Bioprospecting the flora of southern Africa: optimising plant selections

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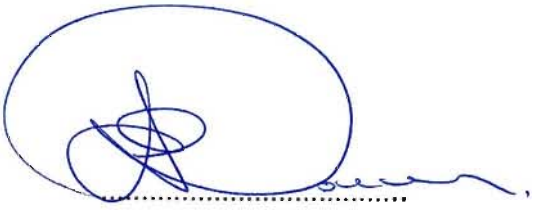
Preface

The work described in this dissertation was carried out at the Ethnobotany Unit, South African National Biodiversity Institute, Durban and at the School of Biological and Conservation Sciences, University of KwaZulu-Natal, Pietermaritzburg from January 2004 to November 2005 under the supervision of Professor T.J. Edwards (School of Biological and Conservation Sciences, University of KwaZulu-Natal, Pietermaritzburg) and Dr N. R. Crouch (Ethnobotany Unit, South African National Biodiversity Institute, Durban).

These studies, submitted for the degree of Master of Science in the School of Biological and Conservation Sciences, University of KwaZulu-Natal, Pietermaritzburg, represent the original work of the author and have not been submitted in any form to another university. Use of the work of others has been duly acknowledged in the text.

We certify that the above statement is correct



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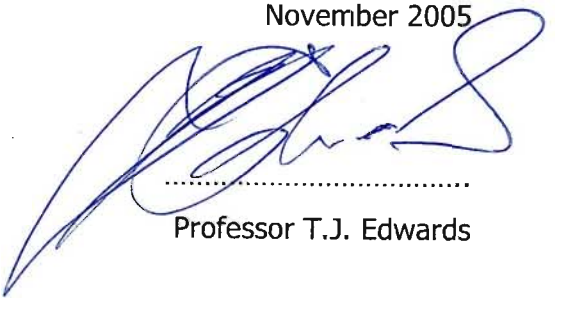

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Abstract

Focused procedures which streamline and optimise plant prioritisation and selection in bioprospecting have the potential to save both time and resources. A variety of semi-quantitative techniques were assessed for their ability to prioritise ethnomedicinal taxa in the *Flora of Southern Africa* (*FSA*) region. These techniques were subsequently expanded upon for application in plant selection for the Novel Drug Development Platform bioprospecting programme.

Least squares regression analyses were used to test the hypothesis that ethnomedicinal plant use in southern Africa is strictly random, i.e. no order or family contains significantly more medicinal plants, than any other order or family. This hypothesis was falsified revealing several 'hot' plant orders. The distribution of southern African ethnomedicinal taxa was investigated, and revealed low ethnomedicinal plant usage in the Western Cape and Northern Cape. The historical settlement of Bantu tribes in the eastern regions of southern Africa was one explanation for this discrepancy. Growth forms of ethnomedicinal taxa in 'hot' orders (identified in the regression analysis) were analysed. The results indicated no clear preferences across orders, but rather a preference for particular growth forms in certain orders. With respect to distribution, endemism and Red Data List status of ethnomedicinal taxa, the Western Cape had the greatest proportion of endemics and Namibia had the highest proportion of Red Data Listed ethnomedicinal taxa. With respect to chemotaxonomy, the Asteraceae contained the highest proportion of terpenoids, the Rubiaceae the highest proportion of alkaloids and the Fabaceae the highest proportion of flavonoids.

The predictive value of regression analyses was tested against an existing analysis of anti-malarials and the subsequent *in vitro* bioassays on *Plasmodium falciparum*. In particular, the ability of these analyses to identify plants with antiplasmodial IC_{50} values of ≤ 10 μg/ml was assessed. Most species in 'hot' genera showed comparatively good antiplasmodial activities ($IC_{50} \leq 10$ μg/ml).

Plant candidates were prioritised for screening anti-tuberculosis, anti-diabetes and immune-modulatory compounds, using a weighting system based on;
their ethnomedicinal application, chemotaxonomic potential, frequency in ethnomedicinal trade, association with the relative disease, toxicity, Red Data status, indigenous or endemic status, and family selection in ethnomedicine (identified through regression analyses). Other taxa were short-listed due to their presence in biodiversity hotspots where few ethnomedicinal plant use records are documented, and still others were incorporated due to their taxonomic association with efficacious exotic allies. Statistical analyses of the weighting processes employed were not possible in the absence of screening results which are due only in December 2006.

The legislation governing bioprospecting in South Africa is discussed and several recommendations are presented to minimise negative impacts on the industry.

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List of abbreviations

ABS	Access and benefit sharing
CBD	Convention on Biological Diversity
CFK	Cape floral kingdom
COP	Conference of Parties
CSIR	Council for Scientific and Industrial Research
DACST	South African Department of Arts, Culture, Science and Technology
DCM	Dichloromethane
DEAT	South African Department of Environmental Affairs and Tourism
DNP	Dictionary of Natural Products
DST	South African Department of Science and Technology
EIA	Environmental impact assessment
EthmedDBM	Ethnomedicinal taxa used to treat diabetes
EthmedIMM	Ethnomedicinal taxa used for immune modulation
EthmedTB	Ethnomedicinal taxa used to treat tuberculosis
FSA	*Flora of southern Africa*
GMO	Genetically modified organisms
IP	Intellectual property
MAFEV	Malaria and fever
MAT	Mutually agreed terms
MEA	Malaria endemic area
MEDBASE	Medicinal Plant Database for South Africa
MeOH	Methanol
MRC	Medical Research Council
MTA	Material transfer agreement
NCI	United States National Cancer Institute
NDDP	Novel Drug Development Platform
NP	Natural products
PBR	Plant breeders' rights
PIA	Prior informed approval
PIC	Prior informed consent
PRECIS	National Herbarium (PRE) Computerised Information System
RAU	Rand Afrikaans University (now University of Johannesburg)
SABONET	South African Botanical Diversity Network
SANBI	South African National Biodiversity Institute
TK	Traditional knowledge
TRAMED	Traditional medicines database
TRIPS	Agreement on Trade Related Aspects of Intellectual Property Rights
UCT	University of Cape Town
UKZN	University of KwaZulu-Natal
UP	University of Pretoria
UPE	University of Port Elizabeth
WTO	World Trade Organisation

Chapter 1

Introduction

All who drink of this remedy recover in a short time, except those whom it does not help, who all die. Therefore, it is obvious that it fails only in incurable cases.

– Galen (130-200 AD)

While Galen's logic may be flawed, his statement carries a warning to all involved in drug development to test thoroughly claims of efficacies which may hold toxic qualities. It also provides an indication that research in medicine is not new to science. Indeed, humans have used therapeutic plants for thousands of years (Hamburger and Hostettmann, 1991; George *et al.*, 2001; Buenz *et al.*, 2004). In developing countries up to 80% of populations remain dependent on plants for primary healthcare (Hostettmann and Marston, 2002). The historical development of pharmaceuticals has been primarily through the extraction and synthesis of efficacious compounds from plants (Farnsworth and Bingel, 1977) identified through a variety of screening programs (Hunter, 2001) and ethnobotanical studies (Farnsworth and Bingel, 1977). The importance of ethno-directed research is significant, having contributed in the region of 74% of the pharmaceutical drugs from plants (Farnsworth *et al.*, 1985). Plant bioprospecting (the search for economically valuable genetic and biochemical resources)(Wynberg and Swiderska, 2001) is likely to continue into the foreseeable future, due to complementary advances in bioassay techniques (Tyler, 1986).

1.1 Bioprospecting – history and current global overview

Bioprospecting when defined in relation to indigenous biological resources includes any research, development and/or application of indigenous biological resources for commercial or industrial exploitation (DEAT, 2004b). This includes: i) searching for, collecting, or making extractions from such resources for research, development or application purposes; ii) utilising information regarding the traditional uses of indigenous biological resources for research or development purposes; or iii) research, application, development and/or modification of traditional uses, for commercial or industrial exploitation (DEAT, 2004b). This comprehensive definition recognises the multifaceted nature of bioprospecting with its many research phases (Figure 1.1).

Typically, pharmaceutical companies or other research institutions investigate plants (or other life forms) for compounds with efficacy against target diseases/organisms. Once suitable plants are identified, the subsequent isolation of active ingredients, toxicity analyses and drug trials may result in the production of new drugs. The process is however, expensive and time consuming. Many useful drugs currently in circulation, such as vincristine, resperpine, quinine and aspirin, originate from plants mentioned in the pharmacopoeias of traditional peoples (Cox, 1990). Natural product drug discovery programs have, however, grown in complexity and diversity, and while traditionally-targeted lead organisms were those that could easily be collected or propagated (plants, marine organisms and culturable microbes)(Quinn *et al.*, 2002), the scope has since broadened considerably. Although marine organisms present a large source of genetic diversity, and research into such organisms is increasing, many are as yet undescribed (Quinn *et al.*, 2002) compared with land-based organisms. The relatively well-described

floras of the world provide inventories that are relatively easy to access and the great diversity and novelty of plant secondary metabolites also holds strong appeal.

A single plant extract may contain several thousand different secondary metabolites, even though most phytochemical analyses reveal only a narrow spectrum of constituents (Hostettmann *et al.*, 2001). A large percentage of plants produce useful bioactive compounds: Cox *et al.* (1989) reported that 86% of species in the Samoan ethnopharmacopoeia showed pharmacological activity in broad *in vitro* and *in vivo* screenings.

The continued use of traditional medicines for healthcare purposes is fortunate for scientists engaged in bioprospecting, as they are still able to access traditional peoples' knowledge directly (Cox, 1990; Farnsworth, 1990). Pharmacological investigations of ethnomedicinal plants are thus likely to continue to: i) provide derivatives of plant extracts requiring no further chemical manipulation, i.e. they can be used (as new drugs) in an unmodified state; ii) provide the provision of 'building blocks' or the 'blueprints' from which other similar or more complex compounds may be synthesised; iii) indicate new modes of pharmacological action (Cox, 1990).

While plants represent a significant resource for novel drug development *per se*, there has been caution with regard to research and development, not only by the pharmaceutical industry, but also by government agencies and scientists (Farnsworth and Bingel, 1977; Dalton, 2004). Bioprospecting was seen as particularly risky in the late 1960's and early 1970's due to significant financial losses being experienced by a number of leading pharmaceutical firms (Farnsworth and Bingel, 1977; Tyler, 1986). This same reason is given for the termination of the United States National Cancer Institute

(NCI) anti-cancer agent plant screening programme (Cragg *et al.*, 1993). The failure of these projects was also reported to be a product of inefficiency in primary screening technology. The uniqueness of many natural product core structures (templates) makes these compounds of particular interest for use as starting points for semi-synthesis and total synthesis of novel drugs (Dickson and Gagnon, 2004). Between 1990 and 1996, ten natural product templates were discovered that have compounds either under clinical investigation or registration (Butler, 2005). Templates discovered since 1996 have not resulted in compounds entering clinical trials. Thus, natural products and natural product-derived drugs currently in clinical trials are derived from a relatively narrow range of templates. The small number of natural product templates discovered over the last 10 years coincides with the significant reduction in screening of natural products by the pharmaceutical industry (Butler, 2005).

With the signing of the Convention on Biological Diversity (CBD) in Rio in 1992 (CBD, 1992), many economically poor nations of the tropics hoped that their natural resources would begin to be utilised in a sustainable way (Dalton, 2004). In addition, they hoped to receive economic benefits from their biological resources (Macilwain, 1998). While there are reports of successful partnerships being forged (e.g. the investment by Merck & Company of Rathway, New Jersey and the government of Costa Rica)(Joyce, 1991), these are few and far between (Macilwain, 1998). No significant increase in bioprospecting has occurred in the ten years following the signing of the CBD. If anything, such interest has decreased: both Monsanto and the New York-based Bristol Myers Squibb shut down their natural product divisions (Dalton, 2004). Merck has halted investment in their Costa Rica project, a spokesperson having stated that no products had been realised from the project. Company officials refused to discuss details of the withdrawal (Dalton, 2004). The push for benefit-sharing by developing nations also likely

gave drug companies the perception that financial risks in bioprospecting currently outweighed the benefits (Dalton, 2004). The recalling of bioprospecting permits by the Mexican government from a multinational project aimed at identifying and preserving Mayan knowledge of plants is an example of how indigenous peoples, even when offered full benefit sharing, may be reluctant to share cultural secrets (Stokes, 2001). In this instance the use of the phrase 'prior informed consent' in the agreement was reportedly the cause for contention (Hardison, 2000). This highlights the need for carefully considered legislation to govern bioprospecting activities as well as the need for good communication between parties involved.

1.2 Bioprospecting in the flora of southern Africa

The *Flora of southern Africa* (*FSA*) includes more than 70 major vegetation units (Acocks, 1953) nested within the subcontinent's seven floristically distinct biomes (Rutherford, 1997)(Figure 1.2). The *FSA* region includes the following countries: Namibia, Botswana, Swaziland, Lesotho and South Africa (Germishuizen and Meyer, 2003). An estimated 80% of the 24,300 plant taxa recorded for the *FSA* are endemic to the region (Goldblatt, 1978). The flora is estimated to constitute approximately 10% of global plant diversity, of which a relatively small percentage has been pharmacologically investigated (Eloff, 1998). A systematic evaluation of the southern African flora began at Noristan Ltd. in 1974, with the aim of isolating and identifying pharmacologically useful compounds (Fourie *et al.*, 1992). If higher plants are indeed 'treasure houses' of phytochemicals that may serve as pharmacological drugs (George *et al.*, 2001), then the potential of the southern African region holds is large.

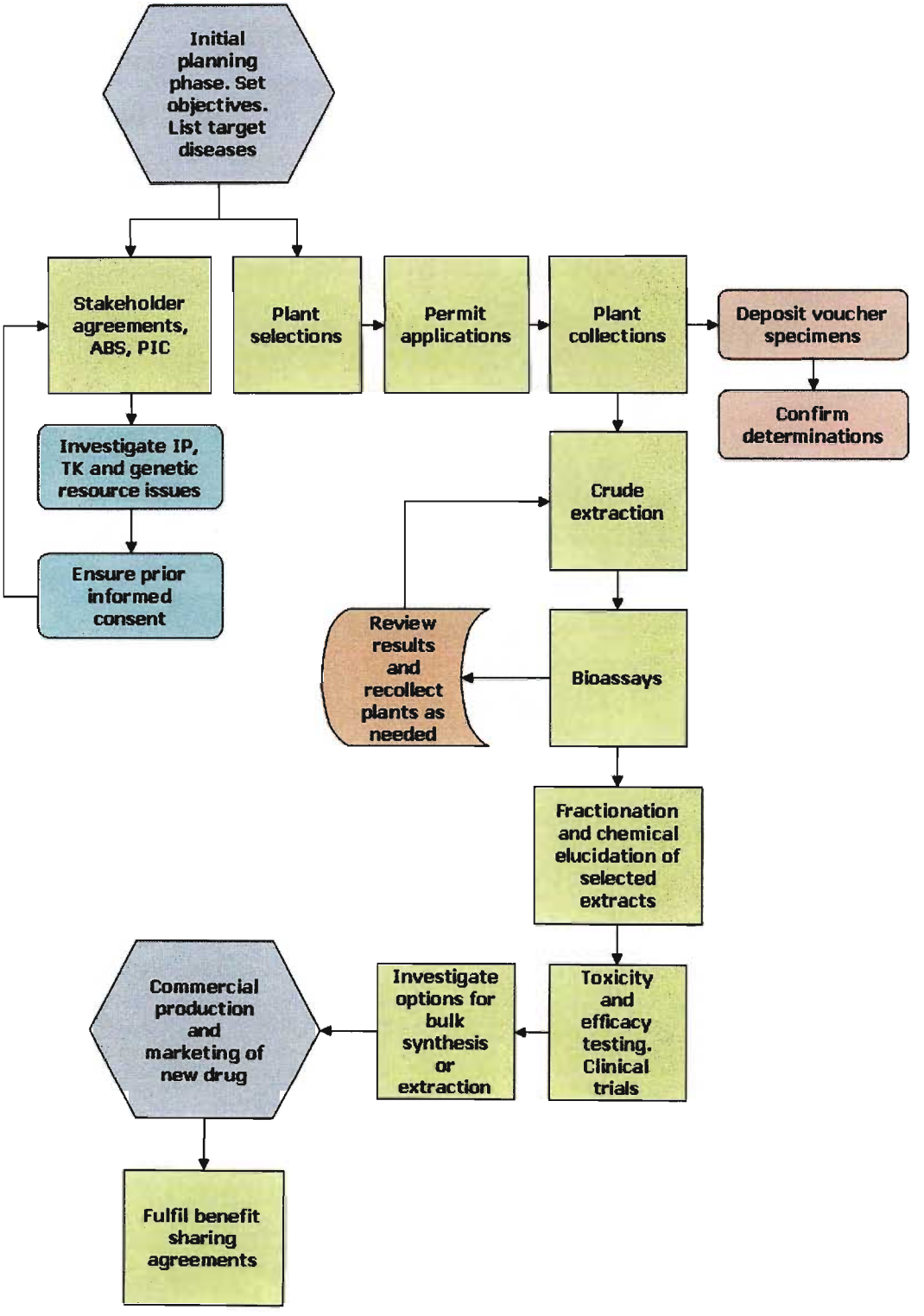

Figure 1.1 Overview of the bioprospecting process (adapted from George and Van Staden, 2000)

The region also contains a wealth of traditional medicinal plant knowledge, much of which has been collected and stored in computer databases (Fourie *et al.*, 1992). These authors report that approximately 81% of the 300 South African plant taxa they evaluated showed biological activity in target assays. This substantiates the notion that plants used in traditional medicine systems are a good starting point for drug development research. However, the sophistication and expense of medicinal chemistry may result in years of research (screening, purifying and identifying the chemical structures) before the compounds responsible for the effects seen in early bioassays are identified. Once identified, compounds still need to be tested for safety and efficacy before being formulated and marketed (Figure 1.1)(Van Rijssen, 1995). These time-consuming and expensive research and development operations are usually undertaken by large pharmaceutical companies, none of which are currently based in South Africa. Noristan Ltd., the only sizable such company to have existed in the region, closed down in the early-1990's after 15 years of bioprospecting operations (Laird and Wynberg, 1996).

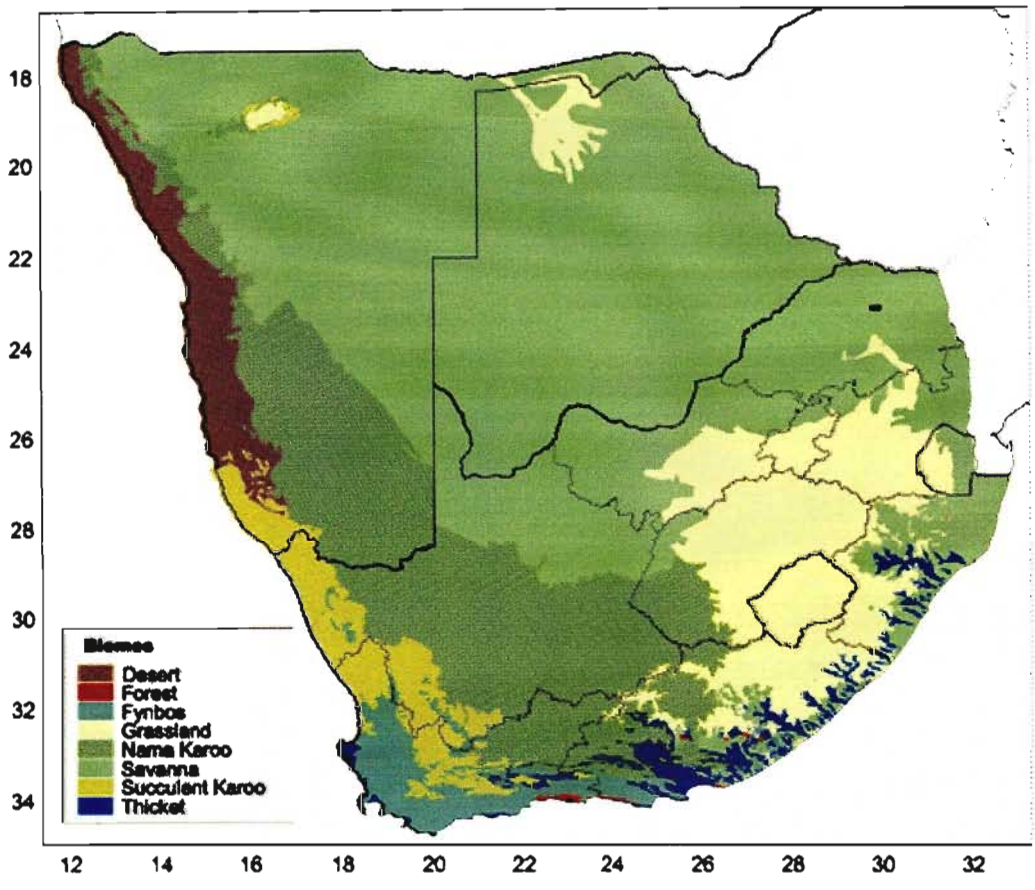

Figure 1.2 The major biomes represented in the *Flora of southern Africa* (*FSA*) region (Rutherford, 1997; SANBI, 2005)

Within South Africa, scientists from universities and other research institutions have collaborated with a view to developing novel pharmaceuticals from local plants. One network with interest and expertise in ethnopharmacology was established at the Department of Pharmacology, University of Cape Town in 1995. A central resource known as the TRAMED (Traditional Medicines Database) Programme, with a database of regularly-updated plant chemistry, toxicology and pharmacology information was constructed to serve as a source of information for collaborators (Van Rijssen, 1995; MRC, 2001). The database (available on the World Wide Web)(TRAMED, 2005) incorporates traditional medicine information donated by Noristan Ltd., which in 1995 added 46 000 anecdotes and the results of selected bioassays for 350 plant taxa. The other regional scientific collaborations have yielded promising results, with a number of phytomedicines commercialised or listed as having good potential (George *et al.*, 2001). These authors provided a detailed short-list of those taxa from which products have been manufactured and marketed in South Africa. In light of these various successes, further regional consortia have since been established.

1.3 The Antimalarials Consortium (Figure 1.3)

Due to a need for efficacious antimalarial agents in the region, the South African Department of Arts, Culture, Science and Technology (DACST)(now Department of Science and Technology, DST) awarded an innovation fund grant to a consortium of five South African institutions to evaluate medicinal plant extracts for antimalarial activity (Clarkson *et al.*, 2004). These institutions included the Council for Scientific and Industrial Research (CSIR), the Medical Research Council (MRC), the National Botanical Institute (NBI)(now South African National Biodiversity Institute, SANBI), the University

of Cape Town (UCT) and the University of Pretoria (UP). As the majority of historical antimalarial drugs have been derived from ethnomedicinal plants, or from structures modelled on plant lead compounds, the consortium opted to investigate local ethnomedicinal plant extracts for the development of novel plant-based antimalarial drugs.

1.3.1 Plant selection for antimalarial drug development

The selection of plants for screening was undertaken by the NBI. A survey of ethnomedicinal plant literature resulted in the compilation of a database, which allowed further interrogation of the data. Plant taxa were selected on the basis of weighted criteria and ranked, using a method similar to that used by Clark *et al.* (1997). These authors selected plant molluscicidal candidates from the *FSA*. The antimalarial plant selection technique was deemed a success, with more than 50% of the plant extracts showing IC_{50} values of ≤10 µg/ml (Clarkson *et al.*, 2004).

1.4 The Novel Drug Development Platform (Figure 1.3)

The establishment of the Novel Drug Development Platform (NDDP) in 2003 was as a result of funding obtained through the Innovation Fund Technology Missions (Department of Science and Technology). Consortium members included the following institutions: the Agricultural Research Council (ARC), Centre for Scientific and Industrial Research (CSIR), Medical Research Council (MRC), University of Johannesburg (UJ)(formerly Rand Afrikaans University), South African National Biodiversity Institute (SANBI), University of Cape Town (UCT), University of KwaZulu-Natal (UKZN), University of the North (UNIN), University of Port Elizabeth (UPE), and the University of Pretoria

(UP). The key objective of the NDDP was to establish a scientific biotechnology infrastructure to collaboratively research and develop novel medicines from indigenous plants in southern Africa. This has involved the identification and screening of candidate plant extracts against (i) tuberculosis and (ii) diabetes, and (iii) for the modulation of human immune systems. Ongoing research into the development of antimalarial drugs (previously undertaken by the Antimalarials Consortium)(Section 1.3)(Figure 1.3) was also incorporated into the NDDP.

1.4.1 Plant selection by the NDDP

The plant selection procedure adopted was based on that used by the Antimalarials Consortium, but was modified in a variety of ways. It also incorporated a regression analysis technique similar to one applied by Moerman (1991). Screening results for the three disease states under investigation are anticipated by December 2006.

1.5 Approaches to selecting plants for bioprospecting

Selection of plants for extract screening can be achieved in two ways (Cox, 1990): i) random selection, where no regard is taken of the taxonomic affinities, ethnobotanical context or other intrinsic qualities; ii) targeted or focused selection, by means of phylogenetic surveys (close relatives of plants known to contain useful compounds are sampled), ecological surveys (plants in particular habitats with particular growth habits), or ethnopharmacological surveys (identifying plants used by indigenous peoples to target specific diseases).

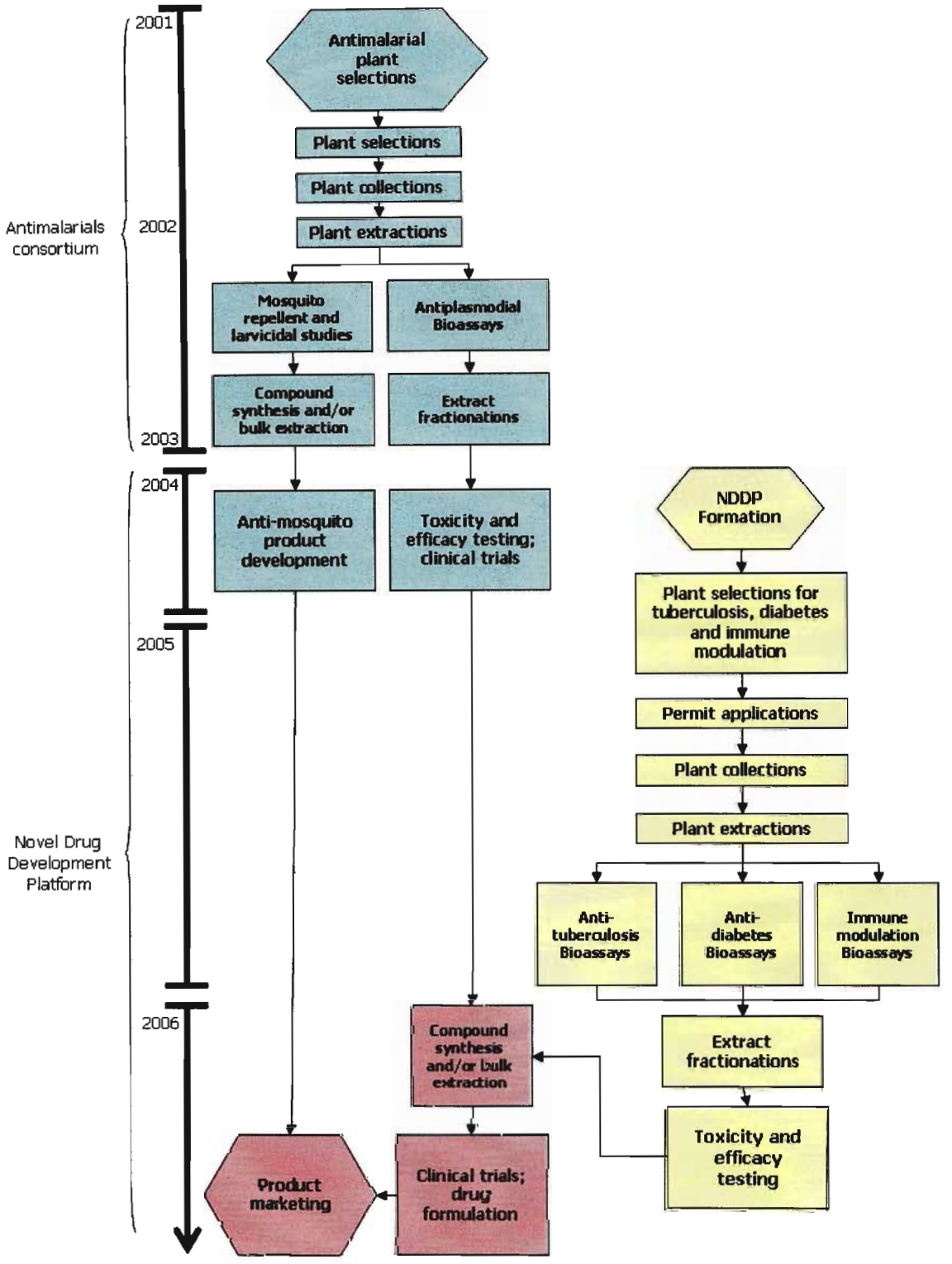

Figure 1.3 Relationship between Antimalarials Project and NDDP, and the respective bioprospecting approaches

Generally, it has been shown that random selection has a low success rate, though not always: Taxol, a compound derived from *Taxus brevifolia* Hort. ex Gord. (Pacific Yew) and approved for treatment of ovarian and metastatic breast cancer, is one of the few drugs developed through use of random-screening (Cragg *et al.*, 1993; Cox and Balick, 1994). Focused selection and ethnobotanical screens in particular, have shown relatively high success rates (Farnsworth *et al.*, 1985; Cox, 1990; Farnsworth, 1990; Cox, 1994).

1.5.1 Focused plant selection methods

Focused methods employed to identify efficacious ethnomedicinal plants worthy of research vary (Trotter, 1986) and include: i) Cross-cultural comparisons, where plant efficacies are inferred from the extent to which they are used across different ethnic groups or cultures; ii) the extent of selective borrowing and diffusion of herbal remedy-use by various ethnic groups or cultures; (iii) market and household garden-based studies which identify popular plants or those with high trade volumes; (iv) the collection and analysis of case histories and related plant-use anecdotes which may prove to be instructive. In addition, Buenz *et al.* (2005) reported that correlations between ancient and current plant use practices suggest that the taxa in question are indeed effective treatments.

The question of how ethnomedicinal practitioners select plants has also often been posed (Moerman, 1979; Moerman, 1991). Adler and Hammett (1973) postulated that such plant selection is undertaken on a strictly symbolic basis, and that reported therapeutic benefits are of a placebo effect. If this is so, it could be assumed that symbolic selection of plant taxa is random, in so far as the proportion of taxa selected from any given family or order will be equal. Moerman (1991) proposed this null-hypothesis in an analysis of the patterns of collective ethnobotanical plant use by Native

Americans. However, by means of a least squares regression analysis, he identified a distinct bias towards the use of certain taxonomic groups by these people in the treatment of particular diseases, and so disproved the hypothesis. Analyses comparing the actual number of medicinal taxa in a family with the probability distribution for numbers of medicinal taxa in that family (using a random test hypothesis) showed comparable results (Moerman and Estabrook, 2003) to the least squares regression analysis. These results demonstrate the advantage of selecting plants from 'hot' families when bioprospecting for efficacious plant extracts. Section 1.5.2 provides further discussion and justification for the use of plant prioritisation techniques which incorporate taxonomic or phylogenetic information.

Methods employed by Clark *et al.* (1997) identified relevant criteria and formulated a scoring system to help streamline plant selection. Examples of desirable characteristics included relative toxicity, availability of plants, plant growth characteristics, localisation of activity (plant part), physical and chemical stability, ethnobotanical use, ease of extraction and ease of application. The procedure of Clark and co-workers allowed for prioritisation of 63 short-listed taxa, of which six were included in preliminary screening. The system aimed to identify taxa that could be used in a relatively crude way by communities and as such has limited application for more sophisticated bioprospecting approaches. However, the objectivity of plant candidate selections and the ease with which the weighting system could be modified were highlighted by the authors as key advantages. The semi-quantitative plant selection procedure used by the antimalarials consortium (Clarkson *et al.*, 2004)(Section 1.3.1) was modelled on that of Clark *et al.* (1997).

1.5.2 Chemotaxonomy, phylogeny and the search for novel drugs

Understanding why different plants produce different secondary metabolites is an important consideration in the field of bioprospecting, as such insights allow for optimising of plant selections. The previously accepted consensus, that secondary metabolite production was primarily related to the effect of enhancing the fitness of the producer, is now being undermined by data from pharmaceutical and agrochemical industries (Firn, 2003). Firn reported that the pharmaceutical and agrochemical industries, through the experience of numerous screening programmes, have realised that a very low probability exists of finding useful compounds from either man-made or naturally made chemicals. This, according to Firn and Jones (2000) is due to the requirement of a very precise three-dimensional match between charge distribution on an efficacious biochemical compound and the surface of the target protein it is required to interact with. Jones and Firn (1991) proposed that evolution favoured organisms that could generate and retain the greatest sustainable chemical diversity at low cost. Such organisms would have an increased likelihood of enhanced fitness due to the greater chances of producing rare chemicals with potent biological activity. As such, the majority of natural products found in plants are unlikely to possess potent biological activity. The task for bioprospectors therefore lies in identifying those taxa with the high chemical diversity as these would likely provide the greatest potential for drug development. This is where a combination of ethnomedicinal and phylogenetic knowledge can focus endeavours.

Native American selections of ethnomedicinal plants show a predilection to some families, regardless of family size (Moerman *et al.*, 2003). This may be due to related plants showing similar efficacy against certain diseases due to heritable similarities in secondary metabolites. Phylogenetic considerations are therefore important in the

bioprospecting process. Although disputed by some influential systematists (Cronquist, 1980) it is generally accepted that related taxa share chemical characteristics, to the extent that phytochemicals can be used as taxonomic characters in classification (Grayer *et al.*, 1999; Waterman, 1999). The early work by Robert Hegnauer is particularly relevant (Grayer *et al.*, 1999) due to his attempt to understand the distribution of secondary (and some primary) metabolites in the plant kingdom and the phylogenetic relationships of plant families based on chemical profiles (Grayer *et al.*, 1999). Hegnauer's early work was controversial but it was later endorsed by a number of systematists (Dahlgren, 1975; Thorne, 1981), who included chemical characters when constructing their classifications.

The structural diversity of plant compounds has likely increased along with other changes observed in the course of plant evolution (Hegnauer, 1967; Heinrich *et al.*, 2004). Chemical characteristics should however only be used in conjunction with other characters (Dahlgren *et al.*, 1981). Certain compounds are restricted taxonomically, e.g. sesquiterpene lactones are limited to the Asteraceae, Apiaceae, Burseraceae, Lauraceae and Magnoliaceae (Dahlgren *et al.*, 1981). Records which document the occurrence of pharmacologically active secondary metabolites within monophyletic assemblages are therefore of particular interest. Homology in such groups, may lead to the evolution of compounds with similar pharmacological activity. Alternatively, the production of the same or similar compounds in unrelated taxa through convergent evolution may be an indicator of endowed selective fitness due to compound efficacy (Dahlgren *et al.*, 1981). Compound classes present across broad polyphyletic groups are generally unlikely to aid bioprospectors identify particularly efficacious taxa. However, convergent clades with known efficacious taxa may prove useful through the provision of independent sets of relatives to investigate. The divergent, convergent or parallelist nature of biosynthetic

pathways producing such compounds may also prove insightful to chemists attempting laboratory syntheses.

Comparative methods (e.g. least squares regression analyses) are common tools for investigating trait correlations (Felsenstein, 1985; Harvey and Pagel, 1991; Westoby *et al.*, 1995). However, comparative tests that seek correlations among phylogenetically conservative variables should establish the phylogenetic independence of any claimed relationships (Silvertown and Dodd, 1996). When this is undertaken, excessive pseudo replication can be avoided (Silvertown and Dodd, 1996). The current lack of detailed phylogenies for the majority of South African taxa will likely generate some degree of pseudo replication where such comparative methods are used.

1.5.3 Plant selection in current bioprospecting programmes

In light of the above, it was considered practical to streamline selection methods used in southern African bioprospecting programmes. The least squares regression analysis proposed by Moerman (1991) has allowed for the testing of the hypothesis that ethnomedicinal plant selection by ethnomedicinal practitioners in southern Africa is undertaken on a purely random basis (Chapter 2). These analyses were also applied to antimalarial plant data (Chapter 3) and to anti-tuberculosis, anti-diabetes and immune modulatory plant data (Chapter 4). Several other methods for identifying candidates are also included in Chapter 4.

1.6 Bioprospecting legislation in South Africa

Advances in bioprospecting are reportedly tempered by the lack of effective co-operation among researchers, inefficient plant selection procedures and poor legislation governing the use of natural resources and traditional knowledge (Farnsworth and Bingel, 1977; Tyler, 1986; Soejarto, 1993). The exorbitant costs associated with laboratory assays and drug trials have also limited the undertaking of bioprospecting activities either to large pharmaceutical companies or to collaborative efforts between research institutions/companies. These expenses, together with the ongoing demise of cultural knowledge in traditional societies (Balick, 1990; Hamilton, 2004), have resulted in the need to use focused bioprospecting methods for identifying candidate taxa most likely to yield efficacious drug products. The use of recorded ethnobotanical knowledge is one of the preferred means of optimising bioprospecting as such knowledge is frequently in published literature in the public domain. Since the signing of the CBD, there has been much contention (Cordell, 2000; Soejarto, 2001; Wynberg, 2004a) over how countries should secure returns from IP rights and ensure equitable sharing of benefits derived from natural resource utilisation (CBD, 1992). It has been recognised that cultural groups who contribute knowledge regarding the use of certain flora/fauna should benefit where such knowledge is the basis of successful new drug development (Aylward, 1995). The issue of knowledge ownership may also be linked to the reduced bioprospecting activities observed at several large pharmaceutical companies (Soejarto *et al.*, 2002b). Risks faced by companies include financial losses, legal conflicts over intellectual property (IP) ownership, and negative publicity linked to perceived biopiracy. The legislative issues were addressed in South Africa by Chapters 6 and 7 of Act 10 of 2004 (DEAT, 2004b) which covers access, benefit-sharing (ABS) and prior informed consent

(PIC) issues. Unfortunately, due to the non-standard and unpredictable nature of bioprospecting, and the difficulties surrounding IP and natural resource ownership, the act (DEAT, 2004b) has fallen short of expectations.

Chapter 2

Prioritisation of ethnomedicinal plants for bioprospecting: a multi-disciplinary approach

He's the best physician that knows the worthlessness of the most medicines.

– Benjamin Franklin (1733)

Abstract

A multidisciplinary analysis of medicinal plant-use in southern Africa has yielded a number of insights which will prove useful for bioprospecting programmes currently underway in the region. Data was sourced from the SANBI MedList database, which is the most comprehensive inventory of ethnomedicinal plants in southern Africa. Taxa were grouped by order, and a least squares regression analysis (after Moerman, 1979) was used to test the hypothesis that ethnomedicinal plant use in the region is strictly random, i.e. no order contains significantly more medicinally-used plant taxa, than any other order. The analysis resulted in the identification of a number of 'hot' plant orders (and families therein) that did contain significantly more ethnomedicinally-used taxa, allowing for the falsification of this hypothesis. The regional distribution of ethnomedicinally-used taxa was investigated, and the results indicated that certain regions, namely the Western Cape and Northern Cape had much lower recorded ethnomedicinal plant usage. This is probably due to higher population densities, longer historical colonisation and better preservation of ethnomedicinal plant-use records from

the eastern regions of southern Africa. Growth forms of ethnomedicinal taxa in 'hot' orders (identified in the regression analysis) were summarised to better understand the role this factor may play in plant selection by ethnomedicinal practitioners. The results indicate no clear preference across orders, but rather a preference for particular growth forms in certain orders. It is likely that growth forms of selected taxa are correlated to the dominant growth forms present in those orders, throughout the region. Distribution, endemicity and Red Data List status of the ethnomedicinal taxa in the *FSA* subregions were investigated. The Western Cape had a particularly low proportion of ethnomedicinal taxa relative to the overall number of taxa in that subregion. However, it had the greatest proportion of endemic ethnomedicinal plants of all regions in South Africa. Namibia had the highest proportion of Red Data Listed ethnomedicinal taxa (16.1%). A data mining trial was undertaken to identify the dominant chemical compound classes from selected 'hot' plant families. The Euphorbiaceae were found to contain notably high proportions of terpenoids, the Rubiaceae had the highest proportion of alkaloids and the Anacardiaceae had the highest proportion of flavonoids. It is feasible that a better understanding of the chemotaxonomy of plant families and the medicinally-used taxa therein will aid in the identification of related taxa with similar, biologically active compounds.

2.1 Introduction

The low probability of finding useful compounds in random plant screening programmes (approx. one plant sample in 10000 will show promising activity of interest to researchers), particularly in areas of high biodiversity, is one reason why private drug companies are reluctant to engage in bioprospecting *de novo* (Soejarto, 1993;

Macilwain, 1998). Methods to streamline and/or optimise the selection of organisms are therefore essential.

The annotated checklist of medicinal and magical plants in southern Africa (Arnold *et al.*, 2002), is a near-comprehensive ethnomedicinal plant-use data set for the region (Grace and Crouch, 2003). One of the key applications to which this data can be put is in the identification of candidate plants for novel drug development from the regional flora. The use of regression analyses (Figure 2.1)(after Moerman, 1979) is a simple yet effective means of reducing copious ethnomedicinal taxa to a small group likely to yield effective bioactivities. Such a reduction is achieved by grouping plant taxa by order or family and then applying a regression analysis to identify outliers. The occurrence of outliers falsifies the null hypothesis, which states that plant-use by traditional peoples is completely random. This implies that the percentage of taxa selected by ethnomedicinal practitioners for ethnomedicinal purposes from different plant orders would approach parity. Outliers above the regression line represent taxonomic groups that are targeted by ethnomedicinal practitioners and as such, should be earmarked for further investigation or prioritisation in bioprospecting. Such orders and families will be referred to as 'hot'. Outlying orders that occur below the regression line are used most infrequently by ethnomedicinal practitioners. The method of prioritising key taxonomic groups presented here is desirable for drug bioprospecting programmes due to improved efficiency.

Once key taxa (primary candidates) have been identified, the plant selection process may be further refined by incorporating chemotaxonomic and/or natural product data. It has been reported that plant secondary metabolites are often specific to taxonomic groups (Hegnauer, 1967; Cronquist, 1980), and close relatives of the primary candidates

may display similar pharmacological activities. The inclusion of related taxa can either be undertaken before initial bioassays or after primary candidate assessment. Molecular trees based on *rbc*L DNA provide a useful framework for assessing the comparative merits of secondary compound classes as chemotaxonomic characters (Grayer *et al.*, 1999), and so plant families and orders (excluding the Pteridophyta) in this analysis were grouped according to recently published phylogenetic trees (Bowe *et al.*, 2000; Chaw *et al.*, 2000; APG II, 2003).

Regional analysis of ethnomedicinal plants in southern Africa is instructive for several reasons, and should influence the planning and execution of drug bioprospecting. For example, biogeographic, habitat and habit information may be scrutinized in a similar way to yield a greater number of promising plant taxa. In addition, the historical settlement patterns and subsequent distribution of indigenous peoples and later migrants in the region may have significantly shaped the current body of recorded traditional plant-use knowledge (as reflected in the SANBI MedList database). This factor could well skew the results of any regression analyses. Similarly, the loss of historical data influences the number of current ethnomedicinal taxa recorded for that region (perhaps through cultural attrition). The presence of botanical hot spots and areas of high endemism should also be noted (Cowling and Hilton-Taylor, 1994), particularly if the goal is to include as many indigenous/endemic plants in a drug bioprospecting programme as possible, for either political, economic or conservation reasons. The patchy distribution and scarcity of many endemic taxa will have resulted in reduced contact with ethnomedicinal practitioners, which may skew results of the regression analyses in terms of both numbers and geographic region. It could be argued that botanical hotspots are under increasing threat due to habitation destruction and these areas should be regarded as priorities for bioprospecting ventures.

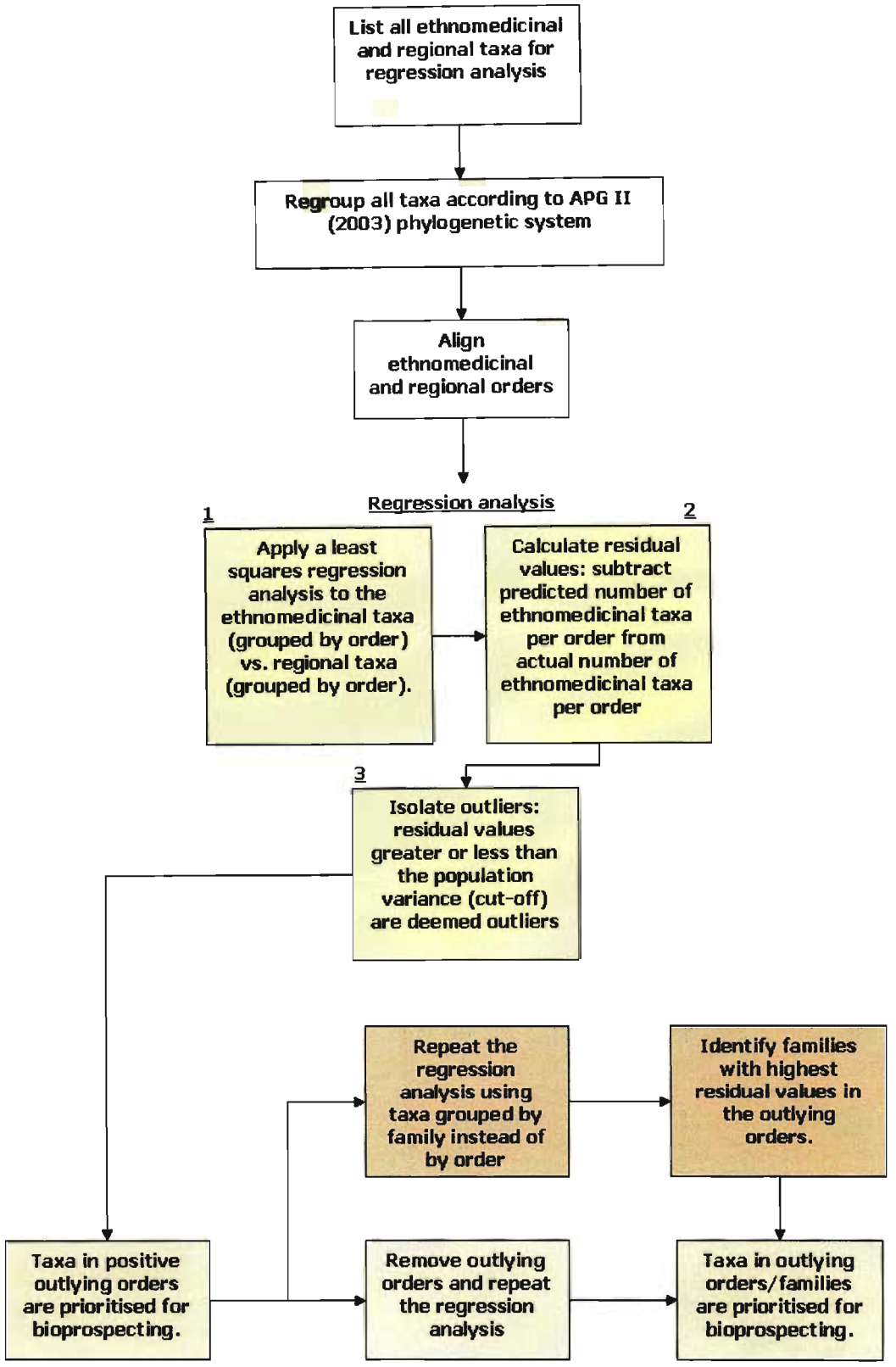

Figure 2.1 Overview of the use of least squares regression analyses for the prioritisation of plant taxa

Etkin (1986) noted that plant selection by ethnomedicinal practitioners may be patterned in accordance with the belief that certain attributes (e.g. leaf shape or colour) serve to indicate utility. This concept is generally referred to as the Doctrine of Signatures in which a plant is considered desirable due to the presence of a physical property that resembles some characteristic associated with the disease of concern. Analysis of ethnomedicinal taxa in the hot families should therefore be performed, with a view to identifying the occurrence of similar plant organ characteristics in utilised taxa. The results may also help to better direct the conservation and sustainable use of plants being harvested, either for traditional or pharmaceutical preparations.

A review of the general phytochemistry of ethnomedicinal plant families may prove beneficial in assessing correlations between the documented pharmacological activities of taxa in those families and their ethnomedicinal use. Records which document the occurrence of pharmacologically active secondary metabolites within monophyletic assemblages will be of particular interest as this may lead to the identification of related taxa with similar efficacies. This due to secondary metabolites (which are generally most active against disease-causing organisms) being considered valuable for taxonomic purposes (Cronquist, 1980). Toxicity of lower or higher ethnomedicinal taxa should also be investigated. A direct comparison of the current results with those presented by Moerman (1991) was not undertaken, due to the very different floras present in the two regions (North America and southern Africa).

2.2 Methods

2.2.1 Data source and organisation

The SANBI MedList database (SANBI, 2004) currently holds 3657 records and 3371 taxa (the difference due to the presence of synonyms in source literature). Of these, 1227 genera are grouped into 211 families. For the purposes of this study, taxonomic groupings at generic and species level conform to the PRECIS database (SANBI, 2005), while groupings at order and family levels follow the APG II (2003) for angiosperms[1], Bowe *et al.* (2000) and Chaw *et al.* (2000) for gymnosperms and Germishuizen and Meyer (2003) for the Pteridophyta. The regrouping resulted in a total of 193 families in 55 orders. Plants in the database include a wide spectrum of growth forms including trees, shrubs, climbers, herbs and geophytes.

2.2.2 Primary regression analyses

A least squares regression analysis (Figure 2.1) measuring the association between the ethnomedicinal taxa, and the total number of taxa present in the *FSA* region (both indigenous and naturalised plants were included), was performed. The entire dataset was incorporated into the primary analysis. A mathematical model for predicting the association between plant orders with ethnomedicinal taxa and the total number of taxa in those orders was obtained from the least-squares regression analysis. Two assumptions are made. Firstly, that due to the extensive literature review conducted during the compilation of the SANBI MedList database, the data constitutes a census rather than a sample of the ethnomedicinal taxa in southern Africa. This assumption eliminates the need for statistical tests of significance which are designed to give

[1] Note that the Balanophoraceae, Bruniaceae and Vahliaceae are not grouped into any order by the APG II (2003). To accommodate this, the Balanophoraceae were grouped with the Santalales, and taxa in the Bruniaceae and Vahliaceae were grouped into the Rosales according to the classification of Cronquist (1988).

confidence that the sample is representative of a larger body of data. Census data implies that all individuals in the population are accounted for. Secondly, that ethnomedicinal taxa used in the analysis are the only plants with any ethnomedicinal potential. Data therefore include (i) all recorded ethnomedicinal taxa in the *FSA* (grouped by order), and (ii) the total number of taxa in the *FSA* (grouped by order). The population correlation coefficient (ρ) indicates the strength of the relationship between these two groups of variables. Total number of orders and families were considered independent variables, and ethnomedicinal taxa as dependant variables.

2.2.2.1 Residual values

Residual values were calculated by subtracting the predicted number of ethnomedicinal taxa used per order from the actual number of ethnomedicinal taxa used per order. The population variance calculated from these residuals was used to identify all outliers, i.e. orders which showed notably different values from those predicted.

2.2.2.2 Plotting regression data

Ethnomedicinal taxa (grouped by order) were plotted against total taxa (grouped by order), and the regression line (equation obtained from the regression analysis) was overlaid to allow for visual assessment of (i) any obvious patterns/relationships and (ii) the position of any outliers. Residual values correspond to the vertical distance from each data point to the regression line ($y-\hat{y}$).

2.2.2.3 Analysis of families within selected orders

Positive outliers (orders selected significantly more often than predicted) were further analysed at family level. This required a regression analysis for all ethnomedicinal taxa

(grouped by family) against total taxa (grouped by family). Data for families within the selected orders were then filtered out for further scrutiny.

2.2.2.4 Secondary regression analyses

Outlying orders and families identified in the primary regression analyses (Section 2.2.1) were removed from the data set, and the regression analyses performed again to allow further partitioning of the data. The population variance of residual values was determined and used as a cut-off to identify outlying orders and families. Total taxa (grouped by orders or families) were considered independent variables and ethnomedicinal taxa (grouped by orders or families) as dependant variables.

2.2.3 Analysis of plant growth forms

In addition to the above analyses, an investigation of plant growth forms of plants present in the highly selected orders was undertaken. Plant growth form data was extracted from Germishuizen and Meyer (2003) and grouped according to four nominal categories, namely: Geophyte, Climber, Tree/Shrub and Herb/Dwarf shrub. All taxa in the respective orders were included, regardless of either annual or perennial status. For this analysis, the chemical defence strategies of annual and perennial taxa were assumed to not differ.

2.2.4 Regional distribution, endemicity and Red Data List status

The number and distribution of indigenous (SANBI, 2005), endemic (Germishuizen *et al.*, 2006) and naturalised (SANBI, 2005) ethnomedicinal taxa were collated and presented along with the proportions of Red Data (SABONET, 2003) ethnomedicinal taxa in the

FSA. Data were assessed for trends which may prove useful to bioprospecting and conservation initiatives in the region.

2.2.5 Evaluation of phytochemical trends in 'hot' families

A data mining exercise which summarised the important compound classes known to occur in selected 'hot' families was undertaken. 'Hot' families were those with the highest residual value in each of the highly selected orders. Compounds known to have been isolated from taxa in the 'hot' families was compiled from the Dictionary of Natural Products (DNP)(DNP, 2005), and then grouped according to class, as defined in the DNP. Proportions of compound classes present in each selected family were determined to assess prevalence. The phytochemical data are limited and do not represent all compounds/compound classes present. However, the DNP was the most comprehensive data source available and data are assumed to be sufficiently representative to allow an overview of the important classes. Compound classes notably absent or infrequently listed for the relevant families were also identified.

2.3 Results

2.3.1 Primary regression analyses

The results of the primary least squares regression analyses (Table 2.1) indicated the presence of a particularly strong linear relationship between ethnomedicinal associated taxa (grouped by order), and the total number of taxa in those orders, i.e. the value of ρ is very close to +1. Figure 1 provides further evidence of this positive relationship. Similar results were obtained for ethnomedicinal taxa grouped by family (Table 2.1).

Table 2.1 Statistics from a least squares regression analysis of ethnomedicinal orders and families

	Coefficient	Constant	ρ	ρ^2	Std. error	Pop. size
Orders	0.107	9.01	0.93	0.86	38.17	55
Families	0.111	1.90	0.88	0.77	20.77	196

2.3.1.1 Residual values

Residual values obtained from the regression analysis of ethnomedicinal taxa grouped by plant order ranged from −118.9 to +103.5 (residual values for each of the 55 orders are not presented). The model was able to account for 86% (ρ^2 = 0.86)(Table 2.1) of the variation in the y-values. As such, it was necessary to distinguish which orders could be considered outliers, i.e. farthest from the regression line. The population variance of all 55 order residuals (37.47) was employed as a cut-off, leaving 12 orders as outliers (seven positive and five negative)(Table 2.2). Plants in these orders were considered to have been selected either far more or far less than plants from other orders in the region. The magnitude of the outlying residuals falsified the null hypothesis.

Table 2.2 Orders used significantly greater or significantly less than predicted for ethnomedicinal purposes

Order	Total *FSA* taxa	Predicted ethnomedicinal taxa	Actual ethnomedicinal taxa	Residual value*
Malpighiales	895	104.5	208	+103.5
Fabales	2636	290.4	393	+102.6
Gentianales	1304	148.2	241	+92.8
Asterales	3179	348.3	414	+65.7
Solanales	515	64.0	127	+63.0
Malvales	732	87.1	132	+44.9
Sapindales	620	75.2	117	+41.8
Rosales	929	108.2	68	-40.2
Proteales	440	56.0	15	-41.0
Poales	1904	212.2	158	-54.2
Asparagales	3888	424.0	338	-86.0
Caryophyllales	2725	299.9	181	-118.9

* Residual values above (+) or below (-) the population variance

2.3.1.2 Plotting regression data

The 55 orders containing ethnomedicinal taxa were plotted against the total number of taxa present within those orders in the *FSA* (Figure 2.2). The strength of the positive relationship (ρ) is particularly evident. The seven positive and five negative outlying orders which influence both the coefficient of determination (ρ^2) and the reliability of predictions made from the line of best fit are particularly evident.

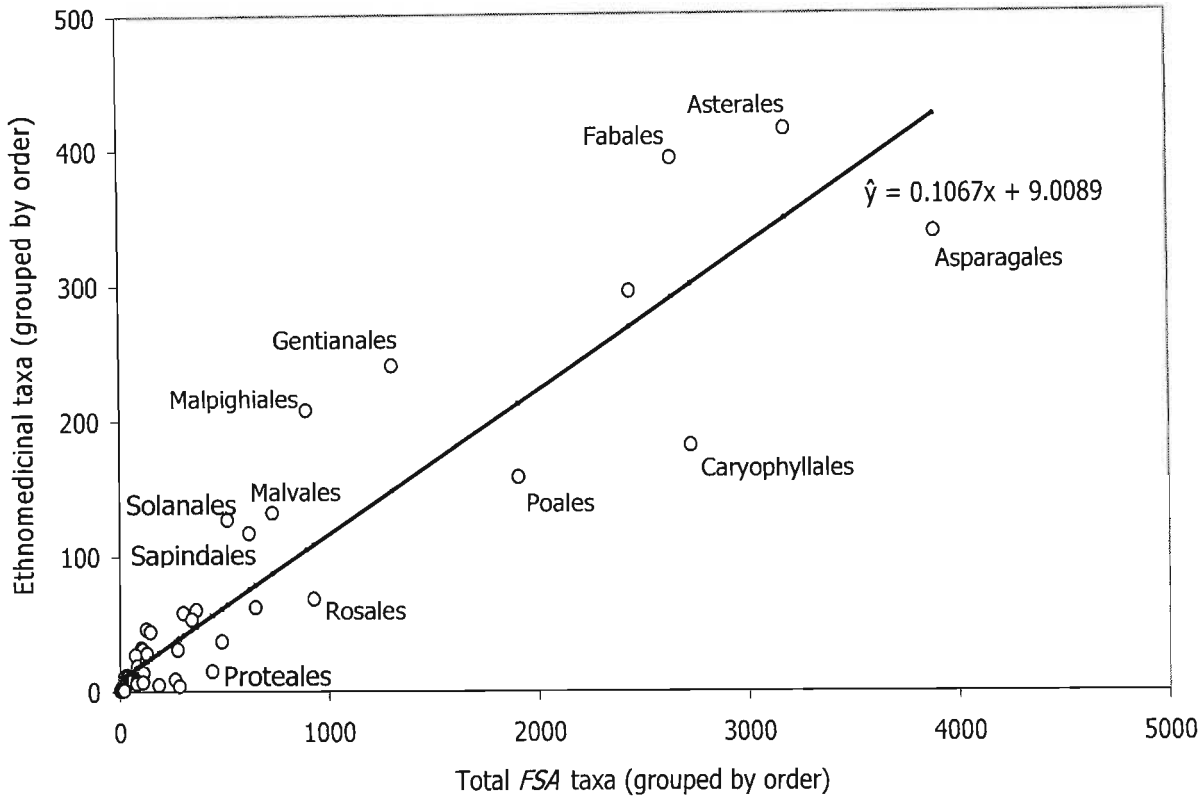

Figure 2.2 Regression plot of ethnomedicinal taxa grouped by order versus total taxa grouped by order

2.3.1.3 Analysis of families within selected orders

To better understand how families constituting the outlying orders contributed towards their popularity in ethnomedicinal use, a regression analysis for all families was performed. Although results of the entire analysis are too large to include, data for families which constitute the positive outlying orders were extracted (Table 2.3 – Table 2.9). Data in these tables are ordered by residual value, which dictates the extent to which the predicted number of medicinal plants varies from the actual number of medicinal plants. Families with high positive residual values contribute most to the outlier status assigned to their respective orders.

Table 2.3 Families in the Malpighiales extracted from a least squares regression analysis of ethnomedicinal taxa and total *FSA* taxa (grouped by family)

Family	Total *FSA* taxa	Predicted ethnomedicinal taxa	Actual ethnomedicinal taxa	Residual value*
Euphorbiaceae	523	60.1	110	+49.9
Phyllanthaceae	49	7.4	18	+10.6
Passifloraceae	37	6.0	13	+7.0
Salicaceae	93	12.3	18	+5.8
Ochnaceae	15	3.6	7	+3.4
Rhizophoraceae	8	2.8	6	+3.2
Hypericaceae	30	5.2	6	+0.8
Violaceae	22	4.4	5	+0.7
Malpighiaceae	16	3.7	4	+0.3
Turneraceae	11	3.1	3	-0.1
Linaceae	21	4.2	4	-0.2
Elatinaceae	13	3.4	3	-0.4
Chrysobalanaceae	5	2.5	2	-0.5
Clusiaceae	6	2.6	2	-0.6
Papaveraceae	28	5.0	4	-1.0
Dichapetalaceae	3	2.2	1	-1.2
Erythroxylaceae	7	2.7	1	-1.7
Picrodendraceae	8	2.8	1	-1.8

* Residual values above (+) or below (-) the population variance

Table 2.4 Families in the Fabales extracted from a least squares regression analysis of ethnomedicinal taxa and total *FSA* taxa (grouped by family)

Family	Total *FSA* taxa	Predicted ethnomedicinal taxa	Actual ethnomedicinal taxa	Residual value*
Fabaceae	2422	271.4	369	+97.6
Polygalaceae	214	25.7	24	-1.7

* Residual values above (+) or below (-) the population variance

Table 2.5 Families in the Gentianales extracted from a least squares regression analysis of ethnomedicinal taxa and total *FSA* taxa (grouped by family)

Family	Total *FSA* taxa	Predicted ethnomedicinal taxa	Actual ethnomedicinal taxa	Residual value*
Rubiaceae	345	40.3	89	+48.7
Apocynaceae	853	96.8	127	+30.2
Loganiaceae	10	3.0	9	+6.0
Gentianaceae	96	12.6	16	+3.4

* Residual values above (+) or below (-) the population variance

Table 2.6 Families in the Asterales extracted from a least squares regression analysis of ethnomedicinal taxa and total *FSA* taxa (grouped by family)

Family	Total *FSA* taxa	Predicted ethnomedicinal taxa	Actual ethnomedicinal taxa	Residual value*
Asteraceae	2681	300.2	387	+86.8
Goodeniaceae	4	2.3	1	-1.4
Menyanthaceae	8	2.8	1	-1.8
Campanulaceae	486	56.0	25	-31.0

* Residual values above (+) or below (-) the population variance

Table 2.7 Families in the Solanales extracted from a least squares regression analysis of ethnomedicinal taxa and total *FSA* taxa (grouped by family)

Family	Total *FSA* taxa	Predicted ethnomedicinal taxa	Actual ethnomedicinal taxa	Residual value*
Convolvulaceae	146	18.1	48	+29.9
Solanaceae	222	26.6	45	+18.4
Boraginaceae	146	18.1	33	+14.9
Montiniaceae	1	2.0	1	-1.0

* Residual values above (+) or below (-) the population variance

Table 2.8 Families in the Malvales extracted from a least squares regression analysis of ethnomedicinal taxa and total *FSA* taxa (grouped by family)

Family	Total *FSA* taxa	Predicted ethnomedicinal taxa	Actual ethnomedicinal taxa	Residual value*
Malvaceae	524	60.2	112	+51.8
Dipterocarpaceae	1	2.0	1	-1.0
Thymelaeaceae	207	24.9	19	-5.9

* Residual values above (+) or below (-) the population variance

Table 2.9 Families in the Sapindales extracted from a least squares regression analysis of ethnomedicinal taxa and total *FSA* taxa (grouped by family)

Family	Total *FSA* taxa	Predicted ethnomedicinal taxa	Actual ethnomedicinal taxa	Residual value*
Anacardiaceae	157	19.4	40	+20.6
Sapindaceae	45	6.9	15	+8.1
Burseraceae	35	5.8	13	+7.2
Meliaceae	30	5.2	12	+6.8
Simaroubaceae	2	2.1	2	-0.1
Rutaceae	351	41.0	35	-6.0

* Residual values above (+) or below (-) the population variance

2.3.1.4 Secondary regression analyses

Outlying orders and families previously identified as outliers were removed from the dataset and the regression analyses performed again. The results indicate a strong linear relationship ($\rho = 0.96$) between ethnomedicinal taxa (grouped by order), and total taxa in those orders (Table 2.10). The population variance of the 43 order residuals (12.03) was employed as a cut-off; seven positive and five negative outlying orders were identified (Table 2.11).

Table 2.10 Statistics from a secondary regression analysis of ethnomedicinal orders and families

	Coefficient	Constant	ρ	ρ^2	Std. error	Pop. size
Orders	0.117	3.28	0.96	0.93	12.31	43
Families	0.108	2.74	0.90	0.80	6.67	176

Table 2.11 Orders used significantly greater or less than predicted for ethnomedicinal purposes as identified in the secondary regression analyses

Order	Total *FSA* taxa	Predicted ethnomedicinal taxa	Actual ethnomedicinal taxa	Residual value*
Cucurbitales	126	18.0	46	+28.0
Ericales	145	20.2	44	+23.8
Brassicales	302	38.6	58	+19.4
Celastrales	102	15.2	32	+16.8
Vitales	73	11.8	27	+15.2
Ranunculales	108	15.9	31	+15.1
Geraniales	364	45.8	60	+14.2
Myrtales	649	79.1	62	-17.1
Coniferales	184	24.8	5	-19.8
Saxifragales	487	60.2	37	-23.2
Oxalidales	263	34.0	9	-25.0
Arecales	284	36.5	4	-32.5

* Residual values above (+) or below (-) the population variance

2.3.2 Analysis of plant growth forms

Growth forms of the positive outlying orders (from Table 2.2) were analysed by means of the stacked bar chart (Figure 2.3). The Asterales and Solanales contain predominantly herb-like plants and/or dwarf shrubs, while the Lamiales and Sapindales have a greater representation of trees and/or shrubs. Other orders such as the Fabales and Malpighiales

have an even mix of growth forms between trees/shrubs and herbs/dwarf shrubs. The Gentianales have the highest percentage of geophytes and climbers within the group.

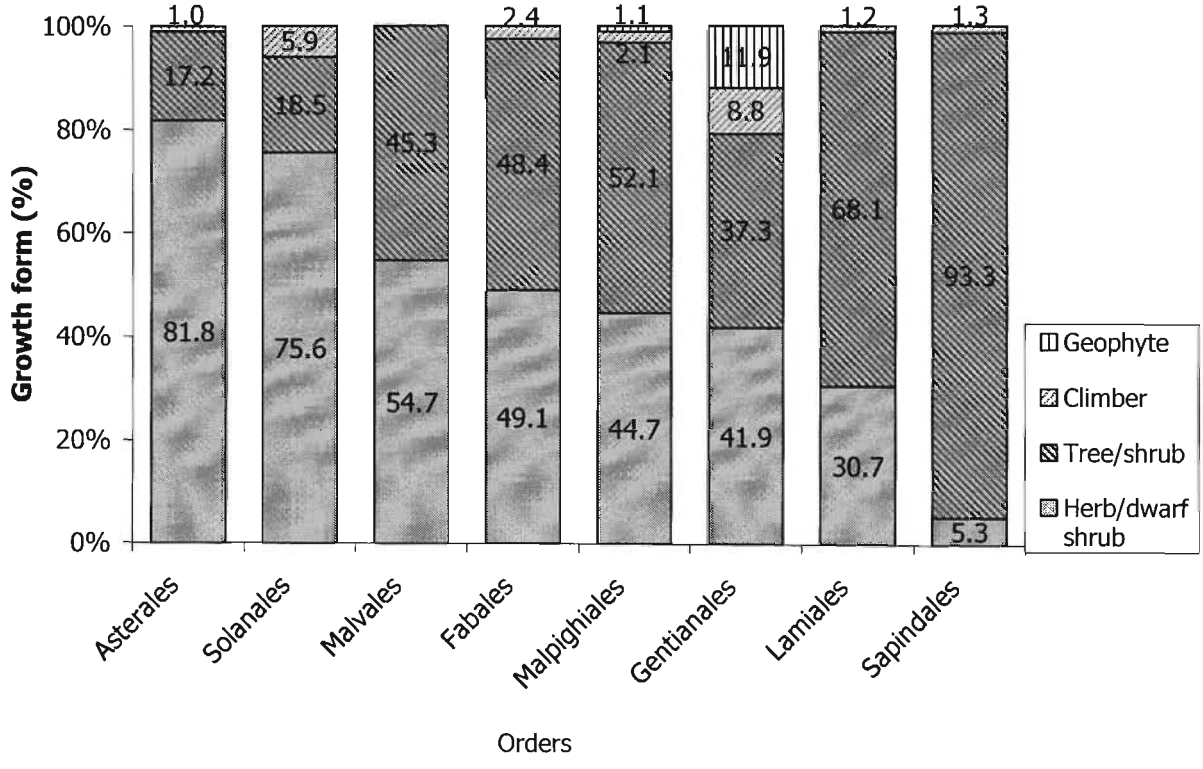

Figure 2.3 Relative proportion of medicinal plant growth forms in the eight ethnomedicinal plant orders with greatest residual values (Note: the Lamiales are included but were not deemed outliers)

2.3.3 Regional distribution, endemicity and Red Data List status

The *FSA* ethnomedicinal taxa (Arnold *et al.*, 2002) are comprised primarily of angiosperms, with a small proportion of gymnosperms and pteridophytes (Table 2.12). This is generally comparable to composition of taxa in the *FSA* regional flora (Table 2.13)(Germishuizen and Meyer, 2003). The ethnomedicinal angiosperms are predominantly dicotyledonous (Table 2.14).

Table 2.12 Proportion of ethnomedicinal angiosperms, gymnosperms and pteridophytes in the *FSA* region.

	Orders	Families	Genera	Taxa
Angiosperms	45 (81.8%)	173 (88.3%)	1192 (97.1%)	3308 (98.1%)
Gymnosperms	3 (5.5%)	6 (3.1%)	6 (0.5%)	14 (0.4%)
Pteridophyta	7 (12.7%)	17 (8.7%)	29 (2.4%)	49 (1.5%)
Total	55	196		3371

Table 2.13 Proportion of angiosperms, gymnosperms and pteridophytes in the *FSA* region.

	Families	Genera	Taxa
Angiosperms	231 (85.2%)	2232 (96.0%)	22805 (98.5%)
Gymnosperms	6 (2.2%)	10 (0.4%)	61 (0.3%)
Pteridophyta	34 (12.5%)	88 (3.8%)	294 (1.3%)
Total	271	2330	23160

Table 2.14 Proportion of dicotyledonous and monocotyledonous ethnomedicinal taxa in the *FSA* region.

	Orders	Families	Genera	Taxa
Dicotyledons	36 (76.6%)	135 (78.0%)	1976 (90.6%)	2746 (83.0%)
Monocotyledons	11 (23.4%)	38 (22.0%)	204 (9.4%)	562 (17.0%)
Total	47	173	2180	3308

Of the ethnomedicinal *FSA* taxa, 341 are naturalised, 26 are cultivated and 2924 are indigenous (SANBI, 2005)(Table 2.15). A comparison of the total ethnomedicinal taxa in each *FSA* subregion to the total taxa in each subregion (Figure 2.4) indicates that

disproportionately few ethnomedicinal taxa occur in the Western Cape Province. Percentages presented in Table 2.15 refer to the proportion of indigenous and naturalised taxa in the *FSA* and in each *FSA* subregion.

Table 2.15 Proportion of indigenous, naturalised and total ethnomedicinal taxa in each *FSA* subregion

FSA subregion	Indigenous ethnomed. taxa	Naturalised ethnomed. taxa	Total ethnomed. taxa
Eastern Cape	1602	184	1786
Free State	879	126	1005
Gauteng	1000	174	1174
KwaZulu-Natal	1849	230	2080
Limpopo	1593	152	1745
Mpumalanga	1642	173	1815
Northern Cape	648	97	745
North West	906	116	1022
Western Cape	900	165	1065
Botswana	930	82	1012
Lesotho	618	81	699
Namibia	971	95	1066
Swaziland	1278	99	1377
Total *FSA* region	2924	341	3371

Table 2.16 Ethnomedicinal taxa endemic to each province in South Africa

Province	Taxa
Eastern Cape	322
Free State	39
Gauteng	31
KwaZulu-Natal	197
Limpopo	43
Mpumalanga	70
Northern Cape	64
North West	23
Western Cape	300
Total ethnomedicinal endemics in South Africa	532

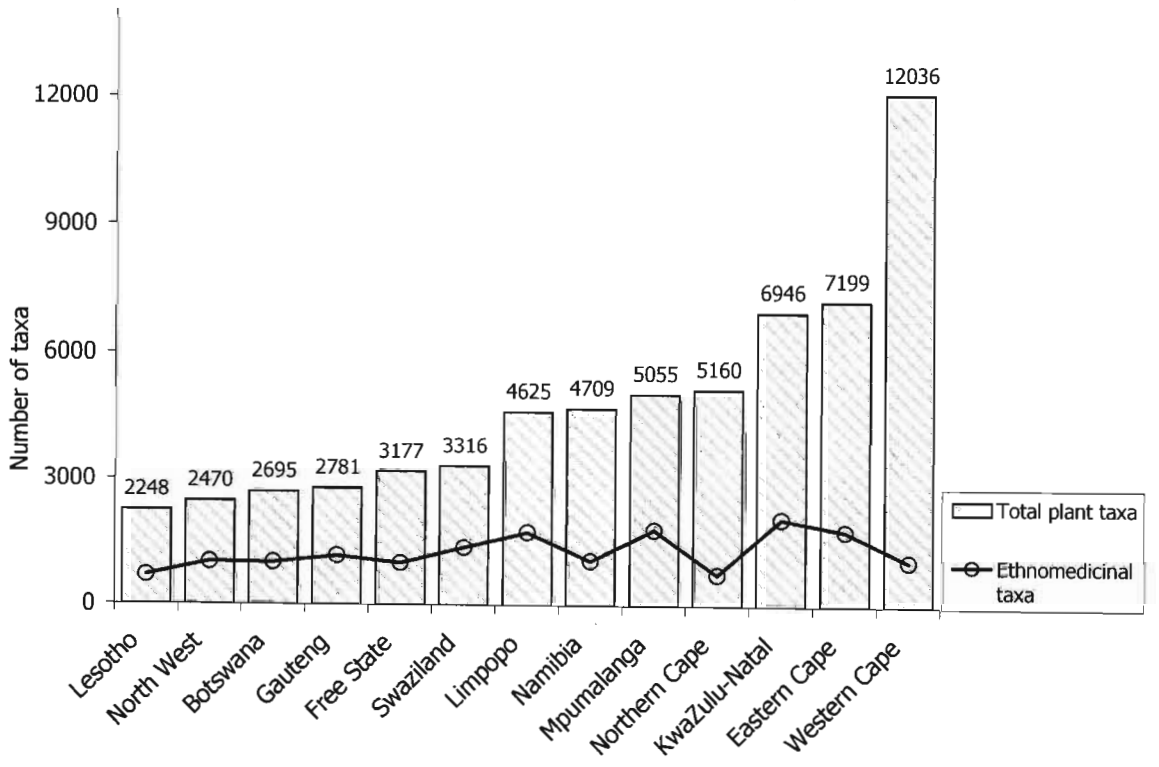

Figure 2.4 Total plant taxa and recorded ethnomedicinal taxa in each *FSA* subregion

Ethnomedicinal taxa that are endemic to South Africa total 531 (15.8% of *FSA* ethnomedicinal taxa)(Germishuizen *et al.*, 2006)(Table 2.15)(Figure 2.5). The Western Cape Province showed the highest percentage of endemic ethnomedicinal taxa (28.3%) relative to the total taxa in that province. The North-West Province had the lowest percentage of endemic ethnomedicinal (2.3%) taxa relative to the total taxa in that province.

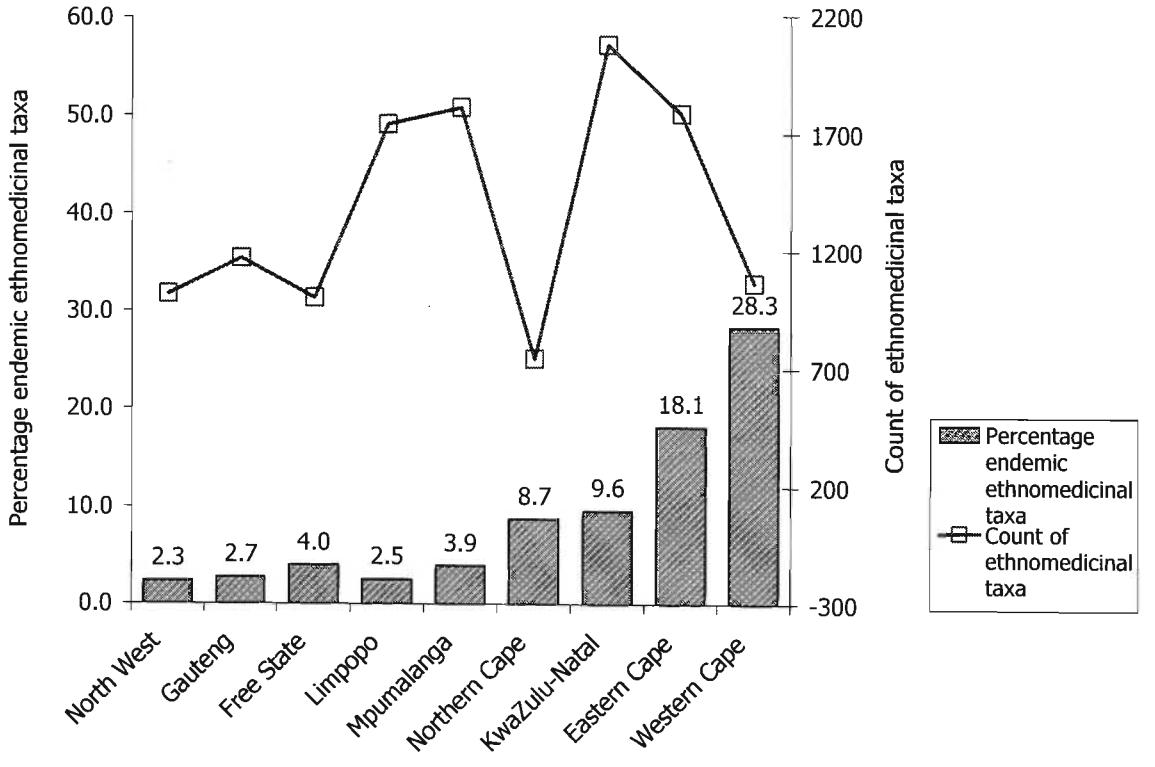

Figure 2.5 Percentage of endemic ethnomedicinal taxa in each of province of South Africa

A total of 447 Red Data Listed ethnomedicinal taxa are reported for the *FSA* region (Golding, 2002; SABONET, 2003) which amounts to 13.3% of the total 3371 ethnomedicinal taxa. Namibia showed the highest percentage (16.1%) and Lesotho the

lowest percentage (6%) of Red Data Listed ethnomedicinal taxa relative to the total taxa in those regions (Figure 2.6).

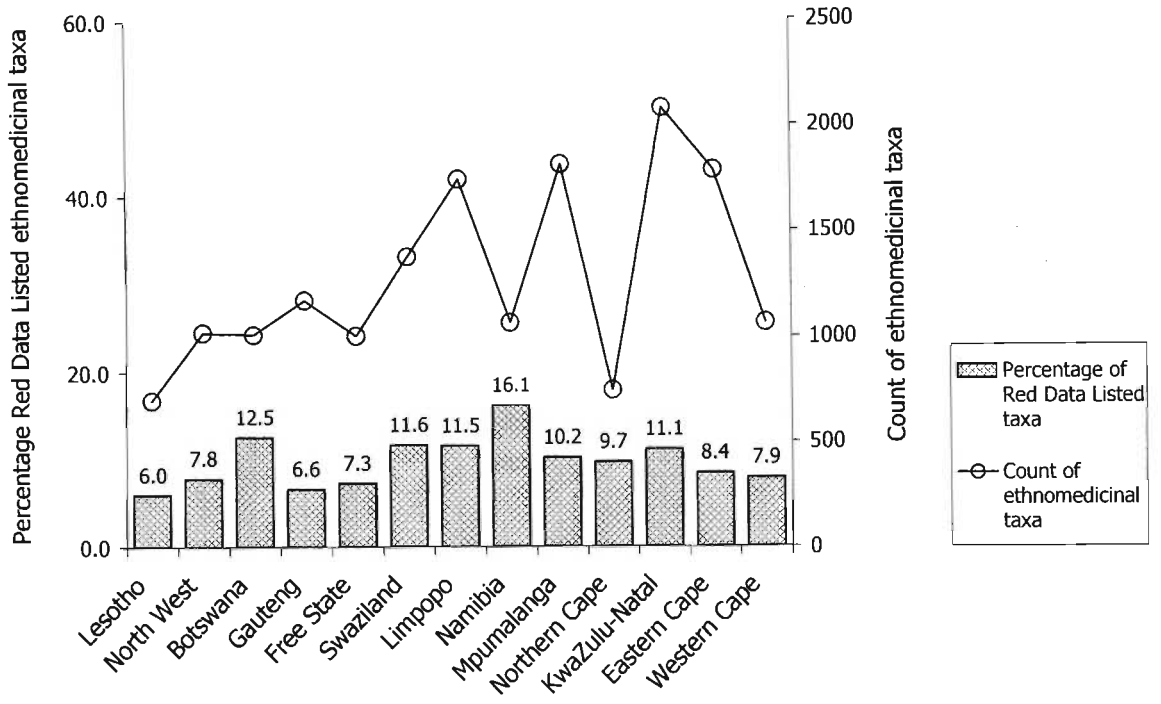

Figure 2.6 Percentage of Red Data Listed ethnomedicinal taxa and count of recorded ethnomedicinal taxa in each *FSA* subregion

2.3.4 Evaluation of phytochemical trends in 'hot' families

Data mining results of compound class data for selected plant families (DNP, 2005) were grouped by class and percentage, relative to the total number of compounds known from each family globally (Table 2.17). Some notable results include the following: the Fabaceae had the greatest percentage of flavonoids, followed by the Anacardiaceae (Figure 2.7); the Rubiaceae had the greatest percentage alkaloids, followed by the Convolvulaceae (Figure 2.8); the Asteraceae had the greatest percentage of terpenoids, followed by the Euphorbiaceae (Figure 2.9).

Table 2.17 Percentage natural product compounds in each class for families with highest residual values in selected outlying orders

Compound Class	Euphorbiaceae	Rubiaceae	Convolvulaceae	Malvaceae	Anacardiaceae	Fabaceae	Asteraceae
Aliphatics	10.2%	2.2%	38.7%	11.1%	27.2%	1.8%	7.4%
Alkaloids	11.3%	29.0%	17.9%	7.4%	0.5%	8.0%	0.4%
Amino Acids and Peptides	2.3%	2.9%	0.5%	2.6%	0.5%	0.8%	0.3%
Benzopyranoids	6.8%	0.5%	1.4%	1.1%	0.9%	1.5%	2.5%
Flavonoids	8.5%	11.7%	20.8%	30.5%	32.4%	59.5%	7.9%
Oxygen heterocycles	1.7%	0.2%	1.4%	2.6%	0.9%	0.3%	0.3%
Polycyclic aromatics	1.7%	22.3%	0.0%	4.2%	1.4%	7.4%	0.0%
Simple aromatics	7.9%	2.2%	4.2%	3.2%	10.3%	5.5%	2.4%
Terpenoids and derivatives	49.7%	29.1%	15.1%	37.4%	25.8%	22.5%	78.8%
Total (%)	100.0%	100.0%	100.0%	100.0%	100.0%	100.0%	100.0%

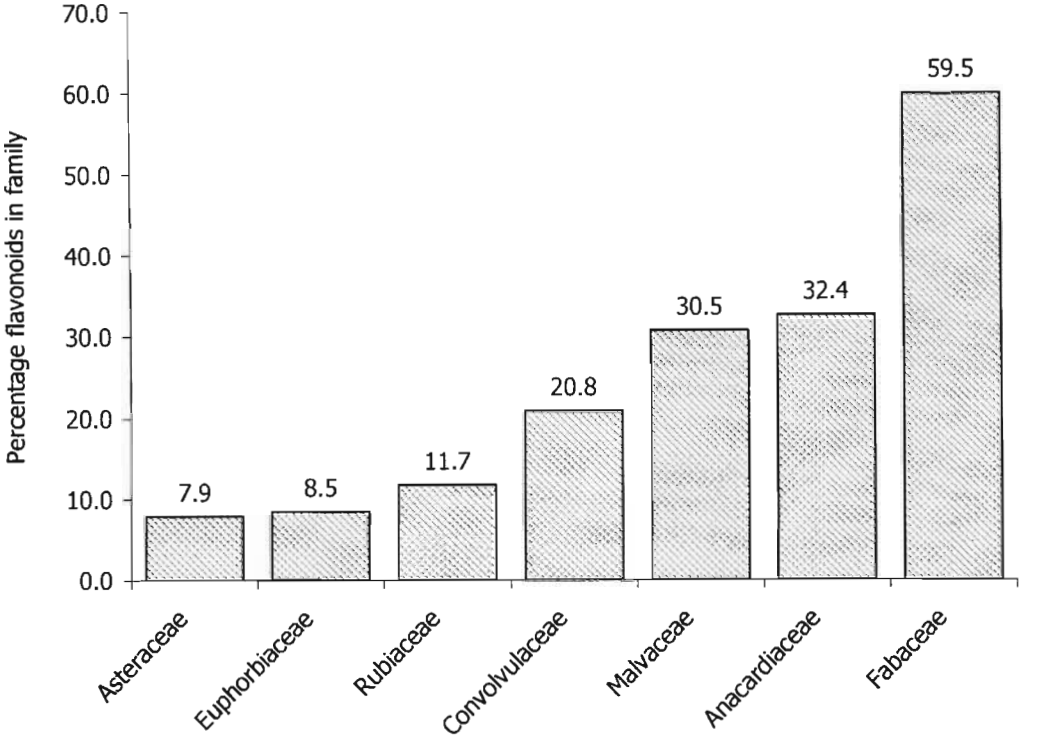

Figure 2.7 Percentage flavonoids in selected outlying families

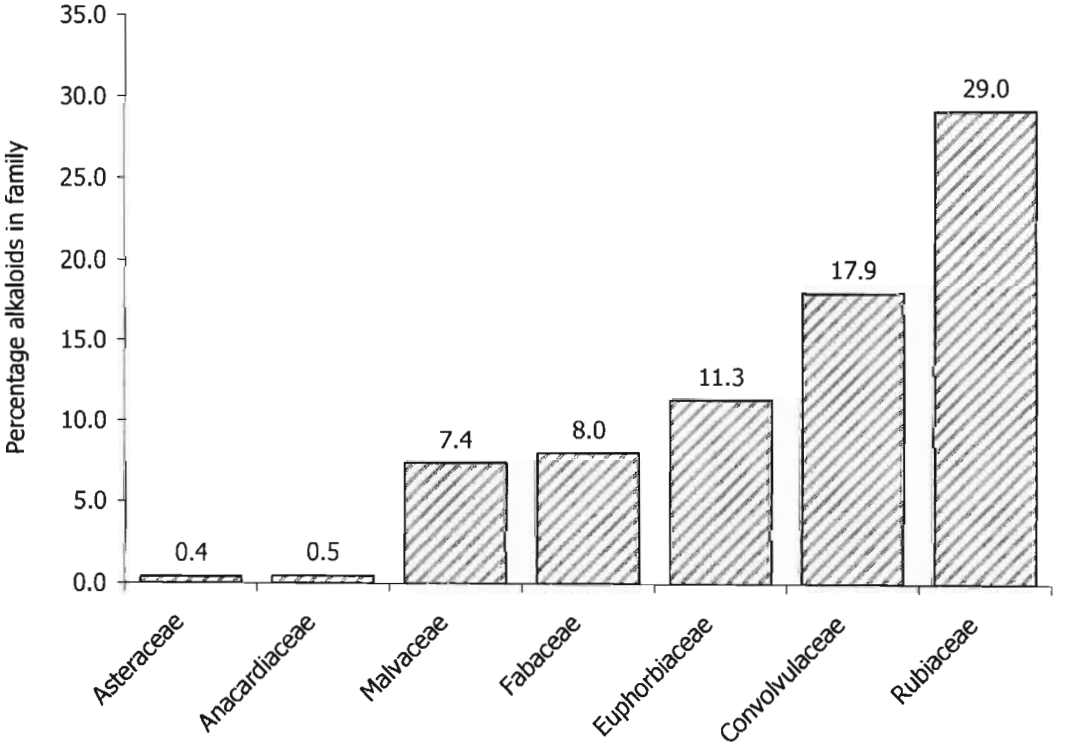

Figure 2.8 Percentage alkaloids in selected outlying families

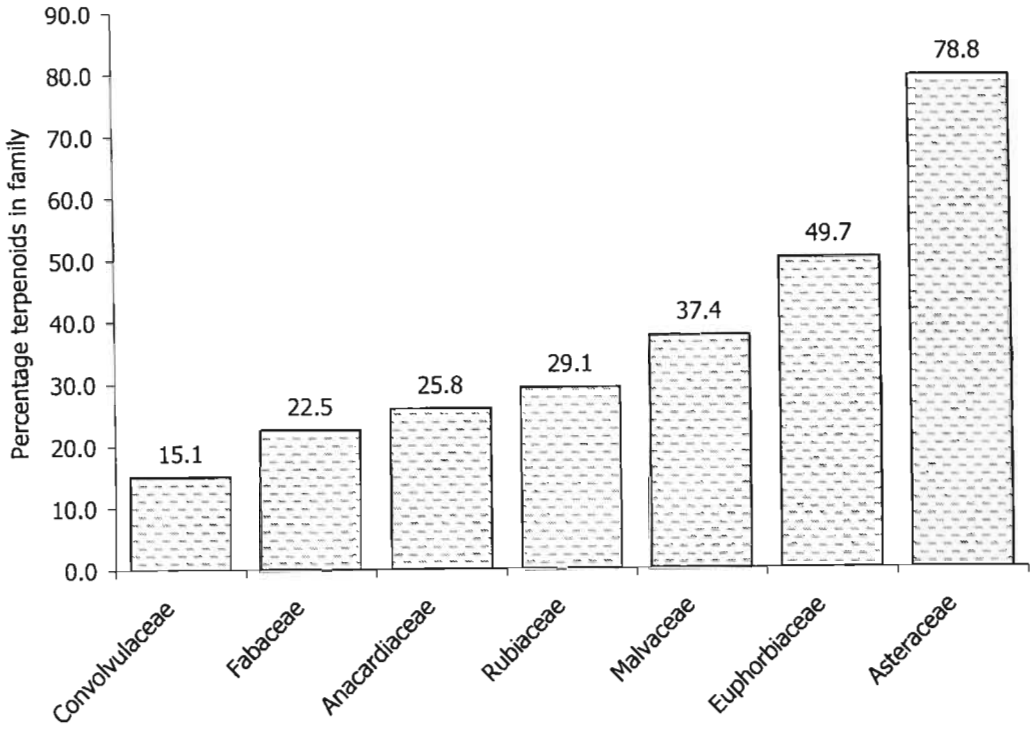

Figure 2.9 Percentage terpenoids (and their derivatives) in selected outlying families

2.4 Discussion

Medicinal plants are primarily used as complex mixtures with a broad range of constituents (from infusions, extracts etc.) or as pure, chemically-defined active principles (Hamburger *et al.*, 1991). Plant-use by traditional people is exclusively by means of complex mixtures, the precise pharmacological activities of which are seldom known, and the association of ethnomedicinal plants with certain diseases gives no assurance that the relevant taxa contain efficacious principles. It may be that only one compound is pharmacologically active, or that various constituents are acting synergistically. There is growing evidence, particularly in immune modulation that drugs

or biological agents capable of modulating single pathways are of limited value. Chemically complex and diverse extracts with appropriate combinations of active principles are preferred due to potential for synergistic action (Patwardhan and Gautam, 2005). For example, herbal medicines are reported to modulate diverse functions such as cytokine secretion, histamine release, immunoglobulin secretion, class switching, cellular coreceptor expression, lymphocyte expression and phagocytosis (Plaeger, 2003).

While there may be a significant rational basis for plant selection by ethnomedicinal practitioners, the nature of that rationale may not be immediately apparent. Ethnomedicinal practitioners may often accept subjective truths which they regard as objective, compared with what can be demonstrated scientifically (Conco, 1972). Moerman (1979) notes that there 'appears to be some kind of order to the collective ethnobotanical wisdom (of Native Americans) in that the plants they use do show a high likelihood of producing biologically active secondary products'. It is possible that the same is true for ethnomedicinal plants in the *FSA* region. The toxicity of certain ethnomedicinal plants should also not be overlooked. While ethnomedicinal poisoning is reportedly relatively rare in southern Africa (less common than for orthodox medicine)(Van Wyk *et al.*, 2002), numerous medicinal taxa are known to be highly toxic (Watt and Breyer-Brandwijk, 1962). Such plants may be lethal to humans in their basic form, but small measured doses, correct preparation, or use in combination with other substances/plants could reduce toxicity and/or maximise therapeutic benefits. Seasonal and climatic changes that govern flowering/fruiting or senescent cycles also influence the chemical constituents of plants (Blaisdell *et al.*, 1952; Li *et al.*, 1996) and should always be considered in bioprospecting. Additionally, different plant parts may produce and store different compounds e.g. the seeds of *Abrus precatorius* Linn. are fatal if ingested (Gunn, 1969; Hutchings *et al.*, 1996; Pooley, 2003), yet the roots and leaves are used in

the treatment of various complaints (Hutchings *et al.*, 1996). Different tissue development stages can also reflect different chemical constituents, e.g. some atropine-producing plants of the Solanaceae have the highest concentration of this chemical in the green fruits (Keeler *et al.*, 1991).

2.4.1 Statistical evaluation

The high percentage of variation that the statistical model was able to account for, and the strong positive correlations observed in the regression plots, signify that the model performed well as a tool for prediction with regard to the number of taxa used ethnomedicinally in each order and family. The identification of outliers nullifies the hypothesis that traditional user-groups in the region select plants for medicinal purposes in a wholly random manner. Such outliers (either orders or families) are considered useful for the prioritisation of taxa deemed more likely to yield extracts with desirable pharmacological activity. Data mining of chemical classes indicates that many 'hot' ethnomedicinal families are rich in chemical classes with known bio-active metabolites such as flavonoids, alkaloids and terpenoids (Balandrin *et al.*, 1985). This result concurs with previous documentation that suggests ethnobotanical plant selections (vs. random selections) yield better results by enhancing hit rates of pharmacologically active compounds (Hamburger and Hostettmann, 1991; Soejarto, 1993; Marles and Farnsworth, 1994; Macilwain, 1998). However, prioritised *FSA* taxa identified through the analysis of plant orders are numerous – far more than could reasonably be included in an average pharmacological screening programme. For this reason, residual values of families within these orders were also calculated (Table 2.3 – Table 2.9). Although analysis at family level provides for additional focus, taxa at this level may still be too numerous e.g. the number of *FSA* taxa in the Asteraceae alone is 2681 (SANBI, 2005), likely too many for a high throughput screening programme on a limited budget. In such

instances, it may be necessary to perform analyses at the generic level to obtain more definition in taxa for screening. Such analyses were not included in this chapter due to the extensive amount of data that would require presentation. However, coupling such studies with disease-specific parameters would greatly enhance the focus, i.e. taxa known to be associated with specific diseases could be extracted from the dataset prior to analysis.

Outlying orders which occur below the regression line (Figure 2.2), and therefore selected less often by ethnomedicinal practitioners, are also of particular interest. Plants in these orders may have characteristics which result in their more modest usage. The Poaceae, for example, which are highly utilised by browsers rely primarily on physical attributes (e.g., sharp awns, high lectin and/or high silica content), growth form and compensatory growth rather than secondary metabolite production for defence (Lindroth, 1988; Peumans and Van Damme, 1995). The Poaceae also contain numerous food plants (e.g. maize, millet, etc.) and as a group may generally produce insufficient quantities of bioactive compounds to be of medicinal interest to humans. If this is the case, the same result is likely to be seen the world over and it is therefore unsurprising that plants most rarely used by Native American people include the Caryophyllaceae and Poaceae (Moerman, 1991). Both these families are selected significantly less often than others by ethnomedicinal practitioners in southern Africa (Table 2.2; Figure 2.2).

2.4.2 Growth form

In the search for additional criteria that may assist in improving the accuracy of plant selection procedures for bioprospecting, it is essential to examine diverse data. Close inspection of the categories of plant growth forms used for ethnomedicinal purposes in South Africa reveals that it is difficult at this level to assign significance to any particular

life forms given that a wide range are utilised (Figure 2.3). It is also likely that the distribution of growth forms of ethnomedicinal taxa in 'hot' orders (Figure 2.3) are representative of the growth forms for each order as a whole. As such, growth forms would not prove useful as criteria to be weighted in the short-listing of plants for bioprospecting. However, plants have many other characteristics such as the colour/shape/smell and size of fruits, seeds, leaves and flowers, any number of which should also be assessed as has been undertaken for growth form. [Further, vernacular names indiating ethnomedicinal applications may prove to be useful criteria following evaluation, as may specific epithets such as *salutaris*, *officinalis* and *athamantica*].

2.4.3 Regional distribution, endemicity and Red Data List status

The high levels of endemism contained within southern Africa's distinct phylogenetic assemblage (Cowling and Hilton-Taylor, 1994) are potentially advantageous in a bio-political sense should a significant percentage show potential for use through bioprospecting. The biodiversity is however, localised at various hot-spots (Figure 2.11)(Cowling and Hilton-Taylor, 1994; Davis and Heywood, 1994; Van Wyk and Smith, 2001). The Cape and Succulent Karoo floras for example (Western Cape and North West Province) are of particular interest, being the richest regions of plant diversity per unit area in the world (Cowling and Hilton-Taylor, 1994). The notably small percentage of medicinal plants recorded for the Western Cape region (9% of taxa) compared with 42% in Swaziland and Gauteng, and 41% in the North West Province (Figure 2.4) suggests a significant under-utilization of plants (for ethnomedicinal purposes) in the western regions of southern Africa (Figure 2.10). This is likely to have influenced the results of the regression analyses, and it is most likely that several Western Cape families are grossly under-represented. This may be due to several reasons including, the loss of ethnomedicinal plant-use knowledge from the region prior to documentation, inadequate

or biased documentation of plant-use knowledge (by ethnographers and ethnobotanists), and/or an historical absence of human habitation with a corresponding absence of historical plant-use. This last point links closely to the observation that many endemic Western Cape taxa (Van Wyk and Smith, 2001) would have had little or only recent contact with Bantu tribes due to migration/settlement patterns in southern Africa (Figure 2.12). If the analyses were performed independently for each region, a very different set of 'hot' orders may well emerge. Furthermore, it is likely that taxa with distributions into regions north of the *FSA* would have been exposed to the attentions of ethnomedicinal practitioners for centuries while taxa confined to the *FSA* would have been used by the majority of Bantu tribes (that migrated southwards)(Thompson, 2001) for a much shorter time.

Considering the above, it is remarkable that the Asterales which have a large portion of their diversity in the deserts of the western seaboard and Fynbos/Renosterveld vegetation types (Van Wyk and Smith, 2001), have gained such a high overall position (third highest outlier out of 55 orders analysed)(Table 2.2). Many desert and Fynbos/Renosterveld species also spend a high percentage of their time in the seedbank (Jürgens and Gotzmann, 1999) and are therefore not likely to be harvested to any large degree. The bias which the broad-scale regression analysis introduces to the data needs to be accounted for, particularly in terms of supra-generic distribution and endemicity in South Africa. Two endemic families, the Greyiaceae and Achariaceae, are restricted to Afromontane and Tonga-Pondoland areas of the eastern seaboard. The other seven endemic families – Bruniaceae, Peneaceae, Stilbaceae, Grubbiaceae, Roridulaceae, Geissolomaceae and Retziaceae – are all endemic or nearly so to the Cape subregion (Cowling and Hilton-Taylor, 1997). In addition, though not strictly endemic, southern Africa also houses the vast majority of taxa in the Mesembryanthemaceae, Selaginaceae,

Ericaceae, Aizoaceae, Amaryllidaceae, Iridaceae and Restionaceae, as well as a high proportion of Geraniaceae, Proteaceae and Rutaceae (Goldblatt, 1978). A further factor which may have skewed the results of the regression analyses is the parochial distribution of many Western Cape endemics (Van Wyk and Smith, 2001). Even in regions of dense human populations, which historically the Cape was not (Thompson, 2001)(Figure 2.12) these species would have been known to relatively few people.

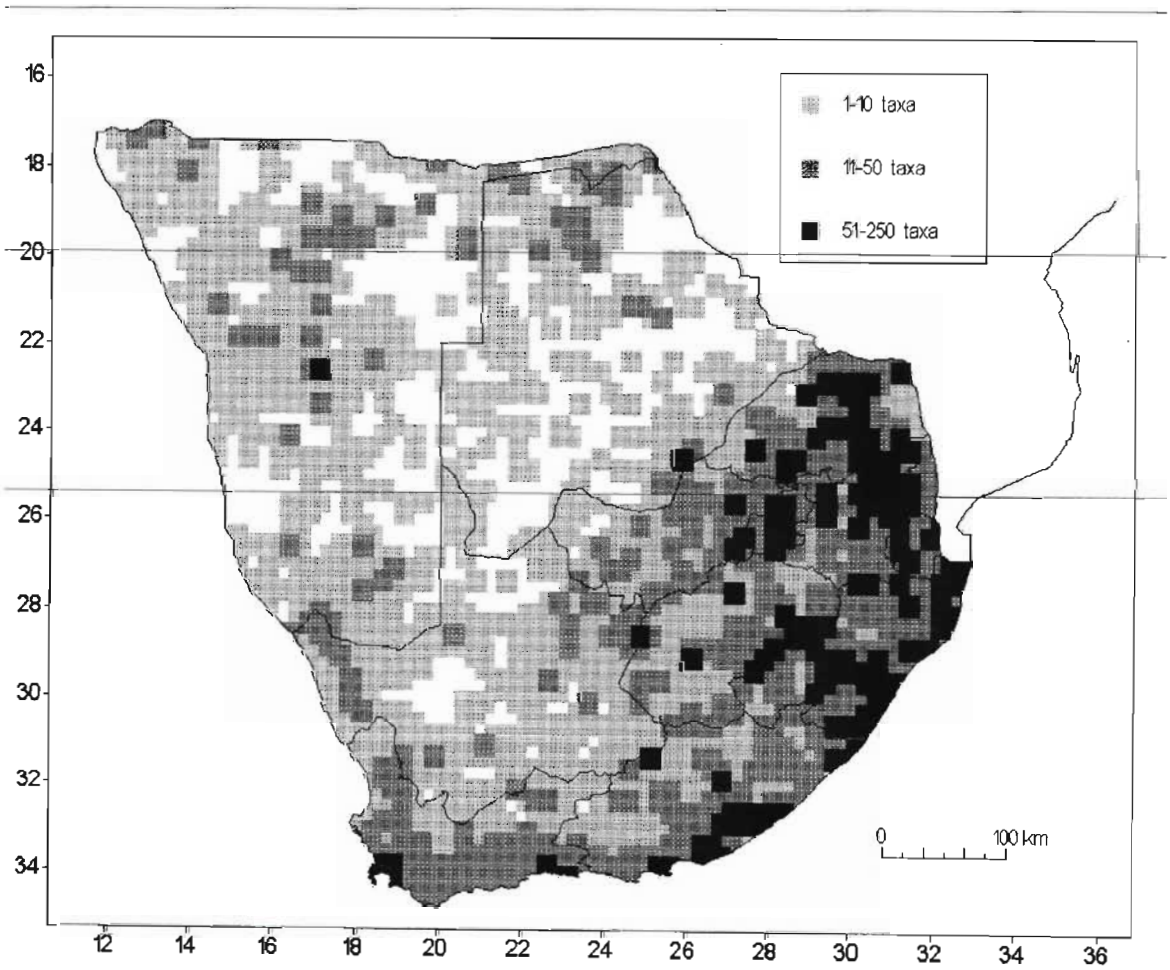

Figure 2.10 Distribution of ethnomedicinal plants, based on records from PRECIS (SANBI, 2005). Areas of highest species concentration are highlighted (Arnold *et al.*, 2002)

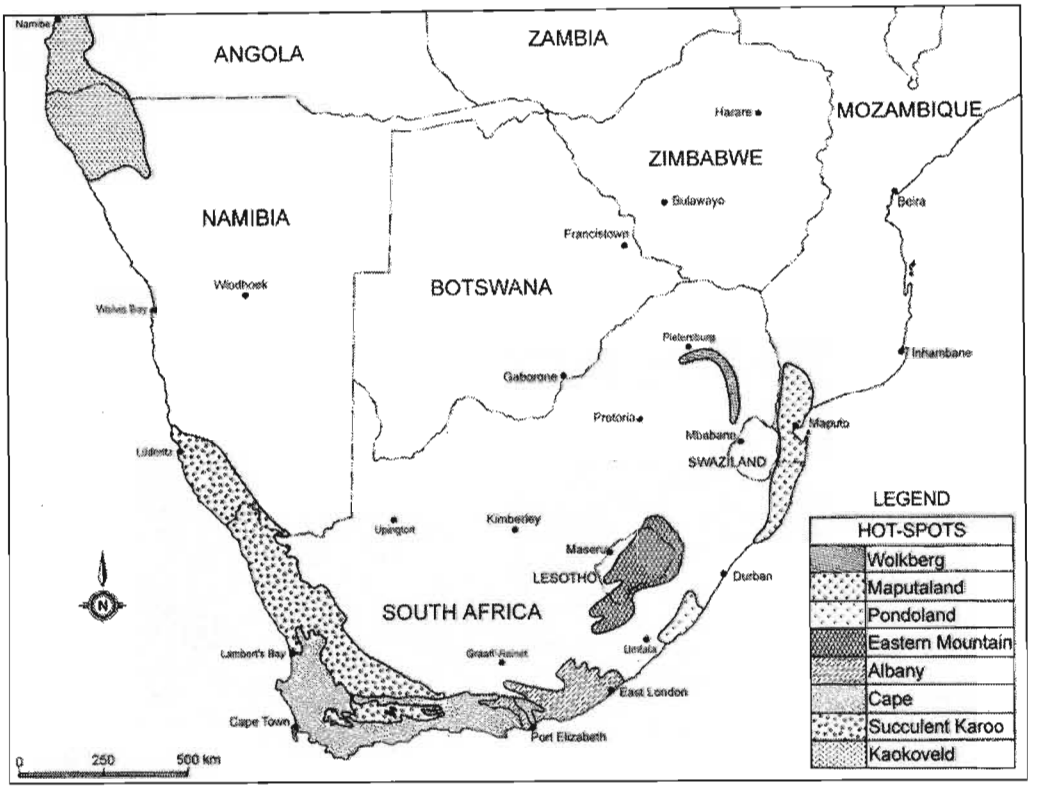

Figure 2.11 Hot-spots of high plant species richness in southern Africa (Cowling and Hilton-Taylor, 1994)

2.4.4 Historical use of ethnomedicinal plants in the *FSA*

Historical use of ethnomedicinals in southern Africa has largely influenced the current body of recorded knowledge, from which a recent checklist was compiled (Arnold *et al.*, 2002). Aboriginal San hunter-gatherers are the earliest recorded inhabitants of southern Africa, and were presumably knowledgeable about the nutritional, medicinal and other uses to which plants in the area could be put (Du Toit, 1998). The demise of their nation has continued steadily during the past 2000 years due to clashes first with Bantu immigrants and later with European settlers (Thompson, 2001). The patterns of interaction, negotiation and conflict between the San and the nomadic Bantu herders and settled farmers were doubtlessly complex, as were the economic, technological and cultural frontiers across which these people fought, shared skills, traded and influenced

each other's lives (Morris, 2004). The Bantu reportedly began moving into southern Africa between c.250 and 500AD (Thompson, 2001), and would likely to have brought much traditional plant-use knowledge with them. They would also undoubtedly have acquired additional knowledge from the San with whom they interacted (Du Toit, 1998). Ethnomedicinal genera known to occur along the eastern axis of Africa would likely have been tried and tested by the Bantu long before they reached South Africa. The likely result being that these genera continued to have preference when Bantu migrants entered the *FSA* region. The distribution patterns of the majority of genera in 'hot' families of the Malpighiales (highest positive outlying order)(Table 2.3) provides evidence for this. It is therefore unsurprising that the current recorded body of traditional plant-use knowledge is primarily from the eastern and central regions of the country (Figure 2.4). This correlates strongly with the distribution of Bantu speaking people (Figure 2.12). Furthermore, plant taxa in the eastern and central regions are likely to be more similar to those from the north from whence the Bantu arrived than with those from the Western Cape region, and so more likely to be used. It is apparent however, that knowledge was lost due to the fragility of oral traditions, rapid urbanisation and cultural attrition (Van Wyk *et al.*, 1997). Ethnomedicinal knowledge from other regions is even scarcer but has not been entirely lost (Liengme, 1983). Indeed, San and Khoikhoi groups still live in the western and north-western parts of the region, and many still practice traditional forms of healing (Liengme, 1983).

Nine native languages are spoken in South Africa by different Bantu tribes (Figure 2.12), whilst English and Afrikaans are the two dominant European languages. The Bantu are classified into four major subgroups (the Nguni, Sotho, Tsonga-Shangaan, and Venda). These subgroups are well represented throughout the region (Thompson, 2001) and each holds much culturally related plant-use knowledge (Liengme, 1983) which has

influenced ethnomedicinal plant use in the region. European settlers have also influenced regional ethnomedicinal practices through dissemination of their medicinal folk lore.

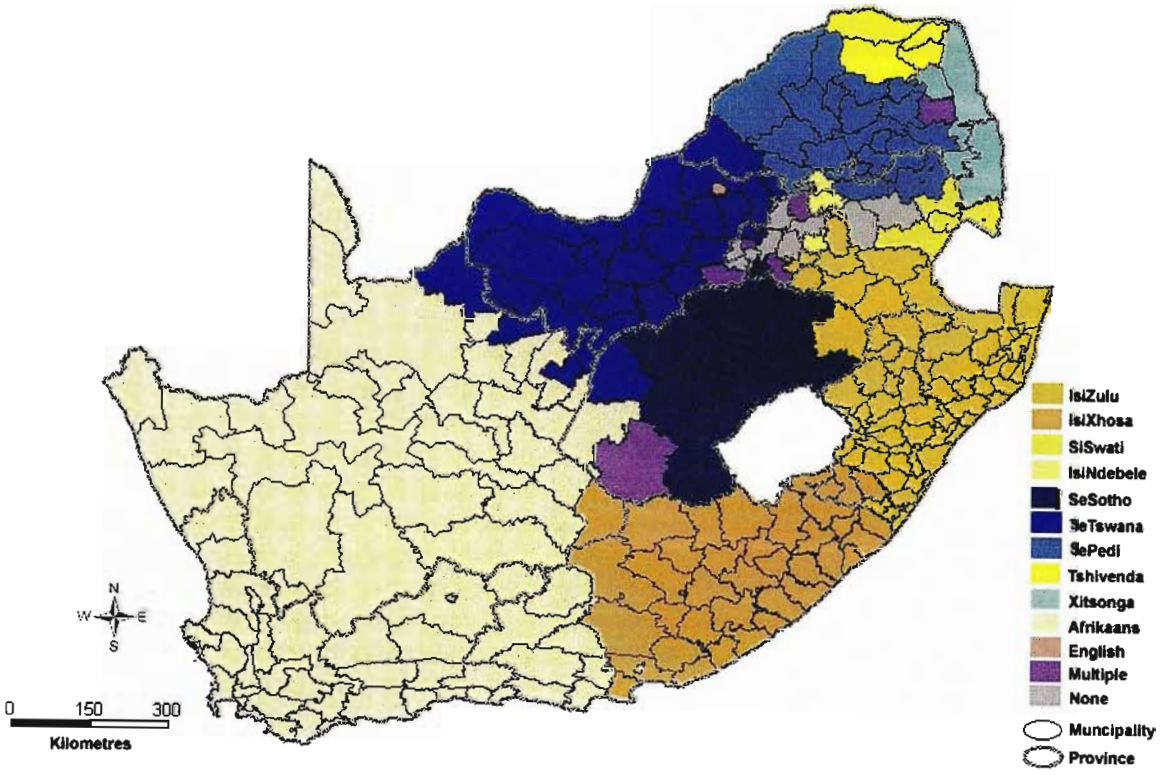

Figure 2.12 Dominant home language in South African municipalities in 2001 (SSA, 2003). The map demonstrates the absence of the main Bantu tribes from the Western Cape

These interactions point to the very dynamic character of traditional healing which continues to evolve in the region today. Evidence of this is provided by Crouch and Hutchings (1999). These authors found that 30% of plants cultivated by Zulu healers for ethnomedicinal purposes were not indigenous to the *FSA* region. In addition, 44% of taxa recorded had not previously been recorded as traditionally used by the Zulu (Hutchings *et al.*, 1996).

2.4.5 Phytochemical evaluation

It was assumed for the purpose of this study that individual ethnomedicinal taxa are efficacious against the diseases for which they are reportedly used. Their phytochemical traits were thus regarded as being correlated through common descent as opposed to convergent evolution. The assumptions were based on reports that most kinds of secondary compounds, including tannins and alkaloids, are phylogenetically conservative in their distribution (Silvertown and Dodd, 1996). The isolation of popular ethnomedicinal orders/families by means of regression analyses was therefore considered appropriate for i) the identification of related taxa with similar bioactive constituents and ii) the prioritisation of taxa for bioprospecting purposes. As detailed phylogenies were not incorporated into the analyses, all species were treated as independent data points. The phylogenetic independence of claimed relationships was therefore not confirmed and some degree of pseudo replication is expected (Silvertown and Dodd, 1996).

The data mining yielded varying results for the families examined. High proportions of flavonoids from families such as the Fabaceae (high positive outlier)(Table 2.4) and Anacardiaceae (Figure 2.7; Table 2.17) were encouraging due to the reported health benefits these compounds may have (Yao *et al.*, 2004; Halliwell *et al.*, 2005). Evidence of their strong antioxidant properties continues to grow (Kris-Etherton and Keen, 2002),

and they are also known to suppress lipid peroxidation in both tissues and subcellular fractions (Yang *et al.*, 2001). Alkaloids were the dominant group in the Rubiaceae (Figure 2.8). They are an extremely diverse group of chemicals, widely known both for their toxic and medicinal uses. Commonly present in plants as salts of malic, tartaric, citric or other acids, the majority of alkaloids act on the nervous system (Kretovish, 1966). In small amounts they are stimulators, but act as depressants when used in large doses (Kretovish, 1966). Alkaloids from the bark of *Cinchona* spp. (Rubiaceae) have been particularly widely researched due to their invaluable role in the treatment of malaria (Warhurst *et al.*, 2003). Terpenoid natural products (Figure 2.9) and their derivatives were the dominant compound class for the Asteraceae and Euphorbiaceae (Table 2.17). Both these families were found to be high positive outliers (Table 2.3; Table 2.6). Terpenoids are formed by the linking of isoprene units, the number of which are used to differentiate between sub-classes, e.g. diterpenoids, triterpenoids etc. The toxicity of many *Euphorbia* taxa is due primarily to the presence of toxic diterpenes (Van Wyk *et al.*, 2002). The relative frequency with which compound classes occur in plants likely has a significant bearing on the way those plants are used traditionally. Plants with high proportions of toxic compounds e.g. cardiac glycosides are almost certainly used more sparingly. A detailed knowledge of compound class proportions in plants can potentially be applied in weighting systems used to prioritise candidate taxa during bioprospecting.

2.5 Conclusion

In bioprospecting, ongoing evaluation and incorporation of updated phytochemical, taxonomic and other plant data is essential for maximising the returns offered by prioritised selection. The analyses of data for prioritised plant selection as here

presented yields several insights into the wide range of factors that bioprospectors need to evaluate and reflect upon prior to plant selection and subsequent collection. Statistical analyses of ethnomedicinal plant-use data are particularly relevant due to the extent of the historical and current medicinal plant trade and consumption in the region: direct trading of medicinal plants and plant derived pharmaceuticals currently on the market is of significant economic value. Mander (1998) estimated that over 20000 tonnes of plant material was informally traded by users of ethnomedicine in that year alone, a trade volume estimated then at US$ 60 million. The extent of this trade also emphasises the urgent need for research on plants which are increasingly under threat from expanding human populations and agriculture. Should such research be neglected it is likely that many important species will disappear or at least their genetic diversity will erode considerably before their potential for wider application can be assessed. Furthermore, should the unsustainable use of these resources continue unchecked, millions of consumers and ethnomedicinal practitioners will lose much in terms of healthcare, financial income and traditional culture.

Both emic (indigenous) and etic (Western biomedical) perspectives have been incorporated into the investigations presented in this chapter. The value of general ethnomedicinal knowledge and the means by which it can be utilised to direct plant selection for bioprospecting has also been demonstrated. Pharmacological investigations based on ethnobotanical information usually require prioritisation of candidates prior to collection of plants for screening. The incorporation of multidisciplinary analyses expands the scope of inquiry for such an evaluation. This more streamlined approach in support of plant selection has the distinct advantage of basic statistical analyses, and the flexibility to include a variety of taxonomic levels.

Chapter 3

Bioprospecting antimalarials in southern Africa: retrospective analyses of plant selections

In seeking absolute truth we aim at the unattainable, and must be content with finding broken portions.

– William Osler (1889)

Abstract

The results of the previous chapter indicate significant potential for the inclusion of regression analyses in the course of selecting plants for bioprospecting. However, it is imperative that such techniques be tested on taxa for which screening results are available in order to further assess their feasibility. The availability of initial *in vitro* screening results for plant extracts against *Plasmodium falciparum* presented such an opportunity. These results, made available by the Innovation-funded Antimalarials Project included plant extract IC_{50} values for plants selected by means of a semi-quantitative selection protocol. A retrospective application of the least squares regression analysis technique to the antimalarial data was deemed useful in evaluating its potential in prioritising candidate taxa. Families and genera selected through regression analyses were compared to available results of the antiplasmodial bioassays. The evaluation allowed for an assessment of how the regression analyses performed in the identification

of plants with *in vitro* antiplasmodial IC_{50} values of ≤ 10 μg/ml. The regression analyses were applied to various higher taxa, including order, family and generic levels. The null hypothesis which stated that there is no difference between taxa available to ethnomedicinal practitioners and taxa selected by them for antimalarial/anti-fever purposes was falsified. It was deemed that ethnomedicinal practitioners do not select antimalarial/anti-fever plants at random. Higher taxa containing species that might show strong antiplasmodial activity were therefore identified. Genera with the most species in 'hot' orders and families were assessed by identifying any of their respective species that had already been screened. The majority of such species were found to have particularly high antiplasmodial activities ($IC_{50} \leq 10$ μg/ml) in the *in vitro* bioassays. The lack of detailed phylogenies for the respective taxa meant that the elimination of phylogenetic noise was not possible except in the most rudimentary way.

3.1 Introduction

Bioprospecting faces numerous challenges today, from legislative issues (Burgener, 2003), to accusations of biopiracy (Van Wijk, 2000; Ready, 2002) to difficulties in identifying taxa from which to source novel pharmacological agents (Macilwain, 1998; Dalton, 2004). However, bioprospecting does offer feasible benefits to humankind. Such benefits include the development of drugs from natural products (Farnsworth *et al.*, 1985), and the use of novel prototype structures and/or mechanisms as the basis for new therapeutic agents (Xue and Zhang, 1998). Many neglected third world diseases, however, receive little research interest from pharmaceutical companies, due to the low profit-generating potential of drugs sold to the poor (Pecoul *et al.*, 1999; Silverstein, 1999; Moran, 2005). It was largely this reason that led to the establishment of the

(DACST Innovation-Funded) Antimalarials Project (Figure 1.3). The project resolved to investigate primarily South African flora in the hope of identifying compounds from which to develop novel antimalarial drugs. Project members included the CSIR, MRC, SANBI, UCT, UP, all of whom participated in the research and development of new antimalarial drugs.

Crude plant extracts were tested for *in vitro* activity against the human pathogen *Plasmodium falciparum* (chloroquine-sensitive D10 strain) using the parasite lactate dehydrogenase assay (Makler *et al.*, 1993). Plant extracts were obtained as follows. Plant samples were separated into different components and oven-dried (30 – 60°C). Dried plant material was coarse-ground and stored at ambient temperature. For each extraction, 100 – 500 g of powdered plant material was sequentially extracted with the following solvents: cold dichloromethane (DCM), dichloromethane/methanol (1:1)(DCM/MeOH), methanol (MeOH) and purified water (Clarkson *et al.*, 2004). The *in vitro* assays were performed as described by Clarkson *et al.* (2003), and IC_{50} values were obtained from dose-response curves, using non-linear dose-response curve fitting analyses with GraphPad Prism v.3.00 software (Clarkson *et al.*, 2004). The plant selection procedure resulted in more than 50% of plants yielding crude extracts with promising antiplasmodial activity ($IC_{50} \leq 10$ μg/ml)(Clarkson *et al.*, 2004). Such success prompted the retrospective analyses of plant selection procedure presented. Extracts showing high antiplasmodial activity were further fractionated for investigation as potential candidates for antimalarial drug development.

Focused plant selection for bioprospecting as used by the Antimalarials Project often incorporates ethnomedicinal knowledge (Cox, 1990; Fourie *et al.*, 1992; Hamilton, 2004) due to the greater likelihood of finding positive leads. In the current study, we used

regression analyses (Figure 2.1) to ask how taxa associated with or used to treat malaria/fever (MAFEV) compare to other available taxa in the region. We also asked if ethnomedicinal practitioners demonstrate preferential bias towards the use of certain taxa in the treatment of MAFEV-related conditions. Our null hypothesis states that no such bias exists, i.e. plant use for MAFEV-related ailments is strictly random and there is no difference between taxa available to, and taxa selected by ethnomedicinal practitioners for curative MAFEV-related purposes.

The analyses aimed to assess the contributory value of applied selection criteria and provide insights into the plant selection patterns of ethnomedicinal practitioners. Ethnobotanical and chemotaxonomic attributes were the principal criteria used. The results were used to provide guidelines for the improvement of plant selection procedures in other/future bioprospecting programmes. Improvements may reduce the total number of plants required for initial collection and screening while simultaneously increasing the number of lead candidates. A reduction in expenses in the initial stages should result and later research, e.g. advanced pharmacology, patent filing and clinical trials (Macilwain, 1998; Garrity and Hunter-Cevera, 1999; Hamilton, 2004), can be fast-tracked (Figure 4.1). Analyses in this chapter were exclusively for plant taxa selected through their associated ethnomedicinal plant-use. Data from other taxa which may have been screened were excluded.

3.2. Methods

The various facets of the Antimalarials Project were undertaken by different members of the consortium (Clarkson *et al.*, 2004). Plant selection undertaken by SANBI (Figure 3.1)

which did not form part of the current thesis work, was based on the selection of plant molluscicidal candidates from the *FSA* region (Clark *et al.*, 1997). The primary aim was the identification of positive antiplasmodial leads. To expedite the anti-plasmodial screening process, extracts from the CSIR plant extract bank were used. This bank contains a range of plant extracts from several thousand regional plant taxa. Bioprospecting for antimalarial drugs occurred between January 2001 and December 2003, after which the Antimalarials Project and its activities were integrated into the NDDP (Figure 1.3).

3.2.1 Selection of plant candidates

A list of keywords was compiled as a means to identify plants used to treat or associated with MAFEV conditions (Table 3.1). Keywords were grouped into two categories, namely malaria and fever. Plant-use records pertaining to the ethnomedicinal treatment of MAFEV-related conditions were captured in a database. Plant taxa were also included if either positively or negatively associated with MAFEV through laboratory screening investigations. Literature sources (30 separate books, monographs and/or theses) from both East and southern Africa, and deemed to sufficiently cover the extent of relevant recorded traditional knowledge in the region were included. To establish if keyword categories (Table 3.1) were biased towards any taxonomic groups, proportions of taxa, families and orders found to be associated with either malaria and fever keywords were determined.

Various criteria were identified and weighted (Table 3.2) and scores (Table 3.3) were allocated to all taxa. Criteria that were weighted included: i) indigenous to the *FSA* region, ii) occurrence in the regional malaria-endemic area, iii) use in ethnomedicine, iv) popularity in the local ethnomedicinal plant trade, v) associated keyword category, and

vi) the documented chemotherapeutic (antiplasmodial) potential of the plant family. Scores allocated to taxa were tallied, yielding a total score which allowed for ranking of taxa.

Table 3.1 Keywords used to identify candidate antimalarial taxa in the antimalarials literature survey

Keyword category	Keywords
Malaria (category 1)	Antimalarial, Antiplasmodium, Antiprotozoa, Blackwater fever, Malaria, Plasmodia, Plasmodium, Protistocidal, Protozoa
Fever (category 2)	Ague, Antifebrifugal, Antifebrile, Antipyretic, Chills, Febrifuge, Febrile, Fever, Quinidine, Quinine, Rigors, Sweating

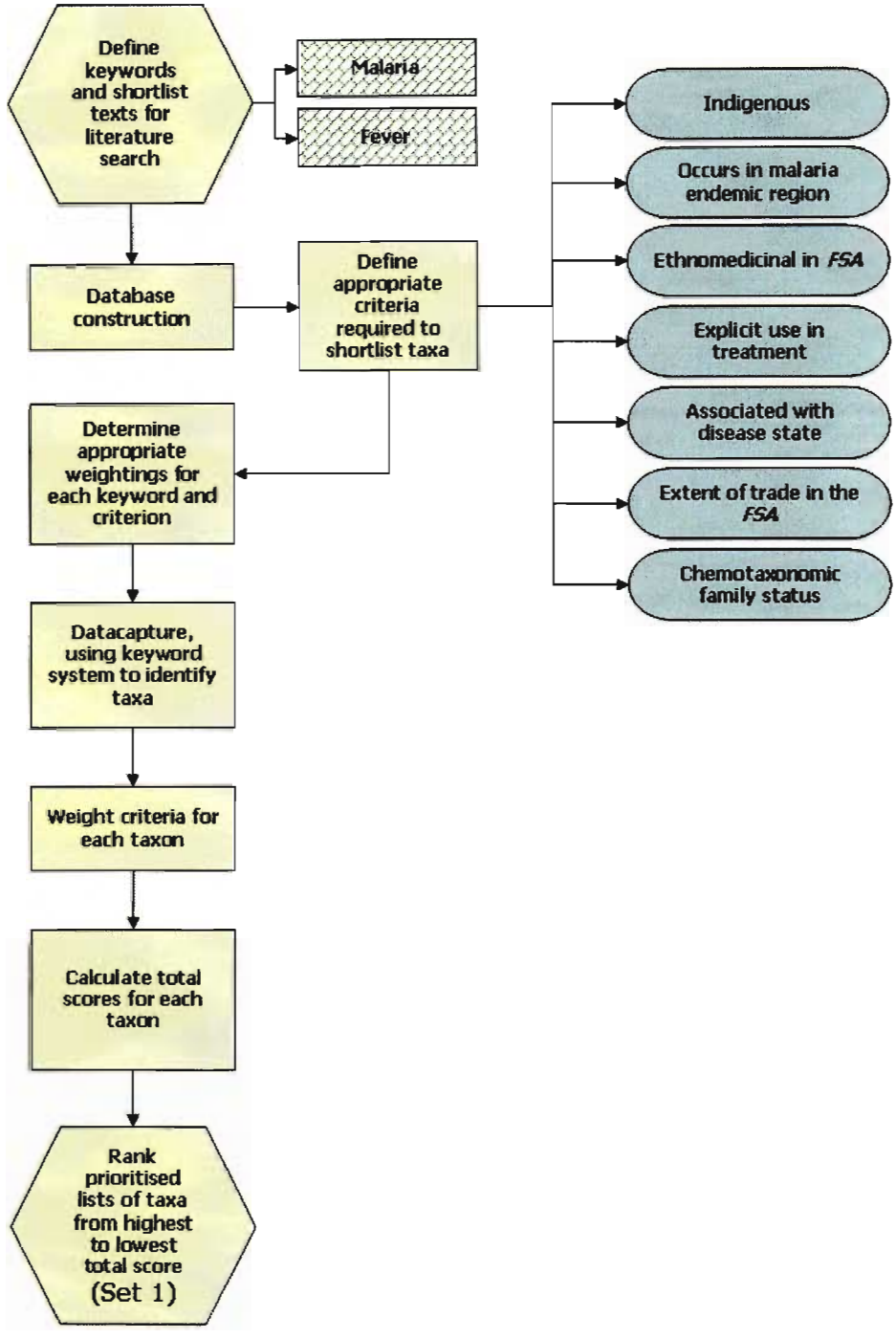

Figure 3.1 The generation of an ethnodirected list of plant candidates for the Antimalarials Project

Table 3.2 Criteria used to identify candidate antimalarial taxa from the FSA flora in the MAFEV literature survey *

Column	Abbreviation	Description
A	Rank no.	Rank to be allocated after totals (column K) have been calculated. Taxa will be ranked by descending order of total score, then alphabetical order by family, genus and species. Rank forms the basis of preference for screening
B	Taxon	Taxon name including genus, species, subspecies and authority (Germishuizen and Meyer, 2003)
C	Family	Plant family to which taxa belong (Germishuizen and Meyer, 2003)
D	Indig.	Taxa indigenous to the *FSA* region were allocated additional weighting. This preference was on the basis that indigenous taxa could present fewer political obstacles if patenting of compounds is required
E	Mal. Endem.	Taxa occurring in the malarial endemic region (defined by the MRC) in the *FSA* were weighted
F	*FSA* (med)	Taxa were weighted if listed in MedList (SANBI, 2004) and/or in Arnold *et al.* (2002) as ethnomedicinal in the *FSA* region
G	Cat. 1 Keyword	Taxa associated with category 1 keywords during the literature search were weighted
H	Cat. 2 Keyword	Taxa associated with category 2 keywords during the literature search were weighted
I	Traded	Taxa weighted according to the number of regional markets where traded (Cunningham, 1988; Mander, 1997; Mander, 1998; Marshall, 1998)
J	HFam	Taxa in phytochemically 'hot' families were weighted according to the number of compound classes in that family known to be used successfully in antimalarial therapy, or with antimalarial activity (Nkunya, 1992)
K	Total	A total score which sums the values of columns D through J

* Details of the associated scoring system are outlined in Table 3.3.

Table 3.3 Weighting of criteria considered important in identifying promising southern African antiplasmodial plant candidates identified in the MAFEV literature survey

Column	Abbreviation*	Weighting
D	Indig.	Weighted 1 if indigenous to the *FSA* region.
E	Mal. endem.	Weighted 1 if occurring in the malarial endemic region.
F	*FSA* (med)	Weighted 2 if the plant is recorded as ethnomedicinal for any purpose.
G	Cat. 1 keyword	Weighted 5 if the plant identified with a category 1 keyword.
H	Cat. 2 keyword	Weighted 3 if the plant identified with a category 2 keyword.
I	Traded	Weighted 0, 1, 2, 3 or 4 according to the number of regional ethnomedicinal markets where the plant is traded.
J	HFam	Weighted 0, 1, 2, 3, or 4 according to the importance assigned to the family: • 0 if family not recorded by Nkunya (1992) to contain efficacious compound classes. • 1 if in the Loganiaceae (Strychnaceae, Gentianaceae, Buddlejaceae), Chenopodiaceae, Rhizophoraceae, Euphorbiaceae, Cyperaceae, Bignoniaceae, Moraceae, Anacardiaceae, Verbenaceae (Avicenniaceae). • Two if in the Asteraceae, Rubiaceae, Lamiaceae • Three if in the Menispermaceae, Rutaceae, Amaryllidaceae • Four if in the Annonaceae, Simaroubaceae (Kirkiaceae), Meliaceae (Ptaeroxylaceae).
K	Total score	A total score which sums the values of columns D through J, with a possible maximum top score of 20 points.

* A full expansion of each abbreviation is presented in Table 3.2

3.2.2. Primary regression analyses

A least squares regression analysis measuring the association between MAFEV plant taxa (grouped by order)(Table 3.1) and the total number of taxa present in those orders in the *FSA* region was performed. Both indigenous and naturalised plant taxa were included. An assumption was made that the literature review conducted during the compilation of the SANBI Malaria database was comprehensive, and that the data constitutes a census rather than a sample of taxa used to treat MAFEV conditions by ethnomedicinal practitioners in southern Africa. Data therefore included i) all taxa used to treat MAFEV conditions in the *FSA* (grouped by order), and ii) the total number of taxa in the *FSA* (grouped by order). The population correlation coefficient (ρ) indicated the strength of the relationship of these two groups of variables. Total numbers of orders or families were designated as independent variables and MAFEV taxa were designated as dependant variables. Taxonomic groupings at generic and species level conform to the PRECIS database (SANBI, 2005), while groupings at order and family levels follow the APG II (2003) for angiosperms, and Bowe *et al.* (2000) and Chaw *et al.* (2000) for gymnosperms.

3.2.2.1 Residual values

Residual values were calculated by subtracting predicted numbers of taxa used per order from the actual number of taxa used per order. The population variance calculated from these residuals was used to identify all outliers, i.e. orders which showed notably different values from those predicted.

3.2.2.2 Plotting regression data

The 44 orders containing MAFEV taxa were plotted against total *FSA* taxa (grouped by order) and the regression line (equation obtained from the regression analysis) was overlaid to allow for visual assessment of i) any notable relationships/patterns, and ii) the position of any outliers. Residual values correspond to the vertical distance from each data point to the regression line ($y- \hat{y}$).

3.2.2.3 Analysis of families within selected orders

A regression analysis of all MAFEV taxa (grouped by family) against total taxa (grouped by family) was performed. Families in outlying positive ('hot') orders were then filtered out to better understand the contribution those families made to the outlier status of 'hot' orders.

3.2.2.4 Assessing bioassay results from taxa in 'hot' families

The most frequently occurring genera in 'hot' families were listed first by rank and then alphabetically. Species of these genera for which bioassay results (from initial antiplasmodial screenings) were available were listed with their respective IC_{50} values to allow an assessment of the plant selection procedure. A near-comprehensive list of all antiplasmodial bioassay findings has been published by Clarkson *et al.* (2004).

3.2.3 Secondary regression analyses

Outlying orders identified in the primary regression analysis were removed from the data set, and the analysis performed again to allow further partitioning of the data. The population variance of the residual values was determined and used as a cut-off to

identify outlying orders. Total taxa (grouped by order) were considered independent variables and ethnomedicinal taxa (grouped by order) as dependant variables.

3.3. Results

3.3.1 Selection of plant candidates

Approximately 616 taxa were short-listed during the literature search and were subsequently ranked according to weighted criteria. Within the list of short-listed candidates 475 taxa attained total scores of seven or more, of which 134 were collected and screened. The top-ranked taxon achieved a total score of 17 out of a possible maximum 20 (Clarkson *et al.*, 2004).

194 (31.5%) out of 616 taxa were identified using malaria keywords, while 404 (65.6%) out of 616 were identified using fever keywords. 99 (16.1%) taxa were identified from both malaria and fever keywords. 31 plant orders contained taxa identified from malaria keywords, while 39 orders contained taxa identified from fever keywords (Table 3.4). The discrimination between 'malaria' and 'fever' keywords was disregarded in subsequent analyses and the taxa from the two groups were combined.

Table 3.4 Proportions of higher taxa identified in the literature survey through either fever or malaria keywords

	Fever	Malaria	Total
Orders	39	31	43
Families	99	73	122
Species and subspecies	404	194	616

3.3.2. Primary regression analyses

The results of the primary least squares regression analysis (Table 3.5) reveal the presence of a strong linear relationship ($\rho = 0.77$) between the MAFEV taxa (grouped by order) and the total number of taxa in those orders. Very similar results ($\rho = 0.75$) were obtained for MAFEV taxa grouped by family.

Table 3.5 Statistics from a least squares regression analysis of MAFEV orders and families

	Coefficient	Constant	ρ	ρ^2	Std. error	Pop. size
Orders	0.015	4.304	0.77	0.59	12.88	43
Families	0.018	1.386	0.75	0.56	6.61	122

3.3.2.1 Residual values

The residual values obtained from the regression analysis of plant orders (Table 3.6) ranged from 37.6 to -27.9, and the model was able to account for 59% ($\rho^2 = 0.59$) of the variation in y-values. It was necessary to distinguish which orders could be considered outliers, i.e. were farthest from the regression line. The population variance of the residuals (12.6) was employed as a cut-off, leaving eight orders as outliers. Five orders showed positive residuals higher than the population variance, and three showed negative residuals below the population variance. Plants in these eight regional MAFEV orders are therefore considered to have been selected either far more or far less than others by ethnomedicinal practitioners. The magnitude of these eight residuals ($> +12.6$ and/or < -12.6) falsifies the null hypothesis.

Table 3.6 Orders used significantly greater or less than predicted against MAFEV conditions

Order	Total *FSA* taxa	Predicted MAFEV taxa	Actual MAFEV taxa	Residual value*
Sapindales	655	14.4	52	+37.6
Fabales	2636	44.9	80	+35.1
Malpighiales	902	18.2	48	+29.8
Lamiales	2457	42.2	58	+15.8
Asterales	3179	53.3	69	+15.7
Caryophyllales	2848	48.2	29	-19.2
Asparagales	3942	65.0	39	-26.0
Poales	2245	38.9	11	-27.9

* Residual values above (+) or below (-) the population variance

3.3.2.2 Plotting regression data

A plot of the 43 orders containing MAFEV taxa against the total number of taxa in these orders (Figure 3.2) showed a positive relationship (ρ). The magnitude of the eight outliers, however, clearly influences the coefficient of determination (ρ^2) and hence any predictions made using the line of best fit. The names of the positive and negative outliers have been included on the plot for easy interpretation. The Sapindales and Fabales were the most notable positive outliers.

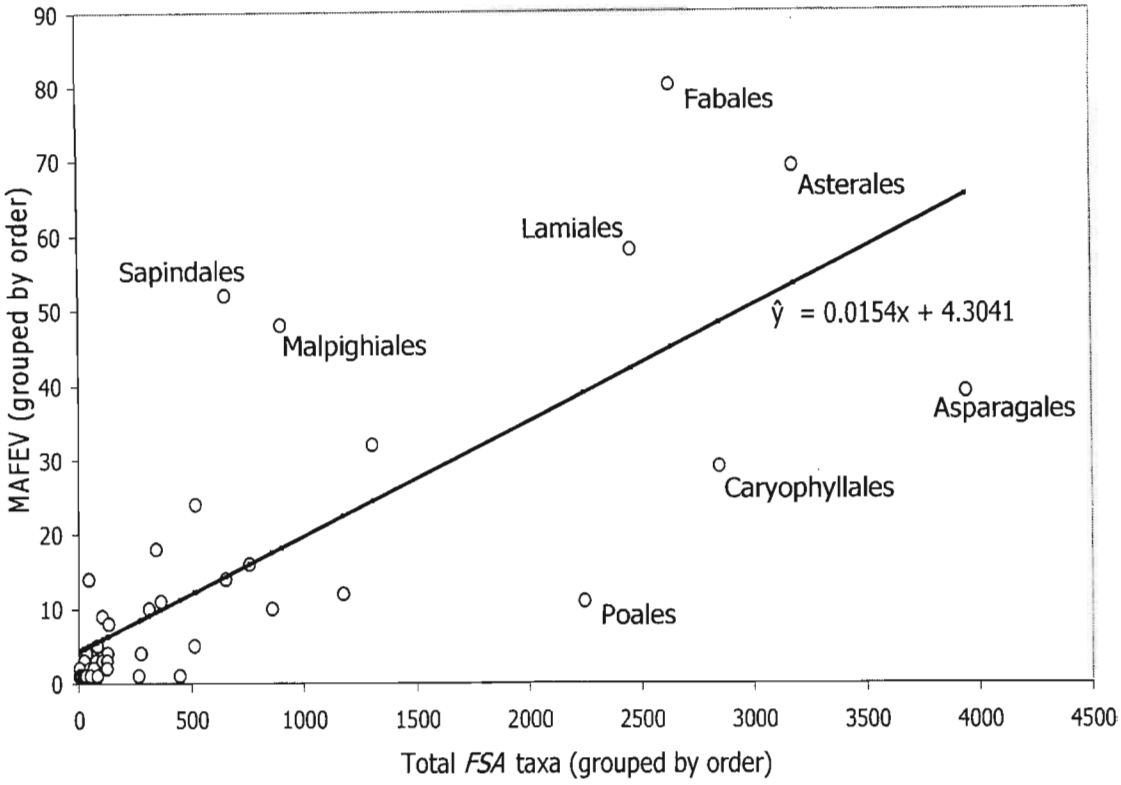

Figure 3.2 Regression plot of MAFEV taxa grouped by order versus the total taxa in those orders

3.3.2.3 Analysis of families within selected orders

The results of the least squares regression analysis of all families containing MAFEV taxa (Table 3.7) indicated that particular families within each order yielded much higher residual values. Residual values presented were calculated as the difference between predicted numbers of MAFEV taxa, and the actual number of taxa in those families. The output of the analysis as shown here was reduced due to the entire dataset being too large for display in this thesis. Only families circumscribed into positive outlying orders (Table 3.6) were included.

Table 3.7 MAFEV families contributing to the positive outlier status of their respective orders

Order	Family	Total number of *FSA* taxa	Predicted MAFEV taxa	Actual MAFEV taxa	Residual values*
Sapindales	Meliaceae	30	1.9	17	+15.1
	Rutaceae	352	7.7	16	+8.3
	Sapindaceae	75	2.7	7	+4.3
	Anacardiaceae	157	4.2	8	+3.8
	Simaroubaceae	3	1.4	3	+1.6
	Burseraceae	35	2.0	1	-1.0
Fabales	Fabaceae	2422	44.6	77	+32.4
	Polygalaceae	214	5.2	3	-2.2
Malpighiales	Euphorbiaceae	536	11.0	24	+13.0
	Phyllanthaceae	37	2.0	8	+6.0
	Salicaceae	93	3.0	4	+1.0
	Rhizophoraceae	8	1.5	2	+0.5
	Ochnaceae	15	1.7	2	+0.3
	Dichapetalaceae	3	1.4	1	-0.4
	Chrysobalanaceae	5	1.5	1	-0.5
	Clusiaceae	6	1.5	1	-0.5
	Elatinaceae	13	1.6	1	-0.6
	Malpighiaceae	16	1.7	1	-0.7
	Papaveraceae	28	1.9	1	-0.9
	Hypericaceae	30	1.9	1	-0.9
	Passifloraceae	37	2.0	1	-1.0
Lamiales	Lamiaceae	464	9.7	32	+22.3
	Verbenaceae	81	2.8	4	+1.2
	Pedaliaceae	42	2.1	3	+0.9
	Plantaginaceae	19	1.7	2	+0.3
	Bignoniaceae	88	3.0	2	-1.0
	Oleaceae	95	3.1	2	-1.1
	Orobanchaceae	98	3.1	1	-2.1

Table 3.7 (continued)

Order	Family	Total number of *FSA* taxa	Predicted MAFEV taxa	Actual MAFEV taxa	Residual values*
	Acanthaceae	436	9.2	7	-2.2
	Scrophulariaceae	1012	19.4	5	-14.4
Asterales	Asteraceae	2681	49.2	66	+16.8
	Goodeniaceae	4	1.5	1	-0.5
	Menyanthaceae	8	1.5	1	-0.5
	Campanulaceae	486	10.1	1	-9.1

* Residual values above (+) or below (-) the population variance

3.3.2.4 Assessing bioassay results from taxa in 'hot' families

Genera appearing most frequently in hot families (from Table 3.7) were listed first according to rank then alphabetically (Table 3.8). Species of these genera with available *in vitro* antiplasmodial bioassay results (IC_{50} values)(Clarkson *et al.*, 2004) are presented (Table 3.9) to allow for assessment of their antiplasmodial activities. Results for all solvent extracts from each species are not shown, but rather the best result obtained for each species. It is notable that each of the species listed obtained an IC_{50} value of $\leq$ 12 μg/ml. Values $\leq$ 10 μg/ml are generally considered favourable and worthy of further investigation. While testing the statistical significance of such results was not considered appropriate, it can be stated that the majority of taxa from hot orders showed good efficacy in the preliminary bioassays.

Table 3.8 The most frequently occurring genera in hot families and orders as determined by the MAFEV regression analyses

Order	Family	Genus	Rank
Sapindales	Meliaceae	*Turraea*	1
		Ekebergia	2
		Entandrophragma	2
		Trichilia	2
Fabales	Fabaceae	*Acacia*	1
		Senna	2
		Albizia	3
Malpighiales	Euphorbiaceae	*Croton*	1
		Euphorbia	1
		Jatropha	2
Lamiales	Lamiaceae	*Salvia*	1
		Leonotis	2
		Ocimum	3
Asterales	Asteraceae	*Vernonia*	1
		Conyza	2
		Dicoma	3

Table 3.9 IC_{50} values obtained for representatives of selected 'hot' genera in the *in vitro* antiplasmodial screen (Clarkson *et al.*, 2004)

Taxon	Plant part	Solvent	IC_{50} (μg/ml)
Turraea floribunda Hochst.	Leaves	DCM/MeOH (1:1)	8.8
Ekebergia capensis Sparrm.	Fruit	DCM/MeOH (1:1)	10.0
Trichilia emetica Vahl subsp. *emetica*	Leaves/Twigs	DCM/MeOH (1:1)	3.5
Acacia tortilis (Forssk.) Hayne subsp. *heteracantha* (Burch.) Brenan	Whole plant	DCM/MeOH (1:1)	4.8
Senna didymobotrya (Fresen.) Irwin & Barneby	Twigs	DCM/MeOH (1:1)	9.5
Croton gratissimus Burch. var. *subgratissimus* (Prain) Burtt Davy	Leaves	DCM	3.5
Euphorbia tirucalli L.	Leaves	DCM	12
Salvia repens Burch. ex Benth. var. *repens*	Whole plant	DCM/MeOH (1:1)	10.8
Leonotis leonurus (L.) R.Br.	Twigs	DCM/MeOH (1:1)	5.4
Ocimum americanum L. var. *americanum*	Whole plant	DCM/MeOH (1:1)	4.2
Vernonia oligocephala (DC.) Sch.Bip. ex Walp.	Leaves	DCM	3.5
Conyza albida Spreng.	Whole plant	DCM/MeOH (1:1)	2.0

3.3.3 Secondary regression analyses

Outlying orders and families identified in the regression analyses in Section 3.3.2.1 were removed from the dataset, and the regression analyses were performed again. The linear relationship ($\rho = 0.74$)(Table 3.10) between MAFEV taxa grouped by order and total taxa in those orders was stronger than the corresponding result obtained prior to removal of the outliers. The population variance of residuals (calculated at 4.90) was

employed as a cut-off, for separation of outlying orders (Table 3.11). These outlying orders are either more or less frequently selected for by ethnomedicinal practitioners.

Table 3.10 Statistics from a secondary regression analysis of MAFEV orders and families

	Coefficient	Constant	ρ	ρ^2	Std. error	Pop. size
Orders	0.016	2.37	0.74	0.54	5.04	35
Families	0.015	1.65	0.73	0.53	2.07	106

Table 3.11 Orders used significantly greater or less than predicted against MAFEV conditions as obtained from the secondary regression analysis

Order	Total *FSA* taxa	Predicted MAFEV taxa	Actual MAFEV taxa	Residual value*
Solanales	519	10.8	24	+13.2
Magnoliales	44	3.1	14	+10.9
Apiales	343	7.9	18	+10.1
Gentianales	1305	23.5	32	+8.5
Celastrales	103	4.0	9	+5.0
Saxifragales	512	10.6	5	-5.6
Oxalidales	265	6.6	1	-5.6
Rosales	859	16.2	10	-6.2
Proteales	447	9.6	1	-8.6
Ericales	1174	21.3	12	-9.3

* Residual values above (+) or below (-) the population variance

3.4. Discussion

That preparations derived from ethnomedicinal plants often show positive pharmacological activities is widely acknowledged (Farnsworth *et al.*, 1985; Fourie *et al.*,

1992; Cox, 1994; Taylor *et al.*, 2001). Considering the diversity of the flora (approximately 24000 taxa in some 368 plant families)(Germishuizen and Meyer, 2003) and ethnomedicinal flora (3434 taxa from 1187 genera and 206 families)(Arnold *et al.*, 2002) in southern Africa, the potential that the region holds in regard to efficacious medicinal plants is considerable. However, even with the recent advances in biodirected assays (Lewis, 2003), screening all regional taxa against ailments such as malaria is currently impractical. When considered in the light of the costs of bioprospecting, the necessity for techniques that prioritise taxa – particularly ethnomedicinal taxa (Farnsworth, 1990) becomes clear.

The preferential use of ethnomedicinal data in drug discovery programmes has several potential spin-offs, such as providing short-term and long-term benefits to the ethnomedicinal knowledge-holders, communities, host countries, and participating institutions (Soejarto *et al.*, 2002a). Furthermore, natural products generally have a great potential for use in their native state, i.e. with little or no structural modification, which can reduce the costs associated with re-engineering structures of complex compounds (Garrity and Hunter-Cevera, 1999). The methods described in this chapter therefore warrant attention from bioprospectors involved in similar projects.

One of the key reasons for incorporating regression analyses in the assessment of antimalarial data is the need to understand if plant selection by ethnomedicinal practitioners in the region is in any way related to current taxonomic constructs. If selection of ethnomedicinal plants is based purely on the placebo effect (Adler and Hammett, 1973) then the hypothesis that such selection is random (Moerman, 1979) would be true. The falsification of the hypothesis, as shown here, indicates a higher than predicted ethnomedicinal use of certain families; plants in such families are likely to be

more efficacious (Moerman and Estabrook, 2003), most likely due to the presence of certain secondary metabolites (Saxena *et al.*, 2003). If so, then the recently validated status of plant families as indicators of evolutionary relationships adds strong support to the argument that closely related plants produce similar chemical compounds (Grayer *et al.*, 1999; Moerman *et al.*, 2003). While it is not the aim of this chapter to expound on the philosophy of plant selection by ethnomedicinal practitioners, the incorporation of such knowledge in the development of bioprospecting methods is seen as essential. This is particularly the case where ethnomedicinal preferences can be correlated with phylogenetic perspectives.

3.4.1 Keyword associations

The keyword system of identifying plants with potentially efficacious anti-malarial extracts is analogous to the use of object attributes in data mining (Westphal and Blaxton, 1998). Keywords are attributes ascribed to certain objects (plant taxa) and as such can be used to identify those objects from the data source. Keywords considered synonymous and analogous with malaria and fever (Table 3.1) were incorporated into text searches on the obvious grounds that recorded ethnomedicinal literature reflects the knowledge of ethnomedicinal practitioners. Of presumed lesser importance is the likelihood that plants may have been used in any number of ways, either singly or in combination with others. It is also unlikely that ethnomedicinal practitioners are familiar with the epidemiological basis of many diseases, including malaria (Randrianarivelojosia *et al.*, 2003), and it is therefore unlikely that ethnomedicinal literature reflects *bona fide* links between the symptoms of the malaria (characterised by cyclic bouts of fever) and the *Plasmodium* pathogen. The assumption is that the occurrence of MAFEV keywords implies that the relative plants are efficacious in the treatment of MAFEV conditions.

It was unsurprising that 'fever' as a keyword showed a greater number of associated taxa (65.6%) relative to those taxa associated with 'malaria' (31.5%) due firstly to the greater number of keywords associated with fever conditions (Table 3.4). Secondly it is likely that fevers are a more ubiquitous phenomenon as opposed to malaria which is normally restricted to certain geographical regions.

3.4.2 Primary regression analyses

The selection of the taxonomic levels used here, was undertaken on the basis of certain published phylogenies (Bowe *et al.*, 2000; Chaw *et al.*, 2000; APG II, 2003) though different classifications may have produced different results. The lack of detailed phylogenies prevented the use of phylogenetic comparative techniques, the disadvantages of which are discussed in Chapter 1.

Certain plant orders and families contained significantly greater numbers of MAFEV taxa (Figure 3.2) than would be expected if ethnomedicinal selection procedures were random. While regression analyses may be considered unbiased, the application of these analyses do provide scope for subjective inputs. In this study, the selection of order and/or family taxonomic levels for analyses was considered subjective, in that other higher or lower taxonomic levels could have been used instead. It is also likely that results would have been different if the initial sampling was based on family level rather than at the level of order.

The use of least squares regression analyses for comparison of ethnomedicinally used anti-MAFEV higher taxa (Table 3.5) resulted in the falsification of the null hypothesis. Ethnomedicinal practitioners may apparently select MAFEV plants at random but the experiential retention of taxa in that capacity is not random. The regression analysis of

families containing MAFEV taxa (Table 3.7) showed that greater residual values were associated with certain families than with others in the same order. This suggests a distinct plant selection bias towards certain taxonomic groups by ethnomedicinal practitioners. Certain 'hot' families clearly contributed more to their respective orders being designated as outliers. Repeated analyses of the same data set at order, family and genus levels would objectify the selection of the optimum taxonomic scale at which to run regressions. Of course none of these categories are equivalent due to different rates of divergence resulting from several suites of selective pressures. Families will be over-represented if the physiological and anatomical machinery required for the manufacture of the particular suite of chemicals evolved as a synapomorphy for the ingroup (the family in question). Reasons for the dominance of certain families are therefore unclear, but the application of detailed phylogenies through additional comparative methods may provide elucidation. This is because details of branch length and/or the evolution of characters on particular branches of a phylogeny should necessarily be factored into the analyses in order to reduce artifactual signals (Felsenstein, 2003). Alternately, it could be that ethnomedicinal practitioners favour particular families due to phenotypic characteristics which they perceive as preferential. Such practices may be particularly common where numerous closely related and similar-looking taxa are available for use in a given region. For example, the genus *Acacia* (Fabales) has 46 taxa (species, subspecies and variants) in the *FSA* region (SANBI, 2005) many of which are ethnomedicinally used (Watt and Breyer-Brandwijk, 1962; Hutchings *et al.*, 1996; Van Wyk *et al.*, 1997). Uses include *inter alia* their inclusion in emetics and in enemas (Watt and Breyer-Brandwijk, 1962).

Comparison of selected taxa in 'hot' families (Table 3.8) from the regression analyses, with the antiplasmodial bioassay results revealed a majority with IC_{50} values $\leq$ 10µg/ml.

It can be concluded that regression analyses are a useful additional tool in bioprospecting.

3.4.3 Secondary regression analyses

The secondary regression analyses (Table 3.10) served to illustrate the potential for identification of additional higher taxa that could be prioritised for bioprospecting purposes. The orders identified (Table 3.11) do however lie closer to the regression line, and as such may not yield candidates with particularly significant efficacies. The repetition of regression analyses after removing outliers may be undertaken several times, but depending on the variability of the data, the data points will tend to move closer to the regression line. Where this is the case, the data will certainly be of reduced value. It is recommended that such analyses are not performed beyond the secondary stage as has been demonstrated.

3.5 Conclusion

Plant selection by ethnomedicinal practitioners often incorporates a complex interplay of factors (Moerman, 1979) including details of the prevailing medical cosmology, concepts of illness, disease aetiology and the expected outcomes of preventative and therapeutic measures (Etkin, 1986). Plant selection is usually not limited to plant availability (Moerman, 1979). Various formulations of the humoral theory of disease in which aetiologies are ascribed to imbalances, and treatments are directed toward restoring harmony, are documented (Etkin, 1986). Furthermore, beliefs that certain tangible attributes of plants serve as signs to indicate utility (Doctrine of Signatures) are common, and demonstrate the strength of symbolism in traditional pharmacology (Etkin,

1986). This is well documented in Zulu and Xhosa ethnomedicinal practices (Hutchings, 1989). Empiricism should also not be ruled out, as remedies that produce both anticipated and therapeutic effects (Trotter, 1986) are likely to become widely known within ethnomedicinal circles. While traditional remedies may not always be allocated on the basis of disease epidemiology, it is possible that through mechanisms such as immune modulation, the targeting of disease organisms, or placebo effects, the body is better able to fight off disease. A key component of any bioprospecting programme is therefore the ability to identify plant candidates most likely to yield positive results from a given array. This is accentuated by low hit rates generally associated with such investigations; one in 250000 samples will likely yield a commercial drug (Macilwain, 1998). The generation of methods which contribute to streamlining the selection process, particularly where numerous factors are being considered and weighted, is therefore essential. Comparative methods, e.g. the regression analyses presented in this chapter, are undoubtedly capable of improving candidate prioritisation. This justifies the need for their inclusion in plant selection programmes. The reliability of the methodology will improve with the advent of more detailed phylogenies, making such analyses even more appealing and advantageous.

Chapter 4

Bioprospecting for anti-tuberculosis, anti-diabetes and immune-modulatory plants in the *FSA*

The use of hypotheses lies not in the display of ingenuity, but in the labour of verification.

– Thomas Clifford Allbutt (1836-1925)

Abstract

Drug discovery can be optimised through the adoption of a focused, easy to implement plant selection procedure. In bioprospecting for anti-tuberculosis, anti-diabetes and immune-modulatory plants, the Novel Drug Development Platform recently incorporated such a focused approach as a means to prioritise plant candidates. The method incorporated various weighted plant selection criteria which allowed for easy prioritisation of candidates once the taxa had been scored. Lists of taxa were compiled in various ways, primarily through ethnobotanical literature searches. Weighted criteria included indigenous and endemic status, ethnomedicinal use, chemotaxonomic potential, frequency of trade at ethnomedicinal markets, direct and/or associated use against the relative disease state, toxicity, Red Data status, perceived importance of plant family according to known chemical properties, and importance of family based on preferences shown by ethnomedicinal practitioners. Certain criteria such as endemism were

incorporated due to the bio-political preference for plants restricted to the *FSA* region. The inclusion of other criteria such as the importance assigned to families by ethnomedicinal practitioners recognised the value of traditional knowledge in bioprospecting. Other taxa were short-listed due to i) their presence in biodiversity hotspots with little known ethnomedicinal tradition, ii) their close taxonomic relationships with other efficacious taxa. The rationale for the selection and weighting is discussed. Statistical analyses of the weighting processes are not possible in absence of screening results, but recommendations for such analyses are detailed.

4.1 Introduction

The establishment of the Novel Drug Development Platform (NDDP) was finalised in South Africa in February 2003. The stated objective of this consortium was to establish a biotechnology infrastructure for research and development of novel medicines from the southern African flora (Figure 4.1). The NDDP took forward development of antimalarial drugs initiated by the Antimalarials Project (Figure 1.3 and Chapter 3) and considered the identification and screening of plant taxa for the development of anti-tuberculosis, anti-diabetes, and immune modulatory drugs (Figure 1.3). Following the success of plant selection procedures used in the Antimalarials Project (Clarkson *et al.*, 2004)(> 50% of taxa showed IC_{50} values of ≤ 10 µg/ml) similar procedures were used in the new programme. However, it was considered necessary to improve upon those selection methods in order to enhance the hit-rate of candidate taxa. As such, several modifications were made to the semi-quantitative approach (after Clark *et al.*, 1997) which ranked plant taxa according to weighted criteria (Figure 4.3). These modifications included the incorporation of regression analysis techniques (Figure 2.1)(after Moerman,

1991) which allowed for additional weighting of 'hot' orders and families, i.e. those shown to be most strongly selected by ethnomedicinal practitioners. The decision to incorporate these regression analyses was also based on their successful application in identifying efficacious antimalarial plant data (Chapter 3). The identification of chemical compound classes known to be efficacious against the relative disease states was incorporated as a means to add weighting to plant families which contained these compound classes. Other additional criteria used to weight plant taxa included toxicity data, endemic status in the *FSA*, and the extent to which taxa were traded at traditional ethnomedicinal markets.

The use of primarily ethnomedicinal data for short-listing plants in Set 1 (Figure 4.2) was considered a limitation due to the significant bias that recorded ethnomedicinal knowledge shows towards plants situated on the eastern seaboard (Chapter 2). This inconsistent use of ethnomedicinal plants in the *FSA* region (Figure 2.10) is most likely due to the skewed historical settlement of Bantu tribes in the moister, more fertile eastern seaboard (Figure 2.12). As such, additional selection methods were incorporated to overcome this bias and to target other taxa which, although not known to be efficacious, may arguably prove to be important considerations. This led to the development of a focused selection of taxa from the Western Cape (Set 5, Figure 4.2), to include at least some of the many (often endemic) taxa in that region. Close relatives of selected ethnomedicinal taxa were targeted because they may share (potentially efficacious) secondary metabolites (Hegnauer, 1967; Cronquist, 1980). Similarly, other non-ethnomedicinal indigenous taxa, but not restricted to the Western Cape, were identified (Set 3, Figure 4.2). Exotic taxa noted to be efficacious against the relative disease states were also short-listed from the literature to allow for the identification of related non-ethnomedicinal indigenous taxa (Set 7, Figure 4.2). While these selection

procedures are based on sound taxonomic principles, a lack of detailed phylogenies for most taxa hampered the process (Harvey and Pagel, 1991).

The modifications incorporated into the plant selection procedures in this chapter are considered central to improving the likelihood of identifying efficacious drug leads. Bioprospecting methodology needs to continually evolve in order to make use of new data and data mining techniques and while the methods presented in this chapter are considered greatly enhanced, they should in turn be evaluated and suitably modified for use in future programmes. The financial overheads and many years required to develop new drugs makes improvement to this research of particular importance. In addition, the many plants in South Africa which are becoming endangered (Van Wyk and Smith, 2001; Golding, 2002), highlights the urgency with which taxa in the region should be assessed.

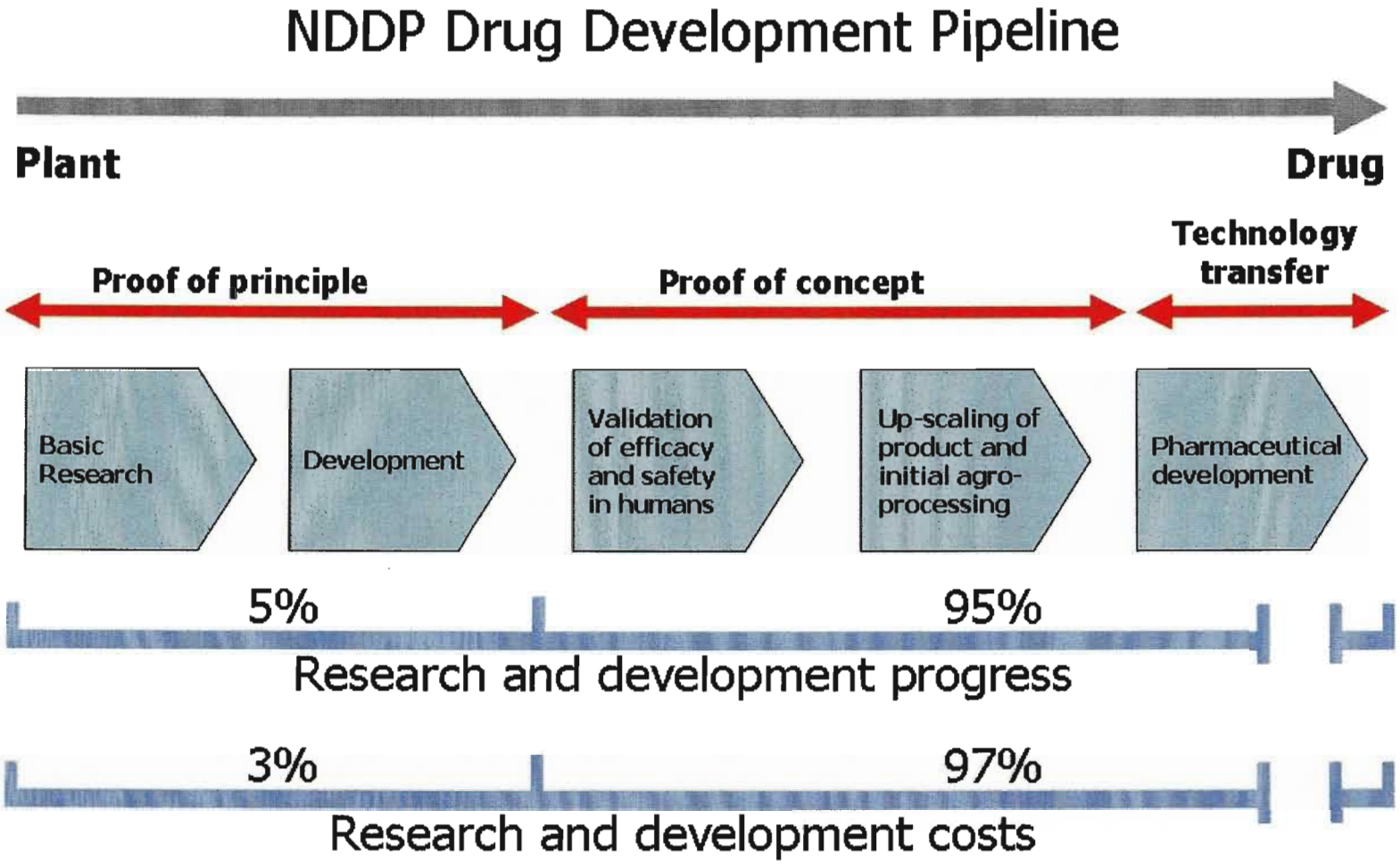

Figure 4.1 A model of the NDDP's proposed drug development pipeline which highlights the financial and research input of various stages

4.2 Methods

The many research facets of the NDDP programme (Figure 1.3) were undertaken by respective consortium members. Plant selections were undertaken by the South African National Biodiversity Institute (SANBI) and were completed in four phases, with four distinct sets of data (Set 1, 3, 5, and 7: Figure 4.2). Each of these sets contained short-lists of taxa potentially useful for the treatment of tuberculosis (EthMedTB taxa) and diabetes (EthMedDBM taxa) and for immune modulation (EthMedIMM taxa). Taxon nomenclature was updated using a current checklist (Germishuizen and Meyer, 2003). Taxa not listed in Germishuizen and Meyer (2003) were substituted with a known indigenous relative of the same genus. Taxa were weighted according to the various criteria and then prioritised by rank. The inconsistent use of ethnomedicinal plants in the *FSA* region (Figure 2.10) necessitated the compilation of taxa in Sets 3 and 5 (Figure 4.2). These two sets of data were primarily non-ethnomedicinal, but were considered closely related to highly ranked ethnomedicinals listed in Set 1. Taxa in Set 7 were compiled due to their close taxonomic relationship with exotic taxa considered efficacious against the respective disease categories. Plant prioritisation techniques outlined in this section are for short-listing candidates for collection. The number of taxa expected to be screened is likely to be significantly less than the total prioritised due to financial and logistical constraints.

4.2.1 Generation of an ethnodirected plant candidate list (Set 1)

The ethnodirected list of plant candidates (Set 1)(Figure 4.3) made use of weighted criteria (Table 4.1) to prioritise plants and was the larger proportion (approx. 70%) of taxa identified. A Microsoft Access database populated from a broad range of

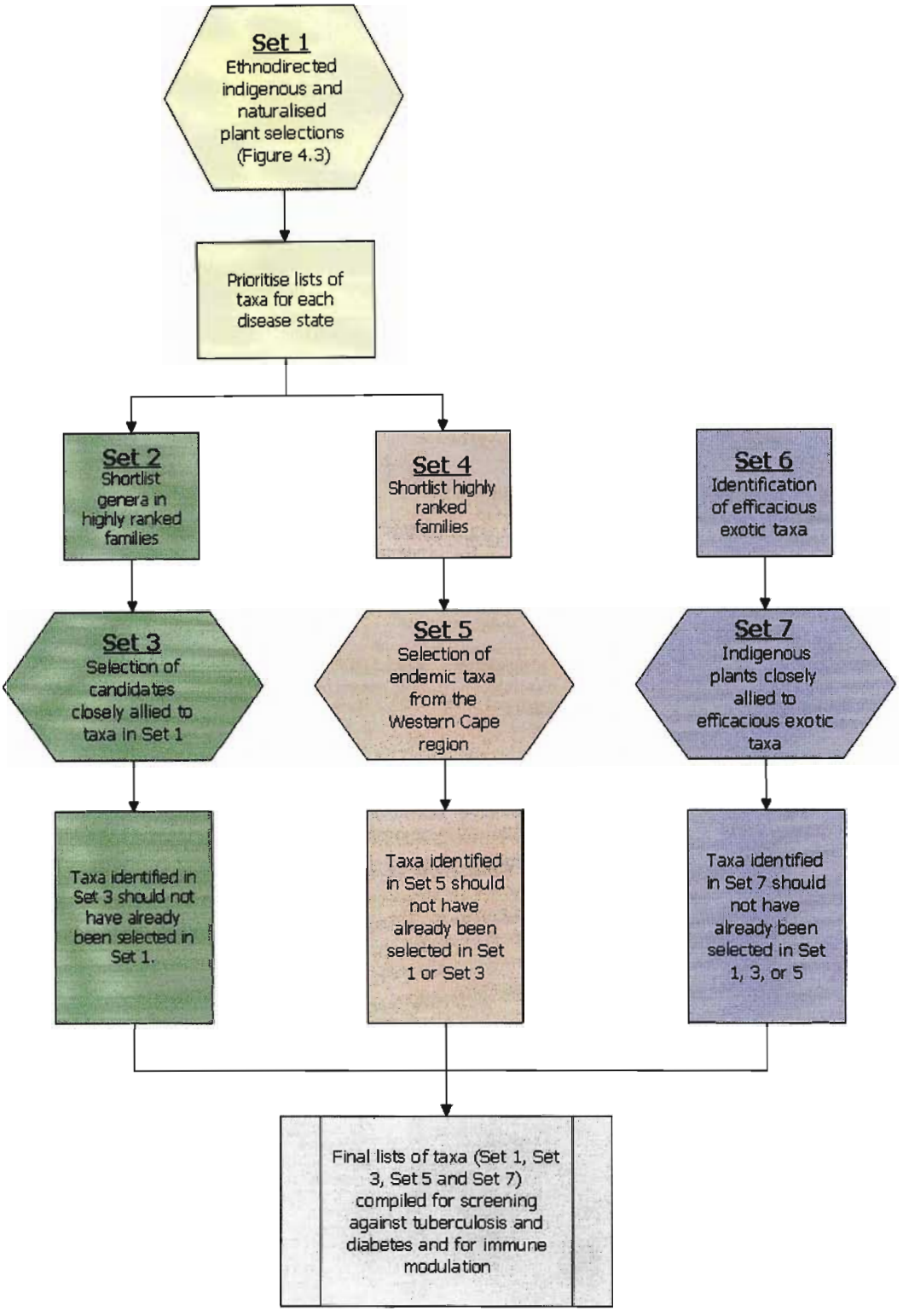

Figure 4.2 Generation of final lists of prioritised taxa for screening by the NDDP

(primarily ethnomedicinal and selected ethnoveterinary) tertiary literature allowed for the compilation of plant data on the basis of predetermined keywords (Section 4.2.1.1).

4.2.1.1 Keywords (Column N)

Keywords used to identify plant taxa from the literature were proposed through consultation of a variety of dictionaries (Friel, 1974; Dent and Nyembezi, 1993; Bloomsbury, 2001; Hyperdictionary, 2005). Each keyword, linked to either tuberculosis (Table 4.3), diabetes (Table 4.4) or immune modulation (Table 4.5), was assigned a weighting (between one and eight) based on its perceived importance for the identification of plant candidates, i.e. plants identified through 'prime' keywords received a higher weighting. The following example refers: the word 'catarrh' was used in the search for anti-tuberculosis candidates and assigned a weighting of two. Ethnomedicines are often used in a general sense and it may be that ethnomedicinal practitioners use the same plant to treat both tuberculosis and catarrh. However, the relatively low score is allocated on the basis that while some of the symptoms of catarrh may also be observed in people infected with tuberculosis, it is not a direct reference to that disease. Similarly, 'respiratory conditions' or 'lung diseases' are likely treated in a general sense as opposed to targeting of the pathogen *Mycobacterium tuberculosis*. A plant directly referenced to treat 'tuberculosis' would have received a full weighting of eight. The keyword scoring system produced lists of candidates that were highly segregated by total score and therefore more easily ranked. Keywords that corresponded to words found in the literature are highlighted (Table 4.3; Table 4.4; Table 4.5).

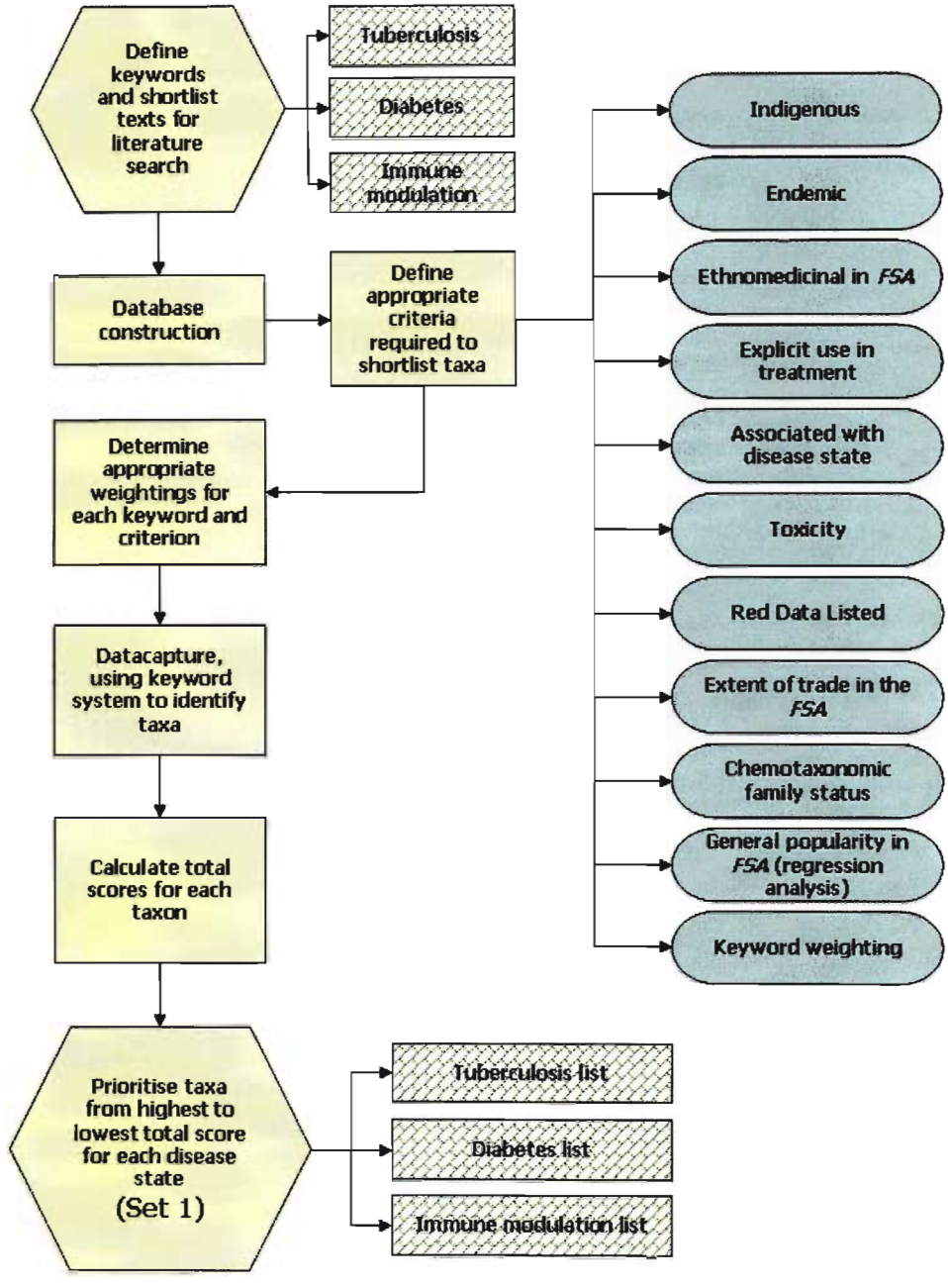

Figure 4.3 Protocol for the generation of ethnodirected list of plant candidates for the NDDP (Set 1)

Table 4.1 Plant characteristics considered important in identification of candidate taxa from the FSA flora *

Column	Abbreviation	Description**
A	Rank No.	Rank number allocated after total scores are calculated
B	Taxon	Genus, species, subspecies and authority
C	Family	The plant family to which taxa belong
D	Indig.	The indigenous status within the *FSA* region
E	End.	The endemic status in South Africa
F	*FSA* (med).	Plants listed as ethnomedicinal in the *FSA* region
G	Treat.	Documented explicit use in treatment of the respective disease categories
H	Assoc.	Documented positive or negative associations (symptomatic relief/supportive therapy/bioassay findings) with the respective disease categories
I	Tox.	Taxa weighted if they or their constituents have been recorded as toxic in literature
J	Red Data	Taxa weighted if Red Data Listed in the *FSA* region
K	Trade	Taxa weighted on the number of regional markets where traded (index of popularity)
L	HFam1	Taxa weighted if in phytochemically 'hot' families
M	HFam2	Taxa weighted if in 'hot' ethnomedicinal families
N	Keyword	Associated literature keyword weighting
O	Total Score	The summed values of columns D through M and used to rank plants in each list

* Details of the associated scoring system are outlined in Table 4.2

** Full details of these brief descriptions are presented in the text (Sections 4.2.1 through to 4.2.4)

Table 4.2 Weighting of characteristics considered important in identifying promising drug-source plant candidates from southern Africa.

Column	Abbreviation*	Weighting
D	Indig.	Weighted 1 if indigenous to the *FSA* region
E	End.	Weighted 1 if endemic to South Africa
F	*FSA*(med)	Weighted 2 if the plant is recorded as ethnomedicinal
G	Treat.	Weighted 15 if the plant has been used explicitly for treating the disease under consideration
H	Ass.	Weighted 8 if the plant is associated with the disease
I	Tox.	Weighted 3 if recorded as toxic
J	Red data	Weighted 2 if the plant has Red Data status
K	Trade	Weighted 0 to 4.5 according to the number of regional ethnomedicinal markets where the plant is traded, i.e. 0.5 points for each market
L	HFam1	Weighted zero, four, six or eight according to the chemotaxonomic importance assigned to the family. 0 if containing no efficacious compound classes, 4 for one efficacious compound class, 6 for two efficacious compound classes and 8 for three or more efficacious compound classes
M	HFam2	Weighted 3 if considered to belong to an important ethnomedicinal family (determined through regression analyses)
N	Keyword	Weighted one to eight according to the keyword with which a plant was associated in the literature search
O	Total score	A total score which sums the values of columns D through N, with a maximum possible score of 52

* A description for each abbreviation is presented Table 4.1

Table 4.3 Tuberculosis keywords and their respective weighting (WT)

Keyword	Brief contextual description of keyword	WT
(i)hubuhubu	Lung	6
(i)phaphu	Lung	6
(i)Xhwala	Lung disease in cattle. Internal ailment	4
(isi)Bele	Pneumonia, with abscess of the lungs	6
(isi)Fuba	Chest/Lung complaint	6
(isi)Khohlela	Expectoration. Phlegm in the throat	6
(isi)khwehlela	Cough	6
Addison's disease	Hypoadrenocorticism. A hormone deficiency caused by damage to the outer layer of the adrenal gland.	1
Alveolitis	Inflammation of the alveoli in the lungs	6
Antimycobacterial	Combating *Mycobacterium*	8
Bacillus tuberculosis	*M. tuberculosis*	8
Bronchitic	Suffering from bronchitis	5
Bronchitis	Inflammation of the membranes lining the bronchial tubes	5
Catarrh	Inflammation of the nose and throat with increased production of mucus	2
Chest ailment (s)	Any ailment in the chest	4
Chest complaint (s)	Any complaint related to the chest	4
Chest pain (s)	Any pain in the chest	4
Consumption	Involving the lungs, with progressive wasting of the body	4
Cough (ing)	To cough	3
Cough remedy	Any remedy for a cough	1
Expectorant	A medicine prompting expectoration	1
Expectoration	The act of spitting or coughing up phlegm	4
Haemoptysis	Coughing up blood from the respiratory tract	6
Koch's bacillus	*M. tuberculosis*	8
Lung (s)	Respiratory organ	4
Lung disease (s)	Disease infecting the lungs	5
MDR tuberculosis	Multi-drug resistant tuberculosis	8
Miliary tuberculosis	Acute tuberculosis characterised by the appearance of tiny tubercles on one or more organs	8
Mycobacterium aurum	Non-tuberculous relative of *M. tuberculosis* (eMedicine.com, 2005)	7
Mycobacterium avium	Usually non-tuberculous but can be life-threatening in people with compromised immune systems (AIDSMEDS.COM, 2005a)	7
Mycobacterium bovis	Usually infects cattle but an unknown proportion of human infections are reported (Cosivi *et al.*, 1998)	7
Mycobacterium kansasii	Usually non-tuberculous but can be life-threatening in people with compromised immune systems (AIDSMEDS.COM, 2005b)	7
Mycobacterium tuberculosis	The primary bacterium causing tuberculosis in humans	8
Phlegm	Saliva mixed with discharges from the respiratory passages	4
Pleurisy	Inflammation of the pleura of the lungs	5
Pthisis	Historical term for tuberculosis	8
Pulmonary abscess (es)	A lung abscess - a confined area of suppuration within the lung parenchyma	4
Pulmonary cavity	The portion of the thoracic cavity lying on either side of the mediastinum and occupied by the lung	4
Respiratory condition (s)	Any condition affecting the respiratory tract	5
Respiratory distress	Pain or suffering associated with the respiratory tract	5
Scrofula	A form of tuberculosis characterised by swelling of the lymphatic glands	8
Sputum	See phlegm	4
TB	Tuberculosis	8
Tubercle	A swelling characteristic of the lesions caused by tuberculosis	7
Tubercle bacillus	Bacillus causing tubercles	7
Tuberculin	A sterile liquid containing a purified derivative of the *M. tuberculosis*. Used for diagnosis	6
Tuberculocidal	Able to kill *M. tuberculosis*	8

Table 4.3 (continued)

Keyword	Brief contextual description of keyword	WT
Tuberculocidin	A substance contained in tuberculin	6
Tuberculoid	Has the appearance of tuberculosis	7
Tuberculose	Having tubercles	7
Tuberculosed	Affected with tuberculosis	8
Tuberculosis	Lung disease caused by *M. tuberculosis*	8
Tuberculous	Afflicted with or caused by tuberculosis	8
Weight loss	Loss of body mass	1

Table 4.4 Diabetes keywords and their respective weighting (WT)

Keyword	Brief contextual description of keyword	WT
(i)dayabhithizi	Diabetes	8
(ne)dayabhithizi	Diabetic	8
(u)shukela	Sugar	2
(uk)oma/-omile	Thirst for liquid	4
(uku)khuluphala	Obesity	4
Acidosis	Too much acid in the body. For a person with diabetes, this can lead to diabetic ketoacidosis.	4
Antidiuretic (hormone)	Hormone that stops the formation of urine	4
Blood sugar	Blood glucose	5
Coma	Unarousable unconsciousness. Can occur if suffering from diabetes	4
Diabetes	Diabetes	8
Diabetes insipidus	Rare form of diabetes resulting from vasopressin deficiency. Characterised by excretion of large amounts of pale, diluted urine which results in dehydration and extreme thirst.	6
Diabetes mellitus	Caused by a relative deficiency of insulin and the resulting defect in transfer of glucose from the blood into cells. Results in abnormally high blood sugar and polyuria.	8
Diabetic	Having diabetes	8
Diabetogenic	Causing diabetes	6
Diabetogenous	Caused by diabetes	6
Diuretic	Any substance that tends to increase the flow of urine	5
Glucose in blood/urine	Excessive glucose in the blood or urine	5
Glucose intolerance	Unable to metabolise glucose normally	6
Glycosuria	The presence of abnormally high levels of sugar in the urine	6
Hemochromatosis	A defect in iron metabolism with a build up of iron in the body	4
Hyperglycaemia	Abnormally high blood sugar usually associated with diabetes	7
Hyperinsulinemia	An endocrine disorder characterised by a failure of the blood sugar control system (bscs)	7
Hypoglycaemia	Blood sugar levels are too low	7
Inosituria	Inositol in the urine	4
Insulin	Hormone secreted by the isles of Langerhans in the pancreas. Regulates storage of glycogen in the liver and accelerates oxidation of sugar in cells	7
Ketoacidosis	Acidosis with an accumulation of ketone bodies	5
Ketosis	Abnormal increase of ketone bodies in the blood - usually during severe diabetes mellitus	5
Metabolic disorder	Any disorder in the metabolic process	2
Metabolism	The sum of all chemical changes that take place in a cell or organism. Production of energy for life processes	1
Obesity	Abnormal body weight - greater than normal.	4
Phosphaturia	Excessive discharge of phosphates in the urine	3
Polydipsia	Excessive thirst - often associated with diabetes	5
Polyuria	Excessive urination	4
Retinopathy	Disease of the small blood vessels in the retina that may cause deterioration of eyesight.	2

Table 4.4 (continued)

Keyword	Brief contextual description of keyword	WT
shobingo/thunda/chama	Urinate	1
Sugar	Sucrose	2
Sugar (in) tolerance	Unable to metabolise glucose normally	7
Sugar dependent (ence)	Reliant on sugar	3
Thirst	Needing to drink	4
Urine	Liquid excretory product	1

Table 4.5 Immune modulatory keywords and their respective weighting (WT)

Keyword	Brief contextual description of keyword	WT
(i)bilo/(im)bilapho	Swelling of glands	5
(i)dlala	Tonsil	2
(i)Dosi	Bee sting	1
(i)thabatha	Invigorating medicine	8
(isi)boko	Soft glandular swelling	5
(isi)fo samadlala	Tonsillitis	3
(isi)hlambezo	Plant infusion sipped by pregnant woman to assist confinement (of pregnancy)	5
-batshwa	itching/burning sensation	5
-cabuza	Itch	5
-nwayiza	Itch	5
Adenitis	Inflammation of a gland or lymph node	5
Angiitis	Inflammation of blood vessel or lymph duct	5
Antibody (ies)	Any of a large variety of immunoglobulins normally present in the body - produced in response to an antigen which it neutralises, thus producing an immune response.	6
Antigen (ic)	Any substance able to provoke an immune response in the body	6
Antitoxin (s)	An antibody which can neutralise a specific toxin	6
Fight infection	Immune response	6
Gland	Lymph gland	5
Immune	Able to resist infectious disease	7
Immune boost (er)	Substance that aids the immune system	8
Immune response	Activities of the immune system against foreign substances	6
Immune system	Network of cells and organs that work to defend the body against attack by 'foreign' objects	6
Immunity	Being resistant to a disease	7
Immunocompromised	A weak immune system	6
Immunodeficiency	Decreased ability of the body to fight infection/disease	6
Immunodiffusion	Technique for analysing antigen and antibody mixtures by watching them as they diffuse toward each other	4
Immunodominance	The part of the antigenic determinant most likely to bind with an antibody.	6
Immunogen	Any substance that provokes an immune response	6
Immunogenetic (s)	A field of genetics that uses a combination of genetic and immunological analyses to study antibody formation and immune response	4
Immunogenic	Any substance that provokes an immune response	6
Immunoglobulin	A protein that acts as an antibody	6
Immunologic	Relating to immunology	4
Immunomodulatory	Controls or influences the immune system	8
Immunopotentiator	Any drug or chemical which increases the body's immune response to an antigen	8
Immunoreaction	Reaction between antigen and antibody	4
Immunosenescence	Aging of the immune system	5
Immunosuppressant	An anti-rejection drug used to prevent the body from rejecting a transplanted organ	8

Table 4.5 (continued)

Keyword	Brief contextual description of keyword	WT
Immunosuppression	See immunosuppressant	8
Immunosuppressive	See immunosuppressant	8
Immunotherapy	A medical technique for stimulating a patient's immune system to attack and destroy disease causing substances/bodies	7
Immunotoxin	An antibody linked to a toxic substance	6
Infection	Invasion of the body by microorganisms that cause disease.	6
Inflammation	Swelling due to immune response	6
Intelezi	Protective charm	5
Itch	Irritation to the cutaneous tissues producing a desire to scratch	5
Joint flexibility	Ability of the joint to move	3
Lymph duct	Tube which channels lymph fluid	3
Lymph fluid	Plasma-like fluid containing lymphocytes	3
Lymph glands/nodes	Cluster of glandular tissue which supplies lymphocytes to the blood stream	3
Lymphatic system	Tissues and organs that produce or store lymphocytes	3
Lymphocyte	Infection fighting, agranulocytic leukocyte	3
Malady	Any disease or impairment of normal physiological function	1
Malaise	Illness or discomfort	1
Mental health	Relating to the well-being of the mind.	1
Node	Lymph gland	2
Pinkeye	Inflammation of the conjunctiva of the eye	2
Quinsy	Painful pus-filled inflammation of the tonsils and surrounding tissues	2
Rash	A red inflammation of the skin	2
Rejection	Immunological response that refuses to accept a substance that is recognised as foreign.	5
Resistant (ance)	Unhealthy, weak state	1
Rubor/Red	Colour of skin on inflammation	1
Sterols/sterolins	Natural steroid alcohols. Some are reportedly beneficial to the immune system	3
Stimulant	Substance such as a drug that quickens certain vital actions in an organism	5
Sting/Bite	Any sting or bite resulting in an immune response	3
Swelling	Becoming puffy due to immune response	3
Tonic	Medicine that strengthens and invigorates	7
Tonsil	Either of two masses of lymphatic tissue on each side of the oral pharynx	2
Tonsillitis	Inflammation of the tonsil	3
Vitality	Healthy and energetic	5
Weakness	Unhealthy, weak state	5
Well-being	A healthy state	3
Wellness	A healthy state	3
White blood cells	Infection fighting, agranulocytic leukocyte	6

4.2.1.2 Taxon names (Column B)

Data were captured from both generalist and specialist sources including books, monographs, journals and theses (Smith, 1895; Gerstner, 1938a; Gerstner, 1938b; Gerstner, 1939b; Gerstner, 1939a; Gerstner, 1941b; Gerstner, 1941a; Hulme, 1954; Williamson, 1955; Watt and Breyer-Brandwijk, 1962; Batten and Bokelman, 1966;

Bryant, 1966; Le Roux, 1971; Malan and Owen-Smith, 1974; Kokwaro, 1976; Lindsay and Hepper, 1978; Broster and Bourn, 1982; Taylor, 1983; Duke, 1985; Gelfand *et al.*, 1985; Johnson and Sokutu, 1985; Rodin, 1985; Ellis, 1989; Hedberg and Staugard, 1989; Mabogo, 1990; Chin, 1992; Van den Eynden *et al.*, 1992; Archer, 1994; Hutchings *et al.*, 1996; ITDG and IIRR, 1996; Neuwinger, 1996; Felhaber, 1997; Maliehe, 1997; Van Wyk *et al.*, 1997; Neuwinger, 2000; Van Wyk and Gericke, 2000; Van Wyk *et al.*, 2002; Giess and Snyman). Taxa were entered into the database as presented in source literature. However, with several taxonomic revisions having been undertaken since the publication of many of the works, Germishuizen and Meyer (2003) was consulted to obtain recent synonyms (including genus, species, subspecies and authority). Current taxon names were added to the database in a separate field, and thereafter used in all analyses.

4.2.1.3 Family (Column C)

Plant family as presented in the source literature was entered into the database, and an additional field was added for recording updated family names, as recognised by Germishuizen and Meyer (2003).

4.2.1.4 Indigenous status of taxa (Column D)

The indigenous status of each taxon was assessed for the *FSA* region (SANBI, 2005) and weighted.

4.2.1.5 Endemic status of taxa (Column E)

Endemism was determined from a checklist of endemic South African plants (Germishuizen *et al.*, 2006) and weighted (Table 4.2).

4.2.1.6 Ethnomedicinal status of taxa in the *FSA* region (Column F)

The ethnomedicinal status of was assessed (Arnold *et al.*, 2002) and weighted (Table 4.2).

4.2.1.7 Explicit use of taxa for disease treatment (Column G)

Taxa documented in the source literature as having been used explicitly for treatment of any of documented diseases were weighted (Table 4.2). Weightings applied to this criterion (15 if explicitly used) were notably high due to the assumption that explicit use indicates high efficacy. Note that this weighting would have been applied to any instances of explicit use, regardless of the keyword used (Section 4.2.1.1) to identify the taxon under consideration.

4.2.1.8 Documented positive or negative associations (Column H)

Taxa documented as being either positively or negatively associated with disease treatment as opposed to being used explicitly were weighted (Table 4.2). Associations included symptomatic relief, supportive therapy and/or bioassay findings. Historical negative associations were included on the grounds that current advanced screening techniques could show positive results. Furthermore, factors such as chemotypes, environmental parameters, harvesting and storage conditions could have influenced historical activity findings (Clarkson *et al.*, 2004). Note that this weighting would have been applied to any instances of associated use, regardless of the keyword used to

identify the taxon under consideration. This effectively created a 'double' weighting system as individual keywords were also weighted (Section 4.2.1.1)

4.2.1.9 Toxicity of recorded taxa (Column I)

Toxicity (Steyn, 1934; Shone and Drummond, 1965; Neuwinger, 1996; Arnold *et al.*, 2002; Van Wyk *et al.*, 2002) was deemed a desirable characteristic due to the medicinal nature of many toxic plants (Watt and Breyer-Brandwijk, 1962; Bruneton, 1999; Arnold *et al.*, 2002). Relative dosage usually determines the extent of therapeutic or toxic effects.

4.2.1.10 Red Data Listed taxa in the *FSA* region (Column J)

Recorded taxa that were listed in the Southern African Plant Red Data Lists Database for the *FSA* region (SABONET, 2003) were weighted (Table 4.2). This database is a compilation of several other published works (Melville, 1970; Lucas and Synge, 1978; Hall *et al.*, 1980; Hall and Ashton, 1983; Hall and Veldhuis, 1985; Hilton-Taylor, 1996a; Hilton-Taylor, 1996b; Hilton-Taylor, 1997; Walter and Gillett, 1998; Scott-Shaw, 1999; Hilton-Taylor, 2000; Golding, 2002).

4.2.1.11 Plant taxa traded in regional markets (Column K)

An index of popularity was used to weight each taxon (Table 4.2) according to the number of regional ethnomedicinal markets (Cunningham, 1988; Mander, 1997; Mander, 1998; Marshall, 1998; Botha *et al.*, 2001; Dold and Cocks, 2002; Williams, 2003) where plants are known to be traded (0.5 points for each market where traded). This weighting may seemingly introduce a bias against rare species and endemics, some Red Data

Listed taxa (e.g. *Warburgia salutaris* (Bertol.f.) Chiov) are widely traded. Plants may occur repeatedly in trade because they are widespread and common, but may have low efficacy. Arguably, the other weighting categories counter this bias. The decision to allocate additional weighting to traded taxa was justified by the assumption that widely traded taxa are in high demand due to greater efficacy.

The seven trade reports accessed reported on trade in nine different regions. These included the countries of Swaziland, Namibia, Botswana, and Lesotho (Marshall, 1998), as well as some South African provinces, including the Eastern Cape (Dold and Cocks, 2002), Limpopo (Botha *et al.*, 2001), Mpumalanga (Mander, 1997), KwaZulu-Natal (Cunningham, 1988; Mander, 1998) and Gauteng (Faraday Market)(Williams, 2003). Trade reports which covered the same regions (Cunningham, 1988; Mander, 1998) would likely have enhanced the sampling from these regions. For the purposes of the analyses, updated synonyms (Germishuizen and Meyer, 2003) of traded taxa were grouped by region traded to eliminate duplication.

4.2.1.12 Taxa in families with biological activity of interest (Column L)

Taxa containing compounds reportedly efficacious against the relevant disease states (Labadie *et al.*, 1989; Wong *et al.*, 1994; Oubré *et al.*, 1997; Van Wyk *et al.*, 1997; Gori and Campbell, 1998; Lall and Meyer, 1999; Newton *et al.*, 2000; Bouic, 2001; Cantrell *et al.*, 2001; Heinrich *et al.*, 2004; DNP, 2005) allowed for lists of priority compound classes in the relevant families to be compiled. The number of efficacious compound classes known to occur in specific plant families was considered a possible means to weight taxa due to the assumption that similar chemical constituents and/or biological activities are observed in taxonomically-related plants (Grayer *et al.*, 1999). Taxa were weighted according to the importance ascribed to their respective families (Table 4.2).

4.2.1.13 Taxa in 'hot' ethnomedicinal families (Column M)

Taxa were weighted by family (Table 4.2) according to the results of the least-squares regression analyses (Figure 2.1). These analyses incorporated a mathematical model for predicting the association between plant-orders containing medicinal taxa and the total number of taxa in those orders (in the *FSA* region) for each disease state. Plant orders and families favoured by ethnomedicinal practitioners were identified as positive outliers in the regression analysis (Figure 2.1). Both indigenous and naturalised plants were scored.

4.2.1.14 Total score (Column O)

A total score that summed the values of columns D through M, with a maximum score of 52, was presented in this column. These totals were used to rank taxa, in order to prioritise collection and screening efforts.

4.2.1.15 Rank Number (Column A)

A rank number was allocated to each taxon after total scores had been calculated and the entire list of taxa ranked in descending order of total score. Alphabetical order of family, genus and species was applied as a secondary ranking. The values in this column formed the basis of preference for selecting taxa to be screened.

4.2.2 Candidates allied to high ranking plants (Set 3)

Plant families from the top 100 taxa in each prioritised list in Set 1 (Section 4.2.1) were short-listed, followed by the identification of high ranking genera in each (Set 2)(Figure

4.2). Indigenous species not previously recorded as ethnomedicinal but of these genera were then randomly identified by means of the Microsoft Excel random number generator (Set 3). Where these ethnomedicinal allies exceeded three in number, such relatives were randomly selected, again by means of the Microsoft Excel random number generator. No more than five species (allies of Set 1) were selected for any genus from Set 2. Although the taxa in Set 3 fall outside the current medicinal plant knowledge-base systems, they may show good bioactivity due to a likelihood of sharing secondary metabolites.

4.2.3 Endemic taxa from the Western Cape subregion (Set 5)

This phase targeted plant taxa endemic to the Western Cape subregion. A preliminary list of South African endemic plants (Germishuizen *et al.*, 2006) was matched against a list of taxa known to occur in the Western Cape region (SANBI, 2005). The result was a list of endemic Western Cape taxa. Plant families from the top 100 taxa in each prioritised list in Set 1 (Section 4.2.1) were short-listed (Set 4). Endemic Western Cape taxa in these select families were then randomly short-listed using the Microsoft Excel random number generator to obtain a quota for each disease state (Set 5). The short-lists contained not more than 25% of the total taxa already selected in Set 1.

4.2.4 Candidate taxa related to efficacious exotics (Set 7)

Exotic candidates potentially useful in the treatment of the listed ailments were identified in current scientific literature for tuberculosis (Lall and Meyer, 1999; Newton *et al.*, 2000; Cantrell *et al.*, 2001), diabetes (Oubré *et al.*, 1997; Gori and Campbell, 1998) and immune modulation (Labadie *et al.*, 1989; Wong *et al.*, 1994; Bouic, 2001)(Set 6). A

quota of indigenous taxa, closely allied to those in Set 6 was short-listed (Set 7). The relationship was defined on the basis of taxa being classified within the same genus.

4.2.5 Selection of randomly identified control taxa

A quota of randomly identified control plants which numbered the same as plants to be screened was compiled. The inclusion of control plants was considered necessary if future evaluations of the plant selection procedures are to be statistically sound. Such evaluations will allow for assessment of the validity of current selection methods, and thus the streamlining of future plant selection approaches.

4.2.6 Proposed statistical evaluation of plant selection methods

Statistical analyses of the plant selection methods were not undertaken due to the lack of initial bioassay results. Such results are only expected in December 2006. The analyses may determine if the ethnodirected bioprospecting approach is indeed more efficient than a random approach within the southern African context. The proposed statistical assessment is outlined below.

4.2.6.1 Normalise the distribution of initial screening results

Initial screening results (e.g. IC_{50} values) can be used to assess the effectiveness of selection criteria. Ineffective criteria should be removed prior to further analyses (Zar, 1999; Jaisingh, 2000; SYSTAT, 2002).

All criteria should be considered independent variables, and the weighting of each reduced to a binary value, e.g. where a taxon received a weighting of two due to

ethnomedicinal status, the value is changed to one. Where not weighted, it will remain zero. Probability plots of screening results versus each of the (now-binary) selection criteria should be prepared and the one-sample Kolmogarov Smirnov statistical test applied to assess the distribution of the screening results (the Lilliefors test option is incorporated to obtain a standard normal distribution). If found to be not normal, a Log_{10} transformation should be applied, and the one-sample Kolmogarov Smirnov test performed again to confirm the normality of data. A two sample t-test should be applied to compare each (now-binary) selection criterion with the normalised (log_{10}) screening results. If the test indicates no significant difference, then the criterion in question has not significantly contributed to the prioritisation of taxa, and should not be included in further analyses.

4.2.6.2 Correlate IC_{50} and total score

A Pearson correlation should be applied using total score and IC_{50} as variables. This test produces a matrix of Pearson product-moment correlation coefficients. Pearson correlations vary between -1 and +1 (SYSTAT, 2002). A perfectly positive linear relationship between the variables will result in a sample correlation coefficient (r) of +1, while a perfectly negative linear relationship will produce an r-value of −1. A value of 0 indicates that neither of two variables can be predicted from the other by using a linear equation (Jaisingh, 2000). If a strong positive relationship is present between total score and the IC_{50} value (obtained in the bioassay), the resulting sample correlation coefficient will be close to +1.

4.2.6.3 Evaluate focused and random plant selection

To evaluate the differences in the means of IC_{50} values between taxa collected through focused selection and those collected through random selection, a t-test should be applied. If the data to be tested are normally distributed (Kolmogarov Smirnov test) then a t-test is applied. The p-level reported represents the probability of error involved in accepting the hypothesis that a difference exists between the two sampling methods. If the data are found to be not-normal, a non-parametric Spearman correlation should be applied (Zar, 1999).

4.3 Results

4.3.1 Ethnodirected plant candidates (Set 1)

The majority of EthmedIMM and EthmedTB taxa were found to be indigenous (>80%)(Table 4.6) as compared with the EthmedDBM taxa where the minority (approx. 43%) were indigenous. Very low proportions of taxa in each disease category were recorded as endemic (Table 4.7). The use of primarily ethnobotanical literature for plant prioritisation (Set 1) yielded high proportions of ethnomedicinal taxa for each disease category (Table 4.8). High proportions of taxa were recorded as explicitly used for all disease categories (Table 4.9). By comparison, the number of positive or negative associations documented was notably few (Table 4.10). Taxa recorded as toxic (Steyn, 1934; Shone and Drummond, 1965; Neuwinger, 1996; Arnold *et al.*, 2002; Van Wyk *et al.*, 2002) ranged from 39.6% (anti-tuberculosis) to 45.3% (immune-modulatory) to 53.8% (anti-diabetes)(Table 4.11). Very low proportions of Red Data Listed taxa were recorded for each disease category (Table 4.12). A marginally greater proportion of EthmedIMM taxa were recorded as traded, followed by EthmedTB and then EthmedDBM taxa (Figure 4.4). Very few taxa were widely traded in all the trade-regions surveyed

(Table 4.13), and overall, the minority of short-listed taxa were recorded as traded (Table 4.14). The Faraday market in the Gauteng region had the greatest proportion of traded taxa (Table 4.15; Figure 4.5; Figure 4.6; Figure 4.7). At least 10% of families (for each disease state) contained three or more efficacious compound classes (Table 4.17).

Taxa short-listed for the three disease states as well as their relative weightings and total scores are presented in Table 4.36 (566 anti-tuberculosis taxa), Table 4.37 (197 anti-diabetes taxa), and Table 4.38 (369 immune modulatory taxa). These taxa were short-listed out of the approximately 24000 taxa available in the region.

Table 4.6 Proportion of indigenous and non-indigenous Set 1 candidates in South Africa

Category	Indigenous	Non-indigenous	Total taxa
EthmedTB	484 (85.5%)	82 (14.5%)	566
EthmedDBM	84 (42.6%)	113 (57.4%)	197
EthmedIMM	301 (81.6%)	68 (18.4%)	369

Table 4.7 Proportion of endemic and non-endemic Set 1 candidates in South Africa

Category	Endemic	Non-endemic	Total taxa
EthmedTB	53 (9.4%)	513 (90.6%)	566
EthmedDBM	15 (7.6%)	182 (92.4%)	197
EthmedIMM	27 (7.3%)	342 (92.7%)	369

Table 4.8 Proportion of reportedly ethnomedicinal and non-ethnomedicinal Set 1 candidates in the *FSA* region

Category	Ethnomedicinal	Non-ethnomedicinal	Total taxa
EthmedTB	428 (75.6%)	138 (24.4%)	566
EthmedDBM	127 (64.5%)	70 (35.5%)	197
EthmedIMM	266 (72.1%)	103 (27.9%)	369

Table 4.9 Proportion of explicitly used Set 1 candidates for each disease category

Category	Explicit used	Not explicitly used	Total taxa
EthmedTB	527 (93.1%)	39 (6.9%)	566
EthmedDBM	135 (68.5%)	62 (31.5%)	197
EthmedIMM	326 (88.3%)	43 (11.7%)	369

Table 4.10 Proportion of Set 1 candidates recorded as either positively or negatively associated for each disease category

Category	Associated	Not associated	Total
EthmedTB	9 (1.6%)	557 (98.4%)	566
EthmedDBM	6 (3.0%)	191 (97.0%)	197
EthmedIMM	5 (1.4%)	364 (98.6%)	369

Table 4.11 Proportion of Set 1 candidates recorded as toxic or not

Category	Toxic	Not recorded as toxic	Total taxa
EthmedTB	224 (39.6%)	342 (60.4%)	566
EthmedDBM	106 (53.8%)	91 (46.2%)	197
EthmedIMM	167 (45.3%)	202 (54.7%)	369

Table 4.12 The proportion of Red Data Listed and non-Red Data Listed Set 1 candidates recorded in the *FSA* flora

Category	Red Data Listed	Non-Red Data Listed	Total
EthmedTB	56 (9.9%)	510 (90.1%)	566
EthmedDBM	15 (7.6%)	182 (92.4%)	197
EthmedIMM	37 (10.0%)	332 (90.0%)	369

Table 4.13 The popularity in trade of Set 1 candidates for each disease state

Category	Traditional markets where plants are traded*									
	0	1	2	3	4	5	6	7	8	Total
EthmedTB	345	104	57	32	17	5	4	1	1	566
EthmedDBM	132	29	21	6	8	0	1	0	0	197
EthmedIMM	213	62	44	31	14	2	1	1	1	369

* Nine market surveys were reviewed but the highest score any plant achieved was eight

Table 4.14 Proportion of Set 1 candidates recorded as traded for each disease category

Category	Total traded taxa	Total taxa
EthmedTB	225 (39.8%)	566
EthmedDBM	65 (33.0%)	197
EthmedIMM	157 (42.5%)	369

Table 4.15 Frequency of taxa traded in the nine markets reviewed

Regional market	EthmedTB	EthmedDBM	EthmedIMM
Namibia	3	2	4
Swaziland	3	0	2
Lesotho	9	2	5
Botswana	14	5	8
Eastern Cape	25	5	14
Limpopo	33	7	22
Mpumalanga	77	26	63
KwaZulu-Natal	116	33	87
Gauteng (Faraday)	150	37	109

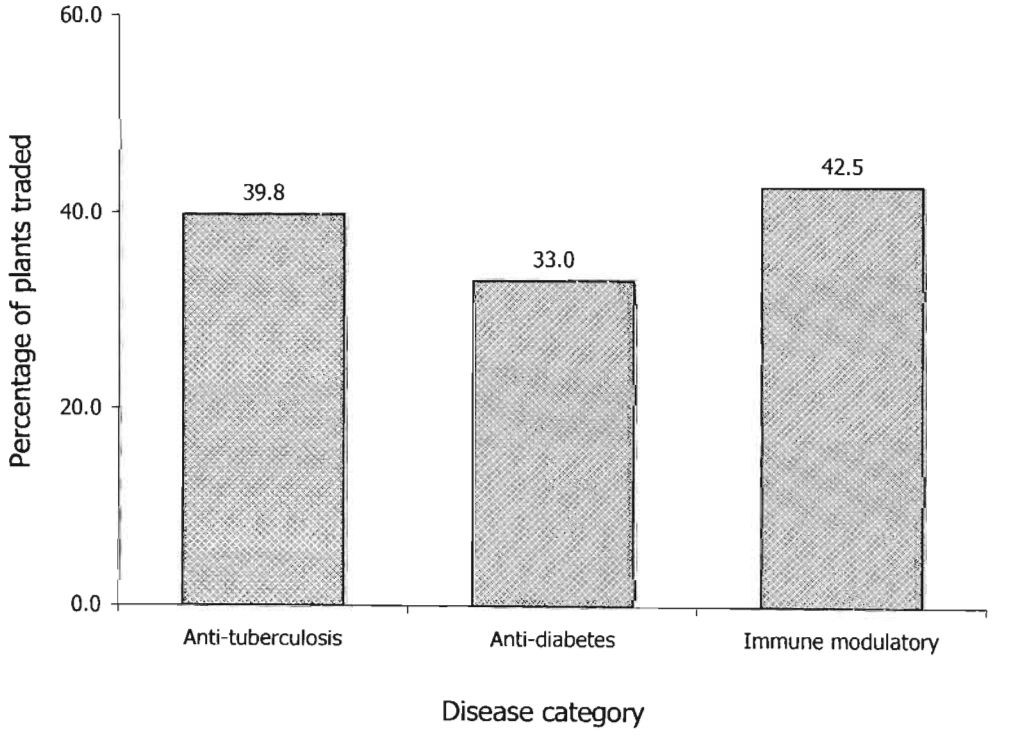

Figure 4.4 Proportion of Set 1 taxa traded, by disease state

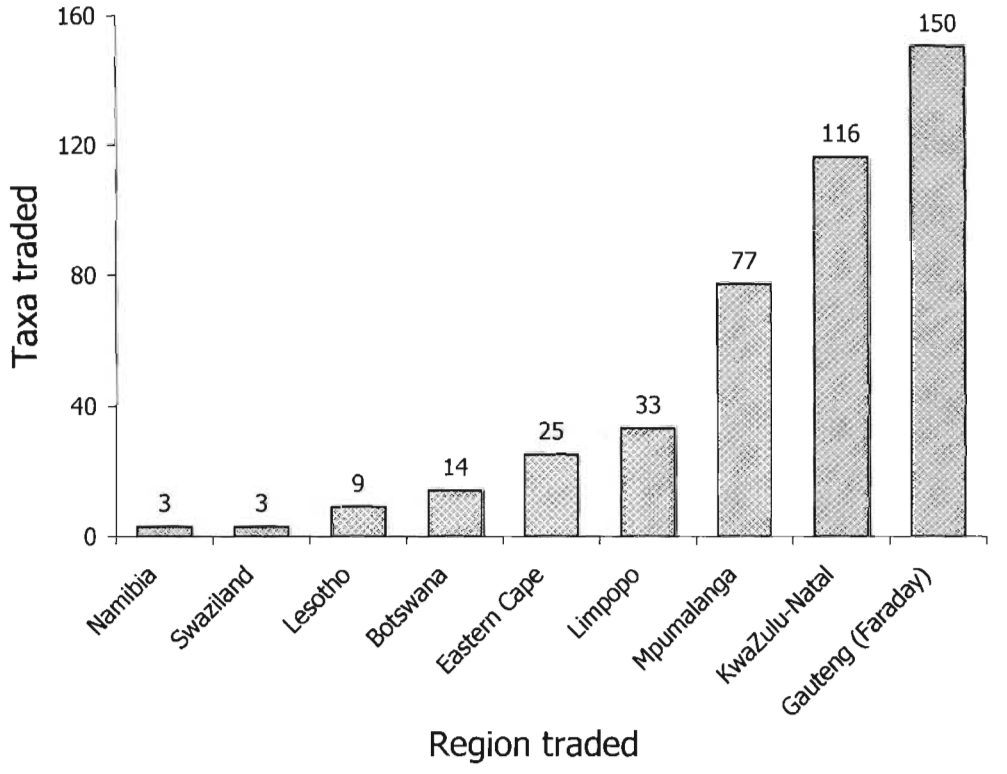

Figure 4.5 Anti-tuberculosis taxa traded in regional markets

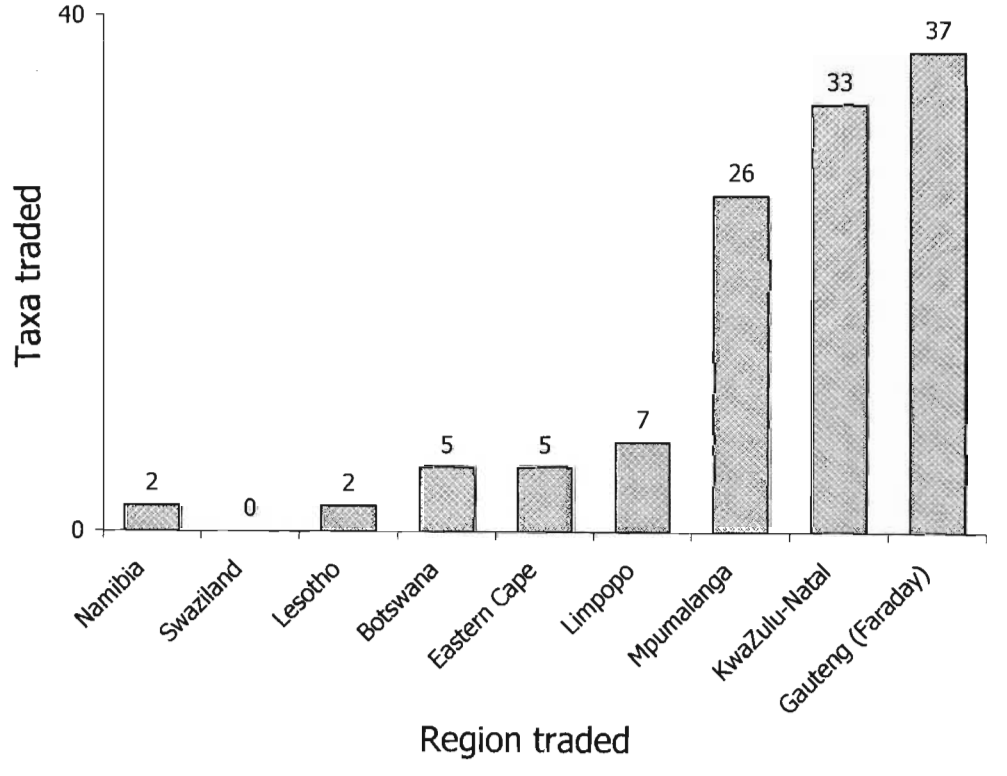

Figure 4.6 Anti-diabetes taxa traded in regional markets

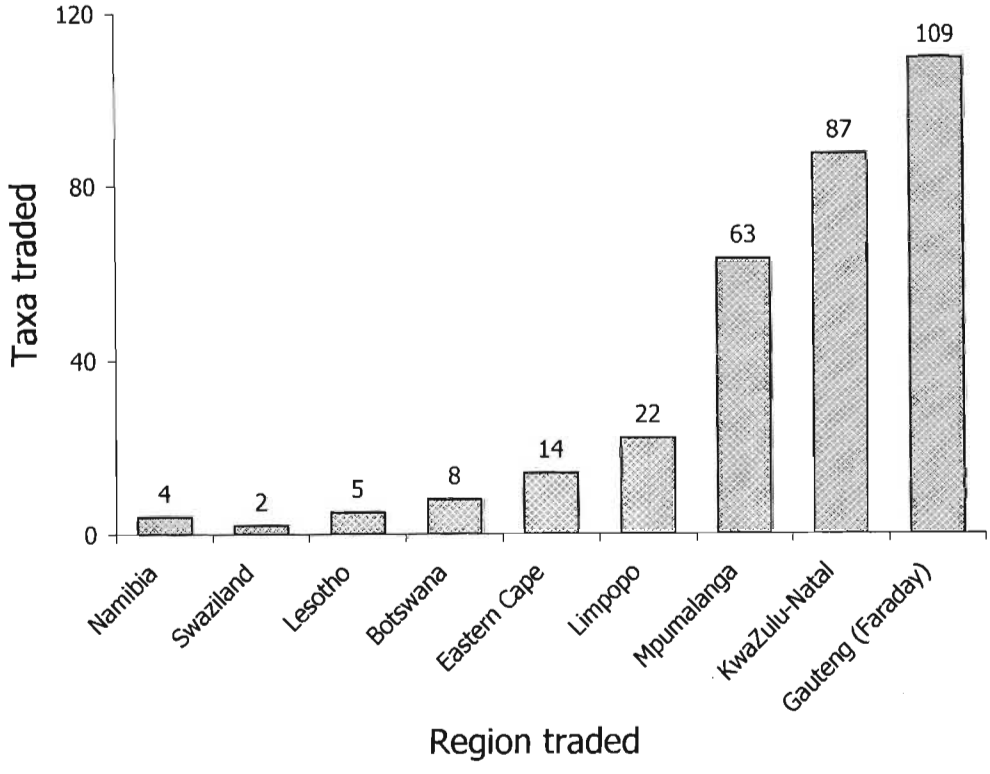

Figure 4.7 Immune modulatory taxa traded in regional markets

Table 4.16 Compound classes identified as containing efficacious compounds

Category	Compound classes
EthmedTB	Diterpenoids; monoterpenoids; flavonoids; alkaloids; sesquiterpenoids
EthmedDBM	Alkaloids; diterpenoids; sesquiterpenoids; triterpenoids
EthmedIMM	Diterpenoids; triterpenoids; alkaloids; sesquiterpenoids; cardiac glycosides

Table 4.17 Proportion of recorded efficacious compound classes in Set 1 taxa

	Efficacious compound classes				
Category	0 classes	1 class	2 classes	3 or more classes	Total taxa
EthmedTB	360 (63.6%)	80 (14.1%)	5 (0.9%)	121 (21%)	566
EthmedDBM	125 (63.5%)	50 (25.4%)	2 (1.0)	20 (10.2%)	197
EthmedIMM	202 (54.7%)	64 (17.3%)	50 (13.6%)	53 (14.4%)	369

Table 4.18 Anti-tuberculosis plant families in relation to the number of reportedly efficacious compound classes

Efficacious compound classes	Families
1 class	Apiaceae, Apocynaceae, Araceae, Bombacaceae, Canellaceae, Geraniaceae, Lauraceae, Meliaceae, Pteridaceae, Rosaceae, Rubiaceae, Rutaceae, Sapindaceae, Scrophulariaceae, Valerianaceae
2 classes	Myrtaceae
3 or more classes	Asteraceae, Euphorbiaceae, Lamiaceae, Verbenaceae

Table 4.19 Anti-diabetes plant families in relation to the number of reportedly efficacious compound classes

Efficacious compound classes	Families
1 class	Apocynaceae, Asteraceae, Apiaceae, Asclepiadaceae, Combretaceae, Cactaceae, Scrophulariaceae, Hyacinthaceae, Dioscoreaceae, Caprifoliaceae, Ranunculaceae
2 classes	Valerianaceae, Oleaceae
3 classes	Araliaceae, Fabaceae

Table 4.20 Immune modulatory plant families in relation to the number of reportedly efficacious compound classes

Efficacious compound classes	Families
1 class	Amaryllidaceae, Anacardiaceae, Apocynaceae, Araliaceae, Caryophyllaceae, Celastraceae, Cucurbitaceae, Lauraceae, Malvaceae, Rhamnaceae, Solanaceae, Strychnaceae, Verbenaceae
2 classes	Apiaceae, Araceae, Fabaceae, Oleaceae, Pedaliaceae
3 classes	Asteraceae, Lamiaceae

4.3.1.1 Taxa in ethnomedicinally 'hot' families

Results of the regression analyses for ethnomedicinal *FSA* taxa grouped by plant order and family are presented separately below.

4.3.1.1.1 Regression analyses for anti-tuberculosis taxa

The model obtained from the regression analysis of plant orders was able to account for 51% ($\rho^2 = 0.51$) of the variation in the y-values (Table 4.21).

Table 4.21 Statistics from a least squares regression analyses of EthmedTB orders and families.

	Coefficient	Constant	ρ	ρ^2	Std. error	Pop. size
Orders	0.023	9.43	0.71	0.51	23.71	38
Families	0.019	1.28	0.76	0.58	6.95	104

Residual values obtained for EthmedTB taxa grouped by plant order ranged from -47.37 to 75.35. The population variance for order residuals was calculated at 23.08. This value

was employed as a cut-off to distinguish outlying orders. Eight orders (four with positive and four with negative residuals) out of a total of 38 orders analysed were outliers. Taxa in these outlying orders are considered to be either far more or far less frequently selected for in use against tuberculosis than taxa from other orders. The magnitude of the outlying residual values (Table 4.22) falsified the null hypothesis.

Table 4.22 Set 1 orders used significantly greater or less than predicted against EthmedTB conditions

Order	Total *FSA* taxa	Predicted EthmedTB taxa	Actual EthmedTB taxa	Residual value*
Fabales	2636	70.7	146	+75.3
Lamiales	2529	68.2	115	+46.8
Malpighiales	904	30.4	69	+38.6
Sapindales	654	24.6	58	+33.4
Ericales	1174	36.7	10	-26.7
Asparagales	3959	101.4	59	-42.4
Poales	2244	61.5	18	-43.5
Caryophyllales	2839	75.4	28	-47.4

* Residual values above (+) or below (-) the population variance

EthmedTB taxa (grouped by order) were plotted against total *FSA* taxa (grouped by order). The magnitude of the outliers, particularly the Fabales are evident, as is the strength of the positive linear relationship ($\rho = 0.71$)(Figure 4.8).

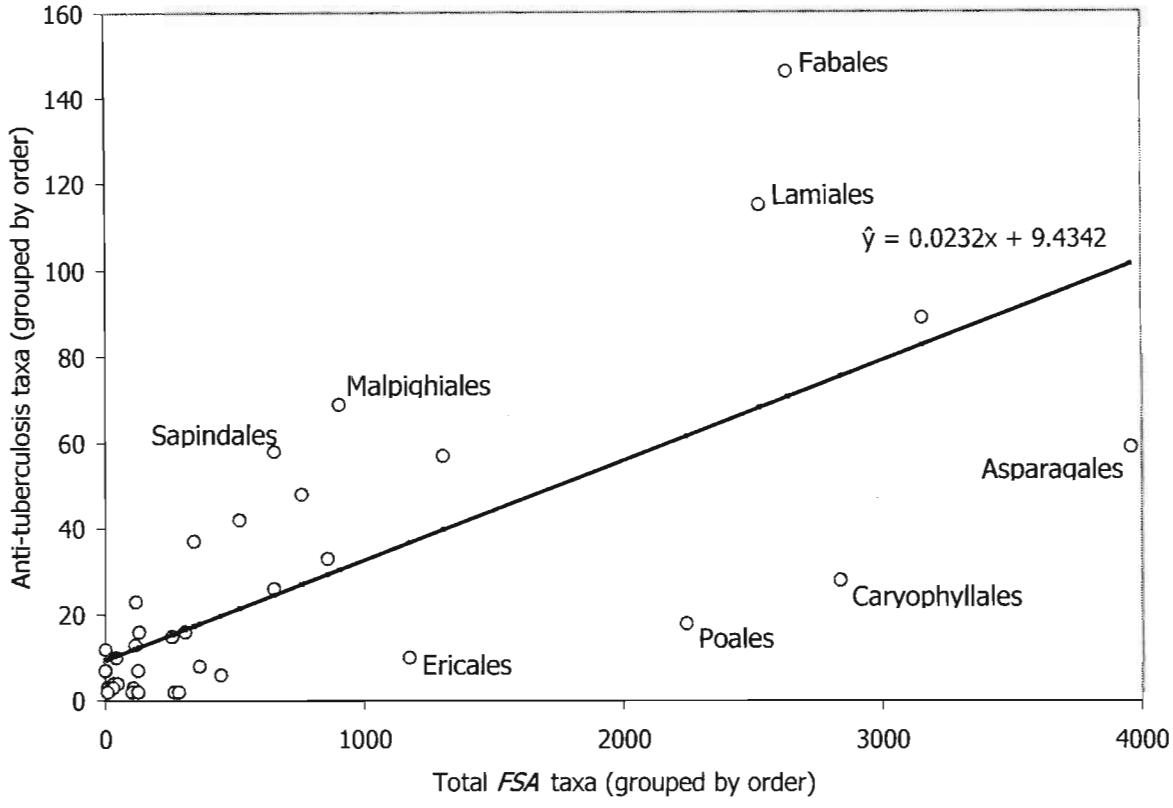

Figure 4.8 Regression plot of EthmedTB taxa grouped by order versus total taxa grouped by order.

Regression data for families which constitute the outlying orders were extracted and ranked by order, family, and residual value. The residual values dictated the extent to which the predicted number of EthmedTB taxa varied from the actual number of taxa in each family (Table 4.23).

Table 4.23 EthmedTB families contributing to the positive outlier status of their respective orders.

Order	Family	EthmedTB taxa	*FSA* taxa	Predicted *FSA* taxa	Residual value *
Fabales	Fabaceae	82	2422	47.3	+34.7
Fabales	Polygalaceae	5	214	5.4	-0.4
Lamiales	Lamiaceae	27	537	11.5	+15.5
Lamiales	Verbenaceae	9	81	2.8	+6.2
Lamiales	Bignoniaceae	4	88	3.0	+1.1
Lamiales	Pedaliaceae	2	42	2.1	-0.1
Lamiales	Plantaginaceae	1	17	1.6	-0.6
Lamiales	Acanthaceae	7	435	9.5	-2.5
Lamiales	Scrophulariaceae	7	1007	20.4	-13.4
Malpighiales	Euphorbiaceae	31	580	12.3	+18.7
Malpighiales	Passifloraceae	3	37	2.0	+1.0
Malpighiales	Salicaceae	4	93	3.1	+1.0
Malpighiales	Ochnaceae	2	15	1.6	+0.4
Malpighiales	Clusiaceae	1	6	1.4	-0.4
Malpighiales	Violaceae	1	22	1.7	-0.7
Malpighiales	Papaveraceae	1	28	1.8	-0.8
Malpighiales	Hypericaceae	1	30	1.9	-0.9
Sapindales	Anacardiaceae	12	157	4.3	+7.7
Sapindales	Sapindaceae	9	45	2.1	+6.9
Sapindales	Meliaceae	3	30	1.9	+1.2
Sapindales	Rutaceae	8	350	7.9	+0.1
Sapindales	Simaroubaceae	1	2	1.3	-0.3

* Residual values above (+) or below (-) the population variance

Upon completion of the above analyses, outlying orders and families were removed from the datasets and a secondary regression analysis performed (Table 4.24). As expected, an even stronger linear relationship was obtained (ρ =0.89) between EthmedTB taxa grouped by order and total *FSA* taxa in those orders. Unexpectedly, the linear

relationship for EthmedTB taxa grouped by family and the total taxa in those families was weaker than before ($\rho = 0.59$).

Table 4.24 Statistics from a secondary regression analysis of EthmedTB orders and families.

	Coefficient	Constant	ρ	ρ^2	Std. error	Pop. size
Orders	0.030	6.00	0.89	0.78	9.68	30
Families	0.009	1.90	0.59	0.34	2.01	88

The population variance for order residuals in the secondary regression analysis was calculated at 9.35. This value was employed as a cut-off which resulted in nine new orders (Table 4.25) being identified as outliers (five positive and four negative). The positive outlying orders identified are considered to be highly selected for by ethnomedicinal practitioners.

Table 4.25 Set 1 orders used significantly greater or less than predicted against EthmedTB conditions as obtained from a secondary of regression analyses

Order	Total *FSA* taxa	Actual EthmedTB taxa	Predicted EthmedTB taxa	Residual value*
Apiales	343.0	37	16.2	+20.8
Solanales	519.0	42	21.4	+20.6
Malvales	759.0	48	28.5	+19.5
Celastrales	119.0	23	9.5	+13.5
Gentianales	1304.0	57	44.7	+12.3
Asterales	3154.0	89	99.7	-10.7
Oxalidales	265.0	2	13.9	-11.9
Arecales	284	2	14.4	-12.4
Proteales	447	6	19.3	-13.3

* Residual values above (+) or below (-) the population variance

4.3.1.1.2 Regression analyses for anti-diabetes taxa

Anti-diabetes taxa are hereafter referred to as EthmedDBM. The model obtained from the regression analysis of plant orders (Table 4.26) was able to account for 59% (ρ^2 = 0.59) of the variation in the y-values.

Table 4.26 Statistics from a least squares regression analysis of EthmedDBM orders and families.

	Coefficient	Constant	ρ	ρ^2	Std. error	Pop. size
Orders	0.006	3.01	0.77	0.59	5.9	33
Families	0.006	1.12	0.81	0.66	2.1	75

Residual values obtained from the regression analysis of EthmedDBM taxa grouped by plant order ranged from -12.4 to 13.2. The population variance for order residuals was calculated at 5.70. This value was employed as a cut-off to distinguish which orders were outliers. Seven orders (five with positive and two with negative residuals) out of 33 orders analysed were found to be outliers. Taxa in these outlying orders were considered to have been selected either far more or far less frequently for use against diabetes than taxa from other orders. The magnitude of the outlying residual values (Table 4.27) falsified the null hypothesis.

Table 4.27 Set 1 orders used significantly greater or less than predicted against EthmedDBM conditions

Order	Total *FSA* taxa	Predicted EthmedDBM taxa	Actual EthmedDBM taxa	Residual value*
Malpighiales	904	8.8	22	+13.2
Asterales	3154	23.2	35	+11.8
Gentianales	1304	11.4	23	+11.6
Sapindales	654	7.2	18	+10.8
Apiales	343	5.2	11	+5.8
Caryophyllales	2839	21.2	12	-9.2
Poales	2244	17.4	5	-12.4

* Residual values above (+) or below (-) the population variance

EthmedDBM taxa (grouped by order) were plotted against total *FSA* taxa (grouped by order)(Figure 4.9). The positive slope provides evidence of the strength of the positive linear relationship ($\rho = 0.77$). The seven outlying orders which influence the coefficient of determination (ρ^2) and therefore the reliability of predictions made from the line of best fit are notable (Figure 4.9).

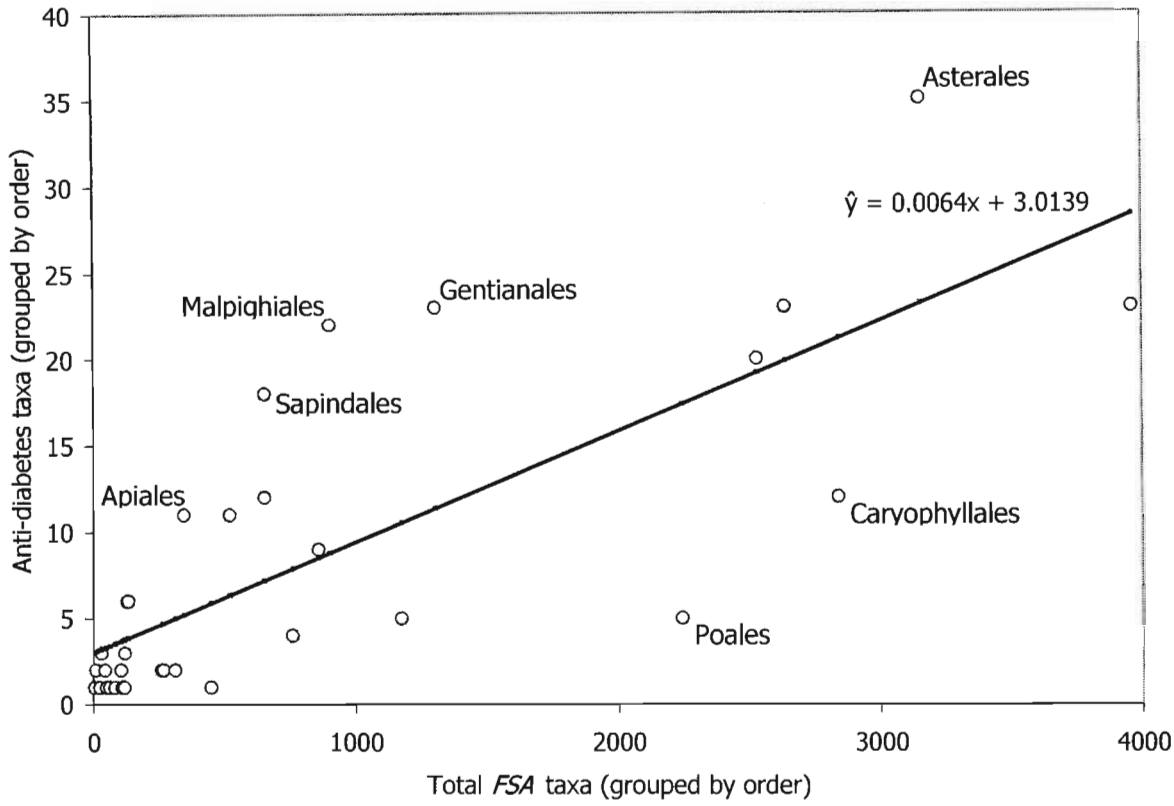

Figure 4.9 Regression plot of EthmedDBM taxa grouped by order versus total taxa grouped by order.

Regression data for families which constitute the outlying orders were extracted and ranked (Table 4.28) by order, family and residual value. The residual values dictated the extent to which the predicted number of EthmedDBM taxa varied from the actual number of taxa in each family.

Table 4.28 EthmedDBM families contributing to the positive outlier status of their respective orders.

Order	Family	Total *FSA* taxa	Predicted EthmedDBM taxa	Actual EthmedDBM taxa	Residual value*
Malpighiales	Euphorbiaceae	580	4.7	11	+6.3
Malpighiales	Papaveraceae	28	1.3	2	+0.7
Malpighiales	Clusiaceae	6	1.2	1	-0.2
Malpighiales	Rhizophoraceae	8	1.2	1	-0.2
Malpighiales	Hypericaceae	30	1.3	1	-0.3
Malpighiales	Salicaceae	36	1.4	1	-0.4
Malpighiales	Passifloraceae	37	1.4	1	-0.4
Magnoliales	Annonaceae	22	1.3	2	+0.7
Asterales	Asteraceae	2681	17.7	24	+6.3
Gentianales	Apocynaceae	854	6.4	8	+1.6
Gentianales	Rubiaceae	345	3.3	4	+0.7
Sapindales	Anacardiaceae	157	2.1	5	+2.9
Sapindales	Rutaceae	350	3.3	4	+0.7
Sapindales	Meliaceae	30	1.3	2	+0.7
Sapindales	Sapindaceae	45	1.4	1	-0.4
Apiales	Apiaceae	276	2.8	6	+3.2
Apiales	Araliaceae	49	1.4	2	+0.6

* Residual values above (+) or below (-) the population variance

Following the above analyses, outlying orders were removed from the datasets and a secondary regression analysis performed (Table 4.29). The results obtained indicate the presence of a strong linear relationship (ρ =0.91) between EthmedDBM taxa grouped by order, and total *FSA* taxa in those orders.

Table 4.29 Statistics from a secondary regression analysis of EthmedDBM orders and families.

	Coefficient	Constant	ρ	ρ^2	Std. error	Pop. size
Orders	0.006	1.81	0.91	0.83	2.85	26
Families	0.007	0.99	0.95	0.91	0.73	65

The population variance for order residuals in the secondary regression analysis was calculated at 2.74. This value was employed as a cut-off which resulted in eight further orders (Table 4.30) being identified as outliers (five positive and three negative). The positive outlying orders were also considered to be highly selected for by ethnomedicinal practitioners.

Table 4.30 Set 1 orders used significantly greater or less than predicted against EthmedDBM conditions (from a secondary regression analysis)

Order	Total *FSA* taxa	Predicted number of EthmedDBM taxa	Actual number of EthmedDBM taxa	Residual value*
Myrtales	653	5.97	12	+6.0
Solanales	519	5.12	11	+5.9
Fabales	2636	18.57	23	+4.4
Cucurbitales	128	2.63	6	+3.4
Ranunculales	132	2.65	6	+3.4
Proteales	447	4.66	1	-3.7
Asparagales	3959	26.98	23	-4.0
Ericales	1174	9.28	5	-4.3

* Residual values above (+) or below (-) the population variance

4.3.1.1.3 Regression analyses for immune modulatory taxa

The model obtained from the regression analysis of plant orders accounted for 58% (ρ^2 = 0.58) of the variation in the y-values (Table 4.31).

Table 4.31 Statistics from a least squares regression analysis of EthmedIMM orders and families.

	Coefficient	Constant	ρ	ρ^2	Std. error	Pop. size
Orders	0.013	4.82	0.76	0.58	11.99	35
Families	0.010	1.29	0.73	0.53	1.50	87

Residual values obtained from the regression analysis of EthmedIMM taxa grouped by plant order ranged from -22.08 to 34.99. The population variance for order residuals was calculated at 11.64 and was employed as a cut-off to distinguish outliers. Eight orders (four with positive and four with negative residuals) out of 35 were outliers. Taxa in these orders are considered to have been targeted or avoided for use in immune modulation. The magnitude of the outlying residual values (Table 4.32) falsified the null hypothesis.

EthmedIMM taxa (grouped by order) were plotted against the total *FSA* taxa (grouped by order)(Figure 4.10). The positive slope provides evidence of the strength of the relationship (ρ = 0.76). The eight outliers which influence the coefficient of determination (ρ^2) and therefore the reliability of predictions made from the line of best fit are notable (Figure 4.10).

Regression data for families which constituted the outliers were extracted and ranked by order, family and residual value (Table 4.32). The residual values dictated the extent to which the predicted number of EthmedIMM taxa varied from the actual number of taxa in each family.

Table 4.32 Set 1 orders used significantly greater or less than predicted for EthmedIMM conditions

Order	Total *FSA* taxa	Predicted EthmedIMM taxa	Actual EthmedIMM taxa	Residual value*
Lamiales	2529	38.0	73	+35.0
Malpighiales	904	16.7	45	+28.3
Gentianales	1304	22.0	43	+21.1
Solanales	519	11.6	31	+19.4
Proteales	447	10.7	2	-8.7
Poales	2244	34.3	15	-19.3
Asparagales	3959	56.8	37	-19.8
Caryophyllales	2839	42.1	20	-22.1

* Residual values above (+) or below (-) the population variance

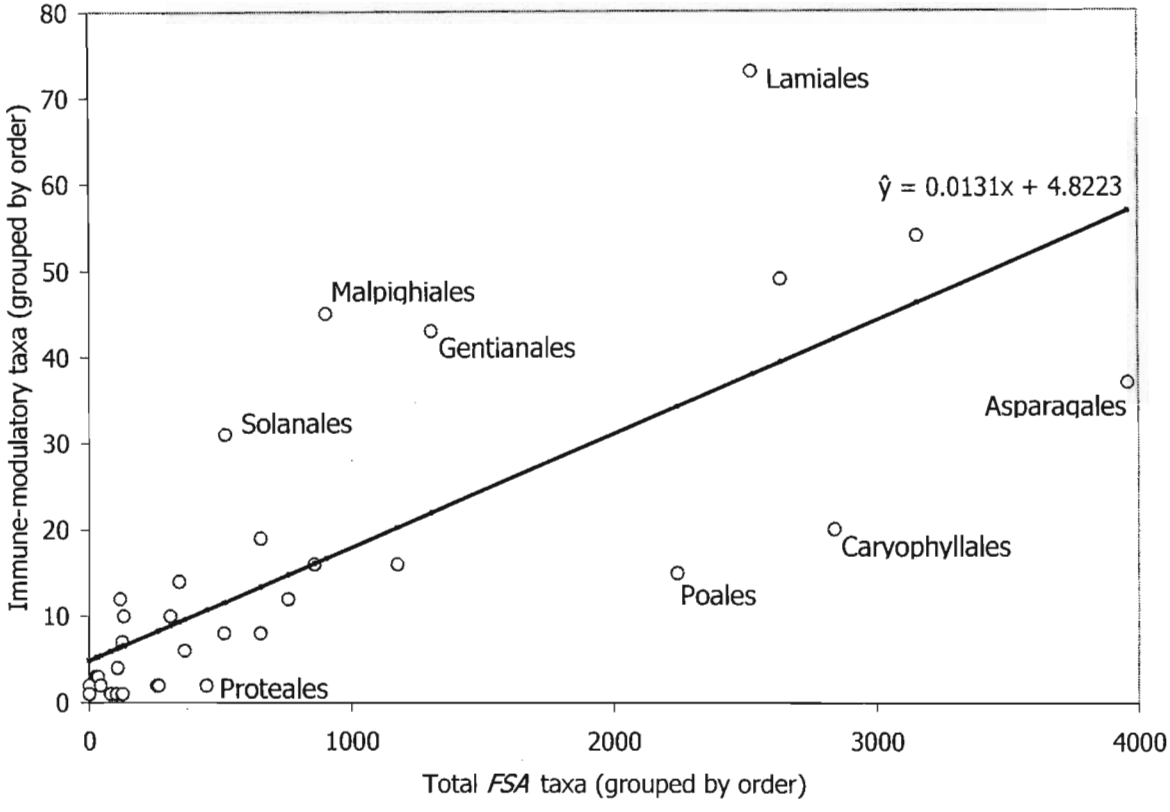

Figure 4.10 Regression plot of EthmedIMM taxa grouped by order versus total taxa grouped by order

Table 4.33 EthmedIMM families contributing to the positive outlier status of their respective orders.

Order	Family	Total *FSA* taxa	Predicted EthmedIMM taxa	Actual EthmedIMM taxa	Residual value*
Lamiales	Lamiaceae	537	7.0	18	+11.0
Lamiales	Verbenaceae	81	2.2	12	+9.8
Lamiales	Oleaceae	95	2.4	5	+2.6
Lamiales	Plantaginaceae	17	1.5	1	-0.5
Lamiales	Pedaliaceae	42	1.8	1	-0.8
Lamiales	Bignoniaceae	88	2.3	1	-1.3
Lamiales	Acanthaceae	435	6.0	3	-3.0
Lamiales	Scrophulariaceae	1007	12.0	4	-8.0
Malpighiales	Euphorbiaceae	580	7.5	25	+17.5
Malpighiales	Salicaceae	93	2.3	3	+0.7
Malpighiales	Violaceae	22	1.6	2	+0.4
Malpighiales	Papaveraceae	28	1.7	2	+0.4
Malpighiales	Turneraceae	11	1.5	1	-0.5
Malpighiales	Ochnaceae	15	1.5	1	-0.5
Malpighiales	Linaceae	21	1.6	1	-0.6
Malpighiales	Passifloraceae	37	1.7	1	-0.7
Gentianales	Rubiaceae	345	5.0	9	+4.0
Gentianales	Apocynaceae	854	10.4	14	+3.6
Gentianales	Gentianaceae	96	2.4	4	+1.6
Gentianales	Loganiaceae	10	1.5	2	+0.5
Solanales	Solanaceae	222	3.7	14	+10.3
Solanales	Convolvulaceae	146	2.9	2	-0.9
Solanales	Unplaced Euasterid I	146	2.9	2	-0.9

* Residual values above (+) or below (-) the population variance

Upon completion of the above analyses, the outlying orders were removed from the dataset and a secondary regression analysis was performed (Table 4.34). The results show a strong linear relationship (ρ =0.96) between EthmedIMM taxa grouped by order, and the total *FSA* taxa in those orders.

Table 4.34 Statistics from a secondary regression analysis of EthmedIMM taxa orders and families.

	Coefficient	Constant	ρ	ρ^2	Std. error	Pop. size
Orders	0.017	1.87	0.96	0.92	3.72	27
Families	0.010	1.29	0.73	0.53	1.50	87

The population variance for order residuals in the secondary regression analysis was calculated at 3.58. This value was employed as a cut-off which resulted in eight further orders (Table 4.35) being identified as outliers (four positive and four negative). The positive outlying orders identified were considered to be targeted by ethnomedicinal practitioners.

Table 4.35 Set 1 orders used significantly greater or less than predicted for EthmedIMM conditions as obtained from a secondary regression analyses

Order	Total *FSA* taxa	Predicted EthmedIMM taxa	Actual EthmedIMM taxa	Residual value*
Celastrales	119	3.9	12	8.1
Apiales	343	7.6	14	6.4
Sapindales	654	12.8	19	6.2
Ranunculales	132	4.1	10	5.9
Santalales	259	6.2	2	-4.2
Oxalidales	265	6.3	2	-4.3
Myrtales	653	12.7	8	-4.7
Ericales	1174	21.4	16	-5.4

Table 4.36 Shortlisted taxa for tuberculosis and the respective scores for weighted criteria

Rank No.	Taxon	Family	Indg.	End.	*FSA* (med)	Treat.	Assoc.	Tox.	Red Data	Trade	HFam1	HFam2	Keyword	Total Score
1	*Croton sylvaticus* Hochst. ex C.Krauss	EUPHORBIACEAE	1	0	2	15	0	3	0	1.5	8	3	8	41.5
2	*Euphorbia ingens* E.Mey. ex Boiss.	EUPHORBIACEAE	1	0	2	15	0	3	2	1	8	3	5	40
3	*Glycyrrhiza glabra* L.	FABACEAE	0	0	2	15	8	3	0	1	0	3	8	40
4	*Tetradenia riparia* (Hochst.) Codd	LAMIACEAE	1	0	2	15	0	3	0	1.5	8	3	6	39.5
5	*Croton pseudopulchellus* Pax	EUPHORBIACEAE	1	0	2	15	0	3	2	1	8	3	4	39
6	*Salvia coccinea* Etl.	LAMIACEAE	0	0	2	15	0	3	0	0	8	3	8	39
7	*Lippia javanica* (Burm.f.) Spreng.	VERBENACEAE	1	0	2	15	0	3	0	2	8	3	5	39
8	*Jatropha capensis* (L.f.) Sond.	EUPHORBIACEAE	1	1	2	15	0	0	0	0	8	3	8	38
9	*Andrachne ovalis* (Sond.) Müll.Arg.	EUPHORBIACEAE	1	0	2	15	0	3	0	1.5	8	3	4	37.5
10	*Leonotis leonurus* (L.) R.Br.	LAMIACEAE	1	0	2	15	0	3	0	0.5	8	3	5	37.5
11	*Clerodendrum glabrum* E.Mey. var. *glabrum*	VERBENACEAE	1	0	2	15	0	0	0	0.5	8	3	8	37.5
12	*Chrysocoma ciliata* L.	ASTERACEAE	1	0	2	15	0	3	0	0	8	0	8	37
13	*Flueggea virosa* (Roxb. ex Willd.) Voigt subsp. *virosa*	EUPHORBIACEAE	1	0	2	15	0	3	0	0	8	3	5	37
14	*Ballota africana* (L.) Benth.	LAMIACEAE	1	0	2	15	0	3	0	0	8	3	5	37
15	*Lippia rehmannii* H.Pearson	VERBENACEAE	1	0	2	15	0	3	0	0	8	3	5	37
16	*Mentha aquatica* L.	LAMIACEAE	1	0	2	15	0	3	0	0.5	8	3	4	36.5
17	*Lantana rugosa* Thunb.	VERBENACEAE	1	0	2	15	0	3	0	0.5	8	3	4	36.5
18	*Artemisia afra* Jacq. ex Willd.	ASTERACEAE	1	0	2	15	0	3	0	2	8	0	5	36
19	*Jatropha curcas* L.	EUPHORBIACEAE	0	0	2	15	0	3	0	0	8	3	5	36

Table 4.36 (continued)

Rank No.	Taxon	Family	Indg.	End.	*FSA* (med)	Treat.	Assoc.	Tox.	Red Data	Trade	HFam1	HFam2	Keyword	Total Score
20	*Monadenium lugardiae* N.E.Br.	EUPHORBIACEAE	1	0	2	15	0	3	0	0	8	3	4	36
21	*Warburgia salutaris* (Bertol.f.) Chiov.	CANELLACEAE	1	0	2	15	0	3	2	3.5	4	0	5	35.5
22	*Bridelia micrantha* (Hochst.) Baill.	EUPHORBIACEAE	1	0	2	15	0	3	0	0.5	8	3	3	35.5
23	*Croton gratissimus* Burch. var. *gratissimus*	EUPHORBIACEAE	1	0	2	15	0	0	0	1.5	8	3	5	35.5
24	*Mentha longifolia* (L.) Huds. subsp. *capensis* (Thunb.) Briq.	LAMIACEAE	1	0	0	15	0	0	0	0.5	8	3	8	35.5
25	*Carpobrotus edulis* (L.) L.Bolus subsp. *edulis*	MESEMBRYANTHEMACEAE	1	1	2	15	8	0	0	0.5	0	0	8	35.5
26	*Syzygium guineense* (Willd.) DC. subsp. *guineense*	MYRTACEAE	1	0	2	15	0	3	0	0.5	6	0	8	35.5
27	*Euphorbia hirta* L.	EUPHORBIACEAE	1	0	0	15	0	3	0	0	8	3	5	35
28	*Pterocarpus angolensis* DC.	FABACEAE	1	0	2	15	0	3	2	1	0	3	8	35
29	*Basilicum polystachyon* (L.) Moench	LAMIACEAE	1	0	2	15	0	3	0	0	8	3	3	35
30	*Hyptis spicigera* Lam.	LAMIACEAE	0	0	2	15	0	0	2	0	8	3	5	35
31	*Salvia africana-caerulea* L.	LAMIACEAE	1	1	2	15	0	0	0	0	8	3	5	35
32	*Gardenia volkensii* K.Schum. subsp. *spatulifolia* (Stapf & Hutch.) Verdc.	RUBIACEAE	1	0	2	15	0	3	0	2	4	0	8	35
33	*Pentanisia prunelloides* (Klotzsch ex Eckl. & Zeyh.) Walp. subsp. *prunelloides*	RUBIACEAE	1	0	2	15	0	3	0	2	4	0	8	35
34	*Zanthoxylum capense* (Thunb.) Harv.	RUTACEAE	1	0	2	15	0	0	0	2	4	3	8	35

Table 4.36 (continued)

Rank No.	Taxon	Family	Indg.	End.	*FSA* (med)	Treat.	Assoc.	Tox.	Red Data	Trade	HFam1	HFam2	Keyword	Total Score
35	*Verbena officinalis* L.	VERBENACEAE	0	0	2	15	0	3	0	0	8	3	4	35
36	*Microglossa mespilifolia* (Less.) B.L.Rob.	ASTERACEAE	1	0	2	15	0	3	0	0.5	8	0	5	34.5
37	*Vernonia mespilifolia* Less.	ASTERACEAE	1	0	2	15	0	0	0	0.5	8	0	8	34.5
38	*Plectranthus madagascariensis* (Pers.) Benth. var. *madagascariensis*	LAMIACEAE	1	1	2	15	0	0	0	0.5	8	3	4	34.5
39	*Heteromorpha arborescens* (Spreng.) Cham. & Schltdl. var. *abyssinica* (A.Rich.) H.Wolff	APIACEAE	1	0	2	15	0	3	0	1	4	0	8	34
40	*Rauvolfia caffra* Sond.	APOCYNACEAE	1	0	2	15	0	3	0	1	4	0	8	34
41	*Eclipta prostrata* (L.) L.	ASTERACEAE	0	0	2	15	0	3	0	1	8	0	5	34
42	*Helichrysum cochleariforme* DC.	ASTERACEAE	1	1	2	15	0	0	2	0	8	0	5	34
43	*Helichrysum pedunculatum* Hilliard & B.L.Burtt	ASTERACEAE	1	0	2	15	0	0	0	0	8	0	8	34
44	*Pechuel-Loeschea leubnitziae* (Kuntze) O.Hoffm.	ASTERACEAE	1	0	2	15	0	0	0	0	8	0	8	34
45	*Senecio speciosus* Willd.	ASTERACEAE	1	0	2	15	0	3	0	1	8	0	4	34
46	*Tarchonanthus camphoratus* L.	ASTERACEAE	1	0	2	15	0	3	0	0	8	0	5	34
47	*Acalypha punctata* Meisn. var. *punctata*	EUPHORBIACEAE	1	0	0	15	0	3	0	0	8	3	4	34
48	*Alchornea hirtella* Benth. forma *glabrata* (Müll.Arg.) Pax & K.Hoffm.	EUPHORBIACEAE	1	0	0	15	0	0	2	0	8	3	5	34
49	*Shirakiopsis elliptica* (Hochst.) Esser	EUPHORBIACEAE	0	0	2	15	0	3	0	0	8	3	3	34

Table 4.36 (continued)

Rank No.	Taxon	Family	Indg.	End.	*FSA* (med)	Treat.	Assoc.	Tox.	Red Data	Trade	HFam1	HFam2	Keyword	Total Score
50	*Salvia chamelaeagnea* P.J.Bergius	LAMIACEAE	1	1	2	15	0	0	0	0	8	3	4	34
51	*Syzygium cordatum* Hochst. ex Sond. var. *cordatum*	MYRTACEAE	1	0	0	15	0	3	0	1	6	0	8	34
52	*Polygala fruticosa* P.J.Bergius	POLYGALACEAE	1	1	2	15	0	3	0	1	0	3	8	34
53	*Lantana camara* L.	VERBENACEAE	0	0	2	15	0	3	0	0	8	3	3	34
54	*Senecio bupleuroides* DC.	ASTERACEAE	1	0	2	15	0	3	0	0.5	8	0	4	33.5
55	*Acalypha peduncularis* E.Mey. ex Meisn.	EUPHORBIACEAE	1	0	2	15	0	0	0	0.5	8	3	4	33.5
56	*Croton gratissimus* Burch. var. *subgratissimus* (Prain) Burtt Davy	EUPHORBIACEAE	1	0	2	15	0	0	0	1.5	8	3	3	33.5
57	*Macaranga capensis* (Baill.) Benth. ex Sim	EUPHORBIACEAE	1	0	2	15	0	0	0	0.5	8	3	4	33.5
58	*Ekebergia capensis* Sparrm.	MELIACEAE	1	0	2	15	0	3	0	1.5	4	3	4	33.5
59	*Toddalia asiatica* (L.) Lam.	RUTACEAE	1	0	2	15	0	3	0	0.5	4	3	5	33.5
60	*Pappea capensis* Eckl. & Zeyh.	SAPINDACEAE	1	0	2	15	0	3	0	1.5	4	3	4	33.5
61	*Urtica urens* L.	URTICACEAE	0	0	2	15	8	0	0	0.5	0	0	8	33.5
62	*Siphonochilus aethiopicus* (Schweinf.) B.L.Burtt	ZINGIBERACEAE	1	0	2	15	0	3	2	2.5	0	0	8	33.5
63	*Carissa edulis* Vahl	APOCYNACEAE	1	0	2	15	0	3	0	0	4	0	8	33
64	*Ageratum conyzoides* L.	ASTERACEAE	0	0	2	15	0	3	0	0	8	0	5	33
65	*Bidens pilosa* L.	ASTERACEAE	0	0	2	15	0	3	0	0	8	0	5	33
66	*Callilepis laureola* DC.	ASTERACEAE	1	0	2	15	0	3	0	1	8	0	3	33
67	*Eriocephalus microphyllus* DC. var. *pubescens* (DC.) M.A.N.Müll.	ASTERACEAE	1	1	0	15	0	0	0	0	8	0	8	33

Table 4.36 (continued)

Rank No.	Taxon	Family	Indg.	End.	*FSA* (med)	Treat.	Assoc.	Tox.	Red Data	Trade	HFam1	HFam2	Keyword	Total Score
68	*Vernonia myriantha* Hook.f.	ASTERACEAE	1	0	2	15	0	3	0	0	8	0	4	33
69	*Capparis tomentosa* Lam.	CAPPARACEAE	1	0	2	15	0	3	2	2	0	0	8	33
70	*Erythrococca menyharthii* (Pax) Prain	EUPHORBIACEAE	1	0	2	15	0	0	0	0	8	3	4	33
71	*Jatropha zeyheri* Sond. var. *zeyheri*	EUPHORBIACEAE	1	0	0	15	0	3	0	0	8	3	3	33
72	*Acacia caffra* (Thunb.) Willd.	FABACEAE	1	0	2	15	0	3	0	1	0	3	8	33
73	*Aspalathus cordata* (L.) R.Dahlgren	FABACEAE	1	1	2	15	8	0	0	0	0	3	3	33
74	*Elephantorrhiza elephantina* (Burch.) Skeels	FABACEAE	1	0	2	15	0	3	2	3	0	3	4	33
75	*Hoslundia opposita* Vahl	LAMIACEAE	1	0	2	15	0	3	0	0	8	3	1	33
76	*Hyptis pectinata* (L.) Poit.	LAMIACEAE	0	0	2	15	0	0	0	0	8	3	5	33
77	*Turraea floribunda* Hochst.	MELIACEAE	1	0	2	15	0	3	2	2	4	3	1	33
78	*Hippobromus pauciflorus* (L.f.) Radlk.	SAPINDACEAE	1	0	2	15	0	3	0	2	4	3	3	33
79	*Helichrysum odoratissimum* (L.) Sweet	ASTERACEAE	1	0	2	15	0	0	0	2.5	8	0	4	32.5
80	*Buddleja saligna* Willd.	BUDDLEJACEAE	1	0	2	15	0	3	0	0.5	0	3	8	32.5
81	*Acalypha villicaulis* Hochst. ex A.Rich.	EUPHORBIACEAE	1	0	2	15	0	0	0	0.5	8	3	3	32.5
82	*Antidesma venosum* auct. non E.Mey. ex Tul.	EUPHORBIACEAE	0	0	0	15	0	3	0	0.5	8	3	3	32.5
83	*Drypetes gerrardii* Hutch. var. *gerrardii*	EUPHORBIACEAE	1	0	0	15	0	0	0	0.5	8	3	5	32.5
84	*Euphorbia davyi* N.E.Br.	EUPHORBIACEAE	1	0	2	15	0	0	0	0.5	8	3	3	32.5

Table 4.36 (continued)

Rank No.	Taxon	Family	Indg.	End.	*FSA* (med)	Treat.	Assoc.	Tox.	Red Data	Trade	HFam1	HFam2	Keyword	Total Score
85	*Margaritaria discoidea* (Baill.) G.L.Webster subsp. *discoidea*	EUPHORBIACEAE	0	0	0	15	0	3	0	0.5	8	3	3	32.5
86	*Phyllanthus meyerianus* Müll.Arg.	EUPHORBIACEAE	1	0	2	15	0	0	0	0.5	8	3	3	32.5
87	*Becium obovatum* (E.Mey. ex Benth.) N.E.Br. subsp. *obovatum* var. *obovatum*	LAMIACEAE	1	0	2	15	0	0	0	0.5	8	3	3	32.5
88	*Clausena anisata* (Willd.) Hook.f. ex Benth. var. *anisata*	RUTACEAE	1	0	0	15	0	0	0	1.5	4	3	8	32.5
89	*Vepris lanceolata* (Lam.) G.Don	RUTACEAE	1	0	2	15	0	3	0	0.5	4	3	4	32.5
90	*Zanthoxylum davyi* (I.Verd.) P.G.Waterman	RUTACEAE	1	0	2	15	0	0		1.5	4	3	4	30.5
91	*Tulbaghia alliacea* L.f.	ALLIACEAE	1	0	2	15	0	3	0	3	0	0	8	32
92	*Lichtensteinia interrupta* (Thunb.) Sond.	APIACEAE	1	1	2	15	0	3	0	1	4	0	5	32
93	*Antiphiona fragrans* (Merxm.) Merxm.	ASTERACEAE	1	0	2	15	0	0	2	0	8	0	4	32
94	*Schkuhria pinnata* (Lam.) Cabrera	ASTERACEAE	0	0	2	15	0	3	0	0	8	0	4	32
95	*Euphorbia clavarioides* Boiss. var. *truncata* (N.E.Br.) A.C.White, R.A.Dyer & B.Sloane	EUPHORBIACEAE	1	1	2	15	0	0	0	1	8	3	1	32
96	*Euphorbia heterophylla* L.	EUPHORBIACEAE	0	0	2	0	8	3	0	0	8	3	8	32
97	*Afzelia quanzensis* Welw.	FABACEAE	1	0	2	15	0	3	2	1	0	3	5	32
98	*Indigofera tinctoria* L. var. *arcuata* J.B.Gillett	FABACEAE	1	0	0	15	8	0	0	0	0	3	5	32

Table 4.36 (continued)

Rank No.	Taxon	Family	Indg.	End.	*FSA* (med)	Treat.	Assoc.	Tox.	Red Data	Trade	HFam1	HFam2	Keyword	Total Score
99	*Sesbania sesban* (L.) Merr. subsp. *sesban* var. *sesban*	FABACEAE	1	0	2	15	0	3	0	0	0	3	8	32
100	*Tephrosia vogelii* Hook.f.	FABACEAE	1	0	2	15	0	3	0	0	0	3	8	32
101	*Leonotis ocymifolia* (Burm.f.) Iwarsson var. *ocymifolia*	LAMIACEAE	1	0	2	15	0	0	0	0	8	3	3	32
102	*Marrubium vulgare* L.	LAMIACEAE	0	0	2	15	0	3	0	0	8	3	1	32
103	*Ocimum gratissimum* L. subsp. *gratissimum* var. *gratissimum*	LAMIACEAE	1	0	2	15	0	0	0	0	8	3	3	32
104	*Plectranthus laxiflorus* Benth.	LAMIACEAE	1	0	2	15	0	0	0	0	8	3	3	32
105	*Salvia africana-lutea* L.	LAMIACEAE	1	0	2	15	0	0	0	0	8	3	3	32
106	*Satureja biflora* (Buch.-Ham. ex D.Don) Briq.	LAMIACEAE	1	0	2	15	0	0	0	0	8	3	3	32
107	*Syzygium gerrardii* (Harv. ex Hook.f.) Burtt Davy	MYRTACEAE	1	0	2	15	0	0	0	0	6	0	8	32
108	*Ruta graveolens* L.	RUTACEAE	0	0	2	15	0	3	0	0	4	3	5	32
109	*Cissus quadrangularis* L. var. *quadrangularis*	VITACEAE	1	0	2	15	0	3	0	0	0	3	8	32
110	*Acalypha depressinerva* (Kuntze) K.Schum.	EUPHORBIACEAE	1	0	0	15	0	0	0	0.5	8	3	4	31.5
111	*Dalbergia melanoxylon* Guill. & Perr.	FABACEAE	1	0	2	15	0	3	2	0.5	0	3	5	31.5
112	*Cardiospermum halicacabum* L. var. *halicacabum*	SAPINDACEAE	1	0	0	15	0	3	0	0.5	4	3	5	31.5
113	*Tulbaghia violacea* Harv.	ALLIACEAE	1	1	2	15	0	3	0	1	0	0	8	31
114	*Arctopus echinatus* L.	APIACEAE	1	1	2	15	0	0	0	0	4	0	8	31

Table 4.36 (continued)

Rank No.	Taxon	Family	Indg.	End.	*FSA* (med)	Treat.	Assoc.	Tox.	Red Data	Trade	HFam1	HFam2	Keyword	Total Score
115	*Aster bakerianus* Burtt Davy ex C.A.Sm.	ASTERACEAE	1	0	0	15	0	3	0	1	8	0	3	31
116	*Dicoma capensis* Less.	ASTERACEAE	1	0	2	15	0	0	2	0	8	0	3	31
117	*Helichrysum appendiculatum* (L.f.) Less.	ASTERACEAE	1	1	2	15	0	0	0	0	8	0	4	31
118	*Helichrysum nudifolium* (L.) Less.	ASTERACEAE	1	0	2	15	0	0	0	1	8	0	4	31
119	*Melanthera scandens* (Schumach. & Thonn.) Roberty subsp. *dregei* (DC.) Wild	ASTERACEAE	1	0	2	15	0	0	0	0	8	0	5	31
120	*Acalypha fruticosa* Forssk. var. *fruticosa*	EUPHORBIACEAE	1	0	0	15	0	0	0	0	8	3	4	31
121	*Phyllanthus glaucophyllus* Sond.	EUPHORBIACEAE	1	0	0	15	0	0	0	0	8	3	4	31
122	*Albizia adianthifolia* (Schumach.) W.Wight var. *adianthifolia*	FABACEAE	1	0	2	15	0	3	0	2	0	3	5	31
123	*Albizia amara* (Roxb.) Boivin subsp. *sericocephala* (Benth.) Brenan	FABACEAE	1	0	2	15	0	0	2	0	0	3	8	31
124	*Faidherbia albida* (Delile) A.Chev.	FABACEAE	1	0	2	15	0	3	2	0	0	3	5	31
125	*Peltophorum africanum* Sond.	FABACEAE	1	0	2	15	0	3	2	1	0	3	4	31
126	*Tephrosia grandiflora* (Aiton) Pers.	FABACEAE	1	1	2	15	0	3	2	0	0	3	4	31
127	*Leonotis randii* S.Moore	LAMIACEAE	1	0	0	15	0	0	0	0	8	3	4	31
128	*Dodonaea viscosa* Jacq. var. *angustifolia* Benth.	SAPINDACEAE	1	0	0	15	0	0	0	0	4	3	8	31
129	*Adenostemma viscosum* J.R.& G.Forst.	ASTERACEAE	1	0	2	15	0	0	0	0.5	8	0	4	30.5

Table 4.36 (continued)

Rank No.	Taxon	Family	Indg.	End.	*FSA* (med)	Treat.	Assoc.	Tox.	Red Data	Trade	HFam1	HFam2	Keyword	Total Score
130	*Conyza aegyptiaca* (L.) Aiton	ASTERACEAE	1	0	2	15	0	0	0	0.5	8	0	4	30.5
131	*Gerbera ambigua* (Cass.) Sch.Bip.	ASTERACEAE	1	0	2	15	0	0	0	1.5	8	0	3	30.5
132	*Helichrysum caespititium* (DC.) Harv.	ASTERACEAE	1	0	2	15	0	0	0	0.5	8	0	4	30.5
133	*Erythrophleum lasianthum* Corbishley	FABACEAE	1	0	2	15	0	3	0	1.5	0	3	5	30.5
134	*Ficus sur* Forssk.	MORACEAE	1	0	2	15	0	3	0	1.5	0	0	8	30.5
135	*Rubia petiolaris* DC.	RUBIACEAE	1	0	2	15	0	0	0	0.5	4	0	8	30.5
136	*Deinbollia oblongifolia* (E.Mey. ex Arn.) Radlk.	SAPINDACEAE	1	0	2	15	0	0	0	0.5	4	3	5	30.5
137	*Withania somnifera* (L.) Dunal	SOLANACEAE	1	0	2	15	0	3	0	1.5	0	0	8	30.5
138	*Gnidia kraussiana* Meisn. var. *kraussiana*	THYMELAEACEAE	1	0	2	15	0	3	0	1.5	0	0	8	30.5
139	*Thunbergia capensis* Retz.	ACANTHACEAE	1	1	2	15	0	0	0	0	0	3	8	30
140	*Crinum macowanii* Baker	AMARYLLIDACEAE	1	0	2	15	0	3	0	1	0	0	8	30
141	*Harpephyllum caffrum* Bernh.	ANACARDIACEAE	1	0	2	15	0	0	0	1	0	3	8	30
142	*Alepidea amatymbica* Eckl. & Zeyh. var. *amatymbica*	APIACEAE	1	0	2	15	0	0	0	4	4	0	4	30
143	*Diplorhynchus condylocarpon* (Müll.Arg.) Pichon	APOCYNACEAE	1	0	2	15	0	0	0	0	4	0	8	30
144	*Zantedeschia aethiopica* (L.) Spreng.	ARACEAE	1	0	2	15	0	3	0	0	4	0	5	30
145	*Asparagus africanus* Lam.	ASPARAGACEAE	1	0	2	15	0	3	0	1	0	0	8	30
146	*Bidens schimperi* Sch.Bip. ex Walp.	ASTERACEAE	1	0	2	15	0	0	0	0	8	0	4	30

Table 4.36 (continued)

Rank No.	Taxon	Family	Indg.	End.	*FSA* (med)	Treat.	Assoc.	Tox.	Red Data	Trade	HFam1	HFam2	Keyword	Total Score
147	*Dicoma anomala* Sond. subsp. *anomala*	ASTERACEAE	1	0	0	15	0	0	0	1	8	0	5	30
148	*Gerbera piloselloides* (L.) Cass.	ASTERACEAE	1	0	2	15	0	0	0	1	8	0	3	30
149	*Pseudolachnostylis maprouneifolia* Pax var. *maprouneifolia*	EUPHORBIACEAE	1	0	0	15	0	0	0	0	8	3	3	30
150	*Cassia abbreviata* Oliv. subsp. *beareana* (Holmes) Brenan	FABACEAE	1	0	2	15	0	3	0	1	0	3	5	30
151	*Eriosema salignum* E.Mey.	FABACEAE	1	0	2	15	0	0	0	1	0	3	8	30
152	*Xeroderris stuhlmannii* (Taub.) Mendonça & E.C.Sousa	FABACEAE	1	0	2	15	0	3	2	0	0	3	4	30
153	*Entandrophragma caudatum* (Sprague) Sprague	MELIACEAE	1	0	0	15	0	0	2	0	4	3	5	30
154	*Dodonaea viscosa* Jacq. subsp. *angustifolia* (L.f.) J.G.West	SAPINDACEAE	0	0	0	15	0	0	0	0	4	3	8	30
155	*Dodonaea viscosa* Jacq. subsp. *viscosa*	SAPINDACEAE	0	0	0	15	0	0	0	0	4	3	8	30
156	*Sutera hispida* (Thunb.) Druce	SCROPHULARIACEAE	1	1	2	15	0	0	0	0	4	3	4	30
157	*Gnidia burchellii* (Meisn.) Gilg	THYMELAEACEAE	1	0	2	15	0	3	0	1	0	0	8	30
158	*Premna mooiensis* (H.Pearson) W.Piep.	VERBENACEAE	1	0	0	15	0	0	0	0	8	3	3	30
159	*Rotheca myricoides* (Hochst.) Steane & Mabb	VERBENACEAE	0	0	0	15	0	0	0	0	8	3	4	30
160	*Tabernaemontana elegans* Stapf	APOCYNACEAE	1	0	2	15	0	3	0	0.5	4	0	4	29.5
161	*Acorus calamus* L.	ARACEAE	0	0	2	15	0	3	0	0.5	4	0	5	29.5
162	*Gomphocarpus physocarpus* E.Mey.	ASCLEPIADACEAE	1	0	2	15	0	3	0	0.5	0	0	8	29.5

Table 4.36 (continued)

Rank No.	Taxon	Family	Indg.	End.	*FSA* (med)	Treat.	Assoc.	Tox.	Red Data	Trade	HFam1	HFam2	Keyword	Total Score
163	*Conyza podocephala* DC.	ASTERACEAE	1	0	2	15	0	0	0	0.5	8	0	3	29.5
164	*Vernonia colorata* (Willd.) Drake subsp. *colorata*	ASTERACEAE	1	0	2	15	0	0	0	0.5	8	0	3	29.5
165	*Begonia homonyma* Steud.	BEGONIACEAE	1	1	2	15	0	3	2	1.5	0	0	4	29.5
166	*Diospyros mespiliformis* Hochst. ex A.DC.	EBENACEAE	1	0	2	15	0	3	0	0.5	0	0	8	29.5
167	*Dichrostachys cinerea* (L.) Wight & Arn. subsp. *africana* Brenan & Brummitt var. *africana*	FABACEAE	1	0	2	15	0	3	2	0.5	0	3	3	29.5
168	*Mentha longifolia* (L.) Huds. subsp. *longifolia*	LAMIACEAE	0	0	0	15	0	0	0	0.5	8	3	3	29.5
169	*Ocotea bullata* (Burch.) Baill.	LAURACEAE	1	0	2	15	0	0	2	2.5	4	0	3	29.5
170	*Cissampelos capensis* L.f.	MENISPERMACEAE	1	0	2	15	0	3	0	0.5	0	0	8	29.5
171	*Cissampelos mucronata* A.Rich.	MENISPERMACEAE	1	0	2	15	0	3	0	0.5	0	0	8	29.5
172	*Adenia digitata* (Harv.) Engl.	PASSIFLORACEAE	1	0	2	15	0	3	0	0.5	0	3	5	29.5
173	*Securidaca longipedunculata* Fresen. var. *longipedunculata*	POLYGALACEAE	0	0	0	15	0	3	0	0.5	0	3	8	29.5
174	*Vangueria infausta* Burch. subsp. *infausta*	RUBIACEAE	1	0	2	15	0	3	0	0.5	4	0	4	29.5
175	*Ozoroa obovata* (Oliv.) R.& A.Fern. var. *obovata*	ANACARDIACEAE	1	0	2	15	0	3	0	1	0	3	4	29
176	*Heteromorpha arborescens* (Thunb.) Cham. & Schltdl. var. *arborescens*	APIACEAE	1	0	0	15	0	0	0	1	4	0	8	29

Table 4.36 (continued)

Rank No.	Taxon	Family	Indg.	End.	*FSA* (med)	Treat.	Assoc.	Tox.	Red Data	Trade	HFam1	HFam2	Keyword	Total Score
177	*Pergularia daemia* (Forssk.) Chiov. var. *daemia*	ASCLEPIADACEAE	1	0	2	15	0	3	2	0	0	0	6	29
178	*Asparagus cooperi* Baker	ASPARAGACEAE	1	0	2	15	0	3	0	0	0	0	8	29
179	*Asparagus plumosus* Baker	ASPARAGACEAE	1	0	2	15	0	3	0	0	0	0	8	29
180	*Baccharoides adoensis* (Sch.Bip. ex Walp.) H.Rob. var. *kotschyana* (Sch.Bip. ex Walp.) Isawumi, El-Ghazaly & B.Nord.	ASTERACEAE	1	0	2	15	0	0	0	0	8	0	3	29
181	*Berkheya rhapontica* (DC.) Hutch. & Burtt Davy subsp. *aristosa* (DC.) Roessler var. *aristosa*	ASTERACEAE	1	0	2	15	0	0	0	0	8	0	3	29
182	*Conyza scabrida* DC.	ASTERACEAE	1	0	2	15	0	0	0	0	8	0	3	29
183	*Conyza ulmifolia* (Burm.f.) Kuntze	ASTERACEAE	1	0	2	15	0	0	0	0	8	0	3	29
184	*Dicoma macrocephala* DC.	ASTERACEAE	1	0	2	15	0	0	0	0	8	0	3	29
185	*Macledium speciosum* (DC.) S.Ortíz	ASTERACEAE	1	1	0	15	0	0	0	0	8	0	4	29
186	*Macledium zeyheri* (Sond.) S.Ortíz subsp. *argyrophylum* (Oliv.) S.Ortíz	ASTERACEAE	1	1	0	15	0	0	0	0	8	0	4	29
187	*Senecio quinquelobus* (Thunb.) DC.	ASTERACEAE	1	0	2	15	0	0	0	0	8	0	3	29
188	*Ursinia tenuiloba* DC.	ASTERACEAE	1	0	2	15	0	0	0	0	8	0	3	29
189	*Vernonia hirsuta* (DC.) Sch.Bip. ex Walp.	ASTERACEAE	1	0	2	15	0	0	0	0	8	0	3	29
190	*Markhamia obtusifolia* (Baker) Sprague	BIGNONIACEAE	1	0	2	15	0	0	0	0	0	3	8	29
191	*Garcinia livingstonei* T.Anderson	CLUSIACEAE	1	0	2	15	0	3	0	1	0	3	4	29

Table 4.36 (continued)

Rank No.	Taxon	Family	Indg.	End.	*FSA* (med)	Treat.	Assoc.	Tox.	Red Data	Trade	HFam1	HFam2	Keyword	Total Score
192	*Acacia nilotica* (L.) Willd. ex Delile subsp. *nilotica*	FABACEAE	0	0	0	15	0	3	0	0	0	3	8	29
193	*Erythrina humeana* Spreng.	FABACEAE	1	0	2	15	0	0	0	0	0	3	8	29
194	*Indigofera confusa* Prain & Baker f.	FABACEAE	0	0	0	15	0	3	0	0	0	3	8	29
195	*Pterolobium stellatum* (Forssk.) Brenan	FABACEAE	1	0	2	15	0	0	0	0	0	3	8	29
196	*Senna siamea* (Lam.) Irwin & Barneby	FABACEAE	0	0	2	15	0	3	0	0	0	3	6	29
197	*Sutherlandia frutescens* (L.) R.Br.	FABACEAE	1	0	2	15	0	3	0	0	0	3	5	29
198	*Oncoba spinosa* Forssk. subsp. *spinosa*	FLACOURTIACEAE	1	0	2	15	0	0	0	0	0	3	8	29
199	*Scilla natalensis* Planch.	HYACINTHACEAE	0	0	2	15	0	3	2	3	0	0	4	29
200	*Hypoxis hemerocallidea* Fisch. & C.A.Mey.	HYPOXIDACEAE	1	0	2	15	0	0	2	1	0	0	8	29
201	*Sida rhombifolia* L. subsp. *rhombifolia*	MALVACEAE	1	0	2	15	0	3	0	0	0	0	8	29
202	*Eucalyptus globulus* Labill. subsp. *globulus*	MYRTACEAE	0	0	0	15	0	3	0	1	6	0	4	29
203	*Psidium guajava* L.	MYRTACEAE	0	0	2	15	0	3	0	0	6	0	3	29
204	*Ochna pulchra* Hook.f.	OCHNACEAE	1	0	2	15	0	3	0	0	0	3	5	29
205	*Plumbago zeylanica* L.	PLUMBAGINACEAE	1	0	2	15	0	3	0	0	0	0	8	29
206	*Polygala amatymbica* Eckl. & Zeyh.	POLYGALACEAE	1	0	2	15	0	0	0	0	0	3	8	29
207	*Agathosma puberula* (Steud.) Fourc.	RUTACEAE	1	1	2	15	0	0	0	0	4	3	3	29
208	*Thamnosma africana* Engl.	RUTACEAE	1	0	2	15	0	0	0	0	4	3	4	29
209	*Thesium hystrix* A.W.Hill	SANTALACEAE	1	0	2	15	0	3	0	0	0	0	8	29
210	*Zanha africana* (Radlk.) Exell	SAPINDACEAE	1	0	2	15	0	0	0	0	4	3	4	29

Table 4.36 (continued)

Rank No.	Taxon	Family	Indg.	End.	*FSA* (med)	Treat.	Assoc.	Tox.	Red Data	Trade	HFam1	HFam2	Keyword	Total Score
211	*Sutera floribunda* (Benth.) Kuntze	SCROPHULARIACEAE	1	0	2	15	0	0	0	0	4	3	4	29
212	*Solanum capense* L.	SOLANACEAE	1	0	2	15	0	3	0	0	0	0	8	29
213	*Gnidia polycephala* (C.A.Mey.) Gilg	THYMELAEACEAE	1	0	2	15	0	3	0	0	0	0	8	29
214	*Lantana trifolia* L.	VERBENACEAE	0	0	2	15	0	0	0	0	8	3	1	29
215	*Stylochiton natalensis* Schott	ARACEAE	1	0	2	15	0	0	0	0.5	4	0	6	28.5
216	*Adansonia digitata* L.	BOMBACACEAE	1	0	2	15	0	0	0	0.5	4	0	6	28.5
217	*Abrus precatorius* L. subsp. *africanus* Verdc.	FABACEAE	1	0	2	15	0	3	0	0.5	0	3	4	28.5
218	*Adenia fruticosa* Burtt Davy subsp. *fruticosa*	PASSIFLORACEAE	1	1	0	15	0	0	0	0.5	0	3	8	28.5
219	*Rubus rigidus* Sm.	ROSACEAE	1	0	2	15	0	3	0	0.5	4	0	3	28.5
220	*Solanum nigrum* L.	SOLANACEAE	0	0	2	15	0	3	0	0.5	0	0	8	28.5
221	*Ozoroa paniculosa* (Sond.) R.& A.Fern. var. *paniculosa*	ANACARDIACEAE	1	0	2	15	0	3	0	0	0	3	4	28
222	*Annona senegalensis* Pers. subsp. *senegalensis*	ANNONACEAE	1	0	2	15	0	3	0	2	0	0	5	28
223	*Nerium oleander* L.	APOCYNACEAE	0	0	2	15	0	3	0	0	4	0	4	28
224	*Borassus aethiopum* Mart.	ARECACEAE	1	0	2	15	0	3	2	0	0	0	5	28
225	*Ambrosia artemisiifolia* L.	ASTERACEAE	0	0	0	15	0	0	0	0	8	0	5	28
226	*Catha edulis* (Vahl) Forssk. ex Endl.	CELASTRACEAE	1	0	2	15	0	3	2	1	0	0	4	28
227	*Gymnosporia senegalensis* (Lam.) Loes.	CELASTRACEAE	0	0	2	15	0	3	0	0	0	0	8	28
228	*Cnestis polyphylla* Lam.	CONNARACEAE	1	0	2	15	0	3	2	0	0	0	5	28
229	*Acacia hebeclada* DC. subsp. *hebeclada*	FABACEAE	1	0	2	15	0	3	0	0	0	3	4	28
230	*Acacia robusta* Burch. subsp. *robusta*	FABACEAE	1	0	2	15	0	3	0	0	0	3	4	28

Table 4.36 (continued)

Rank No.	Taxon	Family	Indg.	End.	*FSA* (med)	Treat.	Assoc.	Tox.	Red Data	Trade	HFam1	HFam2	Keyword	Total Score
231	*Alysicarpus rugosus* (Willd.) DC. subsp. *perennirufus* J.Léonard	FABACEAE	1	0	2	15	0	3	0	0	0	3	4	28
232	*Aspalathus flexuosa* Thunb.	FABACEAE	1	1	0	15	0	0	0	0	0	3	8	28
233	*Caesalpinia pulcherrima* (L.) Sw.	FABACEAE	0	0	2	15	0	3	0	0	0	3	5	28
234	*Cyclopia genistoides* (L.) R.Br. var. *genistoides*	FABACEAE	1	1	0	15	0	0	0	0	0	3	8	28
235	*Smithia erubescens* (E.Mey.) Baker f.	FABACEAE	1	0	0	15	8	0	0	0	0	3	1	28
236	*Geranium canescens* L'Hér.	GERANIACEAE	1	1	2	15	0	0	0	0	4	0	5	28
237	*Monsonia emarginata* (L.f.) L'Hér.	GERANIACEAE	1	0	2	15	0	3	0	0	4	0	3	28
238	*Cryptocarya latifolia* Sond.	LAURACEAE	1	1	2	15	0	0	0	1	4	0	4	28
239	*Dahlgrenodendron natalense* (J.H.Ross) J.J.M.van der Merwe & A.E.van Wyk	LAURACEAE	1	1	0	15	0	0	2	0	4	0	5	28
240	*Ochna arborea* Burch. ex DC. var. *oconnorii* (E.Phillips) Du Toit	OCHNACEAE	1	0	2	15	0	0	2	0	0	3	5	28
241	*Argemone ochroleuca* Sweet subsp. *ochroleuca*	PAPAVERACEAE	0	0	2	15	0	0	0	0	0	3	8	28
242	*Allophylus africanus* P.Beauv.	SAPINDACEAE	1	0	2	15	0	0	0	0	4	3	3	28
243	*Datura metel* L.	SOLANACEAE	0	0	2	15	0	3	0	0	0	0	8	28
244	*Uvaria caffra* E.Mey. ex Sond.	ANNONACEAE	1	0	2	15	0	0	0	1.5	0	0	8	27.5
245	*Bulbine abyssinica* A.Rich.	ASPHODELACEAE	1	0	2	15	0	0	0	1.5	0	0	8	27.5
246	*Athrixia phylicoides* DC.	ASTERACEAE	1	0	2	15	0	0	0	0.5	8	0	1	27.5

Table 4.36 (continued)

Rank No.	Taxon	Family	Indg.	End.	*FSA* (med)	Treat.	Assoc.	Tox.	Red Data	Trade	HFam1	HFam2	Keyword	Total Score
247	*Gerbera viridifolia* (DC.) Sch.Bip.	ASTERACEAE	1	0	2	15	0	0	0	0.5	8	0	1	27.5
248	*Buddleja salviifolia* (L.) Lam.	BUDDLEJACEAE	1	0	2	15	0	3	0	0.5	0	3	3	27.5
249	*Albizia tanganyicensis* Baker f. subsp. *tanganyicensis*	FABACEAE	1	0	2	15	0	3	0	0.5	0	3	3	27.5
250	*Myrothamnus flabellifolius* Welw.	MYROTHAMNACEAE	1	0	2	15	0	0	0	1.5	0	0	8	27.5
251	*Ziziphus mucronata* Willd. subsp. *mucronata*	RHAMNACEAE	1	0	2	15	0	0	0	1.5	0	0	8	27.5
252	*Solanum aculeastrum* Dunal	SOLANACEAE	1	0	2	15	0	3	0	1.5	0	0	5	27.5
253	*Strychnos henningsii* Gilg	STRYCHNACEAE	1	0	2	15	0	3	0	2.5	0	0	4	27.5
254	*Gnidia cuneata* Meisn.	THYMELAEACEAE	1	1	2	15	0	3	0	0.5	0	0	5	27.5
255	*Adhatoda andromeda* (Lindau) C.B.Clarke	ACANTHACEAE	1	0	0	15	0	0	0	0	0	3	8	27
256	*Cyrtanthus obliquus* (L.f.) Aiton	AMARYLLIDACEAE	1	1	2	15	0	0	0	0	0	0	8	27
257	*Scadoxus puniceus* (L.) Friis & Nordal	AMARYLLIDACEAE	1	0	2	15	0	3	2	1	0	0	3	27
258	*Pistia stratiotes* L.	ARACEAE	0	0	2	15	0	3	0	0	4	0	3	27
259	*Asparagus stipulaceus* Lam.	ASPARAGACEAE	1	1	2	15	0	0	0	0	0	0	8	27
260	*Baccharoides adoensis* (Sch.Bip. ex Walp.) H.Rob. var. *mossambiquensis* (Steetz) Isawumi, El-Ghazaly & B.Nord.	ASTERACEAE	1	0	0	15	0	0	0	0	8	0	3	27
261	*Cyanthillium cinereum* (L.) H.Rob. var. *cinereum*	ASTERACEAE	1	0	0	15	0	0	0	0	8	0	3	27

Table 4.36 (continued)

Rank No.	Taxon	Family	Indg.	End.	*FSA* (med)	Treat.	Assoc.	Tox.	Red Data	Trade	HFam1	HFam2	Keyword	Total Score
262	*Dicoma anomala* Sond. subsp. *gerrardii* (Harv. ex F.C.Wilson) S.Ortíz & Rodr.Oubiña	ASTERACEAE	0	0	0	15	0	0	0	1	8	0	3	27
263	*Eriocephalus africanus* L. var. *africanus*	ASTERACEAE	1	0	0	15	0	0	0	0	8	0	3	27
264	*Senecio achilleifolius* DC.	ASTERACEAE	1	0	0	15	0	0	0	0	8	0	3	27
265	*Senecio helminthioides* (Sch.Bip.) Hilliard	ASTERACEAE	1	0	0	15	0	0	0	0	8	0	3	27
266	*Tecoma capensis* (Thunb.) Lindl.	BIGNONIACEAE	0	0	2	15	0	3	0	0	0	3	4	27
267	*Acanthosicyos horridus* Welw. ex Hook.f.	CUCURBITACEAE	1	0	2	15	0	3	2	0	0	0	4	27
268	*Dracaena mannii* Baker	DRACAENACEAE	1	0	2	15	0	3	2	0	0	0	4	27
269	*Acacia nilotica* (L.) Willd. ex Delile subsp. *kraussiana* (Benth.) Brenan	FABACEAE	1	0	2	15	0	3	0	0	0	3	3	27
270	*Chamaecrista mimosoides* (L.) Greene	FABACEAE	1	0	2	15	0	3	0	0	0	3	3	27
271	*Erythrophleum africanum* (Welw. ex Benth.) Harms	FABACEAE	1	0	2	0	8	3	2	0	0	3	8	27
272	*Flacourtia indica* (Burm.f.) Merr.	FLACOURTIACEAE	1	0	2	15	0	0	2	0	0	3	4	27
273	*Carpobrotus acinaciformis* (L.) L.Bolus	MESEMBRYANTHEMACEAE	1	1	2	15	0	0	0	0	0	0	8	27
274	*Pharnaceum lineare* L.f.	MOLLUGINACEAE	1	1	2	15	0	0	0	0	0	0	8	27
275	*Ximenia caffra* Sond. var. *caffra*	OLACACEAE	1	0	2	15	0	3	0	2	0	0	4	27

Table 4.36 (continued)

Rank No.	Taxon	Family	Indg.	End.	*FSA* (med)	Treat.	Assoc.	Tox.	Red Data	Trade	HFam1	HFam2	Keyword	Total Score
276	*Talinum caffrum* (Thunb.) Eckl. & Zeyh.	PORTULACACEAE	1	0	2	15	0	3	0	2	0	0	4	27
277	*Adiantum capillus-veneris* L.	PTERIDACEAE	1	0	2	15	0	0	0	0	4	0	5	27
278	*Agathisanthemum bojeri* Klotzsch subsp. *bojeri*	RUBIACEAE	1	0	2	15	0	0	0	0	4	0	5	27
279	*Spermacoce natalensis* Hochst.	RUBIACEAE	1	0	2	15	0	0	0	1	4	0	4	27
280	*Jamesbrittenia filicaulis* (Benth.) Hilliard	SCROPHULARIACEAE	1	0	0	15	0	0	0	0	4	3	4	27
281	*Trema orientalis* (L.) Blume	ULMACEAE	1	0	2	15	0	3	2	1	0	0	3	27
282	*Agapanthus africanus* (L.) Hoffmanns.	ALLIACEAE	1	0	2	15	0	3	0	1.5	0	0	4	26.5
283	*Haemanthus albiflos* Jacq.	AMARYLLIDACEAE	1	1	2	15	0	3	0	1.5	0	0	3	26.5
284	*Peucedanum caffrum* (Meisn.) E.Phillips	APIACEAE	1	0	2	15	0	0	0	0.5	4	0	4	26.5
285	*Asparagus falcatus* L.	ASPARAGACEAE	1	0	2	15	0	0	0	0.5	0	0	8	26.5
286	*Asparagus suaveolens* Burch.	ASPARAGACEAE	1	0	2	15	0	0	0	0.5	0	0	8	26.5
287	*Dracaena aletriformis* (Haw.) Bos	DRACAENACEAE	1	0	2	15	0	0	0	0.5	0	0	8	26.5
288	*Diospyros lycioides* Desf. subsp. *lycioides*	EBENACEAE	1	0	2	15	0	3	0	0.5	0	0	5	26.5
289	*Dichrostachys cinerea* (L.) Wight & Arn. subsp. *cinerea*	FABACEAE	0	0	0	15	0	0	0	0.5	0	3	8	26.5
290	*Entada rheedii* Spreng.	FABACEAE	1	0	2	15	0	0	2	0.5	0	3	3	26.5
291	*Tephrosia kraussiana* Meisn.	FABACEAE	1	0	2	15	0	0	2	0.5	0	3	3	26.5
292	*Dissotis canescens* (E.Mey. ex R.A.Graham) Hook.f.	MELASTOMATACEAE	1	0	2	15	0	0	0	0.5	0	0	8	26.5

Table 4.36 (continued)

Rank No.	Taxon	Family	Indg.	End.	*FSA* (med)	Treat.	Assoc.	Tox.	Red Data	Trade	HFam1	HFam2	Keyword	Total Score
293	*Ficus ingens* (Miq.) Miq. var. *ingens*	MORACEAE	1	0	2	15	0	3	0	0.5	0	0	5	26.5
294	*Ficus sycomorus* L. subsp. *sycomorus*	MORACEAE	1	0	2	15	0	0	0	0.5	0	0	8	26.5
295	*Pittosporum viridiflorum* Sims	PITTOSPORACEAE	1	0	2	15	0	3	0	1.5	0	0	4	26.5
296	*Cymbopogon excavatus* (Hochst.) Stapf ex Burtt Davy	POACEAE	0	0	2	15	0	3	0	1.5	0	0	5	26.5
297	*Rumex sagittatus* Thunb.	POLYGONACEAE	1	0	2	15	0	0	0	0.5	0	0	8	26.5
298	*Clematis brachiata* Thunb.	RANUNCULACEAE	1	0	2	15	0	3	0	1.5	0	0	4	26.5
299	*Rubia cordifolia* L. subsp. *conotricha* (Gand.) Verdc.	RUBIACEAE	1	0	2	15	0	0	0	0.5	4	0	4	26.5
300	*Cyphostemma barbosae* Wild & R.B.Drumm.	VITACEAE	1	0	0	15	0	0	2	0.5	0	3	5	26.5
301	*Anacardium occidentale* L.	ANACARDIACEAE	0	0	2	15	0	3	0	0	0	3	3	26
302	*Mangifera indica* L.	ANACARDIACEAE	0	0	2	15	0	3	0	0	0	3	3	26
303	*Alepidea pilifera* Weim.	APIACEAE	1	0	2	15	0	0	0	0	4	0	4	26
304	*Alepidea setifera* N.E.Br.	APIACEAE	1	0	2	15	0	0	0	0	4	0	4	26
305	*Centella coriacea* Nannf.	ARALIACEAE	1	0	2	15	0	0	0	0	0	0	8	26
306	*Phoenix reclinata* Jacq.	ARECACEAE	1	0	2	15	0	0	0	0	0	0	8	26
307	*Asparagus exuvialis* Burch. forma *exuvialis*	ASPARAGACEAE	1	0	2	15	0	0	0	0	0	0	8	26
308	*Asparagus retrofractus* L.	ASPARAGACEAE	1	0	2	15	0	0	0	0	0	0	8	26
309	*Asparagus striatus* (L.f.) Thunb.	ASPARAGACEAE	1	0	2	15	0	0	0	0	0	0	8	26
310	*Catophractes alexandri* D.Don	BIGNONIACEAE	1	0	2	15	0	0	2	0	0	3	3	26

Table 4.36 (continued)

Rank No.	Taxon	Family	Indg.	End.	*FSA* (med)	Treat.	Assoc.	Tox.	Red Data	Trade	HFam1	HFam2	Keyword	Total Score
311	*Trichodesma zeylanicum* (Burm.) R.Br.	BORAGINACEAE	1	0	2	15	0	0	0	0	0	0	8	26
312	*Cephalaria zeyheriana* Szabó	DIPSACACEAE	1	0	2	15	0	0	0	0	0	0	8	26
313	*Albizia antunesiana* Harms	FABACEAE	1	0	2	15	0	0	2	0	0	3	3	26
314	*Bauhinia galpinii* N.E.Br.	FABACEAE	1	0	2	15	0	0	0	0	0	3	5	26
315	*Indigofera hirsuta* L. var. *hirsuta*	FABACEAE	1	0	0	15	0	3	0	0	0	3	4	26
316	*Indigofera tenuissima* E.Mey.	FABACEAE	1	1	2	15	0	0	0	0	0	3	4	26
317	*Senna occidentalis* (L.) Link	FABACEAE	0	0	2	15	0	3	0	0	0	3	3	26
318	*Tamarindus indica* L.	FABACEAE	0	0	2	15	0	3	0	0	0	3	3	26
319	*Tephrosia macropoda* (E.Mey.) Harv. var. *macropoda*	FABACEAE	1	0	0	15	0	3	0	0	0	3	4	26
320	*Tephrosia purpurea* (L.) Pers. subsp. *purpurea*	FABACEAE	0	0	2	15	0	3	0	0	0	3	3	26
321	*Pelargonium cucullatum* (L.) L'Hér. subsp. *cucullatum*	GERANIACEAE	1	1	0	15	0	0	0	0	4	0	5	26
322	*Pelargonium graveolens* L'Hér.	GERANIACEAE	1	0	2	15	0	0	0	0	4	0	4	26
323	*Gladiolus dalenii* Van Geel subsp. *dalenii*	IRIDACEAE	1	0	2	15	0	3	0	1	0	0	4	26
324	*Hibiscus micranthus* L.f. var. *micranthus*	MALVACEAE	1	0	2	15	0	3	0	0	0	0	5	26
325	*Olinia rochetiana* Juss.	OLINIACEAE	1	0	2	15	0	3	0	0	0	0	5	26
326	*Phytolacca heptandra* Retz.	PHYTOLACCACEAE	1	0	2	15	0	3	0	0	0	0	5	26
327	*Protea repens* (L.) L.	PROTEACEAE	1	1	2	15	0	3	0	0	0	0	4	26
328	*Cheilanthes eckloniana* (Kunze) Mett.	PTERIDACEAE	1	0	2	15	0	0	0	0	4	0	4	26

Table 4.36 (continued)

Rank No.	Taxon	Family	Indg.	End.	*FSA* (med)	Treat.	Assoc.	Tox.	Red Data	Trade	HFam1	HFam2	Keyword	Total Score
329	*Agrimonia bracteata* E.Mey. ex C.A.Mey.	ROSACEAE	1	0	2	15	0	3	0	0	4	0	1	26
330	*Rubus pinnatus* Willd.	ROSACEAE	1	0	2	15	0	0	0	0	4	0	4	26
331	*Canthium inerme* (L.f.) Kuntze	RUBIACEAE	1	0	2	15	0	0	0	1	4	0	3	26
332	*Galium mucroniferum* Sond. var. *dregeanum* (Sond.) Puff	RUBIACEAE	1	0	2	15	0	0	0	0	4	0	4	26
333	*Solanum americanum* Mill.	SOLANACEAE	1	0	2	15	0	3	0	0	0	0	5	26
334	*Cissus nymphaeifolia* (Welw. ex Baker) Planch.	VITACEAE	1	0	2	15	0	0	0	0	0	3	5	26
335	*Elaeodendron croceum* (Thunb.) DC.	CELASTRACEAE	1	0	2	15	0	3	0	0.5	0	0	4	25.5
336	*Elaeodendron transvaalense* (Burtt Davy) R.H.Archer	CELASTRACEAE	1	0	2	15	0	3	0	1.5	0	0	3	25.5
337	*Abrus precatorius* L. subsp. *precatorius*	FABACEAE	0	0	0	15	0	3	0	0.5	0	3	4	25.5
338	*Piliostigma thonningii* (Schumach.) Milne-Redh.	FABACEAE	1	0	2	15	0	0	0	0.5	0	3	4	25.5
339	*Rhynchosia sublobata* (Schumach.) Meikle	FABACEAE	1	0	2	15	0	0	0	0.5	0	3	4	25.5
340	*Phytolacca americana* L.	PHYTOLACCACEAE	1	0	2	15	0	3	0	0.5	0	0	4	25.5
341	*Ranunculus multifidus* Forssk.	RANUNCULACEAE	1	0	2	15	0	3	0	1.5	0	0	3	25.5
342	*Catunaregam obovata* (Hochst.) Gonc.	RUBIACEAE	1	0	0	15	0	0	0	0.5	4	0	5	25.5
343	*Mimusops zeyheri* Sond.	SAPOTACEAE	1	0	2	15	0	3	0	0.5	0	0	4	25.5
344	*Hypoestes aristata* (Vahl) Sol. ex Roem. & Schult. var. *aristata*	ACANTHACEAE	1	0	2	15	0	0	0	0	0	3	4	25
345	*Pseuderanthemum hildebrandtii* Lindau	ACANTHACEAE	1	1	0	15	0	0	0	0	0	3	5	25

Table 4.36 (continued)

Rank No.	Taxon	Family	Indg.	End.	*FSA* (med)	Treat.	Assoc.	Tox.	Red Data	Trade	HFam1	HFam2	Keyword	Total Score
346	*Ozoroa sphaerocarpa* R.& A.Fern.	ANACARDIACEAE	1	0	2	15	0	0	0	0	0	3	4	25
347	*Rhus burchellii* Sond. ex Engl.	ANACARDIACEAE	1	0	2	15	0	0	0	0	0	3	4	25
348	*Anthriscus sylvestris* (L.) Hoffm. var. *sylvestris*	APIACEAE	0	0	2	15	0	0	0	0	4	0	4	25
349	*Peucedanum capense* (Thunb.) Sond. var. *capense*	APIACEAE	1	0	0	15	0	0	0	0	4	0	5	25
350	*Bulbine asphodeloides* (L.) Spreng.	ASPHODELACEAE	1	0	0	15	0	0	0	1	0	0	8	25
351	*Sphaeranthus peduncularis* DC.	ASTERACEAE	1	0	0	15	0	0	0	0	8	0	1	25
352	*Nuxia floribunda* Benth.	BUDDLEJACEAE	1	0	2	15	0	0	0	1	0	3	3	25
353	*Pterocelastrus rostratus* (Thunb.) Walp.	CELASTRACEAE	1	0	0	15	0	0	0	1	0	0	8	25
354	*Combretum erythrophyllum* (Burch.) Sond.	COMBRETACEAE	1	0	2	15	0	3	0	1	0	0	3	25
355	*Dioscorea sylvatica* (Kunth) Eckl. var. *brevipes* (Burtt Davy) Burkill	DIOSCOREACEAE	1	0	0	15	0	3	0	2	0	0	4	25
356	*Acacia ataxacantha* DC.	FABACEAE	1	0	2	15	0	0	0	0	0	3	4	25
357	*Acacia erioloba* E.Mey.	FABACEAE	1	0	2	15	0	3	0	0	0	3	1	25
358	*Adenopodia spicata* (E.Mey.) C.Presl	FABACEAE	1	0	2	15	0	0	0	0	0	3	4	25
359	*Leucaena leucocephala* (Lam.) de Wit subsp. *leucocephala*	FABACEAE	0	0	0	15	0	3	0	0	0	3	4	25
360	*Lotus discolor* E.Mey. subsp. *discolor*	FABACEAE	1	0	2	15	0	0	0	0	0	3	4	25

Table 4.36 (continued)

Rank No.	Taxon	Family	Indg.	End.	*FSA* (med)	Treat.	Assoc.	Tox.	Red Data	Trade	HFam1	HFam2	Keyword	Total Score
361	*Swartzia madagascariensis* Desv.	FABACEAE	1	0	2	15	0	3	0	0	0	3	1	25
362	*Tephrosia semiglabra* Sond.	FABACEAE	1	0	2	15	0	0	0	0	0	3	4	25
363	*Vigna unguiculata* (L.) Walp. subsp. *unguiculata*	FABACEAE	1	0	2	15	0	0	0	0	0	3	4	25
364	*Aristea ecklonii* Baker	IRIDACEAE	1	0	2	15	0	3	0	1	0	0	3	25
365	*Lycopodium clavatum* L.	LYCOPODIACEAE	1	0	0	15	0	3	0	1	0	0	5	25
366	*Myrsine africana* L.	MYRSINACEAE	1	0	2	15	0	3	0	0	0	0	4	25
367	*Phytolacca octandra* L.	PHYTOLACCACEAE	1	0	2	15	0	3	0	0	0	0	4	25
368	*Adiantum aethiopicum* L.	PTERIDACEAE	1	0	2	15	0	0	0	0	4	0	3	25
369	*Datura innoxia* Mill.	SOLANACEAE	0	0	2	15	0	3	0	0	0	0	5	25
370	*Datura stramonium* L.	SOLANACEAE	0	0	2	15	0	3	0	0	0	0	5	25
371	*Solanum panduriforme* E.Mey.	SOLANACEAE	1	0	2	15	0	3	0	0	0	0	4	25
372	*Gnidia anthylloides* (L.f.) Gilg	THYMELAEACEAE	1	1	2	15	0	3	0	0	0	0	3	25
373	*Balanites maughamii* Sprague subsp. *maughamii*	BALANITACEAE	0	0	2	15	0	3	0	1.5	0	0	3	24.5
374	*Pterocelastrus echinatus* N.E.Br.	CELASTRACEAE	1	0	2	15	0	0	0	1.5	0	0	5	24.5
375	*Pterocarpus rotundifolius* (Sond.) Druce subsp. *rotundifolius*	FABACEAE	1	0	2	15	0	0	0	0.5	0	3	3	24.5
376	*Gerrardina foliosa* Oliv.	FLACOURTIACEAE	1	0	2	15	0	0	0	0.5	0	3	3	24.5
377	*Morella serrata* (Lam.) Killick	MYRICACEAE	1	0	0	15	0	3	2	0.5	0	0	3	24.5
378	*Rapanea melanophloeos* (L.) Mez	MYRSINACEAE	1	0	2	15	0	3	0	2.5	0	0	1	24.5

Table 4.36 (continued)

Rank No.	Taxon	Family	Indg.	End.	*FSA* (med)	Treat.	Assoc.	Tox.	Red Data	Trade	HFam1	HFam2	Keyword	Total Score
379	*Pellaea calomelanos* (Sw.) Link var. *calomelanos*	PTERIDACEAE	1	0	0	15	0	0	0	0.5	4	0	4	24.5
380	*Viscum capense* L.f. subsp. *capense*	VISCACEAE	1	0	0	15	0	3	0	0.5	0	0	5	24.5
381	*Justicia betonica* L.	ACANTHACEAE	1	0	2	15	0	0	0	0	0	3	3	24
382	*Justicia flava* (Vahl) Vahl	ACANTHACEAE	1	0	2	15	0	0	0	0	0	3	3	24
383	*Rhus natalensis* Bernh. ex C.Krauss var. *natalensis*	ANACARDIACEAE	1	0	2	15	0	0	0	0	0	3	3	24
384	*Ceropegia linearis* E.Mey. subsp. *woodii* (Schltr.) H.Huber	ASCLEPIADACEAE	1	0	2	15	0	0	2	0	0	0	4	24
385	*Gomphocarpus fruticosus* (L.) Aiton f. subsp. *fruticosus*	ASCLEPIADACEAE	1	0	0	15	0	0	0	0	0	0	8	24
386	*Aloe asperifolia* A.Berger	ASPHODELACEAE	1	0	2	15	0	0	2	0	0	0	4	24
387	*Aloe dichotoma* Masson var. *dichotoma*	ASPHODELACEAE	1	0	0	15	0	0	0	0	0	0	8	24
388	*Asplenium trichomanes* L.	ASPLENIACEAE	1	0	2	15	0	0	2	0	0	0	4	24
389	*Markhamia zanzibarica* (Bojer ex DC.) K.Schum.	BIGNONIACEAE	1	0	2	15	0	0	0	0	0	3	3	24
390	*Lepidium capense* Thunb.	BRASSICACEAE	1	0	2	15	0	3	0	0	0	0	3	24
391	*Silene burchellii* Otth var. *burchellii*	CARYOPHYLLACEAE	1	0	0	15	0	0	0	0	0	0	8	24
392	*Ipomoea wightii* (Wall.) Choisy	CONVOLVULACEAE	1	0	2	15	0	3	0	0	0	0	3	24
393	*Dioscorea sylvatica* (Kunth) Eckl. var. *sylvatica*	DIOSCOREACEAE	1	0	2	15	0	0	0	2	0	0	4	24
394	*Euclea divinorum* Hiern	EBENACEAE	1	0	2	15	0	0	0	2	0	0	4	24

Table 4.36 (continued)

Rank No.	Taxon	Family	Indg.	End.	*FSA* (med)	Treat.	Assoc.	Tox.	Red Data	Trade	HFam1	HFam2	Keyword	Total Score
395	*Acacia arenaria* Schinz	FABACEAE	1	0	2	15	0	0	0	0	0	3	3	24
396	*Acacia gerrardii* Benth. subsp. *gerrardii* var. *gerrardii*	FABACEAE	1	0	2	15	0	0	0	0	0	3	3	24
397	*Crotalaria laburnifolia* L. subsp. *australis* (Baker f.) Polhill	FABACEAE	1	0	0	15	0	0	2	0	0	3	3	24
398	*Entada wahlbergii* Harv.	FABACEAE	1	0	0	15	0	0	0	0	0	3	5	24
399	*Indigofera spicata* Forssk. var. *spicata*	FABACEAE	1	0	2	15	0	0	0	0	0	3	3	24
400	*Sutherlandia microphylla* Burch. ex DC.	FABACEAE	1	0	2	15	0	0	0	0	0	3	3	24
401	*Tephrosia acaciifolia* Baker	FABACEAE	1	0	2	15	0	0	0	0	0	3	3	24
402	*Tephrosia cephalantha* Welw. ex Baker var. *decumbens* Welw. ex Baker	FABACEAE	1	0	2	15	0	0	0	0	0	3	3	24
403	*Sesamum indicum* L.	PEDALIACEAE	0	0	2	15	0	3	0	0	0	3	1	24
404	*Coix lacryma-jobi* L.	POACEAE	0	0	2	15	0	3	0	0	0	0	4	24
405	*Polygala sphenoptera* Fresen. var. *sphenoptera*	POLYGALACEAE	1	0	2	15	0	0	0	0	0	3	3	24
406	*Anemone caffra* (Eckl. & Zeyh.) Harv.	RANUNCULACEAE	1	1	2	15	0	0	0	1	0	0	4	24
407	*Cliffortia ilicifolia* L. var. *ilicifolia*	ROSACEAE	1	1	0	15	0	0	0	0	4	0	3	24
408	*Galium thunbergianum* Eckl. & Zeyh. var. *thunbergianum*	RUBIACEAE	1	0	0	15	0	0	0	0	4	0	4	24
409	*Pavetta capensis* (Houtt.) Bremek. subsp. *capensis*	RUBIACEAE	1	1	0	15	0	0	0	0	4	0	3	24

Table 4.36 (continued)

Rank No.	Taxon	Family	Indg.	End.	*FSA* (med)	Treat.	Assoc.	Tox.	Red Data	Trade	HFam1	HFam2	Keyword	Total Score
410	*Salix mucronata* Thunb. subsp. *mucronata*	SALICACEAE	1	0	2	15	0	0	0	0	0	3	3	24
411	*Kirkia acuminata* Oliv.	SIMAROUBACEAE	1	0	2	15	0	0	0	0	0	3	3	24
412	*Solanum aculeatissimum* Jacq.	SOLANACEAE	1	0	2	15	0	3	0	0	0	0	3	24
413	*Viscum rotundifolium* L.f.	VISCACEAE	1	0	2	15	0	0	2	0	0	0	4	24
414	*Kniphofia laxiflora* Kunth	ASPHODELACEAE	1	1	2	15	0	0	0	0.5	0	0	4	23.5
415	*Combretum molle* R.Br. ex G.Don	COMBRETACEAE	1	0	2	15	0	0	0	0.5	0	0	5	23.5
416	*Ximenia americana* L. var. *americana*	OLACACEAE	1	0	2	15	0	0	2	0.5	0	0	3	23.5
417	*Isoglossa woodii* C.B.Clarke	ACANTHACEAE	1	1	0	15	0	0	0	0	0	3	3	23
418	*Boophone disticha* (L.f.) Herb.	AMARYLLIDACEAE	1	0	0	15	0	3	0	0	0	0	4	23
419	*Alepidea longifolia* E.Mey. var. *longifolia*	APIACEAE	1	0	0	15	0	0	0	0	4	0	3	23
420	*Balanites aegyptiaca* (L.) Delile var. *aegyptiaca*	BALANITACEAE	1	0	2	15	0	0	0	0	0	0	5	23
421	*Capparis sepiaria* L. var. *citrifolia* (Lam.) Toelken	CAPPARACEAE	1	0	2	15	0	0	0	1	0	0	4	23
422	*Gymnosporia heterophylla* (Eckl. & Zeyh.) Loes.	CELASTRACEAE	1	0	0	15	0	3	0	0	0	0	4	23
423	*Combretum collinum* Fresen. subsp. *gazense* (Swynn. & Baker f.) Okafor	COMBRETACEAE	1	0	2	15	0	0	0	0	0	0	5	23
424	*Cyperus rotundus* L. subsp. *rotundus*	CYPERACEAE	1	0	0	15	0	3	0	0	0	0	4	23

Table 4.36 (continued)

Rank No.	Taxon	Family	Indg.	End.	*FSA* (med)	Treat.	Assoc.	Tox.	Red Data	Trade	HFam1	HFam2	Keyword	Total Score
425	*Acacia brevispica* Harms subsp. *dregeana* (Benth.) Brenan	FABACEAE	1	0	0	15	0	0	0	0	0	3	4	23
426	*Cassia abbreviata* Oliv. subsp. *abbreviata*	FABACEAE	0	0	0	15	0	0	0	1	0	3	4	23
427	*Dialium englerianum* Henriq.	FABACEAE	1	0	0	15	0	3	0	0	0	3	1	23
428	*Tephrosia aequilata* Baker subsp. *australis* Brummitt	FABACEAE	1	0	0	15	0	0	0	0	0	3	4	23
429	*Tephrosia pumila* (Lam.) Pers. var. *pumila*	FABACEAE	1	0	0	15	0	0	0	0	0	3	4	23
430	*Anthocleista grandiflora* Gilg	GENTIANACEAE	1	0	2	15	0	0	0	0	0	0	5	23
431	*Drimia altissima* (L.f.) Ker Gaul.	HYACINTHACEAE	0	0	0	15	0	3	0	0	0	0	5	23
432	*Empodium plicatum* (Thunb.) Garside	HYPOXIDACEAE	1	1	2	15	0	0	0	0	0	0	4	23
433	*Tapinanthus oleifolius* (J.C.Wendl.) Danser	LORANTHACEAE	1	0	2	15	0	0	2	0	0	0	3	23
434	*Plantago major* L.	PLANTAGINACEAE	0	0	2	15	0	0	0	0	0	3	3	23
435	*Cymbopogon marginatus* (Steud.) Stapf ex Burtt Davy	POACEAE	1	0	2	15	0	0	0	1	0	0	4	23
436	*Rumex acetosella* L. subsp. *angiocarpus* (Murb.) Murb.	POLYGONACEAE	0	0	0	15	0	0	0	0	0	0	8	23
437	*Pentas micrantha* Baker subsp. *wyliei* (N.E.Br.) Verdc.	RUBIACEAE	1	0	0	15	0	0	2	0	4	0	1	23
438	*Tarenna pavettoides* (Harv.) Sim subsp. *pavettoides*	RUBIACEAE	1	0	0	15	0	0	0	0	4	0	3	23
439	*Hermannia geniculata* Eckl. & Zeyh.	STERCULIACEAE	1	0	2	15	0	0	0	0	0	0	5	23

Table 4.36 (continued)

Rank No.	Taxon	Family	Indg.	End.	*FSA* (med)	Treat.	Assoc.	Tox.	Red Data	Trade	HFam1	HFam2	Keyword	Total Score
440	*Asparagus setaceus* (Kunth) Jessop	ASPARAGACEAE	1	0	2	15	0	0	0	1.5	0	0	3	22.5
441	*Pterocelastrus tricuspidatus* (Lam.) Walp.	CELASTRACEAE	1	1	0	15	0	0	0	0.5	0	0	5	22.5
442	*Combretum hereroense* Schinz	COMBRETACEAE	1	0	0	15	0	3	0	0.5	0	0	3	22.5
443	*Abutilon angulatum* (Guill. & Perr.) Mast. var. *angulatum*	MALVACEAE	1	0	2	15	0	0	0	0.5	0	0	4	22.5
444	*Hibiscus pusillus* Thunb.	MALVACEAE	1	0	2	15	0	0	0	0.5	0	0	4	22.5
445	*Imperata cylindrica* (L.) Raeusch.	POACEAE	1	0	2	15	0	0	0	0.5	0	0	4	22.5
446	*Grewia flava* DC.	TILIACEAE	1	0	2	15	0	0	0	0.5	0	0	4	22.5
447	*Agave americana* L. subsp. *americana* var. *americana*	AGAVACEAE	0	0	0	15	0	3	0	0	0	0	4	22
448	*Tulbaghia acutiloba* Harv.	ALLIACEAE	1	0	2	15	0	0	0	0	0	0	4	22
449	*Mohria caffrorum* (L.) Desv.	ANEMIACEAE	1	0	2	15	0	0	0	0	0	0	4	22
450	*Aloe hereroensis* Engl. var. *hereroensis*	ASPHODELACEAE	1	0	0	15	0	0	2	0	0	0	4	22
451	*Asplenium monanthes* L.	ASPLENIACEAE	1	0	2	15	0	0	0	0	0	0	4	22
452	*Lepidium pinnatum* Thunb.	BRASSICACEAE	1	1	2	15	0	0	0	0	0	0	3	22
453	*Nuxia congesta* R.Br. ex Fresen.	BUDDLEJACEAE	1	0	2	15	0	0	0	0	0	3	1	22
454	*Rhipsalis baccifera* (J.Mill.) Stearn subsp. *baccifera*	CACTACEAE	0	0	2	15	0	0	0	1	0	0	4	22
455	*Atriplex vestita* (Thunb.) Aellen var. *inappendiculata* Aellen	CHENOPODIACEAE	1	1	0	15	0	0	0	0	0	0	5	22

Table 4.36 (continued)

Rank No.	Taxon	Family	Indg.	End.	*FSA* (med)	Treat.	Assoc.	Tox.	Red Data	Trade	HFam1	HFam2	Keyword	Total Score
456	*Combretum platypetalum* Welw. ex M.A.Lawson subsp. *baumii* (Engl. & Gilg) Exell	COMBRETACEAE	1	0	0	15	0	0	0	0	0	0	6	22
457	*Terminalia sericea* Burch. ex DC.	COMBRETACEAE	1	0	0	15	0	3	0	2	0	0	1	22
458	*Alysicarpus rugosus* (Willd.) DC. subsp. *rugosus*	FABACEAE	1	0	0	15	0	0	0	0	0	3	3	22
459	*Tephrosia noctiflora* Bojer ex Baker	FABACEAE	1	0	2	15	0	0	0	0	0	3	1	22
460	*Trifolium hybridum* L. var. *hybridum*	FABACEAE	0	0	0	0	8	3	0	0	0	3	8	22
461	*Enicostema axillare* (Lam.) A.Raynal subsp. *axillare*	GENTIANACEAE	1	0	2	15	0	0	0	0	0	0	4	22
462	*Hibiscus diversifolius* Jacq. subsp. *diversifolius*	MALVACEAE	1	1	0	15	0	0	0	0	0	0	5	22
463	*Hibiscus sabdariffa* L.	MALVACEAE	0	0	2	15	0	0	0	0	0	0	5	22
464	*Hibiscus tiliaceus* L. subsp. *tiliaceus*	MALVACEAE	1	0	2	15	0	0	0	0	0	0	4	22
465	*Pavonia burchellii* (DC.) R.A.Dyer	MALVACEAE	1	0	2	15	0	0	0	0	0	0	4	22
466	*Basananthe heterophylla* Schinz	PASSIFLORACEAE	1	0	2	15	0	0	0	0	0	3	1	22
467	*Polygala erioptera* DC. subsp. *erioptera*	POLYGALACEAE	1	0	0	15	0	0	0	0	0	3	3	22
468	*Faurea saligna* Harv.	PROTEACEAE	1	0	2	15	0	0	0	1	0	0	3	22
469	*Smilax anceps* Willd.	SMILACACEAE	1	0	0	15	0	3	0	0	0	0	3	22
470	*Solanum anguivi* Lam.	SOLANACEAE	1	0	2	15	0	0	0	0	0	0	4	22
471	*Grewia bicolor* Juss. var. *bicolor*	TILIACEAE	1	0	2	15	0	0	0	0	0	0	4	22
472	*Rinorea ilicifolia* (Welw. ex Oliv.) Kuntze subsp. *ilicifolia* var. *ilicifolia*	VIOLACEAE	1	0	0	15	0	0	0	0	0	3	3	22

Table 4.36 (continued)

Rank No.	Taxon	Family	Indg.	End.	*FSA* (med)	Treat.	Assoc.	Tox.	Red Data	Trade	HFam1	HFam2	Keyword	Total Score
473	*Kniphofia rooperi* (T.Moore) Lem.	ASPHODELACEAE	1	1	0	15	0	0	0	0.5	0	0	4	21.5
474	*Capparis brassii* DC.	CAPPARACEAE	1	0	2	15	0	0	0	0.5	0	0	3	21.5
475	*Euclea crispa* (Thunb.) Gürke subsp. *crispa*	EBENACEAE	1	0	2	15	0	0	0	0.5	0	0	3	21.5
476	*Sideroxylon inerme* L. subsp. *inerme*	SAPOTACEAE	1	0	2	15	0	0	0	0.5	0	0	3	21.5
477	*Smilax kraussiana* Meisn.	SMILACACEAE	0	0	0	15	0	3	0	0.5	0	0	3	21.5
478	*Achyranthes aspera* L. var. *aspera*	AMARANTHACEAE	0	0	2	15	0	0	0	0	0	0	4	21
479	*Celosia argentea* L. forma *argentea*	AMARANTHACEAE	1	0	2	15	0	0	0	0	0	0	3	21
480	*Gomphrena globosa* L.	AMARANTHACEAE	0	0	2	15	0	0	0	0	0	0	4	21
481	*Brunsvigia radulosa* Herb.	AMARYLLIDACEAE	1	0	2	15	0	0	0	0	0	0	3	21
482	*Schefflera umbellifera* (Sond.) Baill.	ARALIACEAE	1	0	2	15	0	0	0	0	0	0	3	21
483	*Calotropis procera* (Aiton) Aiton f.	ASCLEPIADACEAE	1	0	0	15	0	0	0	0	0	0	5	21
484	*Lepidium schinzii* Thell.	BRASSICACEAE	1	0	2	15	0	0	0	0	0	0	3	21
485	*Wahlenbergia abyssinica* (Hochst. ex A.Rich.) Thulin subsp. *abyssinica*	CAMPANULACEAE	1	0	2	15	0	0	0	0	0	0	3	21
486	*Combretum adenogonium* Steud. ex A.Rich.	COMBRETACEAE	1	0	2	15	0	0	0	0	0	0	3	21
487	*Combretum microphyllum* Klotzsch	COMBRETACEAE	1	0	2	15	0	0	0	0	0	0	3	21
488	*Terminalia prunioides* M.A.Lawson	COMBRETACEAE	1	0	2	15	0	0	0	0	0	0	3	21
489	*Philenoptera bussei* (Harms) Schrire	FABACEAE	0	0	2	15	0	0	0	0	0	3	1	21
490	*Drimia elata* Jacq.	HYACINTHACEAE	1	0	2	15	0	0	0	2	0	0	1	21
491	*Lobelia anceps* L.f.	LOBELIACEAE	1	0	2	15	0	0	0	0	0	0	3	21

Table 4.36 (continued)

Rank No.	Taxon	Family	Indg.	End.	*FSA* (med)	Treat.	Assoc.	Tox.	Red Data	Trade	HFam1	HFam2	Keyword	Total Score
492	*Lycopodiella cernua* (L.) Pic.Serm.	LYCOPODIACEAE	1	0	2	15	0	0	0	0	0	0	3	21
493	*Tinospora fragosa* (I.Verd.) I.Verd. & Troupin	MENISPERMACEAE	1	0	2	15	0	0	0	0	0	0	3	21
494	*Oxalis corniculata* L.	OXALIDACEAE	0	0	2	15	0	3	0	0	0	0	1	21
495	*Piper capense* L.f. var. *capense*	PIPERACEAE	1	0	2	15	0	0	0	0	0	0	3	21
496	*Sporobolus festivus* A.Rich.	POACEAE	1	0	2	15	0	0	0	0	0	0	3	21
497	*Oxygonum dregeanum* Meisn. subsp. *dregeanum*	POLYGONACEAE	1	0	2	15	0	0	0	0	0	0	3	21
498	*Salvadora persica* L. var. *persica*	SALVADORACEAE	1	0	0	15	0	0	0	0	0	0	5	21
499	*Nicotiana tabacum* L.	SOLANACEAE	0	0	2	15	0	3	0	0	0	0	1	21
500	*Cola natalensis* Oliv.	STERCULIACEAE	1	0	0	15	0	0	0	0	0	0	5	21
501	*Hermannia coccocarpa* (Eckl. & Zeyh.) Kuntze	STERCULIACEAE	1	0	2	15	0	0	0	0	0	0	3	21
502	*Hermannia depressa* N.E.Br.	STERCULIACEAE	1	0	2	15	0	0	0	0	0	0	3	21
503	*Waltheria indica* L.	STERCULIACEAE	1	0	2	15	0	0	0	0	0	0	3	21
504	*Triumfetta rhomboidea* Jacq. var. *rhomboidea*	TILIACEAE	1	0	2	15	0	0	0	0	0	0	3	21
505	*Stephania abyssinica* (Quart.-Dill. & A.Rich.) Walp. var. *abyssinica*	MENISPERMACEAE	1	0	0	15	0	0	0	0.5	0	0	4	20.5
506	*Hesperantha baurii* Baker subsp. *baurii*	IRIDACEAE	1	0	0	15	0	0	0	0	0	0	4	20
507	*Eleusine coracana* (L.) Gaertn. subsp. *africana* (Kenn.-O'Byrne) Hilu & de Wet	POACEAE	1	0	0	15	0	0	0	0	0	0	4	20
508	*Oxygonum delagoense* Kuntze	POLYGONACEAE	1	0	0	15	0	0	0	0	0	0	4	20

Table 4.36 (continued)

Rank No.	Taxon	Family	Indg.	End.	*FSA* (med)	Treat.	Assoc.	Tox.	Red Data	Trade	HFam1	HFam2	Keyword	Total Score
509	*Protea speciosa* (L.) L.	PROTEACEAE	1	1	2	15	0	0	0	0	0	0	1	20
510	*Solanum lichtensteinii* Willd.	SOLANACEAE	1	0	0	15	0	0	0	0	0	0	4	20
511	*Melhania acuminata* Mast. var. *acuminata*	STERCULIACEAE	1	0	0	15	0	0	0	0	0	0	4	20
512	*Senecio serratuloides* DC. var. *serratuloides*	ASTERACEAE	1	0	2	0	0	3	0	1	8	0	4	19
513	*Polycarpaea eriantha* Hochst. ex A.Rich. var. *eriantha*	CARYOPHYLLACEAE	1	0	0	15	0	0	0	0	0	0	3	19
514	*Gymnosporia tenuispina* (Sond.) Szyszyl.	CELASTRACEAE	1	0	0	15	0	0	0	0	0	0	3	19
515	*Drimia sanguinea* (Schinz) Jessop	HYACINTHACEAE	0	0	0	15	0	3	0	0	0	0	1	19
516	*Abutilon mauritianum* (Jacq.) Medik.	MALVACEAE	1	0	2	15	0	0	0	0	0	0	1	19
517	*Gossypioides kirkii* (Mast.) Hutch.	MALVACEAE	1	0	2	15	0	0	0	0	0	0	1	19
518	*Hibiscus fuscus* Garcke	MALVACEAE	1	0	2	15	0	0	0	0	0	0	1	19
519	*Leersia hexandra* Sw.	POACEAE	1	0	2	15	0	0	0	0	0	0	1	19
520	*Lycium hirsutum* Dunal	SOLANACEAE	1	0	0	15	0	0	0	0	0	0	3	19
521	*Solanum linnaeanum* Hepper & Jaeger	SOLANACEAE	1	0	0	15	0	0	0	0	0	0	3	19
522	*Cannabis sativa* L. var. sativa	CANNABACEAE	0	0	0	15	0	0	0	0.5	0	0	3	18.5
523	*Nymphaea nouchali* Burm.f. var. *caerulea* (Savigny) Verdc.	NYMPHAEACEAE	0	0	0	15	0	0	0	0.5	0	0	3	18.5
524	*Clematis villosa* subsp. *villosa*	RANUNCULACEAE	0	0	0	15	0	0	0	0	0	0	3	18
525	*Struthiola hirsuta* Wikstr.	THYMELAEACEAE	1	1	0	15	0	0	0	0	0	0	1	18
526	*Lopholaena coriifolia* (Sond.) E.Phillips & C.A.Sm.	ASTERACEAE	1	0	2	0	0	3	0	0	8	0	3	17

Table 4.36 (continued)

Rank No.	Taxon	Family	Indg.	End.	*FSA* (med)	Treat.	Assoc.	Tox.	Red Data	Trade	HFam1	HFam2	Keyword	Total Score
527	*Vernonia amygdalina* Delile	ASTERACEAE	1	0	2	0	0	3	0	0	8	0	3	17
528	*Cyperus obtusiflorus* Vahl var. *obtusiflorus*	CYPERACEAE	1	0	0	15	0	0	0	0	0	0	1	17
529	*Eleusine indica* (L.) Gaertn. subsp. *indica*	POACEAE	1	0	0	15	0	0	0	0	0	0	1	17
530	*Thalictrum rhynchocarpum* Quart.-Dill. & A.Rich.	RANUNCULACEAE	1	0	0	15	0	0	0	0	0	0	1	17
531	*Sterculia rogersii* N.E.Br.	STERCULIACEAE	1	0	0	15	0	0	0	0	0	0	1	17
532	*Hypericum perforatum* L.	HYPERICACEAE	0	0	2	0	0	3	0	0.5	0	3	8	16.5
533	*Hoodia currorii* (Hook.) Decne. subsp. *currorii*	ASCLEPIADACEAE	0	0	0	15	0	0	0	0	0	0	1	16
534	*Eleusine indica* (L.) Gaertn. subsp. *africana* (Kenn.-O'Byrne) S.M.Phillips	POACEAE	0	0	0	15	0	0	0	0	0	0	1	16
535	*Harpagophytum procumbens* (Burch.) DC. ex Meisn. subsp. *procumbens*	PEDALIACEAE	1	0	0	0	0	0	2	1	0	3	8	15
536	*Crinum bulbispermum* (Burm.f.) Milne-Redh. & Schweick.	AMARYLLIDACEAE	1	0	2	0	0	3	0	0.5	0	0	8	14.5
537	*Helichrysum cymosum* (L.) D.Don subsp. *cymosum*	ASTERACEAE	1	1	0	0	0	0	0	1	8	0	3	14
538	*Helichrysum kraussii* Sch.Bip.	ASTERACEAE	1	0	2	0	0	0	0	0	8	0	3	14
539	*Pavetta schumanniana* F.Hoffm. ex K.Schum.	RUBIACEAE	1	0	2	0	0	3	0	0	4	0	4	14
540	*Sclerocarya birrea* (A.Rich.) Hochst. subsp. *caffra* (Sond.) Kokwaro	ANACARDIACEAE	1	0	2	0	0	3	0	1.5	0	3	3	13.5

Table 4.36 (continued)

Rank No.	Taxon	Family	Indg.	End.	*FSA* (med)	Treat.	Assoc.	Tox.	Red Data	Trade	HFam1	HFam2	Keyword	Total Score
541	*Pelargonium luridum* (Andrews) Sweet	GERANIACEAE	1	0	2	0	0	0	0	1	4	0	5	13
542	*Osmitopsis asteriscoides* (P.J.Bergius) Less.	ASTERACEAE	0	0	0	0	0	0	0	0	8	0	4	12
543	*Eucomis autumnalis* (Mill.) Chitt. subsp. *autumnalis*	HYACINTHACEAE	1	0	2	0	0	3	0	3	0	0	3	12
544	*Centella asiatica* (L.) Urb.	ARALIACEAE	1	0	2	0	0	0	0	0.5	0	0	8	11.5
545	*Fadogia homblei* De Wild.	RUBIACEAE	1	0	0	0	0	3	0	0	4	0	3	11
546	*Rhus lancea* L.f.	ANACARDIACEAE	1	0	2	0	0	0	0	0	0	3	4	10
547	*Rhus undulata* Jacq.	ANACARDIACEAE	1	0	2	0	0	0	0	0	0	3	4	10
548	*Indigofera dimidiata* Vogel ex Walp.	FABACEAE	1	0	2	0	0	0	0	0	0	3	4	10
549	*Sida acuta* Burm.f. subsp. *acuta*	MALVACEAE	1	0	2	0	0	3	0	0	0	0	4	10
550	*Morella humilis* (Cham. & Schltdl.) Killick	MYRICACEAE	1	1	0	0	0	0	0	0	0	0	8	10
551	*Vetiveria nigritana* (Benth.) Stapf	POACEAE	0	0	2	0	0	0	0	0	0	0	8	10
552	*Vangueriopsis lanciflora* (Hiern) Robyns ex R.D.Good	RUBIACEAE	1	0	2	0	0	0	0	0	4	0	3	10
553	*Dombeya rotundifolia* (Hochst.) Planch. var. *rotundifolia*	STERCULIACEAE	1	0	2	0	0	0	2	1	0	0	4	10
554	*Valeriana capensis* Thunb. var. *capensis*	VALERIANACEAE	1	0	0	0	0	0	0	0	4	0	5	10
555	*Lannea discolor* (Sond.) Engl.	ANACARDIACEAE	1	0	2	0	0	0	0	0	0	3	3	9
556	*Astripomoea malvacea* (Klotzsch) A.Meeuse	CONVOLVULACEAE	1	0	2	0	0	3	0	0	0	0	3	9
557	*Crotalaria laburnifolia* L. subsp. *laburnifolia*	FABACEAE	1	0	2	0	0	0	0	0	0	3	3	9

Table 4.36 (continued)

Rank No.	Taxon	Family	Indg.	End.	*FSA* (med)	Treat.	Assoc.	Tox.	Red Data	Trade	HFam1	HFam2	Keyword	Total Score
558	*Erythrina abyssinica* Lam. ex DC.	FABACEAE	0	0	0	0	0	3	0	0	0	3	3	9
559	*Strychnos potatorum* L.f.	STRYCHNACEAE	1	0	2	0	0	3	0	0	0	0	3	9
560	*Foeniculum vulgare* Mill. var. *vulgare*	APIACEAE	0	0	0	0	0	0	0	1.5	4	0	3	8.5
561	*Aeschynomene indica* L.	FABACEAE	1	0	0	0	0	0	0	0	0	3	4	8
562	*Elaeodendron matabelicum* Loes.	CELASTRACEAE	1	0	2	0	0	0	0	0.5	0	0	4	7.5
563	*Azanza garckeana* (F.Hoffm.) Exell & Hillc.	MALVACEAE	1	0	2	0	0	0	0	0	0	0	4	7
564	*Vahlia digyna* (Retz.) Kuntze	VAHLIACEAE	1	0	2	0	0	0	0	0	0	0	3	6
565	*Annona stenophylla* Engl. & Diels subsp. *nana* (Exell) N.Robson	ANNONACEAE	0	0	0	0	0	0	0	0	0	0	4	4
566	*Agelanthus natalitius* (Meisn.) Polhill & Wiens subsp. *natalitius*	LORANTHACEAE	1	0	0	0	0	0	0	0	0	0	3	4

Table 4.37 Shortlisted taxa for diabetes and the respective scores for weighted criteria

Rank No.	Taxon	Family	Indg.	End.	*FSA* (med)	Treat.	Assoc.	Tox.	Red Data	Trade	HFam1	HFam2	Keyword	Total Score
1	*Catharanthus roseus* (L.) G.Don	APOCYNACEAE	0	0	2	15	8	3	0	0	4	3	8	43
2	*Anacardium occidentale* L.	ANACARDIACEAE	0	0	2	15	8	3	0	0	0	3	8	39
3	*Artemisia afra* Jacq. ex Willd.	ASTERACEAE	1	0	2	15	0	3	0	2	4	3	8	38
4	*Cussonia spicata* Thunb.	ARALIACEAE	1	0	2	15	0	3	0	0.5	8	3	5	37.5
5	*Brachylaena elliptica* (Thunb.) DC.	ASTERACEAE	1	1	2	15	0	3	0	0	4	3	8	37
6	*Indigofera arrecta* Hochst. ex A.Rich.	FABACEAE	1	0	2	15	0	3	0	0	8	0	8	37
7	*Peltophorum africanum* Sond.	FABACEAE	1	0	2	15	0	3	2	1	8	0	5	37
8	*Sutherlandia frutescens* (L.) R.Br.	FABACEAE	1	0	2	15	0	3	0	0	8	0	8	37
9	*Momordica charantia* L.	CUCURBITACEAE	0	0	2	15	8	3	0	0	0	0	8	36
10	*Caesalpinia pulcherrima* (L.) Sw.	FABACEAE	0	0	2	15	0	3	0	0	8	0	8	36
11	*Senna occidentalis* (L.) Link	FABACEAE	0	0	2	15	0	3	0	0	8	0	8	36
12	*Psidium guajava* L.	MYRTACEAE	0	0	2	15	8	3	0	0	0	0	8	36
13	*Erythrophleum lasianthum* Corbishley	FABACEAE	1	0	2	15	0	3	0	1.5	8	0	5	35.5
14	*Cnicus benedictus* L.	ASTERACEAE	0	0	2	15	0	3	0	0	4	3	8	35
15	*Peucedanum galbanum* (L.) Drude	APIACEAE	1	1	2	15	0	3	0	0	4	3	5	34
16	*Brachylaena discolor* DC.	ASTERACEAE	1	0	2	15	0	0	0	1	4	3	8	34
17	*Flemingia grahamiana* Wight & Arn.	FABACEAE	1	0	2	15	0	0	0	0	8	0	8	34

Table 4.37 (continued)

Rank No.	Taxon	Family	Indg.	End.	*FSA* (med)	Treat.	Assoc.	Tox.	Red Data	Trade	HFam1	HFam2	Keyword	Total Score
18	*Leucaena leucocephala* (Lam.) de Wit subsp. *leucocephala*	FABACEAE	0	0	0	15	0	3	0	0	8	0	8	34
19	*Lupinus angustifolius* L.	FABACEAE	0	0	0	15	0	3	0	0	8	0	8	34
20	*Brachylaena ilicifolia* (Lam.) E.Phillips & Schweick.	ASTERACEAE	1	0	2	15	0	0	0	0.5	4	3	8	33.5
21	*Microglossa mespilifolia* (Less.) B.L.Rob.	ASTERACEAE	1	0	2	15	0	3	0	0.5	4	3	5	33.5
22	*Vernonia oligocephala* (DC.) Sch.Bip. ex Walp.	ASTERACEAE	1	0	2	15	0	0	0	0.5	4	3	8	33.5
23	*Hoodia currorii* (Hook.) Decne. subsp. *currorii*	ASCLEPIADACEAE	1	0	0	15	0	0	2	0	4	3	8	33
24	*Taraxacum officinale* Weber	ASTERACEAE	0	0	0	15	0	3	0	0	4	3	8	33
25	*Garcinia gerrardii* Harv. ex Sim	CLUSIACEAE	1	0	2	15	0	3	0	1	0	3	8	33
26	*Terminalia sericea* Burch. ex DC.	COMBRETACEAE	1	0	0	15	0	3	0	2	4	0	8	33
27	*Jatropha gossypifolia* L.	EUPHORBIACEAE	1	1	2	15	0	3	0	0	0	3	8	33
28	*Bridelia micrantha* (Hochst.) Baill.	EUPHORBIACEAE	1	0	2	15	0	3	0	0.5	0	3	8	32.5
29	*Tabernaemontana ventricosa* Hochst. ex A.DC.	APOCYNACEAE	1	0	2	15	0	0	0	0	4	3	7	32
30	*Vinca major* L.	APOCYNACEAE	0	0	2	15	0	3	0	0	4	3	5	32
31	*Cichorium intybus* L.	ASTERACEAE	0	0	2	15	0	3	0	0	4	3	5	32
32	*Dicoma anomala* Sond. subsp. *anomala*	ASTERACEAE	1	0	0	15	0	0	0	1	4	3	8	32
33	*Opuntia vulgaris* Mill.	CACTACEAE	0	0	2	15	0	3	0	0	4	0	8	32
34	*Catha edulis* (Vahl) Forssk. ex Endl.	CELASTRACEAE	1	0	2	15	0	3	2	1	0	0	8	32

Table 4.37 (continued)

Rank No.	Taxon	Family	Indg.	End.	*FSA* (med)	Treat.	Assoc.	Tox.	Red Data	Trade	HFam1	HFam2	Keyword	Total Score
35	*Flueggea virosa* (Roxb. ex Willd.) Voigt subsp. *virosa*	EUPHORBIACEAE	1	0	2	15	0	3	0	0	0	3	8	32
36	*Cassia abbreviata* Oliv. subsp. *abbreviata*	FABACEAE	0	0	0	15	0	0	0	1	8	0	8	32
37	*Gardenia ternifolia* Schumach. & Thonn. subsp. *jovis-tonantis* (Welw.) Verdc. var. *goetzei* (Stapf & Hutch.) Verdc.	RUBIACEAE	1	0	2	15	0	3	0	0	0	3	8	32
38	*Scoparia dulcis* L.	SCROPHULARIACEAE	0	0	2	15	0	3	0	0	4	0	8	32
39	*Piliostigma thonningii* (Schumach.) Milne-Redh.	FABACEAE	1	0	2	15	0	0	0	0.5	8	0	5	31.5
40	*Olax dissitiflora* Oliv.	OLACACEAE	1	0	2	15	0	3	2	0.5	0	0	8	31.5
41	*Mangifera indica* L.	ANACARDIACEAE	0	0	2	15	0	3	0	0	0	3	8	31
42	*Asclepias crispa* P.J.Bergius var. *crispa*	ASCLEPIADACEAE	1	1	2	15	0	0	0	0	4	3	5	31
43	*Gomphocarpus fruticosus* (L.) Aiton f. subsp. *fruticosus*	ASCLEPIADACEAE	1	0	0	15	0	0	0	0	4	3	8	31
44	*Marsdenia sylvestris* (Retz.) P.I.Forst.	ASCLEPIADACEAE	1	0	0	15	0	0	0	0	4	3	8	31
45	*Bulbine alooides* (L.) Willd.	ASPHODELACEAE	1	1	2	15	0	3	0	1	0	0	8	31
46	*Terminalia phanerophlebia* Engl. & Diels	COMBRETACEAE	1	0	2	15	0	0	0	1	4	0	8	31
47	*Jatropha curcas* L.	EUPHORBIACEAE	0	0	2	15	0	3	0	0	0	3	8	31
48	*Cassia occidentalis* L.	FABACEAE	0	0	0	15	0	3	0	0	8	0	5	31
49	*Philenoptera bussei* (Harms) Schrire	FABACEAE	1	0	2	15	0	0	0	0	8	0	5	31
50	*Passiflora edulis* Sims	PASSIFLORACEAE	0	0	2	15	0	3	0	0	0	3	8	31
51	*Ambrosia artemisiifolia* L.	ASTERACEAE	0	0	0	15	0	0	0	0	4	3	8	30
52	*Mikania natalensis* DC.	ASTERACEAE	1	0	2	15	0	0	0	0	4	3	5	30

Table 4.37 (continued)

Rank No.	Taxon	Family	Indg.	End.	*FSA* (med)	Treat.	Assoc.	Tox.	Red Data	Trade	HFam1	HFam2	Keyword	Total Score
53	*Capparis tomentosa* Lam.	CAPPARACEAE	1	0	2	15	0	3	2	2	0	0	5	30
54	*Momordica balsamina* L.	CUCURBITACEAE	1	0	2	15	0	3	0	1	0	0	8	30
55	*Momordica foetida* Schumach.	CUCURBITACEAE	1	0	2	15	0	3	0	1	0	0	8	30
56	*Protea repens* (L.) L.	PROTEACEAE	1	1	2	15	0	3	0	0	0	0	8	30
57	*Bulbine narcissifolia* Salm-Dyck	ASPHODELACEAE	1	0	2	15	0	3	0	0.5	0	0	8	29.5
58	*Cissampelos capensis* L.f.	MENISPERMACEAE	1	0	2	15	0	3	0	0.5	0	0	8	29.5
59	*Rhus lancea* L.f.	ANACARDIACEAE	1	0	2	15	0	0	0	0	0	3	8	29
60	*Drimia elata* Jacq.	HYACINTHACEAE	1	0	2	15	0	0	0	2	4	0	5	29
61	*Sida cordifolia* L.	MALVACEAE	1	0	2	15	0	3	0	0	0	0	8	29
62	*Turraea floribunda* Hochst.	MELIACEAE	1	0	2	15	0	3	2	2	0	3	1	29
63	*Haemanthus coccineus* L.	AMARYLLIDACEAE	1	0	2	15	0	3	2	0.5	0	0	5	28.5
64	*Sclerocarya birrea* (A.Rich.) Hochst. subsp. *birrea*	ANACARDIACEAE	1	0	0	15	0	0	0	1.5	0	3	8	28.5
65	*Foeniculum vulgare* Mill. var. *vulgare*	APIACEAE	0	0	0	15	0	0	0	1.5	4	3	5	28.5
66	*Chenopodium ambrosioides* L.	CHENOPODIACEAE	0	0	2	15	0	3	0	0.5	0	0	8	28.5
67	*Annona senegalensis* Pers. subsp. *senegalensis*	ANNONACEAE	1	0	2	15	0	3	0	2	0	0	5	28
68	*Hexalobus monopetalus* (A.Rich.) Engl. & Diels var. *monopetalus*	ANNONACEAE	1	0	2	15	0	0	2	0	0	0	8	28
69	*Bulbine latifolia* (L.f.) Schult. & Schult.f.	ASPHODELACEAE	1	0	0	15	0	3	0	1	0	0	8	28
70	*Eriocephalus africanus* L. var. *africanus*	ASTERACEAE	1	0	0	15	0	0	0	0	4	3	5	28

Table 4.37 (continued)

Rank No.	Taxon	Family	Indg.	End.	*FSA* (med)	Treat.	Assoc.	Tox.	Red Data	Trade	HFam1	HFam2	Keyword	Total Score
71	*Eriocephalus africanus* L. var. *paniculatus* (Cass.) M.A.N.Müll.,Herman & Kolberg	ASTERACEAE	1	0	0	15	0	0	0	0	4	3	5	28
72	*Eriocephalus ericoides* (L.f.) Druce subsp. *ericoides*	ASTERACEAE	1	0	0	15	0	0	0	0	4	3	5	28
73	*Osteospermum grandiflorum* DC.	ASTERACEAE	1	0	0	15	0	0	0	0	4	3	5	28
74	*Flacourtia indica* (Burm.f.) Merr.	FLACOURTIACEAE	1	0	2	15	0	0	2	0	0	3	5	28
75	*Drimia sanguinea* (Schinz) Jessop	HYACINTHACEAE	1	0	0	15	0	3	0	0	4	0	5	28
76	*Hypoxis colchicifolia* Baker	HYPOXIDACEAE	1	1	2	15	0	3	0	1	0	0	5	28
77	*Ficus glumosa* Delile	MORACEAE	1	0	2	15	0	0	2	0	0	0	8	28
78	*Ensete ventricosum* (Welw.) Cheesman	MUSACEAE	1	0	2	15	0	0	2	0	0	0	8	28
79	*Boerhavia diffusa* L. var. *diffusa*	NYCTAGINACEAE	0	0	2	15	0	3	0	0	0	0	8	28
80	*Oxytenanthera abyssinica* (A.Rich.) Munro	POACEAE	1	0	2	15	0	0	2	0	0	0	8	28
81	*Agathosma crenulata* (L.) Pillans	RUTACEAE	0	0	2	15	0	3	0	0	0	3	5	28
82	*Physalis angulata* L.	SOLANACEAE	0	0	2	15	0	3	0	0	0	0	8	28
83	*Lantana camara* L.	VERBENACEAE	0	0	2	15	0	3	0	0	0	0	8	28
84	*Kigelia africana* (Lam.) Benth.	BIGNONIACEAE	1	0	2	15	0	3	0	1.5	0	0	5	27.5
85	*Euclea natalensis* A.DC. subsp. *natalensis*	EBENACEAE	1	0	2	15	0	3	0	1.5	0	0	5	27.5
86	*Carpobrotus edulis* (L.) L.Bolus subsp. *edulis*	MESEMBRYANTHEMACEAE	1	1	2	15	0	0	0	0.5	0	0	8	27.5

Table 4.37 (continued)

Rank No.	Taxon	Family	Indg.	End.	*FSA* (med)	Treat.	Assoc.	Tox.	Red Data	Trade	HFam1	HFam2	Keyword	Total Score
87	*Securidaca longipedunculata* Fresen. var. *longipedunculata*	POLYGALACEAE	1	0	0	15	0	3	0	0.5	0	0	8	27.5
88	*Euphorbia hirta* L.	EUPHORBIACEAE	1	0	0	15	0	3	0	0	0	3	5	27
89	*Phyllanthus glaucophyllus* Sond.	EUPHORBIACEAE	1	0	0	15	0	0	0	0	0	3	8	27
90	*Harpagophytum procumbens* (Burch.) DC. ex Meisn. subsp. *procumbens*	PEDALIACEAE	1	0	0	15	0	0	2	1	0	0	8	27
91	*Agathosma betulina* (P.J.Bergius) Pillans	RUTACEAE	1	1	2	15	0	0	0	0	0	3	5	27
92	*Dodonaea viscosa* Jacq. subsp. *viscosa*	SAPINDACEAE	1	0	0	15	0	0	0	0	0	3	8	27
93	*Euclea crispa* (Thunb.) Gürke subsp. *crispa*	EBENACEAE	1	0	2	15	0	0	0	0.5	0	0	8	26.5
94	*Phyllanthus meyerianus* Müll.Arg.	EUPHORBIACEAE	1	0	2	15	0	0	0	0.5	0	3	5	26.5
95	*Cissampelos mucronata* A.Rich.	MENISPERMACEAE	1	0	2	15	0	3	0	0.5	0	0	5	26.5
96	*Markhamia zanzibarica* (Bojer ex DC.) K.Schum.	BIGNONIACEAE	1	0	2	15	0	0	0	0	0	0	8	26
97	*Eleocharis dulcis* (Burm.f.) Hensch.	CYPERACEAE	1	0	2	15	0	3	0	0	0	0	5	26
98	*Ocimum gratissimum* L. subsp. *gratissimum* var. *gratissimum*	LAMIACEAE	1	0	2	15	0	0	0	0	0	0	8	26
99	*Teucrium trifidum* Retz.	LAMIACEAE	1	0	2	15	0	0	0	0	0	0	8	26
100	*Zea mays* L.	POACEAE	0	0	0	15	0	3	0	0	0	0	8	26
101	*Rubus apetalus* Poir. var. *apetalus*	ROSACEAE	1	0	2	15	0	0	0	0	0	0	8	26
102	*Coddia rudis* (E.Mey. ex Harv.) Verdc.	RUBIACEAE	1	0	2	15	0	0	0	0	0	3	5	26
103	*Gasteria bicolor* Haw. var. *bicolor*	ASPHODELACEAE	1	1	0	15	0	0	0	0.5	0	0	8	25.5

Table 4.37 (continued)

Rank No.	Taxon	Family	Indg.	End.	*FSA* (med)	Treat.	Assoc.	Tox.	Red Data	Trade	HFam1	HFam2	Keyword	Total Score
104	*Buddleja salviifolia* (L.) Lam.	BUDDLEJACEAE	1	0	2	15	0	3	0	0.5	0	0	4	25.5
105	*Clivia miniata* (Lindl.) Regel var. *miniata*	AMARYLLIDACEAE	0	0	2	15	0	3	2	2	0	0	1	25
106	*Bulbine asphodeloides* (L.) Spreng.	ASPHODELACEAE	1	0	0	15	0	0	0	1	0	0	8	25
107	*Bulbine natalensis* Baker	ASPHODELACEAE	1	0	0	15	0	0	0	1	0	0	8	25
108	*Rhizophora mucronata* Lam.	RHIZOPHORACEAE	1	0	2	15	0	3	0	0	0	3	1	25
109	*Sanguisorba minor* Scop. subsp. *muricata* Briq.	ROSACEAE	1	1	0	15	0	0	0	0	0	0	8	25
110	*Stephania abyssinica* (Quart.-Dill. & A.Rich.) Walp. var. *abyssinica*	MENISPERMACEAE	1	0	0	15	0	0	0	0.5	0	0	8	24.5
111	*Nymphaea nouchali* Burm.f. var. *caerulea* (Savigny) Verdc.	NYMPHAEACEAE	1	0	0	15	0	0	0	0.5	0	0	8	24.5
112	*Agelanthus natalitius* (Meisn.) Polhill & Wiens subsp. *zeyheri* (Harv.) Polhill & Wiens	LORANTHACEAE	1	0	0	15	0	0	0	0	0	0	8	24
113	*Carpobrotus acinaciformis* (L.) L.Bolus	MESEMBRYANTHEMACEAE	1	1	2	15	0	0	0	0	0	0	5	24
114	*Sterculia africana* (Lour.) Fiori var. *africana*	STERCULIACEAE	1	0	0	15	0	0	0	0	0	0	8	24
115	*Dissotis canescens* (E.Mey. ex R.A.Graham) Hook.f.	MELASTOMATACEAE	1	0	2	15	0	0	0	0.5	0	0	5	23.5
116	*Imperata cylindrica* (L.) Raeusch.	POACEAE	1	0	2	15	0	0	0	0.5	0	0	5	23.5
117	*Zephyranthes grandiflora* Lindl.	AMARYLLIDACEAE	0	0	0	15	0	0	0	0	0	0	8	23
118	*Stachys hyssopoides* Burch. ex Benth.	LAMIACEAE	1	0	2	15	0	0	0	0	0	0	5	23

Table 4.37 (continued)

Rank No.	Taxon	Family	Indg.	End.	*FSA* (med)	Treat.	Assoc.	Tox.	Red Data	Trade	HFam1	HFam2	Keyword	Total Score
119	*Elaeodendron transvaalense* (Burtt Davy) R.H.Archer	CELASTRACEAE	1	0	0	15	0	0	0	1	0	0	5	22
120	*Pteridium aquilinum* (L.) Kuhn	DENNSTAEDTIACEAE	1	0	2	15	0	3	0	0	0	0	1	22
121	*Glycyrrhiza glabra* L.	FABACEAE	0	0	2	0	0	3	0	1	8	0	8	22
122	*Plantago major* L.	PLANTAGINACEAE	0	0	2	15	0	0	0	0	0	0	5	22
123	*Dioscorea dregeana* (Kunth) T.Durand & Schinz	DIOSCOREACEAE	1	0	2	0	8	3	0	2	4	0	1	21
124	*Aeollanthus rehmannii* Gürke	LAMIACEAE	1	0	0	15	0	0	0	0	0	0	5	21
125	*Oxalis copiosa* F.Bolus	OXALIDACEAE	1	0	0	15	0	0	0	0	0	0	5	21
126	*Oxalis corniculata* L.	OXALIDACEAE	0	0	2	15	0	3	0	0	0	0	1	21
127	*Pennisetum thunbergii* Kunth	POACEAE	1	0	0	15	0	0	0	0	0	0	5	21
128	*Paederia bojeriana* (A.Rich.) Drake subsp. *foetens* (Hiern) Verdc.	RUBIACEAE	0	0	2	15	0	0	0	0	0	3	1	21
129	*Pavetta capensis* (Houtt.) Bremek. subsp. *capensis*	RUBIACEAE	1	1	0	15	0	0	0	0	0	3	1	21
130	*Solanum lichtensteinii* Willd.	SOLANACEAE	1	0	0	15	0	0	0	0	0	0	5	21
131	*Cannabis sativa* L. var. *sativa*	CANNABACEAE	0	0	0	15	0	0	0	0.5	0	0	5	20.5
132	*Daucus carota* L.	APIACEAE	0	0	2	0	0	3	0	0	4	3	8	20
133	*Lonicera japonica* Thunb. var. *japonica*	CAPRIFOLIACEAE	0	0	0	15	0	0	0	0	4	0	1	20
134	*Convolvulus sagittatus* Thunb.	CONVOLVULACEAE	1	0	2	15	0	0	0	1	0	0	1	20
135	*Bowiea volubilis* Harv. ex Hook.f.	HYACINTHACEAE	1	0	2	0	0	3	2	3	4	0	5	20
136	*Abelmoschus esculentus* (L.) Moench var. *esculentus*	MALVACEAE	0	0	0	15	0	0	0	0	0	0	5	20

Table 4.37 (continued)

Rank No.	Taxon	Family	Indg.	End.	*FSA* (med)	Treat.	Assoc.	Tox.	Red Data	Trade	HFam1	HFam2	Keyword	Total Score
137	*Centella asiatica* (L.) Urb.	ARALIACEAE	1	0	2	0	0	0	0	0.5	8	3	5	19.5
138	*Medicago sativa* L.	FABACEAE	1	0	2	0	0	3	0	0	8	0	5	19
139	*Piper capense* L.f. var. *capense*	PIPERACEAE	1	0	2	15	0	0	0	0	0	0	1	19
140	*Pteris dentata* Forssk.	PTERIDACEAE	1	0	2	15	0	0	0	0	0	0	1	19
141	*Melilotus officinalis* (L.) Pall.	FABACEAE	0	0	2	0	0	3	0	0	8	0	5	18
142	*Robinia pseudoacacia* L.	FABACEAE	0	0	2	0	0	3	0	0	8	0	5	18
143	*Commelina africana* L. var. *africana*	COMMELINACEAE	1	0	0	15	0	0	0	0.5	0	0	1	17.5
144	*Apium graveolens* L.	APIACEAE	0	0	2	0	0	3	0	0	4	3	5	17
145	*Nerium oleander* L.	APOCYNACEAE	0	0	2	0	0	3	0	0	4	3	5	17
146	*Artemisia vulgaris* L.	ASTERACEAE	0	0	2	0	0	3	0	0	4	3	5	17
147	*Lactuca serriola* L.	ASTERACEAE	0	0	2	0	0	3	0	0	4	3	5	17
148	*Arctopus echinatus* L.	APIACEAE	1	1	2	0	0	0	0	0	4	3	5	16
149	*Carica papaya* L.	CARICACEAE	0	0	0	0	8	3	0	0	0	0	5	16
150	*Trifolium pratense* L. var. *pratense*	FABACEAE	0	0	0	0	0	3	0	0	8	0	5	16
151	*Ruta graveolens* L.	RUTACEAE	0	0	2	0	0	3	0	0	0	3	8	16
152	*Artemisia absinthium* L.	ASTERACEAE	0	0	0	0	0	3	0	0	4	3	5	15
153	*Oncosiphon suffruticosum* (L.) Källersjö	ASTERACEAE	1	0	2	0	0	0	0	0	4	3	5	15
154	*Valeriana capensis* Thunb. var. *capensis*	VALERIANACEAE	1	0	0	0	0	0	0	0	6	0	8	15
155	*Olea europaea* L. subsp. *africana* (Mill.) P.S.Green	OLEACEAE	1	0	2	0	0	0	0	0.5	6	0	5	14.5
156	*Anemone caffra* (Eckl. & Zeyh.) Harv.	RANUNCULACEAE	1	1	2	0	0	0	0	1	4	0	5	14
157	*Hypericum perforatum* L.	HYPERICACEAE	0	0	2	0	0	3	0	0.5	0	3	5	13.5
158	*Schinus molle* L.	ANACARDIACEAE	0	0	2	0	0	3	0	0	0	3	5	13
159	*Euphorbia lathyris* L.	EUPHORBIACEAE	0	0	2	0	0	3	0	0	0	3	5	13

Table 4.37 (continued)

Rank No.	Taxon	Family	Indg.	End.	*FSA* (med)	Treat.	Assoc.	Tox.	Red Data	Trade	HFam1	HFam2	Keyword	Total Score
160	*Manihot esculenta* Crantz	EUPHORBIACEAE	0	0	2	0	0	3	0	0	0	3	5	13
161	*Mercurialis annua* L.	EUPHORBIACEAE	0	0	2	0	0	3	0	0	0	3	5	13
162	*Drimia altissima* (L.f.) Ker Gawl.	HYACINTHACEAE	1	0	0	0	0	3	0	0	4	0	5	13
163	*Melia azedarach* L.	MELIACEAE	0	0	2	0	0	3	0	0	0	3	5	13
164	*Eschscholzia californica* Cham. subsp. *californica*	PAPAVERACEAE	0	0	2	0	0	3	0	0	0	3	5	13
165	*Urtica dioica* L.	URTICACEAE	0	0	2	0	0	3	0	0	0	0	8	13
166	*Withania somnifera* (L.) Dunal	SOLANACEAE	1	0	2	0	0	3	0	1.5	0	0	5	12.5
167	*Angelica archangelica* L.	APIACEAE	0	0	0	0	0	0	0	0	4	3	5	12
168	*Achillea millefolium* L.	ASTERACEAE	0	0	0	0	0	0	0	0	4	3	5	12
169	*Arctium lappa* L.	ASTERACEAE	0	0	0	0	0	0	0	0	4	3	5	12
170	*Artemisia dracunculus* L.	ASTERACEAE	0	0	0	0	0	0	0	0	4	3	5	12
171	*Calendula officinalis* L.	ASTERACEAE	0	0	0	0	0	0	0	0	4	3	5	12
172	*Eucalyptus globulus* Labill. subsp. *maidenii* (F.Muell.) Kirkp.	MYRTACEAE	0	0	0	0	0	3	0	1	0	0	8	12
173	*Aquilegia vulgaris* L.	RANUNCULACEAE	0	0	0	0	0	3	0	0	4	0	5	12
174	*Hoslundia opposita* Vahl	LAMIACEAE	1	0	2	0	0	3	0	0	0	0	5	11
175	*Argemone mexicana* auct. non L.	PAPAVERACEAE	0	0	0	0	0	3	0	0	0	3	5	11
176	*Solanum nigrum* L.	SOLANACEAE	0	0	2	0	0	3	0	0.5	0	0	5	10.5
177	*Harpagophytum zeyheri* Decne. subsp. *sublobatum* (Engl.) Ihlenf. & H.E.K.Hartmann	PEDALIACEAE	1	0	0	0	0	0	0	1	0	0	8	10
178	*Polygonum aviculare* L.	POLYGONACEAE	0	0	2	0	0	3	0	0	0	0	5	10
179	*Datura stramonium* L.	SOLANACEAE	0	0	2	0	0	3	0	0	0	0	5	10
180	*Solanum tuberosum* L.	SOLANACEAE	0	0	2	0	0	3	0	0	0	0	5	10

Table 4.37 (continued)

Rank No.	Taxon	Family	Indg.	End.	*FSA* (med)	Treat.	Assoc.	Tox.	Red Data	Trade	HFam1	HFam2	Keyword	Total Score
181	*Duranta erecta* L.	VERBENACEAE	0	0	2	0	0	3	0	0	0	0	5	10
182	*Verbena officinalis* L.	VERBENACEAE	0	0	2	0	0	3	0	0	0	0	5	10
183	*Peganum harmala* L.	ZYGOPHYLLACEAE	0	0	2	0	0	3	0	0	0	0	5	10
184	*Borago officinalis* L.	BORAGINACEAE	0	0	0	0	0	3	0	0	0	0	5	8
185	*Agrostemma githago* L. subsp. *githago*	CARYOPHYLLACEAE	0	0	0	0	0	3	0	0	0	0	5	8
186	*Atropa belladonna* L.	SOLANACEAE	0	0	0	0	0	3	0	0	0	0	5	8
187	*Lycopersicon esculentum* Mill. var. *cerasiforme* Hort.	SOLANACEAE	0	0	0	0	0	3	0	0	0	0	5	8
188	*Stellaria media* (L.) Vill.	CARYOPHYLLACEAE	0	0	2	0	0	0	0	0	0	0	5	7
189	*Euphorbia indica* Lam.	EUPHORBIACEAE	0	0	0	0	0	0	0	0	0	3	4	7
190	*Hibiscus sabdariffa* L.	MALVACEAE	0	0	2	0	0	0	0	0	0	0	5	7
191	*Agrimonia eupatoria* L.	ROSACEAE	0	0	0	0	0	0	0	0.5	0	0	5	5.5
192	*Berberis vulgaris* L.	BERBERIDACEAE	0	0	0	0	0	0	0	0	0	0	5	5
193	*Alnus glutinosa* (L.) Gaertn.	BETULACEAE	0	0	0	0	0	0	0	0	0	0	5	5
194	*Buxus sempervirens* L.	BUXACEAE	0	0	0	0	0	0	0	0	0	0	5	5
195	*Ajuga reptans* L. var. *reptans*	LAMIACEAE	0	0	0	0	0	0	0	0	0	0	5	5
196	*Brunfelsia uniflora* (Pohl) D.Don	SOLANACEAE	0	0	0	0	0	0	0	0	0	0	5	5
197	*Camellia sinensis* (L.) Kuntze	THEACEAE	0	0	0	0	0	0	0	0	0	0	5	5

Table 4.38 Shortlisted taxa for Immune modulation and the respective scores for weighted criteria

Rank No.	Taxon	Family	Indg.	End.	*FSA* (med)	Treat.	Assoc.	Tox.	Red Data	Trade	HFam1	HFam2	Keyword	Total Score
1	*Leonotis leonurus* (L.) R.Br.	LAMIACEAE	1	0	2	15	0	3	0	0.5	8	3	7	39.5
2	*Mentha aquatica* L.	LAMIACEAE	1	0	2	15	0	3	0	0.5	8	3	7	39.5
3	*Ballota africana* (L.) Benth.	LAMIACEAE	1	0	2	15	0	3	0	0	8	3	7	39
4	*Mondia whitei* (Hook.f.) Skeels	APOCYNACEAE	1	0	2	15	0	3	2	1.5	4	3	7	38.5
5	*Artemisia afra* Jacq. ex Willd.	ASTERACEAE	1	0	2	15	0	3	0	2	8	0	7	38
6	*Marrubium vulgare* L.	LAMIACEAE	0	0	2	15	0	3	0	0	8	3	7	38
7	*Strychnos henningsii* Gilg	STRYCHNACEAE	1	0	2	15	0	3	0	2.5	4	3	7	37.5
8	*Callilepis laureola* DC.	ASTERACEAE	1	0	2	15	0	3	0	1	8	0	7	37
9	*Spilanthes mauritiana* (Pers.) DC.	ASTERACEAE	1	0	2	15	0	3	0	1	8	0	7	37
10	*Microglossa mespilifolia* (Less.) B.L.Rob.	ASTERACEAE	1	0	2	15	0	3	0	0.5	8	0	7	36.5
11	*Solanum aculeastrum* Dunal	SOLANACEAE	1	0	2	15	0	3	0	1.5	4	3	7	36.5
12	*Withania somnifera* (L.) Dunal	SOLANACEAE	1	0	2	15	0	3	0	1.5	4	3	7	36.5
13	*Pachypodium lealii* Welw.	APOCYNACEAE	1	0	2	15	0	3	2	0	4	3	6	36
14	*Eclipta prostrata* (L.) L.	ASTERACEAE	0	0	2	15	0	3	0	1	8	0	7	36
15	*Pseudognaphalium luteo-album* (L.) Hilliard & B.L.Burtt	ASTERACEAE	1	0	2	15	0	3	0	0	8	0	7	36
16	*Senecio serratuloides* DC. var. *serratuloides*	ASTERACEAE	1	0	2	15	0	3	0	1	8	0	6	36
17	*Tarchonanthus camphoratus* L.	ASTERACEAE	1	0	2	15	0	3	0	0	8	0	7	36
18	*Stachys rugosa* Aiton	LAMIACEAE	1	0	2	15	0	0	0	0	8	3	7	36
19	*Teucrium africanum* Thunb.	LAMIACEAE	1	0	2	15	0	0	0	0	8	3	7	36
20	*Teucrium trifidum* Retz.	LAMIACEAE	1	0	2	15	0	0	0	0	8	3	7	36
21	*Lippia javanica* (Burm.f.) Spreng.	VERBENACEAE	1	0	2	15	0	3	0	2	4	3	6	36
22	*Lippia scaberrima* Sond.	VERBENACEAE	1	0	2	15	0	3	0	0.5	4	3	7	35.5

Table 4.38 (continued)

Rank No.	Taxon	Family	Indg.	End.	*FSA* (med)	Treat.	Assoc.	Tox.	Red Data	Trade	HFam1	HFam2	Keyword	Total Score
23	*Alepidea amatymbica* Eckl. & Zeyh. var. *amatymbica*	APIACEAE	1	0	2	15	0	0	0	4	6	0	7	35
24	*Bidens pilosa* L.	ASTERACEAE	0	0	2	15	0	3	0	0	8	0	7	35
25	*Cichorium intybus* L.	ASTERACEAE	0	0	2	15	0	3	0	0	8	0	7	35
26	*Cnicus benedictus* L.	ASTERACEAE	0	0	2	15	0	3	0	0	8	0	7	35
27	*Vernonia amygdalina* Delile	ASTERACEAE	1	0	2	15	0	3	0	0	8	0	6	35
28	*Olea woodiana* Knobl.	OLEACEAE	1	0	2	15	0	0	2	1	6	3	5	35
29	*Harpagophytum procumbens* (Burch.) DC. ex Meisn. subsp. *procumbens*	PEDALIACEAE	1	0	0	15	0	0	2	1	6	3	7	35
30	*Lycium ferocissimum* Miers	SOLANACEAE	1	0	2	15	0	3	0	0	4	3	7	35
31	*Strychnos usambarensis* Gilg	STRYCHNACEAE	1	0	2	15	0	3	0	0	4	3	7	35
32	*Gerbera ambigua* (Cass.) Sch.Bip.	ASTERACEAE	1	0	2	15	0	0	0	1.5	8	0	7	34.5
33	*Erythrophleum lasianthum* Corbishley	FABACEAE	1	0	2	15	0	3	0	1.5	6	0	6	34.5
34	*Olea europaea* L. subsp. *africana* (Mill.) P.S.Green	OLEACEAE	1	0	2	15	0	0	0	0.5	6	3	7	34.5
35	*Solanum nigrum* L.	SOLANACEAE	0	0	2	15	0	3	0	0.5	4	3	7	34.5
36	*Acokanthera oblongifolia* (Hochst.) Codd	APOCYNACEAE	1	0	2	15	0	3	0	1	4	3	5	34
37	*Catharanthus roseus* (L.) G.Don	APOCYNACEAE	0	0	2	15	0	3	0	0	4	3	7	34
38	*Nerium oleander* L.	APOCYNACEAE	0	0	2	15	0	3	0	0	4	3	7	34
39	*Gonatopus boivinii* (Decne.) Engl.	ARACEAE	1	0	2	15	0	3	0	0	6	0	7	34
40	*Brachylaena discolor* DC.	ASTERACEAE	1	0	2	15	0	0	0	1	8	0	7	34
41	*Gerbera piloselloides* (L.) Cass.	ASTERACEAE	1	0	2	15	0	0	0	1	8	0	7	34
42	*Helichrysum nudifolium* (L.) Less.	ASTERACEAE	1	0	2	15	0	0	0	1	8	0	7	34
43	*Pulicaria scabra* (Thunb.) Druce	ASTERACEAE	1	0	2	15	0	0	0	1	8	0	7	34
44	*Glycyrrhiza glabra* L.	FABACEAE	0	0	2	15	0	3	0	1	6	0	7	34
45	*Mimosa pigra* L.	FABACEAE	1	0	2	15	0	0	2	1	6	0	7	34
46	*Sutherlandia frutescens* (L.) R.Br.	FABACEAE	1	0	2	15	0	3	0	0	6	0	7	34

Table 4.38 (continued)

Rank No.	Taxon	Family	Indg.	End.	*FSA* (med)	Treat.	Assoc.	Tox.	Red Data	Trade	HFam1	HFam2	Keyword	Total Score
47	*Swertia welwitschii* Engl.	GENTIANACEAE	1	0	0	15	8	0	0	0	0	3	7	34
48	*Agathosma betulina* (P.J.Bergius) Pillans	RUTACEAE	1	1	2	15	8	0	0	0	0	0	7	34
49	*Solanum pseudocapsicum* L.	SOLANACEAE	0	0	2	15	0	3	0	0	4	3	7	34
50	*Vitex mombassae* Vatke	VERBENACEAE	1	0	2	15	0	3	0	0	4	3	6	34
51	*Acorus calamus* L.	ARACEAE	0	0	2	15	0	3	0	0.5	6	0	7	33.5
52	*Athrixia phylicoides* DC.	ASTERACEAE	1	0	2	15	0	0	0	0.5	8	0	7	33.5
53	*Vernonia colorata* (Willd.) Drake subsp. *colorata*	ASTERACEAE	1	0	2	15	0	0	0	0.5	8	0	7	33.5
54	*Vernonia oligocephala* (DC.) Sch.Bip. ex Walp.	ASTERACEAE	1	0	2	15	0	0	0	0.5	8	0	7	33.5
55	*Warburgia salutaris* (Bertol.f.) Chiov.	CANELLACEAE	1	0	2	15	0	3	2	3.5	0	0	7	33.5
56	*Acacia karroo* Hayne	FABACEAE	1	0	2	15	0	3	0	0.5	6	0	6	33.5
57	*Entada rheedii* Spreng.	FABACEAE	1	0	2	15	0	0	2	0.5	6	0	7	33.5
58	*Lantana rugosa* Thunb.	VERBENACEAE	1	0	2	15	0	3	0	0.5	4	3	5	33.5
59	*Vitex rehmannii* Gürke	VERBENACEAE	1	0	2	15	0	0	2	0.5	4	3	6	33.5
60	*Berkheya cirsiifolia* (DC.) Roessler	ASTERACEAE	1	0	2	15	0	0	0	0	8	0	7	33
61	*Chrysanthemum coronarium* L.	ASTERACEAE	0	0	2	15	0	3	0	0	8	0	5	33
62	*Leysera gnaphalodes* (L.) L.	ASTERACEAE	1	0	2	15	0	0	0	0	8	0	7	33
63	*Senecio speciosus* Willd.	ASTERACEAE	1	0	2	15	0	3	0	1	8	0	3	33
64	*Catha edulis* (Vahl) Forssk. ex Endl.	CELASTRACEAE	1	0	2	15	0	3	2	1	4	0	5	33
65	*Swartzia madagascariensis* Desv.	FABACEAE	1	0	2	15	0	3	0	0	6	0	6	33
66	*Tephrosia purpurea* (L.) Pers. subsp. *purpurea*	FABACEAE	0	0	2	15	0	3	0	0	6	0	7	33
67	*Adenia gummifera* (Harv.) Harms var. *gummifera*	PASSIFLORACEAE	1	0	2	15	0	3	0	2	0	3	7	33
68	*Pentanisia prunelloides* (Klotzsch ex Eckl. & Zeyh.) Walp. subsp. *prunelloides*	RUBIACEAE	1	0	2	15	0	3	0	2	0	3	7	33
69	*Capsicum frutescens* L.	SOLANACEAE	0	0	2	15	0	3	0	0	4	3	6	33
70	*Lantana camara* L.	VERBENACEAE	0	0	2	15	0	3	0	0	4	3	6	33

Table 4.38 (continued)

Rank No.	Taxon	Family	Indg.	End.	*FSA* (med)	Treat.	Assoc.	Tox.	Red Data	Trade	HFam1	HFam2	Keyword	Total Score
71	*Acokanthera oppositifolia* (Lam.) Codd	APOCYNACEAE	1	0	2	15	0	3	0	1.5	4	3	3	32.5
72	*Cotula nigellifolia* (DC.) Bremer & Humphries var. *tenuior* (DC.) Herman	ASTERACEAE	1	1	2	15	0	3	0	0.5	8	0	2	32.5
73	*Croton sylvaticus* Hochst. ex C.Krauss	EUPHORBIACEAE	1	0	2	15	0	3	0	1.5	0	3	7	32.5
74	*Calpurnia aurea* (Aiton) Benth. subsp. *aurea*	FABACEAE	1	0	2	15	0	3	0	0.5	6	0	5	32.5
75	*Mentha longifolia* (L.) Huds. subsp. *capensis* (Thunb.) Briq.	LAMIACEAE	1	0	0	15	0	0	0	0.5	8	3	5	32.5
76	*Clivia miniata* (Lindl.) Regel var. *miniata*	AMARYLLIDACEAE	1	0	2	15	0	3	2	2	4	0	3	32
77	*Arctopus echinatus* L.	APIACEAE	1	1	2	15	0	0	0	0	6	0	7	32
78	*Holarrhena pubescens* (Buch.-Ham.) Wall.	APOCYNACEAE	1	0	2	15	0	0	0	0	4	3	7	32
79	*Rauvolfia caffra* Sond.	APOCYNACEAE	1	0	2	15	0	3	0	1	4	3	3	32
80	*Sarcostemma viminale* (L.) R.Br. subsp. *viminale*	ASCLEPIADACEAE	1	0	2	15	0	3	2	0	0	3	6	32
81	*Dicoma anomala* Sond. subsp. *gerrardii* (Harv. ex F.C.Wilson) S.Ortíz & Rodr.Oubiña	ASTERACEAE	1	0	0	15	0	0	0	1	8	0	7	32
82	*Helichrysum pedunculatum* Hilliard & B.L.Burtt	ASTERACEAE	1	0	2	15	0	0	0	0	8	0	6	32
83	*Croton megalobotrys* Müll.Arg.	EUPHORBIACEAE	1	0	2	15	0	3	0	1	0	3	7	32
84	*Caesalpinia bracteata* Germish.	FABACEAE	1	1	0	15	0	0	2	0	6	0	7	32
85	*Lablab purpureus* (L.) Sweet subsp. *purpureus*	FABACEAE	0	0	2	15	0	3	0	0	6	0	6	32
86	*Chironia baccifera* L.	GENTIANACEAE	1	1	2	15	0	3	0	0	0	3	7	32
87	*Tinnea galpinii* Briq.	LAMIACEAE	1	0	0	15	0	0	2	0	8	3	3	32
88	*Chionanthus foveolatus* (E.Mey.) Stearn subsp. *foveolatus*	OLEACEAE	1	0	2	15	0	0	2	0	6	3	3	32
89	*Solanum anguivi* Lam.	SOLANACEAE	1	0	2	15	0	0	0	0	4	3	7	32

Table 4.38 (continued)

Rank No.	Taxon	Family	Indg.	End.	*FSA* (med)	Treat.	Assoc.	Tox.	Red Data	Trade	HFam1	HFam2	Keyword	Total Score
90	*Vitex obovata* E.Mey. subsp. *obovata*	VERBENACEAE	1	0	2	15	0	0	0	0	4	3	7	32
91	*Buddleja salviifolia* (L.) Lam.	BUDDLEJACEAE	1	0	2	15	0	3	0	0.5	0	3	7	31.5
92	*Bridelia micrantha* (Hochst.) Baill.	EUPHORBIACEAE	1	0	2	15	0	3	0	0.5	0	3	7	31.5
93	*Ricinus communis* L.	EUPHORBIACEAE	0	0	2	15	0	3	0	1.5	0	3	7	31.5
94	*Cassytha filiformis* L.	LAURACEAE	0	0	2	15	0	3	0	0.5	4	0	7	31.5
95	*Mangifera indica* L.	ANACARDIACEAE	0	0	2	15	0	3	0	0	4	0	7	31
96	*Hydrocotyle verticillata* Thunb.	APIACEAE	1	0	2	15	0	0	0	0	6	0	7	31
97	*Tabernaemontana ventricosa* Hochst. ex A.DC.	APOCYNACEAE	1	0	2	15	0	0	0	0	4	3	6	31
98	*Ageratum conyzoides* L.	ASTERACEAE	0	0	2	15	0	3	0	0	8	0	3	31
99	*Sphaeranthus peduncularis* DC.	ASTERACEAE	1	0	0	15	0	0	0	0	8	0	7	31
100	*Capparis tomentosa* Lam.	CAPPARACEAE	1	0	2	15	0	3	2	2	0	0	6	31
101	*Caesalpinia bonduc* (L.) Roxb.	FABACEAE	1	0	2	15	0	0	0	0	6	0	7	31
102	*Indigofera bainesii* Baker	FABACEAE	1	0	2	15	0	0	0	0	6	0	7	31
103	*Millettia grandis* (E.Mey.) Skeels	FABACEAE	1	1	2	15	0	3	0	0	6	0	3	31
104	*Sphenostylis angustifolia* Sond.	FABACEAE	1	0	2	15	0	0	0	0	6	0	7	31
105	*Sutherlandia microphylla* Burch. ex DC.	FABACEAE	1	0	2	15	0	0	0	0	6	0	7	31
106	*Gunnera perpensa* L.	HALORAGACEAE	1	0	2	15	0	3	0	3	0	0	7	31
107	*Jasminum fluminense* Vell. subsp. *fluminense*	OLEACEAE	1	0	0	15	0	0	0	0	6	3	6	31
108	*Lycopersicon esculentum* Mill. var. *cerasiforme* Hort.	SOLANACEAE	0	0	0	15	0	3	0	0	4	3	6	31
109	*Solanum capense* L.	SOLANACEAE	1	0	2	15	0	3	0	0	4	3	3	31
110	*Trema orientalis* (L.) Blume	ULMACEAE	1	0	2	15	0	3	2	1	0	0	7	31
111	*Cotula nigellifolia* (DC.) Bremer & Humphries var. *nigellifolia*	ASTERACEAE	1	1	0	15	0	3	0	0.5	8	0	2	30.5

Table 4.38 (continued)

Rank No.	Taxon	Family	Indg.	End.	*FSA* (med)	Treat.	Assoc.	Tox.	Red Data	Trade	HFam1	HFam2	Keyword	Total Score
112	*Colophospermum mopane* (J.Kirk ex Benth.) J.Kirk ex J.Léonard	FABACEAE	1	0	2	15	0	0	0	0.5	6	0	6	30.5
113	*Mimosa pudica* L. var. *hispida* Brenan	FABACEAE	0	0	2	15	0	3	0	1.5	6	0	3	30.5
114	*Harpephyllum caffrum* Bernh.	ANACARDIACEAE	1	0	2	15	0	0	0	1	4	0	7	30
115	*Annona senegalensis* Pers. subsp. *senegalensis*	ANNONACEAE	1	0	2	15	0	3	0	2	0	0	7	30
116	*Amorphophallus abyssinicus* (A.Rich.) N.E.Br.	ARACEAE	1	0	2	15	0	0	0	0	6	0	6	30
117	*Xysmalobium undulatum* (L.) Aiton f.	ASCLEPIADACEAE	1	0	2	15	0	0	0	2	0	3	7	30
118	*Cadaba aphylla* (Thunb.) Wild	CAPPARACEAE	1	0	2	15	0	3	2	0	0	0	7	30
119	*Ipomoea purpurea* (L.) Roth	CONVOLVULACEAE	0	0	2	15	0	3	0	0	0	3	7	30
120	*Euphorbia ingens* E.Mey. ex Boiss.	EUPHORBIACEAE	1	0	2	15	0	3	2	1	0	3	3	30
121	*Jatropha curcas* L.	EUPHORBIACEAE	0	0	2	15	0	3	0	0	0	3	7	30
122	*Acacia erioloba* E.Mey.	FABACEAE	1	0	2	15	0	3	0	0	6	0	3	30
123	*Acacia mellifera* (Vahl) Benth. subsp. *mellifera*	FABACEAE	1	0	0	15	0	0	2	0	6	0	6	30
124	*Crotalaria laburnifolia* L. subsp. *australis* (Baker f.) Polhill	FABACEAE	1	0	0	15	0	0	2	0	6	0	6	30
125	*Erythrina abyssinica* Lam. ex DC.	FABACEAE	0	0	0	15	0	3	0	0	6	0	6	30
126	*Sesbania sesban* (L.) Merr. subsp. *sesban* var. *sesban*	FABACEAE	1	0	2	15	0	3	0	0	6	0	3	30
127	*Flacourtia indica* (Burm.f.) Merr.	FLACOURTIACEAE	1	0	2	15	0	0	2	0	0	3	7	30
128	*Datura stramonium* L.	SOLANACEAE	0	0	2	15	0	3	0	0	4	3	3	30
129	*Nicotiana glauca* Graham	SOLANACEAE	0	0	2	15	0	3	0	0	4	3	3	30
130	*Solanum terminale* Forssk. subsp. *terminale*	SOLANACEAE	1	0	2	15	0	0	0	0	4	3	5	30

Table 4.38 (continued)

Rank No.	Taxon	Family	Indg.	End.	*FSA* (med)	Treat.	Assoc.	Tox.	Red Data	Trade	HFam1	HFam2	Keyword	Total Score
131	*Vitex obovata* E.Mey. subsp. *wilmsii* (Gürke) C.L.Bredenkamp & D.J.Botha	VERBENACEAE	1	0	0	15	0	0	0	0	4	3	7	30
132	*Balanites maughamii* Sprague	BALANITACEAE	1	0	2	15	0	3	0	1.5	0	0	7	29.5
133	*Elaeodendron transvaalense* (Burtt Davy) R.H.Archer	CELASTRACEAE	1	0	2	15	0	3	0	1.5	4	0	3	29.5
134	*Gloriosa superba* L.	COLCHICACEAE	1	0	2	15	0	3	0	1.5	0	0	7	29.5
135	*Cotyledon orbiculata* L. var. *oblonga* (Haw.) DC.	CRASSULACEAE	1	0	2	15	0	3	2	0.5	0	0	6	29.5
136	*Ocotea bullata* (Burch.) Baill.	LAURACEAE	1	0	2	15	0	0	2	2.5	4	0	3	29.5
137	*Embelia ruminata* (E.Mey. ex A.DC.) Mez	MYRSINACEAE	1	1	2	15	0	3	0	0.5	0	0	7	29.5
138	*Clematis brachiata* Thunb.	RANUNCULACEAE	1	0	2	15	0	3	0	1.5	0	0	7	29.5
139	*Ziziphus mucronata* Willd. subsp. *mucronata*	RHAMNACEAE	1	0	2	15	0	0	0	1.5	4	0	6	29.5
140	*Gnidia kraussiana* Meisn. var. *kraussiana*	THYMELAEACEAE	1	0	2	15	0	3	0	1.5	0	0	7	29.5
141	*Boophone disticha* (L.f.) Herb.	AMARYLLIDACEAE	1	0	0	15	0	3	0	0	4	0	6	29
142	*Ancylobotrys capensis* (Oliv.) Pichon	APOCYNACEAE	1	0	0	15	0	3	0	0	4	3	3	29
143	*Berkheya decurrens* (Thunb.) Willd.	ASTERACEAE	1	1	2	15	0	0	0	0	8	0	2	29
144	*Cyanthillium cinereum* (L.) H.Rob. var. *cinereum*	ASTERACEAE	1	0	0	15	0	0	0	0	8	0	5	29
145	*Erlangea misera* (Oliv. & Hiern) S.Moore	ASTERACEAE	1	0	2	15	0	0	0	0	8	0	3	29
146	*Senecio achilleifolius* DC.	ASTERACEAE	1	0	0	15	0	0	0	0	8	0	5	29
147	*Gymnosporia senegalensis* (Lam.) Loes.	CELASTRACEAE	1	0	0	15	0	3	0	0	4	0	6	29
148	*Combretum erythrophyllum* (Burch.) Sond.	COMBRETACEAE	1	0	2	15	0	3	0	1	0	0	7	29
149	*Combretum kraussii* Hochst.	COMBRETACEAE	1	0	2	15	0	3	0	1	0	0	7	29

Table 4.38 (continued)

Rank No.	Taxon	Family	Indg.	End.	*FSA* (med)	Treat.	Assoc.	Tox.	Red Data	Trade	HFam1	HFam2	Keyword	Total Score
150	*Cnestis polyphylla* Lam.	CONNARACEAE	1	0	2	15	0	3	2	0	0	0	6	29
151	*Albizia antunesiana* Harms	FABACEAE	1	0	2	15	0	0	2	0	6	0	3	29
152	*Senna occidentalis* (L.) Link	FABACEAE	0	0	2	15	0	3	0	0	6	0	3	29
153	*Cassytha ciliolata* Nees	LAURACEAE	1	1	2	15	0	3	0	0	4	0	3	29
154	*Nylandtia spinosa* (L.) Dumort. var. *spinosa*	POLYGALACEAE	1	1	2	15	0	3	0	0	0	0	7	29
155	*Ziziphus zeyheriana* Sond.	RHAMNACEAE	1	0	2	15	0	0	0	0	4	0	7	29
156	*Solanum linnaeanum* Hepper & Jaeger	SOLANACEAE	1	0	0	15	0	0	0	0	4	3	6	29
157	*Kigelia africana* (Lam.) Benth.	BIGNONIACEAE	1	0	2	15	0	3	0	1.5	0	3	3	28.5
158	*Acalypha peduncularis* E.Mey. ex Meisn.	EUPHORBIACEAE	1	0	2	15	0	0	0	0.5	0	3	7	28.5
159	*Andrachne ovalis* (Sond.) Müll.Arg.	EUPHORBIACEAE	1	0	2	15	0	3	0	1.5	0	3	3	28.5
160	*Cissampelos mucronata* A.Rich.	MENISPERMACEAE	1	0	2	15	0	3	0	0.5	0	0	7	28.5
161	*Zanthoxylum davyi* (I.Verd.) P.G.Waterman	RUTACEAE	1	0	2	15	0	0	2	1.5	0	0	7	28.5
162	*Rhoicissus tridentata* (L.f.) Wild & R.B.Drumm. subsp. *cuneifolia* (Eckl. & Zeyh.) Urton	VITACEAE	1	0	2	15	0	3	0	1.5	0	3	3	28.5
163	*Heteromorpha arborescens* (Thunb.) Cham. & Schltdl. var. *arborescens*	APIACEAE	1	0	0	15	0	0	0	1	6	0	5	28
164	*Aloe ferox* Mill.	ASPHODELACEAE	1	0	2	15	0	0	2	1	0	0	7	28
165	*Conyza albida* Spreng.	ASTERACEAE	0	0	2	15	0	0	0	0	8	0	3	28
166	*Hypoxis hemerocallidea* Fisch. & C.A.Mey.	HYPOXIDACEAE	1	0	2	15	0	0	2	1	0	0	7	28
167	*Linum thunbergii* Eckl. & Zeyh.	LINACEAE	1	0	2	15	0	0	0	0	0	3	7	28
168	*Sida acuta* Burm.f. subsp. *acuta*	MALVACEAE	1	0	2	15	0	3	0	0	4	0	3	28
169	*Olea capensis* L. subsp. *capensis*	OLEACEAE	1	0	0	15	0	0	0	0	6	3	3	28
170	*Agrimonia bracteata* E.Mey. ex C.A.Mey.	ROSACEAE	1	0	2	15	0	3	0	0	0	0	7	28

Table 4.38 (continued)

Rank No.	Taxon	Family	Indg.	End.	*FSA* (med)	Treat.	Assoc.	Tox.	Red Data	Trade	HFam1	HFam2	Keyword	Total Score
171	*Pentas micrantha* Baker subsp. *wyliei* (N.E.Br.) Verdc.	RUBIACEAE	1	0	0	15	0	0	2	0	0	3	7	28
172	*Aptosimum procumbens* (Lehm.) Steud.	SCROPHULARIACEAE	1	0	2	15	0	0	0	0	0	3	7	28
173	*Solanum torvum* Sw.	SOLANACEAE	0	0	0	15	0	3	0	0	4	3	3	28
174	*Dombeya rotundifolia* (Hochst.) Planch. var. *rotundifolia*	STERCULIACEAE	1	0	2	15	0	0	2	1	0	0	7	28
175	*Vitex ferruginea* Schumach. & Thonn.	VERBENACEAE	1	0	2	15	0	0	0	0	4	3	3	28
176	*Cotyledon orbiculata* L. var. *orbiculata*	CRASSULACEAE	1	0	2	15	0	3	0	0.5	0	0	6	27.5
177	*Coccinia adoensis* (A.Rich.) Cogn.	CUCURBITACEAE	1	0	2	15	0	0	0	0.5	4	0	5	27.5
178	*Euphorbia tirucalli* L.	EUPHORBIACEAE	1	0	2	15	0	3	0	0.5	0	3	3	27.5
179	*Margaritaria discoidea* (Baill.) G.L.Webster subsp. *discoidea*	EUPHORBIACEAE	1	0	0	15	0	3	0	0.5	0	3	5	27.5
180	*Pittosporum viridiflorum* Sims	PITTOSPORACEAE	1	0	2	15	0	3	0	1.5	0	0	5	27.5
181	*Clerodendrum glabrum* E.Mey. var. *glabrum*	VERBENACEAE	1	0	2	15	0	0	0	0.5	4	3	2	27.5
182	*Hedera helix* L. var. *helix*	ARALIACEAE	0	0	0	15	0	3	0	0	4	0	5	27
183	*Conyza attenuata* DC.	ASTERACEAE	1	0	0	15	0	0	0	0	8	0	3	27
184	*Boscia albitrunca* (Burch.) Gilg & Gilg-Ben.	CAPPARACEAE	1	0	2	15	0	3	0	1	0	0	5	27
185	*Silene burchellii* Otth var. *burchellii*	CARYOPHYLLACEAE	1	0	0	15	0	0	0	0	4	0	7	27
186	*Elaeodendron transvaalense* (Burtt Davy) R.H.Archer	CELASTRACEAE	1	0	0	15	0	0	0	1	4	0	6	27
187	*Chenopodium album* L.	CHENOPODIACEAE	0	0	2	15	0	3	0	0	0	0	7	27
188	*Crassula muscosa* L. var. *muscosa*	CRASSULACEAE	1	0	2	15	0	0	2	0	0	0	7	27
189	*Euclea divinorum* Hiern	EBENACEAE	1	0	2	15	0	0	0	2	0	0	7	27
190	*Dalechampia capensis* A.Spreng.	EUPHORBIACEAE	0	0	2	15	0	0	0	0	0	3	7	27

Table 4.38 (continued)

Rank No.	Taxon	Family	Indg.	End.	*FSA* (med)	Treat.	Assoc.	Tox.	Red Data	Trade	HFam1	HFam2	Keyword	Total Score
191	*Excoecaria simii* (Kuntze) Pax	EUPHORBIACEAE	1	1	0	15	0	0	2	0	0	3	5	27
192	*Shirakiopsis elliptica* (Hochst.) Esser	EUPHORBIACEAE	1	0	2	15	0	3	0	0	0	3	3	27
193	*Acacia reficiens* Wawra subsp. *reficiens*	FABACEAE	1	0	0	15	0	0	0	0	6	0	5	27
194	*Indigofera swaziensis* Bolus var. *swaziensis*	FABACEAE	1	0	0	15	0	0	0	0	6	0	5	27
195	*Drimia elata* Jacq.	HYACINTHACEAE	1	0	2	15	0	0	0	2	0	0	7	27
196	*Melia azedarach* L.	MELIACEAE	0	0	2	15	0	3	0	0	0	0	7	27
197	*Syzygium cordatum* Hochst. ex Sond. var. *cordatum*	MYRTACEAE	1	0	0	15	0	3	0	1	0	0	7	27
198	*Argemone ochroleuca* Sweet subsp. *ochroleuca*	PAPAVERACEAE	0	0	2	15	0	0	0	0	0	3	7	27
199	*Plantago major* L.	PLANTAGINACEAE	0	0	2	15	0	0	0	0	0	3	7	27
200	*Plumbago zeylanica* L.	PLUMBAGINACEAE	1	0	2	15	0	3	0	0	0	0	6	27
201	*Elytrigia repens* (L.) Nevski	POACEAE	0	0	2	15	0	3	0	0	0	0	7	27
202	*Rumex crispus* L.	POLYGONACEAE	0	0	2	15	0	3	0	0	0	0	7	27
203	*Canthium inerme* (L.f.) Kuntze	RUBIACEAE	1	0	2	15	0	0	0	1	0	3	5	27
204	*Gardenia ternifolia* Schumach. & Thonn. subsp. *jovis-tonantis* (Welw.) Verdc. var. *goetzei* (Stapf & Hutch.) Verdc.	RUBIACEAE	1	0	2	15	0	3	0	0	0	3	3	27
205	*Tricalysia capensis* (Meisn. ex Hochst.) Sim var. *capensis*	RUBIACEAE	1	1	0	15	0	0	0	0	0	3	7	27
206	*Zanthoxylum capense* (Thunb.) Harv.	RUTACEAE	1	0	2	15	0	0	0	2	0	0	7	27
207	*Salix mucronata* Thunb. subsp. *mucronata*	SALICACEAE	1	0	2	15	0	0	0	0	0	3	6	27
208	*Cissus quadrangularis* L. var. *quadrangularis*	VITACEAE	1	0	2	15	0	3	0	0	0	3	3	27
209	*Cissus rotundifolia* (Forssk.) Vahl	VITACEAE	1	0	2	15	0	0	0	0	0	3	6	27

Table 4.38 (continued)

Rank No.	Taxon	Family	Indg.	End.	*FSA* (med)	Treat.	Assoc.	Tox.	Red Data	Trade	HFam1	HFam2	Keyword	Total Score
210	*Acalypha villicaulis* Hochst. ex A.Rich.	EUPHORBIACEAE	1	0	2	15	0	0	0	0.5	0	3	5	26.5
211	*Tragia rupestris* Sond.	EUPHORBIACEAE	0	0	2	15	0	0	0	1.5	0	3	5	26.5
212	*Cissampelos capensis* L.f.	MENISPERMACEAE	1	0	2	15	0	3	0	0.5	0	0	5	26.5
213	*Myrothamnus flabellifolius* Welw.	MYROTHAMNACEAE	1	0	2	15	0	0	0	1.5	0	0	7	26.5
214	*Polygala virgata* Thunb. var. *decora* (Sond.) Harv.	POLYGALACEAE	1	0	0	15	0	3	0	0.5	0	0	7	26.5
215	*Securidaca longipedunculata* Fresen. var. *longipedunculata*	POLYGALACEAE	1	0	0	15	0	3	0	0.5	0	0	7	26.5
216	*Mimusops zeyheri* Sond.	SAPOTACEAE	1	0	2	15	0	3	0	0.5	0	0	5	26.5
217	*Steganotaenia araliacea* Hochst. var. *araliacea*	APIACEAE	1	0	0	15	0	0	0	1	6	0	3	26
218	*Asclepias humilis* (E.Mey.) Schltr.	ASCLEPIADACEAE	1	0	0	15	0	0	0	0	0	3	7	26
219	*Kalanchoe lanceolata* (Forssk.) Pers.	CRASSULACEAE	1	0	2	15	0	3	0	0	0	0	5	26
220	*Cyperus esculentus* L. var. *esculentus*	CYPERACEAE	1	0	2	15	0	3	0	0	0	0	5	26
221	*Clutia hirsuta* E.Mey. ex Sond. var. *hirsuta*	EUPHORBIACEAE	1	0	0	15	0	0	0	0	0	3	7	26
222	*Flueggea virosa* (Roxb. ex Willd.) Voigt subsp. *virosa*	EUPHORBIACEAE	1	0	2	15	0	3	0	0	0	3	2	26
223	*Tragia dioica* Sond.	EUPHORBIACEAE	0	0	0	15	0	3	0	0	0	3	5	26
224	*Crotalaria brevidens* Benth. var. *intermedia* (Kotschy) Polhill	FABACEAE	0	0	2	15	0	0	0	0	6	0	3	26
225	*Pelargonium ramosissimum* (Cav.) Willd.	GERANIACEAE	1	1	2	15	0	0	0	0	0	0	7	26
226	*Drimia sanguinea* (Schinz) Jessop	HYACINTHACEAE	1	0	0	15	0	3	0	0	0	0	7	26
227	*Dietes iridioides* (L.) Sweet ex Klatt	IRIDACEAE	1	0	2	15	0	0	0	1	0	0	7	26
228	*Phytolacca octandra* L.	PHYTOLACCACEAE	1	0	2	15	0	3	0	0	0	0	5	26
229	*Faurea saligna* Harv.	PROTEACEAE	1	0	2	15	0	0	0	1	0	0	7	26
230	*Rotheca myricoides* (Hochst.) Steane & Mabb	VERBENACEAE	1	0	0	15	0	0	0	0	4	3	3	26

Table 4.38 (continued)

Rank No.	Taxon	Family	Indg.	End.	*FSA* (med)	Treat.	Assoc.	Tox.	Red Data	Trade	HFam1	HFam2	Keyword	Total Score
231	*Hybanthus capensis* (Thunb.) Engl.	VIOLACEAE	1	0	0	15	0	0	0	0	0	3	7	26
232	*Aloe marlothii* A.Berger subsp. *marlothii*	ASPHODELACEAE	1	0	2	15	0	0	0	1.5	0	0	6	25.5
233	*Euclea natalensis* A.DC. subsp. *natalensis*	EBENACEAE	1	0	2	15	0	3	0	1.5	0	0	3	25.5
234	*Hibiscus surattensis* L.	MALVACEAE	1	0	0	15	0	0	0	0.5	4	0	5	25.5
235	*Carpobrotus edulis* (L.) L.Bolus subsp. *edulis*	MESEMBRYANTHEMACEAE	1	1	2	15	0	0	0	0.5	0	0	6	25.5
236	*Brackenridgea zanguebarica* Oliv.	OCHNACEAE	1	0	2	15	0	0	0	1.5	0	3	3	25.5
237	*Imperata cylindrica* (L.) Raeusch.	POACEAE	1	0	2	15	0	0	0	0.5	0	0	7	25.5
238	*Pappea capensis* Eckl. & Zeyh.	SAPINDACEAE	1	0	2	15	0	3	0	1.5	0	0	3	25.5
239	*Sideroxylon inerme* L. subsp. *inerme*	SAPOTACEAE	1	0	2	15	0	0	0	0.5	0	0	7	25.5
240	*Thunbergia capensis* Retz.	ACANTHACEAE	1	1	2	15	0	0	0	0	0	3	3	25
241	*Vinca major* L.	APOCYNACEAE	0	0	2	0	8	3	0	0	4	3	5	25
242	*Asparagus africanus* Lam.	ASPARAGACEAE	1	0	2	15	0	3	0	1	0	0	3	25
243	*Balanites aegyptiaca* (L.) Delile	BALANITACEAE	1	0	0	15	0	3	0	0	0	0	6	25
244	*Maerua schinzii* Pax	CAPPARACEAE	1	0	2	15	0	0	2	0	0	0	5	25
245	*Acalypha ciliata* Forssk.	EUPHORBIACEAE	0	0	2	15	0	0	0	0	0	3	5	25
246	*Euphorbia hirta* L.	EUPHORBIACEAE	1	0	0	15	0	3	0	0	0	3	3	25
247	*Hibiscus mutabilis* L.	MALVACEAE	0	0	0	15	0	0	0	0	4	0	6	25
248	*Eragrostis plana* Nees	POACEAE	1	0	2	15	0	0	0	0	0	0	7	25
249	*Kohautia caespitosa* Schnizl. subsp. *brachyloba* (Sond.) D.Mantell	RUBIACEAE	1	0	0	15	0	0	0	0	0	3	6	25
250	*Cyphostemma subciliatum* (Baker) Desc. ex Wild & R.B.Drumm.	VITACEAE	1	0	0	15	0	0	0	1	0	3	5	25
251	*Ehretia rigida* (Thunb.) Druce subsp. *rigida*	BORAGINACEAE	1	0	0	15	0	0	0	0.5	0	3	5	24.5
252	*Maerua edulis* (Gilg & Gilg-Ben.) DeWolf	CAPPARACEAE	1	0	2	15	0	3	0	0.5	0	0	3	24.5
253	*Maesa lanceolata* Forssk.	MAESACEAE	1	0	2	15	0	0	0	1.5	0	0	5	24.5

Table 4.38 (continued)

Rank No.	Taxon	Family	Indg.	End.	*FSA* (med)	Treat.	Assoc.	Tox.	Red Data	Trade	HFam1	HFam2	Keyword	Total Score
254	*Ekebergia capensis* Sparrm.	MELIACEAE	1	0	2	15	0	3	0	1.5	0	0	2	24.5
255	*Ficus sur* Forssk.	MORACEAE	1	0	2	15	0	3	0	1.5	0	0	2	24.5
256	*Portulaca oleracea* L.	PORTULACACEAE	0	0	2	15	0	0	0	0.5	0	0	7	24.5
257	*Clausena anisata* (Willd.) Hook.f. ex Benth. var. *anisata*	RUTACEAE	1	0	0	15	0	0	0	1.5	0	0	7	24.5
258	*Gnidia capitata* L.f.	THYMELAEACEAE	1	0	2	15	0	3	0	0.5	0	0	3	24.5
259	*Urtica urens* L.	URTICACEAE	0	0	2	15	0	0	0	0.5	0	0	7	24.5
260	*Agapanthus campanulatus* F.M.Leight. subsp. *patens* (F.M.Leight.) F.M.Leight.	ALLIACEAE	1	0	0	15	0	0	0	1	0	0	7	24
261	*Tulbaghia acutiloba* Harv.	ALLIACEAE	1	0	2	15	0	0	0	0	0	0	6	24
262	*Psilotrichum scleranthum* Thwaites	AMARANTHACEAE	1	0	2	15	0	3	0	0	0	0	3	24
263	*Amaryllis belladonna* L.	AMARYLLIDACEAE	1	1	2	0	8	3	0	0	4	0	5	24
264	*Heliotropium ciliatum* Kaplan	BORAGINACEAE	1	0	2	15	0	0	0	0	0	3	3	24
265	*Commiphora africana* (A.Rich.) Engl. var. *africana*	BURSERACEAE	1	0	2	15	0	3	0	0	0	0	3	24
266	*Boscia salicifolia* Oliv.	CAPPARACEAE	1	0	2	15	0	3	0	0	0	0	3	24
267	*Ipomoea ficifolia* Lindl.	CONVOLVULACEAE	1	0	2	15	0	0	0	0	0	3	3	24
268	*Cyperus rotundus* L. subsp. *rotundus*	CYPERACEAE	1	0	0	15	0	3	0	0	0	0	5	24
269	*Euphorbia clavarioides* Boiss. var. *clavarioides*	EUPHORBIACEAE	1	0	2	15	0	0	0	1	0	3	2	24
270	*Phyllanthus delagoensis* Hutch.	EUPHORBIACEAE	1	0	0	15	0	0	0	0	0	3	5	24
271	*Argyrolobium collinum* Eckl. & Zeyh.	FABACEAE	1	0	0	15	0	0	0	0	6	0	2	24
272	*Spartium junceum* L.	FABACEAE	0	0	2	0	8	3	0	0	6	0	5	24
273	*Trimeria grandifolia* (Hochst.) Warb. subsp. *grandifolia*	FLACOURTIACEAE	1	0	2	15	0	0	0	0	0	3	3	24
274	*Sebaea hymenosepala* Gilg	GENTIANACEAE	1	0	2	15	0	0	0	0	0	3	3	24
275	*Morella humilis* (Cham. & Schltdl.) Killick	MYRICACEAE	1	1	0	15	0	0	0	0	0	0	7	24

Table 4.38 (continued)

Rank No.	Taxon	Family	Indg.	End.	*FSA* (med)	Treat.	Assoc.	Tox.	Red Data	Trade	HFam1	HFam2	Keyword	Total Score
276	*Piper capense* L.f. var. *capense*	PIPERACEAE	1	0	2	15	0	0	0	0	0	0	6	24
277	*Chloris virgata* Sw.	POACEAE	1	0	2	15	0	0	0	0	0	0	6	24
278	*Diodia dasycephala*	RUBIACEAE	0	0	0	15	0	0	0	0	0	3	6	24
279	*Jamesbrittenia micrantha* (Klotzsch) Hilliard	SCROPHULARIACEAE	1	0	0	15	0	0	0	0	0	3	5	24
280	*Gnidia polycephala* (C.A.Mey.) Gilg	THYMELAEACEAE	1	0	2	15	0	3	0	0	0	0	3	24
281	*Cissus nymphaeifolia* (Welw. ex Baker) Planch.	VITACEAE	1	0	2	15	0	0	0	0	0	3	3	24
282	*Chenopodium ambrosioides* L.	CHENOPODIACEAE	0	0	2	15	0	3	0	0.5	0	0	3	23.5
283	*Euclea crispa* (Thunb.) Gürke subsp. *crispa*	EBENACEAE	1	0	2	15	0	0	0	0.5	0	0	5	23.5
284	*Osyris compressa* (P.J.Bergius) A.DC.	SANTALACEAE	1	0	0	15	0	0	0	0.5	0	0	7	23.5
285	*Blepharis capensis* (L.f.) Pers. var. *capensis*	ACANTHACEAE	1	1	0	15	0	0	0	0	0	3	3	23
286	*Rourea orientalis* Baill.	CONNARACEAE	1	0	2	15	0	0	2	0	0	0	3	23
287	*Trianoptiles capensis* (Steud.) Harv.	CYPERACEAE	1	1	0	15	0	0	0	0	0	0	6	23
288	*Pteridium aquilinum* (L.) Kuhn	DENNSTAEDTIACEAE	1	0	2	15	0	3	0	0	0	0	2	23
289	*Dioscorea sylvatica* (Kunth) Eckl. var. *sylvatica*	DIOSCOREACEAE	1	0	2	15	0	0	0	2	0	0	3	23
290	*Pelargonium grossularioides* (L.) L'Hér.	GERANIACEAE	1	0	2	15	0	0	0	0	0	0	5	23
291	*Commicarpus pentandrus* (Burch.) Heimerl	NYCTAGINACEAE	1	0	2	15	0	0	0	0	0	0	5	23
292	*Pavetta capensis* (Houtt.) Bremek. subsp. *capensis*	RUBIACEAE	1	1	0	15	0	0	0	0	0	3	3	23
293	*Dodonaea viscosa* Jacq. subsp. *viscosa*	SAPINDACEAE	1	0	0	15	0	0	0	0	0	0	7	23
294	*Hydnora africana* Thunb.	HYDNORACEAE	1	0	2	15	0	0	0	1.5	0	0	3	22.5
295	*Apodytes dimidiata* E.Mey. ex Arn. subsp. *dimidiata*	ICACINACEAE	1	0	0	15	0	0	0	0.5	0	0	6	22.5
296	*Podocarpus falcatus* (Thunb.) R.Br. ex Mirb.	PODOCARPACEAE	1	0	2	15	0	0	2	0.5	0	0	2	22.5
297	*Bulbine natalensis* Baker	ASPHODELACEAE	1	0	0	15	0	0	0	1	0	0	5	22

Table 4.38 (continued)

Rank No.	Taxon	Family	Indg.	End.	*FSA* (med)	Treat.	Assoc.	Tox.	Red Data	Trade	HFam1	HFam2	Keyword	Total Score
298	*Juniperus virginiana* L.	CUPRESSACEAE	0	0	0	15	0	0	0	0	0	0	7	22
299	*Tragiella natalensis* (Sond.) Pax & K.Hoffm.	EUPHORBIACEAE	1	0	0	15	0	0	0	0	0	3	3	22
300	*Muraltia heisteria* (L.) DC.	POLYGALACEAE	1	1	0	15	0	0	0	0	0	0	5	22
301	*Dodonaea viscosa* Jacq. var. *angustifolia* Benth.	SAPINDACEAE	1	0	0	15	0	0	0	0	0	0	6	22
302	*Cycnium adonense* E.Mey. ex Benth. subsp. *adonense*	SCROPHULARIACEAE	1	0	0	15	0	0	0	0	0	3	3	22
303	*Cannabis sativa* L. var. *sativa*	CANNABACEAE	0	0	0	15	0	0	0	0.5	0	0	6	21.5
304	*Combretum molle* R.Br. ex G.Don	COMBRETACEAE	1	0	2	15	0	0	0	0.5	0	0	3	21.5
305	*Cardiospermum halicacabum* L. var. *halicacabum*	SAPINDACEAE	1	0	0	15	0	3	0	0.5	0	0	2	21.5
306	*Celosia argentea* L. forma *argentea*	AMARANTHACEAE	1	0	2	15	0	0	0	0	0	0	3	21
307	*Senecio latifolius* DC.	ASTERACEAE	1	0	2	0	0	3	0	0	8	0	7	21
308	*Lonicera japonica* Thunb. var. *japonica*	CAPRIFOLIACEAE	0	0	0	15	0	0	0	0	0	0	6	21
309	*Pelargonium antidysentericum* (Eckl. & Zeyh.) Kostel. subsp. *antidysentericum*	GERANIACEAE	1	0	0	15	0	0	0	0	0	0	5	21
310	*Endostemon obtusifolius* (E.Mey. ex Benth.) N.E.Br.	LAMIACEAE	1	0	2	0	0	0	0	0	8	3	7	21
311	*Lobelia anceps* L.f.	LOBELIACEAE	1	0	2	15	0	0	0	0	0	0	3	21
312	*Carpobrotus acinaciformis* (L.) L.Bolus	MESEMBRYANTHEMACEAE	1	1	2	15	0	0	0	0	0	0	2	21
313	*Phragmites mauritianus* Kunth	POACEAE	1	0	2	15	0	0	0	0	0	0	3	21
314	*Galium capense* Thunb. subsp. *capense*	RUBIACEAE	1	0	0	15	0	0	0	0	0	3	2	21
315	*Cola natalensis* Oliv.	STERCULIACEAE	1	0	0	15	0	0	0	0	0	0	5	21
316	*Hermannia glanduligera* K.Schum.	STERCULIACEAE	1	0	2	15	0	0	0	0	0	0	3	21
317	*Agapanthus comptonii* F.M.Leight. subsp. *comptonii*	ALLIACEAE	1	1	0	15	0	0	0	0.5	0	0	3	20.5

Table 4.38 (continued)

Rank No.	Taxon	Family	Indg.	End.	*FSA* (med)	Treat.	Assoc.	Tox.	Red Data	Trade	HFam1	HFam2	Keyword	Total Score
318	*Bulbine frutescens* (L.) Willd.	ASPHODELACEAE	1	0	2	15	0	0	0	0.5	0	0	2	20.5
319	*Agapanthus campanulatus* F.M.Leight. subsp. *campanulatus*	ALLIACEAE	1	1	0	15	0	0	0	1	0	0	2	20
320	*Acalypha glabrata* Thunb. var. *glabrata*	EUPHORBIACEAE	0	0	0	15	0	0	0	0	0	3	2	20
321	*Albizia adianthifolia* (Schumach.) W.Wight var. *adianthifolia*	FABACEAE	1	0	2	0	0	3	0	2	6	0	6	20
322	*Samolus valerandi* L.	THEOPHRASTACEAE	1	0	2	15	0	0	0	0	0	0	2	20
323	*Aloe angolensis* Baker	ASPHODELACEAE	1	0	0	15	0	0	0	0.5	0	0	3	19.5
324	*Aloe chabaudii* Schönland var. *chabaudii*	ASPHODELACEAE	1	0	0	15	0	0	0	0.5	0	0	3	19.5
325	*Bulbine asphodeloides* (L.) Spreng.	ASPHODELACEAE	1	0	0	15	0	0	0	1	0	0	2	19
326	*Artemisia vulgaris* L.	ASTERACEAE	0	0	2	0	0	3	0	0	8	0	6	19
327	*Quisqualis parviflora* Gerrard ex Sond.	COMBRETACEAE	1	0	0	15	0	0	0	0	0	0	3	19
328	*Burkea africana* Hook.	FABACEAE	1	0	2	0	0	3	0	0	6	0	7	19
329	*Embelia schimperi* Vatke	MYRSINACEAE	1	0	0	15	0	0	0	0	0	0	3	19
330	*Helichrysum petiolare* Hilliard & B.L.Burtt	ASTERACEAE	1	1	2	0	0	0	0	0.5	8	0	6	18.5
331	*Heteromorpha arborescens* (Spreng.) Cham. & Schltdl. var. *abyssinica* (A.Rich.) H.Wolff	APIACEAE	1	0	2	0	0	3	0	1	6	0	5	18
332	*Dicerothamnus rhinocerotis* (L.f.) Koekemoer	ASTERACEAE	1	0	2	0	0	0	0	0	8	0	7	18
333	*Inula glomerata* Oliv. & Hiern	ASTERACEAE	1	0	2	0	0	0	0	0	8	0	7	18
334	*Casuarina equisetifolia* J.R.& G.Forst.	CASUARINACEAE	0	0	0	15	0	0	0	0	0	0	3	18
335	*Ficus retusa* L.	MORACEAE	0	0	0	15	0	0	0	0	0	0	3	18
336	*Eleusine coracana* (L.) Gaertn. subsp. *africana* (Kenn.-O'Byrne) Hilu & de Wet	POACEAE	1	0	0	15	0	0	0	0	0	0	2	18

Table 4.38 (continued)

Rank No.	Taxon	Family	Indg.	End.	*FSA* (med)	Treat.	Assoc.	Tox.	Red Data	Trade	HFam1	HFam2	Keyword	Total Score
337	*Polygala erioptera* DC. subsp. *erioptera*	POLYGALACEAE	1	0	0	15	0	0	0	0	0	0	2	18
338	*Salvadora persica* L. var. *persica*	SALVADORACEAE	1	0	0	15	0	0	0	0	0	0	2	18
339	*Verbena officinalis* L.	VERBENACEAE	0	0	2	0	0	3	0	0	4	3	6	18
340	*Mentha longifolia* (L.) Huds. subsp. *longifolia*	LAMIACEAE	0	0	0	0	0	0	0	0.5	8	3	6	17.5
341	*Acacia senegal* (L.) Willd. var. *rostrata* Brenan	FABACEAE	1	0	2	0	0	0	2	0	6	0	6	17
342	*Peucedanum galbanum* (L.) Drude	APIACEAE	1	1	2	0	0	3	0	0	6	0	3	16
343	*Osmitopsis asteriscoides* (P.J.Bergius) Less.	ASTERACEAE	1	0	0	0	0	0	0	0	8	0	6	15
344	*Centella asiatica* (L.) Urb.	ARALIACEAE	1	0	2	0	0	0	0	0.5	4	0	7	14.5
345	*Crinum macowanii* Baker	AMARYLLIDACEAE	1	0	2	0	0	3	0	1	4	0	3	14
346	*Manihot esculenta* Crantz	EUPHORBIACEAE	0	0	2	0	0	3	0	0	0	3	6	14
347	*Prosopis glandulosa* Torr. var. *glandulosa*	FABACEAE	0	0	2	0	0	0	0	0	6	0	6	14
348	*Enicostema axillare* (Lam.) A.Raynal subsp. *axillare*	GENTIANACEAE	1	0	2	0	0	0	0	0	0	3	8	14
349	*Crinum bulbispermum* (Burm.f.) Milne-Redh. & Schweick.	AMARYLLIDACEAE	1	0	2	0	0	3	0	0.5	4	0	3	13.5
350	*Terminalia sericea* Burch. ex DC.	COMBRETACEAE	1	0	0	0	0	3	0	2	0	0	7	13
351	*Stellaria media* (L.) Vill.	CARYOPHYLLACEAE	0	0	2	0	0	0	0	0	4	0	6	12
352	*Hybanthus enneaspermus* (L.) F.Muell. var. *enneaspermus*	VIOLACEAE	0	0	2	0	0	0	0	0	0	3	7	12
353	*Pancratium tenuifolium* Hochst. ex A.Rich.	AMARYLLIDACEAE	1	0	0	0	0	0	0	0	4	0	6	11
354	*Drimia altissima* (L.f.) Ker Gaul.	HYACINTHACEAE	1	0	0	0	0	3	0	0	0	0	7	11
355	*Argemone mexicana* L. forma *mexicana*	PAPAVERACEAE	0	0	2	0	0	0	0	0	0	3	6	11
356	*Polygonum aviculare* L.	POLYGONACEAE	0	0	2	0	0	3	0	0	0	0	6	11
357	*Ruta graveolens* L.	RUTACEAE	0	0	2	0	0	3	0	0	0	0	6	11
358	*Viscum rotundifolium* L.f.	VISCACEAE	1	0	2	0	0	0	2	0	0	0	6	11

Table 4.38 (continued)

Rank No.	Taxon	Family	Indg.	End.	*FSA* (med)	Treat.	Assoc.	Tox.	Red Data	Trade	HFam1	HFam2	Keyword	Total Score
359	*Galenia africana* L. var. *africana*	AIZOACEAE	1	0	0	0	0	3	0	0	0	0	6	10
360	*Eucalyptus globulus* Labill. subsp. *maidenii* (F.Muell.) Kirkp.	MYRTACEAE	0	0	0	0	0	3	0	1	0	0	6	10
361	*Turnera oculata* Story var. *oculata*	TURNERACEAE	1	0	0	0	0	0	0	0	0	3	6	10
362	*Crabbea nana* Nees	ACANTHACEAE	1	0	2	0	0	0	0	0	0	3	3	9
363	*Melianthus comosus* Vahl	MELIANTHACEAE	1	0	2	0	0	3	0	0	0	0	3	9
364	*Commelina africana* L. var. *africana*	COMMELINACEAE	1	0	0	0	0	0	0	0.5	0	0	7	8.5
365	*Clematis villosa* subsp. *villosa*	RANUNCULACEAE	1	0	0	0	0	0	0	0	0	0	7	8
366	*Pinus elliotii* Engelm. var. *elliottii*	PINACEAE	0	0	0	0	0	0	0	0	0	0	6	6
367	*Ulmus parvifolia* Jacq.	ULMACEAE	0	0	0	0	0	0	0	0	0	0	6	6
368	*Carpobrotus dimidiatus* (Haw.) L.Bolus	MESEMBRYANTHEMACEAE	1	0	0	0	0	0	0	0	0	0	3	4
369	*Dodonaea viscosa* Jacq. subsp. *angustifolia* (L.f.) J.G.West	SAPINDACEAE	1	0	0	0	0	0	0	0	0	0	2	3

4.3.2 Allies of high ranking taxa (Set 3)

The selection of plant families from the top 100 taxa in each prioritised list, i.e. Set 1 (Table 4.36; Table 4.37; Table 4.38) allowed for the short-listing of Set 3 taxa (Figure 4.2). A total of 26 (Table 4.39), 11 (Table 4.40) and 26 (Table 4.41) taxa closely related to those in Set 1 were selected for anti-tuberculosis, anti-diabetes and immune modulatory candidates respectively.

Table 4.39 Set 3 candidates closely related to prioritised EthmedTB taxa in Set 1

Family	Taxon
Mesembryanthemaceae	*Carpobrotus dimidiatus* (Haw.) L.Bolus
Mesembryanthemaceae	*Carpobrotus quadrifidus* L.Bolus
Asteraceae	*Chrysocoma candelabrum* Ehr.Bayer
Asteraceae	*Chrysocoma longifolia* DC.
Euphorbiaceae	*Croton megalobotrys* Müll.Arg.
Euphorbiaceae	*Croton menyharthii* Pax
Meliaceae	*Ekebergia pterophylla* (C.DC.) Hofmeyr
Euphorbiaceae	*Euphorbia bupleurifolia* Jacq.
Euphorbiaceae	*Euphorbia cooperi* N.E.Br. ex A.Berger var. *cooperi*
Rubiaceae	*Gardenia brachythamnus* (K.Schum.) Launert
Rubiaceae	*Gardenia cornuta* Hemsl.
Apiaceae	*Heteromorpha involucrata* Conrath
Apiaceae	*Heteromorpha pubescens* Burtt Davy
Verbenaceae	*Lippia pearsonii* Moldenke
Verbenaceae	*Lippia wilmsii* H.Pearson
Asteraceae	*Microglossa caffrorum* (Less.) Grau
Rubiaceae	*Pentanisia angustifolia* (Hochst.) Hochst.
Rubiaceae	*Pentanisia sykesii* Hutch. subsp. *otomerioides* Verdc.
Lamiaceae	*Salvia albicaulis* Benth.
Lamiaceae	*Salvia lanceolata* Lam.
Myrtaceae	*Syzygium legatii* Burtt Davy & Greenway
Myrtaceae	*Syzygium pondoense* Engl.
Lamiaceae	*Tetradenia barberae* (N.E.Br.) Codd
Lamiaceae	*Tetradenia brevispicata* (N.E.Br.) Codd
Alliaceae	*Tulbaghia capensis* L.
Alliaceae	*Tulbaghia dregeana* Kunth

Table 4.40 Set 3 candidates closely related to prioritised EthmedDBM taxa in Set 1

Family	Taxon
Asteraceae	*Brachylaena elliptica* (Thunb.) DC.
Asteraceae	*Brachylaena ilicifolia* (Lam.) E.Phillips & Schweick.
Araliaceae	*Cussonia paniculata* Eckl. & Zeyh. subsp. *paniculata*
Araliaceae	*Cussonia sphaerocephala* Strey
Fabaceae	*Erythrophleum africanum* (Welw. ex Benth.) Harms
Fabaceae	*Indigofera annua* Milne-Redh.
Fabaceae	*Indigofera heterophylla* Thunb.
Fabaceae	*Sutherlandia humilis* E.Phillips & R.A.Dyer
Fabaceae	*Sutherlandia tomentosa* Eckl. & Zeyh.
Combretaceae	*Terminalia brachystemma* Welw. ex Hiern subsp. *brachystemma*
Combretaceae	*Terminalia prunioides* M.A.Lawson
Urticaceae	*Urtica lobulata* Blume

Table 4.41 Set 3 candidates closely related to prioritised EthmedIMM taxa in Set 1

Family	Taxon
Apiaceae	*Alepidea acutidens* Weim. var. *acutidens*
Apiaceae	*Alepidea angustifolia* Schltr. & H.Wolff
Asteraceae	*Bidens kirkii* (Oliv. & Hiern) Sherff
Asteraceae	*Bidens schimperi* Sch.Bip. ex Walp.
Asteraceae	*Brachylaena elliptica* (Thunb.) DC.
Asteraceae	*Brachylaena ilicifolia* (Lam.) E.Phillips & Schweick.
Asteraceae	*Callilepis lancifolia* Burtt Davy
Asteraceae	*Callilepis salicifolia* Oliv.
Fabaceae	*Erythrophleum africanum* (Welw. ex Benth.) Harms
Asteraceae	*Gerbera cordata* (Thunb.) Less.
Asteraceae	*Gerbera natalensis* Sch.Bip.
Lamiaceae	*Leonotis dubia* E.Mey.
Lamiaceae	*Leonotis nepetifolia* (L.) R.Br.
Verbenaceae	*Lippia pearsonii* Moldenke
Verbenaceae	*Lippia rehmannii* H.Pearson
Asteraceae	*Microglossa caffrorum* (Less.) Grau
Asteraceae	*Pseudognaphalium oligandrum* (DC.) Hilliard & B.L.Burtt
Asteraceae	*Pseudognaphalium undulatum* (L.) Hilliard & B.L.Burtt
Asteraceae	*Senecio abruptus* Thunb.
Asteraceae	*Senecio cordifolius* L.f.
Strychnaceae	*Strychnos gerrardii* N.E.Br.
Strychnaceae	*Strychnos pungens* Soler.
Asteraceae	*Tarchonanthus littoralis* P.P.J.Herman
Asteraceae	*Tarchonanthus parvicapitulatus* P.P.J.Herman
Asteraceae	*Vernonia africana* (Sond.) Druce
Asteraceae	*Vernonia hirsuta* (DC.) Sch.Bip. ex Walp.

4.3.3 Endemics from the Western Cape (Set 5)

The selection of plant families from the top 100 taxa in each prioritised list in Set 1 allowed random short-listing of 60 (Table 4.42), 49 (Table 4.43) and 60 (Table 4.44) Western Cape endemics (Set 5) for anti-tuberculosis, anti-diabetes and immune modulatory candidates respectively.

Table 4.42 Set 4 candidates closely related to prioritised EthmedTB taxa in Set 1

Family	Taxon
Asteraceae	*Amphiglossa rudolphii* Koekemoer
Asteraceae	*Anderbergia fallax* B.Nord.
Asteraceae	*Arctotis undulata* Jacq.
Asteraceae	*Cotula heterocarpa* DC.
Asteraceae	*Disparago kraussii* Sch.Bip.
Asteraceae	*Euryops erectus* (Compton) B.Nord.
Asteraceae	*Felicia echinata* (Thunb.) Nees
Asteraceae	*Gymnostephium papposum* G.L.Nesom
Asteraceae	*Othonna dentata* L.
Asteraceae	*Pentzia dentata* (L.) Kuntze
Asteraceae	*Pentzia peduncularis* B.Nord.
Asteraceae	*Senecio hollandii* Compton
Asteraceae	*Senecio leucoglossus* Sond.
Asteraceae	*Senecio panduratus* (Thunb.) Less.
Asteraceae	*Steirodiscus speciosus* (Pillans) B.Nord.
Euphorbiaceae	*Clutia alaternoides* L. var. *alaternoides*
Euphorbiaceae	*Clutia laxa* Eckl. ex Sond.
Euphorbiaceae	*Clutia pubescens* Thunb.
Euphorbiaceae	*Clutia sericea* Müll.Arg.
Euphorbiaceae	*Euphorbia ecklonii* (Klotzsch & Garcke) A.Hässl.
Euphorbiaceae	*Euphorbia horrida* Boiss. var. *horrida*
Euphorbiaceae	*Euphorbia horrida* Boiss. var. *striata* A.C.White, R.A.Dyer & B.Sloane
Euphorbiaceae	*Euphorbia mira* L.C.Leach
Euphorbiaceae	*Euphorbia pillansii* N.E.Br. var. *albovirens* A.C.White, R.A.Dyer & B.Sloane
Euphorbiaceae	*Euphorbia pillansii* N.E.Br. var. *pillansii*
Euphorbiaceae	*Euphorbia tuberculata* Jacq. var. *macowani* (N.E.Br.) A.C.White, R.A.Dyer & B.Sloane
Euphorbiaceae	*Lachnostylis bilocularis* R.A.Dyer
Lamiaceae	*Plectranthus ciliatus* E.Mey. ex Benth.
Lamiaceae	*Salvia albicaulis* Benth.
Lamiaceae	*Salvia aurita* L.f. var. *aurita*
Lamiaceae	*Salvia granitica* Hochst.
Lamiaceae	*Salvia lanceolata* Lam.
Lamiaceae	*Salvia muirii* L.Bolus
Lamiaceae	*Salvia repens* Burch. ex Benth. var. *repens*
Lamiaceae	*Salvia thermaruma* Van Jaarsv.
Lamiaceae	*Stachys bolusii* Skan
Lamiaceae	*Stachys cuneata* Banks ex Benth.
Lamiaceae	*Stachys flavescens* Benth.
Lamiaceae	*Stachys scabrida* Skan
Lamiaceae	*Stachys sublobata* Skan
Lamiaceae	*Stachys thunbergii* Benth.
Lamiaceae	*Stachys zeyheri* Skan
Rubiaceae	*Anthospermum bicorne* Puff
Rubiaceae	*Anthospermum dregei* Sond. subsp. *ecklonis*
Rubiaceae	*Anthospermum ericifolium* (Licht. ex Roem. & Schult.) Kuntze
Rubiaceae	*Anthospermum paniculatum* Cruse
Rubiaceae	*Anthospermum prostratum* Sond.
Rubiaceae	*Carpacoce heteromorpha* (H.Buek) L.Bolus

Table 4.42 (continued)

Family	Taxon
Rubiaceae	*Carpacoce scabra* (Thunb.) Sond. subsp. *rupestris*
Rubiaceae	*Carpacoce vaginellata* T.M.Salter
Rubiaceae	*Galium bredasdorpense* Puff
Rubiaceae	*Galium spurium-aparine* complex
Rubiaceae	*Galium subvillosum* Sond. var. *subglabrum* Puff
Rubiaceae	*Galium subvillosum* Sond. var. *subvillosum*
Rubiaceae	*Galium undulatum* Puff
Rubiaceae	*Nenax acerosa* Gaertn. subsp. *acerosa*
Rubiaceae	*Nenax elsieae* Puff
Verbenaceae	*Chascanum cernuum* (L.) E.Mey.
Verbenaceae	*Chascanum integrifolium* (H.Pearson) Moldenke

Table 4.43 Set 4 candidates closely related to prioritised EthmedDBM taxa in Set 1

Family	Taxon
Anacardiaceae	*Heeria argentea* (Thunb.) Meisn.
Anacardiaceae	*Laurophyllus capensis* Thunb.
Anacardiaceae	*Loxostylis alata* A.Spreng. ex Rchb.
Anacardiaceae	*Rhus angustifolia* L.
Anacardiaceae	*Rhus crenata* Thunb.
Anacardiaceae	*Rhus dissecta* Thunb.
Anacardiaceae	*Rhus laevigata* L. var. *laevigata* forma *laevigata*
Anacardiaceae	*Rhus longispina* Eckl. & Zeyh.
Anacardiaceae	*Rhus rimosa* Eckl. & Zeyh.
Anacardiaceae	*Rhus stenophylla* Eckl. & Zeyh.
Apocynaceae	*Asclepias crispa* P.J.Bergius var. *crispa*
Apocynaceae	*Aspidoglossum gracile* (E.Mey.) Kupicha
Apocynaceae	*Brachystelma thunbergii* N.E.Br.
Apocynaceae	*Duvalia elegans* (Masson) Haw.
Apocynaceae	*Eustegia minuta* (L.f.) R.Br.
Apocynaceae	*Hoodia pilifera* (L.f.) Plowes subsp. *annulata* (N.E.Br.) Bruyns
Apocynaceae	*Huernia humilis* (Masson) Haw.
Apocynaceae	*Huernia witzenbergensis* C.A.Lückh.
Apocynaceae	*Pectinaria longipes* (N.E.Br.) Bruyns subsp. *longipes*
Apocynaceae	*Quaqua aurea* (C.A.Lückh.) Plowes
Apocynaceae	*Quaqua marlothii* (N.E.Br.) Bruyns
Apocynaceae	*Stapelia cedrimontana* Frandsen
Apocynaceae	*Stapelia erectiflora* N.E.Br. var. *prostratiflora* L.C.Leach
Apocynaceae	*Stapelia montana* L.C.Leach var. *grossa* L.C.Leach
Apocynaceae	*Tridentea parvipuncta* (N.E.Br.) L.C.Leach subsp. *parvipuncta*
Araliaceae	*Cussonia thyrsiflora* Thunb.
Fabaceae	*Amphithalea ericifolia* (L.) Eckl. & Zeyh. subsp. *minuta* Granby
Fabaceae	*Amphithalea purpurea* (Granby) A.L.Schutte
Fabaceae	*Amphithalea vlokii* (A.L.Schutte & B.-E.van Wyk) A.L.Schutte
Fabaceae	*Argyrolobium molle* Eckl. & Zeyh.
Fabaceae	*Aspalathus aciphylla* Harv.

Table 4.43 (continued)

Family	Taxon
Fabaceae	*Aspalathus capensis* (Walp.) R.Dahlgren
Fabaceae	*Aspalathus cephalotes* Thunb. subsp. *cephalotes*
Fabaceae	*Aspalathus desertorum* Bolus
Fabaceae	*Aspalathus macrantha* Harv.
Fabaceae	*Aspalathus serpens* R.Dahlgren
Fabaceae	*Indigofera guthriei* Bolus
Fabaceae	*Indigofera hantamensis* Diels
Fabaceae	*Liparia myrtifolia* Thunb.
Fabaceae	*Lotononis exstipulata* L.Bolus
Fabaceae	*Otholobium racemosum* (Thunb.) C.H.Stirt.
Fabaceae	*Rafnia angulata* Thunb. subsp. *angulata*
Fabaceae	*Rhynchosia chrysoscias* Benth. ex Harv.
Oleaceae	*Chionanthus foveolatus* (E.Mey.) Stearn subsp. *tomentellus* (I.Verd.) Stearn
Oleaceae	*Jasminum glaucum* (L.f.) Aiton
Oleaceae	*Jasminum tortuosum* Willd.
Oleaceae	*Menodora juncea* Harv.
Oleaceae	*Olea exasperata* Jacq.

Table 4.44 Set 4 candidates closely related to prioritised EthmedIMM taxa in Set 1

Family	Taxon
Family	Taxon
Apiaceae	*Annesorhiza altiscapa* Schltr.
Apiaceae	*Apium inundatum* (L.) Rchb.f.
Apiaceae	*Centella caespitosa* Adamson
Apiaceae	*Centella fusca* (Eckl. & Zeyh.) Adamson
Apiaceae	*Centella laevis* Adamson
Apiaceae	*Centella montana* (Cham. & Schltdl.) Domin
Apiaceae	*Centella ternata* M.T.R.Schub. & B.-E.van Wyk
Apiaceae	*Dasispermum suffruticosum* (P.J.Bergius) B.L.Burtt
Apiaceae	*Lichtensteinia latifolia* Eckl. & Zeyh.
Apiaceae	*Peucedanum capillaceum* Thunb. var. *capillaceum*
Apiaceae	*Peucedanum multiradiatum* Drude
Apiaceae	*Stoibrax capense* (Lam.) B.L.Burtt
Araceae	*Zantedeschia odorata* P.L.Perry
Asteraceae	*Edmondia fasciculata* (Andrews) Hilliard
Asteraceae	*Felicia stenophylla* Grau
Asteraceae	*Gazania linearis* (Thunb.) Druce var. *linearis*
Asteraceae	*Gerbera serrata* (Thunb.) Druce
Asteraceae	*Gibbaria ilicifolia* (L.) Norl.
Asteraceae	*Helichrysum litorale* Bolus
Asteraceae	*Metalasia quinqueflora* DC.
Asteraceae	*Metalasia riparia* T.M.Salter
Asteraceae	*Oedera capensis* (L.) Druce
Asteraceae	*Osteospermum pterigoideum* Klatt

Table 4.44 (continued)

Family	Taxon
Asteraceae	*Othonna macrosperma* DC.
Asteraceae	*Phaneroglossa bolusii* (Oliv.) B.Nord.
Asteraceae	*Senecio articulatus* (L.) Sch.Bip.
Asteraceae	*Syncarpha dregeana* (DC.) B.Nord.
Asteraceae	*Tripteris amplexicaulis* (Thunb.) Less.
Asteraceae	*Ursinia quinquepartita* (DC.) N.E.Br.
Fabaceae	*Aspalathus corrudifolia* P.J.Bergius
Fabaceae	*Aspalathus joubertiana* Eckl. & Zeyh.
Fabaceae	*Aspalathus polycephala* E.Mey. subsp. *rigida* (Schltr.) R.Dahlgren
Fabaceae	*Aspalathus ramosissima* R.Dahlgren
Fabaceae	*Aspalathus wurmbeana* E.Mey.
Fabaceae	*Cyclopia alopecuroides* A.L.Schutte
Fabaceae	*Liparia laevigata* (L.) Thunb.
Fabaceae	*Lotononis acuminata* Eckl. & Zeyh.
Fabaceae	*Lotononis bolusii* Dummer
Fabaceae	*Polhillia canescens* C.H.Stirt.
Fabaceae	*Psoralea tenuifolia* L.
Fabaceae	*Rafnia capensis* (L.) Schinz subsp. *ovata* (P.J.Bergius) G.J.Campbell & B.-E.van Wyk
Fabaceae	*Rafnia globosa* G.J.Campbell & B.-E.van Wyk
Fabaceae	*Virgilia divaricata* Adamson
Lamiaceae	*Plectranthus ciliatus* E.Mey. ex Benth.
Lamiaceae	*Salvia africana-caerulea* L.
Lamiaceae	*Salvia albicaulis* Benth.
Lamiaceae	*Salvia chamelaeagnea* P.J.Bergius
Lamiaceae	*Salvia lanceolata* Lam.
Lamiaceae	*Salvia repens* Burch. ex Benth. var. *repens*
Lamiaceae	*Salvia thermaruma* Van Jaarsv.
Lamiaceae	*Stachys bolusii* Skan
Lamiaceae	*Stachys scabrida* Skan
Lamiaceae	*Stachys thunbergii* Benth.
Lamiaceae	*Stachys zeyheri* Skan
Oleaceae	*Chionanthus foveolatus* (E.Mey.) Stearn subsp. *tomentellus* (I.Verd.) Stearn
Oleaceae	*Jasminum glaucum* (L.f.) Aiton
Oleaceae	*Jasminum tortuosum* Willd.
Oleaceae	*Menodora juncea* Harv.

4.3.4 Allies of efficacious exotic taxa (Set 7)

The literature search for exotic taxa potentially efficacious in the treatment of the relative disease categories (Set 6) resulted in the identification of 67 anti-tuberculosis (Table 4.45), 9 anti-diabetes (Table 4.46) and 13 immune modulatory (Table 4.47) allied indigenous taxa respectively (Set 7).

Table 4.45 Exotic EthmedTB taxa and closely related indigenous allies

Exotic taxon (Set 6)	Literature source	Family	Indigenous taxon (Set 7)
Adhatoda vasica	(Newton *et al.*, 2000)	Acanthaceae	*Adhatoda andromeda* (Lindau) C.B.Clarke
		Acanthaceae	*Adhatoda densiflora* (Hochst.) J.C.Manning
Allium sativum	(Newton *et al.*, 2000)	Alliaceae	*Allium dregeanum* Kunth
Centella asiatica	(Newton *et al.*, 2000)	Apiaceae	*Centella annua* M.T.R.Schubert & B.-E.van Wyk
		Apiaceae	*Centella eriantha* (Rich.) Drude var. *orientalis* Adamson
Tabernaemontana citrifolia	(Newton *et al.*, 2000)	Apocynaceae	*Tabernaemontana elegans* Stapf
		Apocynaceae	*Tabernaemontana ventricosa* Hochst. ex A.DC.
Aloe chinensis	(Newton *et al.*, 2000)	Asphodelaceae	*Aloe arenicola* Reynolds
		Asphodelaceae	*Aloe comosa* Marloth & A.Berger
		Asphodelaceae	*Aloe framesii* L.Bolus
		Asphodelaceae	*Aloe striata* Haw. subsp. *striata*
		Asphodelaceae	*Aloe succotrina* Lam.
Santolina chamaecyparissus	(Newton *et al.*, 2000)	Asteraceae	*Athanasia crenata* (L.) L.
		Asteraceae	*Athanasia dentata* (L.) L.
		Asteraceae	*Athanasia trifurcata* (L.) L.
Arnica montana	(Newton *et al.*, 2000)	Asteraceae	*Gerbera cordata* (Thunb.) Less.
		Asteraceae	*Gerbera crocea* (L.) Kuntze
		Asteraceae	*Gerbera linnaei* Cass.
		Asteraceae	*Gerbera piloselloides* (L.) Cass.
Inula helenium	(Cantrell *et al.*, 2001)	Asteraceae	*Inula glomerata* Oliv. & Hiern
		Asteraceae	*Inula paniculata* (Klatt) Burtt Davy
Terminalia spinosa	(Newton *et al.*, 2000)	Combretaceae	*Terminalia brachystemma* Welw. ex Hiern subsp. *brachystemma*
		Combretaceae	*Terminalia randii* Baker f.
		Combretaceae	*Terminalia stenostachya* Engl. & Diels
Momordica charantia	(Newton *et al.*, 2000)	Cucurbitaceae	*Momordica balsamina* L.
		Cucurbitaceae	*Momordica cardiospermoides* Klotzsch
		Cucurbitaceae	*Momordica kirkii* (Hook.f.) C.Jeffrey
Entada abyssinica	(Newton *et al.*, 2000)	Fabaceae	*Entada arenaria* Schinz subsp. *arenaria*
		Fabaceae	*Entada rheedii* Spreng.
Erythrina gibbosa	(Newton *et al.*, 2000)	Fabaceae	*Erythrina acanthocarpa* E.Mey.
		Fabaceae	*Erythrina mendesii* Torre
Ocimum sanctum	(Newton *et al.*, 2000)	Lamiaceae	*Ocimum gratissimum* L. subsp. *gratissimum* var. *gratissimum*
		Lamiaceae	*Ocimum natalense* Ayob. ex A.J.Paton
Salvia hypargeia	(Newton *et al.*, 2000)	Lamiaceae	*Salvia africana-caerulea* L.
		Lamiaceae	*Salvia repens* Burch. ex Benth. var. *keiensis* Hedge
		Lamiaceae	*Salvia scabra* L.f.
Tetradenia riparia	(Newton *et al.*, 2000)	Lamiaceae	*Tetradenia brevispicata* (N.E.Br.) Codd
		Lamiaceae	*Tetradenia kaokoensis* Van Jaarsv. & A.E. van Wyk
		Lamiaceae	*Tetradenia riparia* (Hochst.) Codd
Teucrium chamaedrys	(Newton *et al.*, 2000)	Lamiaceae	*Teucrium africanum* Thunb.
		Lamiaceae	*Teucrium kraussii* Codd

Table 4.45 (continued)

Exotic taxon (Set 6)	Literature source	Family	Indigenous taxon (Set 7)
		Lamiaceae	*Teucrium trifidum* Retz.
Myrica aspleniflora	(Newton *et al.*, 2000)	Myricaceae	*Morella brevifolia* (E.Mey. ex C.DC.) Killick
		Myricaceae	*Morella diversifolia* (Adamson) Killick
		Myricaceae	*Morella integra* (A.Chev.) Killick
Ximenia caffra	(Newton *et al.*, 2000)	Olacaceae	*Ximenia americana* L. var. *americana*
		Olacaceae	*Ximenia americana* L. var. *microphylla* Welw. ex Oliv.
Piper cubeba	(Newton *et al.*, 2000)	Piperaceae	*Piper capense* L.f. var. *capense*
Clematis integrifolia	(Newton *et al.*, 2000)	Ranunculaceae	*Clematis brachiata* Thunb.
		Ranunculaceae	*Clematis villosa* DC. subsp. *villosa*
Rhamnus cathartica	(Newton *et al.*, 2000)	Rhamnaceae	*Rhamnus prinoides* L'Hér.
Acaena pinnatifida	(Cantrell *et al.*, 2001)	Rosaceae	*Acaena latebrosa* Aiton
Geum macrophyllum Willd. var. *macrophyllum*	(Newton *et al.*, 2000)	Rosaceae	*Geum capense* Thunb.
Prunus mume	(Newton *et al.*, 2000)	Rosaceae	*Prunus africana* (Hook.f.) Kalkman
Sanguisorba officinalis	(Newton *et al.*, 2000)	Rosaceae	*Sanguisorba minor* Scop. subsp. *muricata* Briq.
Pentas longiflora	(Newton *et al.*, 2000)	Rubiaceae	*Pentas angustifolia* (A.Rich. ex DC.) Verdc.
		Rubiaceae	*Pentas micrantha* Baker subsp. *wyliei* (N.E.Br.) Verdc.
Salix caprea	(Newton *et al.*, 2000)	Salicaceae	*Salix mucronata* subsp. *woodii* (Seemen) Immelman
		Salicaceae	*Salix mucronata* Thunb. subsp. *capensis* (Thunb.) Immelman
Antirrhinum majus	(Newton *et al.*, 2000)	Scrophulariaceae	*Nemesia fruticans* (Thunb.) Benth.
		Scrophulariaceae	*Nemesia macrocarpa* (Aiton) Druce
		Scrophulariaceae	*Nemesia pinnata* (L.f.) E.Mey. ex Benth.
Solanum sodomaeum	(Newton *et al.*, 2000)	Solanaceae	*Solanum aculeastrum* Dunal subsp. *aculeastrum*
		Solanaceae	*Solanum burchellii* Dunal
		Solanaceae	*Solanum guineense* L.

Table 4.46 Exotic EthmedDBM taxa and closely related indigenous allies

Exotic taxon (Set 6)	Reference	Family	Indigenous Taxon (Set 7)
Dioscorea opposita	(Gori and Campbell, 1998)	Dioscoreaceae	*Dioscorea cotinifolia* Kunth
		Dioscoreaceae	*Dioscorea dregeana* (Kunth) T.Durand & Schinz
		Dioscoreaceae	*Dioscorea hirtiflora* Benth.
		Dioscoreaceae	*Dioscorea rupicola* Kunth
Galega officinalis	(Oubré *et al.*, 1997)	Fabaceae	*Tephrosia capensis* (Jacq.) Pers. var. *capensis*
		Fabaceae	*Tephrosia grandiflora* (Aiton) Pers.
		Fabaceae	*Tephrosia lupinifolia* DC.

Table 4.47 Exotic immune modulatory taxa and closely related indigenous allies

Exotic taxon (Set 6)	Reference	Family	Indigenous taxon (Set 7)
Adhatoda vasica	(Labadie *et al.*, 1989)	Acanthaceae	*Adhatoda andromeda* (Lindau) C.B.Clarke
		Acanthaceae	*Adhatoda densiflora* (Hochst.) J.C.Manning
Bulpeurum falcatum	(Wong *et al.*, 1994)	Apiaceae	*Bupleurum mundii* Cham. & Schltdl.
		Apiaceae	*Centella asiatica* (L.) Urb.
Centella asiatica	(Labadie *et al.*, 1989)	Apiaceae	*Centella glabrata* L. var. *bracteata* Adamson
		Apiaceae	*Centella stenophylla* Adamson
Asparagus falcata	(Labadie *et al.*, 1989)	Asparagaceae	*Asparagus falcatus* L.
		Asparagaceae	*Asparagus kraussianus* (Kunth) J.F.Macbr.
		Asparagaceae	*Asparagus racemosus* Willd.
Astragalus membranaecus	(Wong *et al.*, 1994)	Asparagaceae	*Astragalus atropilosulus* (Hochst.) Bunge subsp. *burkeanus* (Harv.) J.B.Gillett var. burkeanus
Piper longum	(Labadie *et al.*, 1989)	Piperaceae	*Piper capense* L.f. var. *capense*

4.4 Discussion

Procedures for prioritising plants as is required for bioprospecting are heavily reliant on available data and therefore unsuitable for use in regions with no detailed plant species lists. Such regions will also be unlikely to have checklists with recent synonyms, let alone data on endemism and plant distribution (Golding, 2002). Apart from the budgetary and time constraints involved in obtaining good data, the ability to manipulate data to obtain meaningful insights, i.e. data mining, is essential. These techniques usually require special skills and software (Westphal and Blaxton, 1998; Krallinger *et al.*, 2005). Where it is desirable to analyse phytochemical data for structure-related activities, databases and texts need to be reviewed, and data may require modernization for compatibility purposes. Data sourced for the analyses in this chapter were, with the exception of that captured from ethnobotanical texts, straightforward due to the many comprehensive SANBI electronic databases.

The flexibility of the weighting system used for Set 1 taxa (Table 4.1; Table 4.2) is advantageous as it can be altered according to the perceived importance of the various criteria. The weighting of keywords (Table 4.3; Table 4.4; Table 4.5) facilitated the segregation/partitioning of data important for generating a score hierarchy. The number of taxa short-listed for each disease category (Table 4.36; Table 4.37; Table 4.37) was very low relative to the total number of taxa available in the region. This is considered desirable due to the very low number of taxa that can realistically be screened using current budgets and technology.

That the minority of EthMedDBM taxa were indigenous was unexpected due to the regionally focused literature sources accessed. However, this was not considered to detract from to the study because Set 1 taxa formed the basis for identification of other indigenous allies (Set 3) and Western Cape endemics (Set 5)(Figure 4.2). As such, sufficient indigenous and endemic taxa were included in the final lists for collection. Had the study been limited to indigenous taxa, a much smaller number would have been short-listed resulting in potentially far fewer candidates for screening purposes. The small percentage (<10%) of endemic taxa in each category (Table 4.7) was surprising, as endemic and near-endemic taxa in the *FSA* region reportedly constitute about 80% of all taxa (Cowling and Hilton-Taylor, 1997). This is perhaps due to the majority of *FSA* ethnomedicinal plants being distributed along the eastern seaboard (Figure 2.10), while the main centre of endemism is the Cape Floral Kingdom (Cowling and Hilton-Taylor, 1997). The Cape Floral Kingdom has a relatively small percentage of ethnomedicinal taxa (Figure 2.4) which is further discussed in Chapter 2. The preferential use of endemic taxa for drug development is a politically motivated prioritisation due to the challenge of patenting exogenous biological material (Masood, 1998a).

The high percentage of explicit-use records (Table 4.9) compared with the very low percentage of positive or negative associations (Table 4.10) indicates the explicit manner in which ethnomedicinal plants are used in disease treatment. The relatively high percentage of toxic plants was expected due to the documented toxicity of many medicinal plants (Watt and Breyer-Brandwijk, 1962; Bruneton, 1999; Arnold *et al.*, 2002).

The low percentage of Red Data Listed candidates in each disease category is perhaps reassuring (Table 4.12) and certainly expected in many instances, as rare plants are unlikely to be widely accessible for ethnomedicinal use. The necessity for weighting these taxa is due to: i) the potential extinction these species face prior to adequate assessment, ii) the likelihood of high utilisation – to the point of over-exploitation – by ethnomedicinal practitioners which could indicate high efficacy. *Warburgia salutaris* (Bertol.f.) Chiov. and *Siphonochilus aethiopicus* (Schweinf.) B.L.Burtt are respectively classified as Endangered and Extinct in the KwaZulu-Natal region (Scott-Shaw, 1999). Both taxa are known for their medicinal properties (Hutchings *et al.*, 1996; Van Wyk *et al.*, 1997) and are extensively harvested for this purpose (Cunningham, 1988).

The small percentage of taxa recorded as traded (Table 4.13)(Cunningham, 1988; Mander, 1997; Mander, 1998; Marshall, 1998; Botha *et al.*, 2001; Dold and Cocks, 2002; Williams, 2003) for each disease category has several possible explanations. Firstly, trade reports do not generally aim to provide comprehensive lists of all medicinally used taxa in a region. Instead they highlight certain aspects of trade such as the volumes of material that changes hands. Secondly, plant availability may vary from one season/year to another due to seasonal and/or climate variation, resulting in the likely exclusion of many taxa from trade-reports. Thirdly, evidence exists that ethnomedicinal plant use

continues to evolve within the dynamics of traditional healing cultures (Crouch and Hutchings, 1999; Grace and Crouch, 2003).

Many families identified as having three or more efficacious compound classes (Table 4.17) were also identified as positive outlying families in the regression analyses. The Euphorbiaceae, Lamiaceae, Verbenaceae and Asteraceae were identified as containing three or more compound classes with potential efficacy against tuberculosis (Table 4.36). Of these, the Euphorbiaceae, Lamiaceae, and Asteraceae were also positive outliers in the anti-tuberculosis regression analysis (Table 4.21), while the Verbenaceae showed a high positive residual value close to the cut off point. The Fabaceae contain three or more compound classes with potential against diabetes (Table 4.37), and although this family was not an outlier in the anti-diabetes regression analyses (Table 4.26) it had a positive residual value close to the cut-off point. The Lamiaceae and Asteraceae contain three or more compound classes with potential efficacy in immune modulation (Table 4.38). Both were also positive outliers in the immune modulation regression analyses (Table 4.31).

The overlap of certain positive outlying plant orders in the various disease categories was notable. The Malpighiales were identified in all three categories (Table 4.22; Table 4.27; Table 4.32), the Lamiales in both anti-tuberculosis (Table 4.22) and immune modulatory categories (Table 4.32), the Sapindales in both anti-tuberculosis (Table 4.22) and anti-diabetes categories (Table 4.27), and the Gentianales in both anti-diabetes (Table 4.27) and immune modulatory categories (Table 4.32). This overlap, and the clear focus on these few orders (out of a total 55 orders sampled from the *FSA* region) suggests that taxa in these select orders contain compounds of notable biological activity, or, that they are favoured for other reasons. Many of these orders were also

identified as positive outliers in previous chapters. Anti-malarial orders (Chapter 3) include the Sapindales, Fabales, Malpighiales, Lamiales, and Asterales. Highly selected ethnomedicinal orders (Chapter 2) include the Malpighiales, Fabales, Gentianales, Asterales, Solanales, Malvales, and Sapindales.

Inclusion of plants from the western seaboard of southern Africa, i.e. in the Cape and succulent Karoo 'hot-spot' regions (Figure 2.11) was particularly desirable due to the high plant diversity and endemicity in this region and its isolation from the majority of ethnomedicinal knowledge systems in southern Africa. While the focus on the Western Cape was considered essential, regional data segregation can lead to further anomalies in the data because phylogenetic lines often traverse such boundaries (Carbutt and Edwards, 2001). Figure 2.12 illustrates the significant absence of indigenous cultures from the Cape and succulent Karoo hot spots.

4.5 Conclusion

Prioritised plant selection provides a logical and simple means to target taxa for bioprospecting. Bioassays are required for verification of the positive contribution that the various plant selection criteria may have played. Ultimately, success may be measured by the efficacies of new drugs developed for the relative disease states. The inclusion of control taxa will boost the statistical rigour of analyses that allow for improvements and/or alterations to the selection procedures to be subsequently made. The application of phylogenetic comparative methods (Felsenstein, 1985; Harvey and Pagel, 1991) would complement the selection process, but is hamstrung by the lack of baseline systematic studies which are the keystone for the methodology. The techniques

presented in this chapter should not be considered an end, but rather a means to improve drug development investigations for the reduction of human suffering. The value of the southern African flora should be highlighted as well as the need to better conserve this resource.

Chapter 5

Discussion

You would be surprised at the number of years it took me to see clearly what some of the problems were which had to be solved... Looking back, I think it was more difficult to see what the problems were than to solve them.

– Charles Darwin (1859)

The advantage of incorporating ethnomedicinal knowledge into the search for novel drug compounds is widely acknowledged (Balick, 1990; Cox, 1990; Moerman, 1991; Taniguchi, 1993; Du Toit, 1998). The result is typically a reduction in research overheads if the leads prove viable (Balick, 1990). However, this approach has limitations, particularly in South Africa where ethnomedicinal plant use is not equal in all regions. Notably, the Western Cape contains one of the lowest proportions of ethnomedicinally used taxa in the *FSA* (Figure 2.4). This region, known as the Cape Floristic Kingdom (CFK)(Cowling and Richardson, 1995) or the Cape Floristic Region (CFR) (White, 1983; Hilliard and Burtt, 1987; Van Wyk and Smith, 2001) is one of the six most significant concentrations of plant diversity in the world. Bioprospecting the flora of this region by means of the ethnomedicinal approach will not likely prove optimal. In addition, many taxa that are not recorded to have been used ethnomedicinally may well be suited to drug development.

The success of the regression analyses based on ethnomedicinal knowledge does, however, merit use in other regions. Regions with high proportions of ethnomedicinal

taxa, e.g. Mpumalanga and KwaZulu-Natal (Figure 2.4) are more likely to yield good results. Importantly, the grouping of two regions which contain largely different flora (e.g. the Western Cape and KwaZulu-Natal), with only one of those containing high proportions of recorded ethnomedicinal taxa, will likely produce skewed results. This was shown in Chapter 2 where several families endemic to the Western Cape were completely excluded from the regression analyses. Regional data delimitations are therefore recommended and these can be enhanced by considering general vegetation characteristics and the distribution of people whose knowledge has been recorded. The 68 vegetation types described for southern Africa (Acocks, 1988) in conjunction with major biome information: Forest, Fynbos, Grassland, Nama Karoo, Savanna, Succulent Karoo and Thicket (Rutherford, 1997) may prove useful delimitations. Although plant orders in these regions are variously diverse, the regression analysis techniques do assess the relative popularity of each order. Ultimately, regression analyses are restricted by several base assumptions that are required when working with natural systems, and the likelihood is that many of these will never be met.

Confining regression analyses to particular diseases narrows the field of inquiry and improves resolution. In selecting plants for the NDDP (Chapter 4), only a small percentage of the keywords originally listed were actually matched in the literature. This indicates that a narrow range of keywords can be sufficient as long as they are relevant. Most keywords used in that study would be suitable for similar literature searches in texts from other regions, such as East or Central Africa.

In areas of relatively low documented or actual ethnomedicinal plant use, such as the western seaboard of southern Africa, other methods of plant selection may yield better results. Families and/or genera in these regions may prove comparable (in

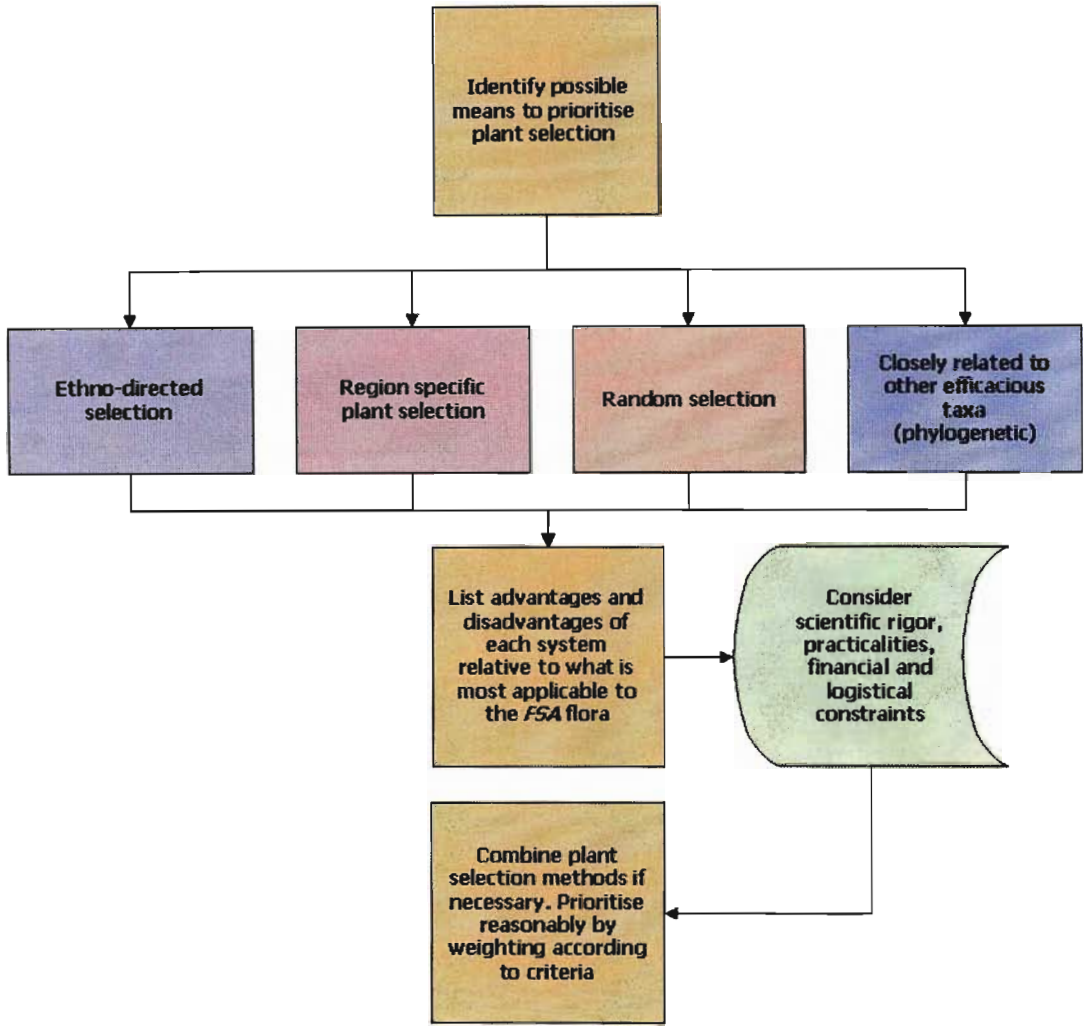

Figure 5.1 A rational decision-making process to optimise bioprospecting the *FSA* flora or regions therein

terms of efficacy) to those in regions of high ethnomedicinal use. In addition, some areas of high endemism, e.g. the Pondoland and the Drakensberg Alpine Centres (Van Wyk and Smith, 2001) may have been excluded from use by ethnomedicinal practitioners due to, for example, inaccessibility. Such rugged environments harbour particularly rich concentrations of certain plant life forms such as cremnophytes, which could otherwise be overlooked. Importantly, the contact between the plant species and traditional healers in these instances is infrequent so plant material is unavailable for regular use and this affects the accumulation of associated knowledge. Desert plants on the western seaboard are also characterised by frequent mortality and their recruitment patterns are driven by moisture availability (Jürgens and Gotzmann, 1999). As these taxa spend a high percentage of their time in the seed bank (Van Wyk and Smith, 2001) and so are unavailable for traditional use, means to ensure their inclusion in bioprospecting should be considered. The low historic human population densities supported by those ecosystems (Thompson, 2001) means that: i) diseases of excess e.g. diabetes (Goodwin *et al.*, 2003) were less prevalent in such communities, ii) the spread of diseases is truncated and iii) longevity of pathogens outside human hosts is severely impaired (Cilimburg *et al.*, 2000). Thus if a disease is not prevalent in an area then there is little motivation or opportunity to seek an herbal cure. The same reason would have contributed to the exclusion of such taxa from checklists compiled by ethnographers and/or ethnobotanists. A further confounding issue is the previous contact the Bantu would have had with plant taxa in areas north of the *FSA*, prior to their southerly migrations. This previous experience would likely have significantly influenced their choice of local taxa, particularly due to their relatively recent colonisation of southern Africa (Thompson, 2001).

The choice of criteria for weighting ethnomedicinal taxa also has implications for bioprospecting outcomes, e.g. where weighting is applied to taxa that are Red Data listed. Many Red Data taxa are 'data deficient', and a robust data set is not guaranteed. The misidentification of plants traded in traditional ethnomedicinal markets may also prove limiting. Traded plants are often severely desiccated and lack reproductive parts required for conclusive identification. Furthermore, regression analyses which highlight potentially 'hot' plant families/orders would be greatly strengthened by more detailed phylogenetic data, as would the identification of taxa on the basis of chemical profiles.

Several issues currently limit bioprospecting opportunities in South Africa, including the legislative environment, biopiracy and mechanisms for equitable benefit sharing. Ethnomedicinal knowledge can be considered the intellectual property of the people from which it was sourced (Gollin, 2002). However, not until the drafting of the CBD (Article 8(j)) has such intellectual property been formally recognised (CBD, 1992). While such recognition is considered a step towards ensuring that traditional peoples partake in commercial benefits from their knowledge, an accepted means of implementing intellectual property recognition is yet to be formulated. Certain provisions made in the World Trade Organisation (WTO) Agreement on Trade Related Aspects of Intellectual Property Rights (TRIPS) in 1995 (Masood, 1998b; Sampath, 2003) were considered to be in conflict with certain ideas proposed by the CBD. The CBD was seen to enshrine equity and accessibility and in particular, acknowledged the collective rights of indigenous and local communities to exchange and develop biodiversity. In contrast, TRIPS strongly favoured private ownership of intellectual property rights and profit-based systems (WTO, 1995; Masood, 1998b). The absence of legislation to protect private ownership of intellectual property rights in developing countries was reported to be costing industrialised countries some US $200 billion in lost royalties per annum (GAIA/GRAIN,

1998). TRIPS attempted to narrow the gaps in the way these rights were globally protected, and to incorporate them into common international rules. The disparity led to much debate, particularly due to WTO members being faced with possible trade sanctions if they chose not to sign the TRIPS agreement. However, the TRIPS agreement did acknowledge the right of countries to decide on the details of their own patent systems (Masood, 1998b) and were thus advised to exclude all life forms and related knowledge from patentability, as was permitted under the WTO (Jha and Vossenaar, 1999).

The issue is pertinent in South Africa where legislation governing bioprospecting was only recently developed (Wynberg and Swiderska, 2001)(Figure 5.2). In May 1997, a White Paper on the Conservation and Sustainable Use of South Africa's Biological Diversity (the White Paper) was gazetted (DEAT, 1997) and following minor modifications by Cabinet was adopted by Parliament (Wynberg and Swiderska, 2001). The policy outlined in detail the necessity for establishing legislation and institutional structures to control access to South Africa's indigenous genetic resources (DEAT, 1997). In addition, the proposed legislation was to ensure that benefits arising from South African resources served the nation. It was in the country's interest to ensure that access to biodiversity was not unnecessarily restrictive and it was recommended that conditions should stimulate economic activity (DEAT, 1997). However, with the promulgation of biodiversity legislation in Act 10 of 2004, this is rendered largely impracticable.

South Africa's Biodiversity Act (Act 10 of 2004) was signed into law on 2 June 2004 and legislates for, *inter alia,* i) the protection of different bio-regions, e.g. the Cape Floristic Kingdom, ii) the establishment of means to protect and regulate the use of South Africa's rare and endangered species, iii) the regulation of Genetically Modified Organisms

(GMO's), iv) benefit sharing by communities where their indigenous biodiversity knowledge and/or resources have been used by third parties, and v) the establishment of sound permitting regulations (DEAT, 2004b). The Act was proclaimed effective as of 1 September 2004, excluding Chapter 7 (permitting systems) which would take effect on 1 April 2005, and Section 105 and Chapter 6 (bioprospecting; benefit sharing; export of biological resources) which would take effect on 1 January 2006 (DEAT, 2004a)(Figure 5.2). The delays were implemented to allow appropriate regulation development by the DEAT.

While Act 10 provides much-needed legislation for bioprospecting activities, several aspects of these activities performed by research institutions and/or commercial organisations appear to be poorly understood. This has resulted in the development of inappropriate and/or unnecessarily restrictive legislation (Figure 5.3). Although this legislation is unlikely to be modified in the foreseeable future, the regulations currently being developed may reflect a deeper insight into the practicalities of bioprospecting based on very recent stakeholder discussions.

Permit issuing authorities will, once the regulations are in place, be required to issue permits only after: i) ensuring that the interests of stakeholders (including indigenous communities) are protected (through benefit sharing and material transfer agreements), ii) that prior informed consent has been obtained, and iii) all information relating to the proposed bioprospecting has been submitted to the stakeholders (Figure 5.3). The Act does not indicate what measures should be taken if no traditional knowledge is involved. In bioprospecting the flora of southern Africa, the NDDP developed a short-list of taxa (Chapter 4), all of which would be included in the collection permit applications.

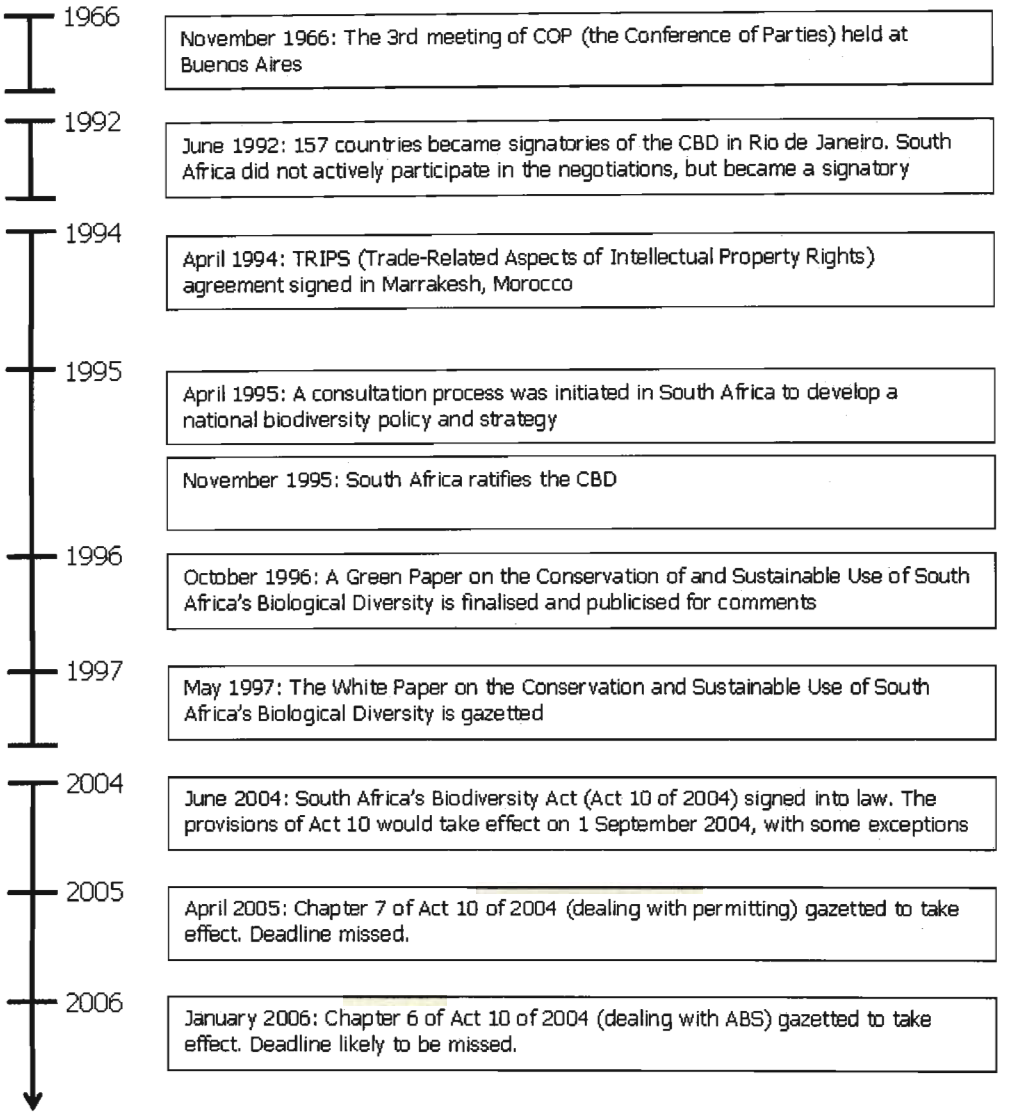

Figure 5.2 The development of policy, legislation and regulations for bioprospecting in South Africa

However, it is unlikely that all such short-listed taxa would be collected due to logistical constraints in locating them. It is also unlikely that all extracts from collected plants will be screened beyond initial pharmacological assays *in vitro*. The question is therefore whether or not it is practical and feasible to identify and communicate with stakeholders and draft benefit sharing agreements for each and every taxon at such early stages in the bioprospecting process (Figure 1.1) as prescribed by Act 10 (Figure 5.3). It would be less restrictive to allow researchers to complete the initial scoping or 'prospecting' studies, prior to engaging in detailed benefit sharing agreements (Figure 5.4). The forthcoming regulations should distinguish between biomining and bioprospecting. Early stages of research (as is presented in this dissertation) are considered the 'prospecting' stage. 'Mining' of biodiversity begins only once suitable candidate taxa have been identified as marketable, commercial subjects. This distinction should provide permit issuing authorities with a better means to assess the activities and impacts of researchers.

Permit issuing authorities can optionally: i) engage with the applicant and/or stakeholders on issues relating to the terms and conditions of the benefit sharing and material transfer agreements, and ii) make recommendations to the Minister. While this is in line with the goals of the CBD the premature identification of stakeholders and the drafting of such agreements (i.e. prior to the 'mining' phase) is severely restrictive and is unlikely to be economical.

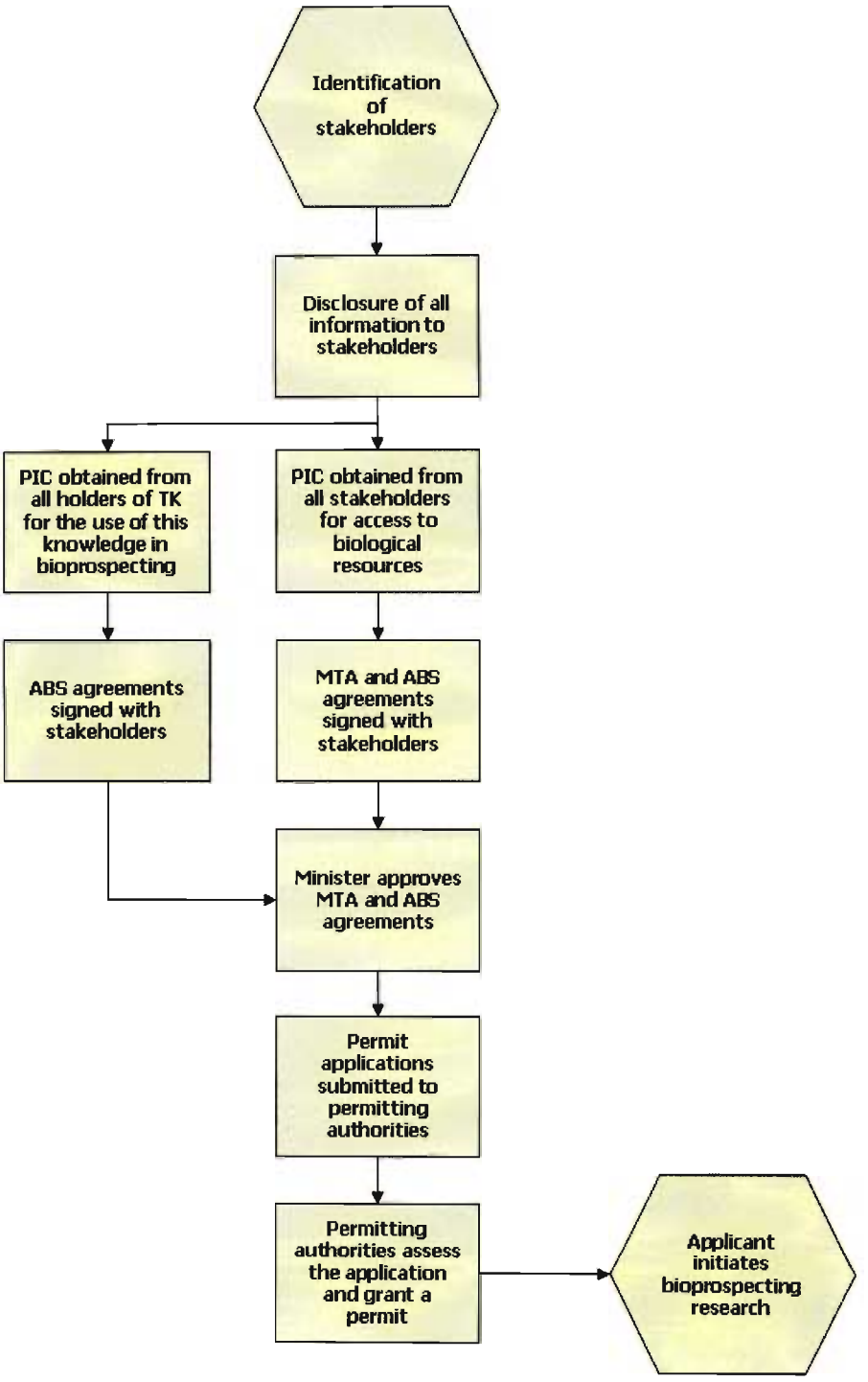

Figure 5.3 Simplified model of bioprospecting procedure as currently prescribed by Act 10 of 2004

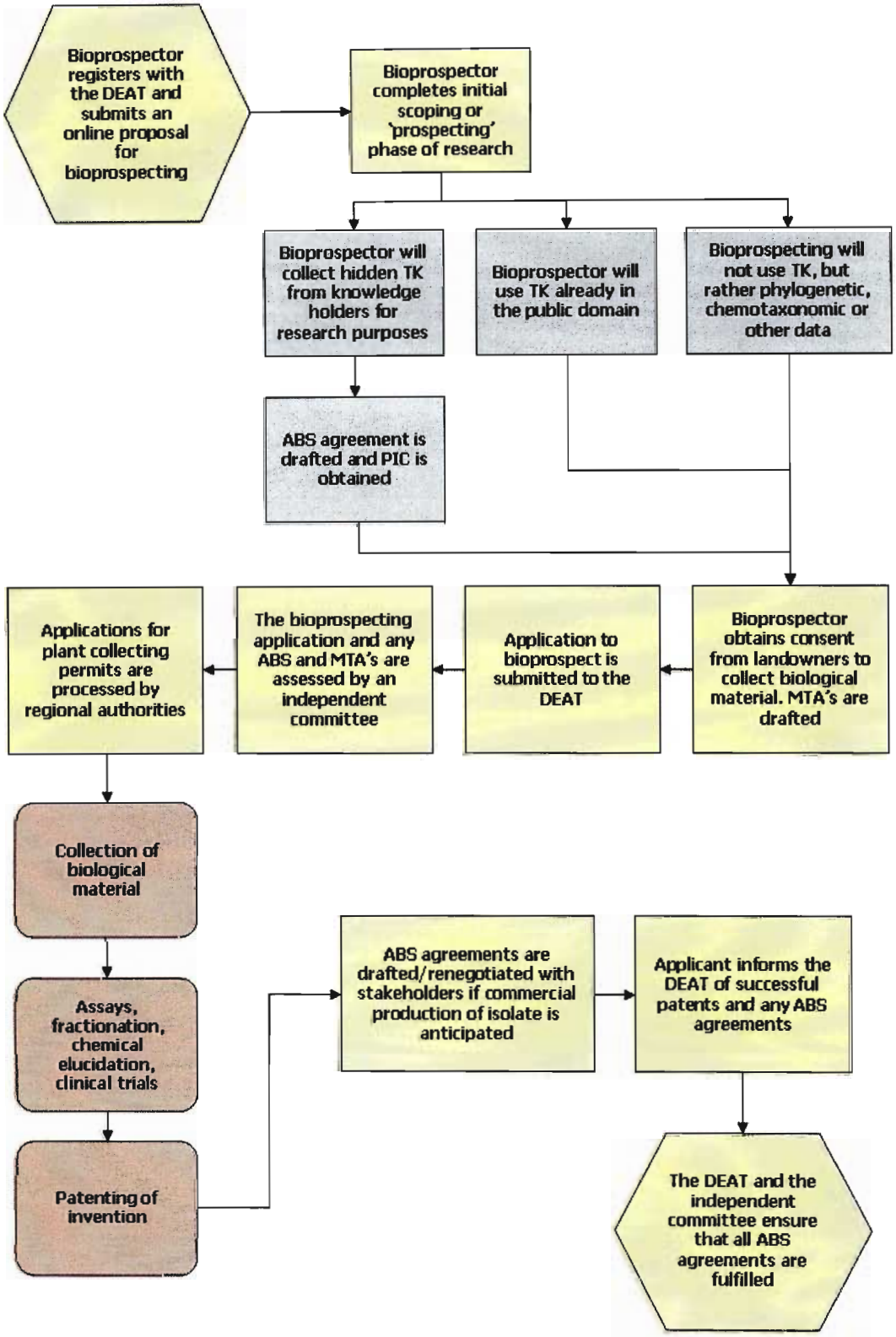

Figure 5.4 Simplified model of a practicable approach to bioprospecting in South Africa

The Act legislates for the establishment of a trust fund into which all money from benefit sharing and material transfer agreements will be deposited. The Director-General will manage and be accountable for the monies therein, and oversee the payment of shares to stakeholders. Benefit-sharing agreements are legislated (regulations yet to be formulated) to specify, *inter alia*, i) the nature and quantity of biological resources as well as the area from which they are to be collected, ii) the known traditional uses and other potential uses, iii) the names of stakeholders, iv) the manner in which resources are to be used, and v) the extent and manner in which stakeholders will benefit. One of the key difficulties is the naming of stakeholders. For example, data for NDDP plant candidates was obtained from published literature and many of the short-listed plants were recorded as being traditionally used by the Zulu. However, the legislation is unclear how the Zulu are to be included as stakeholders, which names should be included in the benefit sharing agreement, and from whom prior informed consent should be obtained. Possible individuals/groups include: i) traditional healers, ii) communities where plants are to be collected, iii) tribal authorities, iv) provincial authorities, or v) from all communities where the plant is known to occur and/or known to be used. Where a plant has been used traditionally by several ethnic groups, the likelihood of several claimants (for benefit-sharing) arising is also likely, e.g. *Pterocarpus angolensis* DC. is reportedly used by the Zulu, the Shangaan and the Sotho people to treat dysentery (Watt and Breyer-Brandwijk, 1962). Problems may also arise due to claimants being located in different countries, e.g. *Hoodia* sp. are used as appetite suppressants by the San who are located in several countries in southern Africa (Germishuizen and Meyer, 2003; Wynberg, 2004b). Regulations should take into account that claims for intellectual property rights may be made from communities located across national or international borders. Some of these communities may give consent while others may not, and others may remain completely uninformed. In this regard, legislation should preferably be

compatible with that in adjacent countries to allow for cross-border benefit sharing. The identification of additional stakeholders during the research period (which could extend for several years) is also a possibility, e.g. experts who through their knowledge of botany/phytochemistry/drug development contribute to research and/or development of drug products. New information may also come to light regarding the previous traditional use of indigenous plants. These are issues which the regulations must deal with if they are to facilitate access to genetic resources and maximize benefits to potential stakeholders and the country as a whole. The regulations should also clarify when exactly bioprospecting is regarded as having commenced, in order that benefit sharing issues are correctly dealt with. It would be advantageous if various categories of benefits are identified as these could be implemented at various stages of the bioprospecting process. For example, commitments to potential stakeholders at the time of the permit applications could include: i) bursaries for students, ii) input into the conservation of community environments, iii) contributions to nature reserves and/or protected areas, iv) training opportunities for local people, e.g. field work/laboratory work, (v) business development opportunities, e.g. agroprocessing of crude drugs developed. Royalties are only tangible at a later stage of the drug development process.

The absence of formalised means of sharing economic benefits derived from the commercial exploitation of biodiversity with land-owners and/or custodians of traditional knowledge, has led to a number of accusations that businesses are committing biopiracy (Fenwick, 1998; Masood, 1998a; Van Wijk, 2000). However, even with the many claims of biopiracy, there is little evidence of economic loss to countries due to misappropriation by pharmaceutical or other research organisations (Hirsch, 2005). It has also become apparent that traditional peoples do not always seek financial rewards (Hardison, 2000; Ready, 2002)(although such a demand may in many instances be considered

reasonable) but may rather seek to be kept informed regarding the use/exploitation of items considered to be of cultural significance (be it knowledge, plants or other). This is especially the case where cultural knowledge leads to the development of products that are patented by drug development agencies without due recognition of the source.

Estimates of as little as one in 250000 plant samples directly yielding commercial drugs have been reported (Macilwain, 1998) and the average minimum weight of plant material required for preliminary bioassays is about one kilogram per sample. Collection, transport and storage costs are estimated at US $500 per sample which makes bioprospecting cost-prohibitive (Macilwain, 1998). In addition, the low hit rates and long time frames for drug development (approx. 8 to 15 years) have made alternative avenues of drug development (e.g. combinatorial chemistry) more attractive. The requirement in Act 10 for bioprospectors to include detailed benefit-sharing agreements in their permit applications may further discourage research and development organisations due to the additional time and financing required. Hirsch (2005) suggests that most cases of biopiracy have in fact been a product of clumsy permit systems that are too costly, time-consuming or simply impossible to work with. Ironically, the ideals contained in the CBD have been promoted as a means to empower the developing world's use of its biodiversity. If South Africa hopes to exploit its wealth of bioresources through bioprospecting, it requires regulations that do not add enormously to costs. They need to be efficiently implemented to encourage potential investors. A national board of trustees (Figure 5.4) dedicated to reviewing both bioprospecting applications and claims relating to intellectual property may be critical in this process. Clear and concise regulations should be implemented which delineate the procedures that businesses need to follow in order to comply with the law (Figure 5.2). Such regulations would necessarily include the preferred means of dealing with communities – and the

use of their intellectual property and/or genetic resources. It would be particularly important to ensure that conservation organisations are included in benefit sharing agreements, to allow improved biodiversity resource monitoring and management as prescribed by the CBD (CBD, 1992). The proposed national trust could be responsible for determining how best to distribute funds received from financially successful bioprospecting programmes. The trustees would necessarily decide how to minimise negative social and economic impacts and conflicts, particularly where beneficiaries occur across geographical and/or political boundaries, and where the sudden influx of large sums of money may be of detriment to existing social structures (Guendling *et al.*, 2003).

Chapter 6

Conclusion

Put forward nothing that cannot be proved simply and conclusively. Venerate the critical spirit... Without it all else is nothing. It always has the last word.

– Louis Pasteur (1888)

Bioprospecting has the potential for considerable development in the near future and advances in large-scale extract screening (Hunter, 2001) and drug template development (Dickson and Gagnon, 2004) will contribute to this end. Rapid shifts in our interpretation of plant phylogenies are being driven by molecular approaches (Davies *et al.*, 2004) and the integration of chemotaxonomy (Grayer *et al.*, 1999) will greatly enhance the predictive capacity of classifications. This will be coupled with a better understanding of the pathways by which secondary metabolites are formed and the DNA dynamics which govern such pathways (Lambert *et al.*, 2005; Yun *et al.*, 2005). Advanced biotechnology and genetic engineering will facilitate faster and cheaper biosynthesis of desired compounds. Improved understanding of pathogen genetic configurations (Ouellette, 2001) will continue to facilitate the treatment of the diseases they cause, even where such pathogens have the propensity to mutate. In addition, the growing collaborations among research institutions (e.g. the NDDP consortium) and the fast, easy access to published results will possibly fuel drug discovery advances in an exponential way (Soejarto *et al.*, 2002a). Digital data mining (Westphal and Blaxton, 1998), data manipulation and plant prioritisation techniques are increasingly necessary in order to accommodate the burgeoning volume of scientific information within the

synthetic field of bioprospecting. This dissertation forms a prototype that could easily be scripted into user-friendly data mining software with options to select diseases and geographical areas of interest allowing efficient automated scans of selected texts for the prioritisation of candidate taxa.

Optimising plant selections in the *FSA* region has provided several insights into the challenges and opportunities of bioprospecting the southern African flora. This region, with its unique and rich flora, could yield many new drug leads and could accommodate various research activities. This is desirable in South Africa which is seeking to exploit its bio-resources in a sustainable manner (DEAT, 2004b). The necessity for sound natural resource conservation is therefore highlighted. However, restrictive legislation and bureaucracy have the potential to severely limit the growth of bioprospecting in the region. Issues surrounding benefit sharing (DEAT, 2004b) are unlikely to be resolved in the near future, despite the gazetted requirement for regulations for ABS (Chapter 6 of Act 10) to be in place by 1 January 2006. Much hinges on decisions made at a global scale, particularly with regard to intellectual property and the patenting of biological material (Ganguli, 1998). It is recommended that South African policy makers implement an interim solution to accommodate bioprospectors and researchers who cannot operate under unnecessarily restrictive legislation. The DEAT should take into account the detrimental effects that local research and development will suffer if facilitatory laws are not implemented. It is ironic that the development of benefit sharing policy in many countries has most hurt those who founded the idea and vision of the CBD, i.e. the scientific and ecological community. These groups, who most strongly advocated against the destruction of habitat and biodiversity, are now effectively unable to continue to study it to promote its value (Hirsch, 2005).

Chapter 7

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