Seed germination and genetic structure of two *Salvia* species in response to environmental variables among phytogeographic regions in Jordan (Part I)

and

Phylogeny of the pan-tropical family Marantaceae (Part II).

Dissertation

Zur Erlangung des akademischen Grades

Doctor rerum naturalium

(Dr. rer. nat)

Vorgelegt der

Naturwissenschaftlichen Fakultät I Biowissenschaften

der Martin-Luther-Universität Halle-Wittenberg

Von

Herrn Mohammad Mufleh Al-Gharaibeh

Geb. am: 18.08.1979 in: Irbid-Jordan

Gutachter/in

1. Prof. Dr. Isabell Hensen

2. Prof. Dr. Martin Roeser

3. Prof. Dr. Regina Classen-Bockhof

Halle (Saale), den 10.01.2017

Copyright notice

CHAPTER 4

Phylogeny of the pantropically distributed family Marantaceae

Al-Gharaibeh M, Borchsenius F, McKechnie L, Sanmartin I, & Ley AC
(Manuscript)

ABSTRACT

Phylogenetic resolution of problematic taxonomic groups can be improved and strengthened by increasing the amount of molecular data and the sampling of ingroup taxa. Here we reassess the phylogeny of the pantropically distributed family Marantaceae compiling a complete genera sampling and using both chloroplast and nuclear markers. Phylogenetic analyses were conducted on a set of four genetic markers (chloroplast markers: *trn*L, *mat*K, *rps*16 and nuclear marker: ITS) for 187 ingroup taxa representing all 29 Marantaceae genera under Maximum Likelihood (ML), Maximum parsimony (MP) criteria and Bayesian Inference (BI). The resulting tree topology focusing on the resolution of major clades was mostly congruent among applied methods and with preexisting family phylogenies. A few relationships within genera or clades were newly resolved here. A genus, *Monophyllanthe*, added to the phylogeny here for the first time appeared within the *Stachyphrynium* clade as sister to the genus *Marantochloa*. Only the affinity of the genus *Haumania* to one of the other major clades still remained uncertain. Four genera, *Calathea*, *Ischnosiphon*, *Maranta* and *Schumannianthus* were identified as being non-monophyletic. Such a robust phylogeny based on multiple molecular markers from both genomes and a complete sampling of Marantaceae genera will be a solid base to investigate in the future the timing of speciation and the migration events leading to the currently observed biogeographical patterns in this family.

Keywords: Backbone, *Haumania*, Marantaceae, *Monophyllanthe*, monophyly.

INTRODUCTION

The Marantaceae family, with approximately 29 genera and 550 species (Andersson 1998, Govaerts & Kennedy 2016), is the second largest family in the order Zingiberales (Sass *et al.* 2016). It has long been recognized as a sister of the family Cannaceae based on results of phylogenetic analyses of morphological (Kress 1990) and molecular (Kress *et al.* 2001; Kress & Specht 2006; Barrett *et al.* 2014) data. Marantaceae species are small to moderate-sized perennial, rhizomatous herbs characterized by a pulvinus (Petersen 1889, Kennedy 2000). The family is distributed throughout the tropics except in Australia. In the Neotropics, the Marantaceae species richness is highest with an estimated 450 species while the remaining species are paleotropical (Africa: ~40 spp., Asia: ~50 spp., Suksathan *et al.* 2009; Dhetchuvi 1996). The morphological diversity found in the Paleotropics was higher than in the Neotropics (Andersson 1981). Only a few genera are found in the temperate regions of South and North America.

Several previous studies estimated the relationships among major clades within the Marantaceae family either based on morphological and anatomical (Petersen 1889; Loesener 1930; Kirchoff 1983; Kress 1990; Andersson 1998; Kress *et al*. 2001) or on molecular data at the family level or for specific taxa (Table 1). Originally, the Marantaceae family has been divided into two tribes based on morphology and the number of fertile locules: Maranteae with one fertile locule, and Phrynieae with three fertile locules per ovary (Petersen1889; Loesener 1930). Later, based on a wider spectrum of morphological characters, Andersson (1998) proposed a world-wide sub division into five informal groups: *Calathea* group, *Donax* group, *Maranta* group, *Myrosma* group and *Phrynium* group. In this wide division, however, four genera were left with unknown affinity (*Haumania*, *Hylaeanthe*, *Thalia* and *Thaumatococus*: Prince & Kress 2006a). Recently, phylogenetic studies provided evidences that the proposed tribes (Petersen1889; Loesener 1930) and the informal groups (Andersson 1998) of the Marantaceae are not monophyletic. Based on a different set of molecular markers and new methods (Table 1), Prince and Kress (2006a and 2006b) proposed a different informal classification of the Marantaceae describing five major clades: *Calathea* clade, *Donax* clade, *Maranta* clade, *Sarcophrynium* clade and *Stachyphrynium* clade.

Table 1. Summary of previous molecular studies on Marantaceae phylogeny.

Target taxa	No. of ingroup genera/species	Molecular marker(s)	Analysis method(s)	Support method(s)	Literature
Marantaceae family	22/59	*rps*16	MP	JK	Andersson &chase 2001
Marantaceae family	27/80	*matK*, *trnL-F*	MP, BI	BS, PP	Prince &Kress 2006a
Marantaceae family	19/25	*matK*, *ndhF*, *rbcL*, *rps*16, *trnL–trnF*, *cox*1 and ITS	MP, BI	BS, PP	Prince &Kress 2006b
Asian Marantaceae taxa	26/79	*rps*16, ITS1 and 5S-NTS	MP, BI	BS, PP	Suksathan *et al*. 2009
***Sarcophrynium* clade, *Marantochloa* clade**	6/43	ITS, 5S, trnL/*trnL-F*	MP, ML, BI	BS, PP	Ley & Claßen-Bockhoff 2011
***Calathea* clade**	6/57	*matK*, *trnK* intron, *trnL* intron, *trnL-F* and ITS	MP	BS	Borchsenius *et al*. 2012

Methods of analysis: BI, Bayesian inference; ML, Maximum likelihood; MP, Maximum parsimony. **Methods of support**: BS, Bootstrap support; JK, Jackknife support; PP, Posterior probability. **Molecular markers**: ITS, internal transcribed spacer.

Resolution and branch support varied among trees produced by both studies, as well as, the placement of the genus *Haumania*. Most recently, Borchsenius *et al*. (2012) proposed a narrowly re-circumscription of the genus *Calathea*. They thereby resurrected the genus *Goeppertia* Nees (1831: 337) to include all members of the former *Calathea* clade I (sensu Prince & Kress 2006a). As a result of this new circumscription and resurrection, *Goeppertia* has become the largest genus in the Marantaceae. Still, all these previous studies are lacking the statistical support for the resolution of the relationships among the five major clades of Marantaceae and the position of the genus *Haumania*.

The evaluation of statistical clade support values is an important aspect of phylogenetic analysis as a function of the explanatory power of a given analysis (Grant & Kluge 2008). These support measures are a prerequisite to identify the well supported clades in a tree as a base for any inference of the evolution of the biological system (Huelsenbeck *et al.* 2000; Lutzoni *et al.* 2001; Pagel & Lutzoni 2002), e.g. to serve as the conceptual framework for the study of trait evolution (Alfaro *et al.* 2003). In both Maximum likelihood (ML) and Maximum parsimony (MP) analyses, tree support can be evaluated by bootstrapping, while the posterior probability support is the evaluation technique in the Bayesian inference (Jill Harrison & Langdale 2006). The bootstrap technique provides an assessment of “confidence” for each clade of an observed tree,

based on the proportion of resampled trees showing that same clade when individual characters in the data set are randomly removed and replaced with data from another character from the same data set (Efron *et al.* 1996). In contrast, the posterior probability is the actual probability of a node being correct (Jill Harrison & Langdale 2006). Bootstrap values > 70% indicate a reasonable support while values of ≥ 95% indicate a high support (Felsenstein 1985; Hillis & Bull 1993). Grant and Kluge (2008) proposed the support measures from parsimony, Maximum likelihood, and Bayesian phylogenetic inference are equivalent. However, when reconstructing the phylogeny of the Marantaceae, Borchsenius *et al*. (2012) found that support values achieved by Maximum likelihood and Bayesian analysis are equivalent, while lower statistical support values achieved in Maximum parsimony analysis. A high support for the accurate resolution in a phylogeny is suggested to be potentially achieved by increasing the total number of characters (Rosenberg and Kumar 2001), taxa (Heath *et al.* 2008; Zwickl & Hillis 2002) or both (Townsend & Lopez-Giraldez 2010).

Currently, the existing studies on the Marantaceae phylogeny could not resolve the relationships of major clades at the back bone of the Marantaceae phylogeny (Prince & Kress 2006a). In addition, the genus *Monophyllanthe* and its affinity to one of the major clades is missing in all previous studies. To overcome these limitations we present here a new phylogenetic analysis using Maximum parsimony (MP) criterion, Maximum likelihood (ML) and Bayesian inference (BI) and three plastid (*matK*, *rps*16 and *trnL-F*) and one nuclear marker (ITS, Internal transcribed spacer). With 187 Marantaceae taxa the full range of morphological variation known in the family is represented and all previously proposed infrageneric entities are covered. By utilizing more additional molecular data and taxa than in the past, the objectives of the current study were: (1) to achieve a higher resolution and support for the branching of the Marantaceae backbone, (2) to ascertain the monophyly of genera and clades, (3) to provide a better statistical support for the placement of the genus *Haumania* and its internal species´ relationships and (4) to locate the genus *Monophyllanthe*.

MATERIALS AND METHODS

Taxon Sequences Assembly

~600 sequences from four genetic markers (chloroplast markers: *trn*L, *mat*K, *rps*16 and nuclear marker: Internal Transcribed Spacer, ITS) covering 188 taxa were included in the analyses, representing all genera within the Marantaceae family and including the outgroup taxon *Canna indica*. All scientific names were updated to the latest synonyms and voucher information for each sample is given in Appendix 1. Datasets were built using on the one hand available published sequences (Andersson & Chase 2001; Prince & Kress 2006a, 2006b; Suksathan *et al.* 2009; Ley & Claßen-Bockhoff 2011; Borchsenius *et al.* 2012; Borchsenius *et al*. in prep.) and on the other hand, 80 sequences of 36 taxa extracted and sequenced newly in the course of this project. However, we could not produce a totally complete dataset. Still, for 16, 14, 17 and 18 taxa out of 188 have no sequence of *matK*, *rps*16, *trnL-F* and ITS, respectively. Furthermore, 18 out of 23 species of the genus *Phrynium* failed to produce the entire matK (mif+867) or ITS (18S+ITS1+5.8S+ITS2+26S) region (Appendix 1).

DNA Extraction, Amplification and Alignment

Total genomic DNA was extracted from leaf tissue using the DNeasy Plant Mini Kit (QIAGEN Inc., California) following the manufacturer's instructions. Amplifications of the target loci *rps16* intron, *matK* gene and *trnL* intron/ *trnL* exon/ *trnLtrnF* intergenic spacer, were conducted in a Mastercycler EP Gradient EPPENDORF via standard PCR. Each 25 µl volume contained 12.5 µl using the PCR mix BioMix (Bioline, Germany) (including the Biotaq DNA polymerase from Ecogen, dNTP Mix, 10x NH4 buffer, MgCl2 solution), 9.5 µl H 2 O and 1 µl genomic DNA extract. Amplification cycles were as follows for *rps16*: one cycle of 2 min at 94°C, 39 cycles of 30 s at 94°C, 60 s at 59°C, 2 min at 72°C with a final extension period of 7 min at 72°C, for *matK*: one cycle of 1.3 min at 94°C, 30 cycles of 1.3 min at 94°C, 2 min at 52°C, 2 min at 72°C with a final extension period of 10 min at 72°C and for *trnL/trnL-F*: one cycle of 2 min at 94°C, 30 cycles of 30 s at 94°C, 60 s at 55°C, 60 s at 72°C with a final extension period of 10 min at 72°C.

Amplification of *rps*16 was performed using the primers *rps*16F and *rps*16R2 (Oxelman *et al.* 1997), for *trnL-F* we used the primers ucp-c and ucp-f (Taberlet *et al.* 1991) and for *matK* the primers *mIF* (Prince & Kress 2006a), *matK*-867F, *matK*-988R and *matK*-1639R (Borchsenius *et al.* 2012). Hereafter, PCR products were purified using ExoSAP-IT™ (USB Corporation) following the

manufactor´s instructions. The products were sent to www.stabvida.com for sequencing in forward and reverse direction.

Sequences from the chloroplast were preliminarily aligned in Muscle 3.6 (Edgar 2004), then manually adjusted in BioEdit 7.2.5 (Hall 1999) and finally exported in Phylip format. Indels were coded with FastGap v. 1.2 (Borchsenius 2007), using the simple indel coding method of Simmons & Ochoterena (2000). Sequences from the highly variable nuclear marker ITS region in the ribosomal RNA gene, including part of the 18S (1-102 bp), through ITS1 (103-390 bp), 5.8S (391-552 bp), ITS2 (553-810 bp), and part of the 26S (811-1048 bp) loci in a single sequence) were aligned by clades identified from our phylogenetic trees reconstructed based solely on the chloroplast sequences. Finally, a partitioned supermatrix dataset of the sequences from *matK*, *rps*16, *trnL-F* and ITS and an indel matrix was prepared manually and exported to the compatible formats for analyses in PAUP, MrBayes and RAxML.

Phylogenetic Analyses and Branch Support

Datasets of the different gene regions were analyzed individually and in combination. The best-fitted model of nucleotide substitution rate for each marker was identified with jModelTest2 2.1.6 (Guindon & Gascuel 2003; Darriba *et al.* 2012) implemented in the CIPRES portal (Miller *et al.* 2010) using default parameters. The Bayesian information criterion (BIC, Schwarz 1978) was used for model choice because of its high accuracy (Darriba *et al.* 2012) and its tendency to favor simpler models than the Akaike information criterion (Posada & Crandall 2001).

Both phylogenetic analyses, Maximum likelihood (ML) and Bayesian inference (BI) were conducted on the CIPRES Science Gateway (Miller *et al*. 2010). Bayesian interferences were calculated including indels in MrBayes 3.2.6 (Ronquist *et al.* 2012). Each analysis consisted of three runs with four sequentially heated chains (temperature set at 0.05) for 5 million generations and sampling a tree every 50 generations with discarding the first 500,000 generations (burnin) prior to the calculation of posterior probability (PP). ML analyses were carried out with default parameters in RAxML-HPC2 BlackBox 8.2.3 (Stamatakis 2006). Maximum Parsimony (MP) analyses were conducted in PAUP* 4.0b10 (Swofford 2002) using a heuristic search with max trees set to 10000 , 100 random addition sequence replicates and branch

swapping algorithm using the tree-bisection-reconnection approach (TBR), holding 2 trees, saving no more than 10 trees per replicate. The consistency (CI), retention (RI) and rescaled consistency (RC) indices were calculated based on the whole data matrix including informative and uninformative characters.

Bootstrap values for Maximum likelihood (with 1,000 fast bootstrap) and Maximum parsimony (BS; Felsenstein 1985) analyses and posterior probabilities (PP) for Bayesian analysis were calculated to estimate branch and clade support. Parsimonious bootstrap percentages were estimated using 1000 replicates (10 random addition replicates, hold 2 trees, saving a maximum of 10 trees per replicate) to maximize the accuracy of the estimation.

RESULTS

DNA sequence summary.

The final data matrix included 688 sequences representing 188 taxa and one outgroup species. The ultimate matrices of aligned regions with indel coding had the following sizes: *matK* - 1375 characters (1362 bp + 13 indels) including 172 taxa*, rps*16 - 1275 characters (1125 bp + 50 indels) including 175 taxa*, trnL-F* - 1131 characters (1039 bp + 92 indels) including 171 taxa for and ITS - 1308 characters (1048 bp + 260 indels) including 170 taxa. Indel events were coded as multistate characters at the end of each data matrix.

Tree topologies.

Tree topologies were almost the same in all combined analyses with only slight variations in branch support, resolution and the placement of the genus *Haumania*. Conflicts in tree topologies among markers were generally for unsupported branches (BS < 50, PP < 0.95) as well as for taxa with a single or two available sequences only. For all Maximum parsimony analyses, tree characteristics and indices are summarized in Table (1). Tree indices indicated lower homoplasy and many more parsimony informative characters in chloroplast markers than in the ITS marker (Table 2).

Table 2. Summary of substitution models and tree scores for each genetic marker in Maximum parsimony analysis.

Maximum parsimony analyses (no. of taxa × no. of characters)	*matK* (173 x1375[a])	*rps*16 (177 x1275[a])	*trnL-F* (172 x1138[a])	ITS (170 x1308 [a])	Combined (188 x 5089 [a])
Substitution Model	TPM1uf+G	TPM1uf+G	TPM1uf+G	TIM1+I+G	
Informative characters	338	325	238	666	1567
Tree length	1032	1103	746	4282	7291
Consistency Index (CI)	0.66	0.65	0.68	0.34	0.46
Retention Index (RI)	0.9	0.88	0.89	0.75	0.81
Rescaled Consistency Index (RCI)	0.59	0.57	0.6	0.25	0.37
Homoplasy Index (HI)	0.34	0.35	0.32	0.66	0.54

[a] Including all characters.

The analyses revealed five well supported clades: *Calathea* clade, *Donax* clade, *Maranta* clade, *Sarcophrynium* clade and *Stachyphrynium* clade. ML-BS and BI-PP revealed a good support for all relationships among these clades except for the *Sarcophrynium* clade and the genus *Haumania*, whereas MP-BS supported only the sister relationship of the *Stachyphrynium* and the *Maranta* clade (BS value: 89, Figure 1).

***Calathea* clade.** The *Calathea* clade was the largest lineage with moderate to high branch support (ML-BS: 71, MP-BS: 85 and BI-PP: 100%). Within the *Calathea* clade there was a highly supported clade in all analyses (ML/MP-BS: 100, BI-PP: 100%) which included the four genera *Calathea* (*Calathea* II sensu Prince & Kress 2006a), *Ischnosiphon*, *Pleiostachya* and *Sanblasia*. The nesting of the two monotypic genera *Sanblasia* and *Pleistachya* within the *Calathea* and *Ischnosiphon* genera, respectively, characterized the latter two genera as non-monophyletic (Fig. 2). The resolution within the *Calathea-Sanblasia* clade was highly supported and formed three groups. The first group included *Sanblasia* and three *Calathea* species (*C. marantina*, *C. plurispicata*, and *C. lutea;* ML/MP-BS: 100 and BI-PP: 100%), where *Sanblasia* was placed at the base. This group was placed as sister (ML-BS: 99, MP-BS: 93 and BI-PP: 100%) to the second *Calathea* group (*C. toroi*, *C. cortalifera*, and *C. utilis;* ML/MP-BS: 100 and BI-PP: 100%). The third *Calathea* group was (*C. guzmanioides*, *C. hagbergi, C. pluriplicata*, and *C. timothei;* ML/MP-BS: 100 and BI-PP: 100%) and placed as sister to the former two groups ML/MP-BS: 100 and BI-PP: 100%). The sister relationship between the *Ischnosiphon-Pleiostachya-Calathea-Sanblasia* clade

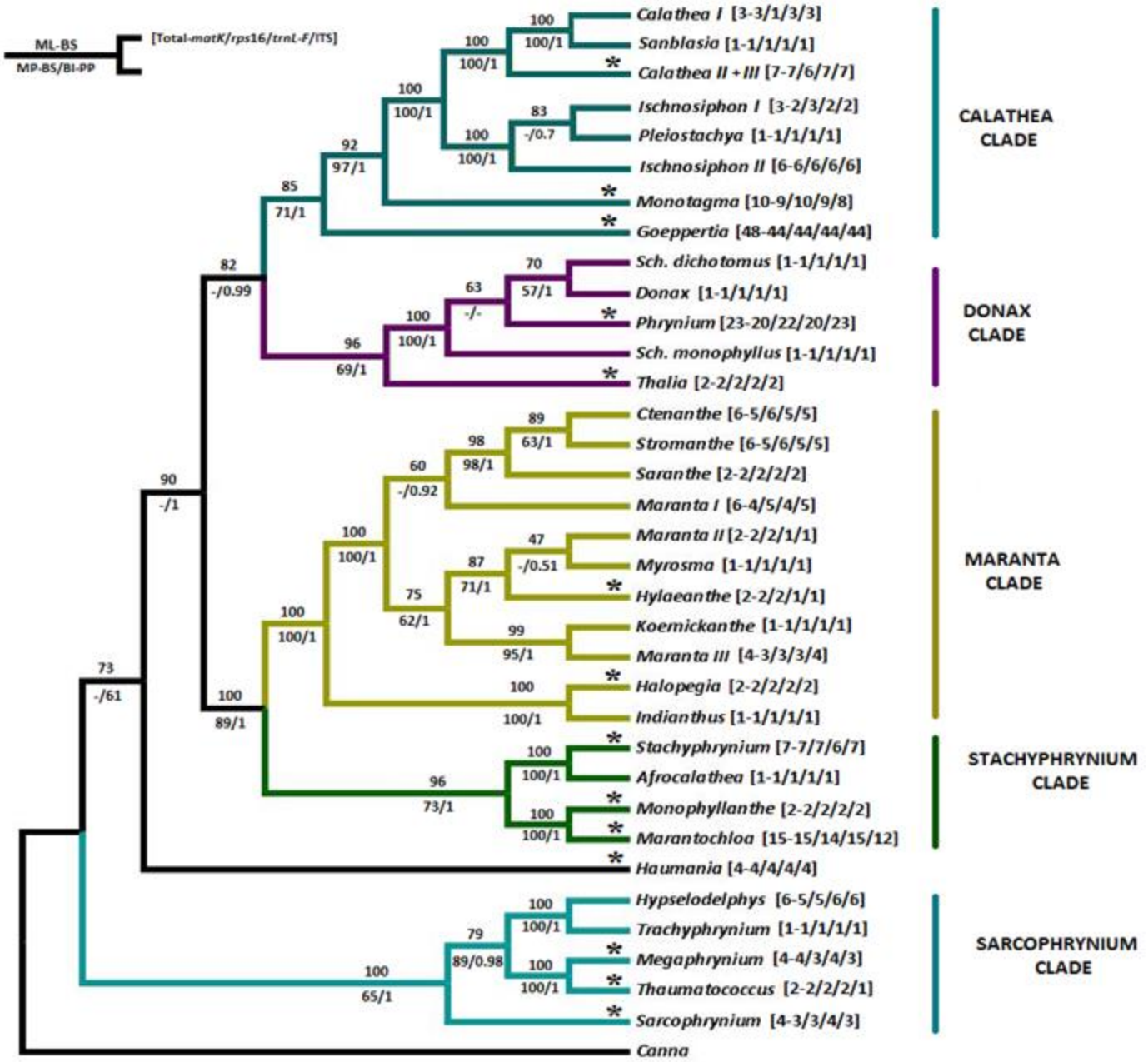

Figure 1. Strict consensus tree (ML) of 188 taxa (here only genera are shown, for the whole tree see Appendix 2.Fig 5a & b) for a combined analysis of the chloroplast markers *matK*, *rps*16 and *trnL-F* and the nuclear marker ITS. Colors indicate major clades (names adopted from Prince and Kress, 2006a). Numbers above and below branches represent support values from ML, MP and BI analyses. -, no branch support in respective analysis. *, high support for the genus or terminal taxa monophyly (ML-BS/BI-PP ≥ 98, MP-BS ≥ 94). Numbers in brackets after the genus name, [total number of known species per genus - number of species with available sequences for *matK*/*rps*16/*trnL-F*/ITS].

and the genus *Monotagma* was highly supported (ML-BS: 92, MP-BS: 97 and BI-PP: 100%), while the sister relationship of the entire clade and the genus *Goeppertia* (*Calathea* I sensu Prince and Kress 1996) was moderately to highly supported (ML-BS: 85, MP-BS: 71 and BI-PP: 100%). The 48 *Goeppertia* species formed a well-supported clade (ML-BS: 96, MP-BS: 98 and BI-PP: 100%). Within this clade, *G. straminea* was placed as sister to all other taxa, which in turn formed five major clades.

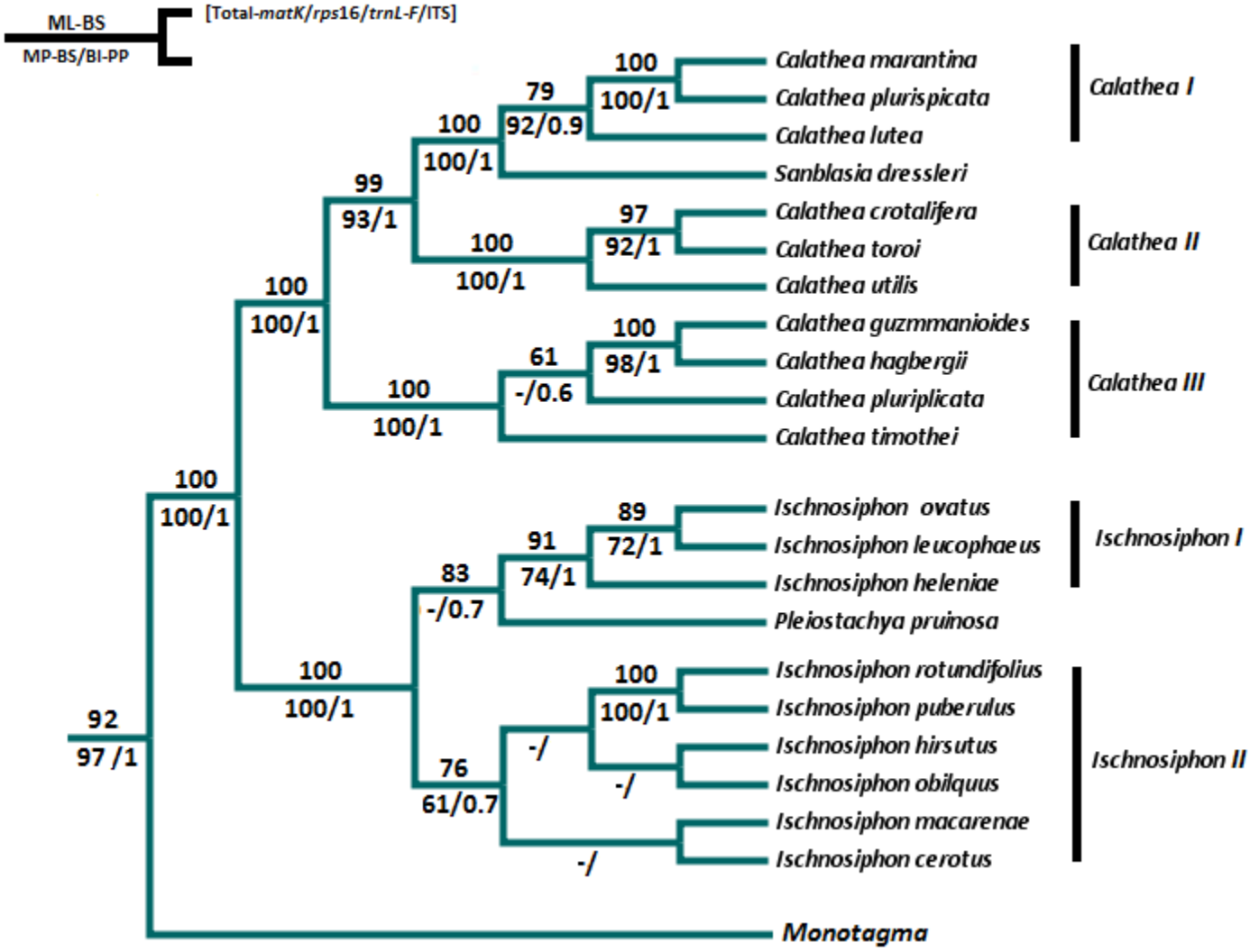

Figure 2. Strict consensus tree (ML, BI) for species relationship within the Ischnosiphon-Pleiostachya-Calathea-Sanblasia clade from a combined analysis. Numbers above and below branches represent support values from ML, MP and BI analyses. -, no branch support in respective analysis. This graph is a selection from the entire tree (Fig. 5a, Appendix 2) and not an independent calculation.

***Donax* clade**. The *Donax* clade included the genera *Donax, Phrynium, Schumannianthus* (two species), and *Thalia.* There was a moderate to high support for the monophyly of the entire clade (ML-BS: 99, MP-BS: 69 and BI-PP: 100%), but low support for the internal branches depicting the relationships among the two *Schumannianthus* species, *Donax* and *Phrynium* expect for the sister relationship of *Thalia* to all other genera of this clade. The monophyly of the genus *Phrynium* including the genera *Cominsia, Monophrynium and Phacelophrynium,* was approved (ML/MP-BS: 99, BI-PP: 100%). The relationships among all species of the genus *Phrynium* were not resolved, however, some subclades and sister relationships were moderately to strongly supported. These relationships were revealed in the subclade including *P. hirtum, P. fissifolium* and *P. villosulum* (ML-BS: 76, MP-BS: 98 and BI-PP: 98 %), the subclade *P. hainanense, P. pedunculiferum* and *P. tokinense* (ML-BS: 100, MP-BS: 97 and BI-PP: 100 %), the subclade *P. imbricatum, P. obscurum, P. pubinerve* and *P. tristachyum* (ML-BS: 93, MP-BS: 77 and BI-PP: 100 %), the sister relationship between *P. kaniense* and *P. macrocephalum* (ML-BS:96, MP-BS: 97 and BI-PP: 100 %), between *P. giganteum* (*Cominsia gigantean* sensu Saksuthan *et al.* 2009) and *P. whitei* (ML-BS:100, MP-BS: 99), between *P. interruptum* and *P. simplex* (*Phacelophrynium interruptum* and *Monophrynium. Simplex,* respectively, sensu Saksuthan *et al.* 2009; ML-BS: 100, MP-BS: 94 and BI-PP: 100 %) and between P*. imbricatum* and *P. pubinerve* (ML/MP-BS: 100 and BI-PP: 100 %; Appendix 2. Fig. 5a). The genus *Schumannianthus* appeared polyphyletic, although, the support of *Schumannianthus dichotomus* as sister to *Donax* was only strong in the BI-PP analysis (100%). Topologies independently from different markers were different with low support regarding the relationships between *Donax*, *S. dichotomous* and *S. monophyllus* (Appendix 2). Only in *rps*16 a moderate support (ML-BS: 79 MP-BS: 75 and BI-PP: 99%) was found for the sister relationship of *Donax* and *S. dichotomous*.

***Maranta* clade**. This clade included the genera *Ctenanthe*, *Halopegia*, *Hylaeanthe*, *Indianthus Koernickanthe*, *Maranta* (in three parts)*, Myrosma, Stromanthe* and *Saranthe*. The monophyly of the *Maranta* clade was strongly support (ML/MP-BS: 100 and BI-PP: 100%). The genus *Maranta* appeared polyphyletic. *Maranta* I (*M. noctiflora, M. rupicola, M. protracta, M. arundinacea, M. sobolifera, M. tuberculate*) was sister to a clade including *Ctenanthe*, *Stromanthe* and *Saranthe* (low support; ML-BS: 60 and BI-PP: 92%). *Maranta* II (*M. ruiziana, M. parvifolia*) formed a

moderate to high supported clade (ML-BS: 87, MP-BS: 71 and BI-PP: 100%) together with the genera *Myrosma* and *Hylaeanthe*. The highest support (ML-BS: 99, MP-BS: 95 and BI-PP: 100%) was found for the clade including *Maranta* III *(M. pohliana, M. friedrichsthaliana, M. humilis, M. leuconeura, M. cristata*) and the genus *Koernickanthe*. A clade including the two genera *Ctenanthe* and *Stromanthe* was moderately supported (ML-BS: 89, MP-BS: 63 and BI-PP: 100%) but with no support for the respective monophyly of the two genera (Appendix 2). *Ctenanthe dasycarpa,* which was represented only by a single *rps*16 sequence, nested with low support within the genus *Stromanthe*. The subclade including *Ctenanthe, Saranthe* and *Stromanthe* was highly supported (Fig. 1). A well supported clade of *Halopegia*/*Indianthus* was placed at the base of the *Maranta* clade.

***Stachyphrynium* clade**. This clade, strongly supported in the combined analysis only by ML and BI analyses (ML-BS: 96 and BI-PP: 100%), included the genera *Afrocalathea, Marantochloa, Monophyllanthe* and *Stachyphrynium*. Analyses conducted independently per markers found only support for the clade monophyly in all chloroplast markers, while this was not confirmed in the analysis of the nuclear marker (ITS). In the three analyses of the ITS region (ML, MP and BI), the two genera *Marantochloa* and *Monophyllanthe* were placed as sister to the *Maranta* clade. The other two genera *Afrocalathea* and *Stachyphrynium* were placed as sister to the *Haumania* clade either at the base of the clade including *Marantochloa*, *Monophyllanthe* and *Maranta* clade (ML), or in a polytomy at the tree base (BI) or apart from *Haumania* in a large polytomy (MP). All genera within this clade were monophyletic with a strong support from all three analyses (Fig. 1). A clear sister relationship was found for *Afrocalathea*/*Stachyphrynium* and for *Monophyllanthe*/*Marantochloa* (Fig. 1 and 3).

***Sarcophrynium* clade.** This strongly supported clade in the ML (BS=100) and BI (PP= 100%) analyses included the genera *Hypselodelphys*, *Megaphrynium*, *Sarcophrynium* and *Thaumatococcus*, *Trachyphrynium*. The sister relationship between *Hypselodelphys*/*Trachyphrynium*, and between *Megaphrynium/Thaumatococcus,* respectively, was highly supported. Topology and support values from the three combined analyses (ML/MP-BS: 100 and BI-PP: 100%) showed the four *Megaphrynium* species clustered in one clade. Within

the clade, *M. trichogynum* was placed at the base while the top branch occupied by both *M. gabonense* and *M. macrostachyum* (Fig. 4).

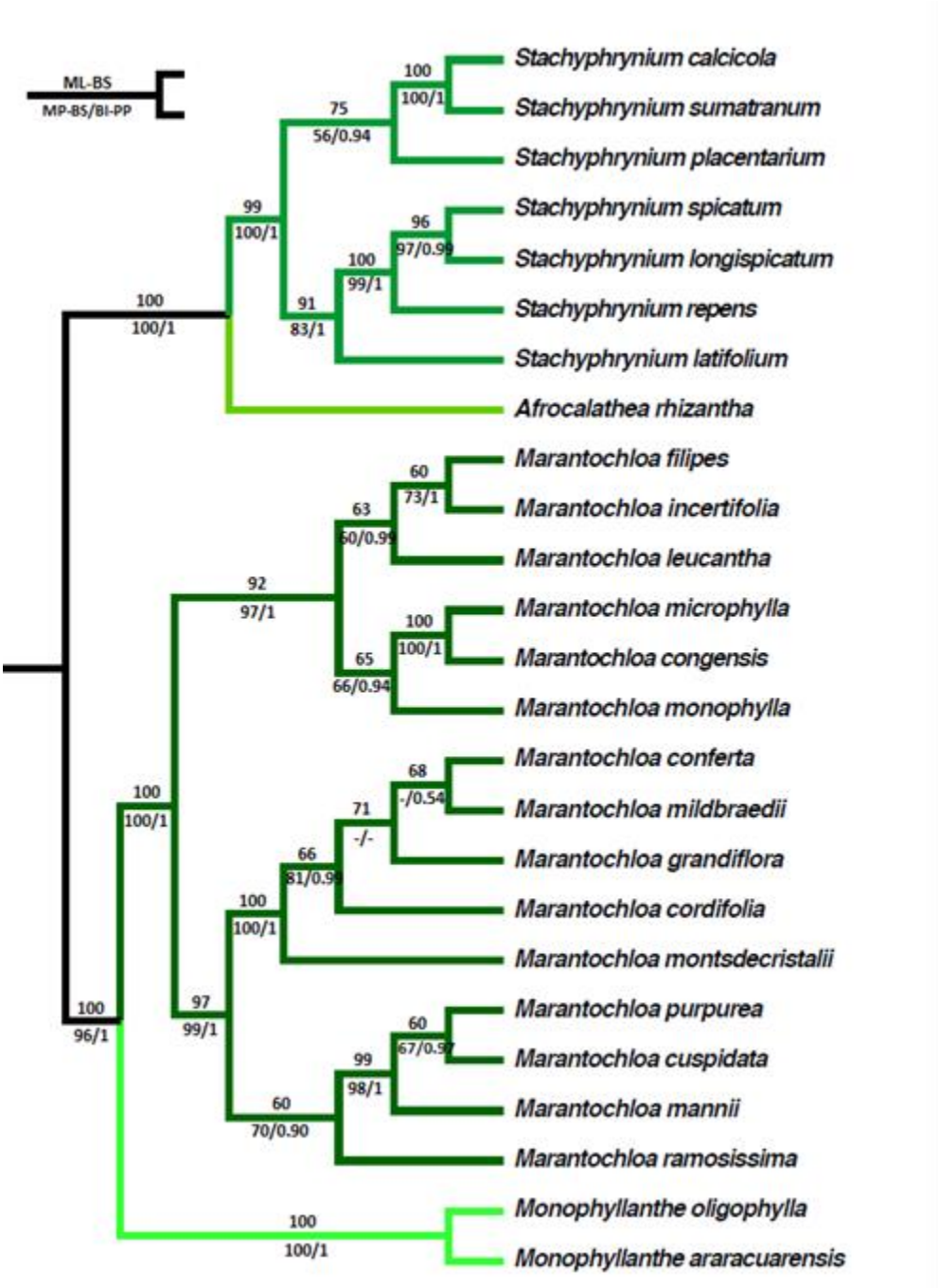

Figure 3. Strict consensus tree (ML) for Species relationship within *Stachyphrynium* clade from combined analyses. Numbers above and below branches represent support values from ML, MP and BI analyses. -, no branch support in respective analysis. This graph is a selection from the entire tree (Fig. 5b, Appendix 2) and not an independent calculation.

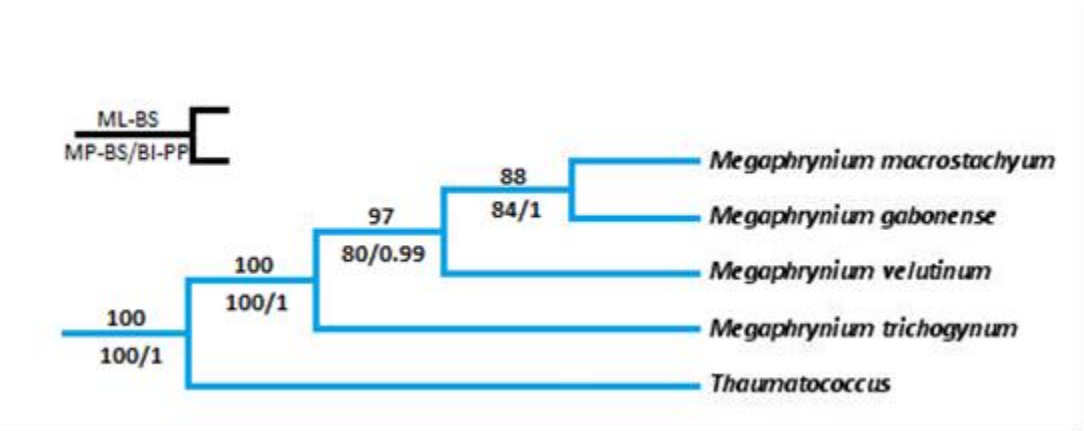

Figure 4. Strict consensus tree (ML, MP and BI) for species relationships within the *Megaphrynium* clade from a combined analyses of all four genetic markers. Numbers above and below branches represent support values from ML, MP and BI analyses. This graph is a selection from the entire tree (Fig. 5b, Appendix 2) and not an independent calculation.

Genus *Haumania*. The genus *Haumania* stood alone in both ML and BI analyses without confirmed affiliation to any of the major clades (Fig. 1), while the MP analysis placed *Haumania* as a member of the *Sarcophrynium* clade (weakly supported, MP-BS: 52). The relationships among the *Haumania* species were fully resolved. In all analyses and for all markers, the unknown *Haumania* species was found closest to *H. dankelmaniana*, where the sister species for both of them was *H. liebrechtsiana* while the species *H. leonardiana* was placed at the base of the *Haumania* clade (Fig. 5).

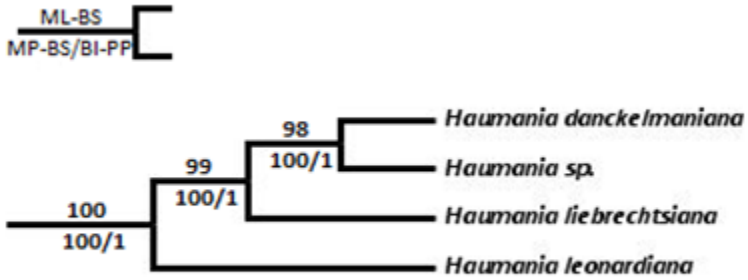

Figure 5. Strict consensus tree (ML, MP and BI) for species relationships within the *Haumania* clade from a combined analyses of all four genetic markers. Numbers above and below branches represent support values from ML, MP and BI analyses. This graph is a selection from the entire tree (Fig. 5b, Appendix 2) and not an independent calculation.

DISCUSSION

The tree topology from this analysis is overall congruent with the topology of the most recent Marantaceae phylogenetic analyses (Andersson & Chase 2001; Prince & Kress 2006a, 2006b) and supports the recognition of the proposed five major lineages. The majority of these lineages were restricted to a single geographical region (continent): tropical America (*Calathea* clade and *Maranta* clade except *Halopegia* from Africa and Asia, *Indianthus* from Asia), tropical Africa (*Sarcophrynium* clade) or tropical Asia (*Donax* clade except *Thalia* from America). While the genera of the *Stachyphrynium* clade can be found in all three tropical regions: Africa (*Afrocalathea* and *Marantochloa*), America (*Monophyllanthe*) and Asia (*Stachyphrynium*). In comparison to the independent marker analyses, the combined analyses improved the Marantaceae backbone support (BS and PP values) and general tree statistics (consistency index, retention index, and rescaled consistency index) against the ITS dataset but not against the chloroplast markers *matK*, *rps*16 and *trnL-F* dataset. Such patterns of higher tree statistics resulting from chloroplast markers rather than from nuclear markers was also found in Ley and Claßen-Bockhoff (2011, *trnL-F* and ITS) and Prince and Kress (2006b, *matK*, *rps*16, *trnL-F* and 18S–26S). Both analyses methods (ML and BI) supported a similar branching of the Marantaceae backbone, but this resolution was not confirmed in the MP analysis. Such results are expected since parsimony and likelihood methods (ML and BI) use different criteria for evaluating topology and choosing the best trees (Kolaczkowski & Thornton 2004). All clade support values (BS and PP) discussed and compared in the following text refer to those of the combined analyses (Fig. 1). If other support values from independent marker analyses are used in the text this is indicated separately in the text.

***Calathea* clade.** The whole clade received a support value of 71 (MP-BS) which is higher than the support values found in previous studies: 65 (Borchsenius *et al.* 2012), 60 (Prince & Kress 2006a) and the MP-JK < 50 (Prince & Kress 2006b). The strong support value (MP-BS: 100) for the *Ischnosiphon-Pleiostachya-Calathea-Sanblasia* clade was also found in (Borchsenius *et al*. 2012). Within this clade, *Calathea* and *Ischnosiphon* are considered potentially paraphyletic with respect to *Sanblasia* and *Pleiostachya,* respectively. The topology of the groups found within the *Calathea-Sanblasia* clade was the same as found by Borchsenius *et al*. (2012) with identical

support values. As more species from *Ischnosiphon* were included in our analyses, more sister species to *Pleiostachya* were found than *I. leucophaeus* (Borchsenius *et al*. 2012). No branch support for the clustering of all *Ischnosiphon* species apart from *Pleiostachya* was found by Prince and Kress (2006a) who used only chloroplast markers. An almost complete sampling of *Monotagma* species (10 species) confirmed the monophyly of the genus found in the previous studies (Andersson and Chase 2001: 2 species, Prince and Kress 2006a: 4 species, Borchsenius *et al*. 2012: 7 species).

The overall clade topology is congruent with the findings of Borchsenius *et al*. (2012), where the *Goeppertia* genus (*Calathea* I sensu Prince and Kress 2006a) was placed as sister to the rest of the clade genera. The support value we found for the *Goeppertia* clade (MP-BS: 98) was higher than in Prince and Kress (2006a, MP-BS: 93) and Borchsenius *et al*. (2012, MP-BS: 90). We could confirm the six major clades within the genus the *Goeppertia: Breviscapus*, *Comosae*, *Microcephalum*, *Ornata, Scapifolia* and *Straminea* found in Borchsenius *et al.* (2012) that supported the infrageneric groupings proposed previously by Kennedy *et al.* (1988). In addition to the similar support value (Appendix 2, Fig. 5a) as in Borchsenius *et al*. (2012) our results added six taxa to the *Comosae* clade (*G. pallidicosta*, *G. picturata*, *G. comosa*, *G. metallica*, *G. neblinensis*, *G. veitchiana*), eight to the *Breviscapus* clade (*G. aemula*, *G. colorata*, *G. concinna*, *G. cylindrical*, *G. laetevirens*, *G. lancifolia*, *G. mirabilis*, *G. zebrine*) and two to the *Ornate* clade (*G. majestica*, *G. splendida*).

***Donax* clade.** Relationships among and within the genera of this clade were not fully resolved. Clade support including 27 taxa was high in both ML and BI analyses (BS: 96 and PP: 100%) but moderate in MP analysis (BS: 69). Our MP support value was higher than in Prince and Kress (2006b, 5 taxa, MP: 53), Borchsenius *et al*. (2012, 4 taxa, MP: 52), slightly lower than in Suksathan *et al*. (2009, 45 taxa, MP: 72) and slightly similar to Prince and Kress (2006a, 9 taxa, MP: 68). The *Donax* clade without the genus *Thalia* was very well supported as in previous studies (Prince & Kress 2006a, 2006b; Suksathan *et al.* 2009; Borchsenius *et al.* 2012). Morphologically, *Thalia* is characterized by one petaloid outer staminode and two equal pendant staminode appendages (Claßen-Bockhoff 1991, see Prince & Kress 2006a) in contrast to all other clade members with two petaloid outer staminodes and one simple appendage at the cucullate staminode. Analyses

at marker level, showed a conflict among markers with respect to the sister relationship of *Donax canniformis* and *Schumannianthus dichotomus* (Appendix 2, Fig. 1a, 2a, 3a, 4b). This resulted in a low support in the ML and MP analyses of the dataset combining all four markers. However, this sister relationship was found strongly supported in the previous studies (Prince & Kress 2006a, 2006b) potentially due to the exclusion of *S. monophyllus* and a reduced taxon sampling within the *Donax* clade. A study with larger sampling from the *Donax* clade but based on *rps*16 only (Suksathan *et al*. 2009) revealed a low supported (MP-BS: 68, BI-PP< 95%) sister relationship between *S. dichotomus* and the genus *Donax* and an unresolved relation to *S. monophyllus*. In the same study but based on a combined analysis of *rps*16 intron + ITS1 + 5SNTS, no sister relationship between *S. dichotomus* and *D. canniformis* was found while *S. monophyllus* was placed at the base of the *Phrynium* clade. Suksathan *et al*. (2006) described *S. monophyllus* by having acaulescent vegetative shoots and short-stemmed, unbranched flowering shoots which is unusual to the stem habit found in *D. canniformis* and *S. dichotomus.* In our data sets probably due to amplification problems in the lab, the whole ITS sequence was of comparable lengths in *S. monophyllus* and the 14 *Phrynium* species (*c*. 240 bp, appendix 1), whereas in *D. canniformis* and *S. dichotomus* it was about 430 and 548 bp longer, respectively. Therefore, we assume that the unique morphology might have placed *S. monophyllus* apart from their closely related species and the low support for this resolution might be due to the variation in sequence length.

The 23 *Phrynium* species formed a well-supported monophyletic group with some resolved internal nodes. This monophyly was also found in Suksathan *et al.* (2009) after the merge of the four genera *Cominsia*, *Monophrynium*, *Phacelophrynium* and *Phrynium* to the genus *Phrynium* (sensu Suksathan *et al.* 2009). Some subclades and sister relationships among the *Phrynium* species were found strongly supported, while the majority was found weakly supported in ML and BI analyses or formed a polytomy in the MP analysis. In general our results support the grouping of the *Phrynium* species based on thier geographical distribution (Suksathan *et al.* 2009) except for the close sister relationships between the two West Malaysian species *P. obscurum* and *P. tristachyum* and the widespread species *P. imbricatum* and *P. pubinerve* (sensu Suksathan *et al.* 2009) rather than to other West Malaysian species *P. hirtum, P. fissifolium* and *P. villosulum*. A new species *P. whitei* was added to the New Guinea clade (see

Suksathan *et al.* 2009) with strong sister relationship to *P. giganteum,* where both species have the same geographical distribution pattern. Variation in the sequences length of ITS and *matK* due to incomplete sequences might have contributed to the poor achieved resolution.

***Maranta* clade.** The Maranta clade received again a high support. This was the first time that all genera of this clade were included in a phylogeny and more than one molecular marker from both chloroplast and nuclear DNA was used (compare to Andersson & Chase 2001; Prince & Kress 2006a, 2006b; Borchsenius *et al.* 2012). For instance, the placement of the genus *Koernickanthe* in the hypothesized tree topology in Prince and Kress (2006a) was based only on the molecular analysis of the *trnL-F* intergenic spacer region and morphological comparisons. Prince and Kress (2006a) further estimated the position of the *Myrosma* genus based on the shared morphological characteristics with other members of *Maranta* clade.

Based on the combined analyses (ML, BI), the 12 *Maranta* species clustered into three groups. This polyphyletic potential was indicated by both chloroplast and nuclear markers independently, as well as in the combined MP analyses but with different topology and support. The monophyly of the genus *Maranta* was already doubted by Andersson and Chase (2001) using only one chloroplast marker (*rps*16) and six *Maranta* species. Based on a limited sampling of *Maranta* (3 species), Prince and Kress (2006a) identified the genus as monophyletic. Polyphyly was neither applicable in Prince and Kress (2006b), as they represented the *Maranta* genus by only one species. Therefore, we assume that *Maranta* in its present circumscription is polyphyletic.

Topologies resulting from ML and BI analyses revealed different sister relationships among the clade taxa than hypothesized by Prince and Kress (2006a). For instance, Prince and Kress (2006a) placed the genus *Koernickanthe* at the base of the *Ctenanth*e-*Hylaeanthe*-*Maranta*-*Myrosma*-*Saranthe*-*Stromanthe* clade, while our analyses strongly supported the sister relationship between *Koernickanthe* and *Maranta III* (ML-BS: 99, MP-BS: 95 and BI-PP: 100%). Moreover, we found that the genus *Saranthe* was more closely related to the two genera *Ctenanthe* and *Stromanthe* than to the genus *Myrosma*. Our results showed a weak (MP-BS: 63) to strong (ML-BS: 89 and BI-PP: 100%) sister relationship for *Ctenanthe* and *Stromanthe*. This

relationship was also found by Andersson & Chase (2001, JK: 60, 8 taxa), Prince and Kress (2006a, BS: 78, 4 taxa), Prince and Kress (2006b, BS: 100, 2 taxa) and Suksathan *et al*. (2009, BS: 87, 3 taxa).

The monophyly of *Ctenanthe* (ML/MP-BS: 100 and BI-PP: 100%) was only supported based on ITS. In the combined analyses, we could only approve the monophyly of the genus when excluding *Ctenanthe dasycarpa* (ML-BS: 93, MP-BS: 99 and BI-PP: 100%) which was only nested with *Stromanthe* genus in the analysis of *rps*16 marker. All study results based only on the *rps*16 marker and including *Ctenanthe dasycarpa* could not show support for the monophyly of the two genera. Here *Ctenanthe dasycarpa* was either placed within the *Stromanthe* clade (Andersson and Chase 2001) or as sister to other *Stromanthe* species rather than *Ctenanthe* species (Suksathan *et al*. 2009). Morphologically, *Ctenanthe* and *Stromanthe* are very similar. While the majority of the species are easily classified at the genus level a few are problematic by sharing characters of both genera (Kennedy 1999). However, Kennedy (1999) found that the placement of the species *Ctenanthe dasycarpa* in *Stromanthe* (sensu Hammel 1986) was incorrect because of the bracts type, as the long and persistent sepals are a characteristic of *Ctenanthe*. However, the corolla tube length in *Ctenanthe dasycarpa* is shorter than in *Ctenanthe* (Kennedy 1978) where this feature is also found in *Stromanthe* (see Prince and Kress 2006a). Therefore, here we suggest to use more genetic markers (chloroplast and nuclear) to reveal the accurate affinity of *Ctenanthe dasycarpa* to the two genera *Ctenanthe* and *Stromanthe.*

The combined analysis very weakly placed the genus *Myrosma* as a sister to the *Maranta* II group and placed the latter taxa moderately supported in one clade with the genus *Hylaeanthe* (ML-BS: 87, MP-BS: 71 and BI-PP: 100%). Analyses based only on *rps*16 data, found no support for the placement of the genus *Myrosma* as sister to the genus *Saranthe* (Andersson & Chase 2001), or placed the five species *Hylaenthe hoffmannii*, *Koernickanthe orbiculata*, *Maranta kerchoviana*, *Maranta massengeana* and *Myrosma cannifolia* in one unsupported polytomy (Suksathan *et al*. 2009). When morphological data was added to the molecular analysis, a sister relationship between *Myrosma* and *Saranthe* was indicated in Prince and Kress (2006a).

***Stachyphrynium* clade**. The monophyly of this clade including the four genera *Afrocalathea, Marantochloa, Monophyllanthe* and *Stachyphrynium* was supported in the chloroplast datasets and the combined analysis. However, a different but only weakly supported clade topology was found in the ITS analysis, where the genera *Marantochloa* and *Monophyllanthe* were always more closely related to the *Maranta* clade than to the genera of the *Stachyphrynium* clade: *Afrocalathea* and *Stachyphrynium.*

The genus *Monophyllanthe* is included here for the first time in the analyses and placed as sister to the genus *Marantochloa*. Thus, the genus *Monophyllanthe* added the American continent to the distribution range of the *Stachyphrynium* clade. Anderson (1998) classified *Monophyllanthe* as a part of the *Maranta* group based on the genus morphology. As this genus was not included in any of the recent molecular studies at the family level (Andersson & Chase 2001; Prince & Kress 2006a, 2006b), no molecular evidence was so far achieved to refute or approve Andersson´s (1998) classification. Despite geographic isolation separating the two genera, *Monophyllanthe* and *Marantochloa* share a number of morphological features, including a solitary and simple cucullate staminode appendage, dehiscent fruits and arillate seeds (see Prince & Kress 2006a). Moreover, stoloniferous rhizomes were found in some *Marantochloa* species (Tomlinson 1961) and in *Monophyllanthe oligophylla* (Andersson 1998).

The here presented combined analyses, confirmed the monophyly of all four included genera. This was not yet the case in Prince and Kress (2006a) where *Ataenidia* was nested within *Marantochloa*, and *Afrocalathea* was embedded within *Stachyphrynium*. However, the genus *Ataenidia* was later included into the genus *Marantochloa* (see Ley & Claßen-Bockhoff 2011): *Marantochloa conferta* (*Ataenidia conferta*). The relationship between *Afrocalathea* and *Stachyphrynium* inferred by Prince and Kress (2006a) was based only on the chloroplast markers (*matK*, *trnL-F*), also a similar result achieved in Suksathan *et al*. (2009) when the analysis was based only on *rps*16. In our study, results from chloroplast markers independently showed also a similar relationship among the two genera. While the nuclear marker (ITS) and later the combined analyses either in our study or in Suksathan *et al.* (2009) confirmed the sister relationship of *Afrocalathea* and *Stachyphrynium*. This result might be achieved because the phylogenetic signal masked by homoplasy in the chloroplast data could be strengthened by a

combined analysis including ITS data which in turn can increases both resolution and support (Karehed *et al.* 2008). However, in our result the Maximum parsimony support value for the monophyly of *Stachyphrynium* genus (BS: 100) was higher than in Suksathan *et al.* (2009, MP-BS: 90). Moreover, the species relationships were almost fully resolved with high support values, while in Suksathan *et al.* (2009) these relationships were not fully resolved with low support values. This example shows, how the addition and concatenation of molecular characters from the chloroplast genome and ribosomal gene regions have a significant impact upon accurate phylogenetic analysis and can improve the resolution of the deep internodes (Townsend & Lopez-Giraldez 2010).

***Sarcophrynium* clade.** The intraclade topology based on all markers from independently evolving genomes (nuclear and chloroplast) are congruent in most parts and confirm the monophyly of all morphologically circumscribed genera within this clade. In addition, the relationships among these genera within the clade are solved with higher support than previously (Ley & Claßen-Bockhoff 2011) potentially due to the addition of further genetic markers. The placement of the genus *Sarcophrynium* at the base of the clade was confirmed by the all analyses (ML, MP and BI) of the combined dataset. This placement was not found in (Prince & Kress 2006b) due to a small sampling but was hypothesized by Prince and Kress (2006a), however, without statistical support.

Concerning the subclade including *Hypselodelphys, Megaphrynium, Thaumatococcus* and *Trachyphrynium,* our results show a moderate support for its monophyly in all three analyses (ML-BS: 79, MP-BS: 89 and BI-PP: 98 %). In a particular study investigating the relationships within the two major African clades (*Sarcophrynium* and *Marantochloa*) based on less molecular data than in our study, Ley and Claßen-Bockhoff (2011) found low support for this subclade (BS > 70). Moreover, the *Megaphrynium* topology was different by placing *M. gabonense* at the base of the genus. This did not yield a morphological support. In our study *Megaphrynium trichogynum* is sister to all other *Megaphrynium* species. In this topology floral (size and arrangement) and pollinator type are congruent between the basal taxon *M. trichogynum* and the sister genus *Thaumatococcus* and shows one shift to bee pollination and its corresponding floral type in the remaining *Megaphrynium* species (see Ley & Claßen-Bockhoff 2011).

Genus *Haumania.* The placement of this African genus *Haumania* as sister to all other major clades (*Calathea*, *Donax*, *Maranta* and *Stachyphrynium* clades) or within the *Sarcophrynium* clade remained unresolved in our analyses, just as in all previous phylogenetic studies. Prince and Kress (2006a) found *Haumania* to be placed at the base of the *Calathea* clade with a poorly supported relationship (less than 50% JK and less than 0.95 PP). However, they found no morphological evidence supporting the inclusion of *Haumania* in the *Calathea* clade. Based on more molecular markers, Prince and Kress (2006b) found *Haumania* in an unresolved polytomy at a more basal position than in the earlier study, or as a weakly supported member of the *Sarcophrynium* clade. To date it is thus still unclear whether the three *Haumania* species belong to the *Sarcophrynium* clade or have to be regarded as the root node for the other four clades. Despite the fact, that our results provide little information concerning the position of *Haumania* the relationships among the *Haumania* species are now fully resolved.

CONCLUSIONS

In conclusion, our results provide a higher resolution and support for the Marantaceae backbone in comparison to what was achieved in all previous studies. The addition of more molecular data and taxa have strengthened the hypothesized topology and suggested generic limits of the relationships within the family Marantaceae (Prince & Kress 2006a; Suksathan *et al.* 2009; Ley & Claßen-Bockhoff 2011; Borchsenius *et al.* 2012). Major new findings include highly supported infrasectional topologies of major clades and many subclades that were not achieved in any of the previous studies. Additionally, our study identified at least four potentially non-monophyletic genera: *Calathea*, *Ischnosiphon*, *Maranta* and *Schumannianthus* and only one genus *Haumania* of uncertain affinity.

Our results strongly supported the monophyly of 12 polytypic genera. The strongly supported sister relationship found between the genera *Monophyllanthe* and *Marantochloa* reveals that the *Stachyphrynium* clade is not restricted to a single geographical region (tropical America, tropical Africa, or tropical Asia). Obtaining a complete and full sequences length for all marker, as well as, more morphological data can enhance the total evidences support Marantaceae phylogeny. Our current results which are based on more molecular data and taxa

can be used in the future to investigate the biogeographical pattern and the timing of divergence in the family Marantaceae.

ACKNOWLEDGMENTS

We gratefully acknowledge the following people for their technical assistance with phylogenetic software: Dr. Natalia Tkach and Sebastian Gebauer and the acquisition of some additional sequences in the laboratory: Bärbel Hildebrandt.

APPENDICES

Appendix 1. Source and voucher information for taxa sampled in a phylogenetic study of Marantaceae based on chloroplast and nuclear DNA sequence data.

NO.	Taxa/Synonyms	*matK*	*rps* 16	*trnL-F*	ITS
1	***Afrocalathea rhizantha*** (K.Schum.) K.Schum.	AY140262	EF382847	ley011	EU605908
2	***Calathea crotalifera*** S.Watson	AU1429	AU1429	AU1429	AU1429
3	***Calathea guzmanioides*** L.B.Sm. & Idrobo	AU1423	AU1423	AU1423	AU1423
4	***Calathea hagbergii*** H.Kenn.	AU1424	AU1424	AU1424	AU1424
5	***Calathea lutea*** (Aubl.) E.Mey. ex Schult.	AU1427	AU1427	AU1427	AU1427
6	***Calathea marantina*** (Willd. ex Körn.) K.Koch	JQ341349	NA	JQ341232	JQ341288
7	***Calathea pluriplicata*** H.Kenn.	AY140280	NA	AY140359	JQ341295
8	***Calathea plurispicata*** H.Kenn.	AU1430	AU1430	AU1430	AU1430
9	***Calathea timothei*** H.Kenn.	AU1425	AU1425	AU1425	AU1425
10	***Calathea toroi*** S.Suárez	AU1426	AU1426	AU1426	AU1426
11	***Calathea utilis*** H.A.Kenn.	AY140282	NA	AY140361	JQ341303
12	***Canna indica*** L.	AM114724	AM116859	AM113702	FJ939505
13	***Ctenanthe burle-marxii*** H.Kenn.	AU1809	AU1809	AU1809	AU1809
14	***Ctenanthe dasycarpa*** (Donn.Sm.) K.Schum.	NA	AF141042	NA	NA
15	***Ctenanthe lubbersiana*** (E.Morren) Eichler ex Petersen	AU1811	AU1811	AU1811	AU1811
16	***Ctenanthe marantifolia*** (Vell.) J.M.A.Braga & H.Gomes	AU1813	AU1813	AU1813	AU1813
17	***Ctenanthe oppenheimiana*** (E.Morren) K.Schum.	AU1812	AU1812	AU1812	AU1812
18	***Ctenanthe setosa*** (Roscoe) Eichler	AU1810	AU1810	AU1810	AU1810
19	***Donax canniformis*** (G.Forst.) K.Schum.	AU650	AY914616	AU1931	AU1931
20	***Goeppertia aemula*** (Körn.) Borchs. & S.Suárez/***Calathea aemula***	AY140265	LP327	AY140344	LP327
21	***Goeppertia altissima*** (Poepp. & Endl.) Borchs. & S.Suárez/***Calathea altissima***	AU1444	AU1444	AU1444	AU1444
22	***Goeppertia attenuata*** (H.Kenn.) Borchs. & S.Suárez/***Calathea attenuata***	AU1448	AU1448	AU1448	AU1448
23	***Goeppertia bella*** (W.Bull) Borchs. & S.Suárez/***Calathea bella***	AY140278	LP348	AY140357	JQ341292
24	***Goeppertia capitata*** (Ruiz & Pav.) Borchs. & S.Suárez/***Calathea capitata***	AU1440	AU1440	AU1440	AU1440
25	***Goeppertia colorata*** (Hook.) Borchs. & S.Suárez/***Calathea colorata***	AY140266	LP343	AY140345	LP343
26	***Goeppertia comosa*** (L.f.) Borchs. & S.Suárez/***Calathea comosa***	AY140267	NA	AY140346	Ley025
27	***Goeppertia concinna*** (W.Bull) Borchs. & S.Suárez/***Calathea concinna*** / ***C. leopardina***	AY140272	LP332	AY140351	LP332
28	***Goeppertia curaraya*** (H.Kenn.) Borchs. & S.Suárez/***Calathea curaraya***	AU1438	AU1438	AU1438	AU1438
29	***Goeppertia cyclophora*** (Baker) Borchs. & S.Suárez/***Calathea cyclophora***	AU1431	AU1431	AU1431	AU1431
30	***Goeppertia cylindrica*** (Roscoe) Borchs. & S.Suárez/***Calathea cylindrica***	NA	AF141028	NA	NA
31	***Goeppertia ecuadoriana*** (H.Kenn.) Borchs. & S.Suárez/***Calathea ecuadoriana***	AY140269	NA	AY140348+JN413126	JQ341275
32	***Goeppertia foliosa*** (Rowlee ex Woodson & Schery) Borchs. & S.Suárez/***Calathea foliosa***	AY140270	LP030	AY140349+LP030	JQ341276
33	***Goeppertia fucata*** (H.Kenn.) Borchs. & S.Suárez/***Calathea fucata***	JQ341340	NA	JQ341223	JQ341277
34	***Goeppertia gymnocarpa*** (H.Kenn.) Borchs. & S.Suárez/***Calathea gymnocarpa***	AY140271	LP339	AY140350+LP339	JQ341279
35	***Goeppertia inocephala*** (Kuntze) Borchs. & S.Suárez/***Calathea inocephala***	AU1446	AU1446	AU1446	AU1446
36	***Goeppertia killipii*** (L.B.Sm. & Idrobo) Borchs. & S.Suárez/***Calathea killipii***	AU1451	AU1451	AU1451	AU1451
37	***Goeppertia laetevirens*** (Huber) Borchs. & S.Suárez/***Calathea laetevirens***	Suarez2655+SG132	AU1922	AU1922	Ley026
38	***Goeppertia lanata*** (Petersen) Borchs. & S.Suárez/***Calathea lanata***	AU1433	AU1433	AU1433	AU1433
39	***Goeppertia lancifolia*** (Boom) Borchs. & S.Suárez/***Calathea lancifolia***	ley046+Ley054	ley002	Ley012	NA
40	***Goeppertia latifolia*** (Willd. ex Link) Borchs. & S.Suárez/***Calathea latifolia***	AU1445	AU1445	AU1445	AU1445
41	***Goeppertia leonia*** (Boom bis) Borchs. & S.Suárez/***Calathea leonia***	AU1447	AU1447	AU1447	AU1447
42	***Goeppertia loeseneri*** (J.F.Macbr.) Borchs. & S.Suárez/***Calathea loeseneri***	AY140273	NA	AY140352	JQ341286
43	***Goeppertia majestica*** (Linden) Borchs. & S.Suárez/***Calathea majestica***	AY140274	LP338	AY140353	LP338
44	***Goeppertia metallica*** (Planch. & Linden) Borchs. & S.Suárez/***Calathea metallica***	AY140275	AY656136	AY140354	AY673046
45	***Goeppertia micans*** (L.Mathieu) Borchs. & S.Suárez/***Calathea micans***	AU1435	AU1435	AU1435	AU1435
46	***Goeppertia microcephala*** (Poepp. & Endl.) Borchs. & S.Suárez/***Calathea microcephala***	AU1436	AU1436	AU1436	AU1436
47	***Goeppertia mirabilis*** (Jacob-Makoy ex E.Morren) Borchs. & S.Suárez/***Calathea mirabilis***	AY140277	LP347	AY140356	LP347
48	***Goeppertia mishuyacu*** (J.F.Macbr.) Borchs. & S.Suárez/***Calathea mishuyacu***	AU1443	AU1443	AU1443	AU1443
49	***Goeppertia neblinensis*** (H.Kenn.) Borchs. & S.Suárez/***Calathea neblinensis***	Castro1152	AU1466	ley013	Ley027
50	***Goeppertia pallidicosta*** (H.Kenn.) Borchs. & S.Suárez/***Calathea pallidicosta***	AY140279	ley004	AY140358	Ley028
51	***Goeppertia pavonii*** (Körn.) Borchs. & S.Suárez/***Calathea pavonii***	AU1492	AU1492	AU1492	AU1492
52	***Goeppertia petersenii*** (Eggers) Borchs. & S.Suárez/***Calathea petersenii***	AU1432	AU1432	AU1432	AU1432
53	***Goeppertia picturata*** (K.Koch & Linden) Borchs. & S.Suárez/***Calathea picturata***	NA	AF141033	NA	NA
54	***Goeppertia propinqua*** (Poepp. & Endl.) Borchs. & S.Suárez/***Calathea propinqua***	AU1441	AU1441	AU1441	AU1441
55	***Goeppertia rufibarba*** (Fenzl) Borchs. & S.Suárez/***Calathea rufibarba***	AY140281	AY656138	AY140360	AY673048
56	***Goeppertia silvosa*** (J.F.Macbr.) Borchs. & S.Suárez/***Calathea silvosa***	AU1439	AU1439	AU1439	AU1439
57	***Goeppertia splendida*** (Lem.) Borchs. & S.Suárez/***Calathea splendida***	NA	AF141036	NA	NA
58	***Goeppertia standleyi*** (J.F.Macbr.) Borchs. & S.Suárez/***Calathea standleyi***	AU1442	AU1442	AU1442	AU1442
59	***Goeppertia straminea*** (Petersen) Borchs. & S.Suárez/***Calathea straminea***	AU1450	AU1450	AU1450	AU1450
60	***Goeppertia undulata*** (Linden & André) Borchs. & S.Suárez/***Calathea undulata***	AU1437	AU1437	AU1437	AU1437

61	***Goeppertia varians*** (K.Koch & Mathieu)Borchs. & S.Suárez/***Calathea varians***	**AU1491**	**AU1491**	**AU1491**	**AU1491**
62	***Goeppertia variegata*** (K.Koch) Borchs. & S.Suárez/***Calathea variegata***	**AU1449**	**AU1449**	**AU1449**	**AU1449**
63	***Goeppertia veitchiana*** (Veitch ex Hook.f.) Borchs. & S.Suárez/***Calathea veitchiana***	**NA**	**AY914604**	**NA**	**AY914651**
64	***Goeppertia villosa*** (Lodd. ex G.Don) Borchs. & S.Suárez./***Calathea villosa***	**AU1462**	**AU1462**	**AU1462**	**AU1462**
65	***Goeppertia vinosa*** (H.Kenn.) Borchs. & S.Suárez/***Calathea vinosa***	**AY140284**	**LP359**	**AY140363+LP359**	**JQ341307**
66	***Goeppertia warscewiczii*** (Lem.) Borchs. & S.Suárez/***Calathea warszewiczii***	**AY140285**	**AY656139**	**AY140364+LP024**	**AY673049**
67	***Goeppertia zebrina*** (Sims) Borchs. & S.Suárez/***Calathea zebrina***	**ley047+Ley055**	**AF141038**	**ley014**	**Ley029**
68	***Halopegia azurea*** (K.Schum.) K.Schum.	**AY140291**	**LP364**	**Ley015**	**LP364**
69	***Halopegia blumei*** (Körn.) K.Schum.	**AU446**	**AU446**	**AU446**	**JQ341258**
70	***Haumania danckelmaniana*** (J.Braun & K.Schum.) Milne-Redh	**Al60**	**AL60**	**AL60**	**Ley031**
71	***Haumania leonardiana*** C.M.Evrard & Bamps	**BEB250**	**BEB250**	**BEB250**	**Ley032**
72	***Haumania liebrechtsiana*** (De Wild. & T.Durand) J.Léonard	**Al50**	**Al50_B03**	**ley016**	**Ley030**
73	***Haumania*** sp.	**AY140293**	**AY656143**	**AY140374+JN413109**	**AY673053**
74	***Hylaeanthe hexantha*** (Poepp. & Endl.) A.M.E.Jonker & Jonker	**AU1825**	**AU1825**	**AU1825**	**AU1825**
75	***Hylaeanthe hoffmannii*** (K.Schum.) A.M.E.Jonker & Jonker ex H.Kenn.	**JQ588304**	**AF141051**	**NA**	**NA**
76	***Hypselodelphys hirsuta*** (Loes.) Koechlin	**AU1219**	**AU1219+AL269**	**Al269**	**AU1219**
77	***Hypselodelphys poggeana*** (K.Schum.) Milne-Redh.	**Al168**	**AL168**	**EU647819**	**EU605912**
78	***Hypselodelphys scandens*** Louis & Mullend.	**Al160**	**AL160**	**EU647824**	**EU605917**
79	***Hypselodelphys triangularis*** Jongkind	**NA**	**vMaesen5275**	**EU647822**	**EU605915**
80	***Hypselodelphys violacea*** (Ridl.) Milne-Redh.	**Al28**	**AF141052**	**EU647821**	**EU605914**
81	***Hypselodelphys velutina*** Jongkind	**Ley078**	**NA**	**EU647818**	**EU605911**
82	***Indianthus virgatus*** (Roxb.) Suksathan & Borchs. /***Schumannianthus virgatus***	**AY140328**	**AY914620**	**AU1921**	**AY914666**
83	***Ischnosiphon cerotus*** Loes.	**AY140297**	**LP366**	**AY140378**	**LP366**
84	***Ischnosiphon heleniae*** L.Andersson	**AY140298**	**AY656145**	**AY140379**	**AY673055**
85	***Ischnosiphon hirsutus*** Petersen	**AU1454**	**AU1454**	**AU1454**	**AU1454**
86	***Ischnosiphon leucophaeus*** (Poepp. & Endl.) Körn.	**AY140299**	**LP367**	**AY140380 +LP367**	**JQ341309**
87	***Ischnosiphon macarenae*** L.Andersson	**AU1455**	**AU1455**	**AU1455**	**AU1455**
88	***Ischnosiphon obliquus*** (Rudge) Körn.	**AU1456**	**AU1456**	**AU1456**	**AU1456**
89	***Ischnosiphon ovatus*** Körn., Bull.	**NA**	**AF141054**	**NA**	**NA**
90	***Ischnosiphon puberulus*** Loes.	**AY140300**	**LP368**	**AY140381+LP368**	**JQ341312**
91	***Ischnosiphon rotundifolius*** (Poepp. & Endl.) Körn.	**AY140301**	**LP440**	**AY140382+LP440**	**JQ341313**
92	***Koernickanthe orbiculata*** (Körn.) L.Andersson	**AU1826**	**AU1826**	**AY140383**	**AU1826**
93	***Maranta arundinacea*** L.	**AU1835**	**AU1835**	**AU1835**	**AU1835**
94	***Maranta cristata*** Nees & Mart. /***Maranta bicolor***	**AY140302**	**AY656146**	**AY140385**	**AY673056**
95	***Maranta friedrichsthaliana*** Körn.	**NA**	**NA**	**NA**	**Ley043**
96	***Maranta humilis*** Aubl.	**AU1845**	**AU1845**	**AU1845**	**AU1845**
97	***Maranta leuconeura*** E.Morren	**AU1831**	**AU1831**	**AU1831**	**AU1831**
98	***Maranta noctiflora*** Regel & Körn.	**AU1840**	**AU1840**	**AU1840**	**AU1840**
99	***Maranta parvifolia*** Petersen	**AU1837**	**AU1837**	**AU1837**	**AU1837**
100	***Maranta pohliana*** Körn.	**AU1839**	**AU1839**	**AU1839**	**AU1839**
101	***Maranta protracta*** Miq.	**AU1877**	**AU1877**	**AU1877**	**AU1877**
102	***Maranta ruiziana*** Körn.	**ley075+ley053**	**AF141060**	**NA**	**NA**
103	***Maranta rupicola*** L.Andersson	**Borchsenius lab.**	**NA**	**NA**	**Ley042**
104	***Maranta sobolifera*** L.Andersson	**NA**	**AF141061**	**NA**	**NA**
105	***Maranta tuberculata*** L.Andersson	**AU1842**	**AU1877**	**AU1842**	**AU1877**
106	***Marantochloa conferta*** (Benth.) A.C.Ley/***Ataenidia conferta***	**AY140263+Al115**	**AY656134**	**AY140342**	**AY673044**
107	***Marantochloa congensis*** (K.Schum.) J.Léonard & Mullend.	**Al107**	**AF141062**	**EU647811**	**EU605903**
108	***Marantochloa cordifolia*** (K.Schum.) Koechlin	**Al63**	**Al63**	**EU647802**	**NA**
109	***Marantochloa cuspidata*** (Roscoe) Milne-Redh.	**AU1221**	**AU1221**	**EU647814**	**EU605906**
110	***Marantochloa filipes*** (Benth.) Hutch.	**AU1222**	**AU1222+AL262**	**AU1222**	**AU1222**
111	***Marantochloa grandiflora*** A.C.Ley	**Ley079**	**WPM017T**	**EU647817**	**NA**
112	***Marantochloa incertifolia*** Dhetchuvi	**Al179**	**NA**	**EU647813**	**NA**
113	***Marantochloa leucantha*** (K.Schum.) Milne-Redh.	**AY140305**	**AF141066**	**EU647809**	**EU605901**
114	***Marantochloa mannii*** (Benth.) Milne-Redh.	**Al638**	**ley005**	**EU647806**	**EU605897**
115	***Marantochloa microphylla*** (Koechlin) Dhetchuvi	**ACL2531**	**ACL2531**	**ACl2531**	**AY673057**
116	***Marantochloa mildbraedii*** Koechlin	**Simons14**	**Simons14**	**Simons14**	**EU605893**
117	***Marantochloa monophylla*** (K.Schum.) D'Orey	**Al45**	**ley006**	**EU647810**	**EU605902**
118	***Marantochloa montsdecristalii*** A.C.Ley	**ley048+ley056**	**AL256**	**ley017**	**Ley033**
119	***Marantochloa purpurea*** (Ridl.) Milne-Redh.	**AY140306**	**AY656147**	**AY140389**	**AY673057**
120	***Marantochloa ramosissima*** (Benth.) Hutch	**Al751**	**ley007**	**ley018**	**Ley034**
121	***Megaphrynium gabonense*** Koechlin	**Al155**	**AL155**	**EU647830**	**EU605924**
122	***Megaphrynium macrostachyum*** (K.Schum.) Milne-Redh.	**AU1217**	**AL260+BEB373**	**AU1217**	**AU1217**
123	***Megaphrynium trichogynum*** Koechlin	**Al22**	**AL22**	**EU647828**	**EU605921**
124	***Megaphrynium velutinum*** (K.Schum.) Koechlin	**Ley059+Ley80**	**NA**	**EU652953**	**NA**
125	***Monophyllanthe araracuarensis*** S.Suárez, Galeano & H.Kenn.	**AU1824**	**AU1824**	**AU1824**	**Ley040**
126	***Monophyllanthe oligophylla*** K.Schum.	**AU1823**	**AU1823**	**AU1823**	**Ley041**
127	***Monotagma densiflorum*** (Körn.) K.Schum.	**Ley049+Ley060**	**ley009**	**Ley019**	**NA**
128	***Monotagma dolosum*** J.F.Macbr	**NA**	**AF141069**	**NA**	**NA**
129	***Monotagma juruanum*** Loes.	**AU1458**	**AU1458**	**AU1458**	**AU1458**
130	***Monotagma laxum*** (Poepp. & Endl.) K.Schum.	**AY140309**	**AY656148**	**AY140392+LP 376**	**AY673058**
131	***Monotagma papillosum*** Hagberg & R.Erikss.	**AY140310**	**LP377**	**AY140393+LP243**	**LP377**
132	***Monotagma parvulum*** Loes.	**AY140311**	**LP378**	**AY140394**	**LP378**
133	***Monotagma secundum*** (Petersen) K.Schum.	**AU1459**	**AU1459**	**AU1459**	**AU1459**
134	***Monotagma smaragdinum*** (Linden & André) K.Schum.	**AY140312**	**LP379**	**AY140395+LP379**	**JQ341318**
135	***Monotagma tomentosum*** K.Schum. ex Loes.	**AU1460**	**AU1460**	**AU1460**	**AU1460**
136	***Monotagma tuberosum*** Hagberg & R.Erikss.	**AU1457**	**AU1457**	**AU1457**	**AU1457**
137	***Myrosma cannifolia*** L.f.	**AU1857**	**AU1857**	**AU1857**	**AU1857**
138	***Phrynium aurantium*** (Clausager & Borchs.) Suksathan & Borchs./***Phacelophrynium aurantium***	**Johannsen12_SG120**	**AY914623**	**Johannsen12**	**AY914668*** **
139	***Phrynium fasciculatum*** (C.Presl) Horan./***Monophrynium fasciculatum***	**Suksathan3419_SG91**	**AY914646**	**Suksathan3419**	**AY914691*** **
140	***Phrynium fissifolium*** Ridl.	**NA**	**EF382851**	**NA**	**EF382843*** **

141	***Phrynium giganteum*** Scheff./***Cominsia gigantea***	**AU1862**	**AU1862**	**AU1862**	**AY673050**
142	***Phrynium grandibracteatum*** Clausager & Borchs.	**SJ11_SG139**	**AY914631+SJ11_SG13**	**SJ11_SG139**	**AU532**
143	***Phrynium hainanense*** T.L.Wu & S.J.Chen	**Suksathan296**	**AY914632**	**AU441**	**AU441**
144	***Phrynium hirtum*** Ridl.	**SJ03_SG336**	**AY914633**	**AU1932**	**Ley035*** **
145	***Phrynium imbricatum*** Roxb.	**AY140319**	**LP384 + AU1923**	**AU1923+AY140401**	**AU1923 + LP384**
146	***Phrynium interruptum*** (K.Schum.) Suksathan & Borchs.	**AU618**	**AY914625**	**AU618**	**AU618**
147	***Phrynium kaniense*** Loes. & G.M.Schulze	**NA**	**NA**	**NA**	**EF382844*** **
148	***Phrynium laxum*** (Clausager & Borchs.) Suksathan & Borchs./***Phacelophrynium laxum***	**SJ16_SG142***	**AY914626**	**AU535**	**AU535**
149	***Phrynium macrocephalum*** K.Schum.	**NA**	**EF382852**	**AU697**	**EF 3EF382845****
150	***Phrynium maximum*** Blume/***Phacelophrynium maximum***	**Poulsen1576+Ley050**	**EF382850**	**AU1933**	**AU555**
151	***Phrynium minutiflorum*** Suksathan & Borchs./***Phacelophrynium cylindricum***	**Suksathan3531_SG245**	**AY914624**	**Suksathan3531**	**AY914669*** **
152	***Phrynium obscurum*** Teijsm. & Binn.	**ley066+Ley051**	**AY914636**	**ley020**	**AY91468*** **
153	***Phrynium pedunculiferum*** D.Fang	**ley67 ***	**AY914637**	**ley021**	**AY914683*** **
154	***Phrynium pubinerve*** Blume/***Phrynium philippinense/ P.rheede***	**AU622**	**AY914639**	**AU622**	**AY914684*** **
155	***Phrynium sapiense*** (Clausager, Mood & Borchs.) Suksathan & Borchs/***Phacelophrynium sapien***	**Johannsen2 ****	**AY914630**	**Johannsen2**	**AY914675*** **
156	***Phrynium simplex*** (Elmer) Suksathan & Borchs./***Monophrynium simplex***	**Suksathan_3525_SG115**	**AY914647**	**Suksathan_3525_SG115**	**AY914692*** **
157	***Phrynium tonkinense*** Gagnep.	**Suksathan3543_SG148+Ley**	**AY914641**	**Suksathan3543**	**AY914682*** **
158	***Phrynium tristachyum*** Ridl.	**ley076***	**AY914642**	**NA**	**Ley044**
159	***Phrynium villosulum*** Miq.	**Johannsen13_SG123**	**AY914643**	**Johannsen13**	**AY914688*** **
160	***Phrynium whitei*** (Ridl.) Suksathan & Borchs.	**AU1224**	**AU1224**	**AU1224**	**AU1224**
161	***Pleiostachya pruinosa*** (Regel) K.Schum.	**AU1366**	**AU1366**	**AU1366**	**AU1366**
162	***Sanblasia dressleri*** L.Andersson	**AU1599**	**AU1599**	**AU1599**	**AU1599**
163	***Saranthe klotzschiana*** (Körn.) Eichler	**AU1822**	**AU1822**	**AU1822**	**AU1822**
164	***Saranthe madagascariensis*** (Benth.) K.Schum./***Saranthe unilateralis***	**AU1878**	**AU1878**	**AU1878**	**AU1878**
165	***Sarcophrynium brachystachyum*** (Benth.) K.Schum.	**Al32**	**AL32**	**EU647831**	**EU605926**
166	***Sarcophrynium prionogonium*** (K.Schum.) K.Schum.	**Al55**	**AL55**	**EU647832**	**EU605929**
167	***Sarcophrynium schweinfurthianum*** (Kuntze) Milne-Redh.	**NA**	**NA**	**EU647833**	**EU605928**
168	***Sarcophrynium villosum*** (Benth.) K.Schum.	**Al759**	**AL759**	**ley022**	**NA**
169	***Schumannianthus dichotomus*** (Roxb.) Gagnep.	**AU649**	**AY914619**	**AU649**	**AU649**
170	***Schumannianthus monophyllus*** Suksathan/***Phrynium griffithii***	**AU653**	**AY914621**	**AU653**	**AY914667**
171	***Stachyphrynium calcicola*** A.D.Poulsen & Clausager	**Poulsen_2026_SG154**	**AY914606**	**Poulsen2026**	**AY914652**
172	***Stachyphrynium latifolium*** (Blume) K.Schum.	**AY140329**	**LP386**	**AY140412 + ley023**	**ley036**
173	***Stachyphrynium longispicatum*** Suksathan & Borchs	**Suksathan3321_SG95**	**AY914609**	**Suksathan3321**	**AY914655**
174	***Stachyphrynium placentarium*** (Lour.) Clausager & Borchs.	**Ley073+Ley077**	**AY914610**	**AU447**	**ley037+Ley045**
175	***Stachyphrynium repens*** (Körn.) Suksathan & Borchs.	**AU616**	**AY914611**	**AU616**	**AU616**
176	***Stachyphrynium spicatum*** (Roxb.) K.Schum	**Suksathan3356_SG90**	**AY914612**	**Suksathan335**	**AY914658**
177	***Stachyphrynium sumatranum*** (Miq.) K.Schum.	**AY140318**	**AY914614**	**NA**	**ley038**
178	***Stromanthe jacquinii*** (Roem. & Schult.) H.Kenn. & Nicolson	**NA**	**AF141087**	**NA**	**NA**
179	***Stromanthe papillosa*** Petersen	**AU1879**	**AU1879**	**AU1879**	**AU1879**
180	***Stromanthe schottiana*** (Körn.) Eichler	**AU1817**	**AU1817**	**AU1817**	**AU1817**
181	***Stromanthe stromanthoides*** (J.F.Macbr.) L.Andersson	**AY140334**	**ley010**	**AY140417**	**Ley039**
182	***Stromanthe thalia*** (Vell.) J.M.A.Braga	**AU1814**	**AU1814**	**AU1814**	**AU1814**
183	***Stromanthe tonckat*** (Aubl.) Eichler	**AU1816**	**AU1816**	**AU1816**	**AU1816**
184	***Thalia dealbata*** Fraser	**AU549**	**AY914648.1**	**JQ341215**	**AY914693**
185	***Thalia geniculata*** L.	**AU916**	**EF382853**	**AU916**	**AU916**
186	***Thaumatococcus daniellii*** (Benn.) Benth.	**AU1218**	**AU1218+AL96**	**EU647826**	**EU605919**
187	***Thaumatococcus flavus*** A.C.Ley	**Al56**	**AL56**	**EU647827**	**NA**
188	***Trachyphrynium braunianum*** (K.Schum.) Baker	**AY140339**	**AL171**	**AY140422+ ley024**	**AY673068**

Abbreviations: Sequences name start with (**Ley**) indicate new sequence or part of sequences obtained from DNA extracted in the Institute of Geobotany and Botanical Garden/Halle (Saale), Germany. **NA**, indicate that this sequence is not available. *****, the *mif matK* part is missing from this sequence (≈ 620 bp); ******, the 867 *matK* part is missing from this sequence (≈ 630 bp); *******, part of the 5.8S and the whole ITS2 are missing from this sequence (≈ 620 bp).

Appendix 2. In the following figures a Maximum Likelihood strict consensus tree for each marker analysis: *matK* (Fig 1a and b), *rps*16 (Fig 2a and b), *trnL-F* (Fig 3a and b), ITS (Fig 4a and b) and combined analysis (Fig 5a and b). Numbers above and below branches denote ML and MP bootstrap support of 50 % or higher, respectively. Bold lines indicated branches with posterior probabilities of 0.95 or higher. Dash sign indicates branches not found in the Maximum parsimony strict consensus tree (-/), in the Bayesian analysis(/-) or in both analyses (-/-). Inset upper left corner shows which clades or branches of the Marantaceae family tree is depicted in the large figure.


A
Thalia
B
C
D
Haumania
E
F
Canna
CALATHEA CLADE (A)
DONAX CLADE (B)
CALATHEA CLADE (C)
SARCOPHRYNIUM CLADE (D)
Goeppertia varians
Goeppertia rufibarba
Goeppertia pavonii
Goeppertia concinna
Goeppertia bella
Goeppertia lancifolia
Goeppertia colorata
Goeppertia zebrina
Goeppertia aemula
Goeppertia mishuyacu
Goeppertia standleyi
Goeppertia laetevirens
Goeppertia propinqua
Goeppertia mirabilis
Goeppertia loeseneri
Goeppertia lanata
Goeppertia neblinensis
Goeppertia petersenii
Goeppertia attenuata
Goeppertia metallica
Goeppertia silvosa
Goeppertia pallidicosta
Goeppertia ecuadoriana
Goeppertia villosa
Goeppertia capitata
Goeppertia leonia
Goeppertia comosa
Goeppertia cyclophora
Goeppertia micans
Goeppertia curaraya
Goeppertia fucata
Goeppertia killipii
Goeppertia undulata
Goeppertia microcephala
Goeppertia latifolia
Goeppertia vinosa
Goeppertia warscewiczii
Goeppertia foliosa
Goeppertia altissima
Goeppertia inocephala
Goeppertia variegata
Goeppertia majestica
Goeppertia gymnocarpa
Goeppertia striminea
Thalia geniculata
Thalia dealbata
Phrynium simplex
Phrynium interruptum
Phrynium fascicultatum
Phrynium laxum
Phrynium maximum
phrynium giganteum
Phrynium whitei
Phrynium minutiflorum
Phrynium tonkinense
Phrynium hainanense
Phrynium pedunculiferum
Phrynium villosulum
Phrynium pubinerve
Phrynium imbricatum
Phrynium tristachyum
Phrynium obscurum
Phrynium hirtum
Phrynium aurantium
Phrynium sapiense
Phrynium grandibracteatum
Schumanniathus monophyllus
Donax canniformis
Schumanniathus dichotomus
Calathea timothei
Calathea hagbergii
Calathea guzmanioides
Calathea pluriplicata
Calathea marantina
Calathea crotalifera
Calathea toroi
Calathea utilis
Saniblasia dressleri
Calathea lutea
Calathea plurispicata
Ischnosiphon heleniae
Ischnosiphon leucophaeus
Ischnosiphon obliquus
Pleiostachya pruinosa
Ischnosiphon cerotus
Ischnosiphon macarenae
Ischnosiphon hirsutus
Ischnosiphon puberulus
Ischnosiphon rotundifolius
Monotagma smaragdinum
Monotagma parvulum
Monotagma secundum
Monotagma tomentosum
Monotagma densiflorum
Monotagma papillosum
Monotagma laxum
Monotagma juruanum
Monotagma tuberosum
Hypseladelphys hirsuta
Hypseladelphys scandens
Hypseladelphys poggeana
Hypseladelphys violacea
Trachyphrynium brauniianum
Hypseladelphys velutina
Sarcophrynium villosum
Sarcophrynium prionogonium
Sarcophrynium brachystachyum
Megaphrynium velutinum
Megaphrynium trichogynum
Megaphrynium gabonense
Megaphrynium macrostachyum
Thaumatococcus flavus
Thaumatococcus daniellii
Haumania danckelmaniana
Haumania sp
Haumania liebrechtsiana
Haumania leonardiana

Figure 1a

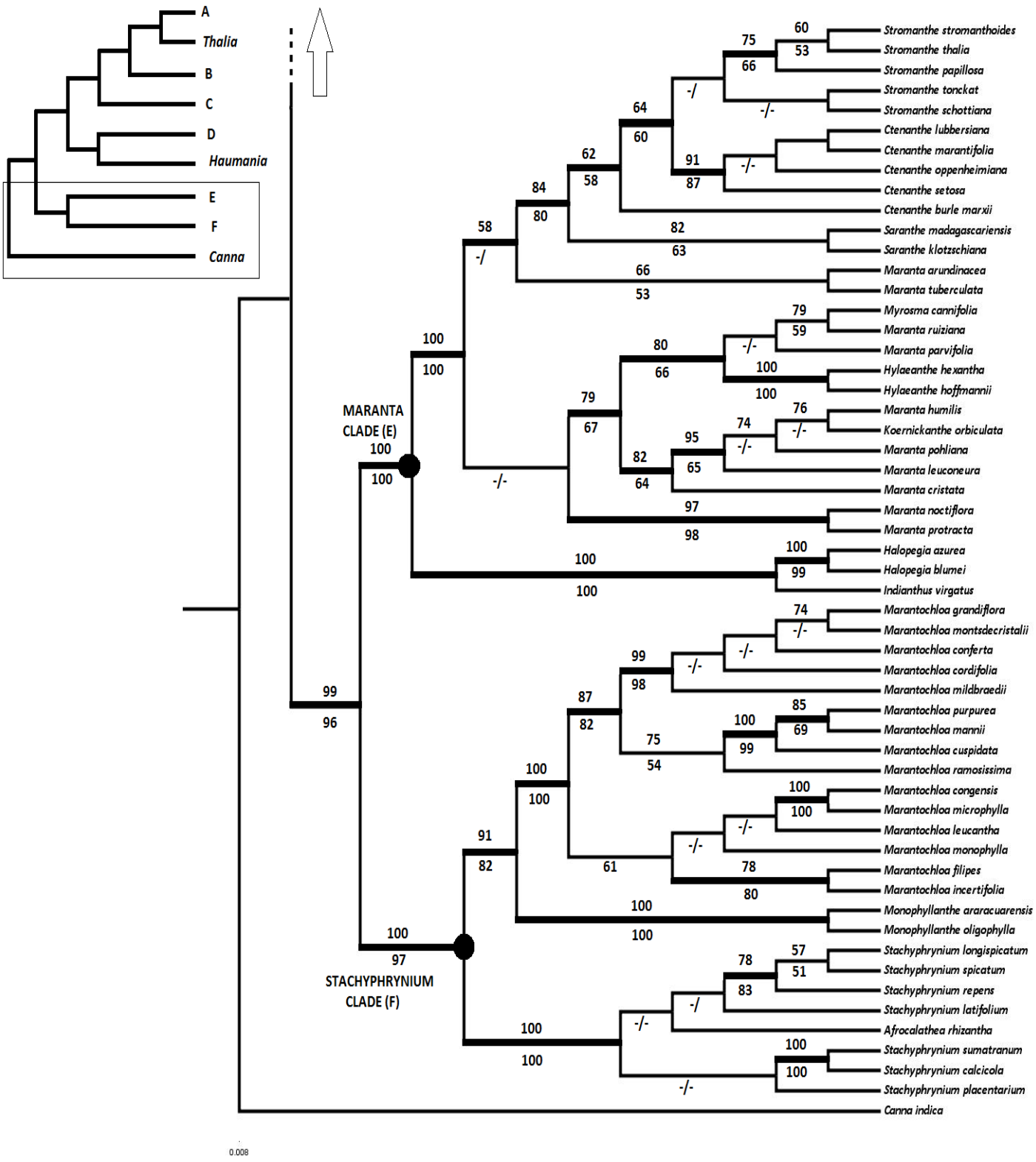
A
Thalia
B
C
D
Haumania
E
F
Canna
MARANTA CLADE (E)
STACHYPHRYNIUM CLADE (F)
Stromanthe stromanthoides
Stromanthe thalia
Stromanthe papillosa
Stromanthe tonckat
Stromanthe schottiana
Ctenanthe lubbersiana
Ctenanthe marantifolia
Ctenanthe oppenheimiana
Ctenanthe setosa
Ctenanthe burle marxii
Saranthe madagascariensis
Saranthe klotzschiana
Maranta arundinacea
Maranta tuberculata
Myrosma cannifolia
Maranta ruiziana
Maranta parvifolia
Hylaeanthe hexantha
Hylaeanthe hoffmannii
Maranta humilis
Koernickanthe orbiculata
Maranta pohliana
Maranta leuconeura
Maranta cristata
Maranta noctiflora
Maranta protracta
Halopegia azurea
Halopegia blumei
Indianthus virgatus
Marantochloa grandiflora
Marantochloa montsdecristalii
Marantochloa conferta
Marantochloa cordifolia
Marantochloa mildbraedii
Marantochloa purpurea
Marantochloa mannii
Marantochloa cuspidata
Marantochloa ramosissima
Marantochloa congensis
Marantochloa microphylla
Marantochloa leucantha
Marantochloa monophylla
Marantochloa filipes
Marantochloa incertifolia
Monophyllanthe araracuarensis
Monophyllanthe oligophylla
Stachyphrynium longispicatum
Stachyphrynium spicatum
Stachyphrynium repens
Stachyphrynium latifolium
Afrocalathea rhizantha
Stachyphrynium sumatranum
Stachyphrynium calcicola
Stachyphrynium placentarium
Canna indica
0.008

Figure 1b

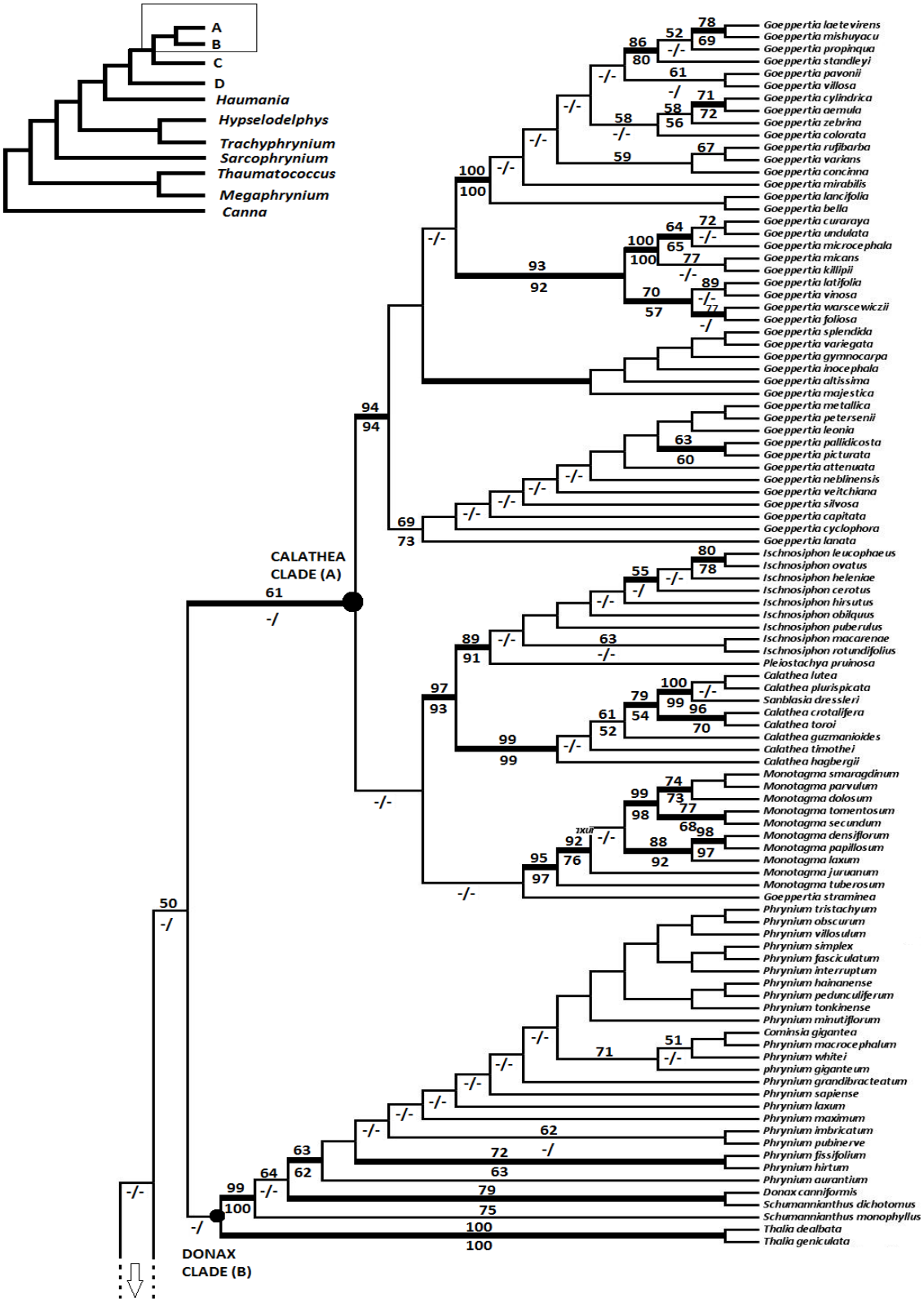
A
B
C
D
Haumania
Hypselodelphys
Trachyphrynium
Sarcophrynium
Thaumatococcus
Megaphrynium
Canna
CALATHEA CLADE (A)
DONAX CLADE (B)
Goeppertia laetevirens
Goeppertia mishuyacu
Goeppertia propinqua
Goeppertia standleyi
Goeppertia pavonii
Goeppertia villosa
Goeppertia cylindrica
Goeppertia aemula
Goeppertia zebrina
Goeppertia colorata
Goeppertia rufibarba
Goeppertia varians
Goeppertia concinna
Goeppertia mirabilis
Goeppertia lancifolia
Goeppertia bella
Goeppertia curaraya
Goeppertia undulata
Goeppertia microcephala
Goeppertia micans
Goeppertia killipii
Goeppertia latifolia
Goeppertia vinosa
Goeppertia warscewiczii
Goeppertia foliosa
Goeppertia splendida
Goeppertia variegata
Goeppertia gymnocarpa
Goeppertia inocephala
Goeppertia altissima
Goeppertia majestica
Goeppertia metallica
Goeppertia petersenii
Goeppertia leonia
Goeppertia pallidicosta
Goeppertia picturata
Goeppertia attenuata
Goeppertia neblinensis
Goeppertia weitchiana
Goeppertia silvosa
Goeppertia capitata
Goeppertia cyclophora
Goeppertia lanata
Ischnosiphon leucophaeus
Ischnosiphon ovatus
Ischnosiphon heleniae
Ischnosiphon cerotus
Ischnosiphon hirsutus
Ischnosiphon obilquus
Ischnosiphon puberulus
Ischnosiphon macarenae
Ischnosiphon rotundifolius
Pleiostachya pruinosa
Calathea lutea
Calathea plurispicata
Sanblasia dressleri
Calathea crotalifera
Calathea toroi
Calathea guzmanioides
Calathea timothei
Calathea hagbergii
Monotagma smaragdinum
Monotagma parvulum
Monotagma dolosum
Monotagma tomentosum
Monotagma secundum
Monotagma densiflorum
Monotagma papillosum
Monotagma laxum
Monotagma juruanum
Monotagma tuberosum
Goeppertia straminea
Phrynium tristachyum
Phrynium obscurum
Phrynium villosulum
Phrynium simplex
Phrynium fasciculatum
Phrynium interruptum
Phrynium hainanense
Phrynium pedunculiferum
Phrynium tonkinense
Phrynium minutiflorum
Cominsia gigantea
Phrynium macrocephalum
Phrynium whitei
phrynium giganteum
Phrynium grandibracteatum
Phrynium sapiense
Phrynium laxum
Phrynium maximum
Phrynium imbricatum
Phrynium pubinerve
Phrynium fissifolium
Phrynium hirtum
Phrynium aurantium
Donax canniformis
Schumannianthus dichotomus
Schumannianthus monophyllus
Thalia dealbata
Thalia geniculata

Figure 2a

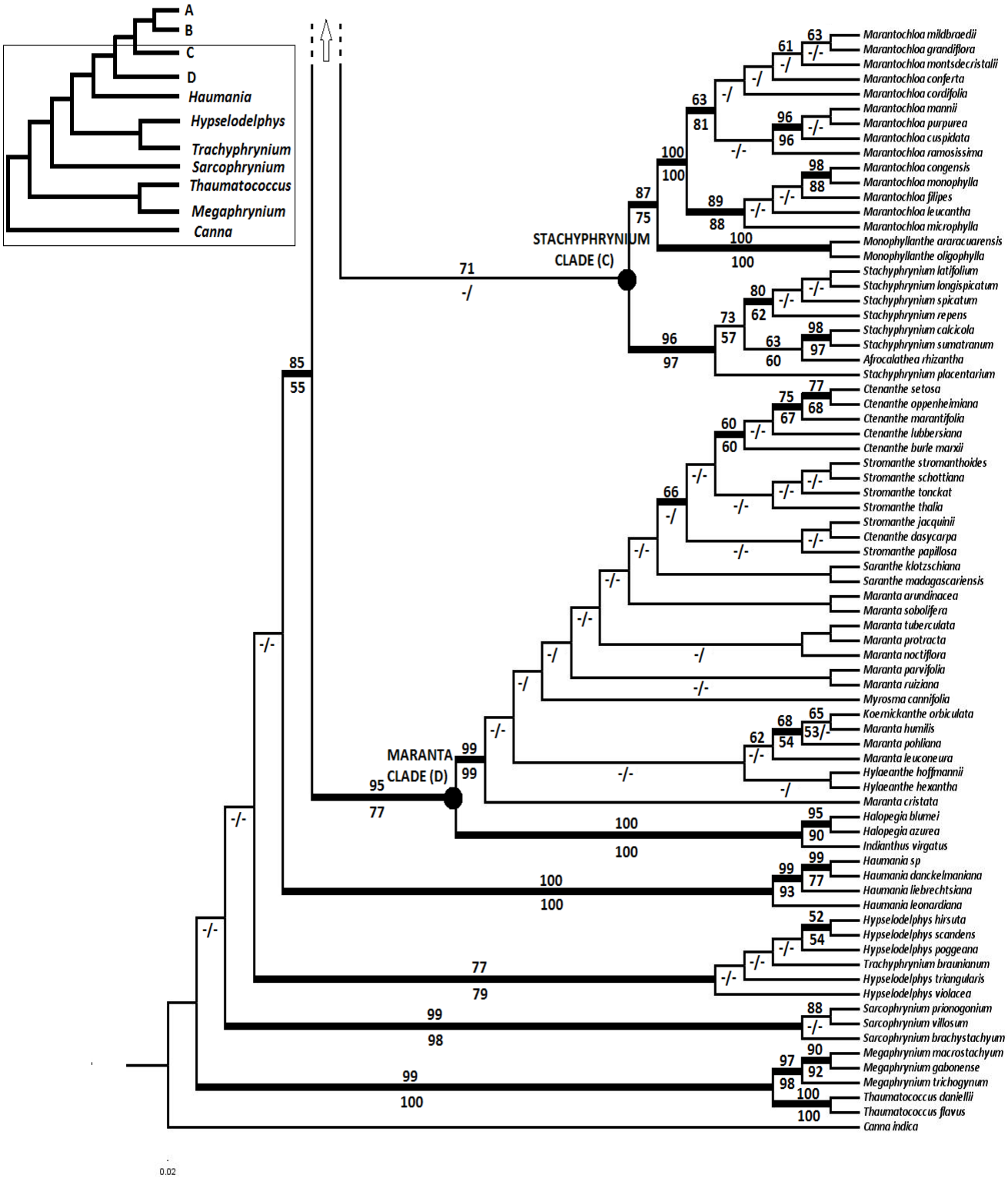
A
B
C
D
Haumania
Hypselodelphys
Trachyphrynium
Sarcophrynium
Thaumatococcus
Megaphrynium
Canna
STACHYPHRYNIUM CLADE (C)
MARANTA CLADE (D)
Marantochloa mildbraedii
Marantochloa grandiflora
Marantochloa montsdecristalii
Marantochloa conferta
Marantochloa cordifolia
Marantochloa mannii
Marantochloa purpurea
Marantochloa cuspidata
Marantochloa ramosissima
Marantochloa congensis
Marantochloa monophylla
Marantochloa filipes
Marantochloa leucantha
Marantochloa microphylla
Monophyllanthe araracuarensis
Monophyllanthe oligophylla
Stachyphrynium latifolium
Stachyphrynium longispicatum
Stachyphrynium spicatum
Stachyphrynium repens
Stachyphrynium calcicola
Stachyphrynium sumatranum
Afrocalathea rhizantha
Stachyphrynium placentarium
Ctenanthe setosa
Ctenanthe oppenheimiana
Ctenanthe marantifolia
Ctenanthe lubbersiana
Ctenanthe burle marxii
Stromanthe stromanthoides
Stromanthe schottiana
Stromanthe tonckat
Stromanthe thalia
Stromanthe jacquinii
Ctenanthe dasycarpa
Stromanthe papillosa
Saranthe klotzschiana
Saranthe madagascariensis
Maranta arundinacea
Maranta sobolifera
Maranta tuberculata
Maranta protracta
Maranta noctiflora
Maranta parvifolia
Maranta ruiziana
Myrosma cannifolia
Koernickanthe orbiculata
Maranta humilis
Maranta pohliana
Maranta leuconeura
Hylaeanthe hoffmannii
Hylaeanthe hexantha
Maranta cristata
Halopegia blumei
Halopegia azurea
Indianthus virgatus
Haumania sp
Haumania danckelmaniana
Haumania liebrechtsiana
Haumania leonardiana
Hypselodelphys hirsuta
Hypselodelphys scandens
Hypselodelphys poggeana
Trachyphrynium braunianum
Hypselodelphys triangularis
Hypselodelphys violacea
Sarcophrynium prionogonium
Sarcophrynium villosum
Sarcophrynium brachystachyum
Megaphrynium macrostachyum
Megaphrynium gabonense
Megaphrynium trichogynum
Thaumatococcus daniellii
Thaumatococcus flavus
Canna indica
0.02

Figure 2b

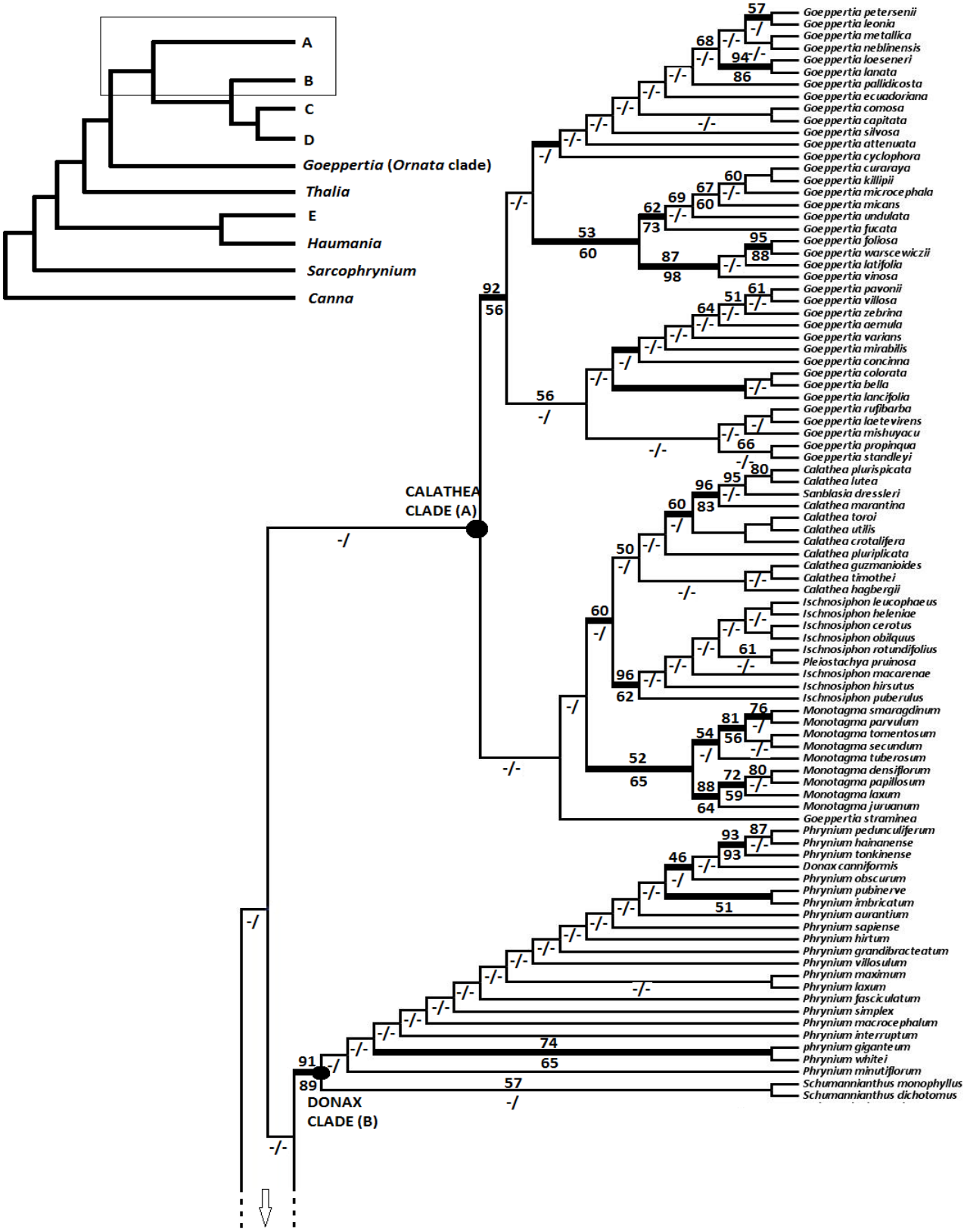
A
B
C
D
Goeppertia (Ornata clade)
Thalia
E
Haumania
Sarcophrynium
Canna
CALATHEA CLADE (A)
DONAX CLADE (B)
Goeppertia petersenii
Goeppertia leonia
Goeppertia metallica
Goeppertia neblinensis
Goeppertia loeseneri
Goeppertia lanata
Goeppertia pallidicosta
Goeppertia ecuadoriana
Goeppertia comosa
Goeppertia capitata
Goeppertia silvosa
Goeppertia attenuata
Goeppertia cyclophora
Goeppertia curaraya
Goeppertia killipii
Goeppertia microcephala
Goeppertia micans
Goeppertia undulata
Goeppertia fucata
Goeppertia foliosa
Goeppertia warscewiczii
Goeppertia latifolia
Goeppertia vinosa
Goeppertia pavonii
Goeppertia villosa
Goeppertia zebrina
Goeppertia aemula
Goeppertia varians
Goeppertia mirabilis
Goeppertia concinna
Goeppertia colorata
Goeppertia bella
Goeppertia lancifolia
Goeppertia rufibarba
Goeppertia laetevirens
Goeppertia mishuyacu
Goeppertia propinqua
Goeppertia standleyi
Calathea plurispicata
Calathea lutea
Sanblasia dressleri
Calathea marantina
Calathea toroi
Calathea utilis
Calathea crotalifera
Calathea pluriplicata
Calathea guzmanioides
Calathea timothei
Calathea hagbergii
Ischnosiphon leucophaeus
Ischnosiphon heleniae
Ischnosiphon cerotus
Ischnosiphon obilquus
Ischnosiphon rotundifolius
Pleiostachya pruinosa
Ischnosiphon macarenae
Ischnosiphon hirsutus
Ischnosiphon puberulus
Monotagma smaragdinum
Monotagma parvulum
Monotagma tomentosum
Monotagma secundum
Monotagma tuberosum
Monotagma densiflorum
Monotagma papillosum
Monotagma laxum
Monotagma juruanum
Goeppertia straminea
Phrynium pedunculiferum
Phrynium hainanense
Phrynium tonkinense
Donax canniformis
Phrynium obscurum
Phrynium pubinerve
Phrynium imbricatum
Phrynium aurantium
Phrynium sapiense
Phrynium hirtum
Phrynium grandibracteatum
Phrynium villosulum
Phrynium maximum
Phrynium laxum
Phrynium fasciculatum
Phrynium simplex
Phrynium macrocephalum
Phrynium interruptum
phrynium giganteum
Phrynium whitei
Phrynium minutiflorum
Schumannianthus monophyllus
Schumannianthus dichotomus

Figure 3a

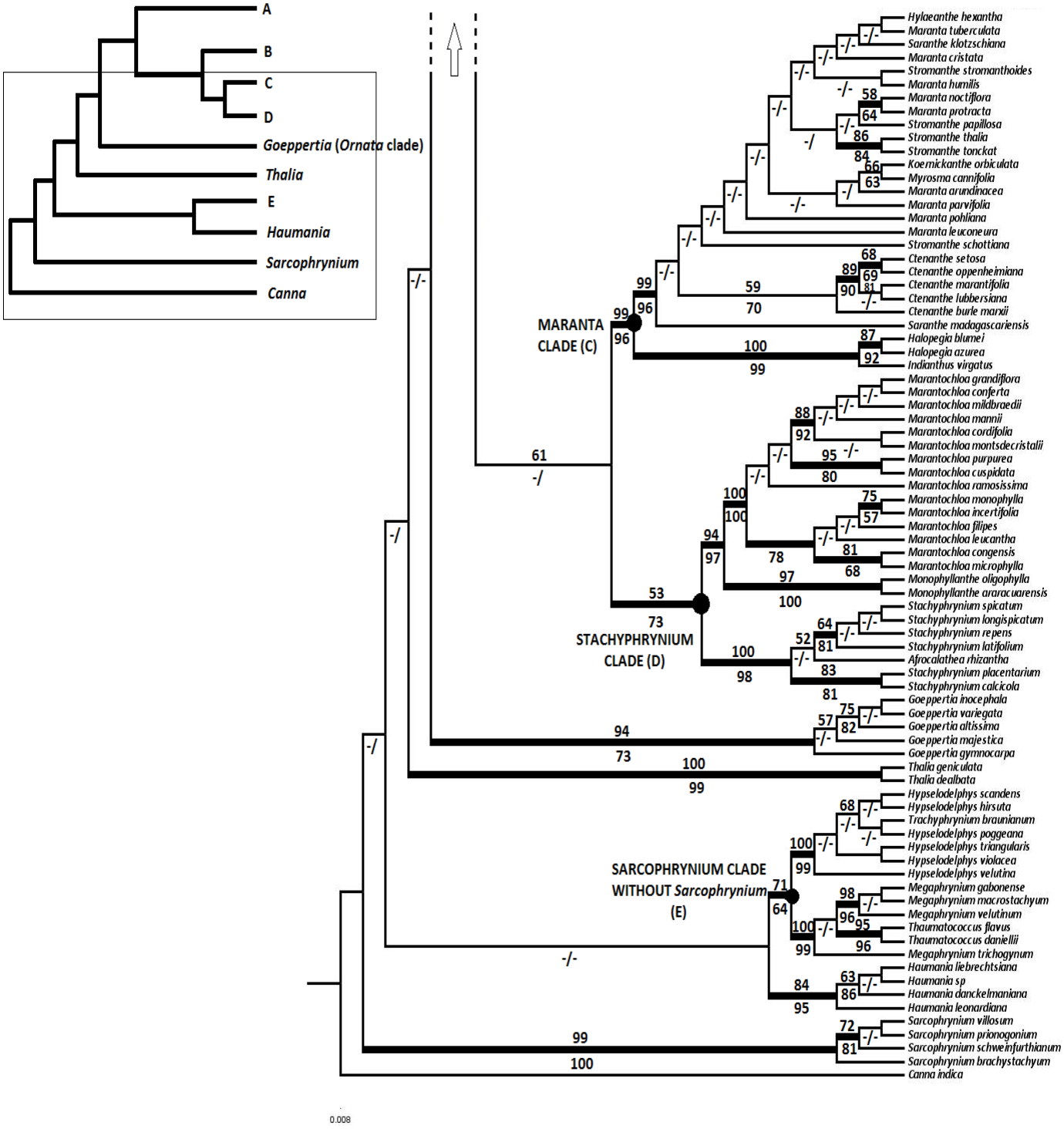
A
B
C
D
Goeppertia (Ornata clade)
Thalia
E
Haumania
Sarcophrynium
Canna
MARANTA CLADE (C)
STACHYPHRYNIUM CLADE (D)
SARCOPHRYNIUM CLADE WITHOUT Sarcophrynium (E)
Hylaeanthe hexantha
Maranta tuberculata
Saranthe klotzschiana
Maranta cristata
Stromanthe stromanthoides
Maranta humilis
Maranta noctiflora
Maranta protracta
Stromanthe papillosa
Stromanthe thalia
Stromanthe tonckat
Koernickanthe orbiculata
Myrosma cannifolia
Maranta arundinacea
Maranta parvifolia
Maranta pohliana
Maranta leuconeura
Stromanthe schottiana
Ctenanthe setosa
Ctenanthe oppenheimiana
Ctenanthe marantifolia
Ctenanthe lubbersiana
Ctenanthe burle marxii
Saranthe madagascariensis
Halopegia blumei
Halopegia azurea
Indianthus virgatus
Marantochloa grandiflora
Marantochloa conferta
Marantochloa mildbraedii
Marantochloa mannii
Marantochloa cordifolia
Marantochloa montsdecristalii
Marantochloa purpurea
Marantochloa cuspidata
Marantochloa ramosissima
Marantochloa monophylla
Marantochloa incertifolia
Marantochloa filipes
Marantochloa leucantha
Marantochloa congensis
Marantochloa microphylla
Monophyllanthe oligophylla
Monophyllanthe araracuarensis
Stachyphrynium spicatum
Stachyphrynium longispicatum
Stachyphrynium repens
Stachyphrynium latifolium
Afrocalathea rhizantha
Stachyphrynium placentarium
Stachyphrynium calcicola
Goeppertia inocephala
Goeppertia variegata
Goeppertia altissima
Goeppertia majestica
Goeppertia gymnocarpa
Thalia geniculata
Thalia dealbata
Hypselodelphys scandens
Hypselodelphys hirsuta
Trachyphrynium braunianum
Hypselodelphys poggeana
Hypselodelphys triangularis
Hypselodelphys violacea
Hypselodelphys velutina
Megaphrynium gabonense
Megaphrynium macrostachyum
Megaphrynium velutinum
Thaumatococcus flavus
Thaumatococcus daniellii
Megaphrynium trichogynum
Haumania liebrechtsiana
Haumania sp
Haumania danckelmaniana
Haumania leonardiana
Sarcophrynium villosum
Sarcophrynium prionogonium
Sarcophrynium schweinfurthianum
Sarcophrynium brachystachyum
Canna indica
0.008

Figure 3b


Goeppertia
Calathea
Sanblasia
Ischnosiphon
Pleiostachya
A
Monotagama
B
Monophyllanthe
Marantochloa
Haumania
Stachyphrynium
Afrocalathea
C
Canna
SARCOPHRYNIUM CLADE (A)
Goeppertia pavonii
Goeppertia villosa
Goeppertia zebrina
Goeppertia aemula
Goeppertia concinna
Goeppertia colorata
Goeppertia varians
Goeppertia rufibarba
Goeppertia laetevirens
Goeppertia mishuyacu
Goeppertia standleyi
Goeppertia propinqua
Goeppertia mirabilis
Goeppertia bella
Goeppertia warscewiczii
Goeppertia foliosa
Goeppertia latifolia
Goeppertia vinosa
Goeppertia lanata
Goeppertia neblinensis
Goeppertia loeseneri
Goeppertia veitchiana
Goeppertia metallica
Goeppertia leonia
Goeppertia petersenii
Goeppertia pallidicosta
Goeppertia ecuadoriana
Goeppertia silvosa
Goeppertia attenuata
Goeppertia capitata
Goeppertia comosa
Goeppertia cyclophora
Goeppertia micans
Goeppertia curaraya
Goeppertia fucata
Goeppertia microcephala
Goeppertia undulata
Goeppertia killipii
Goeppertia altissima
Goeppertia variegata
Goeppertia inocephala
Goeppertia majestica
Goeppertia gymnocarpa
Goeppertia straminea
Calathea plurispicata
Calathea marantina
Calathea lutea
Sanblasia dressleri
Calathea crotalifera
Calathea toroi
Calathea utilis
Calathea hagbergii
Calathea guzmanioides
Calathea pluriplicata
Calathea timothei
Ischnosiphon obilquus
Ischnosiphon hirsutus
Ischnosiphon rotundifolius
Ischnosiphon puberulus
Ischnosiphon macarenae
Ischnosiphon cerotus
Ischnosiphon leucophaeus
Pleiostachya pruinosa
Ischnosiphon heleniae
Megaphrynium trichogynum
Megaphrynium gabonense
Megaphrynium macrostachyum
Thaumatococcus daniellii
Sarcophrynium prionogonium
Sarcophrynium schweinfurthianum
Sarcophrynium brachystachyum
Hypselodelphys violacea
Hypselodelphys scandens
Hypselodelphys triangularis
Hypselodelphys velutina
Hypselodelphys hirsuta
Hypselodelphys poggeana
Trachyphrynium braunianum
Monotagma secundum
Monotagma tomentosum
Monotagma parvulum
Monotagma smaragdinum
Monotagma papillosum
Monotagma laxum
Monotagma juruanum
Monotagma tuberosum

Figure 4a

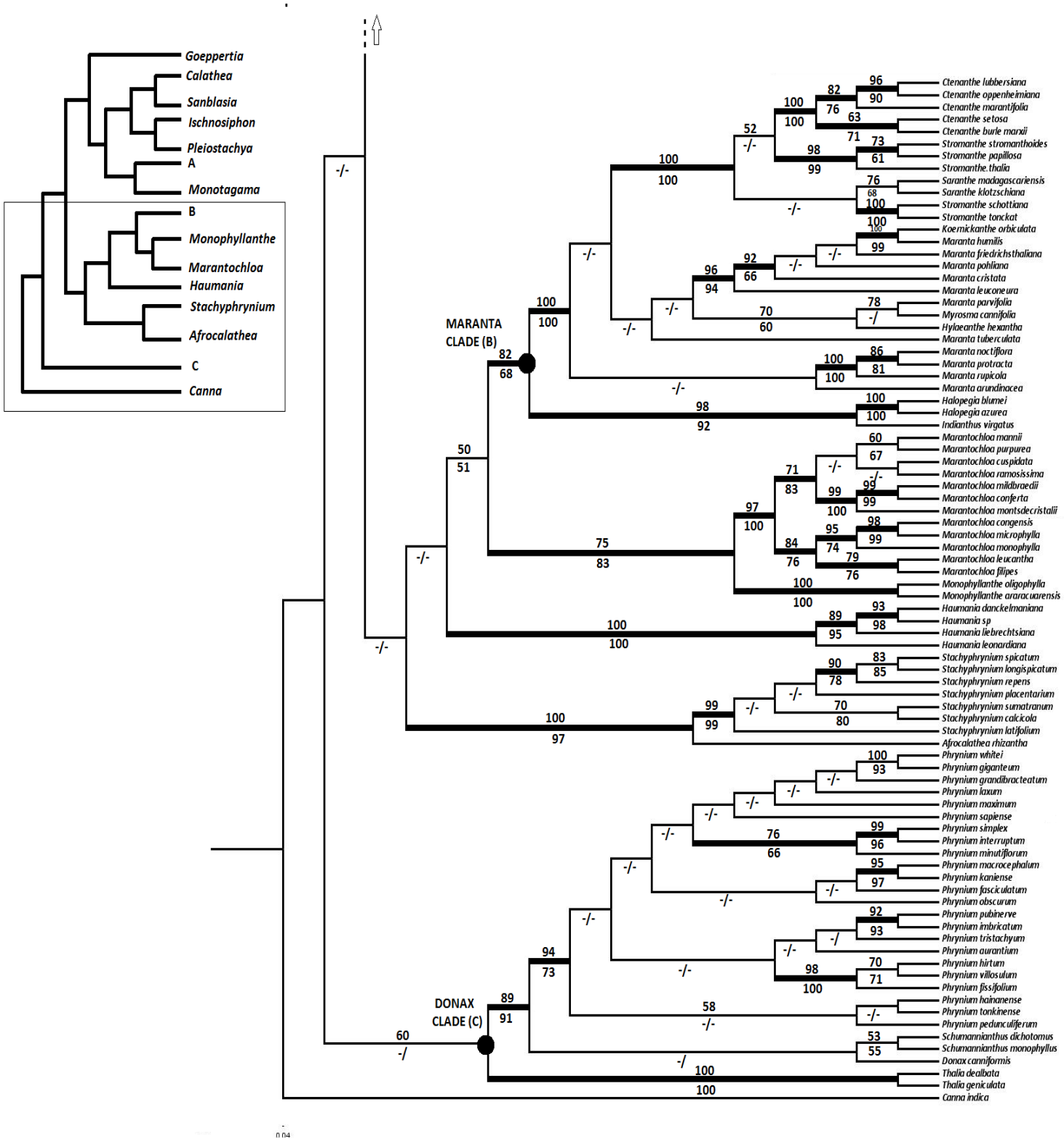
Goeppertia
Calathea
Sanblasia
Ischnosiphon
Pleiostachya
A
Monotagama
B
Monophyllanthe
Marantochloa
Haumania
Stachyphrynium
Afrocalathea
C
Canna
MARANTA CLADE (B)
DONAX CLADE (C)
Ctenanthe lubbersiana
Ctenanthe oppenheimiana
Ctenanthe marantifolia
Ctenanthe setosa
Ctenanthe burle marxii
Stromanthe stromanthoides
Stromanthe papillosa
Stromanthe thalia
Saranthe madagascariensis
Saranthe klotzschiana
Stromanthe schottiana
Stromanthe tonckat
Koernickanthe orbiculata
Maranta humilis
Maranta friedrichsthaliana
Maranta pohliana
Maranta cristata
Maranta leuconeura
Maranta parvifolia
Myrosma cannifolia
Hylaeanthe hexantha
Maranta tuberculata
Maranta noctiflora
Maranta protracta
Maranta rupicola
Maranta arundinacea
Halopegia blumei
Halopegia azurea
Indianthus virgatus
Marantochloa mannii
Marantochloa purpurea
Marantochloa cuspidata
Marantochloa ramosissima
Marantochloa mildbraedii
Marantochloa conferta
Marantochloa montsdecristalii
Marantochloa congensis
Marantochloa microphylla
Marantochloa monophylla
Marantochloa leucantha
Marantochloa filipes
Monophyllanthe oligophylla
Monophyllanthe araracuarensis
Haumania danckelmaniana
Haumania sp
Haumania liebrechtsiana
Haumania leonardiana
Stachyphrynium spicatum
Stachyphrynium longispicatum
Stachyphrynium repens
Stachyphrynium placentarium
Stachyphrynium sumatranum
Stachyphrynium calcicola
Stachyphrynium latifolium
Afrocalathea rhizantha
Phrynium whitei
Phrynium giganteum
Phrynium grandibracteatum
Phrynium laxum
Phrynium maximum
Phrynium sapiense
Phrynium simplex
Phrynium interruptum
Phrynium minutiflorum
Phrynium macrocephalum
Phrynium kaniense
Phrynium fasciculatum
Phrynium obscurum
Phrynium pubinerve
Phrynium imbricatum
Phrynium tristachyum
Phrynium aurantium
Phrynium hirtum
Phrynium villosulum
Phrynium fissifolium
Phrynium hainanense
Phrynium tonkinense
Phrynium pedunculiferum
Schumanniathus dichotomus
Schumanniathus monophyllus
Donax cannifformis
Thalia dealbata
Thalia geniculata
Canna indica

Figure 4b

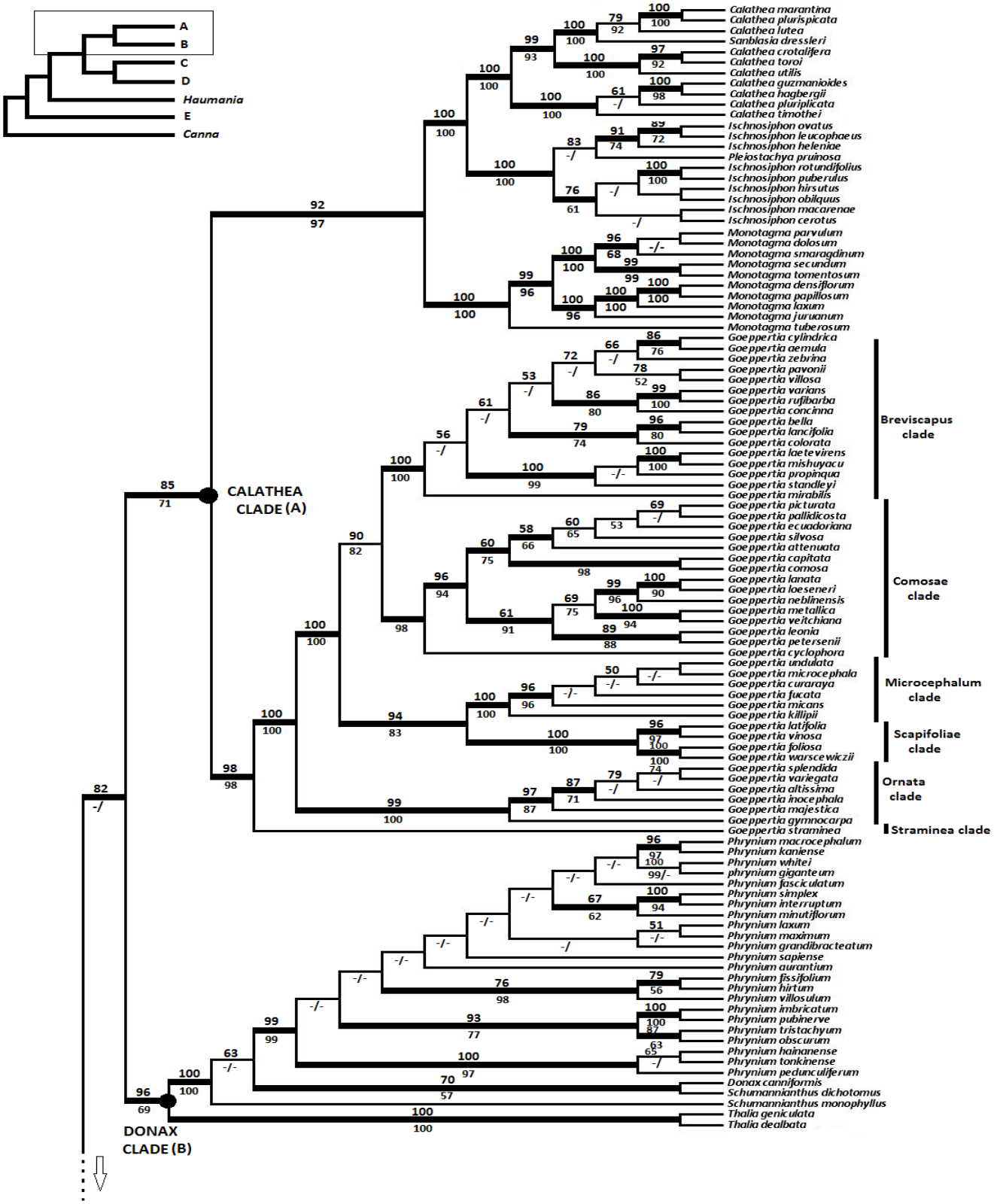
A
B
C
D
Haumania
E
Canna
CALATHEA CLADE (A)
DONAX CLADE (B)
Calathea marantina
Calathea plurispicata
Calathea lutea
Sanblasia dressleri
Calathea crotalifera
Calathea toroi
Calathea utilis
Calathea guzmanioides
Calathea hagbergii
Calathea pluriplicata
Calathea timothei
Ischnosiphon ovatus
Ischnosiphon leucophaeus
Ischnosiphon heleniae
Pleiostachya pruinosa
Ischnosiphon rotundifolius
Ischnosiphon puberulus
Ischnosiphon hirsutus
Ischnosiphon obilquus
Ischnosiphon macarenae
Ischnosiphon cerotus
Monotagma parvulum
Monotagma dolosum
Monotagma smaragdinum
Monotagma secundum
Monotagma tomentosum
Monotagma densiflorum
Monotagma papillosum
Monotagma laxum
Monotagma juruanum
Monotagma tuberosum
Goeppertia cylindrica
Goeppertia aemula
Goeppertia zebrina
Goeppertia pavonii
Goeppertia villosa
Goeppertia varians
Goeppertia rufibarba
Goeppertia concinna
Goeppertia bella
Goeppertia lancifolia
Goeppertia colorata
Goeppertia laetevirens
Goeppertia mishuyacu
Goeppertia propinqua
Goeppertia standleyi
Goeppertia mirabilis
Goeppertia picturata
Goeppertia pallidicosta
Goeppertia ecuadoriana
Goeppertia silvosa
Goeppertia attenuata
Goeppertia capitata
Goeppertia comosa
Goeppertia lanata
Goeppertia loeseneri
Goeppertia neblinensis
Goeppertia metallica
Goeppertia veitchiana
Goeppertia leonia
Goeppertia petersenii
Goeppertia cyclophora
Goeppertia undulata
Goeppertia microcephala
Goeppertia curaraya
Goeppertia fucata
Goeppertia micans
Goeppertia killipii
Goeppertia latifolia
Goeppertia vinosa
Goeppertia foliosa
Goeppertia warscewiczii
Goeppertia splendida
Goeppertia variegata
Goeppertia altissima
Goeppertia inocephala
Goeppertia majestica
Goeppertia gymnocarpa
Goeppertia straminea
Phrynium macrocephalum
Phrynium kaniense
Phrynium whitei
phrynium giganteum
Phrynium fasciculatum
Phrynium simplex
Phrynium interruptum
Phrynium minutiflorum
Phrynium laxum
Phrynium maximum
Phrynium grandibracteatum
Phrynium sapiense
Phrynium aurantium
Phrynium fissifolium
Phrynium hirtum
Phrynium villosulum
Phrynium imbricatum
Phrynium pubinerve
Phrynium tristachyum
Phrynium obscurum
Phrynium hainanense
Phrynium tonkinense
Phrynium pedunculiferum
Donax canniformis
Schumannianthus dichotomus
Schumannianthus monophyllus
Thalia geniculata
Thalia dealbata
Breviscapus clade
Comosae clade
Microcephalum clade
Scapifoliae clade
Ornata clade
Straminea clade

Figure 5a

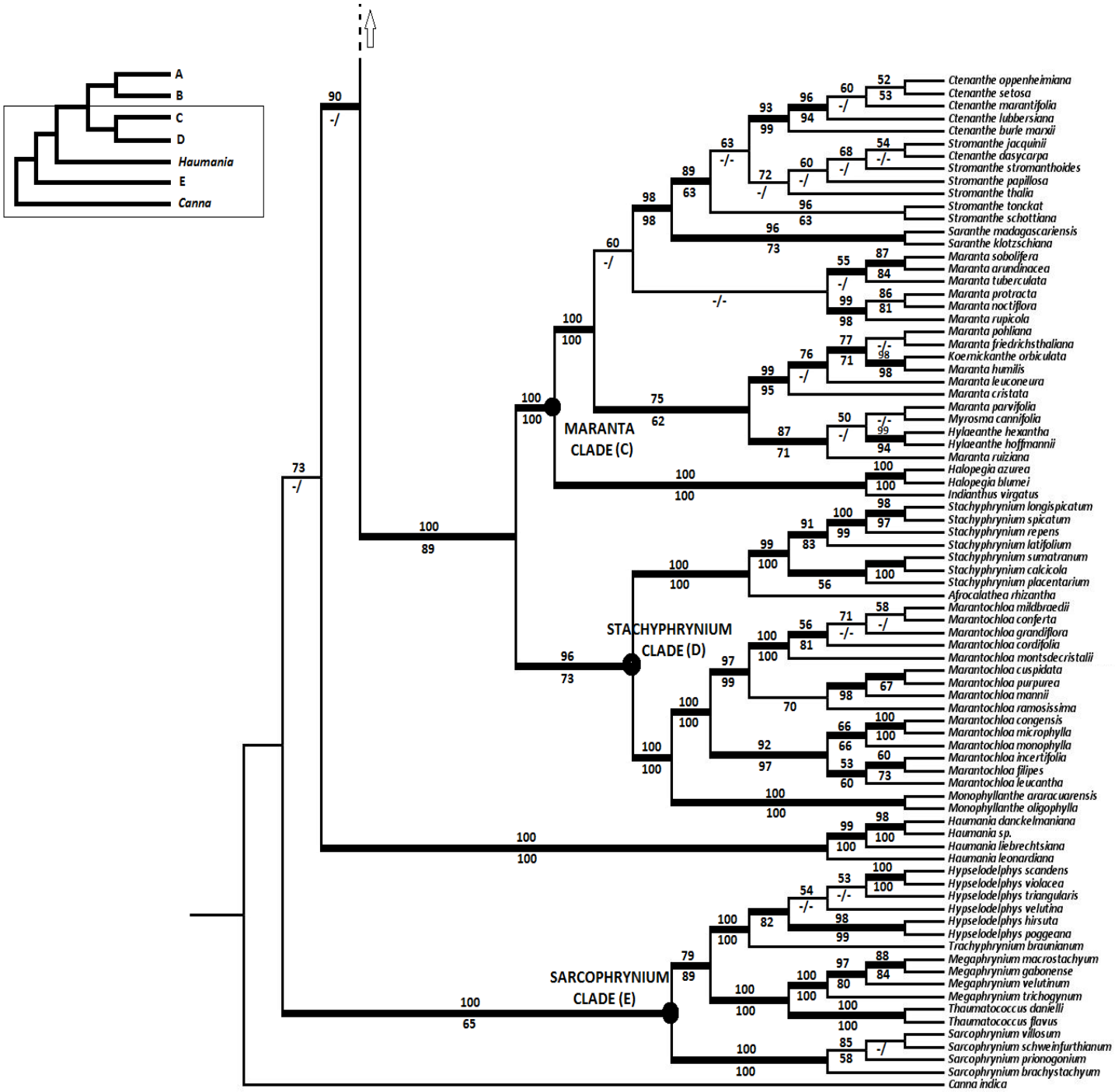
A
B
C
D
Haumania
E
Canna
MARANTA CLADE (C)
STACHYPHRYNIUM CLADE (D)
SARCOPHRYNIUM CLADE (E)
Ctenanthe oppenheimiana
Ctenanthe setosa
Ctenanthe marantifolia
Ctenanthe lubbersiana
Ctenanthe burle marxii
Stromanthe jacquinii
Ctenanthe dasycarpa
Stromanthe stromanthoides
Stromanthe papillosa
Stromanthe thalia
Stromanthe tonckat
Stromanthe schottiana
Saranthe madagascariensis
Saranthe klotzschiana
Maranta sobolifera
Maranta arundinacea
Maranta tuberculata
Maranta protracta
Maranta noctiflora
Maranta rupicola
Maranta pohliana
Maranta friedrichsthaliana
Koernickanthe orbiculata
Maranta humilis
Maranta leuconeura
Maranta cristata
Maranta parvifolia
Myrosma cannifolia
Hylaeanthe hexantha
Hylaeanthe hoffmannii
Maranta ruiziana
Halopegia azurea
Halopegia blumei
Indianthus virgatus
Stachyphrynium longispicatum
Stachyphrynium spicatum
Stachyphrynium repens
Stachyphrynium latifolium
Stachyphrynium sumatranum
Stachyphrynium calcicola
Stachyphrynium placentarium
Afrocalathea rhizantha
Marantochloa mildbraedii
Marantochloa conferta
Marantochloa grandiflora
Marantochloa cordifolia
Marantochloa montsdecristalii
Marantochloa cuspidata
Marantochloa purpurea
Marantochloa mannii
Marantochloa ramosissima
Marantochloa congensis
Marantochloa microphylla
Marantochloa monophylla
Marantochloa incertifolia
Marantochloa filipes
Marantochloa leucantha
Monophyllanthe araracuarensis
Monophyllanthe oligophylla
Haumania danckelmaniana
Haumania sp.
Haumania liebrechtsiana
Haumania leonardiana
Hypselodelphys scandens
Hypselodelphys violacea
Hypselodelphys triangularis
Hypselodelphys velutina
Hypselodelphys hirsuta
Hypselodelphys poggeana
Trachyphrynium braunianum
Megaphrynium macrostachyum
Megaphrynium gabonense
Megaphrynium velutinum
Megaphrynium trichogynum
Thaumatococcus daniellii
Thaumatococcus flavus
Sarcophrynium villosum
Sarcophrynium schweinfurthianum
Sarcophrynium prionogonium
Sarcophrynium brachystachyum
Canna indica

Figure 5b

Declaration of own contributions to the original article /Erklärung über den persönlichen Anteil an den Publikationen

Study (Chapter 2):

Al-Gharaibeh M, Hamasha H, Lachmuth S, & Hensen I (2016) Local adaptation to different phytogeographic regions: habitat-related variations in seed germination in response to temperature and salinity for two medicinal *Salvia* species from Jordan. ***Plant Species Biology***. doi: 10.1111/1442-1984.12123

Field work:	**Mohammad Al-Gharaibeh:** 100 %
Laboratory work:	**Mohammad Al-Gharaibeh:** 90 %
Analysis:	**Mohammad Al-Gharaibeh:** 50 % (Susanna Lachmuth 50 %)
Writing:	**Mohammad Al-Gharaibeh:** 80 % (Corrections by all co-authors)

Study (Chapter 3):

Al-Gharaibeh M, Hamasha H, Rosche C, Lachmuth S, Wesche K & Hensen I (in review) Environmental gradients shape the genetic structure of two medicinal *Salvia* species in Jordan. ***Plant Biology****.*

Field work:	**Mohammad Al-Gharaibeh:** 100 %
Laboratory work:	**Mohammad Al-Gharaibeh:** 90 %
Analysis:	**Mohammad Al-Gharaibeh:** 70 % (Susanna Lachmuth, Karsten Wasche and Christoph Rosche 30 %)
Writing:	**Mohammad Al-Gharaibeh:** 80 % (Corrections by all co-authors)

Study (Chapter 4):

Al-Gharaibeh M, Borchsenius F, McKechnie L, Sanmartin I, & Ley A (manuscript) Phylogeny of the pantropically distributed family Marantaceae.

Genebank sequences assembly:	**Mohammad Al-Gharaibeh:** 100 %
Laboratory work:	Alexandra Ley: 20 %, Co-authors: 80 %
Phylogenetic Analysis:	**Mohammad Al-Gharaibeh:** 100 %
Writing:	**Mohammad Al-Gharaibeh:** 80 % (Alexandra Ley 20%)

Declaration of self-contained work / Eigenständigkeitserklärung

Hiermit erkläre ich, dass diese Arbeit nicht bereits zu einem früheren Zeitpunkt der Naturwissenschaftlichen Fakultät I – Biowissenschaften der Martin-Luther-Universität Halle-Wittenberg oder einer anderen wissenschaftlichen Einrichtung zum Zweck der Promotion vorgelegt wurde. Darüber hinaus erkläre ich, dass ich die vorliegende Arbeit eigenständig und ohne fremde Hilfe verfasst sowie keine anderen als die im Text angegebenen Quellen und Hilfsmittel verwendet habe. Textstellen, welche aus verwendeten Werken wörtlich oder inhaltlich übernommen wurden, wurden von mir als solche kenntlich gemacht. Im Übrigen erkläre ich, dass ich mich bisher noch nie um einen Doktorgrad beworben habe.

Halle (Saale), den

Unterschrift: .....

(Mohammad Al-Gharaibeh)