTTAAGCC TC-CGGACCG TTCGCCCCGA   [283]
K. gracilis SR321                  GGCCGGAGGG AGACGGCGTG CCT-CCGGGG GCTTTAAGCC TC-CGGACCG TTCGCCCCGA   [283]
K. gracilis NNBG                   GGCCGGAGGG AGACGGCGTG CCT-CCGGGG GCTTTAAGCC TC-CGGACCG TTCGCCCCGA   [283]
K. grantii CP4154                  GGCCGGAGGG AGACGGCGTG CCT-CCGGGG GCTTTAAGCC TCTCGGACCG TTCGCCCCGA   [284]
K. hirsuta SR282                   GGCCGGAGGG AGACGGCGTG CCT-CCGGGG GCTTTAAGCC TC-CGGACCG TTCGCCCCGA   [283]
K. ichopensis SR242                GGCCGGAGGG AGACGGCGTG CCT-CCGGGG GCTTTAAGCC TC-CGGACCG TTCGCCCCGA   [283]
K. ichopensis SR286                GGCCGGAGGG AGACGGCGTG CCT-CCGGGG GCTTTAAGCC TC-CGGACCG TTCGCCCCGA   [283]
K. ichopensis SR289                GGCCGGAGGG AGACGGCGTG CCT-CCGGGG GCTTTAAGCC TC-CGGACCG TTCGCCCCGA   [283]
K. insignis SRsn                   GGTCGGAGGG AGACGGCGTG CCT-ACGGGG GCTTTAAGCC TC-CGGACCG TTCGCCCCGA   [283]
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K. isoetofolia SR386               GGCCGGAGGG AGACGGCGTG CCT-ACGGGG GCTTTAAGCC TC-CGGACCG TTCGCCCCGA   [283]
K. isoetifolia SR388               GGTCGGAGGG AGACGGCGTG CCT-ACGGGG GCTTTAAGCC TC-CGGACCG TTCGCCCCGA   [283]
K. isoetifolia SR393               GGTCGGAGGG AGACGGCGTG CCT-ACGGGG GCTTTAAGCC TC-CGGACCG TTCGCCCCGA   [283]
K. latifolia RSSsn                 GGCCGGAGGG AGACGGCGTG CCT-CCGGGG GCTTTAAGCC TC-CGGACCG TTCGCCCCGA   [283]
K. laxiflora SR283                 GGCCGGAGGG AGACGGCGTG CCT-CCGGGG GCTTTAAGCC TC-CGGACCG TTCGCCCCGA   [283]
K. laxifolia SR295                 GGCCGGAGGG AGACGGCGTG CCT-CCGGGG GCTTTAAGCC TC-CGGACCG TTCGCCCCGA   [283]
K. laxiflora SR467                 GGCCGGAGGG AGACGGCGTG CCT-CCGGGG GCTTTAAGCC TC-CGGACCG TTCGCCCCGA   [283]
K. laxiflora SR468                 GGCCGGAGGG AGACGGCGTG CCT-CCGGGG GCTTTAAGCC TC-CGGACCG TTCGCCCCGA   [283]
K. laxifloraC SRsn                 GGCCGGAGGG AGACGGCGTG CCT-CCGGGG GCTTTAAGCC TC-CGGACCG TTCGCCCCGA   [283]
K. laxiflora NPB1810               GGCCGGAGGG AGACGGCGTG CCT-CCGGGG GCTTTAAGCC TC-CGGACCG TTCGCCCCGA   [283]
K. leucocephala NNBG               GGCCGGAGGG AGACGGCGTG CCT-CCGGGG GCTTTAAGCC TC-CGGACCG TTCGCCCCGA   [283]
K. linearifolia SR170              GGCCGGAGGG AGACGGCGTG CCT-CCGGGG GCTTTAAGCC TC-CGGACCG TTCGCCCCGA   [283]
K. linearifolia SR269              GGCCGGAGGG AGACGGCGTG CCT-CCGGGG GCTTTAAGCC TC-CGGACCG TTCGCCCCGA   [283]
K. linearifolia SR290              GGCCGGAGGG AGACGGCGTG CCT-CCGGGG GCTTTAAGCC TC-CGGACCG TTCGCCCCGA   [283]
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K. linearifolia SR313              GGCCGGAGGG AGACGGCGTG CCT-CCGGGG GCTTTAAGCC TC-CGGACCG TTCGCCCCGA   [283]
K. linearifolia SR328              GGCCGGAGGG AGACGGCGTG CCT-CCGGGG GCTTTAAGCC TC-CGGACCG TTCGCCCCGA   [283]
K. linearifolia SR343              GGCCGGAGGG AGACGGCGTG CCT-CCGGGG GCTTTAAGCC TC-CGGACCG TTCGCCCCGA   [283]
K. littoralis SR200                GGCCGGAGGG AGACGGCGTG CCT-CCGGGG GCTTTAAGCC TC-CGGACCG TTCGCCCCGA   [283]
K. multiflora SR310                GGCCGGAGGG AGACGGCGTG CCT-CCGGGG GCTTTAAGCC TC-CGGACCG TTCGCCCCGA   [283]
K. multiflora SR315                GGCCGGAGGG AGACGGCGTG CCT-CCGGGG GCTTTAAGCC TC-CGGACCG TTCGCCCCGA   [283]
K. northiae SR263                  GGCCGGAGGG AGACGGCGTG CCT-CCGGGG GCTTTAAGCC TC-CGGACCG TTCGCCCCGA   [283]
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K. parviflora SR268                GGCCGGAGGG AGACGGCGTG CCT-CCGGGG GCTTTAAGCC TC-CGGACCG TTCGCCCCGA   [283]
K. paviflora SR330                 GGCCGGAGGG AGACGGCGTG CCT-CCGGGG GCTTTAAGCC TC-CGGACCG TTCGCCCCGA   [283]
K. pauciflora HBsn                 GGCCGGAGGG AGACGGCGTG CCT-CCGGGG GCTTTAAGCC TC-CGGACCG TTCGCCCCGA   [283]
K. porphyantha SRsn                GGCCGGAGGG AGACGGCGTG CCT-CCGGGG GCTTTAAGCC TC-CGGATCG TTCGCCCCGA   [283]
K. praecox SR529                   GGCCGGAGGG AGACGGCGTG CCT-CCGGGG GCTTTAAGCC TC-CGGACCG TTCGCCCCGA   [283]
K. rigidifolia SRsn                GGCCGGAGGG AGACGGCGTG CCT-CCGGGG GCTTTAAGCC TC-CGGACCG TTCGCCCCGA   [283]
K. ritualis SR300                  GGCCGGAGGG AGACGGCGTG CCT-CCGGGG GCTTTAAGCC TC-CGGACCG TTCGCCCCGA   [283]
K. rooperi SR237                   GGCCGGAGGG AGACGGCGTG CCT-CCGGGG GCTTTAAGCC TC-CGGACCG TTCGCCCCGA   [283]
K. rooperi SR485                   GGCCGGAGGG AGACGGCGTG CCT-CCGGGG GCTTTAAGCC TC-CGGACCG TTCGCCCCGA   [283]
K. sarmentosa SR207                GGCCGGAGGG AGACGGCGTG CCT-CCGGGG GCTTTACGCC TC-CGGACTG TCCGCCCCGA   [283]
K. schemperi SR391                 GGTCGGAGGG AGACGGCGTG CCT-ACGGGG GCTTTAAGCC TC-CGGACCG TTCGCCCCGA   [283]
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K. splendida SR548                 GGCCGGAGGG AGACGGCGTG CCT-CCGGGG GCTTTAAGCC TC-CGGACCG TTCGCCCCGA   [283]
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K. thomsonii CK4821                GGCCGGAGGG AGACGGCGTG CCT-CCGGGG GCTTTAAGCC TC-CGGACCG TTCGCCCCGA   [283]
K. triangularis SR264              GGCCGGAGGG AGACGGCGTG CCT-CCGGGG GCTTTAAGCC TC-CGGACCG TTCGCCCCGA   [283]
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K. triangularis obtusiloba SRsn    GGCCGGAGGG AGACGGCGTG CCT-CCGGGG GCTTTAAGCC TC-CGGACCG TTCGCCCCGA   [283]
K. typhoides JB8084                GGCCGGAGGG AGACGGCGTG CCT-CCGGGG GCTTTAAGCC TC-CGGACCG TTCGCCCCGA   [283]
K. typhoides NNBG                  GGCCGGAGGG AGACGGCGTG CCT-CCGGGG GCTTTAAGCC TC-CGGACCG TTCGCCCCGA   [283]
K. tysonii SR302                   GGCCGGAGGG AGACGGCGTG CCT-CCGGGG GCTTTAAGCC TC-CGGACCG TTCGCCCCGA   [283]
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K. umbrina RGsn                    GGCCGGAGGG AGACGGCGTG CCT-CCGGGG GCTTTAAGCC TC-CGGACCG TTCGCCCCGA   [283]
K. uvaria SR186                    GGCCGGAGGG AGACGGCGTG CCT-CCGGGG GCTTTAAGCC TC-CGGACCG TTCGCCCCGA   [283]
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K. uvaria SR203                    GGCCGGAGGG AGACGGCGTG CCT-CCGGGG GCTTTAAGCC TC-CGGACCG TTCGCCCCGA   [283]
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K. uvaria SR342                    GGCCGGAGGG AGACGGCGTG CCT-CCGGGG GCTTTAAGCC TC-CGGACCG TTCGCCCCGA   [283]
K. uvaria SR344                    GGCCGGAGGG AGACGGCGTG CCT-CCGGGG GCTTTAAGCC TC-CGGACCG TTCGCCCCGA   [283]
K. uvaria SR477                    GGCCGGAGGG AGACGGCGTG CCT-CCGGGG GCTTTAAGCC TC-CGGACCG TTCGCCCCGA   [283]

[                                            310         320         330         340         350        360]
[                                             .          .          .          .          .         .]

Bulbine latifolia SR61             CCTCCGCAAC CGTACACTAT ATGAATTTTA TGACTCTCGG CAACGGATAT CTCGGCTCTC   [333]
Bulbinella cauda-felis SR204       CCTCCGCAAC CGGACACTAT ATTAATTTTA TGACTCTCGG CAACGGATAT CTCGGCTCTC   [344]
K. acreae TD4626                   CCTCCGCAAC CGAACACTAC ATAAACTGTA TGACTCTCGG CAACGGATAT CTCGGCTCTC   [343]
K. albescens SR314                 CCTCCGCAAC CGAACACTAC ATAAACTGTA TGACTCTCGG CAACGGATAT CTCGGCTCTC   [343]
K. albomontana SR149               CCTCCGCAAC CGAACACTAC ATAAACTGTA TGACTCTCGG CAACGGATAT CTCGGCTCTC   [343]
K. angustifolia SR453              CCTCCGCAAC CGAACACTAC ATAAACTGTA TGACTCTCGG CAACGGATAT CTCGGCTCTC   [343]
K. angustifolia SR542              CCTCCGCAAC CGAACACTAC ATAAACTGTA TGACTCTCGG CAACGGATAT CTCGGCTCTC   [343]
K. ankaratrensis PBP5676           CCTCCGCAAC CGAACACTAC ATAAACTGTA TGACTCTCGG CAACGGATAT CTCGGCTCTC   [343]
K. baurii SR275                    CCTCCGCAAC CGAACACTAC ATAAACTGTA TGACTCTCGG CAACGGATAT CTCGGCTCTC   [343]
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K. brevifolia SR452                CCTCCGCAAC CGAACACTAC ATAAACTGTA TGACTCTCGG CAACGGATAT CTCGGCTCTC   [343]
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K. caulescens SR270                CCTCCGCAAC CGAACACTAC ATAAACTGTA TGACTCTCGG CAACGGATAT CTCGGCTCTC   [343]
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K. coddiana SRsn                   CCTCCGCAAC CGAACACTAC ATAAACTGTA TGACTCTCGG CAACGGATAT CTCGGCTCTC   [343]
K. corraligemma SR549              CCTCCGCAAC CGAACACTAC ATAAACTGTA TGACTCTCGG CAACGGATAT CTCGGCTCTC   [343]
K. drepanophylla RAL4816           CCTCCGCAAC CGAACACTAC ATAAACTGTA TGACTCTCGG CAACGGATAT CTCGGCTCTC   [343]
K. ensifolia ensifolia JBsn        CCTCCGCAAC CGAACACTAC ATAAACTGTA TGACTCTCGG CAACGGATAT CTCGGCTCTC   [343]
K. ensifolia autumnalis SR448      CCTCCGCAAC CGAACACTAC ATAAACTGTA TGACTCTCGG CAACGGATAT CTCGGCTCTC   [343]
K. fibrosa SR297                   CCTCCGCAAC CGAACACTAC ATAAACTGTA TGACTCTCGG CAACGGATAT CTCGGCTCTC   [343]
K. fluvitalis SRsn                 CCTCCGCAAC CGAACACTAC ATAAACTGTA TGACTCTCGG CAACGGATAT CTCGGCTCTC   [343]
K. foliosa SR383                   CCTCCGCAAC CGAACACTAC ATAAACTGTA TGACTCTCGG CAACGGATAT CTCGGCTCTC   [343]
K. foliosa SR387                   CCTCCGCAAC CGAACACTAC ATAAACTGTA TGACTCTCGG CAACGGATAT CTCGGCTCTC   [343]
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K. gracilis SR321                  CCTCCGCAAC CGAACACTAC ATAAACTGTA TGACTCTCGG CAACGGATAT CTCGGCTCTC   [343]
K. gracilis NNBG                   CCTCCGCAAC CGAACACTAC ATAAACTGTA TGACTCTCGG CAACGGATAT CTCGGCTCTC   [343]
K. grantii CP4154                  CCTCCGCAAC CGAACACTAC ATAAACTGTA TGACTCTCGG CAACGGATAT CTCGGCTCTC   [344]
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K. isoetifolia SR393               CCTCCGCAAC CGAACACTAC ATAAACTGTA TGACTCTCGG CAACGGATAT CTCGGCTCTC   [343]
K. latifolia RSSsn                 CCTCCGCAAC CGAACACTAC ATAAACTGTA TGACTCTCGG CAACGGATAT CTCGGCTCTC   [343]
K. laxiflora SR283                 CCTCCGCAAC CGAACACTAC ATAAACTGTA TGACTCTCGG CAACGGATAT CTCGGCTCTC   [343]
K. laxifolia SR295                 CCTCCGCAAC CGAACACTAC ATAAACTGTA TGACTCTCGG CAACGGATAT CTCGGCTCTC   [343]
K. laxiflora SR467                 CCTCCGCAAC CGAACACTAC ATAAACTGTA TGACTCTCGG CAACGGATAT CTCGGCTCTC   [343]
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K. laxiflora NPB1810               CCTCCGCAAC CGAACACTAC ATAAACTGTA TGACTCTCGG CAACGGATAT CTCGGCTCTC   [343]
K. leucocephala NNBG               CCTCCGCAAC CGAACACTAC ATAAACTGTA TGACTCTCGG CAACGGATAT CTCGGCTCTC   [343]
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K. linearifolia SR290              CCTCCGCAAC CGAACACTAC ATAAACTGTA TGACTCTCGG CAACGGATAT CTCGGCTCTC   [343]
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K. linearifolia SR328              CCTCCGCAAC CGAACACTAC ATAAACTGTA TGACTCTCGG CAACGGATAT CTCGGCTCTC   [343]
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K. paviflora SR330                 CCTCCGCAAC CGAACACTAC ATAAACTGTA TGACTCTCGG CAACGGATAT CTCGGCTCTC   [343]
K. pauciflora HBsn                 CCTCCGCAAC CGAACACTAC ATAAACTGTA TGACTCTCGG CAACGGATAT CTCGGCTCTC   [343]
K. porphyantha SRsn                CCTCCGCAAC CGAACACTAC ACAAACTGTA TGACTCTCGG CAACGGATAT CTCGGCTCTC   [343]
K. praecox SR529                   CCTCCGCAAC CGAACACTAC ATAAACTGTA TGACTCTCGG CAACGGATAT CTCGGCTCTC   [343]
K. rigidifolia SRsn                CCTCCGCAAC CGAACACTAC ATAAACTGTA TGACTCTCGG CAACGGATAT CTCGGCTCTC   [343]
K. ritualis SR300                  CCTCCGCAAC CGAACACTAC ATAAACTGTA TGACTCTCGG CAACGGATAT CTCGGCTCTC   [343]
K. rooperi SR237                   CCTCCGCAAC CGAACACTAC ATAAACTGTA TGACTCTCGG CAACGGATAT CTCGGCTCTC   [343]
K. rooperi SR485                   CCTCCGCAAC CGAACACTAC ATAAACTGTA TGACTCTCGG CAACGGATAT CTCGGCTCTC   [343]
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K. schemperi SR391                 CCTCCGCAAC CGAACACTAC ATAAACTGTA TGACTCTCGG CAACGGATAT CTCGGCTCTC   [343]
K. schemperi JMG036                CCTCCGCAAC CGAACACTAC ATAAACTGTA TGACTCTCGG CAACGGATAT CTCGGCTCTC   [343]
K. splendida SR548                 CCTCCGCAAC CGAACACTAC ATAAACTGTA TGACTCTCGG CAACGGATAT CTCGGCTCTC   [343]
K. stricta SR279                   CCTCCGCAAC CGAACACTAC ATAAACTGTA TGACTCTCGG CAACGGATAT CTCGGCTCTC   [343]
K. thodei SR407                    CCTCCGCAAC CGAACACTAC ATAAACTGTA TGACTCTCGG CAACGGATAT CTCGGCTCTC   [343]
K. thomsonii JMG031                CCTCCGCAAC CGAACACTAC ATAAACTGTA TGACTCTCGG CAACGGATAT CTCGGCTCTC   [343]
K. thomsonii AMM                   CCTCCGCAAC CGAACACTAC ATAAACTGTA TGACTCTCGG CAACGGATAT CTCGGCTCTC   [343]
K. thomsonii CK4821                CCTCCGCAAC CGAACACTAC ATAAACTGTA TGACTCTCGG CAACGGATAT CTCGGCTCTC   [343]
K. triangularis SR264              CCTCCGCAAC CGAACACTAC ATAAACTGTA TGACTCTCGG CAACGGATAT CTCGGCTCTC   [343]
K. triangularis SR266              CCTCCGCAAC CGAACACTAC ATAAACTGTA TGACTCTCGG CAACGGATAT CTCGGCTCTC   [343]
K. triangularis SR299              CCTCCGCAAC CGAACACTAC ATAAACTGTA TGACTCTCGG CAACGGATAT CTCGGCTCTC   [343]
K. triangularis obtusiloba SRsn    CCTCCGCAAC CGAACACTAC ATAAACTGTA TGACTCTCGG CAACGGATAT CTCGGCTCTC   [343]
K. typhoides JB8084                CCTCCGCAAC CGAACACTAC ATAAACTGTA TGACTCTCGG CAACGGATAT CTCGGCTCTC   [343]
K. typhoides NNBG                  CCTCCGCAAC CGAACACTAC ATAAACTGTA TGACTCTCGG CAACGGATAT CTCGGCTCTC   [343]
K. tysonii SR302                   CCTCCGCAAC CGAACACTAC ATAAACTGTA TGACTCTCGG CAACGGATAT CTCGGCTCTC   [343]
K. tysonii SR303                   CCTCCGCAAC CGAACACTAC ATAAACTGTA TGACTCTCGG CAACGGATAT CTCGGCTCTC   [343]
K. umbrina RGsn                    CCTCCGCAAC CGAACACTAC ATAAACTGTA TGACTCTCGG CAACGGATAT CTCGGCTCTC   [343]
K. uvaria SR186                    CCTCCGCAAC CGAACACTAC ATAAACTGTA TGACTCTCGG CAACGGATAT CTCGGCTCTC   [343]
K. uvaria SR201                    CCTCCGCAAC CGAACACTAC ATAAACTGTA TGACTCTCGG CAACGGATAT CTCGGCTCTC   [343]
K. uvaria SR203                    CCTCCGCAAC CGAACACTAC ATAAACTGTA TGACTCTCGG CAACGGATAT CTCGGCTCTC   [343]
K. uvaria SR211                    CCTCCGCAAC CGAACACTAC ATAAACTGTA TGACTCTCGG CAACGGATAT CTCGGCTCTC   [343]
K. uvaria SR342                    CCTCCGCAAC CGAACACTAC ATAAACTGTA TGACTCTCGG CAACGGATAT CTCGGCTCTC   [343]
K. uvaria SR344                    CCTCCGCAAC CGAACACTAC ATAAACTGTA TGACTCTCGG CAACGGATAT CTCGGCTCTC   [343]
K. uvaria SR477                    CCTCCGCAAC CGAACACTAC ATAAACTGTA TGACTCTCGG CAACGGATAT CTCGGCTCTC   [343]

[                                            370         380         390         400         410        420]
[                                             .          .          .          .          .         .]

Bulbine latifolia SR61             GCATCGATGA AGAACGTAGC GAAATGCGAT ACTTGGTGTG AATTGCAGAA TCCCGTGAAC   [393]
Bulbinella cauda-felis SR204       GCATCGATGA AGAACGTAGC TAAATGCGAT ACTTGGTGTG AATTGCAGAA TCCCGTGAAT   [404]
K. acreae TD4626                   GCATCGATGA AGAACGTAGC GAAATGCGAT ACTTGGTGTG AATTGCAGAA TCCCGTGAAC   [403]
K. albescens SR314                 GCATCGATGA AGAACGTAGC GAAATGCGAT ACTTGGTGTG AATTGCAGAA TCCCGTGAAC   [403]
K. albomontana SR149               GCATCGATGA AGAACGTAGC GAAATGCGAT ACTTGGTGTG AATTGCAGAA TCCCGTGAAC   [403]
K. angustifolia SR453              GCATCGATGA AGAACGTAGC GAAATGCGAT ACTTGGTGTG AATTGCAGAA TCCCGTGAAC   [403]
K. angustifolia SR542              GCATCGATGA AGAACGTAGC GAAATGCGAT ACTTGGTGTG AATTGCAGAA TCCCGTGAAC   [403]
K. ankaratrensis PBP5676           GCATCGATGA AGAACGTAGC GAAATGCGAT ACTTGGTGTG AATTGCAGAA TCCCGTGAAC   [403]
K. baurii SR275                    GCATCGATGA AGAACGTAGC GAAATGCGAT ACTTGGTGTG AATTGCAGAA TCCCGTGAAC   [403]
K. baurii SR285                    GCATCGATGA AGAACGTAGC GAAATGCGAT ACTTGGTGTG AATTGCAGAA TCCCGTGAAC   [403]
K. baurii SR360                    GCATCGATGA AGAACGTAGC GAAATGCGAT ACTTGGTGTG AATTGCAGAA TCCCGTGAAC   [403]
K. baurii SR382                    GCATCGATGA AGAACGTAGC GAAATGCGAT ACTTGGTGTG AATTGCAGAA TCCCGTGAAC   [403]
K. baurii NPB1923                  GCATCGATGA AGAACGTAGC GAAATGCGAT ACTTGGTGTG AATTGCAGAA TCCCGTGAAC   [403]
K. brachystachya SRsn              GCATCGATGA AGAACGTAGC AAAATGCGAT ACTTGGTGTG AATTGCAGAA TCCCGTGAAC   [403]
K. brevifolia SR452                GCATCGATGA AGAACGTAGC GAAATGCGAT ACTTGGTGTG AATTGCAGAA TCCCGTGAAC   [403]
K. bruceae SR171                   GCATCGATGA AGAACGTAGC GAAATGCGAT ACTTGGTGTG AATTGCAGAA TCCCGTGAAC   [403]
K. buchananii SR307                GCATCGATGA AGAACGTAGC GAAATGCGAT ACTTGGTGTG AATTGCAGAA TCCCGTGAAC   [403]
K. caulescens SR270                GCATCGATGA AGAACGTAGC GAAATGCGAT ACTTGGTGTG AATTGCAGAA TCCCGTGAAC   [403]
K. caulescens SR278                GCATCGATGA AGAACGTAGC GAAATGCGAT ACTTGGTGTG AATTGCAGAA TCCCGTGAAC   [403]
K. caulescens NPB1821              GCATCGATGA AGAACGTAGC GAAATGCGAT ACTTGGTGTG AATTGCAGAA TCCCGTGAAC   [403]
K. citrina SR176                   GCATCGATGA AGAACGTAGC GAAATGCGAT ACTTGGTGTG AATTGCAGAA TCCCGTGAAC   [403]
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K. coddiana SRsn                   GCATCGATGA AGAACGTAGC GAAATGCGAT ACTTGGTGTG AATTGCAGAA TCCCGTGAAC   [403]
K. corraligemma SR549              GCATCGATGA AGAACGTAGC GAAATGCGAT ACTTGGTGTG AATTGCAGAA TCCCGTGAAC   [403]
K. drepanophylla RAL4816           GCATCGATGA AGAACGTAGC GAAATGCGAT ACTTGGTGTG AATTGCAGAA TCCCGTGAAC   [403]
K. ensifolia ensifolia JBsn        GCATCGATGA AGAACGTAGC GAAATGCGAT ACTTGGTGTG AATTGCAGAA TCCCGTGAAC   [403]
K. ensifolia autumnalis SR448      GCATCGATGA AGAACGTAGC GAAATGCGAT ACTTGGTGTG AATTGCAGAA TCCCGTGAAC   [403]
K. fibrosa SR297                   GCATCGATGA AGAACGTAGC GAAATGCGAT ACTTGGTGTG AATTGCAGAA TCCCGTGAAC   [403]
K. fluvitalis SRsn                 GCATCGATGA AGAACGTAGC GAAATGCGAT ACTTGGTGTG AATTGCAGAA TCCCGTGAAC   [403]
K. foliosa SR383                   GCATCGATGA AGAACGTAGC GAAATGCGAT ACTTGGTGTG AATTGCAGAA TCCCGTGAAC   [403]
K. foliosa SR387                   GCATCGATGA AGAACGTAGC GAAATGCGAT ACTTGGTGTG AATTGCAGAA TCCCGTGAAC   [403]
K. foliosa SR389                   GCATCGATGA AGAACGTAGC GAAATGCGAT ACTTGGTGTG AATTGCAGAA TCCCGTGAAC   [403]
K. foliosa SR390                   GCATCGATGA AGAACGTAGC GAAATGCGAT ACTTGGTGTG AATTGCAGAA TCCCGTGAAC   [403]
K. foliosa JMG034                  GCATCGATGA AGAACGTAGC GAAATGCGAT ACTTGGTGTG AATTGCAGAA TCCCGTGAAC   [403]
K. foliosa JMG038                  GCATCGATGA AGAACGTAGC GAAATGCGAT ACTTGGTGTG AATTGCAGAA TCCCGTGAAC   [403]
K. galpinii SR312                  GCATCGATGA AGAACGTAGC GAAATGCGAT ACTTGGTGTG AATTGCAGAA TCCCGTGAAC   [403]
K. gracilis SR321                  GCATCGATGA AGAACGTAGC GAAATGCGAT ACTTGGTGTG AATTGCAGAA TCCCGTGAAC   [403]
K. gracilis NNBG                   GCATCGATGA AGAACGTAGC GAAATGCGAT ACTTGGTGTG AATTGCAGAA TCCCGTGAAC   [403]
K. grantii CP4154                  GCATCGATGA AGAACGTAGC GAAATGCGAT ACTTGGTGTG AATTGCAGAA TCCCGCGAAC   [404]
K. hirsuta SR282                   GCATCGATGA AGAACGTAGC GAAATGCGAT ACTTGGTGTG AATTGCAGAA TCCCGTGAAC   [403]
K. ichopensis SR242                GCATCGATGA AGAACGTAGC GAAATGCGAT ACTTGGTGTG AATTGCAGAA TCCCGTGAAC   [403]
K. ichopensis SR286                GCATCGATGA AGAACGTAGC GAAATGCGAT ACTTGGTGTG AATTGCAGAA TCCCGTGAAC   [403]
K. ichopensis SR289                GCATCGATGA AGAACGTAGC GAAATGCGAT ACTTGGTGTG AATTGCAGAA TCCCGTGAAC   [403]
K. insignis SRsn                   GCATCGATGA AGAACGTAGC GAAATGCGAT ACTTGGTGTG AATTGCAGAA TCCCGTGAAC   [403]
K. isoetofolia SR386               GCATCGATGA AGAACGTAGC GAAATGCGAT ACTTGGTGTG AATTGCAGAA TCCCGTGAAC   [403]
K. isoetifolia SR388               GCATCGATGA AGAACGTAGC GAAATGCGAT ACTTGGTGTG AATTGCAGAA TCCCGTGAAC   [403]
K. isoetifolia SR393               GCATCGATGA AGAACGTAGC GAAATGCGAT ACTTGGTGTG AATTGCAGAA TCCCGTGAAC   [403]
K. latifolia RSSsn                 GCATCGATGA AGAACGTAGC GAAATGCGAT ACTTGGTGTG AATTGCAGAA TCCCGTGAAC   [403]
K. laxiflora SR283                 GCATCGATGA AGAACGTAGC GAAATGCGAT ACTTGGTGTG AATTGCAGAA TCCCGTGAAC   [403]
K. laxifolia SR295                 GCATCGATGA AGAACGTAGC GAAATGCGAT ACTTGGTGTG AATTGCAGAA TCCCGTGAAC   [403]
K. laxiflora SR467                 GCATCGATGA AGAACGTAGC GAAATGCGAT ACTTGGTGTG AATTGCAGAA TCCCGTGAAC   [403]
K. laxiflora SR468                 GCATCGATGA AGAACGTAGC GAAATGCGAT ACTTGGTGTG AATTGCAGAA TCCCGTGAAC   [403]
K. laxifloraC SRsn                 GCATCGATGA AGAACGTAGC GAAATGCGAT ACTTGGTGTG AATTGCAGAA TCCCGTGAAC   [403]
K. laxiflora NPB1810               GCATCGATGA AGAACGTAGC GAAATGCGAT ACTTGGTGTG AATTGCAGAA TCCCGTGAAC   [403]
K. leucocephala NNBG               GCATCGATGA AGAACGTAGC GAAATGCGAT ACTTGGTGTG AATTGCAGAA TCCCGTGAAC   [403]
K. linearifolia SR170              GCATCGATGA AGAACGTAGC GAAATGCGAT ACTTGGTGTG AATTGCAGAA TCCCGTGAAC   [403]
K. linearifolia SR269              GCATCGATGA AGAACGTAGC GAAATGCGAT ACTTGGTGTG AATTGCAGAA TCCCGTGAAC   [403]
K. linearifolia SR290              GCATCGATGA AGAACGTAGC GAAATGCGAT ACTTGGTGTG AATTGCAGAA TCCCGTGAAC   [403]
K. linearifolia SR291              GCATCGATGA AGAACGTAGC GAAATGCGAT ACTTGGTGTG AATTGCAGAA TCCCGTGAAC   [403]
K. linearifolia SR311              GCATCGATGA AGAACGTAGC GAAATGCGAT ACTTGGTGTG AATTGCAGAA TCCCGTGAAC   [403]
K. linearifolia SR313              GCATCGATGA AGAACGTAGC GAAATGCGAT ACTTGGTGTG AATTGCAGAA TCCCGTGAAC   [403]
K. linearifolia SR328              GCATCGATGA AGAACGTAGC GAAATGCGAT ACTTGGTGTG AATTGCAGAA TCCCGTGAAC   [403]
K. linearifolia SR343              GCATCGATGA AGAACGTAGC GAAATGCGAT ACTTGGTGTG AATTGCAGAA TCCCGTGAAC   [403]
K. littoralis SR200                GCATCGATGA AGAACGTAGC GAAATGCGAT ACTTGGTGTG AATTGCAGAA TCCCGTGAAC   [403]
K. multiflora SR310                GCATCGATGA AGAACGTAGC GAAATGCGAT ACTTGGTGTG AATTGCAGAA TCCCGTGAAC   [403]
K. multiflora SR315                GCATCGATGA AGAACGTAGC GAAATGCGAT ACTTGGTGTG AATTGCAGAA TCCCGTGAAC   [403]
K. northiae SR263                  GCATCGATGA AGAACGTAGC GAAATGCGAT ACTTGGTGTG AATTGCAGAA TCCCGTGAAC   [403]
K. northiae SR446                  GCATCGATGA AGAACGTAGC GAAATGCGAT ACTTGGTGTG AATTGCAGAA TCCCGTGAAC   [403]
K. parviflora SR268                GCATCGATGA AGAACGTAGC GAAATGCGAT ACTTGGTGTG AATTGCAGAA TCCCGTGAAC   [403]
K. paviflora SR330                 GCATCGATGA AGAACGTAGC GAAATGCGAT ACTTGGTGTG AATTGCAGAA TCCCGTGAAC   [403]
K. pauciflora HBsn                 GCATCGATGA AGAACGTAGC GAAATGCGAT ACTTGGTGTG AATTGCAGAA TCCCGTGAAC   [403]
K. porphyantha SRsn                GCATCGATGA AGAACGTAGC GAAATGCGAT ACTTGGTGTG AATTGCAGAA TCCCGTGAAC   [403]
K. praecox SR529                   GCATCGATGA AGAACGTAGC GAAATGCGAT ACTTGGTGTG AATTGCAGAA TCCCGTGAAC   [403]
K. rigidifolia SRsn                GCATCGATGA AGAACGTAGC GAAATGCGAT ACTTGGTGTG AATTGCAGAA TCCCGTGAAC   [403]
K. ritualis SR300                  GCATCGATGA AGAACGTAGC GAAATGCGAT ACTTGGTGTG AATTGCAGAA TCCCGTGAAC   [403]
K. rooperi SR237                   GCATCGATGA AGAACGTAGC GAAATGCGAT ACTTGGTGTG AATTGCAGAA TCCCGTGAAC   [403]
K. rooperi SR485                   GCATCGATGA AGAACGTAGC GAAATGCGAT ACTTGGTGTG AATTGCAGAA TCCCGTGAAC   [403]
K. sarmentosa SR207                GCATCGATGA AGAACGTAGC GAAATGCGAT ACTTGGTGTG AATTGCAGAA TCCCGTGAAC   [403]
K. schemperi SR391                 GCATCGATGA AGAACGTAGC GAAATGCGAT ACTTGGTGTG AATTGCAGAA TCCCGTGAAC   [403]
K. schemperi JMG036                GCATCGATGA AGAACGTAGC GAAATGCGAT ACTTGGTGTG AATTGCAGAA TCCCGTGAAC   [403]
K. splendida SR548                 GCATCGATGA AGAACGTAGC GAAATGCGAT ACTTGGTGTG AATTGCAGAA TCCCGTGAAC   [403]
K. stricta SR279                   GCATCGATGA AGAACGTAGC GAAATGCGAT ACTTGGTGTG AATTGCAGAA TCCCGTGAAC   [403]
K. thodei SR407                    GCATCGATGA AGAACGTAGC GAAATGCGAT ACTTGGTGTG AATTGCAGAA TCCCGTGAAC   [403]
K. thomsonii JMG031                GCATCGATGA AGAACGTAGC GAAATGCGAT ACTTGGTGTG AATTGCAGAA TCCCGTGAAC   [403]
K. thomsonii AMM                   GCATCGATGA AGAACGTAGC GAAATGCGAT ACTTGGTGTG AATTGCAGAA TCCCGTGAAC   [403]
K. thomsonii CK4821                GCATCGATGA AGAACGTAGC GAAATGCGAT ACTTGGTGTG AATTGCAGAA TCCCGTGAAC   [403]
K. triangularis SR264              GCATCGATGA AGAACGTAGC GAAATGCGAT ACTTGGTGTG AATTGCAGAA TCCCGTGAAC   [403]
K. triangularis SR266              GCATCGATGA AGAACGTAGC GAAATGCGAT ACTTGGTGTG AATTGCAGAA TCCCGTGAAC   [403]
K. triangularis SR299              GCATCGATGA AGAACGTAGC GAAATGCGAT ACTTGGTGTG AATTGCAGAA TCCCGTGAAC   [403]
K. triangularis obtusiloba SRsn    GCATCGATGA AGAACGTAGC GAAATGCGAT ACTTGGTGTG AATTGCAGAA TCCCGTGAAC   [403]
K. typhoides JB8084                GCATCGATGA AGAACGTAGC AAAATGCGAT ACTTGGTGTG AATTGCAGAA TCCCGTGAAC   [403]
K. typhoides NNBG                  GCATCGATGA AGAACGTAGC AAAATGCGAT ACTTGGTGTG AATTGCAGAA TCCCGTGAAC   [403]
K. tysonii SR302                   GCATCGATGA AGAACGTAGC GAAATGCGAT ACTTGGTGTG AATTGCAGAA TCCCGTGAAC   [403]
K. tysonii SR303                   GCATCGATGA AGAACGTAGC GAAATGCGAT ACTTGGTGTG AATTGCAGAA TCCCGTGAAC   [403]
K. umbrina RGsn                    GCATCGATGA AGAACGTAGC GAAATGCGAT ACTTGGTGTG AATTGCAGAA TCCCGTGAAC   [403]
K. uvaria SR186                    GCATCGATGA AGAACGTAGC GAAATGCGAT ACTTGGTGTG AATTGCAGAA TCCCGTGAAC   [403]
K. uvaria SR201                    GCATCGATGA AGAACGTAGC GAAATGCGAT ACTTGGTGTG AATTGCAGAA TCCCGTGAAC   [403]
K. uvaria SR203                    GCATCGATGA AGAACGTAGC GAAATGCGAT ACTTGGTGTG AATTGCAGAA TCCCGTGAAC   [403]
K. uvaria SR211                    GCATCGATGA AGAACGTAGC GAAATGCGAT ACTTGGTGTG AATTGCAGAA TCCCGTGAAC   [403]
K. uvaria SR342                    GCATCGATGA AGAACGTAGC GAAATGCGAT ACTTGGTGTG AATTGCAGAA TCCCGTGAAC   [403]
K. uvaria SR344                    GCATCGATGA AGAACGTAGC GAAATGCGAT ACTTGGTGTG AATTGCAGAA TCCCGTGAAC   [403]
K. uvaria SR477                    GCATCGATGA AGAACGTAGC GAAATGCGAT ACTTGGTGTG AATTGCAGAA TCCCGTGAAC   [403]

[                                            430         440         450         460         470        480]
[                                             .          .          .          .          .         .]

Bulbine latifolia SR61             CATCGAGTCT TTGAACGCAA GTTGCGCCCG AGGCCACCCG GCCGAGGGCA CGCCTGCCTG   [453]
Bulbinella cauda-felis SR204       CATCGAGTTT TTGAACGCAA GTTGCGCCCG AGGCCACCCG GCCGAGGGCA CGCCTGCCTG   [464]
K. acreae TD4626                   CATCGAGTCT TTGAACGCAA GTTGCGCCCG AAGCCACTCG GCTGAGGGCA CGCCTGCCTG   [463]
K. albescens SR314                 CATCGAGTCT TTGAACGCAA GTTGCGCCCG AAGCCACTCG GCTGAGGGCA CGCCTGCCTG   [463]
K. albomontana SR149               CATCGAGTCT TTGAACGCAA GTTGCGCCCG AAGCCACTCG GCTGAGGGCA CGCCTGCCTG   [463]
K. angustifolia SR453              CATCGAGTCT TTGAACGCAA GTTGCGCCCG AAGCCACTCG GCTGAGGGCA CGCCTGCCTG   [463]
K. angustifolia SR542              CATCGAGTCT TTGAACGCAA GTTGCGCCCG AAGCCACTCG GCTGAGGGCA CGCCTGCCTG   [463]
K. ankaratrensis PBP5676           CATCGAGTCT TTGAACGCAA GTTGCGCCCG AAGCCACTCG GCTGAGGGCA CGCCTGCCTG   [463]
K. baurii SR275                    CATCGAGTCT TTGAACGCAA GTTGCGCCCG AAGCCACTCG GCTGAGGGCA CGCCTGCCTG   [463]
K. baurii SR285                    CATCGAGTCT TTGAACGCAA GTTGCGCCCG AAGCCACTCG GCTGAGGGCA CGCCTGCCTG   [463]
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K. baurii SR360                    CATCGAGTCT TTGAACGCAA GTTGCGCCCG AAGCCACTCG GCTGAGGGCA CGCCTGCCTG   [463]
K. baurii SR382                    CATCGAGTCT TTGAACGCAA GTTGCGCCCG AAGCCACTCG GCTGAGGGCA CGCCTGCCTG   [463]
K. baurii NPB1923                  CATCGAGTCT TTGAACGCAA GTTGCGCCCG AAGCCACTCG GCTGAGGGCA CGCCTGCCTG   [463]
K. brachystachya SRsn              CATCGAGTCT TTGAACGCAA GTTGCGCCCG AAGCCACTCG GCTGAGGGCA CGCCTGCCTG   [463]
K. brevifolia SR452                CATCGAGTCT TTGAACGCAA GTTGCGCCCG AAGCCACTCG GCTGAGGGCA CGCCTGCCTG   [463]
K. bruceae SR171                   CATCGAGTCT TTGAACGCAA GTTGCGCCCG AAGCCACTCG GCTGAGGGCA CGCCTGCCTG   [463]
K. buchananii SR307                CATCGAGTCT TTGAACGCAA GTTGCGCCCG AAGCCACTCG GCTGAGGGCA CGCCTGCCTG   [463]
K. caulescens SR270                CATCGAGTCT TTGAACGCAA GTTGCGCCCG AAGCCACTCG GCTGAGGGCA CGCCTGCCTG   [463]
K. caulescens SR278                CATCGAGTCT TTGAACGCAA GTTGCGCCCG AAGCCACTCG GCTGAGGGCA CGCCTGCCTG   [463]
K. caulescens NPB1821              CATCGAGTCT TTGAACGCAA GTTGCGCCCG AAGCCACTCG GCTGAGGGCA CGCCTGCCTG   [463]
K. citrina SR176                   CATCGAGTCT TTGAACGCAA GTTGCGCCCG AAGCCACTCG GCTGAGGGCA CGCCTGCCTG   [463]
K. coddiana SRsn                   CATCGAGTCT TTGAACGCAA GTTGCGCCCG AAGCCACTCG GCTGAGGGCA CGCCTGCCTG   [463]
K. corraligemma SR549              CATCGAGTCT TTGAACGCAA GTTGCGCCCG AAGCCACTCG GCTGAGGGCA CGCCTGCCTG   [463]
K. drepanophylla RAL4816           CATCGAGTCT TTGAACGCAA GTTGCGCCCG AAGCCACTCG GCTGAGGGCA CGCCTGCCTG   [463]
K. ensifolia ensifolia JBsn        CATCGAGTCT TTGAACGCAA GTTGCGCCCG AAGCCACTCG GCTGAGGGCA CGCCTGCCTG   [463]
K. ensifolia autumnalis SR448      CATCGAGTCT TTGAACGCAA GTTGCGCCCG AAGCCACTCG GCTGAGGGCA CGCCTGCCTG   [463]
K. fibrosa SR297                   CATCGAGTCT TTGAACGCAA GTTGCGCCCG AAGCCACTCG GCTGAGGGCA CGCCTGCCTG   [463]
K. fluvitalis SRsn                 CATCGAGTCT TTGAACGCAA GTTGCGCCCG AAGCCACTCG GCTGAGGGCA CGCCTGCCTG   [463]
K. foliosa SR383                   CATCGAGTCT TTGAACGCAA GTTGCGCCCG AAGCCACTCG GCTGAGGGCA CGCCTGCCTG   [463]
K. foliosa SR387                   CATCGAGTCT TTGAACGCAA GTTGCGCCCG AAGCCACTCG GCTGAGGGCA CGCCTGCCTG   [463]
K. foliosa SR389                   CATCGAGTCT TTGAACGCAA GTTGCGCCCG AAGCCACTCG GCTGAGGGCA CGCCTGCCTG   [463]
K. foliosa SR390                   CATCGAGTCT TTGAACGCAA GTTGCGCCCG AAGCCACTCG GCTGAGGGCA CGCCTGCCTG   [463]
K. foliosa JMG034                  CATCGAGTCT TTGAACGCAA GTTGCGCCCG AAGCCACTCG GCTGAGGGCA CGCCTGCCTG   [463]
K. foliosa JMG038                  CATCGAGTCT TTGAACGCAA GTTGCGCCCG AAGCCACTCG GCTGAGGGCA CGCCTGCCTG   [463]
K. galpinii SR312                  CATCGAGTCT TTGAACGCAA GTTGCGCCCG AAGCCACTCG GCTGAGGGCA CGCCTGCCTG   [463]
K. gracilis SR321                  CATCGAGTCT TTGAACGCAA GTTGCGCCCG AAGCCACTCG GCTGAGGGCA CGCCTGCCTG   [463]
K. gracilis NNBG                   CATCGAGTCT TTGAACGCAA GTTGCGCCCG AAGCCACTCG GCTGAGGGCA CGCCTGCCTG   [463]
K. grantii CP4154                  CATCGAGTCT TTGAACGCAA GTTGCGCCCG AAGCCACTCG GCTGAGGGCA CGCCTGCCTG   [464]
K. hirsuta SR282                   CATCGAGTCT TTGAACGCAA GTTGCGCCCG AAGCCACTCG GCTGAGGGCA CGCCTGCCTG   [463]
K. ichopensis SR242                CATCGAGTCT TTGAACGCAA GTTGCGCCCG AAGCCACTCG GCTGAGGGCA CGCCTGCCTG   [463]
K. ichopensis SR286                CATCGAGTCT TTGAACGCAA GTTGCGCCCG AAGCCACTCG GCTGAGGGCA CGCCTGCCTG   [463]
K. ichopensis SR289                CATCGAGTCT TTGAACGCAA GTTGCGCCCG AAGCCACTCG GCTGAGGGCA CGCCTGCCTG   [463]
K. insignis SRsn                   CATCGAGTCT TTGAACGCAA GTTGCGCCCG AAGCCACTCG GCTGAGGGCA CGCCTGCCTG   [463]
K. isoetofolia SR386               CATCGAGTCT TTGAACGCAA GTTGCGCCCG AAGCCACTCG GCTGAGGGCA CGCCTGCCTG   [463]
K. isoetifolia SR388               CATCGAGTCT TTGAACGCAA GTTGCGCCCG AAGCCACTCG GCTGAGGGCA CGCCTGCCTG   [463]
K. isoetifolia SR393               CATCGAGTCT TTGAACGCAA GTTGCGCCCG AAGCCACTCG GCTGAGGGCA CGCCTGCCTG   [463]
K. latifolia RSSsn                 CATCGAGTCT TTGAACGCAA GTTGCGCCCG AAGCCACTCG GCTGAGGGCA CGCCTGCCTG   [463]
K. laxiflora SR283                 CATCGAGTCT TTGAACGCAA GTTGCGCCCG AAGCCACTCG GCTGAGGGCA CGCCTGCCTG   [463]
K. laxifolia SR295                 CATCGAGTCT TTGAACGCAA GTTGCGCCCG AAGCCACTCG GCTGAGGGCA CGCCTGCCTG   [463]
K. laxiflora SR467                 CATCGAGTCT TTGAACGCAA GTTGCGCCCG AAGCCACTCG GCTGAGGGCA CGCCTGCCTG   [463]
K. laxiflora SR468                 CATCGAGTCT TTGAACGCAA GTTGCGCCCG AAGCCACTCG GCTGAGGGCA CGCCTGCCTG   [463]
K. laxifloraC SRsn                 CATCGAGTCT TTGAACGCAA GTTGCGCCCG AAGCCACTCG GCTGAGGGCA CGCCTGCCTG   [463]
K. laxiflora NPB1810               CATCGAGTCT TTGAACGCAA GTTGCGCCCG AAGCCACTCG GCTGAGGGCA CGCCTGCCTG   [463]
K. leucocephala NNBG               CATCGAGTCT TTGAACGCAA GTTGCGCCCG AAGCCACTCG GCTGAGGGCA CGCCTGCCTG   [463]
K. linearifolia SR170              CATCGAGTCT TTGAACGCAA GTTGCGCCCG AAGCCACTCG GCTGAGGGCA CGCCTGCCTG   [463]
K. linearifolia SR269              CATCGAGTCT TTGAACGCAA GTTGCGCCCG AAGCCACTCG GCTGAGGGCA CGCCTGCCTG   [463]
K. linearifolia SR290              CATCGAGTCT TTGAACGCAA GTTGCGCCCG AAGCCACTCG GCTGAGGGCA CGCCTGCCTG   [463]
K. linearifolia SR291              CATCGAGTCT TTGAACGCAA GTTGCGCCCG AAGCCACTCG GCTGAGGGCA CGCCTGCCTG   [463]
K. linearifolia SR311              CATCGAGTCT TTGAACGCAA GTTGCGCCCG AAGCCACTCG GCTGAGGGCA CGCCTGCCTG   [463]
K. linearifolia SR313              CATCGAGTCT TTGAACGCAA GTTGCGCCCG AAGCCACTCG GCTGAGGGCA CGCCTGCCTG   [463]
K. linearifolia SR328              CATCGAGTCT TTGAACGCAA GTTGCGCCCG AAGCCACTCG GCTGAGGGCA CGCCTGCCTG   [463]
K. linearifolia SR343              CATCGAGTCT TTGAACGCAA GTTGCGCCCG AAGCCACTCG GCTGAGGGCA CGCCTGCCTG   [463]
K. littoralis SR200                CATCGAGTCT TTGAACGCAA GTTGCGCCCG AAGCCACTCG GCTGAGGGCA CGCCTGCCTG   [463]
K. multiflora SR310                CATCGAGTCT TTGAACGCAA GTTGCGCCCG AAGCCACTCG GCTGAGGGCA CGCCTGCCTG   [463]
K. multiflora SR315                CATCGAGTCT TTGAACGCAA GTTGCGCCCG AAGCCACTCG GCTGAGGGCA CGCCTGCCTG   [463]
K. northiae SR263                  CATCGAGTCT TTGAACGCAA GTTGCGCCCG AAGCCACTCG GCTGAGGGCA CGCCTGCCTG   [463]
K. northiae SR446                  CATCGAGTCT TTGAACGCAA GTTGCGCCCG AAGCCACTCG GCTGAGGGCA CGCCTGCCTG   [463]
K. parviflora SR268                CATCGAGTCT TTGAACGCAA GTTGCGCCCG AAGCCACTCG GCTGAGGGCA CGCCTGCCTG   [463]
K. paviflora SR330                 CATCGAGTCT TTGAACGCAA GTTGCGCCCG AAGCCACTCG GCTGAGGGCA CGCCTGCCTG   [463]
K. pauciflora HBsn                 CATCGAGTCT TTGAACGCAA GTTGCGCCCG AAGCCACTCG GCTGAGGGCA CGCCTGCCTG   [463]
K. porphyantha SRsn                CATCGAGTCT TTGAACGCAA GTTGCGCCCG AAGCCACTCG GCTGAGGGCA CGCCTGCCTG   [463]
K. praecox SR529                   CATCGAGTCT TTGAACGCAA GTTGCGCCCG AAGCCACTCG GCTGAGGGCA CGCCTGCCTG   [463]
K. rigidifolia SRsn                CATCGAGTCT TTGAACGCAA GTTGCGCCCG AAGCCACTCG GCTGAGGGCA CGCCTGCCTG   [463]
K. ritualis SR300                  CATCGAGTCT TTGAACGCAA GTTGCGCCCG AAGCCACTCG GCTGAGGGCA CGCCTGCCTG   [463]
K. rooperi SR237                   CATCGAGTCT TTGAACGCAA GTTGCGCCCG AAGCCACTCG GCTGAGGGCA CGCCTGCCTG   [463]
K. rooperi SR485                   CATCGAGTCT TTGAACGCAA GTTGCGCCCG AAGCCACTCG GCTGAGGGCA CGCCTGCCTG   [463]
K. sarmentosa SR207                CATCGAGTCT TTGAACGCAA GTTGCGCCCG AAGCCACTCG GCTGAGGGCA CGCCTGCCTG   [463]
K. schemperi SR391                 CATCGAGTCT TTGAACGCAA GTTGCGCCCG AAGCCACTCG GCTGAGGGCA CGCCTGCCTG   [463]
K. schemperi JMG036                CATCGAGTCT TTGAACGCAA GTTGCGCCCG AAGCCACTCG GCTGAGGGCA CGCCTGCCTG   [463]
K. splendida SR548                 CATCGAGTCT TTGAACGCAA GTTGCGCCCG AAGCCACTCG GCTGAGGGCA CGCCTGCCTG   [463]
K. stricta SR279                   CATCGAGTCT TTGAACGCAA GTTGCGCCCG AAGCCACTCG GCTGAGGGCA CGCCTGCCTG   [463]
K. thodei SR407                    CATCGAGTCT TTGAACGCAA GTTGCGCCCG AAGCCACTCG GCTGAGGGCA CGCCTGCCTG   [463]
K. thomsonii JMG031                CATCGAGTCT TTGAACGCAA GTTGCGCCCG AAGCCACTCG GCTGAGGGCA CGCCTGCCTG   [463]
K. thomsonii AMM                   CATCGAGTCT TTGAACGCAA GTTGCGCCCG AAGCCACTCG GCTGAGGGCA CGCCTGCCTG   [463]
K. thomsonii CK4821                CATCGAGTCT TTGAACGCAA GTTGCGCCCG AAGCCACTCG GCTGAGGGCA CGCCTGCCTG   [463]
K. triangularis SR264              CATCGAGTCT TTGAACGCAA GTTGCGCCCG AAGCCACTCG GCTGAGGGCA CGCCTGCCTG   [463]
K. triangularis SR266              CATCGAGTCT TTGAACGCAA GTTGCGCCCG AAGCCACTCG GCTGAGGGCA CGCCTGCCTG   [463]
K. triangularis SR299              CATCGAGTCT TTGAACGCAA GTTGCGCCCG AAGCCACTCG GCTGAGGGCA CGCCTGCCTG   [463]
K. triangularis obtusiloba SRsn    CATCGAGTCT TTGAACGCAA GTTGCGCCCG AAGCCACTCG GCTGAGGGCA CGCCTGCCTG   [463]
K. typhoides JB8084                CATCGAGTCT TTGAACGCAA GTTGCGCCCG AAGCCACTCG GCTGAGGGCA CGCCTGCCTG   [463]
K. typhoides NNBG                  CATCGAGTCT TTGAACGCAA GTTGCGCCCG AAGCCACTCG GCTGAGGGCA CGCCTGCCTG   [463]
K. tysonii SR302                   CATCGAGTCT TTGAACGCAA GTTGCGCCCG AAGCCACTCG GCTGAGGGCA CGCCTGCCTG   [463]
K. tysonii SR303                   CATCGAGTCT TTGAACGCAA GTTGCGCCCG AAGCCACTCG GCTGAGGGCA CGCCTGCCTG   [463]
K. umbrina RGsn                    CATCGAGTCT TTGAACGCAA GTTGCGCCCG AAGCCACTCG GCTGAGGGCA CGCCTGCCTG   [463]
K. uvaria SR186                    CATCGAGTCT TTGAACGCAA GTTGCGCCCG AAGCCACTCG GCTGAGGGCA CGCCTGCCTG   [463]
K. uvaria SR201                    CATCGAGTCT TTGAACGCAA GTTGCGCCCG AAGCCACTCG GCTGAGGGCA CGCCTGCCTG   [463]
K. uvaria SR203                    CATCGAGTCT TTGAACGCAA GTTGCGCCCG AAGCCACTCG GCTGAGGGCA CGCCTGCCTG   [463]
K. uvaria SR211                    CATCGAGTCT TTGAACGCAA GTTGCGCCCG AAGCCACTCG GCTGAGGGCA CGCCTGCCTG   [463]
K. uvaria SR342                    CATCGAGTCT TTGAACGCAA GTTGCGCCCG AAGCCACTCG GCTGAGGGCA CGCCTGCCTG   [463]
K. uvaria SR344                    CATCGAGTCT TTGAACGCAA GTTGCGCCCG AAGCCACTCG GCTGAGGGCA CGCCTGCCTG   [463]
K. uvaria SR477                    CATCGAGTCT TTGAACGCAA GTTGCGCCCG AAGCCACTCG GCTGAGGGCA CGCCTGCCTG   [463]
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[                                            490         500         510         520         530        540]
[                                            .          .          .          .          .         .]

Bulbine latifolia SR61             GGCGTCACGC ATCGCGTCGC TCCGCCAA-C CCTAACCCGG GCACAACGTG CTCCGCGGA-   [511]
Bulbinella cauda-felis SR204       GGCGTCACGC CTCGCGTCGC TCCGCTCACC CCT--CCCTT T-AGCAC-TA CGTGCTGGAG   [520]
K. acreae TD4626                   GGCGTCACGC CTCACGTCGC TCCGCGCAGC CCGCCACT-G GCACAATGTG CTTGTCGGCG   [522]
K. albescens SR314                 GGCGTCACGC CTCACGTCGC TCCGCGCAGC CCGCCACT-G GCACAATGTG CTTGTCGGCG   [522]
K. albomontana SR149               GGCGTCACGC CTCACGTCGC TCCGCGCAGC CCGCCACT-G GCACAATGTG CTTGTCGGCG   [522]
K. angustifolia SR453              GGCGTCACGC CTCACGTCGC TCCGCGCAGC CCGCCACT-G GCACAATGTG CTTGTCGGCG   [522]
K. angustifolia SR542              GGCGTCACGC CTCACGTCGC TCCGCGCAGC CCGCCACT-G GCACAATGTG CTTGTCGGCG   [522]
K. ankaratrensis PBP5676           GGCGTCACGC CTCACGTCGC TCCGCGCAGC CCGCCACT-G GCACAATGTG CTTGTCGGCG   [522]
K. baurii SR275                    GGCGTCACGC CTCACGTCGC TCCGCGCAGC CCGCCACT-G GCACAATGTG CTTGTCGGCG   [522]
K. baurii SR285                    GGCGTCACGC CTCACGTCGC TCCGCGCAGC CCGCCACT-G GCACAATGTG CTTGTCGGCG   [522]
K. baurii SR360                    GGCGTCACGC CTCACGTCGC TCCGCGCAGC CCGCCACT-G GCACAATGTG CTTGTCGGCG   [522]
K. baurii SR382                    GGCGTCACGC CTCACGTCGC TCCGCGCAGC CCGCCACT-G GCACAATGTG CTTGTCGGCG   [522]
K. baurii NPB1923                  GGCGTCACGC CTCACGTCGC TCCGCGCAGC CCGCCACT-G GCACAATGTG CTTGTCGGCG   [522]
K. brachystachya SRsn              GGCGTCACGC CTCGCGTCGC TCCGCGCAGC CCGCCACA-G GCACAATGTG CTTGTCGGCG   [522]
K. brevifolia SR452                GGCGTCACGC CTCACGTCGC TCCGCGCAGC CCGCCACT-G GCACAATGTG CTTGTCGGCG   [522]
K. bruceae SR171                   GGCGTCACGC CTCACGTCGC TCCGCGCAGC CCGCCACT-G GCACAATGTG CTTGTCGGCG   [522]
K. buchananii SR307                GGCGTCACGC CTCACGTCGC TCCGCGCAGC CCGCCACT-G GCACAATGTG CTTGTCGGCG   [522]
K. caulescens SR270                GGCGTCACGC CTCACGTCGC TCCGCGCACC CCGCCACT-G GCACAATGTG CTTGTCGGCG   [522]
K. caulescens SR278                GGCGTCACGC CTCACGTCGC TCCGCGCAGC CCGCCACT-G GCACAATGTG CTTGTCGGCG   [522]
K. caulescens NPB1821              GGCGTCACGC CTCACGTCGC TCCGCGCACC CCGCCACT-G GCACAATGTG CTTGTCGGCG   [522]
K. citrina SR176                   GGCGTCACGC CTCACGTCGC TCCGCGCAGC CCGCCACT-G GCACAATGTG CTTGTCGGCG   [522]
K. coddiana SRsn                   GGCGTCACGC CTCACGTCGC TCCGCGCAGC CCGCCACT-G GCACAATGTG CTTGTCGGCG   [522]
K. corraligemma SR549              GGCGTCACGC CTCACGTCGC TCCGCGCAGC CCGCCACT-G GCACAATGTG CTTGTCGGCG   [522]
K. drepanophylla RAL4816           GGCGTCACGC CTCACGTCGC TCCGCGCAGC CCGCCACT-G GCACAATGTG CTTGTCGGCG   [522]
K. ensifolia ensifolia JBsn        GGCGTCACGC CTCACGTCGC TCCGCGCAGC CCGCCACT-G GCACAATGTG CTTGTCGGCG   [522]
K. ensifolia autumnalis SR448      GGCGTCACGC CTCACGTCGC TCCGCGCAGC CCGCCACT-G GCACAATGTG CTTGTCGGCG   [522]
K. fibrosa SR297                   GGCGTCACGC CTCACGTCGC TCCGCGCAGC CCGCCACT-G GCACAATGTG CTTGTCGGCG   [522]
K. fluvitalis SRsn                 GGCGTCACGC CTCACGTCGC TCCGCGCAGC CCGCCACT-G GCACAATGTG CTTGTCGGCG   [522]
K. foliosa SR383                   GGCGTCACGC CTCACGTCGC TCCGCGCAGC CCGCCACT-A GCACAGTGTG CTTGTCGGCG   [522]
K. foliosa SR387                   GGCGTCACGC CTCACGTCGC TCCGCGCAGC CCGCCACT-A GCACAGTGTG CTTGTCGGCG   [522]
K. foliosa SR389                   GGCGTCACGC CTCACGTCGC TCCGCGCAGC CCGCCACT-A GCACAGTGTG CTTGTCGGCG   [522]
K. foliosa SR390                   GGCGTCACGC CTCACGTCGC TCCGCGCAGC CCGCCACT-A GCACAGTGTG CTTGTCGGCG   [522]
K. foliosa JMG034                  GGCGTCACGC CTCACGTCGC TCCGCGCAGC CCGCCACT-A GCACAGTGTG CTTGTCGGCG   [522]
K. foliosa JMG038                  GGCGTCACGC CTCACGTCGC TCCGCGCAGC CCGCCACT-A GCACAGTGTG CTTGTCGGCG   [522]
K. galpinii SR312                  GGCGTCACGC CTCACGTCGC TCCGCGCAGC CCGCCACT-G GCACAATGTG CTTGTCGGCG   [522]
K. gracilis SR321                  GGCGTCACGC CTCACGTCGC TCCGCGCAGC CCGCCACT-G GCACAATGTG CTTGTCGGCG   [522]
K. gracilis NNBG                   GGCGTCACGC CTCACGTCGC TCCGCGCAGC CCGCCACT-G GCACAATGTG CTTGTCGGCG   [522]
K. grantii CP4154                  GGCGTCACGC CTCACGTCGC TCCGCGCAGC CCGCCACT-G GCACAATGTG CTTGTCGGCG   [523]
K. hirsuta SR282                   GGCGTCACGC CTCACGTCGC TCCGCGCAGC CCGCCACT-G GCACAATGTG CTTGTCGGCG   [522]
K. ichopensis SR242                GGCGTCACGC CTCACGTCGC TCCGCGCAGC CCGCCACT-G GCACAATGTG CTTGTCGGCG   [522]
K. ichopensis SR286                GGCGTCACGC CTCACGTCGC TCCGCGCAGC CCGCCACT-G GCACAATGTG CTTGTCGGCG   [522]
K. ichopensis SR289                GGCGTCACGC CTCACGTCGC TCCGCGCAGC CCGCCACT-G GCACAATGTG CTTGTCGGCG   [522]
K. insignis SRsn                   GGCGTCACGC CTCACGTCGC TCCGCGCAGC CCGCCACT-A GCACAGTGTG CTTGTCGGCG   [522]
K. isoetofolia SR386               GGCGTCACGC CTCACGTCGC TCCGCGCAGC CCGCCACT-A GCACAGTGTG CTTGTCGGCG   [522]
K. isoetifolia SR388               GGCGTCACGC CTCACGTCGC TCCGCGCAGC CCGCCACT-A GCACAGTGTG CTTGTCGGCG   [522]
K. isoetifolia SR393               GGCGTCACGC CTCACGTCGC TCCGCGCAGC CCGCCACT-A GCACAGTGTG CTTGTCGGCG   [522]
K. latifolia RSSsn                 GGCGTCACGC CTCACGTCGC TCCGCGCAGC CCGCCACT-G GCACAATGTG CTTGTCGGCG   [522]
K. laxiflora SR283                 GGCGTCACGC CTCACGTCGC TCCGCGCAGC CCGCCACT-G GCACAATGTG CTTGTCGGCG   [522]
K. laxifolia SR295                 GGCGTCACGC CTCACGTCGC TCCGCGCAGC CCGCCACT-G GCACAATGTG CTTGTCGGCG   [522]
K. laxiflora SR467                 GGCGTCACGC CTCACGTCGC TCCGCGCAGC CCGCCACT-G GCACAATGTG CTTGTCGGCG   [522]
K. laxiflora SR468                 GGCGTCACGC CTCACGTCGC TCCGCGCAGC CCGCCACT-G GCACAATGTG CTTGTCGGCG   [522]
K. laxifloraC SRsn                 GGCGTCACGC CTCACGTCGC TCCGCGCAGC CCGCCACT-G GCACAATGTG CTTGTCGGCG   [522]
K. laxiflora NPB1810               GGCGTCACGC CTCACGTCGC TCCGCGCAGC CCGCCACT-G GCACAATGTG CTTGTCGGCG   [522]
K. leucocephala NNBG               GGCGTCACGC CTCACGTCGC TCCGCGCAGC CCGCCACT-G GCACAATGTG CTTGTCGGCG   [522]
K. linearifolia SR170              GGCGTCACGC CTCACGTCGC TCCGCGCAGC CCGCCACT-G GCACAATGTG CTTGTCGGCG   [522]
K. linearifolia SR269              GGCGTCACGC CTCACGTCGC TCCGCGCAGC CCGCCACT-G GCACAATGTG CTTGTCGGCG   [522]
K. linearifolia SR290              GGCGTCACGC CTCACGTCGC TCCGCGCAGC CCGCCACT-G GCACAATGTG CTTGTCGGCG   [522]
K. linearifolia SR291              GGCGTCACGC CTCACGTCGC TCCGCGCAGC CCGCCACT-G GCACAATGTG CTTGTCGGCG   [522]
K. linearifolia SR311              GGCGTCACGC CTCACGTCGC TCCGCGCAGC CCGCCACT-G GCACAATGTG CTTGTCGGCG   [522]
K. linearifolia SR313              GGCGTCACGC CTCACGTCGC TCCGCGCAGC CCGCCACT-G GCACAATGTG CTTGTCGGCG   [522]
K. linearifolia SR328              GGCGTCACGC CTCACGTCGC TCCGCGCAGC CCGCCACT-G GCACAATGTG CTTGTCGGCG   [522]
K. linearifolia SR343              GGCGTCACGC CTCACGTCGC TCCGCGCAGC CCGCCACT-G GCACAATGTG CTTGTCGGCG   [522]
K. littoralis SR200                GGCGTCACGC CTCACGTCGC TCCGCGCAGC CCGCCACT-G GCACAATGTG CTTGTCGGCG   [522]
K. multiflora SR310                GGCGTCACGC CTCACGTCGC TCCGCGCAGC CCGCCACT-G GCACAATGTG CTTGTCGGCG   [522]
K. multiflora SR315                GGCGTCACGC CTCACGTCGC TCCGCGCAGC CCGCCACT-G GCACAATGTG CTTGTCGGCG   [522]
K. northiae SR263                  GGCGTCACGC CTCACGTCGC TCCGCGCAGC CCGCCACT-G GCACAATGTG CTTGTCGGCG   [522]
K. northiae SR446                  GGCGTCACGC CTCACGTCGC TCCGCGCAGC CCGCCACT-G GCACAATGTG CTTGTCGGCG   [522]
K. parviflora SR268                GGCGTCACGC CTCACGTCGC TCCGCGCAGC CCGCCACT-G GCACAATGTG CTTGTCGGCG   [522]
K. paviflora SR330                 GGCGTCACGC CTCACGTCGC TCCGCGCAGC CCGCCACT-G GCACAATGTG CTTGTCGGCG   [522]
K. pauciflora HBsn                 GGCGTCACGC CTCACGTCGC TCCGCGCAGC CCGCCACT-G GCACAATGTG CTTGTCGGCG   [522]
K. porphyantha SRsn                GGCGTCACGC CTCACGTCGC TCCGCGCAGC CCGCCACT-G GCACAATGTG CTTGTCGGCG   [522]
K. praecox SR529                   GGCGTCACGC CTCACGTCGC TCCGCGCAGC CCGCCACT-G GCACAATGTG CTTGTCGGCG   [522]
K. rigidifolia SRsn                GGCGTCACGC CTCACGTCGC TCCGCGCAGC CCGCCACT-G GCACAATGTG CTTGTCGGCG   [522]
K. ritualis SR300                  GGCGTCACGC CTCACGTCGC TCCGCGCAGC CCGCCACT-G GCACAATGTG CTTGTCGGCG   [522]
K. rooperi SR237                   GGCGTCACGC CTCACGTCGC TCCGCGCAGC CCGCCACT-G GCACAATGTG CTTGTCGGCG   [522]
K. rooperi SR485                   GGCGTCACGC CTCACGTCGC TCCGCGCAGC CCGCCACT-G GCACAATGTG CTTGTCGGCG   [522]
K. sarmentosa SR207                GGCGTCACGC CTCGCGTCGC TCCGCGCAGC CCGCCGCT-G GCACAATGTG CTTGTCGGCG   [522]
K. schemperi SR391                 GGCGTCACGC CTCACGTCGC TCCGCGCAGC CCGCCACT-A GCACAGTGTG CTTGTCGGCG   [522]
K. schemperi JMG036                GGCGTCACGC CTCACGTCGC TCCGCGCAGC CCGCCACT-A GCACAGTGTG CTTGTCGGCG   [522]
K. splendida SR548                 GGCGTCACGC CTCACGTCGC TCCGCGCAGC CCGCCACT-G GCACAATGTG CTTGTCGGCG   [522]
K. stricta SR279                   GGCGTCACGC CTCACGTCGC TCCACGCACC CCGCCACT-G GCACAATGTG CTTGTCGGCG   [522]
K. thodei SR407                    GGCGTCACGC CTCACGTCGC TCCGCGCAGC CCGCCACT-G GCACAATGTG CTTGTCGGCG   [522]
K. thomsonii JMG031                GGCGTCACGC CTCACGTCGC TCCGCGCAGC CCGCCACT-A GCACAGTGTG CTTGTCGGCG   [522]
K. thomsonii AMM                   GGCGTCACGC CTCACGTCGC TCCGCGCAGC CCGCCACT-G GCACAATGTG CTTGTCGGCG   [522]
K. thomsonii CK4821                GGCGTCACGC CTCACGTCGC TCCGCGCAGC CCGCCACT-G GCACAATGTG CTTGTCGGCG   [522]
K. triangularis SR264              GGCGTCACGC CTCACGTCGC TCCGCGCAGC CCGCCACT-G GCACAATGTG CTTGTCGGCG   [522]
K. triangularis SR266              GGCGTCACGC CTCACGTCGC TCCGCGCAGC CCGCCACT-G GCACAATGTG CTTGTCGGCG   [522]
K. triangularis SR299              GGCGTCACGC CTCACGTCGC TCCGCGCAGC CCGCCACT-G GCACAATGTG CTTGTCGGCG   [522]
K. triangularis obtusiloba SRsn    GGCGTCACGC CTAACGTCGC TCCGCGCAGC CCGCCACT-G GCACAATGTG CTTGTCGGCG   [522]
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K. typhoides JB8084                GGCGTCACGC CTCGCGTCGC TCCGCGCAGC CCGCCACA-G GCACAATGTG CTTGTCGGCG   [522]
K. typhoides NNBG                  GGCGTCACGC CTCGCGTCGC TCCGCGCAGC CCGCCACA-G GCACAATGTG CTTGTCGGCG   [522]
K. tysonii SR302                   GGCGTCACGC CTCACGTCGC TCCGCGCAGC CCGCCACT-G GCACAATGTG CTTGTCGGCG   [522]
K. tysonii SR303                   GGCGTCACGC CTCACGTCGC TCCGCGCAGC CCGCCACT-G GCACAATGTG CTTGTCGGCG   [522]
K. umbrina RGsn                    GGCGTCACGC CTCACGTCGC TCCGCGCAGC CCGCCACT-G GCACAATGTG CTTGTCGGCG   [522]
K. uvaria SR186                    GGCGTCACGC CTCACGTCGC TCCGCGCAGC CCGCCACT-G GCACAATGTG CTTGTCGGCG   [522]
K. uvaria SR201                    GGCGTCACGC CTCACGTCGC TCCGCGCAGC CCGCCACT-G GCACAATGTG CTTGTCGGCG   [522]
K. uvaria SR203                    GGCGTCACGC CTCACGTCGC TCCGCGCAGC CCGCCACT-G GCACAATGTG CTTGTCGGCG   [522]
K. uvaria SR211                    GGCGTCACGC CTCACGTCGC TCCGCGCAGC CCGCCACT-G GCACAATGTG CTTGTCGGCG   [522]
K. uvaria SR342                    GGCGTCACGC CTCACGTCGC TCCGCGCAGC CCGCCACT-G GCACAATGTG CTTGTCGGCG   [522]
K. uvaria SR344                    GGCGTCACGC CTCACGTCGC TCCGCGCAGC CCGCCACT-G GCACAATGTG CTTGTCGGCG   [522]
K. uvaria SR477                    GGCGTCACGC CTCACGTCGC TCCGCGCAGC CCGCCACT-G GCACAATGTG CTTGTCGGCG   [522]

[                                            550         560         570         580         590        600]
[                                            .          .          .          .          .         .]

Bulbine latifolia SR61             ---------G G--GCGGCGG ACGCGGAGAT TGACCCTCCG TGCCTCCCGG CGCGGTGGGT   [560]
Bulbinella cauda-felis SR204       TG--GCGGCG G-T-CGGCGG ACGCGGAGAT TGGCCCTCCG TGCCTCGCGG TGCGGTGGGT   [576]
K. acreae TD4626                   TCCCGCGTCG GATGCGG--- ------AGAT TGGCCCTCCG TGCCTCGCGG TGCGGTGGGT   [573]
K. albescens SR314                 TCCCGCGTCG GATGCGG--- ------AGAT TGGCCCTCCG TGCCTCGCGG TGCGGTGGGT   [573]
K. albomontana SR149               TCCCGCGTCG GATGCGG--- ------AGAT TGGCCCTCCG TGCCTCGCGG TGCGGTGGGT   [573]
K. angustifolia SR453              TCCCGCGTCG GATGCGG--- ------AGAT TGGCCCTCCG TGCCTCGCGG TGCGGTGGGT   [573]
K. angustifolia SR542              TCCCGCGTCG GATGCGG--- ------AGAT TGGCCCTCCG TGCCTCGCGG TGCGGTGGGT   [573]
K. ankaratrensis PBP5676           TCCCGCGTCG GATGCGG--- ------AGAT TGGCCCTCCG TGCCTCGCGG TGCGGTGGGT   [573]
K. baurii SR275                    TCCCGCGTCG GATGCGG--- ------AGAT TGGCCCTCCG TGCCTCGCGG TGCGGTGGGT   [573]
K. baurii SR285                    TCCCGCGTCG GATGCGG--- ------AGAT TGGCCCTCCG TGCCTCGCGG TGCGGTGGGT   [573]
K. baurii SR360                    TCCCGCGTCG GATGCGG--- ------AGAT TGGCCCTCCG TGCCTCGCGG TGCGGTGGGT   [573]
K. baurii SR382                    TCCCGCGTCG GATGCGG--- ------AGAT TGGCCCTCCG TGCCTCGCGG TGCGGTGGGT   [573]
K. baurii NPB1923                  TCCCGCGTCG GATGCGG--- ------AGAT TGGCCCTCCG TGCCTCGCGG TGCGGTGGGT   [573]
K. brachystachya SRsn              TCCCGCGTCG GATGCGG--- ------AGAT TGGCCCTCCG TGCCTCGCGG TGCGGTGGGT   [573]
K. brevifolia SR452                TCCCGCGTCG GATGCGG--- ------AGAT TGGCCCTCCG TGCCTCGCGG TGCGGTGGGT   [573]
K. bruceae SR171                   TCCCGCGTCG GATGCGG--- ------AGAT TGGCCCTCCG TGCCTCGCGG TGCGGTGGGT   [573]
K. buchananii SR307                TCCCGCGTCG GATGCGG--- ------AGAT TGGCCCTCCG TGCCTCGCGG TGCGGTGGGT   [573]
K. caulescens SR270                TCCCGCGTCG GATGCGG--- ------AGAT TGGCCCTCCG TGCCTCGCGG TGCGGTGGGT   [573]
K. caulescens SR278                TCCCGCGTCG GATGCGG--- ------AGAT TGGCCCTCCG TGCCTCGCGG TGCGGTGGGT   [573]
K. caulescens NPB1821              TCCCGCGTCG GATGCGG--- ------AGAT TGGCCCTCCG TGCCTCGCGG TGCGGTGGGT   [573]
K. citrina SR176                   TCCCGCGTCG GATGCGG--- ------AGAT TGGCCCTCCG TGCCTCGCGG TGCGGTGGGT   [573]
K. coddiana SRsn                   TCCCGCGTCG GATGCGG--- ------AGAT TGGCCCTCCG TGCCTCGCGG TGCGGTGGGT   [573]
K. corraligemma SR549              TCCCGCGTCG GATGCGG--- ------AGAT TGGCCCTCCG TGCCTCGCGG TGCGGTGGGT   [573]
K. drepanophylla RAL4816           TCCCGCGTCG GATGCGG--- ------AGAT TGGCCCTCCG TGCCTCGCGG TGCGGTGGGT   [573]
K. ensifolia ensifolia JBsn        TCCCGCGTCG GATGCGG--- ------AGAT TGGCCCTCCG TGCCTCGCGG TGCGGTGGGT   [573]
K. ensifolia autumnalis SR448      TCCCGCGTCG GATGCGG--- ------AGAT TGGCCCTCCG TGCCTCGCGG TGCGGTGGGT   [573]
K. fibrosa SR297                   TCCCGCGTCG GATGCGG--- ------AGAT TGGCCCTCCG TGCCTCGCGG TGCGGTGGGT   [573]
K. fluvitalis SRsn                 TCCCGCGTCG GATGCGG--- ------AGAT TGGCCCTCCG TGCCTCGCGG TGCGGTGGGT   [573]
K. foliosa SR383                   TCCCGCGTCG GATGCGG--- ------AGAT TGGCCCTCCG TGCCTCGCGG TGCGGTGGGT   [573]
K. foliosa SR387                   TCCCGCGTCG GATGCGG--- ------AGAT TGGCCCTCCG TGCCTCGCGG TGCGGTGGGT   [573]
K. foliosa SR389                   TCCCGCGTCG GATGCGG--- ------AGAT TGGCCCTCCG TGCCTCGCGG TGCGGTGGGT   [573]
K. foliosa SR390                   TCCCGCGTCG GATGCGG--- ------AGAT TGGCCCTCCG TGCCTCGCGG TGCGGTGGGT   [573]
K. foliosa JMG034                  TCCCGCGTCG GATGCGG--- ------AGAT TGGCCCTCCG TGCCTCGCGG TGCGGTGGGT   [573]
K. foliosa JMG038                  TCCCGCGTCG GATGCGG--- ------AGAT TGGCCCTCCG TGCCTCGCGG TGCGGTGGGT   [573]
K. galpinii SR312                  TCCCGCGTCG GATGCGG--- ------AGAT TGGCCCTCCG TGCCTCGCGG TGCGGTGGGT   [573]
K. gracilis SR321                  TCCCGCGTCG GATGCGG--- ------AGAT TGGCCCTCCG TGCCTCGCGG TGCGGTGGGT   [573]
K. gracilis NNBG                   TCCCGCGTCG GATGCGG--- ------AGAT TGGCCCTCCG TGCCTCGCGG TGCGGTGGGT   [573]
K. grantii CP4154                  TCCCGCGTCG GATGCGG--- ------AGAT TGGCCCTCCG TGCCTCGCGG TGCGGTGGGT   [574]
K. hirsuta SR282                   TCCCGCGTCG GATGCGG--- ------AGAT TGGCCCTCCG TGCCTCGCGG TGCGGTGGGT   [573]
K. ichopensis SR242                TCCCGCGTAG GATGCGG--- ------AGAT TGGCCCTCCG TGCCTCGCGG TGCGGTGGGT   [573]
K. ichopensis SR286                TCCCGCGTCG GATGCGG--- ------AGAT TGGCCCTCCG TGCCTCGCGG TGCGGTGGGT   [573]
K. ichopensis SR289                TCCCGCGTCG GATGCGG--- ------AGAT TGGCCCTCCG TGCCTCGCGG TGCGGTGGGT   [573]
K. insignis SRsn                   TCCCGCGTCG GATGCGG--- ------AGAT TGGCCCTCCG TGCCTCGCGG TGCGGTGGGT   [573]
K. isoetofolia SR386               TCCCGCGTCG GATGCGG--- ------AGAT TGGCCCTCCG TGCCTCGCGG TGCGGTGGGT   [573]
K. isoetifolia SR388               TCCCGCGTCG GATGCGG--- ------AGAT TGGCCCTCCG TGCCTCGCGG TGCGGTGGGT   [573]
K. isoetifolia SR393               TCCCGCGTCG GATGCGG--- ------AGAT TGGCCCTCCG TGCCTCGCGG TGCGGTGGGT   [573]
K. latifolia RSSsn                 TCCCGCGTCG GATGCGG--- ------AGAT TGGCCCTCCG TGCCTCGCGG TGCGGTGGGT   [573]
K. laxiflora SR283                 TCCCGCGTCG GATGCGG--- ------AGAT TGGCCCTCCG TGCCTCGCGG TGCGGTGGGT   [573]
K. laxifolia SR295                 TCCCGCGTCG GATGCGG--- ------AGAT TGGCCCTCCG TGCCTCGCGG TGCGGTGGGT   [573]
K. laxiflora SR467                 TCCCGCGTCG GATGCGG--- ------AGAT TGGCCCTCCG TGCCTCGCGG TGCGGTGGGT   [573]
K. laxiflora SR468                 TCCCGCGTCG GATGCGG--- ------AGAT TGGCCCTCCG TGCCTCGCGG TGCGGTGGGT   [573]
K. laxifloraC SRsn                 TCCCGCGTCG GATGCGG--- ------AGAT TGGCCCTCCG TGCCTCGCGG TGCGGTGGGT   [573]
K. laxiflora NPB1810               TCCCGCGTCG GATGCGG--- ------AGAT TGGCCCTCCG TGCCTCGCGG TGCGGTGGGT   [573]
K. leucocephala NNBG               TCCCGCGTCG GATGCGG--- ------AGAT TGGCCCTCCG TGCCTCGCGG TGCGGTGGGT   [573]
K. linearifolia SR170              TCCCGCGTCG GATGCGG--- ------AGAT TGGCCCTCCG TGCCTCGCGG TGCGGTGGGT   [573]
K. linearifolia SR269              TCCCGCGTCG GATGCGG--- ------AGAT TGGCCCTCCG TGCCTCGCGG TGCGGTGGGT   [573]
K. linearifolia SR290              TCCCGCGTCG GATGCGG--- ------AGAT TGGCCCTCCG TGCCTCGCGG TGCGGTGGGT   [573]
K. linearifolia SR291              TCCCGCGTCG GATGCGG--- ------AGAT TGGCCCTCCG TGCCTCGCGG TGCGGTGGGT   [573]
K. linearifolia SR311              TCCCGCGTCG GATGCGG--- ------AGAT TGGCCCTCCG TGCCTCGCGG TGCGGTGGGT   [573]
K. linearifolia SR313              TCCCGCGTCG GATGCGG--- ------AGAT TGGCCCTCCG TGCCTCGCGG TGCGGTGGGT   [573]
K. linearifolia SR328              TCCCGCGTCG GATGCGG--- ------AGAT TGGCCCTCCG TGCCTCGCGG TGCGGTGGGT   [573]
K. linearifolia SR343              TCCCGCGTCG GATGCGG--- ------AGAT TGGCCCTCCG TGCCTCGCGG TGCGGTGGGT   [573]
K. littoralis SR200                TCCCGCGTCG GATGCGG--- ------AGAT TGGCCCTCCG TGCCTCGCGG TGCGGTGGGT   [573]
K. multiflora SR310                TCCCGCGTCG GATGCGG--- ------AGAT TGGCCCTCCG TGCCTCGCGG TGCGGTGGGT   [573]
K. multiflora SR315                TCCCGCGTCG GATGCGG--- ------AGAT TGGCCCTCCG TGCCTCGCGG TGCGGTGGGT   [573]
K. northiae SR263                  TCCCGCGTCG GATGCGG--- ------AGAT TGGCCCTCCG TGCCTCGCGG TGCGGTGGGT   [573]
K. northiae SR446                  TCCCGCGTCG GATGCGG--- ------AGAT TGGCCCTCCG TGCCTCGCGG TGCGGTGGGT   [573]
K. parviflora SR268                TCCCGCGTCG GATGCGG--- ------AGAT TGGCCCTCCG TGCCTCGCGG TGCGGTGGGT   [573]
K. paviflora SR330                 TCCCGCGTCG GATGCGG--- ------AGAT TGGCCCTCCG TGCCTCGCGG TGCGGTGGGT   [573]
K. pauciflora HBsn                 TCCCGCGTAG GATGCGG--- ------AGAT TGGCCCTCCG TGCCTCGCGG TGCGGTGGGT   [573]
K. porphyantha SRsn                TCCCGCGTCG GATGCGG--- ------AGAT TGGCCCTCCG TGCCTCGCGG TGCGGTGGGT   [573]
K. praecox SR529                   TCCCGCGTCG GATGCGG--- ------AGAT TGGCCCTCCG TGCCTCGCGG TGCGGTGGGT   [573]
K. rigidifolia SRsn                TCCCGCGTCG GATGCGG--- ------AGAT TGGCCCTCCG TGCCTCGCGG TGCGGTGGGT   [573]
K. ritualis SR300                  TCCCGCGTCG GATGCGG--- ------AGAT TGGCCCTCCG TGCCTCGCGG TGCGGTGGGT   [573]
K. rooperi SR237                   TCCCGCGTCG GATGCGG--- ------AGAT TGGCCCTCCG TGCCTCGCGG TGCGGTGGGT   [573]
K. rooperi SR485                   TCCCGCGTCG GATGCGG--- ------AGAT TGGCCCTCCG TGCCTCGCGG TGCGGTGGGT   [573]
K. sarmentosa SR207                TCCCGCGTCG GATGCGG--- ------AGAT TGGCCCTCCG TGCCTCGCGG TGCGGTGGGT   [573]
K. schemperi SR391                 TCCCGCGTCG GATGCGG--- ------AGAT TGGCCCTCCG TGCCTCGCGG TGCGGTGGGT   [573]
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K. schemperi JMG036                TCCCGCGTCG GATGCGG--- ------AGAT TGGCCCTCCG TGCCTCGCGG TGCGGTGGGT   [573]
K. splendida SR548                 TCCCGCGTCG GATGCGG--- ------AGAT TGGCCCTCCG TGCCTCGCGG TGCGGTGGGT   [573]
K. stricta SR279                   TCCCGCGTCG GATGCGG--- ------AGAT TGGCCCTCCG TGCCTCGCGG TGCGGTGGGT   [573]
K. thodei SR407                    TCCCGCGTCG GATGCGG--- ------AGAT TGGCCCTCCG TGCCTCGCGG TGCGGTGGGT   [573]
K. thomsonii JMG031                TCCCGCGTCG GATGCGG--- ------AGAT TGGCCCTCCG TGCCTCGCGG TGCGGTGGGT   [573]
K. thomsonii AMM                   TCTCGCGTCG GATGCGG--- ------AGAT TGGCCCTCCG TGCCTCGCGG TGCGGTGGGT   [573]
K. thomsonii CK4821                TCTCGCGTCG GATGCGG--- ------AGAT TGGCCCTCCG TGCCTCGCGG TGCGGTGGGT   [573]
K. triangularis SR264              TCCCGCGTCG GATGCGG--- ------AGAT TGGCCCTCCG TGCCTCGCGG TGCGGTGGGT   [573]
K. triangularis SR266              TCCCGCGTCG GATGCGG--- ------AGAT TGGCCCTCCG TGCCTCGCGG TGCGGTGGGT   [573]
K. triangularis SR299              TCCCGCGTCG GATGCGG--- ------AGAT TGGCCCTCCG TGCCTCGCGG TGCGGTGGGT   [573]
K. triangularis obtusiloba SRsn    TCCCGCGTCG GATGCGG--- ------AGAT TGGCCCTCCG TGCCTCGCGG TGCGGTGGGT   [573]
K. typhoides JB8084                TCCCGCGTCG GATGCGG--- ------AGAT TGGCCCTCCG TGCCTCGCGG TGCGGTGGGT   [573]
K. typhoides NNBG                  TCCCGCGTCG GATGCGG--- ------AGAT TGGCCCTCCG TGCCTCGCGG TGCGGTGGGT   [573]
K. tysonii SR302                   TCCCGCGTCG GATGCGG--- ------AGAT TGGCCCTCCG TGCCTCGCGG TGCGGTGGGT   [573]
K. tysonii SR303                   TCCCGCGTCG GATGCGG--- ------AGAT TGGCCCTCCG TGCCTCGCGG TGCGGTGGGT   [573]
K. umbrina RGsn                    TCCCGCGTCG GATGCGG--- ------AGAT TGGCCCTCCG TGCCTCGCGG TGCGGTGGGT   [573]
K. uvaria SR186                    TCCCGCGTCG GATGCGG--- ------AGAT TGGCCCTCCG TGCCTCGCGG TGCGGTGGGT   [573]
K. uvaria SR201                    TCCCGCGTCG GATGCGG--- ------AGAT TGGCCCTCCG TGCCTCGCGG TGCGGTGGGT   [573]
K. uvaria SR203                    TCCCGCGTCG GATGCGG--- ------AGAT TGGCCCTCCG TGCCTCGCGG TGCGGTGGGT   [573]
K. uvaria SR211                    TCCCGCGTCG GATGCGG--- ------AGAT TGGCCCTCCG TGCCTCGCGG TGCGGTGGGT   [573]
K. uvaria SR342                    TCCCGCGTCG GATGCGG--- ------AGAT TGGCCCTCCG TGCCTCGCGG TGCGGTGGGT   [573]
K. uvaria SR344                    TCCCGCGTCG GATGCGG--- ------AGAT TGGCCCTCCG TGCCTCGCGG TGCGGTGGGT   [573]
K. uvaria SR477                    TCCCGCGTCG GATGCGG--- ------AGAT TGGCCCTCCG TGCCTCGCGG TGCGGTGGGT   [573]

[                                            610         620         630         640         650        660]
[                                            .          .          .          .          .         .]

Bulbine latifolia SR61             CGAAGTGTCG GTCGTCGGTC GAGCTTGGCA CGGCGAGTGG TGGACGGACA TGATCCTGAG   [620]
Bulbinella cauda-felis SR204       CAAAGTGCCG GTCGCCGGCC GGGCTTGGCA CGGCGAGTGG TGGACGGACA TGCTCCTGAG   [636]
K. acreae TD4626                   TGAAGTTTCT CACGCCGGTC GGGCCGGGCA CGGCGAGTGG TGGACGGACA CGCTCCTGAT   [633]
K. albescens SR314                 TGAAGTTTCT CACGCCGGTC GGGCCGGGCA CGGCGAGTGG TGGACGGACA CGCTCCTGAT   [633]
K. albomontana SR149               TGAAGTTTCT CACGCCGGTC GGGCCGGGCA CGGCGAGTGG TGGACGGACA CGCTCCTGAT   [633]
K. angustifolia SR453              TGAAGTTTCT CACGCCGGTC GGGCCGGGCA CGGCGAGTGG TGGACGGACA CGCTCCTGAT   [633]
K. angustifolia SR542              TGAAGTTTCT CACGCCGGTC GGGCCGGGCA CGGCGAGTGG TGGACGGACA CGCTCCTGAT   [633]
K. ankaratrensis PBP5676           TGAAGTTTCT CACGCCGGTC GGGCCGGGCA CGGCGAGTGG TGGACGGACA CGCTCCTGAT   [633]
K. baurii SR275                    TGAAGTTTCT CACGCCGGTC GGGCCGGGCA CGGCGAGTGG TGGACGGACA CGCTCCTGAT   [633]
K. baurii SR285                    TGAAGTTTCT CACGCCGGTC GGGCCGGGCA CGGCGAGTGG TGGACGGACA CGCTCCTGAT   [633]
K. baurii SR360                    TGAAGTTTCT CACGCCGGTC GGGCCGGGCA CGGCGAGTGG TGGACGGACA CGCTCCTGAT   [633]
K. baurii SR382                    TGAAGTTTCT CACGCCGGTC GGGCCGGGCA CGGCGAGTGG TGGACGGACA CGCTCCTGAT   [633]
K. baurii NPB1923                  TGAAGTTTCT CACGCCGGTC GGGCCGGGCA CGGCGAGTGG TGGATGGACA CGCTCCTGAT   [633]
K. brachystachya SRsn              TGAAGTTTCT CACGTCGGTC GGGCCGGGCA CGGCGAGTGG TGGACGGACA CGCTCCTGAT   [633]
K. brevifolia SR452                TGAAGTTTCT CACGCCGGTC GGGCCGGGCA CGGCGAGTGG TGGACGGACA CGCTCCTGAT   [633]
K. bruceae SR171                   TGAAGTTTCT CACGCCGGTC GGGCCGGGCA CGGCGAGTGG TGGACGGACA CGCTCCTGAT   [633]
K. buchananii SR307                TGAAGTTTCT CACGCCGGTC GGGCCGGGCA CGGCGAGTGG TGGACGGACA CGCTCCTGAT   [633]
K. caulescens SR270                TGAAGTTTCT CACGCCGGTC GGGCCGGGCA CGGCGAGTGG TGGACGGACA CGCTCCTGAT   [633]
K. caulescens SR278                TGAAGTTTCT CACGCCGGTC GGGCCGGGCA CGGCGAGTGG TGGACGGACA CGCTCCTGAT   [633]
K. caulescens NPB1821              TGAAGTTTCT CACGCCGGTC GGGCCGGGCA CGGCGAGTGG TGGACGGACA CGCTCCTGAT   [633]
K. citrina SR176                   TGAAGTTTCT CACGCCGGTC GGGCCGGGCA CGGCGAGTGG TGGACGGACA CGCTCCTGAT   [633]
K. coddiana SRsn                   TGAAGTTTCT CACGCCGGTC GGGCCGGGCA CGGCGAGTGG TGGACGGACA CGCTCCTGAT   [633]
K. corraligemma SR549              TGAAGTTTCT CACGCCGGTC GGGCCGGGCA CGGCGAGTGG TGGACGGACA CGCTCCTGAT   [633]
K. drepanophylla RAL4816           TGAAGTTTCT CACGCCGGTC GGGCCGGGCA CGGCGAGTGG TGGACGGACA CGCTCCTGAT   [633]
K. ensifolia ensifolia JBsn        TGAAGTTTCT CACGCCGGTC GGGCCGGGCA CGGCGAGTGG TGGACGGACA CGCTCCTGAT   [633]
K. ensifolia autumnalis SR448      TGAAGTTTCT CACGCCGGTC GGGCCGGGCA CGGCGAGTGG TGGACGGACA CGCTCCTGAT   [633]
K. fibrosa SR297                   TGAAGTTTCT CACGCCGGTC GGGCCGGGCA CGGCGAGTGG TGGACGGACA CGCTCCTGAT   [633]
K. fluvitalis SRsn                 TGAAGTTTCT CACGCCGGTC GGGCCGGGCA CGGCGAGTGG TGGACGGACA CGCTCCTGAT   [633]
K. foliosa SR383                   TGAAGTTTCT CACGCCGGTC GGGCCGGGCA CGGCGAGTGG TGGACGGACA CGCTCCTGAT   [633]
K. foliosa SR387                   TGAAGTTTCT CACGCCGGTC GGGCCGGGCA CGGCGAGTGG TGGACGGACA CGCTCCTGAT   [633]
K. foliosa SR389                   TGAAGTTTCT CACGCCGGTC GGGCCGGGCA CGGCGAGTGG TGGACGGACA CGCTCCTGAT   [633]
K. foliosa SR390                   TGAAGTTTCT CACGCCGGTC GGGCCGGGCA CGGCGAGTGG TGGACGGACA CGCTCCTGAT   [633]
K. foliosa JMG034                  TGAAGTTTCT CACACCGGTC GGGCCAGGCA CGGCGAGTGG TGGACGGACA CGCTCCTGAT   [633]
K. foliosa JMG038                  TGAAGTTTCT CACGCCGGTC GGGCCGGGCA CGGCGAGTGG TGGACGGACA CGCTCCTGAT   [633]
K. galpinii SR312                  TGAAGTTTCT CACGCCGGTC GGGCCGGGCA CGGCGAGTGG TGGACGGACA CGCTCCTGAT   [633]
K. gracilis SR321                  TGAAGTTTCT CACGCCGGTC GGGCCGGGCA CGGCGAGTGG TGGACGGACA CGCTCCTGAT   [633]
K. gracilis NNBG                   TGAAGTTTCT CACGCCGGTC GGGCCGGGCA CGGCGAGTGG TGGACGGACA CGCTCCTGAT   [633]
K. grantii CP4154                  TGAAGTTTCT CACGCCGGTC GGGCCGGGCA CGGCGAGTGG TGGACGGACA CGCTCCTGAT   [634]
K. hirsuta SR282                   TGAAGTTTCT CACGCCGGTC GGGCCGGGCA CGGCGAGTGG TGGACGGACA CGCTCCTGAT   [633]
K. ichopensis SR242                TGAAGTTTCT CACGCCGGTC GGGCCGGGCA CGGCGAGTGG TGGACGGACA CGCTCCTGAT   [633]
K. ichopensis SR286                TGAAGTTTCT CACGCCGGTC GGGCCGGGCA CGGCGAGTGG TGGACGGACA CGCTCCTGAT   [633]
K. ichopensis SR289                TGAAGTTTCT CACGCCGGTC GGGCCGGGCA CGGCGAGTGG TGGACGGACA CGCTCCTGAT   [633]
K. insignis SRsn                   TGAAGTTTCT CACGCCGGTC GGGCCGGGCA CGGCGAGTGG TGGACGGACA CGCTCCTGAT   [633]
K. isoetofolia SR386               TGAAGTTTCT CACGCCGGTC GGGCCGGGCA CGGCGAGTGG TGGACGGACA CGCTCCTGAT   [633]
K. isoetifolia SR388               TGAAGTTTCT CACGCCGGTC GGGCCGGGCA CGGCGAGTGG TGGACGGACA CGCTCCTGAT   [633]
K. isoetifolia SR393               TGAAGTTTCT CACGCCGGTC GGGCCGGGCA CGGCGAGTGG TGGACGGACA CGCTCCTGAT   [633]
K. latifolia RSSsn                 TGAAGTTTCT CACGCCGGTC GGGCCGGGCA CGGCGAGTGG TGGACGGACA CGCTCCTGAT   [633]
K. laxiflora SR283                 TGAAGTTTCT CACGCCGGTC GGGCCGGGCA CGGCGAGTGG TGGACGGACA CGCTCCTGAT   [633]
K. laxifolia SR295                 TGAAGTTTCT CACGCCGGTC GGGCCGGGCA CGGCGAGTGG TGGACGGACA CGCTCCTGAT   [633]
K. laxiflora SR467                 TGAAGTTTCT CACGCCGGTC GGGCCGGGCA CGGCGAGTGG TGGACGGACA CGCTCCTGAT   [633]
K. laxiflora SR468                 TGAAGTTTCT CACGCCGGTC GGGCCGGGCA CGGCGAGTGG TGGACGGACA CGCTCCTGAT   [633]
K. laxifloraC SRsn                 TGAAGTTTCT CACGCCGGTC GGGCCGGGCA CGGCGAGTGG TGGACGGACA CGCTCCTGAT   [633]
K. laxiflora NPB1810               TGAAGTTTCT CACGCCGGTC GGGCCGGGCA CGGCGAGTGG TGGACGGACA CGCTCCTGAT   [633]
K. leucocephala NNBG               TGAAGTTTCT CACGCCGGTC GGGCCGGGCA CGGCGAGTGG TGGACGGACA CGCTCCTGAT   [633]
K. linearifolia SR170              TGAAGTTTCT CACGCCGGTC GGGCCGGGCA CGGCGAGTGG TGGACGGACA CGCTCCTGAT   [633]
K. linearifolia SR269              TGAAGTTTCT CACGCCGGTC GGGCCGGGCA CGGCGAGTGG TGGACGGACA CGCTCCTGAT   [633]
K. linearifolia SR290              TGAAGTTTCT CACGCCGGTC GGGCCGGGCA CGGCGAGTGG TGGACGGACA CGCTCCTGAT   [633]
K. linearifolia SR291              TGAAGTTTCT CACGCCGGTC GGGCCGGGCA CGGCGAGTGG TGGACGGACA CGCTCCTGAT   [633]
K. linearifolia SR311              TGAAGTTTCT CACGCCGGTC GGGCCGGGCA CGGCGAGTGG TGGACGGACA CGCTCCTGAT   [633]
K. linearifolia SR313              TGAAGTTTCT CACGCCGGTC GGGCCGGGCA CGGCGAGTGG TGGACGGACA CGCTCCTGAT   [633]
K. linearifolia SR328              TGAAGTTTCT CACGCCGGTC GGGCCGGGCA CGGCGAGTGG TGGACGGACA CGCTCCTGAT   [633]
K. linearifolia SR343              TGAAGTTTCT CACGCCGGTC GGGCCGGGCA CGGCGAGTGG TGGACGGACA CGCTCCTGAT   [633]
K. littoralis SR200                TGAAGTTTCT CACGCCGGTC GGGCCGGGCA CGGCGAGTGG TGGACGGACA CGCTCCTGAT   [633]
K. multiflora SR310                TGAAGTTTCT CACGCCGGTC GGGCCGGGCA CGGCGAGTGG TGGACGGACA CGCTCCTGAT   [633]
K. multiflora SR315                TGAAGTTTCT CACGCCGGTC GGGCCGGGCA CGGCGAGTGG TGGACGGACA CGCTCCTGAT   [633]
K. northiae SR263                  TGAAGTTTCT CACGCCGGTC GGGCCGGGCA CGGCGAGTGG TGGACGGACA CGCTCCTGAT   [633]
K. northiae SR446                  TGAAGTTTCT CACGCCGGTC GGGCCGGGCA CGGCGAGTGG TGGACGGACA CGCTCCTGAT   [633]
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K. parviflora SR268                TGAAGTTTCT CACGCCGGTC GGGCCGGGCA CGGCGAGTGG TGGACGGACA CGCTCCTGAT   [633]
K. paviflora SR330                 TGAAGTTTCT CACGCCGGTC GGGCCGGGCA CGGCGAGTGG TGGACGGACA CGCTCCTGAT   [633]
K. pauciflora HBsn                 TGAAGTTTCT CACGCCGGTC GGGCCGGGCA CGGCGAGTGG TGGACGGACA CGCTCCTGAT   [633]
K. porphyantha SRsn                TGAAGTTTCT CACGCCGGTC GGGCCGGGCA CGGCGAGTGG TGGACGGACA CGCTCCTGAT   [633]
K. praecox SR529                   TGAAGTTTCT CACGCCGGTC GGGCCGGGCA CGGCGAGTGG TGGACGGACA CGCTCCTGAT   [633]
K. rigidifolia SRsn                TGAAGTTTCT CACGCCGGTC GGGCCGGGCA CGGCGAGTGG TGGACGGACA CGCTCCTGAT   [633]
K. ritualis SR300                  TGAAGTTTCT CACGCCGGTC GGGCCGGGCA CGGCGAGTGG TGGACGGACA CGCTCCTGAT   [633]
K. rooperi SR237                   TGAAGTTTCT CACGCCGGTC GGGCCGGGCA CGGCGAGTGG TGGACGGACA CGCTCCTGAT   [633]
K. rooperi SR485                   TGAAGTTTCT CACGCCGGTC GGGCCGGGCA CGGCGAGTGG TGGACGGACA CGCTCCTGAT   [633]
K. sarmentosa SR207                TGAAGTTTCT CACGCCGGTC GGGCCGGGCA CGGCGAGTGG TGGACGGACA CGCTCCTGAT   [633]
K. schemperi SR391                 TGAAGTTTCT CACGCCGGTC GGGCCGGGCA CGGCGAGTGG TGGACGGACA CGCTCCTGAT   [633]
K. schemperi JMG036                TGAAGTTTCT CACGCCGGTC GGGCCGGGCA CGGCGAGTGG TGGACGGACA CGCTCCTGAT   [633]
K. splendida SR548                 TGAAGTTTCT CACGCCGGTC GGGCCGGGCA CGGCGAGTGG TGGACGGACA CGCTCCTGAT   [633]
K. stricta SR279                   TGAAGTTTCT CACGCCGGTC GGGCCGGGCA CGGCGAGTGG TGGACGGACA CGCTCCTGAT   [633]
K. thodei SR407                    TGAAGTTTCT CACGCCGGTC GGGCCGGGCA CGGCGAGTGG TGGACGGACA CGCTCCTGAT   [633]
K. thomsonii JMG031                TGAAGTTTCT CACGCCGGTC GGGCCGGGCA CGGCGAGTGG TGGACGGACA CGCTCCTGAT   [633]
K. thomsonii AMM                   TGAAGTTTCT CACGCCGGTC GGGCCGGGCA CGGCGAGTGG TGGACGGACA CGCTCCTGAT   [633]
K. thomsonii CK4821                TGAAGTTTCT CACGCCGGTC GGGCCGGGCA CGGCGAGTGG TGGACGGACA CGCTCCTGAT   [633]
K. triangularis SR264              TGAAGTTTCT CACGCCGGTC GGGCCGGGCA CGGCGAGTGG TGGACGGACA CGCTCCTGAT   [633]
K. triangularis SR266              TGAAGTTTCT CACGCCGGTC GGGCCGGGCA CGGCGAGTGG TGGACGGACA CGCTCCTGAT   [633]
K. triangularis SR299              TGAAGTTTCT CACGCCGGTC GGGCCGGGCA CGGCGAGTGG TGGACGGACA CGCTCCTGAT   [633]
K. triangularis obtusiloba SRsn    TGAAGTTTCT CACGCCGGTC GGGCCGGGCA CGGCGAGTGG TGGACGGACA CGCTCCTGAT   [633]
K. typhoides JB8084                TGAAGTTTCT CACGTCGGTC GGGCCGGGCA CGGCGAGTGG TGGACGGACA CGCTCCTGAT   [633]
K. typhoides NNBG                  TGAAGTTTCT CACGTCGGTC GGGCCGGGCA CGGCGAGTGG TGGACGGACA CGCTCCTGAT   [633]
K. tysonii SR302                   TGAAGTTTCT CACGCCGGTC GGGCCGGGCA CGGCGAGTGG TGGACGGACA CGCTCCTGAT   [633]
K. tysonii SR303                   TGAAGTTTCT CACGCCGGTC GGGCCGGGCA CGGCGAGTGG TGGACGGACA CGCTCCTGAT   [633]
K. umbrina RGsn                    TGAAGTTTCT CACGCCGGTC GGGCCGGGCA CGGCGAGTGG TGGACGGACA CGCTCCTGAT   [633]
K. uvaria SR186                    TGAAGTTTCT CACGCCGGTC GGGCCGGGCA CGGCGAGTGG TGGACGGACA CGCTCCTGAT   [633]
K. uvaria SR201                    TGAAGTTTCT CACGCCGGTC GGGCCGGGCA CGGCGAGTGG TGGACGGACA CGCTCCTGAT   [633]
K. uvaria SR203                    TGAAGTTTCT CACGCCGGTC GGGCCGGGCA CGGCGAGTGG TGGACGGACA CGCTCCTGAT   [633]
K. uvaria SR211                    TGAAGTTTCT CACGCCGGTC GGGCCGGGCA CGGCGAGTGG TGGACGGACA CGCTCCTGAT   [633]
K. uvaria SR342                    TGAAGTTTCT CACGCCGGTC GGGCCGGGCA CGGCGAGTGG TGGACGGACA CGCTCCTGAT   [633]
K. uvaria SR344                    TGAAGTTTCT CACGCCGGTC GGGCCGGGCA CGGCGAGTGG TGGACGGACA CGCTCCTGAT   [633]
K. uvaria SR477                    TGAAGTTTCT CACGCCGGTC GGGCCGGGCA CGGCGAGTGG TGGACGGACA CGCTCCTGAT   [633]

[                                            670         680         690         700         710        720]
[                                            .          .          .          .          .          .]

Bulbine latifolia SR61             CGCCGGACGC CGTGGAATCC CAGCTCGACG TCTG-ATACG GGACCGAG-A TGATAA-GAA   [677]
Bulbinella cauda-felis SR204       CGCCGGACGC CGTGGAAACC TAGCCCGATG CCGG-ATGTA TGACCGAGAA CAA-AA-GAA   [693]
K. acreae TD4626                   CGCCGGGCGC CGTGTAAACC CAGCCCGATG CCGG------ ---------A C-ATAATGAA   [677]
K. albescens SR314                 CGCCGGGCGC CGTGTAAACC CAGCCCGATG CCGG------ ---------A C-ATAATGAA   [677]
K. albomontana SR149               CGCCGGGCGC CGTGTAAACC CAGCCCGATG CCGG------ ---------A C-ATAATGAA   [677]
K. angustifolia SR453              CGCCGGGCGC CGTGTAAACC CAGCCCGATG CCGG------ ---------A C-ATAATGAA   [677]
K. angustifolia SR542              CGCCGGGCGC CGTGTAAACC CAGCCCGATG CCGG------ ---------A C-ATAATGAA   [677]
K. ankaratrensis PBP5676           CGCCGGGCGC CGTGTAAACC CAGTCCGATG CCGG------ ---------A C-ATAATGAA   [677]
K. baurii SR275                    CGCCGGGCGC CGTGTAAACC CAGCCCGATG CCGG------ ---------A C-ATAATGAA   [677]
K. baurii SR285                    CGCCGGGCGC CGTGTAAACC CAGCCCGATG CCGG------ ---------A C-ATAATGAA   [677]
K. baurii SR360                    CGCCGGGCGC CGTGTAAACC CAGCCCGATG CCGG------ ---------A C-ATAATGAA   [677]
K. baurii SR382                    CGCCGGGCGC CGTGTAAACC CAGCCCGATG CCGG------ ---------A C-ATAATGAA   [677]
K. baurii NPB1923                  CGCTGGGCGC CGTGTAAACC CAGCCCGATG CCGG------ ---------A C-ATAATGAA   [677]
K. brachystachya SRsn              CGCCGGGCGC CGTGCAAACC CAGCCCGATG CCGGG----- ---------A C-ATAATGAA   [678]
K. brevifolia SR452                CGCCGGGCGC CGTGTAAACC CAGCCCGATG CCGG------ ---------A C-ATAATGAA   [677]
K. bruceae SR171                   CGCCGGGCGC CGTGTAAACC CAGCCCGATG CCGG------ ---------A C-ATAATGAA   [677]
K. buchananii SR307                CGCCGGGCGC CGTGTAAACC CAGCCCGATG CCGG------ ---------A C-ATAATGAA   [677]
K. caulescens SR270                CGCCGGGCGC CGTGTAAACC CAGCCCGATG CCGG------ ---------A C-ATAATGAA   [677]
K. caulescens SR278                CGCCGGGCGC CGTGTAAACC CAGCCCGATG CCGG------ ---------A C-ATAATGAA   [677]
K. caulescens NPB1821              CGCCGGGCGC CGTGTAAACC CAGCCCGATG CCGG------ ---------A C-ATAATGAA   [677]
K. citrina SR176                   CGCCGGGCGC CGTGTAAACC CAGCCCGATG CCGG------ ---------A C-ATAATGAA   [677]
K. coddiana SRsn                   CGCCGGGCGC CGTGTAAACC CAGCCCGATG CCGG------ ---------A C-ATAATGAA   [677]
K. corraligemma SR549              CGCCGGGCGC CGTGTAAACC CAGCCCGATG CCGG------ ---------A C-ATAATGAA   [677]
K. drepanophylla RAL4816           CGCCGGGCGC CGTGTAAACC CAGCCCGATG CCGG------ ---------A C-ATAATGAA   [677]
K. ensifolia ensifolia JBsn        CGCCGGGCGC CGTGTAAACC CAGCCCGATG CCGG------ ---------A C-ATAATGAA   [677]
K. ensifolia autumnalis SR448      CGCCGGGCGC CGTGTAAACC CAGCCCGATG CCGG------ ---------A C-ATAATGAA   [677]
K. fibrosa SR297                   CGCCGGGCGC CGTGTAAACC CAGCCCGATG CCGG------ ---------A C-ATAATGAA   [677]
K. fluvitalis SRsn                 CGCCGGGCGC CGTGTAAACC CAGCCCGATG CCGG------ ---------A C-ATAATGAA   [677]
K. foliosa SR383                   CGCCGGGCGT CGTGTAAACC TAGCCCGATG CCGG------ ---------A C-ATAATGAA   [677]
K. foliosa SR387                   CGCCGGGCGT CGTGTAAACC TAGCCCGATG CCGG------ ---------A C-ATAATGAA   [677]
K. foliosa SR389                   CGCCGGGCGT CGTGTAAACC TAGCCCGATG CCGG------ ---------A C-ATAATGAA   [677]
K. foliosa SR390                   CGCCGGGCGT CGTGTAAACC TAGCCCGATG CCGG------ ---------A C-ATAATGAA   [677]
K. foliosa JMG034                  CGCCGGGCGT CGTGTAAACC TAGCCCGATG CCGG------ ---------A C-ATAATGAA   [677]
K. foliosa JMG038                  CGCCGGGCGT CGTGTAAACC TAGCCCGATG CCGG------ ---------A C-ATAATGAA   [677]
K. galpinii SR312                  CGCCGGGCGC CGTGTAAACC CAGCCCGATG CCGG------ ---------A C-ATAATGAA   [677]
K. gracilis SR321                  CGCCGGGCGC CGTGTAAACC CAGCCCGATG CCGG------ ---------A C-ATAATGAA   [677]
K. gracilis NNBG                   CGCCGGGCGC CGTGTAAACC CAGCCCGATG CCGG------ ---------A C-ATAATGAA   [677]
K. grantii CP4154                  CGCCGGGCGC CGTGTAAACC CAGCCCGATG CCGG------ ---------A C-ACAATGAA   [678]
K. hirsuta SR282                   CGCCGGGCGC CGTGTAAACC CAGCCCGATG CCGG------ ---------A C-ATAATGAA   [677]
K. ichopensis SR242                CGCCGGGCGC CGTGTAAACC CAGCCCGATG CCGG------ ---------A C-ATAATGAA   [677]
K. ichopensis SR286                CGCCGGGCGC CGTGTAAACC CAGCCCGATG CCGG------ ---------A C-ATAATGAA   [677]
K. ichopensis SR289                CGCCGGGCGC CGTGTAAACC CAGCCCGATG CCGG------ ---------A C-ATAATGAA   [677]
K. insignis SRsn                   CGCCGGGCGT CGTGTAAACC TAGCCCGATG CCGG------ ---------A C-ATAATGAA   [677]
K. isoetofolia SR386               CGCCGGGCGT CGTGTAAACC CAGCCCGATG CCGG------ ---------A C-ATAATGAA   [677]
K. isoetifolia SR388               CGCCGGGCGT CGTGTAAACC TAGCCCGATG CCGG------ ---------A C-ATAATGAA   [677]
K. isoetifolia SR393               CGCCGGGCGT CGTGTAAACC TAGCCCGATG CCGG------ ---------A C-ATAATGAA   [677]
K. latifolia RSSsn                 CGCCGGGCGC CGTGTAAACC CAGCCCGATG CCGG------ ---------A C-ATAATGAA   [677]
K. laxiflora SR283                 CGCCGGGCGC CGTGTAAACC CAGCCCGATG CCGG------ ---------A C-ATAATGAA   [677]
K. laxifolia SR295                 CGCCGGGCGC CGTGTAAACC CAGCCCGATG CCGG------ ---------A C-ATAATGAA   [677]
K. laxiflora SR467                 CGCCGGGCGC CGTGTAAACC CAGCCCGATG CCGG------ ---------A C-ATAATGAA   [677]
K. laxiflora SR468                 CGCCGGGCGC CGTGTAAACC CAGCCCGATG CCGG------ ---------A C-ATAATGAA   [677]
K. laxifloraC SRsn                 CGCCGGGCGC CGTGTAAACC CAGCCCGATG CCGG------ ---------A C-ATAATGAA   [677]
K. laxiflora NPB1810               CGCCGGGCGC CGTGTAAACC CAGCCCGATG CCGG------ ---------A C-ATAATGAA   [677]
K. leucocephala NNBG               CGCCGGGCGC CGTGTAAACC CAGCCCGATG CCGG------ ---------A C-ATAATGAA   [677]
K. linearifolia SR170              CGCCGGGCGC CGTGTAAACC CAGCCCGATG CCGG------ ---------A C-ATAATGAA   [677]
K. linearifolia SR269              CGCCGGGCGC CGTGTAAACC CAGCCCGATG CCGG------ ---------A C-ATAATGAA   [677]
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K. linearifolia SR290              CGCCGGGCGC CGTGTAAACC CAGCCCGATG CCGG------ ---------A C-ATAATGAA   [677]
K. linearifolia SR291              CGCCGGGCGC CGTGTAAACC CAGCCCGATG CCGG------ ---------A C-ATAATGAA   [677]
K. linearifolia SR311              CGCCGGGCGC CGTGTAAACC CAGCCCGATG CCGG------ ---------A C-ATAATGAA   [677]
K. linearifolia SR313              CGCCGGGCGC CGTGTAAACC CAGCCCGATG CCGG------ ---------A C-ATAATGAA   [677]
K. linearifolia SR328              CGCCGGGCGC CGTGTAAACC CAGCCCGATG CCGG------ ---------A C-ATAATGAA   [677]
K. linearifolia SR343              CGCCGGGCGC CGTGTAAACC CAGCCCGATG CCGG------ ---------A C-ATAATGAA   [677]
K. littoralis SR200                CGCCGGGCGC CGTGTAAACC CAGCCCGATG CCGG------ ---------A C-ATAATGAA   [677]
K. multiflora SR310                CGCCGGGCGC CGTGTAAACC CAGCCCGATG CCGG------ ---------A C-ATAATGAA   [677]
K. multiflora SR315                CGCCGGGCGC CGTGTAAACC CAGCCCGATG CCGG------ ---------A C-ATAATGAA   [677]
K. northiae SR263                  CGCCGGGCGC CGTGTAAACC CAGCCCGATG CCGG------ ---------A C-ATAATGAA   [677]
K. northiae SR446                  CGCCGGGCGC CGTGTAAACC CAGCCCGATG CCGG------ ---------A C-ATAATGAA   [677]
K. parviflora SR268                CGCCGGGCGC CGTGTAAACC CAGCCCGATG CCGG------ ---------A C-ATAATGAA   [677]
K. paviflora SR330                 CGCCGGGCGC CGTGTAAACC CAGCCCGATG CCGG------ ---------A C-ATAATGAA   [677]
K. pauciflora HBsn                 CGCCGGGCGC CGTGTAAACC CAGCCCGATG CCGG------ ---------A C-ATAATGAA   [677]
K. porphyantha SRsn                CGCCGGGCGC CGTGTAAACC CAGCCCGATG CCGG------ ---------A C-ATAATGAA   [677]
K. praecox SR529                   CGCCGGGCGC CGTGTAAACC CAGCCCGATG CCGG------ ---------A C-ATAATGAA   [677]
K. rigidifolia SRsn                CGCCGGGCGC CGTGTAAACC CAGCCCGATG CCGG------ ---------A C-ATAATGAA   [677]
K. ritualis SR300                  CGCCGGGCGC CGTGTAAACC CAGCCCGATG CCGG------ ---------A C-ATAATGAA   [677]
K. rooperi SR237                   CGCCGGGCGC CGTGTAAACC CAGCCCGATG CCGG------ ---------A C-ATAATGAA   [677]
K. rooperi SR485                   CGCCGGGCGC CGTGTAAACC CAGCCCGATG CCGG------ ---------A C-ATAATGAA   [677]
K. sarmentosa SR207                CGCCGGGCGC CGTGTAAACC CAGCCCGATG CCGG------ ---------A C-ATGACGAA   [677]
K. schemperi SR391                 CGCCGGGCGT CGTGTAAACC TAGCCCGATG CCGG------ ---------A C-ATAATGAA   [677]
K. schemperi JMG036                CGCCGGGCGT CGTGTAAACC TAGCCCGATG CCGG------ ---------A C-ATAATGAA   [677]
K. splendida SR548                 CGCCGGGCGC CGTGTAAACC CAGCCCGATG CCGG------ ---------A C-ATAATGAA   [677]
K. stricta SR279                   CGCCGGGCGC CGTGTAAACC CAGCCCGATG CCGG------ ---------A C-ATAATGAA   [677]
K. thodei SR407                    CGCCGGGCGC CGTGTAAACC CAGCCCGATG CCGG------ ---------A C-ATAATGAA   [677]
K. thomsonii JMG031                CGCCGGGCGT CGTGTAAACC TAGCCCGATG CCGG------ ---------A C-ATAATGAA   [677]
K. thomsonii AMM                   CGCCGGGCGC CGTGTAAACC CAGCCCGATG CCGG------ ---------A C-ATAATGAA   [677]
K. thomsonii CK4821                CGCCGGGCGC CGTGTAAACC CAGCCCGATG CCGG------ ---------A C-ATAATGAA   [677]
K. triangularis SR264              CGCCGGGCGC CGTGTAAACC CAGCCCGATG CCGG------ ---------A C-ATAATGAA   [677]
K. triangularis SR266              CGCCGGGCGC CGTGTAAACC CAGCCCGATG CCGG------ ---------A C-ATAATGAA   [677]
K. triangularis SR299              CGCCGGGCGC CGTGTAAACC CAGCCCGATG CCGG------ ---------A C-ATAATGAA   [677]
K. triangularis obtusiloba SRsn    CGCCGGGCGC CGTGTAAACC CAGCCCGATG CCGG------ ---------A C-ATAATGAA   [677]
K. typhoides JB8084                CGCCGGGCGC CGTGTAAACC CAGCCCGATG CCGGG----- ---------A C-ATAATGAA   [678]
K. typhoides NNBG                  CGCCGGGCGC CGTGTATACC CAGCCCGATG CCGGG----- ---------A C-ATAATGAA   [678]
K. tysonii SR302                   CGCCGGGCGC CGTGTAAACC CAGCCCGATG CCGG------ ---------A C-ATAATGAA   [677]
K. tysonii SR303                   CGCCGGGCGC CGTGTAAACC CAGCCCGATG CCGG------ ---------A C-ATAATGAA   [677]
K. umbrina RGsn                    CGCCGGGCGC CGTGTAAACC CAGCCCGATG CCGG------ ---------A C-ATAATGAA   [677]
K. uvaria SR186                    CGCCGGGCGC CGTGTAAACC CAGCCCGATG CCGG------ ---------A C-ATAATGAA   [677]
K. uvaria SR201                    CGCCGGGCGC CGTGTAAACC CAGCCCGATG CCGG------ ---------A C-ATAATGAA   [677]
K. uvaria SR203                    CGCCGGGCGC CGTGTAAACC CAGCCCGATG CCGG------ ---------A C-ATAATGAA   [677]
K. uvaria SR211                    CGCCGGGCGC CGTGTAAACC CAGCCCGATG CCGG------ ---------A C-ATAATGAA   [677]
K. uvaria SR342                    CGCCGGGCGC CGTGTAAACC CAGCCCGATG CCGG------ ---------A C-ATAATGAA   [677]
K. uvaria SR344                    CGCCGGGCGC CGTGTAAACC CAGCCCGATG CCGG------ ---------A C-ATAATGAA   [677]
K. uvaria SR477                    CGCCGGGCGC CGTGTAAACC CAGCCCGATG CCGG------ ---------A C-ATAATGAA   [677]

[                                            730         740         750         760         770        780]
[                                            .          .          .          .          .         .]

Bulbine latifolia SR61             CCCAAACCGA AGGGCGCA-C GCGCCATCGG ACCGCGACCC CAGGTCAGGC GGGACTACCC   [736]
Bulbinella cauda-felis SR204       CCCAAACCGA CAGGCGCATC GCGCCATCGG ATCGCGACCC CAGGTCAGGC GGGACTACCC   [753]
K. acreae TD4626                   CCCAAACCGA AGGGCGCAAC GCGCCATCGG ATCGCGACCC CAGGTCAGGC GGGACCACCC   [737]
K. albescens SR314                 CCCAAACCGA AGGGCGCAAC GCGCCATCGG ATCGCGACCC CAGGTCAGGC GGGACCACCC   [737]
K. albomontana SR149               CCCAAACCGA AGGGCGCAAC GCGCCATCGG ATCGCGACCC CAGGTCAGGC GGGACCACCC   [737]
K. angustifolia SR453              CCCAAACCGA AGGGCGCAAC GCGCCATCGG ATCGCGACCC CAGGTCAGGC GGGACCACCC   [737]
K. angustifolia SR542              CCCAAACCGA AGGGCGCAAC GCGCCATCGG ATCGCGACCC CAGGTCAGGC GGGACCACCC   [737]
K. ankaratrensis PBP5676           CCCAAACCGA AGGGCGCAAC GCGCCATCGG ATCGCGACCC CAGGTCAGGC GGGACCACCC   [737]
K. baurii SR275                    CCCAAACCGA AGGGCGCAAC GCGCCATCGG ATCGCGACCC CAGGTCAGGC GGGACCACCC   [737]
K. baurii SR285                    CCCAAACCGA AGGGCGCAAC GCGCCATCGG ATCGCGACCC CAGGTCAGGC GGGACCACCC   [737]
K. baurii SR360                    CCCAAACCGA AGGGCGCAAC GCGCCATCGG ATCGCGACCC CAGGTCAGGC GGGACCACCC   [737]
K. baurii SR382                    CCCAAACCGA AGGGCGCAAC GCGCCATCGG ATCGCGACCC CAGGTCAGGC GGGACCACCC   [737]
K. baurii NPB1923                  CCCAAACCGA AGGGCGCAAC GCGCCATCGG ATCGCGACCC CAGGTCAGGC GGGACCACCC   [737]
K. brachystachya SRsn              CCCAAACCGA AGGGCGCAAC GCGCCATCGG ATCGCGACCC CAGGTCAGGC GGGACCACCC   [738]
K. brevifolia SR452                CCCAAACCGA AGGGCGCAAC GCGCCATCGG ATCGCGACCC CAGGTCAGGC GGGACCACCC   [737]
K. bruceae SR171                   CCCAAACCGA AGGGCGCAAC GCGCCATCGG ATCGCGACCC CAGGTCAGGC GGGACCACCC   [737]
K. buchananii SR307                CCCAAACCGA AGGGCGCAAC GCGCCATCGG ATCGCGACCC CAGGTCAGGC GGGACCACCC   [737]
K. caulescens SR270                CCCAAACCGA AGGGCGCAAC GCGCCATCGG ATCGCGACCC CAGGTCAGGC GGGACCACCC   [737]
K. caulescens SR278                CCCAAACCGA AGGGCGCAAC GCGCCATCGG ATCGCGACCC CAGGTCAGGC GGGACCACCC   [737]
K. caulescens NPB1821              CCCAAACCGA AGGGCGCAAC GCGCCATCGG ATCGCGACCC CAGGTCAGGC GGGACCACCC   [737]
K. citrina SR176                   CCCAAACCGA AGGGCGCAAC GCGCCATCGG ATCGCGACCC CAGGTCAGGC GGGACCACCC   [737]
K. coddiana SRsn                   CCCAAACCGA AGGGCGCAAC GCGCCATCGG ATCGCGACCC CAGGTCAGGC GGGACCACCC   [737]
K. corraligemma SR549              CCCAAACCGA AGGGCGCAAC GCGCCATCGG ATCGCGACCC CAGGTCAGGC GGGACCACCC   [737]
K. drepanophylla RAL4816           CCCAAACCGA AGGGCGCAAC GCGCCATCGG ATCGCGACCC CAGGTCAGGC GGGACCACCC   [737]
K. ensifolia ensifolia JBsn        CCCAAACCGA AGGGCGCAAC GCGCCATCGG ATCGCGACCC CAGGTCAGGC GGGACCACCC   [737]
K. ensifolia autumnalis SR448      CCCAAACCGA AGGGCGCAAC GCGCCATCGG ATCGCGACCC CAGGTCAGGC GGGACCACCC   [737]
K. fibrosa SR297                   CCCAAACCGA AGGGCGCAAC GCGCCATCGG ATCGCGACCC CAGGTCAGGC GGGACCACCC   [737]
K. fluvitalis SRsn                 CCCAAACCGA AGGGCGCAAC GCGCCATCGG ATCGCGACCC CAGGTCAGGC GGGATCACCC   [737]
K. foliosa SR383                   CCCAAACCGA AGGGCGCAAC GCGCCATCGG ATCGCGACCC CAGGTCAGGC GGGACCACCC   [737]
K. foliosa SR387                   CCCAAACCGA AGGGCGCAAC GCGCCATCGG ATCGCGACCC CAGGTCAGGC GGGACCACCC   [737]
K. foliosa SR389                   CCCAAACCGA AGGGCGCAAC GCGCCATCGG ATCGCGACCC CAGGTCAGGC GGGACCACCC   [737]
K. foliosa SR390                   CCCAAACCGA AGGGCGCAAC GCGCCATCGG ATCGCGACCC CAGGTCAGGC GGGACCACCC   [737]
K. foliosa JMG034                  CCCAAACCGA AGGGCGCAAC GCGCCATCGG ATCGCGACCC CAGGTCAGGC GGGACCACCC   [737]
K. foliosa JMG038                  CCCAAACCGA AGGGCGCAAC GCGCCATCGG ATCGCGACCC CAGGTCAGGC GGGACCACCC   [737]
K. galpinii SR312                  CCCAAACCGA AGGGCGCAAC GCGCCATCGG ATCGCGACCC CAGGTCAGGC GGGATCACCC   [737]
K. gracilis SR321                  CCCAAACCGA AGGGCGCAAC GCGCCATCGG ATCGCGACCC CAGGTCAGGC GGGACCACCC   [737]
K. gracilis NNBG                   CCCAAACCGA AGGGCGCAAC GCGCCATCGG ATCGCGACCC CAGGTCAGGC GGGACCACCC   [737]
K. grantii CP4154                  CCCAAACCGA AGGGCGCAAC GCGCCATCGG ATCGCGACCC CAGGTCAGGC GGGACCACCC   [738]
K. hirsuta SR282                   CCCAAACCGA AGGGCGCAAC GCGCCATCGG ATCGCGACCC CAGGTCAGGC GGGACCACCC   [737]
K. ichopensis SR242                CCCAAACCGA AGGGCGCAAC GCGCCATCGG ATCGCGACCC CAGGTCAGGC GGGACCACCC   [737]
K. ichopensis SR286                CCCAAACCGA AGGGCGCAAC GCGCCATCGG ATCGCGACCC CAGGTCAGGC GGGACCACCC   [737]
K. ichopensis SR289                CCCAAACCGA AGGGCGCAAC GCGCCATCGG ATCGCGACCC CAGGTCAGGC GGGACCACCC   [737]
K. insignis SRsn                   CCCAAACCGA AGGGCGCAAC GCGCCATCGG ATCGCGACCC CAGGTCAGGC GGGACCACCC   [737]
K. isoetofolia SR386               CCCAAACCGA AGGGCGCAAC GCGCCATCGG ATCGCGACCC CAGGTCAGGC GGGACCACCC   [737]
K. isoetifolia SR388               CCCAAACCGA AGGGCGCAAC GCGCCATCGG ATCGCGACCC CAGGTCAGGC GGGACCACCC   [737]
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K. isoetifolia SR393               CCCAAACCGA AGGGCGCAAC GCGCCATCGG ATCGCGACCC CAGGTCAGGC GGGACCACCC   [737]
K. latifolia RSSsn                 CCCAAACCGA AGGGCGCAAC GCGCCATCGG ATCGCGACCC CAGGTCAGGC GGGACCACCC   [737]
K. laxiflora SR283                 CCCAAACCGA AGGGCGCAAC GCGCCATCGG ATCGCGACCC CAGGTCAGGC GGGACCACCC   [737]
K. laxifolia SR295                 CCCAAACCGA AGGGCGCAAC GCGCCATCGG ATCGCGACCC CAGGTCAGGC GGGACCACCC   [737]
K. laxiflora SR467                 CCCAAACCGA AGGGCGCAAC GCGCCATCGG ATCGCGACCC CAGGTCAGGC GGGACCACCC   [737]
K. laxiflora SR468                 CCCAAACCGA AGGGCGCAAC GCGCCATCGG ATCGCGACCC CAGGTCAGGC GGGACCACCC   [737]
K. laxifloraC SRsn                 CCCAAACCGA AGGGCGCAAC GCGCCATCGG ATCGCGACCC CAGGTCAGGC GGGACCACCC   [737]
K. laxiflora NPB1810               CCCAAACCGA AGGGCGCAAC GCGCCATCGG ATCGCGACCC CAGGTCAGGC GGGACCACCC   [737]
K. leucocephala NNBG               CCCAAACCGA AGGGCGCAAC CCGCCATCGG ATCGCGACCC CAGGTCAGGC GGGACCACCC   [737]
K. linearifolia SR170              CCCAAACCGA AGGGCGCAAC GCGCCATCGG ATCGCGACCC CAGGTCAGGC GGGACCACCC   [737]
K. linearifolia SR269              CCCAAACCGA AGGGCGCAAC GCGCCATCGG ATCGCGACCC CAGGTCAGGC GGGACCACCC   [737]
K. linearifolia SR290              CCCAAACCGA AGGGCGCAAC GCGCCATCGG ATCGCGACCC CAGGTCAGGC GGGACCACCC   [737]
K. linearifolia SR291              CCCAAACCGA AGGGCGCAAC GCGCCATCGG ATCGCGACCC CAGGTCAGGC GGGACCACCC   [737]
K. linearifolia SR311              CCCAAACCGA AGGGCGCAAC GCGCCATCGG ATCGCGACCC CAGGTCAGGC GGGACCACCC   [737]
K. linearifolia SR313              CCCAAACCGA AGGGCGCAAC GCGCCATCGG ATCGCGACCC CAGGTCAGGC GGGACCACCC   [737]
K. linearifolia SR328              CCCAAACCGA AGGGCGCAAC GCGCCATCGG ATCGCGACCC CAGGTCAGGC GGGACCACCC   [737]
K. linearifolia SR343              CCCAAACCGA AGGGCGCAAC GCGCCATCGG ATCGCGACCC CAGGTCAGGC GGGACCACCC   [737]
K. littoralis SR200                CCCAAACCGA AGGGCGCAAC GCGCCATCGG ATCGCGACCC CAGGTCAGGC GGGACCACCC   [737]
K. multiflora SR310                CCCAAACCGA AGGGCGCAAC GCGCCATCGG ATCGCGACCC CAGGTCAGGC GGGATCACCC   [737]
K. multiflora SR315                CCCAAACCGA AGGGCGCAAC GCGCCATCGG ATCGCGACCC CAGGTCAGGC GGGATCACCC   [737]
K. northiae SR263                  CCCAAACCGA AGGGCGCAAC GCGCCATCGG ATCGCGACCC CAGGTCAGGC GGGACCACCC   [737]
K. northiae SR446                  CCCAAACCGA AGGGCGCAAC GCGCCATCGG ATCGCGACCC CAGGTCAGGC GGGACCACCC   [737]
K. parviflora SR268                CCCAAACCGA AGGGCGCAAC GCGCCATCGG ATCGCGACCC CAGGTCAGGC GGGACCACCC   [737]
K. paviflora SR330                 CCCAAACCGA AGGGCGCAAC GCGCCATCGG ATCGCGACCC CAGGTCAGGC GGGACCACCC   [737]
K. pauciflora HBsn                 CCCAAACCGA AGGGCGCAAC GCGCCATCGG ATCGCGACCC CAGGTCAGGC GGGACCACCC   [737]
K. porphyantha SRsn                CCCAAACCGA AGGGCGCAAC GCGCCATCGG ATCGCGACCC CAGGTCAGGC GGGATCACCC   [737]
K. praecox SR529                   CCCAAACCGA AGGGCGCAAC GCGCCATCGG ATCGCGACCC CAGGTCAGGC GGGACCACCC   [737]
K. rigidifolia SRsn                CCCAAACCGA AGGGCGCAAC GCGCCATCGG ATCGCGACCC CAGGTCAGGC GGGACCACCC   [737]
K. ritualis SR300                  CCCAAACCGA AGGGCGCAAC GCGCCATCGG ATCGCGACCC CAGGTCAGGC GGGACCACCC   [737]
K. rooperi SR237                   CCCAAACCGA AGGGCGCAAC GCGCCATCGG ATCGCGACCC CAGGTCAGGC GGGACCACCC   [737]
K. rooperi SR485                   CCCAAACCGA AGGGCGCAAC GCGCCATCGG ATCGCGACCC CAGGTCAGGC GGGACCACCC   [737]
K. sarmentosa SR207                CCCAAACCGA AGGGCGCAAC GCGCCATCGG ATCGCGACCC CAGGTCAGGC GGGACCACCC   [737]
K. schemperi SR391                 CCCAAACCGA AGGGCGCAAC GCGCCATCGG ATCGCGACCC CAGGTCAGGC GGGACCACCC   [737]
K. schemperi JMG036                CCCAAACCGA AGGGCGCAAC GCGCCATCGG ATCGCGACCC CAGGTCAGGC GGGACCACCC   [737]
K. splendida SR548                 CCCAAACCGA AGGGCGCAAC GCGCCATCGG ATCGCGACCC CAGGTCAGGC GGGACCACCC   [737]
K. stricta SR279                   CCCAAACCGA AGGGCGCAAC GCGCCATCGG ATCGCGACCC CAGGTCAGGC GGGACCACCC   [737]
K. thodei SR407                    CCCAAACCGA AGGGCGCAAC GCGCCATCGG ATCGCGACCC CAGGTCAGGC GGGACCACCC   [737]
K. thomsonii JMG031                CCCAAACCGA AGGGCGCAAC GCGCCATCGG ATCGCGACCC CAGGTCAGGC GGGACCACCC   [737]
K. thomsonii AMM                   CCCAAACCGA AGGGCGCAAC GCGCCATCGG ATCGCGACCC CAGGTCAGGC GGGACCACCC   [737]
K. thomsonii CK4821                CCCAAACCGA AGGGCGCAAC GCGCCATCGG ATCGCGACCC CAGGTCAGGC GGGACCACCC   [737]
K. triangularis SR264              CCCAAACCGA AGGGCGCAAC GCGCCATCGG ATCGCGACCC CAGGTCAGGC GGGACCACCC   [737]
K. triangularis SR266              CCCAAACCGA AGGGCGCAAC GCGCCATCGG ATCGCGACCC CAGGTCAGGC GGGACCACCC   [737]
K. triangularis SR299              CCCAAACCGA AGGGCGCAAC GCGCCATCGG ATCGCGACCC CAGGTCAGGC GGGACCACCC   [737]
K. triangularis obtusiloba SRsn    CCCAAACCGA AGGGCGCAAC GCGCCATCGG ATCGCGACCC CAGGTCAGGC GGGATCACCC   [737]
K. typhoides JB8084                CCCAAACCGA AGGGCGCAAC GCGCCATCGG ATCGCGACCC CAGGTCAGGC GGGACCACCC   [738]
K. typhoides NNBG                  CCCAAACCGA AGGGCGCAAC GCGCCATCGG ATCGCGACCC CAGGTCAGGC GGGACCACCC   [738]
K. tysonii SR302                   CCCAAACCGA AGGGCGCAAC GCGCCATCGG ATCGCGACCC CAGGTCAGGC GGGACCACCC   [737]
K. tysonii SR303                   CCCAAACCGA AGGGCGCAAC GCGCCATCGG ATCGCGACCC CAGGTCAGGC GGGACCACCC   [737]
K. umbrina RGsn                    CCCAAACCGA AGGGCGCAAC GCGCCATCGG ATCGCGACCC CAGGTCAGGC GGGATCACCC   [737]
K. uvaria SR186                    CCCAAACCGA AGGGCGCAAC GCGCCATCGG ATCGCGACCC CAGGTCAGGC GGGACCACCC   [737]
K. uvaria SR201                    CCCAAACCGA AGGGCGCAAC GCGCCATCGG ATCGCGACCC CAGGTCAGGC GGGACCACCC   [737]
K. uvaria SR203                    CCCAAACCGA AGGGCGCAAC GCGCCATCGG ATCGCGACCC CAGGTCAGGC GGGACCACCC   [737]
K. uvaria SR211                    CCCAAACCGA AGGGCGCAAC GCGCCATCGG ATCGCGACCC CAGGTCAGGC GGGACCACCC   [737]
K. uvaria SR342                    CCCAAACCGA AGGGCGCAAC GCGCCATCGG ATCGCGACCC CAGGTCAGGC GGGACCACCC   [737]
K. uvaria SR344                    CCCAAACCGA AGGGCGCAAC GCGCCATCGG ATCGCGACCC CAGGTCAGGC GGGACCACCC   [737]
K. uvaria SR477                    CCCAAACCGA AGGGCGCAAC GCGCCATCGG ATCGCGACCC CAGGTCAGGC GGGACCACCC   [737]

[                                            790         800         810         820        830]
[                                            .          .          .          .          .]

Bulbine latifolia SR61             GCTGAGCTTA AGCATATCAA TAAGCGGAGG AGAAGAAACT AACAAGGATT   [786]
Bulbinella cauda-felis SR204       GCTGAGTTTA AGCATATCAA TAAGCGGAGG AGAAGAAACT AACAAGGATT   [803]
K. acreae TD4626                   GCTGAGTTTA AGCATATCAA TAAGCGGAGG AGAAGAAACT AACAAGGATT   [787]
K. albescens SR314                 GCTGAGTTTA AGCATATCAA TAAGCGGAGG AGAAGAAACT AACAAGGATT   [787]
K. albomontana SR149               GCTGAGTTTA AGCATATCAA TAAGCGGAGG AGAAGAAACT AACAAGGATT   [787]
K. angustifolia SR453              GCTGAGTTTA AGCATATCAA TAAGCGGAGG AGAAGAAACT AACAAGGATC   [787]
K. angustifolia SR542              GCTGAGTTTA AGCATATCAA TAAGCGGAGG AGAAGAAACT AACAAGGATT   [787]
K. ankaratrensis PBP5676           GCTGAGTTTA AGCATATCAA TAAGCGGAGG AGAAGAAACT AACAAGGATT   [787]
K. baurii SR275                    GCTGAGTTTA AGCATATCAA TAAGCGGAGG AGAAGAAACT AACAAGGATT   [787]
K. baurii SR285                    GCTGAGTTTA AGCATATCAA TAAGCGGAGG AGAAGAAACT AACAAGGATT   [787]
K. baurii SR360                    GCTGAGTTTA AGCATATCAA TAAGCGGAGG AGAAGAAACT AACAAGGATT   [787]
K. baurii SR382                    GCTGAGTTTA AGCATATCAA TAAGCGGAGG AGAAGAAACT AACAAGGATT   [787]
K. baurii NPB1923                  GCTGAGTTTA AGCATATCAA TAAGCGGAGG AGAAGAAACT AACAAGGATT   [787]
K. brachystachya SRsn              GCTGAGTTTA AGCATATCAA TAAGCGGAGG AGAAGAAACT AACAAGGATT   [788]
K. brevifolia SR452                GCTGAGTTTA AGCATATCAA TAAGCGGAGG AGAAGAAACT AACAAGGATT   [787]
K. bruceae SR171                   GCTGAGTTTA AGCATATCAA TAAGCGGAGG AGAAGAAACT AACAAGGATT   [787]
K. buchananii SR307                GCTGAGTTTA AGCATATCAA TAAGCGGAGG AGAAGAAACT AACAAGGATT   [787]
K. caulescens SR270                GCTGAGTTTA AGCATATCAA TAAGCGGAGG AGAAGAAACT AACAAGGATT   [787]
K. caulescens SR278                GCTGAGTTTA AGCATATCAA TAAGCGGAGG AGAAGAAACT AACAAGGATT   [787]
K. caulescens NPB1821              GCTGAGTTTA AGCATATCAA TAAGCGGAGG AGAAGAAACT AACAAGGATT   [787]
K. citrina SR176                   GCTGAGTTTA AGCATATCAA TAAGCGGAGG AGAAGAAACT AACAAGGATT   [787]
K. coddiana SRsn                   GCTGAGTTTA AGCATATCAA TAAGCGGAGG AGAAGAAACT AACAAGGATT   [787]
K. corraligemma SR549              GCTGAGTTTA AGCATATCAA TAAGCGGAGG AGAAGAAACT AACAAGGATT   [787]
K. drepanophylla RAL4816           GCTGAGTTTA AGCATATCAA TAAGCGGAGG AGAAGAAACT AACAAGGATT   [787]
K. ensifolia ensifolia JBsn        GCTGAGTTTA AGCATATCAA TAAGCGGAGG AGAAGAAACT AACAAGGATT   [787]
K. ensifolia autumnalis SR448      GCTGAGTTTA AGCATATCAA TAAGCGGAGG AGAAGAAACT AACAAGGATT   [787]
K. fibrosa SR297                   GCTGAGTTTA AGCATATCAA TAAGCGGAGG AGAAGAAACT AACAAGGATT   [787]
K. fluvitalis SRsn                 GCTGAGTTTA AGCATATCAA TAAGCGGAGG AGAAGAAACT AACAAGGATT   [787]
K. foliosa SR383                   GCTGAGTTTA AGCATATCAA TAAGCGGAGG AGAAGAAACT AACAAGGATT   [787]
K. foliosa SR387                   GCTGAGTTTA AGCATATCAA TAAGCGGAGG AGAAGAAACT AACAAGGATT   [787]
K. foliosa SR389                   GCTGAGTTTA AGCATATCAA TAAGCGGAGG AGAAGAAACT AACAAGGATT   [787]
K. foliosa SR390                   GCTGAGTTTA AGCATATCAA TAAGCGGAGG AGAAGAAACT AACAAGGATT   [787]
K. foliosa JMG034                  GCTGAGTTTA AGCATATCAA TAAGCGGAGG AGAAGAAACT AACAAGGATT   [787]
K. foliosa JMG038                  GCTGAGTTTA AGCATATCAA TAAGCGGAGG AGAAGAAACT AACAAGGATT   [787]
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K. galpinii SR312                  GCTGAGTTTA AGCATATCAA TAAGCGGAGG AGAAGAAACT AACAAGGATT   [787]
K. gracilis SR321                  GCTGAGTTTA AGCATATCAA TAAGCGGAGG AGAAGAAACT AACAAGGATT   [787]
K. gracilis NNBG                   GCTGAGTTTA AGCATATCAA TAAGCGGAGG AGAAGAAACT AACAAGGATT   [787]
K. grantii CP4154                  GCTGAGTTTA AGCATATCAA TAAGCGGAGG AGAAGAAACT AACAAGGATT   [788]
K. hirsuta SR282                   GCTGAGTTTA AGCATATCAA TAAGCGGAGG AGAAGAAACT AACAAGGATT   [787]
K. ichopensis SR242                GCTGAGTTTA AGCATATCAA TAAGCGGAGG AGAAGAAACT AACAAGGATT   [787]
K. ichopensis SR286                GCTGAGTTTA AGCATATCAA TAAGCGGAGG AGAAGAAACT AACAAGGATT   [787]
K. ichopensis SR289                GCTGAGTTTA AGCATATCAA TAAGCGGAGG AGAAGAAACT AACAAGGATT   [787]
K. insignis SRsn                   GCTGAGTTTA AGCATATCAA TAAGCGGAGG AGAAGAAACT AACAAGGATT   [787]
K. isoetofolia SR386               GCTGAGTTTA AGCATATCAA TAAGCGGAGG AGAAGAAACT AACAAGGATT   [787]
K. isoetifolia SR388               GCTGAGTTTA AGCATATCAA TAAGCGGAGG AGAAGAAACT AACAAGGATT   [787]
K. isoetifolia SR393               GCTGAGTTTA AGCATATCAA TAAGCGGAGG AGAAGAAACT AACAAGGATT   [787]
K. latifolia RSSsn                 GCTGAGTTTA AGCATATCAA TAAGCGGAGG AGAAGAAACT AACAAGGATT   [787]
K. laxiflora SR283                 GCTGAGTTTA AGCATATCAA TAAGCGGAGG AGAAGAAACT AACAAGGATT   [787]
K. laxifolia SR295                 GCTGAGTTTA AGCATATCAA TAAGCGGAGG AGAAGAAACT AACAAGGATT   [787]
K. laxiflora SR467                 GCTGAGTTTA AGCATATCAA TAAGCGGAGG AGAAGAAACT AACAAGGATT   [787]
K. laxiflora SR468                 GCTGAGTTTA AGCATATCAA TAAGCGGAGG AGAAGAAACT AACAAGGATT   [787]
K. laxifloraC SRsn                 GCTGAGTTTA AGCATATCAA TAAGCGGAGG AGAAGAAACT AACAAGGATT   [787]
K. laxiflora NPB1810               GCTGAGTTTA AGCATATCAA TAAGCGGAGG AGAAGAAACT AACAAGGATT   [787]
K. leucocephala NNBG               GCTGAGTTTA AGCATATCAA TAAGCGGAGG AGAAGAAACT AACAAGGATT   [787]
K. linearifolia SR170              GCTGAGTTTA AGCATATCAA TAAGCGGAGG AGAAGAAACT AACAAGGATT   [787]
K. linearifolia SR269              GCTGAGTTTA AGCATATCAA TAAGCGGAGG AGAAGAAACT AACAAGGATT   [787]
K. linearifolia SR290              GCTGAGTTTA AGCATATCAA TAAGCGGAGG AGAAGAAACT AACAAGGATT   [787]
K. linearifolia SR291              GCTGAGTTTA AGCATATCAA TAAGCGGAGG AGAAGAAACT AACAAGGATT   [787]
K. linearifolia SR311              GCTGAGTTTA AGCATATCAA TAAGCGGAGG AGAAGAAACT AACAAGGATT   [787]
K. linearifolia SR313              GCTGAGTTTA AGCATATCAA TAAGCGGAGG AGAAGAAACT AACAAGGATT   [787]
K. linearifolia SR328              GCTGAGTTTA AGCATATCAA TAAGCGGAGG AGAAGAAACT AACAAGGATT   [787]
K. linearifolia SR343              GCTGAGTTTA AGCATATCAA TAAGCGGAGG AGAAGAAACT AACAAGGATT   [787]
K. littoralis SR200                GCTGAGTTTA AGCATATCAA TAAGCGGAGG AGAAGAAACT AACAAGGATT   [787]
K. multiflora SR310                GCTGAGTTTA AGCATATCAA TAAGCGGAGG AGAAGAAACT AACAAGGATT   [787]
K. multiflora SR315                GCTGAGTTTA AGCATATCAA TAAGCGGAGG AGAAGAAACT AACAAGGATT   [787]
K. northiae SR263                  GCTGAGTTTA AGCATATCAA TAAGCGGAGG AGAAGAAACT AACAAGGATT   [787]
K. northiae SR446                  GCTGAGTTTA AGCATATCAA TAAGCGGAGG AGAAGAAACT AACAAGGATT   [787]
K. parviflora SR268                GCTGAGTTTA AGCATATCAA TAAGCGGAGG AGAAGAAACT AACAAGGATT   [787]
K. paviflora SR330                 GCTGAGTTTA AGCATATCAA TAAGCGGAGG AGAAGAAACT AACAAGGATT   [787]
K. pauciflora HBsn                 GCTGAGTTTA AGCATATCAA TAAGCGGAGG AGAAGAAACT AACAAGGATT   [787]
K. porphyantha SRsn                GCTGAGTTTA AGCATATCAA TAAGCGGAGG AGAAGAAACT AACAAGGATT   [787]
K. praecox SR529                   GCTGAGTTTA AGCATATCAA TAAGCGGAGG AGAAGAAACT AACAAGGATT   [787]
K. rigidifolia SRsn                GCTGAGTTTA AGCATATCAA TAAGCGGAGG AGAAGAAACT AACAAGGATT   [787]
K. ritualis SR300                  GCTGAGTTTA AGCATATCAA TAAGCGGAGG AGAAGAAACT AACAAGGATT   [787]
K. rooperi SR237                   GCTGAGTTTA AGCATATCAA TAAGCGGAGG AGAAGAAACT AACAAGGATT   [787]
K. rooperi SR485                   GCTGAGTTTA AGCATATCAA TAAGCGGAGG AGAAGAAACT AACAAGGATT   [787]
K. sarmentosa SR207                GCTGAGTTTA AGCATATCAA TAAGCGGAGG AGAAGAAACT AACAAGGATT   [787]
K. schemperi SR391                 GCTGAGTTTA AGCATATCAA TAAGCGGAGG AGAAGAAACT AACAAGGATT   [787]
K. schemperi JMG036                GCTGAGTTTA AGCATATCAA TAAGCGGAGG AGAAGAAACT AACAAGGATT   [787]
K. splendida SR548                 GCTGAGTTTA AGCATATCAA TAAGCGGAGG AGAAGAAACT AACAAGGATT   [787]
K. stricta SR279                   GCTGAGTTTA AGCATATCAA TAAGCGGAGG AGAAGAAACT AACAAGGATT   [787]
K. thodei SR407                    GCTGAGTTTA AGCATATCAA TAAGCGGAGG AGAAGAAACT AACAAGGATT   [787]
K. thomsonii JMG031                GCTGAGTTTA AGCATATCAA TAAGCGGAGG AGAAGAAACT AACAAGGATT   [787]
K. thomsonii AMM                   GCTGAGTTTA AGCATATCAA TAAGCGGAGG AGAAGAAACT AACAAGGATT   [787]
K. thomsonii CK4821                GCTGAGTTTA AGCATATCAA TAAGCGGAGG AGAAGAAACT AACAAGGATT   [787]
K. triangularis SR264              GCTGAGTTTA AGCATATCAA TAAGCGGAGG AGAAGAAACT AACAAGGATT   [787]
K. triangularis SR266              GCTGAGTTTA AGCATATCAA TAAGCGGAGG AGAAGAAACT AACAAGGATT   [787]
K. triangularis SR299              GCTGAGTTTA AGCATATCAA TAAGCGGAGG AGAAGAAACT AACAAGGATT   [787]
K. triangularis obtusiloba SRsn    GCTGAGTTTA AGCATATCAA TAAGCGGAGG AGAAGAAACT AACAAGGATT   [787]
K. typhoides JB8084                GCTGAGTTTA AGCATATCAA TAAGCGGAGG AGAAGAAACT AACAAGGATT   [788]
K. typhoides NNBG                  GCTGAGTTTA AGCATATCAA TAAGCGGAGG AGAAGAAACT AACAAGGATT   [788]
K. tysonii SR302                   GCTGAGTTTA AGCATATCAA TAAGCGGAGG AGAAGAAACT AACAAGGATT   [787]
K. tysonii SR303                   GCTGAGTTTA AGCATATCAA TAAGCGGAGG AGAAGAAACT AACAAGGATT   [787]
K. umbrina RGsn                    GCTGAGTTTA AGCATATCAA TAAGCGGAGG AGAAGAAACT AACAAGGATT   [787]
K. uvaria SR186                    GCTGAGTTTA AGCATATCAA TAAGCGGAGG AGAAGAAACT AACAAGGATT   [787]
K. uvaria SR201                    GCTGAGTTTA AGCATATCAA TAAGCGGAGG AGAAGAAACT AACAAGGATT   [787]
K. uvaria SR203                    GCTGAGTTTA AGCATATCAA TAAGCGGAGG AGAAGAAACT AACAAGGATT   [787]
K. uvaria SR211                    GCTGAGTTTA AGCATATCAA TAAGCGGAGG AGAAGAAACT AACAAGGATT   [787]
K. uvaria SR342                    GCTGAGTTTA AGCATATCAA TAAGCGGAGG AGAAGAAACT AACAAGGATT   [787]
K. uvaria SR344                    GCTGAGTTTA AGCATATCAA TAAGCGGAGG AGAAGAAACT AACAAGGATC   [787]
K. uvaria SR477                    GCTGAGTTTA AGCATATCAA TAAGCGGAGG AGAAGAAACT AACAAGGATT   [787]
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Appendix 7: List of haplotype generated by the TCS analysis for full data set

A total of 56 haplotype were recognised by TCS of which 15 were internal node haplotypes. The remaining 41 are characterised below:

1. Haplotype SR549 (n=1): SR 549
2. Haplotype SR548 (n=1): SR 548
3. Haplotype SR468 (n=1): SR 468
4. Haplotype SR467 (n=3): SR 467, SR 330, SR398
5. Haplotype SR283 (n=1): SR 283
6. Haplotype SR311 (n=1): SR 311
7. Haplotype laxiCSRsn (n=1): *K. laxiflora C* SR *sn*
8. Haplotype SR211 (n=4): SR 211, SR 201, RJM 1026, SR530
9. Haplotype TD4477 (n=1): TD 4477
10. Haplotype KtypNNBG (n=11): *K. typhoides* NNBG, SR186, *K. brachystachya* SR *sn*, SR 176, SR 529, SR 207, SR 203, SR 202, SR 532, SR 528, SR 166
11. Haplotype CP4154 (n=1): CP 4154
12. Haplotype PBP5676 (n=1): PBP 5676
13. Haplotype SR275 (n=1): SR 275
14. Haplotype SR314 (n=8): SR 314, SR 452, SR 360, SR 382, SR 448, SR 485, SR 344, SR 477
15. Haplotype NPB1923 (n=1): NPB 1923
16. Haplotype NPB1821 (n=1): NPB 1821
17. Haplotype RAL4816 (n=1): RAL 4816
18. Haplotype SR285 (n=5): SR 285, SR 171, *K. coddiana* SR *sn*, TD 4638, RAL 4227
19. Haplotype SR328 (n=1): SR 328
20. Haplotype SR282 (n=2): SR 282, SR 295
21. Haplotype SR300 (n=27): SR 300, SR 279, SR 299, SR 302, SR 149, SR 542, SR 297, SR 321, *K. gracilis* NNBG, SR 242, SR 289, *K. latifolia* RSS *sn*, NPB 1810, SR 291, SR 290, SR 200, *K. pauciflora* HB *sn*, SR 407, SR 305, SR 485, RJM 1100, SR 561, SR 409, SR 441, SR 442, SR 558, SR 460
22. Haplotype SR286 (n=1): SR 286
23. Haplotype SR400 (n=1): SR 400
24. Haplotype SR287 (n=1): SR 287
25. Haplotype SR269 (n=2): SR 269; SR 264
26. Haplotype TD4626 (n=11): TD 4626, SR 446, SR 268, SR 342, SR 263, SR 237, SR 266, PBP 5579,SR 172, SR 337, SR 471
27. Haplotype SR391 (n=1): SR 391
28. Haplotype SR388 (n=4): SR 388, JMG 031, SR 389, SR 390
29. Haplotype SR174 (n=1): SR 174
30. Haplotype SR307 (n=1): SR 307
31. Haplotype Chap9061 (n=1): Chapman & Chapman 9061
32. Haplotype insiSRsn (n=3): SR *sn K. insignis*, AMM 2647, CK 4821
33. Haplotype JMG034 (n=6): JMG 034, JMG 036, SR 387, JMG 038, SR 386, SR 393
34. Haplotype SR310 (n=1): SR 310
35. Haplotype SR312 (n=1): SR 312
36. Haplotype SR383 (n=1): SR 310
37. Haplotype KporphSRsn (n=1): *K. porphyantha* SR *sn*
38. Haplotype RGsn (n=5): RG *sn*, *K. ensifolia* JB *sn*, *K. leucocephala* NNBG, *K. rigidifolia* SR *sn*, *K. triangularis* subsp. *obtusifolia* SR *sn*

39. Haplotype SR303 (n=1): SR 303
40. Haplotype SR453 (n=1): SR 453
41. Haplotype SR278 (n=4): SR 278, SR 270, RJM 974, SR 274

Appendix 8: List of haplotype generated by the TCS analysis for South African samples

A total of 42 haplotype were recognised by TCS of which nine were internal node haplotypes. The remaining 33 are characterised below:

1. Haplotype SR549 (n=1): SR 549
2. Haplotype SR549 (n=1): SR 549
3. Haplotype SR468 (n=1): SR 468
4. Haplotype SR467 (n=3): SR 467, SR 330, SR398
5. Haplotype SR283 (n=1): SR 283
6. Haplotype SR311 (n=1): SR 311
7. Haplotype laxiCSRsn (n=1): *K. laxiflora C* SR *sn*
8. Haplotype SR211 (n=4): SR 211, SR 201, RJM 1026, SR530
9. Haplotype KtypNNBG (n=11): *K. typhoides* NNBG, SR186, *K. brachystachya* SR *sn*, SR 176, SR 529, SR 207, SR 203, SR 202, SR 532, SR 528, SR 166
10. Haplotype TD4477 (n=1): TD 4477
11. Haplotype SR275 (n=1): SR 275
12. Haplotype NPB1923 (n=1): NPB 1923
13. Haplotype SR314 (n=8): SR 314, SR 452, SR 360, SR 382, SR 448, SR 485, SR 344, SR 477
14. Haplotype NPB1821 (n=1): NPB 1821
15. Haplotype RAL4816 (n=1): RAL 4816
16. Haplotype SR285 (n=5): SR 285, SR 171, *K. coddiana* SR *sn*, TD 4638, RAL 4227
17. Haplotype SR328 (n=1): SR 328
18. Haplotype SR282 (n=2): SR 282, SR 295
19. Haplotype SR286 (n=1): SR 286
20. Haplotype SR300 (n=27): SR 300, SR 279, SR 299, SR 302, SR 149, SR 542, SR 297, SR 321, *K. gracilis* NNBG, SR 242, SR 289, *K. latifolia* RSS *sn*, NPB 1810, SR 291, SR 290, SR 200, *K. pauciflora* HB *sn*, SR 407, SR 305, SR 485, RJM 1100, SR 561, SR 409, SR 441, SR 442, SR 558, SR 460
21. Haplotype SR287 (n=1): SR 287
22. Haplotype SR400 (n=1): SR 400
23. Haplotype SR269 (n=2): SR 269; SR 264
24. Haplotype TD4626 (n=11): TD 4626, SR 446, SR 268, SR 342, SR 263, SR 237, SR 266, PBP 5579,SR 172, SR 337, SR 471
25. Haplotype SR174 (n=1): SR 174
26. Haplotype SR307 (n=1): SR 307
27. Haplotype SR310 (n=1): SR 310
28. Haplotype SR312 (n=1): SR 312
29. Haplotype SR303 (n=1): SR 303
30. Haplotype SR453 (n=1): SR 453
31. Haplotype RGsn (n=5): RG *sn*, *K. ensifolia* JB *sn*, *K. leucocephala* NNBG, *K. rigidifolia* SR *sn*, *K. triangularis* subsp. *obtusifolia* SR *sn*
32. Haplotype KporphSRsn (n=1): *K. porphyantha* SR *sn*
33. Haplotype SR278 (n=4): SR 278, SR 270, RJM 974, SR 274

Appendix 9: GeoDis input file at half degree grid scale (NCA: South African samples)

```
Kniphofia cpDNA
39
Iron Crown
2 24 00 00 S 29 30 00 E
Witbank
1 25 30 00 S 29 00 00 E
3 Lydenberg
4 25 00 00 S 30 00 00 E
4 Long Toms
1 25 00 00 S 30 30 00 E
5 Forbes reef
1 26 00 00 S 31 00 00 E
6 Wakkerstroom
2 27 00 00 S 30 00 00 E
7 Vryheid
1 27 30 00 S 30 30 00 E
8 Cath Peak
7 28 30 00 S 29 00 00 E
9 Estcourt
2 28 30 00 S 29 30 00 E
10 Rich Bay
1 28 30 00 S 32 00 00 E
11 Kamberg
5 29 00 00 S 29 30 00 E
12 Sani Pass
2 29 30 00 S 29 00 00 E
13 Pervensey
3 29 30 00 S 29 30 00 E
14 Howick
7 29 00 00 S 30 00 00 E
15 Greytown
4 29 00 00 S 30 30 00 E
16 Durban
4 29 30 00 S 30 30 00 E
17 Rhodes
2 30 30 00 S 27 30 00 E
18 Naudes Nek
7 30 30 00 S 28 00 00 E
19 Franklin
2 30 00 00 S 29 00 00 E
20 Weza
2 30 30 00 S 29 30 00 E
21 Ixopo
2 30 00 00 S 30 00 00 E
22 Scottburgh
1 30 00 00 S 30 30 00 E
23 Elliot
1 31 00 00 S 27 30 00 E
24 Mkambati
3 31 00 00 S 29 30 00 E
25 Post Chalmers
1 32 00 00 S 25 00 00 E
26 Seymour
8 32 30 00 S 26 30 00 E
27 Stutterheim
1 32 30 00 S 27 00 00 E
28 Komga
2 32 30 00 S 27 30 00 E
29 The haven
1 32 00 00 S 28 30 00 E
30 Matroosberg
2 33 00 00 S 19 30 00 E
31 George
1 33 30 00 S 22 00 00 E
32 The Crags
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2 33 30 00 S 23 00 00 E
33 Joubertina
1 33 30 00 S 23 30 00 E
34 Kareedouw
3 33 30 00 S 23 30 00 E
35 Port Eliza
4 33 30 00 S 25 30 00 E
36 Grahamstown
5 33 00 00 S 26 30 00 E
37 East london
1 33 00 00 S 27 30 00 E
38 Fish River Mouth
1 33 30 00 S 27 00 00 E
39 Humansdorp
3 34 00 00 S 24 30 00 E
21
Clade 1-2
3
4 5 6
0 0 1
4
20 19 14 18
1  0  0  0
1  1  1  0
0  0  0  1
Clade 1-3
2
7 8
1 0
2
3 6
1 0
0 1
Clade 1-4
3
9 10 11
1 0  1
9
34 32 33 7 9 39 30 31 35
2  1  1  0 0 0  0  0  0
1  1  0  1 1 2  2  1  2
0  0  0  0 0 0  0  0  1
Clade 1-6
2
13 14
0  1
5
36 6 8 35 38
1  0 0 0 0
3  1 2 1 1
Clade 1-8
4
16 17 18 19
0  1  0  0
7
24 18 28 23 29 19 11
1  0  0  0  0  0  0
1  1  1  1  1  0  0
0  0  0  0  0  1  0
0  1  0  0  0  0  1
Clade 1-9
4
20 21 22 23
1  0  1  1
13
11 13 17 21 15 8 16 9 14 26 12 24 22
1  0  0  0  0  0 0  0 0  0  0  0  0
3  3  1  1  3  2 4  1 5  1  1  1  1
0  0  0  0  0  0 0  0 1  0  0  0  0
```

```
0  0  0  0  0  1 0  0 0  0  0  0  0
Clade 1-10
2
24 25
1  0
6
26 25 37 27 28 36
2  0  0  0  0  0
6  1  1  1  1  1
Clade 1-11
2
26 27
1  0
2
39 15
1  0
0  1
Clade 1-12
2
28 29
0  0
2
3 4
1 0
0 1
Clade 1-13
2
30 31
0  0
2
8 21
1 0
0 1
Clade 1-14
2
32 33
0  0
5
3 5 2 10 4
1 0 0 0  0
1 1 1 1  1
Clade 2-1
2
1-1 1-4
1   1
10
1 34 32 33 7 9 39 30 31 35
2 0  0  0  0 0 0  0  0  0
0 3  2  1  1 1 2  2  1  2
Clade 2-2
2
1-2 1-9
1   0
16
20 19 14 18 11 13 17 21 15 8 16 9 26 12 24 22
2  1  1  1  0  0  0  0  0  0 0  0 0  0  0  0
0  0  6  0  4  3  1  1  3  3 4  1 1  1  1  1
Clade 2-3
2
1-3 1-12
0   0
3
3 6 4
1 1 0
1 0 1
Clade 2-4
2
1-5 1-8
1   0
```

```
7
18 24 28 23 29 19 11
0  1  0  0  0  0  0
2  2  1  1  1  1  1
Clade 2-5
2
1-6 1-13
0   0
6
36 6 8 35 38 21
4  1 2 1  1  0
0  0 1 0  0  1
Clade 2-6
3
1-7 1-15 1-10
0   0    1
9
12 17 18 26 25 37 27 28 36
1  0  0  0  0  0  0  0  0
0  1  2  0  0  0  0  0  0
0  0  0  8  1  1  1  1  1
Clade 2-7
2
1-11 1-14
0    0
7
39 15 3 5 2 10 4
1  1  0 0 0 0  0
0  0  2 1 1 1  1
Clade 3-1
2
2-1 2-7
1   0
16
1 34 32 33 7 9 39 30 31 35 15 3 5 2 10 4
2 3  2  1  1 1 2  2  1  2  0  0 0 0 0  0
0 0  0  0  0 0 1  0  0  0  1  2 1 1 1  1
Clade 3-2
2
2-2 2-4
1   0
19
20 19 14 18 11 13 17 21 15 8 16 9 26 12 24 22 28 23 29
2  1  7  1  5  3  1  1  3  3  4 1 1  1  1  1  0  0  0
0  1  0  3  1  0  0  0  0  0  0 0 0  0  3  0  1  1  1
Clade 3-3
3
2-3 2-5 2-6
1   0   1
16
3 6 4 36 8 35 38 21 12 17 18 26 25 37 27 28
2 1 1 0  0 0  0  0  0  0  0  0  0  0  0  0
0 1 0 4  3 1  1  2  0  0  0  0  0  0  0  0
0 0 0 1  0 0  0  0  1  1  3  8  1  1  1  1
Total Cladogram
3
3-1 3-2 3-3
1   1   1
39
1 34 32 33 7 9 39 30 31 35 15 3 5 2 10 4 20 19 14 18 11 13 17 21 8 16
26 12 24 22 28 23 29 6 36 38 25 37 27
2 3  2  1  1 1 3  2  1  2  1  2 1 1 1  1 0  0  0  0  0  0  0  0  0 0  0
0  0  0  0  0  0  0 0  0  0  0  0
0 0  0  0  0 1 0  0  0  0  3  0 0 0 0  0 2  2  7  4  6  3  1  1  3 4  1
1  4  1  1  1  1  0 0  0  0  0  0
0 0  0  0  0 0 0  0  0  1  0  2 0 0 0  0 1  0  0  3  0  0  1  2  3 0  8
1  0  0  1  0  0  2 5  2  1  1  1
END
```

Appendix 10: GeoDis input file at full degree grid scale (NCA: South African samples)

```
Kniphofia FullcpDNA
25
1 Iron Crown
2 24 00 00 S 29 00 00 E
2 Witbank
1 25 00 00 S 29 00 00 E
3 Lydenberg
7 25 00 00 S 30 00 00 E
4 Wakkerstroom
3 27 00 00 S 30 00 00 E
5 Cath Peak
9 28 00 00 S 29 00 00 E
6 Kamberg
10 29 00 00 S 29 00 00 E
7 Howick
15 29 00 00 S 30 00 00 E
8 Naudes Nek
9 30 00 00 S 28 00 00 E
9 Kokstad
6 30 00 00 S 29 00 00 E
10 Elloit
1 31 00 00 S 27 00 00 E
11 Mkambati
3 31 00 00 S 29 00 00 E
12 Seymour
10 32 00 00 S 26 00 00 E
13 Komga
3 33 00 00 S 27 00 00 E
14 Matroosberg
2 33 00 00 S 19 00 00 E
15 Joubertina
3 33 00 00 S 23 00 00 E
16 Kareedouw
2 33 00 00 S 24 00 00 E
17 Port Eliza
4 33 00 00 S 25 00 00 E
18 Grahamstown
5 33 00 00 S 26 00 00 E
19 East London
2 33 00 00 S 27 00 00 E
20 Humansdorp
4 34 00 00 S 24 00 00 E
21 Richards Bay
1 28 00 00 S 32 00 00 E
22 Scottbrough
1 30 00 00 S 30 00 00 E
23 Cradock
1 32 00 00 S 25 00 00 E
24 The Haven
1 32 00 00 S 28 00 00 E
25 George
1 33 00 00 S 22 00 00 E
20
Clade 1-2
3
4 5 6
0 1 0
3
9 7 8
1 0 0
2 1 0
0 0 1
Clade 1-3
2
7 8
```

```
0 1
2
3 4
1 0
0 1
Clade 1-4
3
9 10 11
1 1  0
8
20 16 15 4 5 14 25 17
1  1  2  0 0 0  0  0
2  1  1  1 1 2  1  2
0  0  0  0 0 0  0  1
Clade 1-6
2
13 14
0  1
5
18 4 5 17 2
1  0 0 0  0
3  1 2 1  1
Clade 1-8
4
16 17 18 19
0  0  0  1
7
11 8 13 10 24 9 6
1  0 0  0  0  0 0
1  1 1  1  1  0 0
0  0 0  0  0  1 0
0  1 0  0  0  0 1
Calde 1-9
4
20 21 22 23
1  1  1  0
8
6 8 9 7  5 12 11 22
1 0 0 0  0 0  0  0
7 1 1 12 3 1  1  1
0 0 0 1  0 0  0  0
0 0 0 0  1 0  0  0
Clade 1-10
2
24 25
0  1
5
12 23 19 13 18
2  0  0  0  0
6  1  1  2  1
Clade1-11
2
26 27
0  1
2
20 7
1  0
0  1
Clade 1-13
2
30 31
0  0
2
5 9
1 0
0 1
Clade 1-14
2
32 33
```

```
0  0
3
3 2 21
1 0 0
3 1 1
Clade 2-1
2
1-1 1-4
1   1
9
1 20 16 15 4 5 14 25 17
2 0  0  0  0 0 0  0  0
0 3  2  3  1 1 2  1  3
Clade 2-2
2
1-2 1-9
1   0
8
9 7  8 6 5 12 11 22
3 1  1 0 0 0  0  0
1 13 1 8 4 1  1  1
Clade 2-3
2
1-3 1-12
0   0
2
3 4
1 1
2 0
Clade 2-4
2
1-5 1-8
1   0
7
8 11 13 10 24 9 6
1 0  0  0  0  0 0
2 2  1  1  1  1 1
Clade 2-5
2
1-6 1-13
0   0
6
18 4 5 17 2 9
4  1 2 1  1 0
0  0 1 0  0 1
Clade 2-6
3
1-7 1-15 1-10
0   0    1
7
6 8 12 23 19 13 18
1 0 0  0  0  0  0
0 4 0  0  0  0  0
0 0 8  1  1  2  1
Clade 2-7
2
1-11 1-14
0    0
5
20 7 3 2 21
1  1 0 0 0
0  0 4 1 1
Clade 3-1
2
2-1 2-7
1   0
13
1 20 16 15 4 5 14 25 17 7 3 2 21
2 3  2  3  1 1 2  1  3  0 0 0 0
```

```
0 1  0  0  0 0 0  0  0  1 4 1 1
Clade 3-2
2
2-2 2-4
0   1
11
9 7  8 6 5 12 11 22 13 10 24
4 14 2 8 4 1  1  1  0  0  0
1 0  3 1 0 0  2  0  1  1  1
Clade 3-3
3
2-3 2-5 2-6
1   0   1
13
3 4 18 5 17 2 9 6 8 12 23 19 13
3 1 0  0 0  0 0 0 0 0  0  0  0
0 1 4  3 1  1 1 0 0 0  0  0  0
0 0 1  0 0  0 0 1 4 8  1  1  2
Total Cladogram
3
3-1 3-2 3-3
1   1   1
25
1 20 16 15 4 5 14 25 17 7 3 2 21 9 8 6 12 11 23 13 10 24 18 23 19
2 4  2  3  1 1 2  1  3  1 4 1 1  0 0 0 0  0  0  0  0  0  0  0  0
0 0  0  0  0 4 14 0  0  0 0 0 0  5 5 9 1  3  1  1  1  1  0  0  0
0 0  0  0  2 3 0  0  1  0 3 1 0  1 4 1 8  0  0  2  0  0  5  1  1
END
```

Appendix 11: GeoDis output file at half degree grid scale (NCA: South African samples)

```
Differentiating population structure from history - Geodis  2.4
(c) Copyright, 1999-2005 David Posada and Alan Templeton
Contact: David Posada, University of Vigo, Spain (dposada@uvigo.es)
________________________________________________________________________


Input file:
/Applications/phylosoft/GeoDis2.4/SYD/Half_deg/geodis_half.txt
Kniphofia cpDNA

Tue Jan 31 12:11:33 SAST 2006


PERMUTATION ANALYSIS OF Clade 1-2
   BASED ON 1000 RESAMPLES


PART I.  PERMUTATIONAL CONTINGENCY TEST:


  OBSERVED CHI-SQUARE STATISTIC =     6.6667

  THE PROBABILITY OF A RANDOM CHI-SQUARE BEING GREATER THAN
    OR EQUAL TO THE OBSERVED CHI-SQUARE =     0.8820


PART II.  GEOGRAPHIC DISTANCE ANALYSIS:

GEOGRAPHICAL CENTERS    LATITUDE      LONGITUDE
       Clade 1-2       -30 14'24"     29 16'48"
               4      -30 30'00"     29 30'00"
               5      -30 05'38"     29 20'38"
               6      -30 30'00"     28 00'00"

CLADE 4 (Interior)
 TYPE OF DISTANCE       DISTANCE      PROB.<=      PROB.>=
     WITHIN CLADE        0.0000       1.0000       1.0000
     NESTED CLADE       35.7612       0.4260       1.0000

CLADE 5 (Interior)
 TYPE OF DISTANCE       DISTANCE      PROB.<=      PROB.>=
     WITHIN CLADE       53.0996       0.7970       0.3900
     NESTED CLADE       51.5050       0.6790       0.5080

CLADE 6 (Tip)
 TYPE OF DISTANCE       DISTANCE      PROB.<=      PROB.>=
     WITHIN CLADE        0.0000       1.0000       1.0000
     NESTED CLADE      126.0358       0.8100       0.3980


PART III.  TEST OF INTERIOR VS. TIP CLADES:

 TYPE OF DISTANCE   I-T DISTANCE      PROB.<=      PROB.>=
     WITHIN CLADE       39.8247       0.7970       0.3900
     NESTED CLADE      -78.4667       0.3370       0.7610




PERMUTATION ANALYSIS OF Clade 1-3
   BASED ON 1000 RESAMPLES


PART I.  PERMUTATIONAL CONTINGENCY TEST:


  OBSERVED CHI-SQUARE STATISTIC =     2.0000

  THE PROBABILITY OF A RANDOM CHI-SQUARE BEING GREATER THAN
    OR EQUAL TO THE OBSERVED CHI-SQUARE =     1.0000


PART II.  GEOGRAPHIC DISTANCE ANALYSIS:

GEOGRAPHICAL CENTERS    LATITUDE      LONGITUDE
       Clade 1-3       -26 19'60"     30 00'00"
```

```
           7      -25 00'00"    30 00'00"
           8      -27 00'00"    30 00'00"

CLADE 7 (Tip)
 TYPE OF DISTANCE      DISTANCE     PROB.<=     PROB.>=
     WITHIN CLADE        0.0000      1.0000      1.0000
     NESTED CLADE      148.1194      1.0000      0.5270

CLADE 8 (Interior)
 TYPE OF DISTANCE      DISTANCE     PROB.<=     PROB.>=
     WITHIN CLADE        0.0000      1.0000      1.0000
     NESTED CLADE       74.0597      0.5270      1.0000


PART III.  TEST OF INTERIOR VS. TIP CLADES:

 TYPE OF DISTANCE   I-T DISTANCE     PROB.<=     PROB.>=
     WITHIN CLADE        0.0000      1.0000      1.0000
     NESTED CLADE      -74.0597      0.5270      1.0000




PERMUTATION ANALYSIS OF Clade 1-4
   BASED ON 1000 RESAMPLES


PART I.  PERMUTATIONAL CONTINGENCY TEST:


  OBSERVED CHI-SQUARE STATISTIC =    14.0000

  THE PROBABILITY OF A RANDOM CHI-SQUARE BEING GREATER THAN
    OR EQUAL TO THE OBSERVED CHI-SQUARE =     0.7430


PART II.  GEOGRAPHIC DISTANCE ANALYSIS:

GEOGRAPHICAL CENTERS    LATITUDE      LONGITUDE
      Clade 1-4       -32 24'19"    24 16'44"
           9      -33 30'00"    23 23'05"
          10       -31 55'27"    24 34'33"
          11       -33 30'00"    25 30'00"

CLADE 9 (Tip)
 TYPE OF DISTANCE      DISTANCE     PROB.<=     PROB.>=
     WITHIN CLADE       16.4443      0.0050      0.9980
     NESTED CLADE      148.2542      0.0190      0.9840

CLADE 10 (Interior)
 TYPE OF DISTANCE      DISTANCE     PROB.<=     PROB.>=
     WITHIN CLADE      414.2011      0.9550      0.0500
     NESTED CLADE      394.7397      0.9680      0.0370

CLADE 11 (Tip)
 TYPE OF DISTANCE      DISTANCE     PROB.<=     PROB.>=
     WITHIN CLADE        0.0000      1.0000      1.0000
     NESTED CLADE      166.5674      0.4710      0.7360


PART III.  TEST OF INTERIOR VS. TIP CLADES:

 TYPE OF DISTANCE   I-T DISTANCE     PROB.<=     PROB.>=
     WITHIN CLADE      401.0457      0.9970      0.0040
     NESTED CLADE      242.8228      0.9910      0.0100




PERMUTATION ANALYSIS OF Clade 1-6
   BASED ON 1000 RESAMPLES


PART I.  PERMUTATIONAL CONTINGENCY TEST:


  OBSERVED CHI-SQUARE STATISTIC =     1.4063

  THE PROBABILITY OF A RANDOM CHI-SQUARE BEING GREATER THAN
```

```
   OR EQUAL TO THE OBSERVED CHI-SQUARE =     1.0000


PART II.  GEOGRAPHIC DISTANCE ANALYSIS:

GEOGRAPHICAL CENTERS    LATITUDE      LONGITUDE
       Clade 1-6       -31 42'33"     27 27'26"
             13       -33 00'00"     26 30'00"
             14       -31 36'40"     27 31'47"

CLADE 13 (Interior)
 TYPE OF DISTANCE       DISTANCE      PROB.<=      PROB.>=
      WITHIN CLADE        0.0000       1.0000       1.0000
      NESTED CLADE      169.2154       0.4420       1.0000

CLADE 14 (Tip)
 TYPE OF DISTANCE       DISTANCE      PROB.<=      PROB.>=
      WITHIN CLADE      297.8284       0.8840       0.5580
      NESTED CLADE      292.8996       0.8840       0.5580


PART III.  TEST OF INTERIOR VS. TIP CLADES:

 TYPE OF DISTANCE   I-T DISTANCE      PROB.<=      PROB.>=
      WITHIN CLADE     -297.8284       0.5580       0.8840
      NESTED CLADE     -123.6842       0.5580       0.8840




PERMUTATION ANALYSIS OF Clade 1-8
   BASED ON 1000 RESAMPLES


PART I.  PERMUTATIONAL CONTINGENCY TEST:


  OBSERVED CHI-SQUARE STATISTIC =    18.4500

  THE PROBABILITY OF A RANDOM CHI-SQUARE BEING GREATER THAN
   OR EQUAL TO THE OBSERVED CHI-SQUARE =     0.7940


PART II.  GEOGRAPHIC DISTANCE ANALYSIS:

GEOGRAPHICAL CENTERS    LATITUDE      LONGITUDE
       Clade 1-8       -31 10'13"     28 22'24"
             16       -31 00'00"     29 30'00"
             17       -31 33'50"     28 05'02"
             18       -30 00'00"     28 59'60"
             19       -29 37'30"     28 52'30"

CLADE 16 (Interior)
 TYPE OF DISTANCE       DISTANCE      PROB.<=      PROB.>=
      WITHIN CLADE        0.0000       1.0000       1.0000
      NESTED CLADE      108.8491       0.6800       0.5260

CLADE 17 (Tip)
 TYPE OF DISTANCE       DISTANCE      PROB.<=      PROB.>=
      WITHIN CLADE       91.1247       0.1770       0.8490
      NESTED CLADE      104.4307       0.2000       0.8260

CLADE 18 (Interior)
 TYPE OF DISTANCE       DISTANCE      PROB.<=      PROB.>=
      WITHIN CLADE        0.0000       1.0000       1.0000
      NESTED CLADE      143.1576       0.7440       0.3620

CLADE 19 (Interior)
 TYPE OF DISTANCE       DISTANCE      PROB.<=      PROB.>=
      WITHIN CLADE      107.2991       0.9020       0.1500
      NESTED CLADE      188.5663       0.9790       0.0730


PART III.  TEST OF INTERIOR VS. TIP CLADES:

 TYPE OF DISTANCE   I-T DISTANCE      PROB.<=      PROB.>=
      WITHIN CLADE      -37.4751       0.9120       0.0910
      NESTED CLADE       52.8541       0.9060       0.0970
```

```
PERMUTATION ANALYSIS OF Clade 1-9
  BASED ON 1000 RESAMPLES


PART I.  PERMUTATIONAL CONTINGENCY TEST:


  OBSERVED CHI-SQUARE STATISTIC =    20.0000

  THE PROBABILITY OF A RANDOM CHI-SQUARE BEING GREATER THAN
    OR EQUAL TO THE OBSERVED CHI-SQUARE =     0.8990


PART II.  GEOGRAPHIC DISTANCE ANALYSIS:

GEOGRAPHICAL CENTERS    LATITUDE      LONGITUDE
       Clade 1-9       -29 29'57"     29 41'30"
              20       -28 59'60"     29 30'00"
              21       -29 32'22"     29 42'13"
              22       -28 59'60"     30 00'00"
              23       -28 30'00"     28 59'60"

CLADE 20 (Tip)
 TYPE OF DISTANCE      DISTANCE      PROB.<=      PROB.>=
      WITHIN CLADE        0.0000       1.0000       1.0000
      NESTED CLADE       58.4769       0.2170       0.9030

CLADE 21 (Interior)
 TYPE OF DISTANCE      DISTANCE      PROB.<=      PROB.>=
      WITHIN CLADE       94.4665       0.5080       0.5120
      NESTED CLADE       94.0461       0.4690       0.5510

CLADE 22 (Tip)
 TYPE OF DISTANCE      DISTANCE      PROB.<=      PROB.>=
      WITHIN CLADE        0.0000       1.0000       1.0000
      NESTED CLADE       62.9922       0.4050       0.7740

CLADE 23 (Tip)
 TYPE OF DISTANCE      DISTANCE      PROB.<=      PROB.>=
      WITHIN CLADE        0.0000       1.0000       1.0000
      NESTED CLADE      129.7500       0.8990       0.2060


PART III.  TEST OF INTERIOR VS. TIP CLADES:

 TYPE OF DISTANCE   I-T DISTANCE      PROB.<=      PROB.>=
      WITHIN CLADE       94.4665       0.5080       0.5120
      NESTED CLADE       10.3064       0.4960       0.5240



PERMUTATION ANALYSIS OF Clade 1-10
  BASED ON 1000 RESAMPLES


PART I.  PERMUTATIONAL CONTINGENCY TEST:


  OBSERVED CHI-SQUARE STATISTIC =     1.4773

  THE PROBABILITY OF A RANDOM CHI-SQUARE BEING GREATER THAN
    OR EQUAL TO THE OBSERVED CHI-SQUARE =     1.0000


PART II.  GEOGRAPHIC DISTANCE ANALYSIS:

GEOGRAPHICAL CENTERS    LATITUDE      LONGITUDE
      Clade 1-10       -32 31'17"     26 36'23"
              24       -32 30'00"     26 30'00"
              25       -32 31'21"     26 36'44"

CLADE 24 (Tip)
 TYPE OF DISTANCE      DISTANCE      PROB.<=      PROB.>=
      WITHIN CLADE        0.0000       0.3640       1.0000
      NESTED CLADE       10.2425       0.3640       1.0000
```

```
CLADE 25 (Interior)
 TYPE OF DISTANCE      DISTANCE     PROB.<=     PROB.>=
     WITHIN CLADE      80.3518      0.8640      0.5000
     NESTED CLADE       80.4357      0.8640      0.5000


PART III.  TEST OF INTERIOR VS. TIP CLADES:

 TYPE OF DISTANCE   I-T DISTANCE     PROB.<=     PROB.>=
     WITHIN CLADE      80.3518      1.0000      0.3640
     NESTED CLADE       70.1932      1.0000      0.3640




PERMUTATION ANALYSIS OF Clade 1-11
   BASED ON 1000 RESAMPLES


PART I.  PERMUTATIONAL CONTINGENCY TEST:


  OBSERVED CHI-SQUARE STATISTIC =    2.0000

  THE PROBABILITY OF A RANDOM CHI-SQUARE BEING GREATER THAN
    OR EQUAL TO THE OBSERVED CHI-SQUARE =    1.0000


PART II.  GEOGRAPHIC DISTANCE ANALYSIS:

GEOGRAPHICAL CENTERS    LATITUDE     LONGITUDE
     Clade 1-11      -31 51'26"    27 04'17"
             26      -34 00'00"    24 30'00"
             27      -28 59'60"    30 30'00"

CLADE 26 (Tip)
 TYPE OF DISTANCE      DISTANCE     PROB.<=     PROB.>=
     WITHIN CLADE       0.0000      1.0000      1.0000
     NESTED CLADE      337.8429      0.5270      1.0000

CLADE 27 (Interior)
 TYPE OF DISTANCE      DISTANCE     PROB.<=     PROB.>=
     WITHIN CLADE       0.0000      1.0000      1.0000
     NESTED CLADE      456.6681      1.0000      0.5270


PART III.  TEST OF INTERIOR VS. TIP CLADES:

 TYPE OF DISTANCE   I-T DISTANCE     PROB.<=     PROB.>=
     WITHIN CLADE       0.0000      1.0000      1.0000
     NESTED CLADE      118.8253      1.0000      0.5270




PERMUTATION ANALYSIS OF Clade 1-12
   BASED ON 1000 RESAMPLES


PART I.  PERMUTATIONAL CONTINGENCY TEST:


  OBSERVED CHI-SQUARE STATISTIC =    2.0000

  THE PROBABILITY OF A RANDOM CHI-SQUARE BEING GREATER THAN
    OR EQUAL TO THE OBSERVED CHI-SQUARE =    1.0000


PART II.  GEOGRAPHIC DISTANCE ANALYSIS:

GEOGRAPHICAL CENTERS    LATITUDE     LONGITUDE
     Clade 1-12      -25 00'00"    30 24'00"
             28      -25 00'00"    30 00'00"
             29      -25 00'00"    30 30'00"

CLADE 28 (Interior)
 TYPE OF DISTANCE      DISTANCE     PROB.<=     PROB.>=
     WITHIN CLADE       0.0000      1.0000      1.0000
```

```
    NESTED CLADE      40.2725      1.0000      0.5270

CLADE 29 (Interior)
 TYPE OF DISTANCE      DISTANCE     PROB.<=     PROB.>=
    WITHIN CLADE       0.0000      1.0000      1.0000
    NESTED CLADE      10.0681      0.5270      1.0000


NO INTERIOR/TIP CLADES EXIST IN THIS GROUP




PERMUTATION ANALYSIS OF Clade 1-13
  BASED ON 1000 RESAMPLES


PART I.  PERMUTATIONAL CONTINGENCY TEST:


 OBSERVED CHI-SQUARE STATISTIC =    2.0000

 THE PROBABILITY OF A RANDOM CHI-SQUARE BEING GREATER THAN
   OR EQUAL TO THE OBSERVED CHI-SQUARE =    1.0000


PART II.  GEOGRAPHIC DISTANCE ANALYSIS:

GEOGRAPHICAL CENTERS    LATITUDE     LONGITUDE
    Clade 1-13      -29 40'00"    29 46'40"
          30       -28 30'00"    28 59'60"
          31       -30 00'00"    30 00'00"

CLADE 30 (Interior)
 TYPE OF DISTANCE      DISTANCE     PROB.<=     PROB.>=
    WITHIN CLADE       0.0000      1.0000      1.0000
    NESTED CLADE     149.9950      1.0000      0.5270

CLADE 31 (Interior)
 TYPE OF DISTANCE      DISTANCE     PROB.<=     PROB.>=
    WITHIN CLADE       0.0000      1.0000      1.0000
    NESTED CLADE      42.7763      0.5270      1.0000


NO INTERIOR/TIP CLADES EXIST IN THIS GROUP




PERMUTATION ANALYSIS OF Clade 1-14
  BASED ON 1000 RESAMPLES


PART I.  PERMUTATIONAL CONTINGENCY TEST:


 OBSERVED CHI-SQUARE STATISTIC =    2.4000

 THE PROBABILITY OF A RANDOM CHI-SQUARE BEING GREATER THAN
   OR EQUAL TO THE OBSERVED CHI-SQUARE =    1.0000


PART II.  GEOGRAPHIC DISTANCE ANALYSIS:

GEOGRAPHICAL CENTERS    LATITUDE     LONGITUDE
    Clade 1-14      -26 06'40"    30 33'20"
          32       -25 00'00"    30 00'00"
          33       -26 10'35"    30 35'18"

CLADE 32 (Interior)
 TYPE OF DISTANCE      DISTANCE     PROB.<=     PROB.>=
    WITHIN CLADE       0.0000      1.0000      1.0000
    NESTED CLADE     135.4090      0.6840      0.6560

CLADE 33 (Interior)
 TYPE OF DISTANCE      DISTANCE     PROB.<=     PROB.>=
    WITHIN CLADE     160.3158      0.6560      0.6840
    NESTED CLADE     158.6916      0.6560      0.6840
```

```
NO INTERIOR/TIP CLADES EXIST IN THIS GROUP



PERMUTATION ANALYSIS OF Clade 2-1
   BASED ON 1000 RESAMPLES


PART I.  PERMUTATIONAL CONTINGENCY TEST:


  OBSERVED CHI-SQUARE STATISTIC =     1.0000

  THE PROBABILITY OF A RANDOM CHI-SQUARE BEING GREATER THAN
    OR EQUAL TO THE OBSERVED CHI-SQUARE =     0.0810


PART II.  GEOGRAPHIC DISTANCE ANALYSIS:

GEOGRAPHICAL CENTERS    LATITUDE      LONGITUDE
       Clade 2-1       -31 24'14"     24 50'46"
             1-1       -24 00'00"     29 30'00"
             1-4       -32 22'10"     24 14'21"

CLADE 1-1 (Tip)
 TYPE OF DISTANCE       DISTANCE      PROB.<=      PROB.>=
      WITHIN CLADE        0.0000       0.0910       1.0000
      NESTED CLADE      940.9851       1.0000       0.0070

CLADE 1-4 (Tip)
 TYPE OF DISTANCE       DISTANCE      PROB.<=      PROB.>=
      WITHIN CLADE      325.7980       0.0180       0.9890
      NESTED CLADE      390.5675       0.0180       0.9890


NO INTERIOR/TIP CLADES EXIST IN THIS GROUP



PERMUTATION ANALYSIS OF Clade 2-2
   BASED ON 1000 RESAMPLES


PART I.  PERMUTATIONAL CONTINGENCY TEST:


  OBSERVED CHI-SQUARE STATISTIC =    28.0000

  THE PROBABILITY OF A RANDOM CHI-SQUARE BEING GREATER THAN
    OR EQUAL TO THE OBSERVED CHI-SQUARE =     0.0180


PART II.  GEOGRAPHIC DISTANCE ANALYSIS:

GEOGRAPHICAL CENTERS    LATITUDE      LONGITUDE
       Clade 2-2       -29 37'49"     29 37'07"
             1-2       -30 14'24"     29 16'48"
             1-9       -29 29'57"     29 41'30"

CLADE 1-2 (Tip)
 TYPE OF DISTANCE       DISTANCE      PROB.<=      PROB.>=
      WITHIN CLADE       53.0592       0.1470       0.8530
      NESTED CLADE       95.7345       0.5580       0.4420

CLADE 1-9 (Interior)
 TYPE OF DISTANCE       DISTANCE      PROB.<=      PROB.>=
      WITHIN CLADE       93.2685       0.2080       0.7920
      NESTED CLADE       97.1396       0.4450       0.5550


PART III.  TEST OF INTERIOR VS. TIP CLADES:

 TYPE OF DISTANCE   I-T DISTANCE      PROB.<=      PROB.>=
      WITHIN CLADE       40.2093       0.7770       0.2230
      NESTED CLADE        1.4050       0.4420       0.5580
```

```
PERMUTATION ANALYSIS OF Clade 2-3
   BASED ON 1000 RESAMPLES


PART I.  PERMUTATIONAL CONTINGENCY TEST:


  OBSERVED CHI-SQUARE STATISTIC =     2.0000

  THE PROBABILITY OF A RANDOM CHI-SQUARE BEING GREATER THAN
    OR EQUAL TO THE OBSERVED CHI-SQUARE =     1.0000


PART II.  GEOGRAPHIC DISTANCE ANALYSIS:

GEOGRAPHICAL CENTERS    LATITUDE      LONGITUDE
       Clade 2-3       -25 29'60"     30 15'00"
             1-3       -26 19'60"     30 00'00"
            1-12       -25 00'00"     30 24'00"

CLADE 1-3 (Interior)
 TYPE OF DISTANCE       DISTANCE      PROB.<=      PROB.>=
     WITHIN CLADE       98.7463       0.8480       0.4840
     NESTED CLADE      132.6438       1.0000       0.3320

CLADE 1-12 (Interior)
 TYPE OF DISTANCE       DISTANCE      PROB.<=      PROB.>=
     WITHIN CLADE       16.1090       0.4840       0.8480
     NESTED CLADE       60.9604       0.4840       1.0000


NO INTERIOR/TIP CLADES EXIST IN THIS GROUP




PERMUTATION ANALYSIS OF Clade 2-4
   BASED ON 1000 RESAMPLES


PART I.  PERMUTATIONAL CONTINGENCY TEST:


  OBSERVED CHI-SQUARE STATISTIC =     2.5926

  THE PROBABILITY OF A RANDOM CHI-SQUARE BEING GREATER THAN
    OR EQUAL TO THE OBSERVED CHI-SQUARE =     1.0000


PART II.  GEOGRAPHIC DISTANCE ANALYSIS:

GEOGRAPHICAL CENTERS    LATITUDE      LONGITUDE
       Clade 2-4       -31 09'28"     28 27'25"
             1-5       -31 00'00"     29 30'00"
             1-8       -31 10'13"     28 22'24"

CLADE 1-5 (Tip)
 TYPE OF DISTANCE       DISTANCE      PROB.<=      PROB.>=
     WITHIN CLADE        0.0000       1.0000       1.0000
     NESTED CLADE      100.7671       0.7070       0.6140

CLADE 1-8 (Interior)
 TYPE OF DISTANCE       DISTANCE      PROB.<=      PROB.>=
     WITHIN CLADE      116.3956       0.6140       0.7070
     NESTED CLADE      117.1260       0.8150       0.5060


PART III.  TEST OF INTERIOR VS. TIP CLADES:

 TYPE OF DISTANCE   I-T DISTANCE      PROB.<=      PROB.>=
     WITHIN CLADE      116.3956       0.6140       0.7070
     NESTED CLADE       16.3589       0.6140       0.7070
```

```
PERMUTATION ANALYSIS OF Clade 2-5
   BASED ON 1000 RESAMPLES


PART I.  PERMUTATIONAL CONTINGENCY TEST:


  OBSERVED CHI-SQUARE STATISTIC =     6.5185

  THE PROBABILITY OF A RANDOM CHI-SQUARE BEING GREATER THAN
    OR EQUAL TO THE OBSERVED CHI-SQUARE =     0.3740


PART II.  GEOGRAPHIC DISTANCE ANALYSIS:

GEOGRAPHICAL CENTERS    LATITUDE      LONGITUDE
       Clade 2-5       -31 19'54"     27 53'10"
             1-6       -31 42'33"     27 27'26"
            1-13       -29 40'00"     29 46'40"

CLADE 1-6 (Interior)
 TYPE OF DISTANCE       DISTANCE      PROB.<=      PROB.>=
      WITHIN CLADE      284.1763       0.2180       0.8330
      NESTED CLADE      308.4686       0.6580       0.3930

CLADE 1-13 (Interior)
 TYPE OF DISTANCE       DISTANCE      PROB.<=      PROB.>=
      WITHIN CLADE       66.6027       0.3900       0.6610
      NESTED CLADE      268.5802       0.3770       0.6740


NO INTERIOR/TIP CLADES EXIST IN THIS GROUP




PERMUTATION ANALYSIS OF Clade 2-6
   BASED ON 1000 RESAMPLES


PART I.  PERMUTATIONAL CONTINGENCY TEST:


  OBSERVED CHI-SQUARE STATISTIC =     1.0000

  THE PROBABILITY OF A RANDOM CHI-SQUARE BEING GREATER THAN
    OR EQUAL TO THE OBSERVED CHI-SQUARE =     0.0190


PART II.  GEOGRAPHIC DISTANCE ANALYSIS:

GEOGRAPHICAL CENTERS    LATITUDE      LONGITUDE
       Clade 2-6       -32 00'13"     26 56'51"
             1-7       -29 30'00"     28 59'60"
            1-15       -30 30'00"     27 40'55"
            1-10       -32 31'17"     26 36'23"

CLADE 1-7 (Interior)
 TYPE OF DISTANCE       DISTANCE      PROB.<=      PROB.>=
      WITHIN CLADE        0.0000       1.0000       1.0000
      NESTED CLADE      340.1983       1.0000       0.0480

CLADE 1-15 (Interior)
 TYPE OF DISTANCE       DISTANCE      PROB.<=      PROB.>=
      WITHIN CLADE       22.1496       0.1150       0.8860
      NESTED CLADE      182.1967       0.8410       0.1600

CLADE 1-10 (Tip)
 TYPE OF DISTANCE       DISTANCE      PROB.<=      PROB.>=
      WITHIN CLADE       76.7020       0.0070       0.9930
      NESTED CLADE      104.6628       0.0300       0.9700


PART III.  TEST OF INTERIOR VS. TIP CLADES:

 TYPE OF DISTANCE   I-T DISTANCE      PROB.<=      PROB.>=
      WITHIN CLADE     -60.0898        0.5430       0.4570
      NESTED CLADE     117.0343        0.9690       0.0310
```

```
PERMUTATION ANALYSIS OF Clade 2-7
   BASED ON 1000 RESAMPLES


PART I.  PERMUTATIONAL CONTINGENCY TEST:


  OBSERVED CHI-SQUARE STATISTIC =     1.0000

  THE PROBABILITY OF A RANDOM CHI-SQUARE BEING GREATER THAN
    OR EQUAL TO THE OBSERVED CHI-SQUARE =     0.5790


PART II.  GEOGRAPHIC DISTANCE ANALYSIS:

GEOGRAPHICAL CENTERS    LATITUDE      LONGITUDE
       Clade 2-7       -26 46'14"     30 09'21"
            1-11       -31 51'26"     27 04'17"
            1-14       -26 06'40"     30 33'20"

CLADE 1-11 (Interior)
 TYPE OF DISTANCE       DISTANCE      PROB.<=      PROB.>=
     WITHIN CLADE      388.7680       0.8210       0.2060
     NESTED CLADE      660.5346       1.0000       0.0270

CLADE 1-14 (Interior)
 TYPE OF DISTANCE       DISTANCE      PROB.<=      PROB.>=
     WITHIN CLADE      157.3981       0.0770       0.9500
     NESTED CLADE      192.1723       0.0770       0.9500


NO INTERIOR/TIP CLADES EXIST IN THIS GROUP




PERMUTATION ANALYSIS OF Clade 3-1
   BASED ON 1000 RESAMPLES


PART I.  PERMUTATIONAL CONTINGENCY TEST:


  OBSERVED CHI-SQUARE STATISTIC =    21.9363

  THE PROBABILITY OF A RANDOM CHI-SQUARE BEING GREATER THAN
    OR EQUAL TO THE OBSERVED CHI-SQUARE =     0.0410


PART II.  GEOGRAPHIC DISTANCE ANALYSIS:

GEOGRAPHICAL CENTERS    LATITUDE      LONGITUDE
       Clade 3-1       -29 41'27"     26 48'33"
             2-1       -31 24'14"     24 50'46"
             2-7       -26 46'14"     30 09'21"

CLADE 2-1 (Tip)
 TYPE OF DISTANCE       DISTANCE      PROB.<=      PROB.>=
     WITHIN CLADE      454.0772       0.0010       0.9990
     NESTED CLADE      559.8725       0.5590       0.4410

CLADE 2-7 (Interior)
 TYPE OF DISTANCE       DISTANCE      PROB.<=      PROB.>=
     WITHIN CLADE      245.9188       0.0100       0.9900
     NESTED CLADE      555.0712       0.4470       0.5530


PART III.  TEST OF INTERIOR VS. TIP CLADES:

 TYPE OF DISTANCE   I-T DISTANCE      PROB.<=      PROB.>=
     WITHIN CLADE    -208.1584       0.0280       0.9720
     NESTED CLADE      -4.8014       0.4450       0.5550
```

```
PERMUTATION ANALYSIS OF Clade 3-2
   BASED ON 1000 RESAMPLES


PART I.  PERMUTATIONAL CONTINGENCY TEST:


  OBSERVED CHI-SQUARE STATISTIC =    31.1949

  THE PROBABILITY OF A RANDOM CHI-SQUARE BEING GREATER THAN
    OR EQUAL TO THE OBSERVED CHI-SQUARE =     0.0020


PART II.  GEOGRAPHIC DISTANCE ANALYSIS:

GEOGRAPHICAL CENTERS    LATITUDE      LONGITUDE
       Clade 3-2       -30 05'23"     29 15'07"
             2-2       -29 37'05"     29 36'59"
             2-4       -31 08'14"     28 26'34"

CLADE 2-2 (Tip)
 TYPE OF DISTANCE       DISTANCE      PROB.<=      PROB.>=
     WITHIN CLADE       96.2076       0.0000       1.0000
     NESTED CLADE      117.4931       0.0190       0.9810

CLADE 2-4 (Interior)
 TYPE OF DISTANCE       DISTANCE      PROB.<=      PROB.>=
     WITHIN CLADE      114.9561       0.3850       0.6150
     NESTED CLADE      167.2213       0.9450       0.0550


PART III.  TEST OF INTERIOR VS. TIP CLADES:

 TYPE OF DISTANCE   I-T DISTANCE      PROB.<=      PROB.>=
     WITHIN CLADE       18.7485       0.7740       0.2260
     NESTED CLADE       49.7281       0.9580       0.0420




PERMUTATION ANALYSIS OF Clade 3-3
   BASED ON 1000 RESAMPLES


PART I.  PERMUTATIONAL CONTINGENCY TEST:


  OBSERVED CHI-SQUARE STATISTIC =    58.5556

  THE PROBABILITY OF A RANDOM CHI-SQUARE BEING GREATER THAN
    OR EQUAL TO THE OBSERVED CHI-SQUARE =     0.0000


PART II.  GEOGRAPHIC DISTANCE ANALYSIS:

GEOGRAPHICAL CENTERS    LATITUDE      LONGITUDE
       Clade 3-3       -30 38'08"     27 54'04"
             2-3       -25 30'00"     30 15'00"
             2-5       -31 09'51"     28 09'06"
             2-6       -31 58'07"     26 58'19"

CLADE 2-3 (Tip)
 TYPE OF DISTANCE       DISTANCE      PROB.<=      PROB.>=
     WITHIN CLADE       87.8417       0.1030       0.8970
     NESTED CLADE      615.9515       0.9980       0.0020

CLADE 2-5 (Interior)
 TYPE OF DISTANCE       DISTANCE      PROB.<=      PROB.>=
     WITHIN CLADE      295.2833       0.5470       0.4530
     NESTED CLADE      304.9098       0.5300       0.4700

CLADE 2-6 (Tip)
 TYPE OF DISTANCE       DISTANCE      PROB.<=      PROB.>=
     WITHIN CLADE      137.2891       0.0020       0.9980
     NESTED CLADE      216.0606       0.0000       1.0000


PART III.  TEST OF INTERIOR VS. TIP CLADES:
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```
 TYPE OF DISTANCE   I-T DISTANCE      PROB.<=      PROB.>=
      WITHIN CLADE      166.9847       0.9580       0.0420
      NESTED CLADE       16.1418       0.6110       0.3890


** ANALYSIS FINISHED **
It took 1.0600 seconds.
```

Appendix 12: GeoDis output file at full degree grid scale (NCA: South African samples)

```
Differentiating population structure from history - Geodis  2.4
(c) Copyright, 1999-2005 David Posada and Alan Templeton
Contact: David Posada, University of Vigo, Spain (dposada@uvigo.es)
________________________________________________________________________

Input file: /Applications/phylosoft/GeoDis2.4/SYD/FULL Deg/geo_full2.txt
Kniphofia FullcpDNA

Tue Dec 06 18:16:50 SAST 2005




PERMUTATION ANALYSIS OF Clade 1-2
   BASED ON 1000 RESAMPLES


PART I.  PERMUTATIONAL CONTINGENCY TEST:


  OBSERVED CHI-SQUARE STATISTIC =     5.5556

  THE PROBABILITY OF A RANDOM CHI-SQUARE BEING GREATER THAN
    OR EQUAL TO THE OBSERVED CHI-SQUARE =     0.6790


PART II.  GEOGRAPHIC DISTANCE ANALYSIS:

GEOGRAPHICAL CENTERS    LATITUDE      LONGITUDE
       Clade 1-2       -29 54'06"     28 56'04"
               4       -30 00'00"     28 59'60"
               5       -29 50'00"     29 10'00"
               6       -30 00'00"     28 00'00"

CLADE 4 (Interior)
 TYPE OF DISTANCE       DISTANCE      PROB.<=      PROB.>=
      WITHIN CLADE        0.0000       1.0000       1.0000
      NESTED CLADE       12.6188       0.6160       1.0000

CLADE 5 (Tip)
 TYPE OF DISTANCE       DISTANCE      PROB.<=      PROB.>=
      WITHIN CLADE       40.8798       0.6790       0.6040
      NESTED CLADE       34.4699       0.6790       0.6040

CLADE 6 (Interior)
 TYPE OF DISTANCE       DISTANCE      PROB.<=      PROB.>=
      WITHIN CLADE        0.0000       1.0000       1.0000
      NESTED CLADE       90.6033       0.8100       0.3980


PART III.  TEST OF INTERIOR VS. TIP CLADES:

 TYPE OF DISTANCE   I-T DISTANCE      PROB.<=      PROB.>=
      WITHIN CLADE      -40.8798       0.6040       0.6790
      NESTED CLADE       17.1411       0.6040       0.6790




PERMUTATION ANALYSIS OF Clade 1-3
   BASED ON 1000 RESAMPLES


PART I.  PERMUTATIONAL CONTINGENCY TEST:


  OBSERVED CHI-SQUARE STATISTIC =     2.0000

  THE PROBABILITY OF A RANDOM CHI-SQUARE BEING GREATER THAN
    OR EQUAL TO THE OBSERVED CHI-SQUARE =     1.0000


PART II.  GEOGRAPHIC DISTANCE ANALYSIS:
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```
GEOGRAPHICAL CENTERS    LATITUDE      LONGITUDE
       Clade 1-3       -26 23'60"     30 00'00"
               7       -25 00'00"     30 00'00"
               8       -27 00'00"     30 00'00"

CLADE 7 (Interior)
 TYPE OF DISTANCE       DISTANCE      PROB.<=      PROB.>=
      WITHIN CLADE        0.0000       1.0000       1.0000
      NESTED CLADE      155.5254       1.0000       0.5270

CLADE 8 (Tip)
 TYPE OF DISTANCE       DISTANCE      PROB.<=      PROB.>=
      WITHIN CLADE        0.0000       1.0000       1.0000
      NESTED CLADE       66.6537       0.5270       1.0000


PART III.  TEST OF INTERIOR VS. TIP CLADES:

 TYPE OF DISTANCE   I-T DISTANCE      PROB.<=      PROB.>=
      WITHIN CLADE        0.0000       1.0000       1.0000
      NESTED CLADE       88.8717       1.0000       0.5270




PERMUTATION ANALYSIS OF Clade 1-4
   BASED ON 1000 RESAMPLES


PART I.  PERMUTATIONAL CONTINGENCY TEST:


  OBSERVED CHI-SQUARE STATISTIC =    10.3636

  THE PROBABILITY OF A RANDOM CHI-SQUARE BEING GREATER THAN
    OR EQUAL TO THE OBSERVED CHI-SQUARE =     0.9380


PART II.  GEOGRAPHIC DISTANCE ANALYSIS:

GEOGRAPHICAL CENTERS    LATITUDE      LONGITUDE
       Clade 1-4       -32 41'47"     23 12'37"
               9       -33 10'35"     23 31'46"
              10       -32 31'10"     22 59'60"
              11       -33 00'00"     25 00'00"

CLADE 9 (Tip)
 TYPE OF DISTANCE       DISTANCE      PROB.<=      PROB.>=
      WITHIN CLADE       59.7725       0.0300       0.9740
      NESTED CLADE       75.6220       0.0100       0.9940

CLADE 10 (Tip)
 TYPE OF DISTANCE       DISTANCE      PROB.<=      PROB.>=
      WITHIN CLADE      265.7729       0.8940       0.1140
      NESTED CLADE      261.8151       0.8900       0.1180

CLADE 11 (Interior)
 TYPE OF DISTANCE       DISTANCE      PROB.<=      PROB.>=
      WITHIN CLADE        0.0000       1.0000       1.0000
      NESTED CLADE      170.4019       0.7680       0.4390


PART III.  TEST OF INTERIOR VS. TIP CLADES:

 TYPE OF DISTANCE   I-T DISTANCE      PROB.<=      PROB.>=
      WITHIN CLADE     -210.8395       0.5940       0.4070
      NESTED CLADE      -41.7617       0.7140       0.2870




PERMUTATION ANALYSIS OF Clade 1-6
   BASED ON 1000 RESAMPLES


PART I.  PERMUTATIONAL CONTINGENCY TEST:


  OBSERVED CHI-SQUARE STATISTIC =     1.4063
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```
  THE PROBABILITY OF A RANDOM CHI-SQUARE BEING GREATER THAN
    OR EQUAL TO THE OBSERVED CHI-SQUARE =     1.0000


PART II.  GEOGRAPHIC DISTANCE ANALYSIS:

GEOGRAPHICAL CENTERS    LATITUDE      LONGITUDE
       Clade 1-6       -28 44'08"     27 49'23"
              13       -33 00'00"     26 00'00"
              14       -28 22'52"     27 58'29"

CLADE 13 (Interior)
 TYPE OF DISTANCE       DISTANCE      PROB.<=      PROB.>=
      WITHIN CLADE        0.0000       1.0000       1.0000
      NESTED CLADE      504.5870       0.8990       0.5430

CLADE 14 (Tip)
 TYPE OF DISTANCE       DISTANCE      PROB.<=      PROB.>=
      WITHIN CLADE      403.9716       0.6590       0.7830
      NESTED CLADE      414.5933       0.5430       0.8990


PART III.  TEST OF INTERIOR VS. TIP CLADES:

 TYPE OF DISTANCE   I-T DISTANCE      PROB.<=      PROB.>=
      WITHIN CLADE     -403.9716       0.7830       0.6590
      NESTED CLADE       89.9936       0.8990       0.5430




PERMUTATION ANALYSIS OF Clade 1-8
   BASED ON 1000 RESAMPLES


PART I.  PERMUTATIONAL CONTINGENCY TEST:


  OBSERVED CHI-SQUARE STATISTIC =    18.4500

  THE PROBABILITY OF A RANDOM CHI-SQUARE BEING GREATER THAN
    OR EQUAL TO THE OBSERVED CHI-SQUARE =     0.7940


PART II.  GEOGRAPHIC DISTANCE ANALYSIS:

GEOGRAPHICAL CENTERS    LATITUDE      LONGITUDE
       Clade 1-8       -31 18'32"     27 53'07"
              16       -31 00'00"     28 59'60"
              17       -31 33'36"     27 38'24"
              18       -30 00'00"     28 59'60"
              19       -29 31'35"     28 28'25"

CLADE 16 (Interior)
 TYPE OF DISTANCE       DISTANCE      PROB.<=      PROB.>=
      WITHIN CLADE        0.0000       1.0000       1.0000
      NESTED CLADE      111.3849       0.4440       0.7620

CLADE 17 (Interior)
 TYPE OF DISTANCE       DISTANCE      PROB.<=      PROB.>=
      WITHIN CLADE       97.5123       0.4630       0.5630
      NESTED CLADE      104.4916       0.2490       0.7770

CLADE 18 (Interior)
 TYPE OF DISTANCE       DISTANCE      PROB.<=      PROB.>=
      WITHIN CLADE        0.0000       1.0000       1.0000
      NESTED CLADE      180.2473       0.7440       0.3620

CLADE 19 (Tip)
 TYPE OF DISTANCE       DISTANCE      PROB.<=      PROB.>=
      WITHIN CLADE       73.4280       0.7640       0.2880
      NESTED CLADE      208.4031       0.9590       0.0930


PART III.  TEST OF INTERIOR VS. TIP CLADES:

 TYPE OF DISTANCE   I-T DISTANCE      PROB.<=      PROB.>=
      WITHIN CLADE       -3.7763       0.2810       0.7220
      NESTED CLADE      -92.1045       0.0710       0.9320
```

```
PERMUTATION ANALYSIS OF Calde 1-9
   BASED ON 1000 RESAMPLES


PART I.  PERMUTATIONAL CONTINGENCY TEST:


  OBSERVED CHI-SQUARE STATISTIC =    10.7265

  THE PROBABILITY OF A RANDOM CHI-SQUARE BEING GREATER THAN
    OR EQUAL TO THE OBSERVED CHI-SQUARE =     0.5830


PART II.  GEOGRAPHIC DISTANCE ANALYSIS:

GEOGRAPHICAL CENTERS    LATITUDE      LONGITUDE
       Calde 1-9       -29 28'15"     29 22'51"
              20       -28 59'60"     28 59'60"
              21       -29 32'21"     29 23'31"
              22       -28 59'60"     30 00'00"
              23       -28 00'00"     28 59'60"

CLADE 20 (Tip)
 TYPE OF DISTANCE       DISTANCE      PROB.<=      PROB.>=
      WITHIN CLADE        0.0000       1.0000       1.0000
      NESTED CLADE       64.0286       0.2430       1.0000

CLADE 21 (Tip)
 TYPE OF DISTANCE       DISTANCE      PROB.<=      PROB.>=
      WITHIN CLADE      106.5239       0.4680       0.6280
      NESTED CLADE      106.2516       0.4350       0.6610

CLADE 22 (Tip)
 TYPE OF DISTANCE       DISTANCE      PROB.<=      PROB.>=
      WITHIN CLADE        0.0000       1.0000       1.0000
      NESTED CLADE       79.6219       0.7450       0.7140

CLADE 23 (Interior)
 TYPE OF DISTANCE       DISTANCE      PROB.<=      PROB.>=
      WITHIN CLADE        0.0000       1.0000       1.0000
      NESTED CLADE      167.5621       0.9390       0.2010


PART III.  TEST OF INTERIOR VS. TIP CLADES:

 TYPE OF DISTANCE   I-T DISTANCE      PROB.<=      PROB.>=
      WITHIN CLADE      -99.1774       0.6280       0.4680
      NESTED CLADE       63.6848       0.8940       0.1360



PERMUTATION ANALYSIS OF Clade 1-10
   BASED ON 1000 RESAMPLES


PART I.  PERMUTATIONAL CONTINGENCY TEST:


  OBSERVED CHI-SQUARE STATISTIC =     1.4773

  THE PROBABILITY OF A RANDOM CHI-SQUARE BEING GREATER THAN
    OR EQUAL TO THE OBSERVED CHI-SQUARE =     1.0000


PART II.  GEOGRAPHIC DISTANCE ANALYSIS:

GEOGRAPHICAL CENTERS    LATITUDE      LONGITUDE
      Clade 1-10       -32 25'54"     26 03'09"
              24       -32 00'00"     26 00'00"
              25       -32 27'38"     26 03'22"

CLADE 24 (Interior)
 TYPE OF DISTANCE       DISTANCE      PROB.<=      PROB.>=
      WITHIN CLADE        0.0000       0.4010       1.0000
      NESTED CLADE       48.1984       0.3640       1.0000
```

```
CLADE 25 (Tip)
 TYPE OF DISTANCE       DISTANCE      PROB.<=      PROB.>=
      WITHIN CLADE       94.0316       1.0000       0.3640
      NESTED CLADE       93.8446       0.8920       0.4720


PART III.  TEST OF INTERIOR VS. TIP CLADES:

 TYPE OF DISTANCE   I-T DISTANCE      PROB.<=      PROB.>=
      WITHIN CLADE      -94.0316       0.3640       1.0000
      NESTED CLADE      -45.6462       0.3640       1.0000




PERMUTATION ANALYSIS OF Clade1-11
   BASED ON 1000 RESAMPLES


PART I.  PERMUTATIONAL CONTINGENCY TEST:


  OBSERVED CHI-SQUARE STATISTIC =     2.0000

  THE PROBABILITY OF A RANDOM CHI-SQUARE BEING GREATER THAN
    OR EQUAL TO THE OBSERVED CHI-SQUARE =     1.0000


PART II.  GEOGRAPHIC DISTANCE ANALYSIS:

GEOGRAPHICAL CENTERS    LATITUDE      LONGITUDE
       Clade1-11       -32 56'51"     25 15'47"
              26       -34 00'00"     24 00'00"
              27       -28 59'60"     30 00'00"

CLADE 26 (Interior)
 TYPE OF DISTANCE       DISTANCE      PROB.<=      PROB.>=
      WITHIN CLADE        0.0000       1.0000       1.0000
      NESTED CLADE      165.4498       0.5270       1.0000

CLADE 27 (Tip)
 TYPE OF DISTANCE       DISTANCE      PROB.<=      PROB.>=
      WITHIN CLADE        0.0000       1.0000       1.0000
      NESTED CLADE      629.0113       1.0000       0.5270


PART III.  TEST OF INTERIOR VS. TIP CLADES:

 TYPE OF DISTANCE   I-T DISTANCE      PROB.<=      PROB.>=
      WITHIN CLADE        0.0000       1.0000       1.0000
      NESTED CLADE     -463.5615       0.5270       1.0000




PERMUTATION ANALYSIS OF Clade 1-13
   BASED ON 1000 RESAMPLES


PART I.  PERMUTATIONAL CONTINGENCY TEST:


  OBSERVED CHI-SQUARE STATISTIC =     2.0000

  THE PROBABILITY OF A RANDOM CHI-SQUARE BEING GREATER THAN
    OR EQUAL TO THE OBSERVED CHI-SQUARE =     1.0000


PART II.  GEOGRAPHIC DISTANCE ANALYSIS:

GEOGRAPHICAL CENTERS    LATITUDE      LONGITUDE
      Clade 1-13       -29 11'60"     28 59'60"
              30       -28 00'00"     28 59'60"
              31       -30 00'00"     28 59'60"

CLADE 30 (Interior)
 TYPE OF DISTANCE       DISTANCE      PROB.<=      PROB.>=
      WITHIN CLADE        0.0000       1.0000       1.0000
      NESTED CLADE      133.3075       1.0000       0.5270
```

```
CLADE 31 (Interior)
 TYPE OF DISTANCE       DISTANCE      PROB.<=      PROB.>=
      WITHIN CLADE        0.0000       1.0000       1.0000
      NESTED CLADE       88.8717       0.5270       1.0000


NO INTERIOR/TIP CLADES EXIST IN THIS GROUP




PERMUTATION ANALYSIS OF Clade 1-14
   BASED ON 1000 RESAMPLES


PART I.  PERMUTATIONAL CONTINGENCY TEST:


  OBSERVED CHI-SQUARE STATISTIC =     0.6000

  THE PROBABILITY OF A RANDOM CHI-SQUARE BEING GREATER THAN
    OR EQUAL TO THE OBSERVED CHI-SQUARE =     1.0000


PART II.  GEOGRAPHIC DISTANCE ANALYSIS:

GEOGRAPHICAL CENTERS    LATITUDE      LONGITUDE
      Clade 1-14       -26 09'60"     30 23'20"
              32       -25 00'00"     30 00'00"
              33       -26 14'07"     30 24'42"

CLADE 32 (Interior)
 TYPE OF DISTANCE       DISTANCE      PROB.<=      PROB.>=
      WITHIN CLADE        0.0000       1.0000       1.0000
      NESTED CLADE      135.3351       0.6790       1.0000

CLADE 33 (Interior)
 TYPE OF DISTANCE       DISTANCE      PROB.<=      PROB.>=
      WITHIN CLADE      209.8508       1.0000       0.6790
      NESTED CLADE      208.6634       0.8380       0.8410


NO INTERIOR/TIP CLADES EXIST IN THIS GROUP




PERMUTATION ANALYSIS OF Clade 2-1
   BASED ON 1000 RESAMPLES


PART I.  PERMUTATIONAL CONTINGENCY TEST:


  OBSERVED CHI-SQUARE STATISTIC =    18.0000

  THE PROBABILITY OF A RANDOM CHI-SQUARE BEING GREATER THAN
    OR EQUAL TO THE OBSERVED CHI-SQUARE =     0.0450


PART II.  GEOGRAPHIC DISTANCE ANALYSIS:

GEOGRAPHICAL CENTERS    LATITUDE      LONGITUDE
       Clade 2-1       -31 26'38"     24 02'38"
             1-1       -24 00'00"     28 59'60"
             1-4       -32 41'47"     23 12'37"

CLADE 1-1 (Tip)
 TYPE OF DISTANCE       DISTANCE      PROB.<=      PROB.>=
      WITHIN CLADE        0.0000       0.0750       1.0000
      NESTED CLADE      959.5455       1.0000       0.0050

CLADE 1-4 (Tip)
 TYPE OF DISTANCE       DISTANCE      PROB.<=      PROB.>=
      WITHIN CLADE      213.5975       0.0050       1.0000
      NESTED CLADE      305.2983       0.0050       1.0000


NO INTERIOR/TIP CLADES EXIST IN THIS GROUP
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PERMUTATION ANALYSIS OF Clade 2-2
   BASED ON 1000 RESAMPLES


PART I.  PERMUTATIONAL CONTINGENCY TEST:


  OBSERVED CHI-SQUARE STATISTIC =    17.2083

  THE PROBABILITY OF A RANDOM CHI-SQUARE BEING GREATER THAN
    OR EQUAL TO THE OBSERVED CHI-SQUARE =     0.0230


PART II.  GEOGRAPHIC DISTANCE ANALYSIS:

GEOGRAPHICAL CENTERS    LATITUDE      LONGITUDE
       Clade 2-2       -29 32'09"     29 18'49"
             1-2       -29 54'06"     28 56'04"
             1-9       -29 28'15"     29 22'51"

CLADE 1-2 (Tip)
 TYPE OF DISTANCE       DISTANCE      PROB.<=      PROB.>=
      WITHIN CLADE       38.2989       0.0100       0.9900
      NESTED CLADE       75.2995       0.1340       0.8660

CLADE 1-9 (Interior)
 TYPE OF DISTANCE       DISTANCE      PROB.<=      PROB.>=
      WITHIN CLADE      106.4647       0.7900       0.2100
      NESTED CLADE      108.2847       0.8700       0.1300


PART III.  TEST OF INTERIOR VS. TIP CLADES:

 TYPE OF DISTANCE   I-T DISTANCE      PROB.<=      PROB.>=
      WITHIN CLADE       68.1658       0.9840       0.0160
      NESTED CLADE       32.9852       0.8970       0.1030




PERMUTATION ANALYSIS OF Clade 2-3
   BASED ON 1000 RESAMPLES


PART I.  PERMUTATIONAL CONTINGENCY TEST:


  OBSERVED CHI-SQUARE STATISTIC =     1.3333

  THE PROBABILITY OF A RANDOM CHI-SQUARE BEING GREATER THAN
    OR EQUAL TO THE OBSERVED CHI-SQUARE =     1.0000


PART II.  GEOGRAPHIC DISTANCE ANALYSIS:

GEOGRAPHICAL CENTERS    LATITUDE      LONGITUDE
       Clade 2-3       -25 52'30"     30 00'00"
             1-3       -26 23'60"     30 00'00"
            1-12       -25 00'00"     30 00'00"

CLADE 1-3 (Interior)
 TYPE OF DISTANCE       DISTANCE      PROB.<=      PROB.>=
      WITHIN CLADE       93.3152       1.0000       0.5100
      NESTED CLADE      116.6440       1.0000       0.5100

CLADE 1-12 (Interior)
 TYPE OF DISTANCE       DISTANCE      PROB.<=      PROB.>=
      WITHIN CLADE        0.0000       0.5100       1.0000
      NESTED CLADE       97.2034       0.5100       1.0000


NO INTERIOR/TIP CLADES EXIST IN THIS GROUP



PERMUTATION ANALYSIS OF Clade 2-4
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   BASED ON 1000 RESAMPLES


PART I.  PERMUTATIONAL CONTINGENCY TEST:


  OBSERVED CHI-SQUARE STATISTIC =     2.5926

  THE PROBABILITY OF A RANDOM CHI-SQUARE BEING GREATER THAN
    OR EQUAL TO THE OBSERVED CHI-SQUARE =     1.0000


PART II.  GEOGRAPHIC DISTANCE ANALYSIS:

GEOGRAPHICAL CENTERS    LATITUDE      LONGITUDE
       Clade 2-4       -31 16'07"     27 53'20"
             1-5       -30 00'00"     28 00'00"
             1-8       -31 18'32"     27 53'07"

CLADE 1-5 (Tip)
 TYPE OF DISTANCE       DISTANCE      PROB.<=      PROB.>=
      WITHIN CLADE        0.0000       1.0000       1.0000
      NESTED CLADE      141.3188       0.7070       0.5990

CLADE 1-8 (Interior)
 TYPE OF DISTANCE       DISTANCE      PROB.<=      PROB.>=
      WITHIN CLADE      115.0567       0.5990       0.7070
      NESTED CLADE      115.4667       0.5990       0.7070


PART III.  TEST OF INTERIOR VS. TIP CLADES:

 TYPE OF DISTANCE   I-T DISTANCE      PROB.<=      PROB.>=
      WITHIN CLADE      115.0567       0.5990       0.7070
      NESTED CLADE      -25.8520       0.5990       0.7070




PERMUTATION ANALYSIS OF Clade 2-5
   BASED ON 1000 RESAMPLES


PART I.  PERMUTATIONAL CONTINGENCY TEST:


  OBSERVED CHI-SQUARE STATISTIC =     6.5185

  THE PROBABILITY OF A RANDOM CHI-SQUARE BEING GREATER THAN
    OR EQUAL TO THE OBSERVED CHI-SQUARE =     0.3740


PART II.  GEOGRAPHIC DISTANCE ANALYSIS:

GEOGRAPHICAL CENTERS    LATITUDE      LONGITUDE
       Clade 2-5       -28 46'49"     27 56'11"
             1-6       -28 44'08"     27 49'23"
            1-13       -29 11'60"     28 59'60"

CLADE 1-6 (Interior)
 TYPE OF DISTANCE       DISTANCE      PROB.<=      PROB.>=
      WITHIN CLADE      421.5012       0.9200       0.1310
      NESTED CLADE      420.9898       0.9200       0.1310

CLADE 1-13 (Interior)
 TYPE OF DISTANCE       DISTANCE      PROB.<=      PROB.>=
      WITHIN CLADE      106.6460       0.4210       0.6300
      NESTED CLADE      156.2353       0.1090       0.9420


NO INTERIOR/TIP CLADES EXIST IN THIS GROUP




PERMUTATION ANALYSIS OF Clade 2-6
   BASED ON 1000 RESAMPLES


PART I.  PERMUTATIONAL CONTINGENCY TEST:
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  OBSERVED CHI-SQUARE STATISTIC =    36.0000

  THE PROBABILITY OF A RANDOM CHI-SQUARE BEING GREATER THAN
    OR EQUAL TO THE OBSERVED CHI-SQUARE =     0.0000


PART II.  GEOGRAPHIC DISTANCE ANALYSIS:

GEOGRAPHICAL CENTERS    LATITUDE      LONGITUDE
       Clade 2-6       -32 02'52"     26 21'55"
             1-7       -28 59'60"     28 59'60"
            1-15       -30 00'00"     28 00'00"
            1-10       -32 25'54"     26 03'09"

CLADE 1-7 (Interior)
 TYPE OF DISTANCE       DISTANCE      PROB.<=      PROB.>=
      WITHIN CLADE        0.0000       1.0000       1.0000
      NESTED CLADE      422.1125       1.0000       0.0620

CLADE 1-15 (Interior)
 TYPE OF DISTANCE       DISTANCE      PROB.<=      PROB.>=
      WITHIN CLADE        0.0000       0.0230       1.0000
      NESTED CLADE      275.6257       0.9990       0.0010

CLADE 1-10 (Tip)
 TYPE OF DISTANCE       DISTANCE      PROB.<=      PROB.>=
      WITHIN CLADE       90.9617       0.0030       0.9970
      NESTED CLADE      101.1576       0.0010       0.9990


PART III.  TEST OF INTERIOR VS. TIP CLADES:

 TYPE OF DISTANCE   I-T DISTANCE      PROB.<=      PROB.>=
      WITHIN CLADE      -90.9617       0.1480       0.8520
      NESTED CLADE      203.7655       1.0000       0.0000




PERMUTATION ANALYSIS OF Clade 2-7
   BASED ON 1000 RESAMPLES


PART I.  PERMUTATIONAL CONTINGENCY TEST:


  OBSERVED CHI-SQUARE STATISTIC =     1.0000

  THE PROBABILITY OF A RANDOM CHI-SQUARE BEING GREATER THAN
    OR EQUAL TO THE OBSERVED CHI-SQUARE =     0.2030


PART II.  GEOGRAPHIC DISTANCE ANALYSIS:

GEOGRAPHICAL CENTERS    LATITUDE      LONGITUDE
       Clade 2-7       -26 54'37"     29 49'37"
            1-11       -32 56'51"     25 15'47"
            1-14       -26 09'60"     30 23'20"

CLADE 1-11 (Interior)
 TYPE OF DISTANCE       DISTANCE      PROB.<=      PROB.>=
      WITHIN CLADE      263.0417       0.7710       0.2560
      NESTED CLADE      810.6780       1.0000       0.0270

CLADE 1-14 (Interior)
 TYPE OF DISTANCE       DISTANCE      PROB.<=      PROB.>=
      WITHIN CLADE      204.5896       0.1050       0.9220
      NESTED CLADE      231.5518       0.0550       0.9720


NO INTERIOR/TIP CLADES EXIST IN THIS GROUP




PERMUTATION ANALYSIS OF Clade 3-1
   BASED ON 1000 RESAMPLES
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PART I.  PERMUTATIONAL CONTINGENCY TEST:


  OBSERVED CHI-SQUARE STATISTIC =    22.4792

  THE PROBABILITY OF A RANDOM CHI-SQUARE BEING GREATER THAN
    OR EQUAL TO THE OBSERVED CHI-SQUARE =     0.0040


PART II.  GEOGRAPHIC DISTANCE ANALYSIS:

GEOGRAPHICAL CENTERS    LATITUDE      LONGITUDE
       Clade 3-1       -30 06'44"     25 44'33"
             2-1       -31 26'38"     24 02'38"
             2-7       -26 54'37"     29 49'37"

CLADE 2-1 (Tip)
 TYPE OF DISTANCE       DISTANCE      PROB.<=      PROB.>=
      WITHIN CLADE      399.5099       0.0190       0.9810
      NESTED CLADE      508.8250       0.0490       0.9510

CLADE 2-7 (Interior)
 TYPE OF DISTANCE       DISTANCE      PROB.<=      PROB.>=
      WITHIN CLADE      295.0503       0.0840       0.9160
      NESTED CLADE      640.8546       0.9700       0.0300


PART III.  TEST OF INTERIOR VS. TIP CLADES:

 TYPE OF DISTANCE   I-T DISTANCE      PROB.<=      PROB.>=
      WITHIN CLADE     -104.4596       0.2540       0.7460
      NESTED CLADE      132.0296       0.9720       0.0280




PERMUTATION ANALYSIS OF Clade 3-2
   BASED ON 1000 RESAMPLES


PART I.  PERMUTATIONAL CONTINGENCY TEST:


  OBSERVED CHI-SQUARE STATISTIC =    24.4286

  THE PROBABILITY OF A RANDOM CHI-SQUARE BEING GREATER THAN
    OR EQUAL TO THE OBSERVED CHI-SQUARE =     0.0020


PART II.  GEOGRAPHIC DISTANCE ANALYSIS:

GEOGRAPHICAL CENTERS    LATITUDE      LONGITUDE
       Clade 3-2       -30 18'21"     28 40'49"
             2-2       -29 32'09"     29 18'49"
             2-4       -31 16'07"     27 53'20"

CLADE 2-2 (Interior)
 TYPE OF DISTANCE       DISTANCE      PROB.<=      PROB.>=
      WITHIN CLADE      103.3165       0.0010       0.9990
      NESTED CLADE      144.6634       0.1360       0.8640

CLADE 2-4 (Tip)
 TYPE OF DISTANCE       DISTANCE      PROB.<=      PROB.>=
      WITHIN CLADE      116.2646       0.3350       0.6650
      NESTED CLADE      164.5546       0.6510       0.3490


PART III.  TEST OF INTERIOR VS. TIP CLADES:

 TYPE OF DISTANCE   I-T DISTANCE      PROB.<=      PROB.>=
      WITHIN CLADE      -12.9481       0.2510       0.7490
      NESTED CLADE      -19.8912       0.3010       0.6990




PERMUTATION ANALYSIS OF Clade 3-3
   BASED ON 1000 RESAMPLES
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PART I.  PERMUTATIONAL CONTINGENCY TEST:


  OBSERVED CHI-SQUARE STATISTIC =    56.5083

  THE PROBABILITY OF A RANDOM CHI-SQUARE BEING GREATER THAN
    OR EQUAL TO THE OBSERVED CHI-SQUARE =     0.0000


PART II.  GEOGRAPHIC DISTANCE ANALYSIS:

GEOGRAPHICAL CENTERS    LATITUDE      LONGITUDE
       Clade 3-3       -30 07'40"     27 21'27"
             2-3       -25 52'30"     30 00'00"
             2-5       -28 46'49"     27 56'11"
             2-6       -32 02'52"     26 21'55"

CLADE 2-3 (Tip)
 TYPE OF DISTANCE       DISTANCE      PROB.<=      PROB.>=
      WITHIN CLADE      109.3538       0.1200       0.8800
      NESTED CLADE      541.5202       0.9930       0.0070

CLADE 2-5 (Interior)
 TYPE OF DISTANCE       DISTANCE      PROB.<=      PROB.>=
      WITHIN CLADE      395.4836       0.8380       0.1620
      NESTED CLADE      426.7021       0.9110       0.0890

CLADE 2-6 (Tip)
 TYPE OF DISTANCE       DISTANCE      PROB.<=      PROB.>=
      WITHIN CLADE      130.7005       0.0010       0.9990
      NESTED CLADE      267.6463       0.0000       1.0000


PART III.  TEST OF INTERIOR VS. TIP CLADES:

 TYPE OF DISTANCE   I-T DISTANCE      PROB.<=      PROB.>=
      WITHIN CLADE      268.6643       1.0000       0.0000
      NESTED CLADE      109.2606       0.9020       0.0980


** ANALYSIS FINISHED **
It took 0.9330 seconds.
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Appendix 13: Data matrix used for the leaf transectional phenetic analysis

K. acraea TD4626	10?0000111 1011111112 0020010010 1010100010 1110001111 0000000110
K. albesens SR314	1210010011 1011111112 0010010011 1110101110 1110101111 0000000110
K. angustfolia SR453	1000000111 1011111112 0010020011 1111101110 1110111111 0000000110
K. baurii SR174	1211010111 1011111111 0010010011 1111101110 1110101111 0000100110
K. baurii SR285	1010010111 1011111111 0010010011 1011101110 1110101111 0000000110
K. baurii SR360	1011100111 1011111112 0010010011 1111101110 1110101111 0000001110
K. baurii NPB1923	1110000111 1011111112 0010010011 1111101110 1110101111 0000000110
K. brachystachya SRsn	1210000111 1011111112 0020020011 1111101110 1110111111 0000000110
K. breviflora SR452	10?1000111 1011111112 0020010011 1111101110 1110101111 0000000110
K. bruceae SR171	1010110111 1011111111 0010010011 1111101110 1110101111 0000001110
K. buchananii SR305	1000000111 1011111112 0020010010 1010101110 1110101111 0000000110
K. buchananii SR307	1001010111 1011111112 0010020011 1111101110 1110111111 0000000110
K. buchananii SR458	1200010111 1011111112 0020010010 1010101110 1110101111 0000000110
K. caulescens SR270	1200000111 1011111111 0010010011 1111000000 0000001111 1010100110
K. caulescens SR278	1200010111 1011111111 0010010011 1010000000 0000001111 11111101?1
K. citrina SR176	1000110111 1011111111 0010010011 1111101110 1110101111 0000001110
K. coddiana SRsn	1200010?11 1011111112 0010010010 1011101110 1110001111 0000000110
K. coddiana RAL4820	1210010?11 1011111111 0010010011 1011101110 1110101111 0000000110
K. coralligemma SR549	1011010111 1011111112 0010010011 1110101110 1110001111 1111110111
K. drepanophylla RJM1100	1000010?11 1011111111 0010010011 1111101110 1110101111 0000000110
K. ensifolia autumnalis SR448	1110000111 1011111112 0020010011 1111101110 1110101111 0000000110
K. ensifolia ensifolia JBsn	1011000111 1011111111 0020010011 1111101110 1110101111 0000000110
K. fibrosa SR297	2200000111 1001111112 0020020011 1111101110 1110101111 0000000110
K. fibrosa PBP 5579	2201000111 1011111111 0010010011 1111101110 1110111111 0000000110
K. fluviatilis SRsn	1001010111 1001111112 0010010011 1111101110 1110111111 0000000110
K. gracilis SR308	10?1000111 1011111111 0010010011 1111101110 1110101111 0000000110
K. gracilis SR321	1211000111 1111111111 0010010011 1111101110 1110101111 0000000110
K. galpinii SR312	10??000111 1011111112 0010010011 1111101110 1110101111 0000000110
K. hirsuta SR282	1100010111 1011111111 0010010011 1111101110 1110101111 0000000110
K. ichopenesis SR241	1211000111 1011111111 0010010011 1111101110 1110101111 0000000110
K. ichopenesis SR242	1211000111 1011111111 0020010011 1111101110 1110101111 0000000110
K. ichopensis SR409	1110000111 1011111111 0010010011 1111101110 1110101111 0000000110
K. latifolia RSSsn	1011010111 1011111111 0010010011 1111101110 1110101111 0000000110
K. laxiflora SR253	1210000111 1011111111 0010010011 1111101110 1110101111 0000000110
K. laxiflora SR283	1011000111 1011111111 0010010011 1111101110 1110111111 0000000110
K. laxiflora SR295	1010000111 1011111111 0020010011 1111101110 1110101111 00000001?0
K. laxiflora SR441	1010010111 1111111112 0020010010 1010101110 1110101111 0000000110
K. laxiflora SR442	1011010111 1111111112 0010010010 1010101110 1110101111 0000000110
K. laxiflora SR468	1110000111 1111111111 0020010011 1111111110 1110101111 0000000110
K. laxifloraC SRsn	1010000111 1011111112 0010010011 1111101110 1110101111 0000000110
K. leucocephala NNBG	2200000111 1011111111 0010010011 1111101110 1100001111 0000000000
K. linearifolia SR151	1011010111 1001111112 0020010011 1111101110 1110101111 0000000110
K. linearifolia SR170	1111110111 1011111112 0010010011 1111101110 1110101111 0000000110
K. linearifolia SR182	1211100111 1011111112 0020010011 1111101110 1110001111 0000001110
K. linearifolia SR269	1010110111 1011111111 0010010011 1111101110 1110001111 1010101111
K. linearifolia SR287	1110100111 1011111111 0010010011 1111101110 1110101111 0000000110
K. linearifolia SR290	1010010111 1011111112 0010010011 1111101110 1110001111 1010100110
K. linearifolia SR291	1010010111 1011100111 0010010011 1111101110 1110001111 0010100110
K. linearifolia SR311	1010000111 1011111111 0010010011 1111101110 1110001111 0010100110
K. linearifolia SR328	1010010111 1011111112 0010010011 1111101110 1110101111 0000100110
K. linearifolia SR343	1011010111 1011111111 0010010011 1111101110 0010101111 0000000110
K. linearifolia SR400	1010000111 1011111112 0020010011 1111101110 1110101111 0000000110
K. linearifolia JPsn	1010010111 1011111112 0010010011 1111101110 1110001111 1010100100
K. littoralis SR200	1010000111 1011111112 0000010011 1111101110 1110001111 0000000110
K. multiflora SR310	1010100111 1111111111 0010010011 1111101110 1110101111 0000000110
K. northiae SR263	0000010110 1000011110 0010010000 1011000010 1110100111 0000000010
K. northiae SR274	0000010110 1000011110 0010010000 1010000010 1110101111 0000000010
K. parviflora SR268	1010010111 1011111111 0010010011 1111101110 1110111111 0000000110
K. parviflora SR330	2200000111 1011111111 0010010011 1111101110 1110111111 0000000110
K. pauciflora HBsn	2200000101 1001111111 0010010011 1110101110 1110001111 0000000110
K. porphyantha SRsn	121?000111 1011111112 0010010010 1?1?101110 1110111111 0000000110
K. praecox SR529	1010000111 1011111111 0010010011 1111101110 1110101111 0000000001
K. praecox TD4461	1010010111 1111111112 0020010010 1011101110 1110101111 0000000110
K. rigidifolia SRsn	1010010111 1011111111 0010010011 1111101110 1110001111 0000100110
K. ritualis SR300	1010010111 1011111111 0010010011 1111101110 1110001111 0010100110
K. rooperi SR237	1211000111 1101111111 0000010011 1111101110 1110101111 0000000110
K. sarmentosa SR207	1200000111 1011111112 0020010010 1?1?101110 1100001111 1010100??1
K. splendida SR548	1210010111 1011111112 0010010010 1110101110 1110101111 0000000110
K. stricta SR279	00000001?0 1000011110 0020010000 1111000010 1110110111 0000000010
K. thodei SR407	1110000111 1011111112 0010010011 1111101110 1110111111 0000000110
K. triangularis SR264	1010000111 1010000101 0010010011 1111101110 1110111111 0000000110
K. triangularis SR266	1010000111 1011111112 0010020011 1111101110 1110111111 0000000110
K. triangularis SR267	1010000111 1011111112 0010010011 1111101110 1110111111 0000000110
K. triangularis SR299	1010000111 1010011112 0020020011 1111101110 1110111111 0000000110
K. triangularis SR304	1211010111 1011111112 0010010011 1111101110 1110111111 0000000110
K. triangularis obtusiloba SRsn	1110000111 1011111111 0010010011 1111101110 1110111111 0000000110
K. typhoides JB8084	1210000111 1011111111 0010010011 1111101110 1110111111 0000000100
K. tysonii SR199	1211010111 1011111111 0000010011 1111101110 1110101111 0000000110
K. tysonii SR302	1010010111 1011111111 0010010011 1111101110 1110101111 1010100110
K. tysonii SR303	1010010111 1111111111 0010010011 1111101110 1110001111 1010100111
K. tysonii SR460	1010010111 1111111111 0010010011 1011101110 1110101111 0010100110
K. umbrina RGsn	1011010111 1011111111 0010010011 1111101110 1110111111 0000000010
K. uvaria SR166	1011110111 1011111112 0010010011 1111101110 1110101111 0000001110
K. uvaria SR186	101?000111 1011111112 0020010011 1111101110 1110101111 0000000110
K. uvaria SR201	1201010111 101111111? ??20010011 1111101110 1110101111 0000000110
K. uvaria SR203	1200010110 1011111112 0010010011 1111101110 1110001111 1010100111
K. uvaria SR211	1101010111 1011111112 0020010011 1111101110 1110101111 0000000110
K. uvaria TD4477	1010110111 1011111112 0020020011 1111101110 1110111111 0000001110
K. uvaria SR337	1010110111 1011111111 0020010011 1111101110 1110101111 0000001110

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K. uvaria SR342                    1011110111 1011111112 0020010011 1111101110 1110001111 0000100110
K. uvaria SR471                    1210110111 1011111111 0020010011 1111101110 1110101111 0000000110
K. uvaria SR172                    1010000111 1011111112 0010010011 1111101110 1110101111 0000000110
K. uvaria SR477                    1011100111 1011111112 0020010011 1111101111 1110101111 0000001110
K. uvaria SR344                    1001110111 1011111112 0020010011 1111101110 1110101111 0000001110


K. acraea TD4626                   0?000
K. albesens SR314                  0?000
K. angustfolia SR453               00000
K. baurii SR174                    01000
K. baurii SR285                    00000
K. baurii SR360                    01000
K. baurii NPB1923                  01000
K. brachystachya SRsn              0?000
K. breviflora SR452                01000
K. bruceae SR171                   01010
K. buchananii SR305                0?000
K. buchananii SR307                0?000
K. buchananii SR458                0?000
K. caulescens SR270                0?000
K. caulescens SR278                1?000
K. citrina SR176                   01000
K. coddiana SRsn                   0?000
K. coddiana RAL4820                01000
K. coralligemma SR549              1?000
K. drepanophylla RJM1100           0?000
K. ensifolia autumnalis SR448      0?000
K. ensifolia ensifolia JBsn        01000
K. fibrosa SR297                   00000
K. fibrosa PBP 5579                00000
K. fluviatilis SRsn                0?000
K. gracilis SR308                  0?000
K. gracilis SR321                  01000
K. galpinii SR312                  0?000
K. hirsuta SR282                   0?000
K. ichopenesis SR241               0?000
K. ichopenesis SR242               01000
K. ichopensis SR409                0?000
K. latifolia RSSsn                 01000
K. laxiflora SR253                 01000
K. laxiflora SR283                 00000
K. laxiflora SR295                 01000
K. laxiflora SR441                 01000
K. laxiflora SR442                 01000
K. laxiflora SR468                 0?000
K. laxifloraC SRsn                 0?000
K. leucocephala NNBG               00000
K. linearifolia SR151              01100
K. linearifolia SR170              01000
K. linearifolia SR182              01000
K. linearifolia SR269              11000
K. linearifolia SR287              01000
K. linearifolia SR290              11000
K. linearifolia SR291              11000
K. linearifolia SR311              11000
K. linearifolia SR328              01000
K. linearifolia SR343              00000
K. linearifolia SR400              01000
K. linearifolia JPsn               11000
K. littoralis SR200                01000
K. multiflora SR310                01000
K. northiae SR263                  00100
K. northiae SR274                  00000
K. parviflora SR268                0?000
K. parviflora SR330                00000
K. pauciflora HBsn                 00000
K. porphyantha SRsn                0?000
K. praecox SR529                   00000
K. praecox TD4461                  01000
K. rigidifolia SRsn                0?000
K. ritualis SR300                  01000
K. rooperi SR237                   00000
K. sarmentosa SR207                1?000
K. splendida SR548                 01000
K. stricta SR279                   00001
K. thodei SR407                    0?000
K. triangularis SR264              01000
K. triangularis SR266              01000
K. triangularis SR267              0?000
K. triangularis SR299              01000
K. triangularis SR304              00000
K. triangularis obtusiloba SRsn    01000
K. typhoides JB8084                00000
K. tysonii SR199                   01000
K. tysonii SR302                   1?000
K. tysonii SR303                   1?000
K. tysonii SR460                   11000
K. umbrina RGsn                    01000
K. uvaria SR166                    00000
K. uvaria SR186                    0?000
K. uvaria SR201                    00000
K. uvaria SR203                    10000
K. uvaria SR211                    0?000
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K. uvaria TD4477                   0?000
K. uvaria SR337                    01000
K. uvaria SR342                    01000
K. uvaria SR471                    01000
K. uvaria SR172                    01000
K. uvaria SR477                    010?0
K. uvaria SR344                    01000
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Appendix 14: Data matrix used for the SEM leaf surface phenetic analysis

K. acraea TD4626	1001110110 0002200
K. albescens SR314	0001010110 0002200
K. angustifolia SR453	0000000110 0002200
K. angustifolia SR542	0001010110 0002200
K. ankaratrensis PBP5676	1000010010 1002200
K. baurii SR174	0110000110 0001100
K. baurii SR275	0001111111 1002200
K. baurii SR285	1001111110 0002211
K. brachystachya SRsn	0001010110 0001100
K. breviflora SR452	1000010110 0002200
K. breviflora SRsn	0000000110 0002200
K. bruceae SR171	1001000111 1001100
K. buchananii SR307	1000010110 0002200
K. caulescens SR270	0001010110 0002200
K. citrina SR176	0000000111 1001100
K. coddiana SRsn	1000010110 0001100
K. coralligemma SR549	1001111110 0002201
K. drepanophylla RJM1100	1000010111 1002100
K. ensifolia autumnalis SR448	1001010110 0002200
K. ensifolia ensifolia JBsn	1001010110 0002200
K. fibrosa PBP5579	0000000000 0001100
K. fluvialitis SRsn	0110000110 0002200
K. foliosa JMG034	0??1010110 0002200
K. galpinii SR312	1001000101 1002100
K. gracilis SR308	1000010111 0001100
K. gracilis SR321	1001010011 0002200
K. grantii CIP4154	0001010110 0001100
K. hirsuta SR282	1001111111 0111200
K. ichopensis SR242	0001010110 0002200
K. insignis SRsn	1001000000 0002200
K. insignis TT30	1001010000 0001100
K. isoetifolia JMG033	0001010000 0002100
K. latifolia RSSsn	1000010010 0001100
K. laxiflora SR253	0001010110 0002200
K. laxiflora SR295	0001010110 0002200
K. leucocephala NNBG	0000000110 0001100
K. linearifolia SR151	0000000000 0002200
K. linearifolia SR170	1001010111 1001100
K. linearifolia SR182	0000000111 1001100
K. linearifolia SR269	1000010110 0001100
K. linearifolia SR287	0001010110 0001100
K. linearifolia SR290	1000010001 1001100
K. linearifolia SR291	1000011000 0001100
K. linearifolia SR311	1000000010 0001100
K. linearifolia SR328	1001011111 1002100
K. linearifolia SR343	1001011011 0001100
K. linearifolia SR400	0000000001 1002100
K. linearifolia JPSsn	1110010000 0001100
K. littoralis SR200	1000010010 0002200
K. multiflora SR310	1000011011 0001200
K. northiae SR263	1000100111 0002200
K. parviflora SR268	0??0000000 0002200
K. pauciflora HBsn	0001010110 0001200
K. porphyantha SRsn	1001011110 0001100
K. praecox SR529	0001010111 1001100
K. praecox TD4461	1000011111 0001200
K. pumila Friss1079	1001010100 0001100
K. rigidifolia SRsn	0000000000 0001100
K. ritualis SR300	1??0010010 0001100
K. rooperii SR237	1001100111 1002200
K. rooperii SRsn	10?1011110 0002200
K. sarmentosa SR207	0000000110 0002200
K. schemperi JMG036	1000010110 0001100
K. splendida SR548	1001010111 0001200
K. stricta SR279	0000000111 1002100
K. thodei SR407	0000000110 0002200
K. thomsonii JMG031	0001010110 0001100
K. thomsonii AMM2647	1001010110 0002200
K. thomsonii CK4821	0001010110 0001100
K. triangularis SR264	1000010000 0002200
K. triangulari sSR266	1000010000 0001100
K. triangularis SR267	1001010000 0001200
K. triangularis SR299	1000010111 0001100
K. triangularis SR304	0000000110 0002200
K. triangularis obtusifolia SRsn	1000010010 0002200
K. typhoides JB8084	0000000110 0002200
K. tysonii SR199	1001010111 1002200
K. tysonii SR303	1001010101 0001100
K. umbrina RGsn	1000010110 0002200
K. uvaria SR165	0000000110 0002200
K. uvaria SR172	1000011111 0001200
K. uvaria SR186	1000010111 1001100
K. uvaria SR201	1000010110 1001100
K. uvaria SR203	1000000011 1001100
K. uvaria SR211	1000000110 0002201
K. uvaria SR337	1001010110 0002211
K. uvaria SR342	1?01111111 1002201
K. uvaria SR344	0000000110 0002200
K. uvaria SR471	1?00011111 0001200

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K. uvaria SR477                     0000000110 0002200
K. uvaria TD4477                    0000000110 0001100
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