

A taxonomic revision of the southern African endemic
genus *Gazania* (Asteraceae) based on morphometric,
genetic and phylogeographic data.

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Abstract

Gazania is a small genus of the subtribe Gorteriinae, tribe Arctoteae, that is endemic to southern Africa. The genus was last revised in 1959 by Roessler, who noted that delimitation of the species of *Gazania* can be “extraordinarily difficult”.

Morphometric data was collected to test the reality of the 16 species as delimited by Roessler, who based species boundaries on morphological characters. Only six taxa were found to be morphologically distinct, while the remaining samples showed no species cohesion.

DNA sequence data from two nuclear spacer regions (ITS and ETS) and four chloroplast noncoding regions (the *trnL* and *rpS16* introns, and the *psbA-trnH* and *trnL-F* spacers) of 43 samples were utilised to create a species level phylogeny and to investigate correlations between genetically delimited units and morphologically defined taxa. DNA sequence data reveal that seven species (as delimited by Roessler) are morphologically and genetically distinct. The remaining nine of Roessler’s species fall into a morphologically and genetically overlapping continuum that forms an ochlopecies.

Phylogeographic methods (based on an expanded ITS and ETS DNA sequence data set from 169 samples) were employed to further resolve the limits of species, with special focus on the clades within the ochlopecies. These genetically defined clades were correlated with their geographical distributions, and in combination with molecular dating techniques, used to elucidate the recent climatic or environmental factors that may have shaped the phylogeographic structure of the genus.

Phylogeographic patterns and molecular dating reveals that the genus *Gazania* is an example of a South African endemic clade that has undergone episodic cladogenesis in response to fluctuating climatic conditions over the last seven million years. The ochlopecies within *Gazania* is a result of repeated cycles of climate driven isolation in refugia and subsequent expansion and hybridization events during the Pliocene and Pleistocene. Comparisons with phylogeographic studies on other organisms reveal a common pattern indicative of the presence and evolutionary importance of an ancestral refugium in the arid Richtersveld / Namib region of southern Africa.

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Contents

Abstract

Acknowledgements

Chapter 1: General introduction1

Aims7

Chapter 2: Morphometric species delimitations

Introduction8

 Morphometrics9

 Sources and types of character data10

 Character selection13

 Analyses methods13

 Cluster Analysis14

 Principle Component Analysis14

Methods15

 Morphological character selection and data collection15

 Discarded characters24

 Analysis of herbarium versus live specimens25

 Data sets26

 Data analysis26

 Normalization of data26

 Cluster Analysis27

 Principle Component Analysis27

Results28

 Test of normality28

 Cluster Analysis28

 Principle Component Analysis41

 Eigen values49

 Uninformative characters49

Discussion57

 Non-distinct taxa58

 Comparative data signal between ratios and size data59

 Comparative analysis methods for morphometric analysis59

 Conclusion59

Chapter 3: Molecular systematics of *Gazania* at the species level

Introduction61

 DNA sequence data as a tool for reviewing existing taxonomy62

 The nuclear genome: Multicopy nuclear markers (ITS and ETS)63

 The chloroplast genome65

Methods68

 Study samples68

 PCR amplification and sequencing68

 Primer development for ITS and ETS amplification and sequencing69

 Sequence checking and alignment73

 Treatment of gaps74

 Testing for incongruence74

Phylogenetic analyses	76
Parsimony analysis	76
Bayesian analysis	77
Results and Discussion	78
Choice of data sets	78
Combining data sets	78
Testing for incongruence	79
Final data set composition, variability and informativeness	80
Analyses results: nrDNA data set	80
Parsimony analysis	80
Bayesian analysis	83
Correspondence between molecular phylogeny and taxonomy	83
Analyses results: cpDNA data set	85
Parsimony analysis	85
Bayesian analysis	85
Correspondence between molecular phylogeny and taxonomy	85
Composite total evidence phylogeny	88
Gaps in relation to species phylogeny	88
Polytomies	89
Gene trees vs species trees	93
Polyploidy	94
Caveats	94
Conclusion	95

Chapter 4: Phylogeography of *Gazania*

Introduction	96
Sources of genetic data	97
Application of phylogeographic methods to <i>Gazania</i>	98
Methods	99
Sampling	99
Neighbor-Joining	99
Neighbor-Net analysis	99
Distribution maps	100
Morphometric comparison	100
Results and Discussion	107
Genetically discrete species	107
Neighbor-Joining analysis	107
Bayesian analysis	107
K-R clade	112
Neighbor Joining analysis	112
Bayesian analysis	127
Neighbor-Net analysis	135
Morphometric comparison	137
Caveats	144
Conclusions	144

Chapter 5: Recent evolutionary history of *Gazania*

Introduction	146
Geography and climate as driving factors in speciation	146
Population growth history	146

Methods	148
Geographical mapping	148
Divergence time estimation	148
Pairwise sequence divergences	149
Results and Discussion	150
Maps of genetically cohesive species	150
K-R clade	155
Divergence date estimates	158
The effects of Pleistocene climate change	163
Population history	165
Congruent patterns in SA fauna/flora	167
East-West split	167
North-South split	170
Caveats	172
Conclusions	173
Chapter 6: General conclusions	
Recent evolutionary history	178
Caveats	179
Morphological characters and species phylogeny	179
Valid taxonomic entities with genetic and morphological distinction	181
Problematic “species” lacking genetic and morphological distinction	181
Morphological key to taxonomic entities within <i>Gazania</i>	184
References	186
Appendix 1: Morphological characters for each of Roessler's species	200
Appendix 2: Morphometric data set for Chapter 2.	209
Appendix 3: Details of cpDNA primer screening for Chapter 3.	223
Appendix 4: nrDNA sequence data for Chapter 3.	225
Appendix 5: cpDNA sequence data for Chapter 3.	239
Appendix 6: Additional nrDNA sequence data for Chapter 4.	261

Chapter 1.

General introduction

“The existing treatment for *Gazania* can only be a preliminary revision, and can make no claims to finality.” (Roessler, 1959, pp 100, translated from the original German).

Gazania Gaert. is a small genus of 16 species endemic to Southern Africa. The genus was named in honour of Theodorus Gaza, a 15th-century Italian scholar and translator of the works of Theophrastus, a man often called the “father of taxonomy” due to his works “On the History of Plants” and “On the Causes of Plants” which are considered by some to constitute the most important contributions to botanical science during antiquity and the middle ages.

The genus was last revised in 1959 by Helmut Roessler, although not with any overwhelming certainty, as the opening quote illustrates. The most commonly listed number of species for *Gazania* is 17, but Roessler indicated that the 17th species (*G. thermalis*) is *nomen subnudum*, and disregarded it as a valid species. No subsequent authors have lobbied for a revalidation of this species or offered a species description or type specimen. Roessler based his taxonomy on morphological characters from herbarium specimens, in conjunction with geographical distribution of these samples, and from this he outlined 16 species and ten subspecies.

The delimitation of both the genus *Gazania* itself and the species within it have long been and continue to be problematic. Many of the species in *Gazania*, and in the associated genera of the Gorteriinae (see below for details), have been moved from genus to genus, and many of them have multiple instances of synonymy. The species as accepted by Roessler are laid out in Table 1.1.

Gazania is a member of the tribe Arctoteae, subtribe Gorteriinae. The Gorteriinae also includes seven other genera: *Berkheya*, *Gorteria*, *Cuspida*, *Didelta*, *Heterorachis*, *Cullumia* and *Hirpicium*. Whilst Roessler noted that it is difficult to differentiate between “primitive” and “advanced” characters within a highly advanced family like the Asteraceae, he still used certain morphological features to rank the eight genera of the Gorteriinae from primitive to advanced. A graphical representation of the genera within the Gorteriinae based on Roessler’s description of their relationships, ranked according to their morphological criteria, is presented in Figure 1.1.

Table 1.1: Gazania species and subspecies as accepted by Roessler

Species	Subspecies
<i>G. maritima</i> Levyn	
<i>G. rigens</i> L.	<i>uniflora</i> (L.f) Roessler
	<i>rigens</i>
	<i>leucolaena</i> (DC.) Roessler
<i>G. pectinata</i> (Thunb.) Spreng	
<i>G. linearis</i> (Thunb.) Druce	<i>linearis</i>
	<i>ovalis</i> (Harv.) Roessler
<i>G. ciliaris</i> DC.	
<i>G. caespitosa</i> Bolus	
<i>G. heterochaeta</i> DC.	
<i>G. schenckii</i> O.Hoffm.	
<i>G. leiopoda</i> (DC.) Roessler	
<i>G. othonnites</i> (Thunb.) Less.	
<i>G. jurineifolia</i> DC.	<i>jurineifolia</i>
	<i>scabra</i> (DC.) Roessler
<i>G. lichtensteinii</i> Less.	
<i>G. tenuifolia</i> Less.	
<i>G. rigida</i> (Burm.f.) Roessler	
<i>G. serrata</i> DC.	
<i>G. krebsiana</i> Less.	<i>krebsiana</i>
	<i>arctotoides</i> (Less.) Roessler
	<i>serrulata</i> (DC.) Roessler

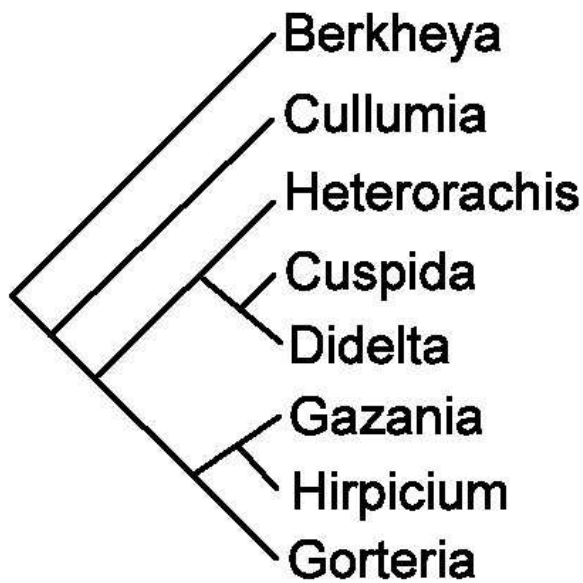


Figure 1.1: Graphical representation of the genera within the Gorteriinae based on Roessler's description of their relationships, ranked according to their morphological criteria.

He considered *Berkheya* as the most primitive genus, with *Cullumia* was ranked as the next most primitive. *Didelta*, *Cuspida* and *Heterorachis* were grouped together due to the uniformity of their achenes. He likewise groups *Gorteria*, *Hirpicium* and *Gazania* together. He considered *Gazania* as representing the endpoint of development, as the involucre shows the highest degree of fusion, in combination with the presence of “a remarkable capitulum with multicoloured petals, with basal eyespots at the base of the ray florets” (Roessler, 1959: p. 101).

While morphological data suggest that *Gazania* and *Hirpicium* are closely related genera (Roessler, 1959), genetic data suggests that *Gazania* is nested within *Hirpicium* (see Figure 1.2, Funk *et al.*, 2004). More recent molecular work by McKenzie on the placement of *Gazania* within the Gorteriinae shows the same result (Figure 1.3, McKenzie, unpublished data). The review by Karis (2006) of the genera of Gorteriinae, based on morphological characters, placed *Gazania* as sister to *Gorteria* and *Hirpicium*, rather than nestled within the latter genus (Figure 1.4).

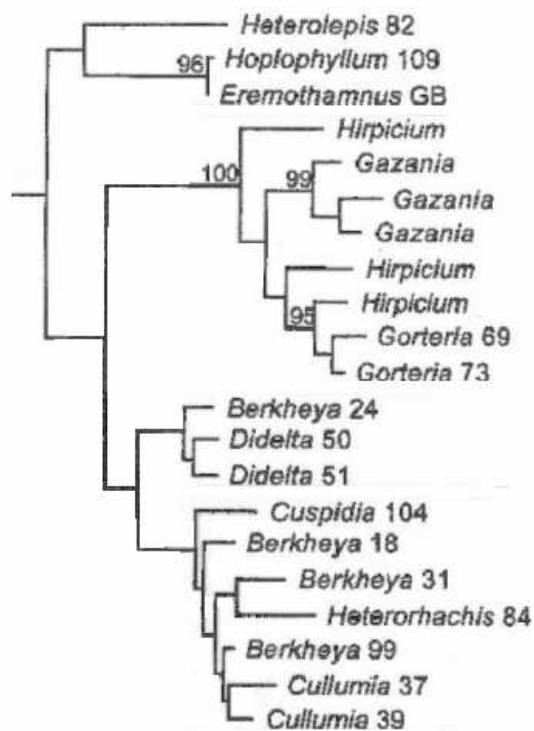


Figure 1.2: Relationships of the genera of the Gorteriinae (from Funk *et al.*, 2004.)

Roessler (1959) described *Gazania* as having two main habits. The presence of a shortened stem, with the leaves crowded into dense rosettes at the base, out of which a leafless unbranched stem arises to bear solitary inflorescences is found in 11 species (see Appendix 1); the other habit (shown by five species, see Appendix 1) is a developed stem, with leaves present more or less evenly along the stem. Roessler commented that the rosette habit was a characteristic of *Gazania* (but also observed in a few *Hirpicium* species) and the developed stem habit was a characteristic of *Hirpicium* (but also observed in a few *Gazania* species).

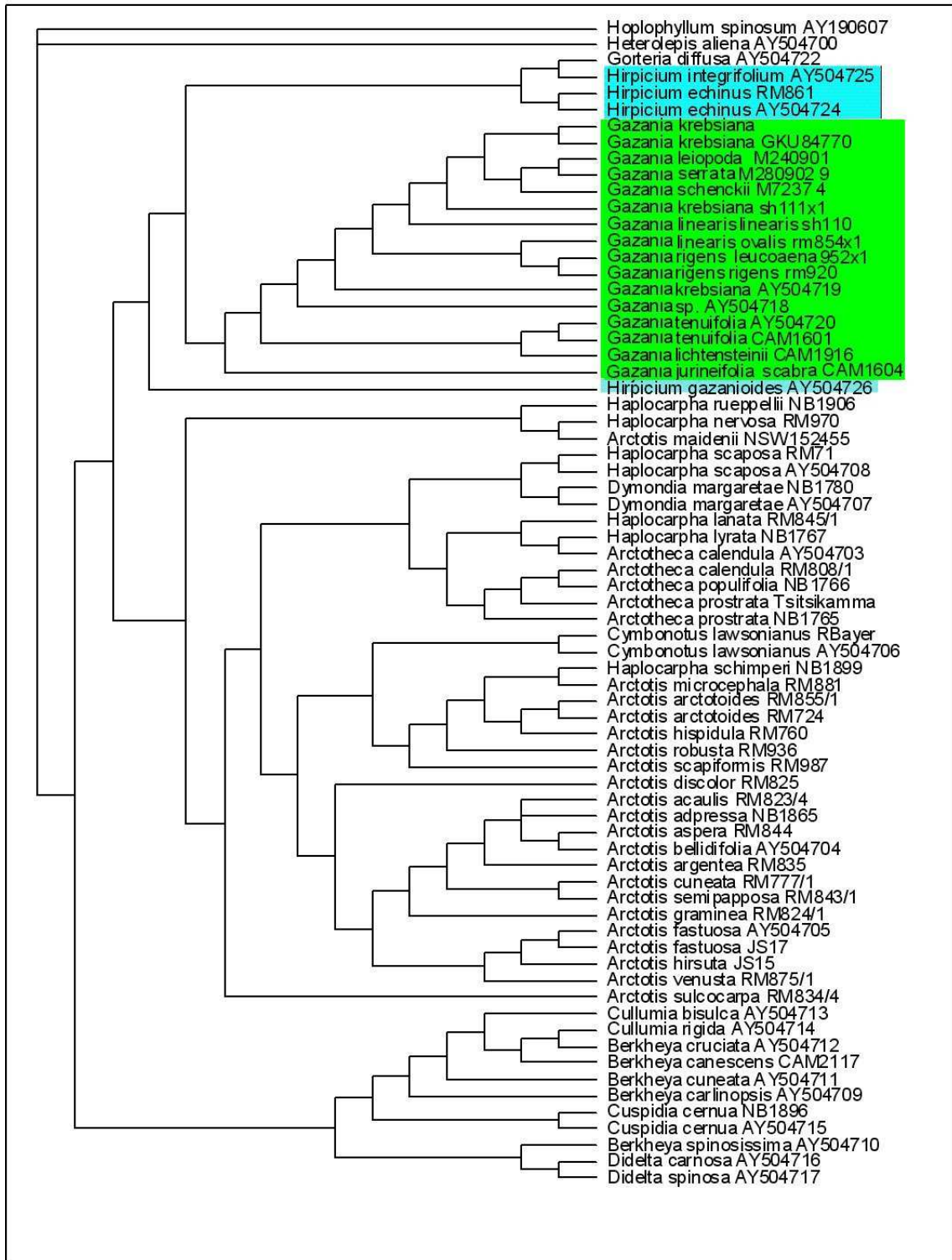


Figure 1.3: Relationships of the genera of the Gorteriinae, based on ITS data from McKenzie, unpublished.

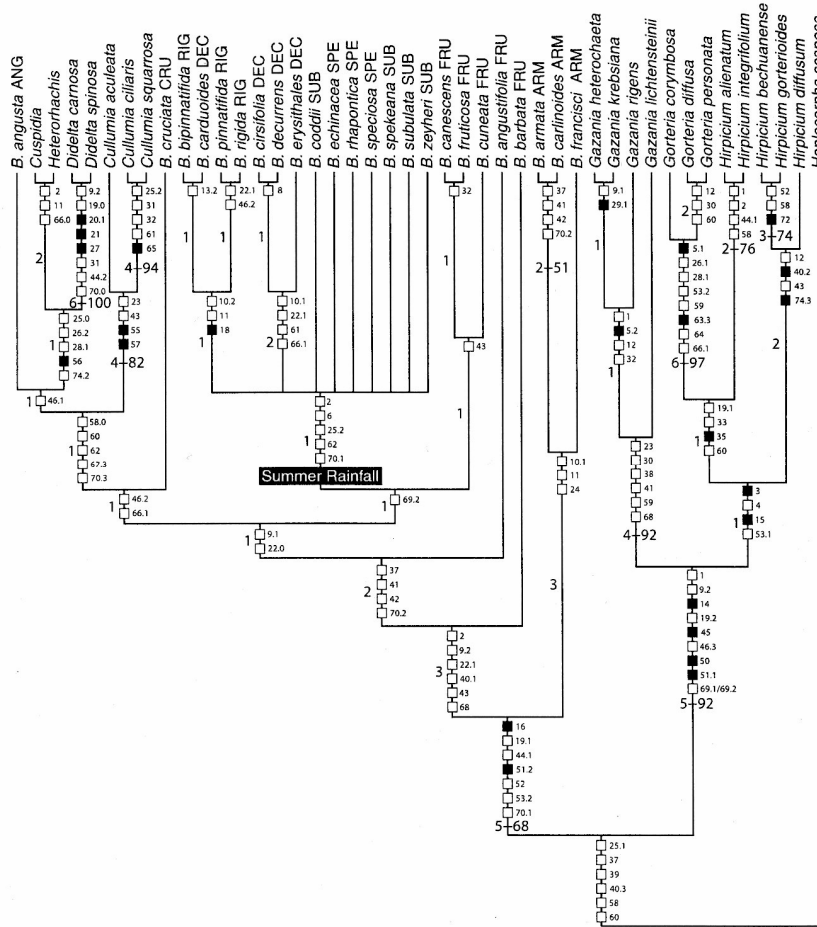


Figure 1.4: Relationships of the genera of the Gorteriinae, based on morphological data (from Karis, 2006, Figure 4).

He separated *Hirpicium* and *Gazania* on the basis of two characters: pappus scales and involucre fusion. The number of rows of pappus scales differentiates the two genera, as *Gazania* has two rows of fully developed pappus scales, while *Hirpicium* has either one row, or one row of full developed scales with a second inner row of smaller scales. He noted that within the genus *Hirpicium* it could be assumed that the species without internal rows of pappus scales are derived in relation to the species with two rows, which is suggested by the occurrence of transition rows that should “certainly be considered as degenerated rows” (Roessler, 1959: p. 101).

Gazania has generalist pollinators (pers. obsv.) and wind dispersed seeds (pers. obsv.). It frequently colonizes disturbed areas, and grows well in poor soils. It has a short period between germination and seedset (under a year).

Aims of this research

All studies to date, be they molecular or morphological, have indicated that *Gazania* is monophyletic. However, within *Gazania*, species delimitations and relationships are not at all clear. Roessler recognised and delimited 16 species in *Gazania*, based on morphology. Some of these species are clearly morphologically and geographically distinct, but some species show overlaps in both morphology and geography. The overall aim of this research is to investigate Roessler's "preliminary revision" (Roessler, 1959) by means of three different approaches to the problem.

- 1) To use a morphometric data set of *Gazania* samples to test the validity of Roessler's species delimitations.**

- 2) To use DNA sequence data to determine the status and relationships of the taxonomic entities ("species") as delimited by Roessler and the morphometric analysis conducted in Chapter 2.**

- 3) To undertake a phylogeographic study of the genetic entities within *Gazania*.**

Chapter 2.

Morphometric species delimitations

“The abundance of forms regarding systematically rather unimportant (but obvious) characters ... with simultaneous uniformity of the habit and the poverty of useful characteristics for type distinction make the development and delimitation of the types extraordinarily difficult.”
(Roessler, 1959, pp 100, translated from the original German).

Aim: To use a morphometric data set of *Gazania* samples to test the validity of Roessler’s species delimitations.

Introduction

Morphological data is the major basis of most systematic descriptions and delimitations, and morphological variation in size and shape has physiological, ecological and taxonomic significance (Somers, 1989). Jensen (2003) observes that the majority of systematic studies begin by grouping organisms on the basis of morphological similarity and, once they are so grouped, then the study of relationships among the groups can begin, often by careful examination of variation in morphological features, but increasingly more often by using these morphologically defined groups as the basis for conducting studies of molecular variation.

The advent of modern computing (and the associated increase in the volume of data that can be analyzed) has afforded systematists the chance to statistically test the observed trends in plant morphological variability. Additionally, the availability of high speed electronic computers permits calculations (and statistical methodologies) that previously would have been far too time-consuming to be practical (Mayr, 1965).

Gazania has a two-fold problem, in that the genus possesses a low number of taxonomically informative characters (Roessler, 1959), and that those characters that are potentially useful display a high level of variability within, but not necessarily between, taxonomic entities. A further complication is the observed presence of some phenotypic plasticity in certain characteristics in response to changes in environmental conditions (discussed individually in more detail in the justification for choice of characters in the Methods section). Abdel Khalik *et al.* (2002) note that problems in classification can arise when taxa display a large amount of variability, due to

phenotypic plasticity, or when they demonstrate very little variability at all. Further problems occur if the variability that is present lacks any correlation with taxonomic designation.

Morphometrics

There are alternative approaches to the morphometric (phenetic) approach employed here. One such alternative is cladistics, which relies on synapomorphies to define clades. Morphometric data that is continuous in nature creates difficulties in defining binary "present/absent" data necessary to define synapomorphies. There are very few binary characters that could be used to investigate *Gazania*, as most defining characteristics for taxa rely on quantitative measurements of size, rather than presence/absence data. While some may also argue that morphometrics does not allow for the translation of results into meaningful phylogenetic hypotheses (Crowe, 1994), that is not required for this particular investigation. This morphometric study is aimed only at searching for morphological clusters that may or may not correlate with recognized species delimitations.

Even a brief survey of the morphometric literature reveals a large amount of, often heated, debate (see Atchley & Anderson, 1978, for a particularly strident rebuttal to criticism). The debate in the literature covers subjects ranging from the very initial stages of character selection and the measurement of those characters, to the final stages of data analysis (the discussions of the finer details of the methods of morphometric analysis could be most charitably described as contentious).

Morphometrics is defined by Rohlf (1990) as the quantitative description, analyses, and interpretation of shape and shape variation in biology. Bookstein (1982) provides a narrower definition of morphometrics as the assignment of quantities to biological shapes.

The approach now referred to as traditional morphometrics (or multivariate morphometrics) is characterized by the application of multivariate statistical methods to sets of variables (Rohlf & Marcus, 1993). The selected variables usually correspond to various measured distances on an organism; commonly lengths and widths of structures and distances between certain landmarks, as well as angles and ratios (Rohlf & Marcus, 1993). One can then apply cluster-finding procedures to the statistics resulting from the multivariate statistical analysis of data (Oxnard, 1978).

The combined application of various multivariate statistical and clustering methods to morphometric data has been used extensively to tackle both new and old biological problems (Oxnard, 1978). The use of multivariate statistical methods stem from the fact that two (or more) variables taken singly

may not separate two groups, but when taken together they may indeed separate the groups (Oxnard, 1978). Multivariate techniques summarize these patterns of morphometric covariation (Somers, 1986) and this provides statistical methods for study of the joint relationships of variables in data that contain intercorrelations (James & McCulloch, 1990). Because several variables can be considered simultaneously, interpretations can be made that are not possible with univariate statistics (James & McCulloch, 1990).

Sources and types of character data

Various measurements can be taken in the pursuit of morphometric data sets. There are two main types of data: quantitative and qualitative. A qualitative character consists of either binary presence or absence of a particular morphological structure/trait (e.g. leaf setae: present or absent), or discrete forms of a character (e.g. leaf shape could be whole, pinnate or lobed). There are two types of quantitative characters: continuous (e.g. leaf length; in which individual measurements are not necessarily integers and potentially form a continuum) or discrete (e.g. ray number, in which any individual measurement is an integer) (Stevens, 1991). Some authors, however, consider the two main types of data to be interchangeable, noting that continuous quantitative characters can be coded and treated as discrete qualitative characters by the delimitation of intervals (e.g. $0 = <5\text{mm}$, $1 = >5\text{mm}$), and that most qualitative variation, when examined carefully, will be found to describe an underlying continuum that has been transformed into discrete classes (Stevens, 1991).

Biological shapes have been characterized most often by means of a single measure or other descriptor, or by a very small number of measurements (Oxnard, 1978). A scheme of measured distances is inadequate if it does not permit the reconstruction of the polygon it purports to measure, since information is thereby lost (Bookstein, 1982). The more complicated the shape, the greater the number of measurements necessary to encapsulate the information contained in that shape (Oxnard, 1978).

One can measure the more basic shapes by means of ratios. Figure 2.1.1 illustrates this process with a simple length/width ratio of triangular involucral scales. Both involucral scales are 1 unit of length wide, but A is 6 units long, while B is 1 unit long. The longer scale (A) will have a ratio of “6 units / 1 unit” (i.e. 6), whilst the shorter scale (B) will have a ratio of “1 unit / 1 unit” (1). The lower the ratio, the more obtuse the scale.

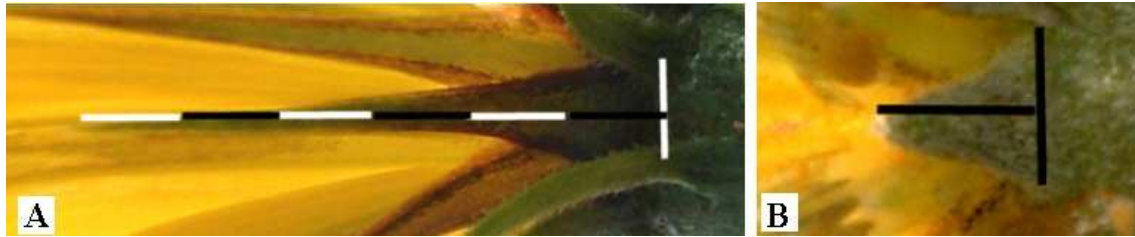


Figure 2.1.1: Comparison of differently shaped involucral scales, overlaid with length units in black and white. All black and white bars are equal in length.

The age of a physical characteristic (e.g. the age of a leaf) can have an effect on the size of the leaf (the older a leaf, the bigger it may be), but not necessarily the shape. Ratios can be useful for comparing shape across size gradients, without letting raw size skew the analysis. Figure 2.1.2 illustrates an example: If length were used as a grouping character, the leaves would group by age rather than species. The use of ratios to encapsulate basic shape (length/width) allows for differentiation based on shape rather than simply length.

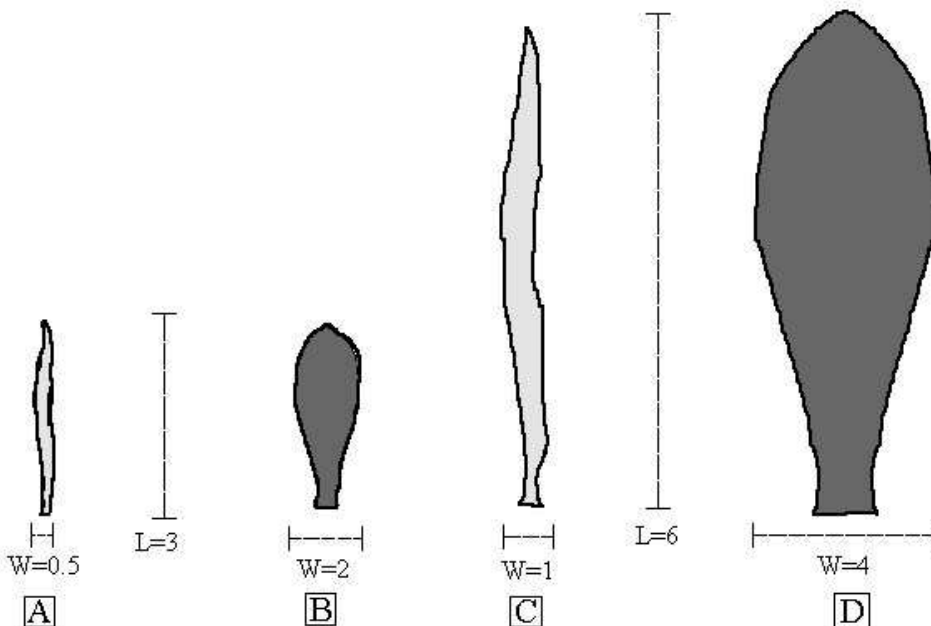


Figure 2.1.2: Use of ratios eliminates size but retains shape. Comparison of four leaves from two species (Species 1 = A,C; Species 2 = B,D). Two leaves are young (A,B) and two old (C,D). The lengths of the younger leaves are the same ($L=3$), as are the lengths of the older leaves ($L=6$), but the ratios are different (Species 1: $A = 3/0.5 = 6$, $C = 6/1 = 6$; Species 2: $B = 3/2 = 1.5$, $D = 6/4 = 1.5$)

Phillips (1983) notes that measurements taken with the use of ratios may be affected by allometric growth. But he notes that this usually only applies in the earliest stages of growth, and by the time the organ is large enough to be measured, allometric growth has stabilized. Phillips (1983) holds that while ratios are inherently correlated with size, there is still a large amount of information about shape within that ratio. As an alternative to ratios, he posits the use of regression analysis. However, this method is computationally intensive. The other problem with regression analysis is the requirement of at least two samples per taxon, to allow for the regression line to be calculated. For some taxa in *Gazania*, this was not possible. Given that there is only an average of 10 samples per taxon, this may not be sufficient to utilize regression analysis properly.

The other alternative to ratios is the use of shape charts. These charts, however, are an attempt to put names to discrete intervals of shapes, whereas in *Gazania* there are no such clear intervals. The shapes of leaves fall along a continuum of variation; categorization of certain leaves into definite shape categories must become subjective when they straddle the uncomfortable interval between two shapes. Actual measurements of ratios allow for the quantification of this continuum of shape variation, rather than the pigeon-holing of samples into the nearest possible fit of shape.

Some analytical methods are sensitive to size effects, and some authors insist that ratios can be a good way to deal with size, and have been useful for some studies (Oxnard, 1978), whilst others indicate that the traditional use of ratios is often criticized (Rohlf, 1990) and that the use of ratios does not always eliminate size from the raw variables (Albrecht, 1978; Phillips, 1983). Hillis (1978) firmly states that “of the many myths about the use of the ratio of two linear measurements perhaps the most widespread is that such ratios are improper in some statistical sense”. He continues by noting that ratios are widely used in taxonomy as measure of shape, and that the statistical difficulties associated with ratios arise because X/Y is not a linear function of X and Y ; the difficulties disappear if one transforms ratios using logs (Hillis, 1978). James & McCulloch (1990) agree, stating that ratios must be log transformed.

The inclusion of both ratios and the original measurements that the ratios were calculated could be theorized to lead to double weighting for those characters. Castro *et al.* (2005) however included both size data as well as shape ratios in their data to no ill effect.

Character selection

The major task in selecting characters is to construct measures optimal for particular explanatory purposes (trends, contrasts, comparisons) (Bookstein, 1982). Some authors maintain that as many characters as possible should be used (Presch, 1979), while others insist that the goal in the selection of variable characters is to reduce the volume of data as much as possible, while still retaining the ability to adequately represent the variability (Rohlf, 1990). Scotland *et al.* (2003) support the latter reductionist view, indicating that rigorous and critical anatomical studies of fewer morphological characters is preferable to compiling larger data matrices of increasingly ambiguous and problematic morphological characters.

Combinations of genetic and environmental factors modify growth processes, inducing morphometric variation (Somers, 1986). Good characters are those that are not susceptible to environmental modification, as phenotypic plasticity diminishes a character's taxonomic utility because the environmental contribution to phenotypic variation can obscure genetically based relationships (Davis, 1983). An example of the effects of environment on plant morphology was detected in the analysis of repeat sampling of the same populations of *Lupinus nanus* over several years, which revealed variation due to annual water availability, such that the primary clustering of samples was an annual pattern of variation, rather than taxonomic grouping (Riggins *et al.*, 1977). Davis (1983) does, however, indicate that plastic characters (traditionally considered problematic and useless) are not completely useless as, in some cases, some states are limited to fewer than all genotypes, and the characters therefore exhibit some discriminatory information.

Analyses methods

James & McCulloch (1990) rather understate the case when they observe that researchers do not always agree on the best methods of analysis. There are a multitude of methods available for the multivariate analysis of morphometric data and James & McCulloch (1990) provide an overview of some of the various methods, survey their uses in cases in the literature, and list each method's objectives and limitations. Two of the most widely utilized of those techniques were Principal Component Analysis (PCA) and Cluster Analysis (CA). Each of these methods has certain practical applications and objectives for which they are ideal, but each method has its limitations. Both methods can be utilized for descriptive purposes, i.e. they can suggest causes for patterns, but derived factors and clusters do not necessarily reflect biological factors or clusters in nature (James & McCulloch, 1990). James & McCulloch (1990) limit CA to classification purposes only and PCA to ordination purposes only.

Cluster Analysis

This method places objects in groups according to a similarity measure and then a grouping algorithm (James & McCulloch, 1990). A pairwise similarity matrix is created and used to join the two most similar objects together, then the similarity of this group to all others is calculated, and the closest two groups are again combined until only a single group remains (James & McCulloch, 1990). Although Crompton *et al.* (1990) regard CA as the numerical taxonomic technique most widely used for obtaining groupings, James & McCulloch (1990) caution that CA is most appropriate for categorical rather than continuous data, and may be less efficient than PCA.

Principal Component Analysis

The main purpose of PCA is to describe the total variation in a sample in a few dimensions (Borazan & Babac, 2003). PCA reduces the number of dimensions of a single group of data by producing a smaller number of abstract variables (linear combinations of the original variables, called principal components), such that most of the variation can be summarized by only a few components, so data with many variables can be displayed effectively on a two- or three dimensional graph that uses the components as axes (James & McCulloch, 1990). Not all principal components are needed to summarize the data adequately and, in practice, only the first few components that account for the major patterns of variation need be retained (Borazan & Babac, 2003).

Somers (1986) cautions that PCA is not infallible, since it assumes linearity and multivariate normality of all the variables, and may inefficiently summarize nonlinear patterns. If the distribution of ratios or proportions is reasonably near to normal the analysis can be useful, but without transformations principal components analysis cannot capture nonlinear relationships (James & McCulloch, 1990). PCA is also sensitive to outliers (James & McCulloch, 1990).

Methods

Morphological character selection and data collection

The descriptions of species from Roessler's (1959) review provide a good basis for character selection, as these were the characters that he used to delimit his morphospecies. As such, many of these have been chosen for this morphometric analysis. Appendix 1 contains the character descriptions for each character for each species delimited by Roessler. Data is missing from the table where Roessler gives no details.

Morphometric data was collected for 21 characters from 170 herbarium specimens (both those collected and pressed for this project as well as preexisting herbarium specimens). Although an average number of ten samples per taxa is rather low, the selection of samples was such that a comparison between morphometric and DNA data was made possible. All sample details (including collection localities and herbarium details where appropriate) are listed in Table 2.1.1. Two samples from a putative new species were included as well. Details of characters are given below. Also see Appendix 2 for complete table of morphometric data.

Some characters are inherently difficult to classify quantitatively (e.g. shades of colour). An attempt was made to reduce other characters (e.g. involucre scale shape, leaf shape) that are described by subjective shape descriptive terms (e.g. acuminate, obtuse) to quantitative data values (by means of a ratio). Due to the paucity of measurements that could be taken, the simpler measures were investigated; the simplest way to describe shape quantitatively is to measure length and width and then compare those two measurements as a ratio.

In the case of the involucre scales, the measurement of the length from point of attachment to tip, divided by the width at the point of attachment, provides a numerical estimate of shape. The difference between an acuminate scale (with a ratio of 6:1) and an obtuse scale (with a ratio of 1:1) is clearly illustrated in Figure 2.1.1.

Leaf shape is more difficult to quantify, especially when it comes to including data on pinnate leaves. The basic leaf shape was encapsulated in a length:width ratio. However, as mentioned in the introduction to this chapter, ratios are considered problematic. Shape alone may not be sufficient to discriminate taxa; therefore the actual size of the leaves is included in some data sets to investigate the different effects of actual size versus relative shape ratio on multivariate methods.

Table 2.1.1: List of all samples used in morphometric analyses, including collection locality data.

Sample Name	Species Name	Collection number	Collection site	South	East
Cil1	<i>ciliaris</i>	M270805_12	South Africa. Worcester: Tulbagh, below Waterfall near CapeNature office.	33° 20' 31"	19° 06' 53"
Cil2	<i>ciliaris</i>	RM1230	South Africa. Cape Town: Paarlberg.	33° 45' 8.3"	18° 57' 5.2"
Cil3	<i>ciliaris</i>	RM1382	South Africa. Clan William: Piketberg plateau	32° 48' 41"	18° 42' 40"
Cil4	<i>ciliaris</i>	Galpin 4263	Herbarium (GRA)		
Cil5	<i>ciliaris</i>	Schlechter 5286	Herbarium (GRA)		
Cil6	<i>ciliaris</i>	Schlechter 5286	Herbarium (GRA)		
Cil7	<i>ciliaris</i>	SR705	South Africa. Peddie: Fish River, near Port Alfred. Seven seas.	33° 28' 58"	27° 04' 48"
Het1	<i>heterochaeta</i>	Schlechter 11318	Herbarium (GRA)		
Het2	<i>heterochaeta</i>	Schlechter 11318	Herbarium (GRA)		
Het3	<i>heterochaeta</i>	Archibald 2714	Herbarium (GRA)		
Het4	<i>heterochaeta</i>	Archibald 2715	Herbarium (GRA)		
Het5	<i>heterochaeta</i>	M160901/5G	South Africa. Gamoep: Goegap Nat Res, 4x4 tracks N of Res. Headquarters.	29° 39' 33"	18° 00' 29"
Het6	<i>heterochaeta</i>	RM1451	South Africa. Springbok: 5km N Steinkopf, beside N7 highway	29° 14' 04"	17° 45' 20"
Het7	<i>heterochaeta</i>	RM1255	South Africa. Worcester: beside R355, North of Karooport.	33° 9' 40.8"	19° 45' 2.8"
Het8	<i>heterochaeta</i>	RM1429_1	South Africa. Steytlerville: T2 road Steytlerville - Grootrivierpoort; 5km N Rietfontein turnoff.	33° 22' 30"	24° 22' 30"
Het9	<i>heterochaeta</i>	RM1348	South Africa. Springbok: Roadside, 80km east of Port Nolloth	29° 14' 58"	17° 40' 33"
Jur1	<i>jurineifolia</i>	CAM1604	Namibia. Witputz: Karas	27° 22' 30"	16° 07' 30"
Jur2	<i>jurineifolia</i>	CAM1953	Namibia. Aus: Klein Aus Vista.	26° 37'	16° 22'
Jur3	<i>jurineifolia</i>	Gess 01/02/141	Herbarium (GRA)		
Jur4	<i>jurineifolia</i>	Barber 638	Herbarium (GRA)		
Jur5	<i>jurineifolia</i>	Daly 90	Herbarium (GRA)		
Jur6	<i>jurineifolia</i>	Dyer 1014	Herbarium (GRA)		
Jur7	<i>jurineifolia</i>	Barber 474	Herbarium (GRA)		
Jur8	<i>jurineifolia</i>	Galpin 5564	Herbarium (GRA)		
Jur9	<i>jurineifolia</i>	SR682	South Africa. Gamoep: 18km W of Aggeney's (between Springbok & Pofadder)	29° 22' 46"	18° 38' 53"
KrbA1	<i>krebsiana</i> subsp <i>arctotoides</i>	RM868/1	South Africa. Kenhardt: Rooipan, southeast of Lime Acres.	29° 47'	21° 56'
KrbA10	<i>krebsiana</i> subsp <i>arctotoides</i>	RM831_2	South Africa. Oudtshoorn: south of Oudtshoorn on N12 highway.	33° 35'	22° 11'
KrbA12	<i>krebsiana</i> subsp <i>arctotoides</i>	RM860_1	South Africa. Steynburg: south of Joubertsberge	31° 45' 19"	25° 04' 53"
KrbA2	<i>krebsiana</i> subsp <i>arctotoides</i>	RM770_2	South Africa. Willowmore: Prince Alfred's Pass.	33° 45'	23° 08'
KrbA4	<i>krebsiana</i> subsp <i>arctotoides</i>	M071001/3GP	South Africa. Queenstown: Stormberg Plateau, Penhoek Pass, rest place 3km North of pass.	31° 25' 33"	26° 41' 29"
KrbA5	<i>krebsiana</i> subsp <i>arctotoides</i>	RM903	South Africa. Graaff-Rienet: southwest of Aberdeen on N9 highway.	32° 31'	24° 00'

KrbA6	<i>krebsiana</i> subsp <i>arctotoides</i>	RM904	South Africa. Graaff-Rienet: between Graaff-Reinet and Adendorp on R75 road.	32° 15'	24° 33'
KrbA8	<i>krebsiana</i> subsp <i>arctotoides</i>	RM862_1	South Africa. Worcester; east of Potmasburg, West Cape, Dassiehoek	33° 50'	19° 30'
KrbA9	<i>krebsiana</i> subsp <i>arctotoides</i>	RM876_1	South Africa. Aliwal North: Bloemfontein	30° 19'	26° 48'
KrbK10	<i>krebsiana</i> subsp <i>krebsiana</i>	NB1465	South Africa. Steytlerville: Graaff-Rienet. Farm Welgmoed. Track to Nardousberg plateaux.	32° 47'	24° 32'
KrbK11	<i>krebsiana</i> subsp <i>krebsiana</i>	M261001/2	South Africa. Queenstown: Stormberg, Penhoek Pass.	31° 15' 34"	26° 44' 51"
KrbK12	<i>krebsiana</i> subsp <i>krebsiana</i>	M071001/1G	South Africa. Port Elizabeth: Coega salt works.	33° 46' 35"	25° 40' 05"
KrbK13	<i>krebsiana</i> subsp <i>krebsiana</i>	M071001/3GL	South Africa. Queenstown: Stormberg Plateau, Penhoek Pass, rest place 3km North of the pass.	31° 25' 33"	26° 41' 29"
KrbK14	<i>krebsiana</i> subsp <i>krebsiana</i>	M230803/8	South Africa. Port Shepstone: Umtamvuna Nature Reserve, Beacon hill.	30° 48'	30* 11'
KrbK16	<i>krebsiana</i> subsp <i>krebsiana</i>	RM874	South Africa. Kimberley: SE of Kimberley on N8 highway.	28° 47'	24° 47'
KrbK17	<i>krebsiana</i> subsp <i>krebsiana</i>	RM929	South Africa. Witbank: Middelburg, Agter-Renosterberg, near Uitsig hut, Transkaroo hiking trail.	25° 43'	29° 25'
KrbK18	<i>krebsiana</i> subsp <i>krebsiana</i>	RM968	South Africa. Matatiele: Carlisle's Hoek, beside road to Tiffindell Ski resort.	30° 40'	28° 03'
KrbK19	<i>krebsiana</i> subsp <i>krebsiana</i>	RM962	South Africa. Queenstown: NE of Queenstown on R359 road.	31° 49'	26° 55'
KrbK2	<i>krebsiana</i> subsp <i>krebsiana</i>	RM949	South Africa. Humansdorp: Eskom substation 500m north of N2 on R330 to Hankey.	34° 08' 38*	24° 10' 41"
KrbK20	<i>krebsiana</i> subsp <i>krebsiana</i>	RM960	South Africa. Fort Beaufort: SW of Seymour, junction R67 & road to Katberg Pass.	32° 35'	26° 44'
KrbK22	<i>krebsiana</i> subsp <i>krebsiana</i>	RM856	South Africa. Willowmore: Bloukrans River.	33° 58'	23° 39'
KrbK23	<i>krebsiana</i> subsp <i>krebsiana</i>	RM906	South Africa. Fort Beaufort: south of Bedford.	32° 41'	26° 05'
KrbK24	<i>krebsiana</i> subsp <i>krebsiana</i>	RM852_1	South Africa. Grahamstown: south of Bathurst	33° 30' 43"	26° 49' 44"
KrbK25	<i>krebsiana</i> subsp <i>krebsiana</i>	RM713_3	South Africa. Port Elizabeth: Coega.	33° 46'	25° 40'
KrbK26	<i>krebsiana</i> subsp <i>krebsiana</i>	SR564	South Africa. Port Edward: Umtamvuna Nature Rserve.	31° 04'	30° 11'
KrbK27	<i>krebsiana</i> subsp <i>krebsiana</i>	SR520	South Africa. Underberg: Estcourt.	29° 02' 35"	29° 52' 19"
KrbK28	<i>krebsiana</i> subsp <i>krebsiana</i>	SR480	South Africa. Grahamstown: Fort Brown, resolution hatchery.	33° 09' 53"	26° 37' 18"
KrbK3	<i>krebsiana</i> subsp <i>krebsiana</i>	SH110	South Africa. Grahamstown: 100m from Great Fish River Bridge.	33° 29'	26° 55'
KrbK4	<i>krebsiana</i> subsp <i>krebsiana</i>	SH112	South Africa. Stutterheim: Road out of Kaiskammahoek.	32° 49'	27° 11'
KrbK5	<i>krebsiana</i> subsp <i>krebsiana</i>	SH111	South Africa. Peddie: 10km East Peddie.	33° 12'	27° 07'
KrbK7	<i>krebsiana</i> subsp <i>krebsiana</i>	RM992_2	South Africa. Lady Frere: Baster Voetpad. Near Elliot. Roadside bank.	31° 19'	27° 57'
KrbK8	<i>krebsiana</i> subsp <i>krebsiana</i>	M210902_1	South Africa. Fort Beaufort: N of Fort Brown, road to Fort Beaufort.	32° 55' 43"	26° 37' 28"
KrbK9	<i>krebsiana</i> subsp <i>krebsiana</i>	RM804_2	South Africa. Grahamstown: Riebeek East, 'Willowfontein' farm.	33° 12'	26° 09'
KrbS1	<i>krebsiana</i> subsp <i>serrulata</i>	RM1150	South Africa. Colesberg: Free State, Gariep Dam, day visitor area.	30° 36' 14"	25° 29' 24"
KrbS2	<i>krebsiana</i> subsp <i>serrulata</i>	RM1137	South Africa. Bloemfontein: Bayswater area, junction of N1 + R400 roads.	29° 10'	26° 13'
KrbS3	<i>krebsiana</i> subsp <i>serrulata</i>	RM866	South Africa. Griekwastad: north of Danielskuil	28° 10' 50"	23° 32' 11"
KrbS4	<i>krebsiana</i> subsp <i>serrulata</i>	RM863_1	South Africa. Olifantshoek: southeast of Beeshoek	27° 45'	22° 37'
KrbS5	<i>krebsiana</i> subsp <i>serrulata</i>	RM877_1	South Africa. Aliwal North: north of Rouxville.	30° 25'	26° 49'
KrbS6	<i>krebsiana</i> subsp <i>serrulata</i>	RM965	South Africa. Lady Frere: 13km SW Elliot on R56 road.	31° 19'	27° 57'

Leio1	<i>leiopoda</i>	RM1320	<u>South Africa. Hondeklipbaai: Kamiesberg.</u>	30° 11' 16"	17° 59' 21"
Leio10	<i>leiopoda</i>	RM1309	<u>South Africa. Kamiesberg: Roadside.</u>	30° 24' 38"	18° 3' 9"
Leio11	<i>leiopoda</i>	RM1466	<u>South Africa. Hondeklipbaai: Namakarroo National Park, W of Kamieskroon.</u>	30° 05' 47"	17° 35' 03"
Leio2	<i>leiopoda</i>	M200901/22G	<u>South Africa. Hondeklipbaai: Kamieskroon, Arakop Farm.</u>	30° 05' 31"	17° 54' 33"
Leio3	<i>leiopoda</i>	M230901/7G	<u>South Africa. Vanrhynsdorp: Knersvlakte, Vanrhynsdorp, Quaggaskop Farm.</u>	31° 24' 46"	18° 38' 33"
Leio4	<i>leiopoda</i>	M240901/19	<u>South Africa. Calvinia: Nieuwoudtville, near turnoff to Rondekop.</u>	31° 23' 23"	19° 11' 00"
Leio5	<i>leiopoda</i>	M210901/22	<u>South Africa. Hondeklipbaai: Kamieskroon, Arakop Farm, edge of dirt road.</u>	30° 05' 31"	17° 54' 33"
Leio6	<i>leiopoda</i>	M160704/5	<u>South Africa. Hondeklipbaai: Namaqualand, Kamieskroon, on N7.</u>	30° 14' 15"	17° 53' 43"
Leio7	<i>leiopoda</i>	RM1291	<u>South Africa. Hondeklipbaai: roadside.</u>	30° 18' 37"	17° 53' 37"
Leio8	<i>leiopoda</i>	M250901/34	<u>South Africa. Vanrhynsdorp: road from Vredendal to Strandfontein, Papendorp turnoff.</u>	31° 42' 06"	18° 13' 32"
Leio9	<i>leiopoda</i>	RM1063	<u>South Africa. Vanrhynsdorp: SW of Lutzville, R362 between Papendorp & Lutzville.</u>	31° 33'	18° 21'
Lict1	<i>lichtensteinii</i>	M7249/15	<u>South Africa. Springbok: Kamieskroon, at bridge of N7 over Haasrivier</u>	29° 59' 312"	17° 52' 31"
Lict10	<i>lichtensteinii</i>	RM1323	<u>South Africa. Kamiesberg: Road north east of Kamieskroon.</u>	30° 7' 44"	18° 13' 40"
Lict11	<i>lichtensteinii</i>	Schlechter 4501	Herbarium (GRA)		
Lict3	<i>lichtensteinii</i>	M150704/10	<u>South Africa. Vioolsdrif: N7, between Steinkopf and Vioolsdrif.</u>	28° 57' 24"	17° 46' 17"
Lict4	<i>lichtensteinii</i>	M020803/8	<u>South Africa. Merweville: Leeuw-Gamka, Shell petrol station</u>	32° 47' 13"	21° 59' 00"
Lict5	<i>lichtensteinii</i>	M060605_22	<u>South Africa. Gamoep: Namaqualand, Aggeneys, Kangas farm, gate on N14</u>	29° 30' 10"	18° 18' 48"
Lict6	<i>lichtensteinii</i>	RM1249	<u>South Africa. Wuppertal: beside R355 road near Tankwa Karoo National Park.</u>	32° 10' 30"	19° 42' 47"
Lict8	<i>lichtensteinii</i>	RM1265	<u>South Africa. Calvinia: flats South of Botterkloof Pass.</u>	31° 56' 59"	19° 14' 34"
Linlin1	<i>linearis</i> subsp <i>linearis</i>	RM1013	<u>South Africa. Port St Johns: North of Mbotyi river mouth.</u>	31° 26'	29° 43'
Linlin10	<i>linearis</i> subsp <i>linearis</i>	RM794_2	<u>South Africa. Stutterheim: south of King William's Town on N2 highway.</u>	32° 52'	27° 23'
Linlin13	<i>linearis</i> subsp <i>linearis</i>	RM787_1	<u>South Africa. Umtata: between Umtata and Umlambo Mputi on N2 highway.</u>	31° 59'	28° 40'
Linlin15	<i>linearis</i> subsp <i>linearis</i>	RM916_1	<u>South Africa. Fort Beaufort: Katberg Pass</u>	32° 26' 46"	26° 38' 26"
Linlin2	<i>linearis</i> subsp <i>linearis</i>	RM1061	<u>South Africa. Capetown: Clanwilliam. Possible garden escape growing wild and profusely.</u>	32° 11' 45"	18° 54' 32"
Linlin21	<i>linearis</i> subsp <i>linearis</i>	RM885_1	<u>South Africa. Fort Beaufort: Tor Doone, Hogsback.</u>	32° 34'	26° 56'
Linlin23	<i>linearis</i> subsp <i>linearis</i>	RM789	<u>South Africa. Umtata: between Umtata and Umlambo Mputi on N2 highway.</u>	31° 35'	28° 47'
Linlin24	<i>linearis</i> subsp <i>linearis</i>	RM951_1	<u>South Africa. Humansdorp: St Francis bay, R330 road, St Francis Bay village turnoff.</u>	34° 11'	24° 50'
Linlin25	<i>linearis</i> subsp <i>linearis</i>	RM1182	<u>South Africa. Humansdorp: on N2, Seekooi river.</u>	34° 02'	24* 46'
Linlin26	<i>linearis</i> subsp <i>linearis</i>	SR571	<u>South Africa. Port Shepstone: Port Shepstone. Roadside.</u>	30° 44'	30° 27'
Linlin27	<i>linearis</i> subsp <i>linearis</i>	SR523	<u>South Africa. Humansdorp: Maitlands, road between Seaview and Maitlands River.</u>	34° 00'	25° 41'
Linlin28	<i>linearis</i> subsp <i>linearis</i>	SH131	<u>South Africa. Stutterheim: Road between Hogsback and Cathcart, 7km out.</u>	32° 33'	27° 04'
Linlin29	<i>linearis</i> subsp <i>linearis</i>	SH132	<u>South Africa. Stutterheim: Road between Hogsback and Cathcart, 14km out.</u>	32° 22'	27° 07'
Linlin3	<i>linearis</i> subsp <i>linearis</i>	RM1010	<u>South Africa. Calvinia: Mzimpunzi river mouth, Pondoland.</u>	31° 19'	29° 56'

Chapter 2: Methods

Linlin4	<i>linearis</i> subsp <i>linearis</i>	SH113	South Africa. <u>Stutterheim</u> : 10km out of Stutterheim.	32° 34'	27° 25'
Linlin5	<i>linearis</i> subsp <i>linearis</i>	RM1092	South Africa. <u>Port St Johns</u> : Coffee Bay, Bumvu river mouth.	31° 58'	29° 09'
Linlin6	<i>linearis</i> subsp <i>linearis</i>	RM1103	South Africa. <u>Port Edward</u> : Mkambati Nature Reserve, N of the Msikaba River Mouth.	31° 01' 24"	30° 13' 48"
Linlin9	<i>linearis</i> subsp <i>linearis</i>	RM780	South Africa. <u>Fort Beaufort</u> : between East London and Cintsa turnoff on N2 highway.	32° 53'	28° 04'
LinO1	<i>linearis</i> subsp <i>ovalis</i>	RM854	South Africa. <u>Grahamstown</u> : north of Bathurst.	33° 29'	26° 49'
LinO10	<i>linearis</i> subsp <i>ovalis</i>	Britten 2691	Herbarium (GRA)		
LinO2	<i>linearis</i> subsp <i>ovalis</i>	M041001_2G	South Africa. <u>Grahamstown</u> : Thornycroft, road between Alexandria and Port Elizabeth.	33° 36' 42"	26° 01' 43"
LinO3	<i>linearis</i> subsp <i>ovalis</i>	ND_haven	South Africa. <u>Butterworth</u> : The Haven, Transkei.	32° 14'	28° 54'
LinO4	<i>linearis</i> subsp <i>ovalis</i>	Potts 220	Herbarium (GRA)		
LinO5	<i>linearis</i> subsp <i>ovalis</i>	Galpin 2953	Herbarium (GRA)		
LinO6	<i>linearis</i> subsp <i>ovalis</i>	Daly 717	Herbarium (GRA)		
LinO7	<i>linearis</i> subsp <i>ovalis</i>	White 70	Herbarium (GRA)		
LinO8	<i>linearis</i> subsp <i>ovalis</i>	Britten 5239	Herbarium (GRA)		
LinO9	<i>linearis</i> subsp <i>ovalis</i>	Britten 2691	Herbarium (GRA)		
Marit	<i>maritima</i>	RM1038	South Africa. <u>Bredasdorp</u> : Cape Agulhas, about 2km E of actual cape, on shoreline.	34° 48' 48"	20° 02' 48"
Oth	<i>othomites</i>	RM1306	South Africa. <u>Springbok</u> : Kleinzee, Molyneux trail	29° 41' 27"	17° 05' 40"
Pct1	<i>pectinata</i>	M120903/5	South Africa. <u>Clan William</u> : Western Cape Province, Piketberg, Sauer, Uitvlug turnoff.	32° 50' 17"	18° 33' 14"
Pct2	<i>pectinata</i>	M260901/2G	South Africa. <u>Clanwilliam</u> : Cederberg, Pakhuis pass.	32° 08' 11"	18° 58' 15"
Pct3	<i>pectinata</i>	M180904/5	South Africa. <u>Bredasdorp</u> : De Hoop Nature Reserve., Koppie Alleen.	34° 28 ' 41"	20° 30' 39"
Pct4	<i>pectinata</i>	RM1044_3	South Africa. <u>Caledon</u> : Agulhas peninsula, Bredasdorpberge.	34° 29' 47'	19° 53' 39"
Pct5	<i>pectinata</i>	RM1044_1	South Africa. <u>Caledon</u> : Agulhas peninsula, Bredasdorpberge.	34° 29' 47"	19° 53' 39"
Pct6	<i>pectinata</i>	M250901_37	South Africa. <u>Vanrhynsdorp</u> : Strandfontein, on road to Doringbaai.	31° 45' 18"	18° 14' 02"
Pct7	<i>pectinata</i>	Rogers 11067a	Herbarium (GRA)		
Pct8	<i>pectinata</i>	RM1390	South Africa. <u>Caledon</u> : Franschoek Pass, summit of pass.	33° 54' 27"	19° 09' 19"
Rigid1	<i>rigida</i>	RM1210	South Africa. <u>Bredasdorp</u> : 14.5km North of Bredasdorp on R319 road.	34° 25' 50"	20° 7' 22"
Rigid12	<i>rigida</i>	M110805_10	South Africa. <u>Bredasdorp</u> : De Hoop Nature Reserve, Potberg, Melkosheuwel.	34° 22' 50"	20° 29' 16"
Rigid13	<i>rigida</i>	RM1270	South Africa. <u>Wuppertal</u> : North of base of Pakhuis Pass.	32° 03' 37"	19° 10' 10"
Rigid14	<i>rigida</i>	RM1254	South Africa. <u>Wuppertal</u> : base of Katbakkies Pass, Swaruggens.	32° 52' 58"	19° 44' 27"
Rigid3	<i>rigida</i>	M280902/9	South Africa. <u>Oudtshoorn</u> : Oudtshoorn, turn off to Zebra	33° 45' 45"	22° 20' 07"
Rigid4	<i>rigida</i>	M100903/4	South Africa. <u>Cape Town</u> : Darling, Tienie Versveld Flower Reserve.	33° 20' 07"	18° 16' 16"
Rigid5	<i>rigida</i>	M100904/4	South Africa. <u>Beaufort West</u> : Uniondale, bridge over Keurboomsrivier.	33° 45' 39"	22° 57' 44"
Rigid6	<i>rigida</i>	RM1044_2	South Africa. <u>Caledon</u> : Agulhas peninsula, Bredasdorpberge. Ex-pine plantation.	34° 29' 47"	19° 53' 39"
Rigid7	<i>rigida</i>	M120805_80	South Africa. <u>Sutherland</u> : De Hoop Nature Reserve, Potberg, NE of the Potberg gate.	34° 22' 10"	20° 31' 32"

Rigid8	<i>rigida</i>	Rogers 2889	Herbarium (GRA)		
Rigid9	<i>rigida</i>	JacotGuillarmard 7662	Herbarium (GRA)		
Rigs10	<i>rigens</i>	RM782_2	South Africa. Port St Johns: Second Beach.	31° 37'	29° 32'
Rigs11	<i>rigens</i>	RM772_2	South Africa. Knysna: Plettenberg Bay.	34° 02'	23° 22'
Rigs16	<i>rigens</i>	RM919	South Africa. Grahamstown: SE of Cannon Rocks.	33° 44'	26° 33'
Rigs17	<i>rigens</i>	RM920	South Africa. Grahamstown: SE of Cannon Rocks.	33° 44'	26° 33'
Rigs19	<i>rigens</i>	SR625	South Africa. Skoemakerskop: Cape Riecefé (Between PE and seaview).	34° 00'	25° 39'
Rigs2	<i>rigens</i>	M7298/2	South Africa. Humansdorp: St Francis Bay, bridge over Kromme river, tidal salt marsh.	34° 08' 15"	24° 48' 28"
Rigs20	<i>rigens</i>	SR581	South Africa. Grahamstown: Kowie river.	33° 36'	26° 53'
Rigs21	<i>rigens</i>	SR 575	South Africa. Stanger: Durban, Blue Lagoon.	29° 48'	31° 02'
Rigs22	<i>rigens</i>	SR 574	South Africa. Port Shepstone: Umkomaas, Warner Beach, Baggies Beach, 10km N Durban.	30° 04'	30° 52'
Rigs23	<i>rigens</i>	SR463	South Africa. Stanger: Tugela River mouth	29° 13'	31° 30'
Rigs3	<i>rigens</i>	M7293/1	South Africa. Humansdorp: Jeffereys Bay, beach south of Kabeljous River mouth.	34° 00' 53"	24° 55' 42"
Rigs4	<i>rigens</i>	M070704/1	South Africa. Simonstown: Miller's Point.	34° 13' 57.8"	18° 28' 32"
Rigs5	<i>rigens</i>	M7257/2	South Africa. Riversdale: Gouritzmond, coast, parking lot, leeward slope dune.	34° 21' 01"	21° 53' 00"
Rigs6	<i>rigens</i>	RM952_1	South Africa. Humansdorp: Cape St Francis, in sand rocky shoreline	34° 12'	24° 50'
Rigs7	<i>rigens</i>	RM952_3	South Africa. Humansdorp: Cape St Francis, in sandon rocky shoreline	34° 12'	24° 50'
Rigs9	<i>rigens</i>	RM783	South Africa. Port St Johns: Third Beach.	31° 37'	29° 32'
Serr1	<i>serrata</i>	RM1216	South Africa. Caledon: 1km SW of Caledon on R320 road.	34° 16' 24"	19° 26' 09"
Serr2	<i>serrata</i>	RM1260	South Africa. Worcester: Calvinia.	33° 30' 21"	19° 44' 23"
Serr3	<i>serrata</i>	M250904/15	South Africa. Simonstown: Helderberg strand, R44 between Nautilus and Octopus streets	34° 08' 31"	18° 51' 06"
Serr4	<i>serrata</i>	RM821_1	South Africa. Worcester: Robertson aerodrome.	33° 48'	19° 53'
Serr6	<i>serrata</i>	RM812	South Africa. Worcester: Dassiehoek Nature Reserve.	33° 50'	19° 30'
Serr7	<i>serrata</i>	RM1245	South Africa. Worcester: Skurweberg.	33° 14' 11"	19° 17' 42"
Serr8	<i>serrata</i>	RM1280	South Africa. Calvinia: 5km East of Nieuwoudtville.	31° 23'	19° 06'
Serr9	<i>serrata</i>	RM1374	South Africa. Clanwilliam: Piketberg, near top of Versveld Pass.	32° 50' 59"	18° 44' 02"
sp. nov1	<i>species nova</i>	M040906_33	South Africa. Hondeklipbaai: Hondeklipbaai, coast at police station	30° 19' 22"	17° 16' 21"
sp. nov2	<i>species nova</i>	MSG7237/4	South Africa. Port Nolloth: South of McDougalls Bay. Strandveld.	29° 17' 39"	16° 52' 45"
sp. nov3	<i>species nova</i>	M050905_02	South Africa. Springbok: Kleinzee, Rooikoppies	29° 43' 52"	17° 03' 40"
Ten1	<i>tenuifolia</i>	M7230/2	South Africa. Springbok: Goegap Nature Reserve, Bleshoek	29° 41' 31"	17° 58' 46"
Ten2	<i>tenuifolia</i>	M7219_10	South Africa. Gamoep: Goegap Nature Reserve, SE of Carolusberg.	29° 39' 23"	18° 00' 32"
Ten3	<i>tenuifolia</i>	RM1352	South Africa. Springbok: 40km east of Port Nolloth	29° 17' 56"	17° 12' 21"
Ten4	<i>tenuifolia</i>	CAM1601	Namibia. Witputz: Arras	27° 22' 30"	16° 7' 30"

Chapter 2: Methods

Ten5	<i>tenuifolia</i>	Schlechter 8109	Herbarium (GRA)		
Ten6	<i>tenuifolia</i>	Esterhuysen 5984	Herbarium (GRA)		
Ten7	<i>tenuifolia</i>	Esterhuysen 5985	Herbarium (GRA)		
Ten8	<i>tenuifolia</i>	Esterhuysen 5986	Herbarium (GRA)		
Ten9	<i>tenuifolia</i>	Esterhuysen 5987	Herbarium (GRA)		
Ten10	<i>tenuifolia</i>	Schlechter 8109	Herbarium (GRA)		

Collector abbreviations: RM = Robert McKenzie, M = Laco Mucina, MSG = Mucina & Santos Guerra, CAM = Colleen Mannheimer, SR = Syd Ramdhani, ND = Nico Devos.

A list of characters, an explanation of each character, a description of how each character was quantified/qualified and the possible characters states follows:

Qualitative characters:

Binary characters:

1) Habit:

- 0 = Leaves alternate, capitula scapose.
- 1 = Leaves rosulate, capitula pedunculate.

2) Involucre furry/setose:

- 0 – no
- 1 – yes

Multistate characters:

3) Presence of parietal scales on involucre:

Not all the tips of the fused involucre scales are inserted at the terminal edge of the involucre, some are parietal.

- 0 = No scales
- 1 = Some few single scales
- 2 = Multiple rows of scales

4) Base of involucre truncated/annulated:

See Figure 2.2.1 for illustration of each state.

- 0 – No
- 1 – annulated
- 2 – subinserted
- 3 – truncate

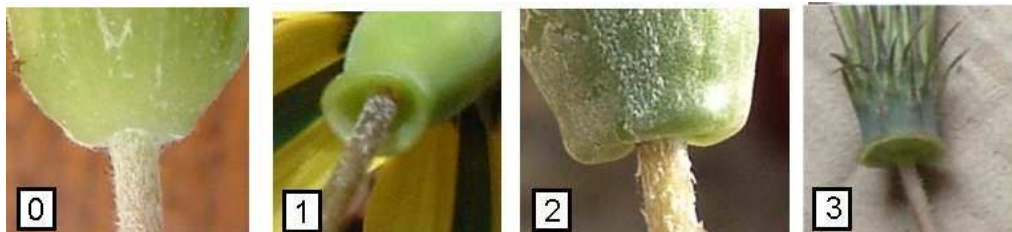


Figure 2.2.1: Involucre base states in *Gazania*: 0 = no modification, 1 = annulated, 2 = subinserted, 3 = truncate.

5) Adaxial leaf indumentum:

Some leaves are very scabrid to touch and others have only a light coat of hairs.

0 – smooth

1 – lightly setose/ciliate

2 – densely roughly setose/ciliate

6) Leaf margin ciliate/smooth:

0 = smooth

1 = ciliate at terminal upper half

2 = ciliate at basal lower half

3 = ciliate along entire edge.

7) Leaf dissectedness:

1 – all leaves on plant entire, no division

2 – all leaves on plant lobed

3 – all leaves on plant pinnatisect (deeply incised)

4 – some leaves on plant whole, some leaves on plant lobed

5 – some leaves on plant whole, some leaves on plant pinnatisect

6 – lobed, pinnatisect and whole all present on plant

7 – minute lobes present all along edges of leaves

Quantitative characters:

8) Outer involucre scale length (mm):

Length from point of attachment to tip.

9) Outer involucre scale width (mm):

Width of scale at point of attachment.

10) Inner involucre scale length (mm):

Length from point of attachment to tip.

11) Inner involucre scale width (mm):

Width of scale at point of attachment.

12) Involucre length (mm):

Length from point of stem attachment to start of terminal scales.

13) Width of involucre at terminal edge (mm):

Width of the involucre at terminal edge where terminal scales are inserted.

14) Leaf length (mm):

Average length of three longest adult leaves on plant.

15) Leaf width (mm):

Average width at widest part of three longest adult leaves on plant.

16) Involucre scape/peduncle length (mm):

Measured from last major leaf, to point of attachment to involucre (solitary linear bracts were ignored as a starting point for the measurement).

Ratio characters:

17) Outer involucre scale:

Length / Width.

18) Inner involucre scale:

Length / Width.

19) Outer involucre scale length/Inner involucre scale length:

Some species are noted for having inner scales longer than the other scales.

20) Involucre length/width

21) Leaf length/width

Discarded characters

Roessler (1959) included “the width of the capitula with the ligules expanded” as a character in his species delimitations. The length of ray floret ligules were investigated for potential data signal during the data collection process. However, the length of ray floret ligules is subject to water

availability (water stress results in smaller inflorescences; pers. obs. on greenhouse plants) and also shows little useful signal.

Roessler (1959) noted that certain species have only divided leaves or only whole leaves, thus leaf dissectedness was investigated. However, the inclusion of leaf dissectedness (whole, lobed or pinnate) as an informative character is debatable. The difference between leaves that are whole, pinnate or lobed can either be species specific (certain species are always pinnate; others are commonly, but not always, whole) or environmentally responsive (excess water can either result in more pinnate leaves in rigens, or more whole leaves in some commonly pinnate western cape species, pers. obs.).

Roessler (1959) listed ray spot patterns in his species descriptions, but the extraordinary variability of ray spot patterns precluded any easy delimitation of character states. Likewise, the large variety of spot patterns, colours and colour combinations that occur within species likewise advised against using this character. Samples of the same subspecies co-occurring within centimeters of each other have been observed to have different spot patterns (pers. obs. & R. McKenzie, pers. comm.).

Roessler (1959) included comments on comparative length of terminal pinnules relative to side pinnules. However, the length of the pinnules (or only the terminal pinnule) was found to be highly variable, not only within species, but also on individual plants, making it very difficult to determine with any accuracy. The lack of pinnules in some samples also made this a dubious character.

Many taxonomists consider colour characters dubious, since colour characters are considered unstable, the measurement is dependent on the colour vision of the observer, and is very hard to quantify (Chandler & Crisp, 1998). In addition, the change in colour that herbarium specimens may undergo over time makes ray colour a very difficult character to judge for *Gazania* specimens.

Analysis of herbarium versus live specimens

The pressing of herbarium samples does not affect the leaves in terms of length and width, nor does it appear to affect involucre scale characters. However, the pressing of herbarium specimens can change the width of the involucre slightly (as the cylindrical involucre becomes rather more two-dimensional). Since all the herbarium specimens are pressed, the measurements are directly comparable with each other, but probably not directly with living material.

Data sets

To compare the effects of ratio data versus raw size data on various analytical methods three data sets were constructed. All three data sets contained the binary and qualitative characters 1-7.

- 1) “RAW”, which contains characters 8-16, i.e. all the raw size data of the qualitative characters but no ratio characters.
- 2) “RAT”, which contains character 17-21, i.e. all the ratio characters but none of the raw size data characters.
- 3) “TOTAL”, which contains both raw size and ratio characters, i.e. characters 8-21.

Data analysis

All data analyses were conducted in NTSYS-pc version 2.02k (Applied Biostatistics, Inc.).

Normalization of data

Certain analyses require that continuous variables be normally distributed. When a variable is not normally distributed a transformation, such as taking the log of the variable, eliminates the undesirable characteristic and improves the symmetry about the mean and the approximation to a normal distribution to provide more natural expressions of the characteristics being studied (Borazan & Babac, 2003). Test of normality were conducted in STATISTICA 6.1 (StatSoft, Inc), using the Lilliefors test (Lilliefors, 1967) of normality, where a significant result ($p < 0.05$) indicates that data is not normally distributed. All quantitative data were converted to their log values prior to PCA analysis.

Albrecht (1978) noted that analysis (specifically PCA) of raw data which contains both size and shape components of variation should yield different results than an analysis of this same data after elimination of the size variation by some appropriate scaling procedure. The data sets were standardized to eliminate the distorting effects of different scales of measurement on the output results (Cupido, 2003; Borazan & Babac, 2003), using the STAND function. As the data was mixed (binary, qualitative, and quantitative/ratio, depending on the data set) the SIMINT function (with the Manhattan distance option) was used to compute a variety of similarity and dissimilarity coefficients for interval measure (quantitative) data, generating a correlation matrix. The most commonly used distance function is the Euclidean distance, but this is also the simplest and may be dependent on scales (Atchley *et al.*, 1982). The Manhattan distance is rather used when the data set contained mixed (metric and binary) data (Cupido, 2003). The Manhattan distance method is the most effective

measure for continuous variables (Pimentel, 1981; Crisp & Weston, 1993), and its stepwise form of measurement suits the assumed hierarchical nature of taxonomic data (Chandler & Crisp, 1998).

Cluster Analysis

The Clustering analysis utilized the SAHN (Sequential Agglomerative Hierarchical Nested Cluster Analysis) function. James & McCulloch (1990) note that it has become conventional in systematics to use the UPGMA (unweighted pair-group method using averages), which distributes the objects into a reasonable number of groups by calculating differences between clusters as the average of all the point-to-point distances between a point in one cluster and a point in the other. The resulting phenogram was plotted using the TREEPLOT function in NTSYS.

The COPH function takes a hierarchical system of clusters and produces a symmetrical matrix of "cophenetic" (ultrametric) similarity or dissimilarity values, which can be used to test for the goodness of fit of a clustering to a set of data. The MXCOMP function takes two symmetric similarity or dissimilarity matrices and plots one matrix against the other element by element, and also computes the product-moment correlation, r , and the Mantel test statistic, Z , (Mantel, 1967) to measure the degree of relationship between the two matrices. The correlation can be used as a measure of goodness of fit for a cluster analysis (the subjective interpretation is roughly $r > 0.9$ indicates a very good fit, $r < 0.7$ indicates a very poor fit).

Principle Component Analysis

The principal components of a matrix are computed by its eigenvalues and eigenvectors, which describe the relationship between operational taxonomic units (Borazan & Babac, 2003). The EIGEN function was used to extract the first three PCA axes from the correlation matrix, along with the eigenvectors and values. The PROJ function was used to project objects onto PCA axes and the 2D PLOT option was used to produce scatterplots of the first three PCA axes. Colours were inserted into the plot circles using PaintShopPro version 4.12 (JASC, Inc).

Results

Tests of normality

The results of the Lilliefors test of normality on all continuous variables are presented in Table 2.3.1 below. The significant p-values for several variables indicate that those variables are not normally distributed, and that logging the data was therefore necessary. Non-normal data does not affect CA, but the logging of data was necessary for PCA.

Table 2.3.1: Table of Lilliefors test of normality p-values for all continuous size variables. Asterisks indicate significant values.

Variable	P-value
Outer Involucral scale length	p<0.01*
Outer Involucral scale width	p<0.15
Inner Involucral scale length	p<0.01*
Inner Involucral scale width	p<0.15
Involucre length	p>0.2
Involucre width	p>0.2
Leaf Length	p<0.01*
Leaf Width	p<0.01*
Stem Length	p<0.01*

Cluster Analysis

The dendrograms from Cluster Analysis of the RAW, RAT and TOTAL data sets are presented in Figures 2.3.1 to 2.3.12. Two species (*G. tenuifolia* and *G. lichtensteinii*) are clearly clustered together in all three analyses regardless as to whether size data or ratio data are used (Figures 2.3.2, 2.3.6 and 2.3.10). Two taxa (*G. rigens* and *G. linearis* subsp *ovalis*) always cluster together in their own branches, but are also always interspersed with one or two additional samples from other species (Figures 2.3.2, 2.3.3, 2.3.6, 2.3.8, 2.3.10 and 2.3.11). Most *G. heterochaeta* samples cluster clearly together, while one or two samples were scattered through the phenogram (Figures 2.3.3, 2.3.8 and 2.3.11). The same holds for most *G. jurineifolia* samples, which cluster together in the same branch, but are sometimes interspersed with some few samples from other taxa (Figures 2.3.3, 2.3.8 and 2.3.11). The remaining taxa samples do not show any clear groupings and are interspersed with each other. Although there are a few small *G. krebsiana* and *G. linearis* clusters (Figures 2.3.8, 2.3.10 and 2.3.11), these clusters do not include all examples of the species and are not retrieved in all three data set analyses.

Figure 2.3.2 contains a cluster (named “A” on the dendrogram) that is composed of a mix of samples from several taxa: *G. linearis* subsp *ovalis*, *G. linearis* subsp *linearis*, *G. pectinata* and *G. ciliaris*.

All of these species are characterised by extremely long and thin acuminate involucre scales. The use of raw size data, rather than shape data from ratios, is the most likely reason that these samples are clustering together.

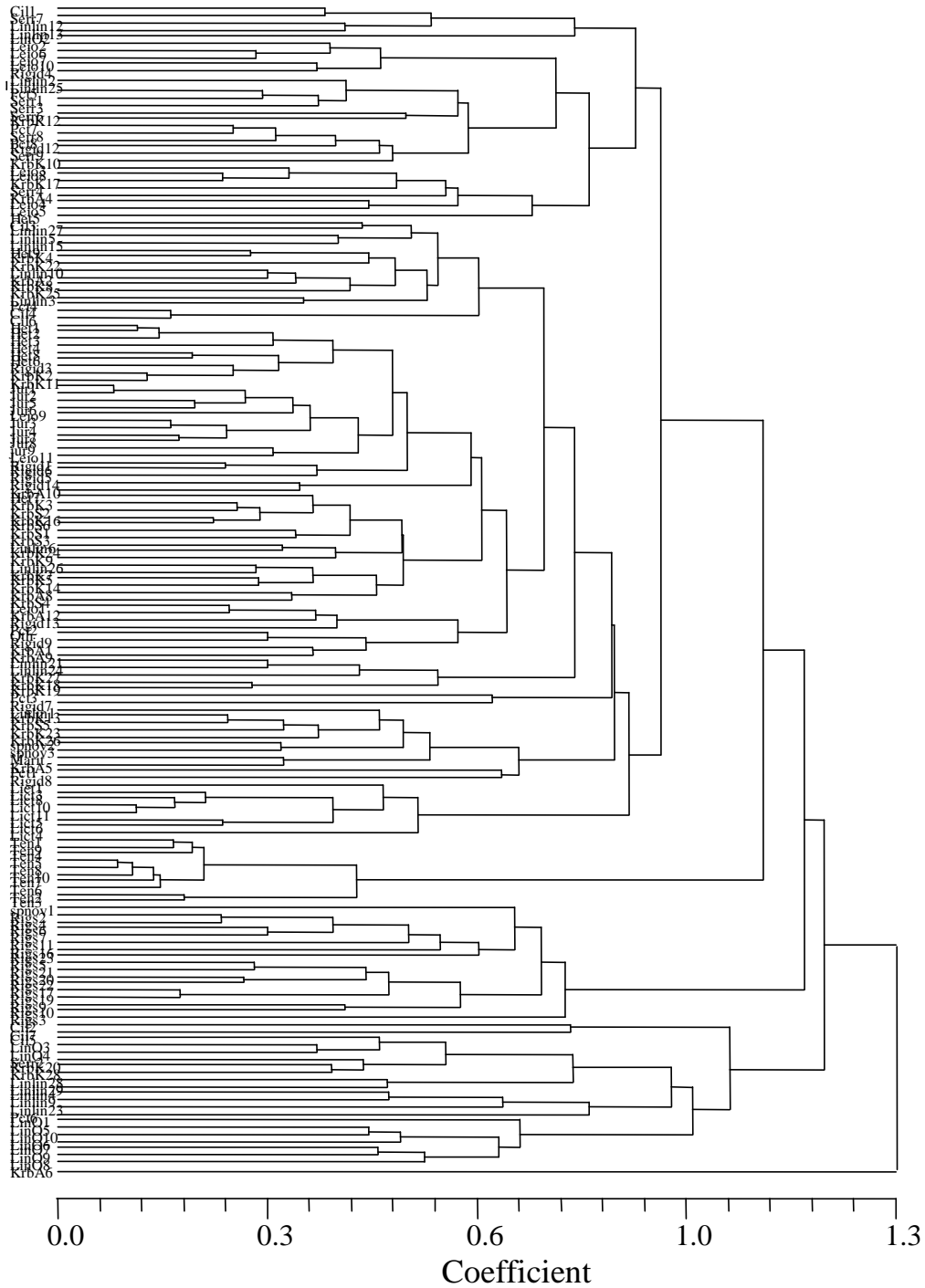


Figure 2.3.1: Cluster Analysis phenogram of RAW data (standardized, Manhattan distance, UPGMA, $r=0.67$). Detailed expansion of branches is provided in next three figures.

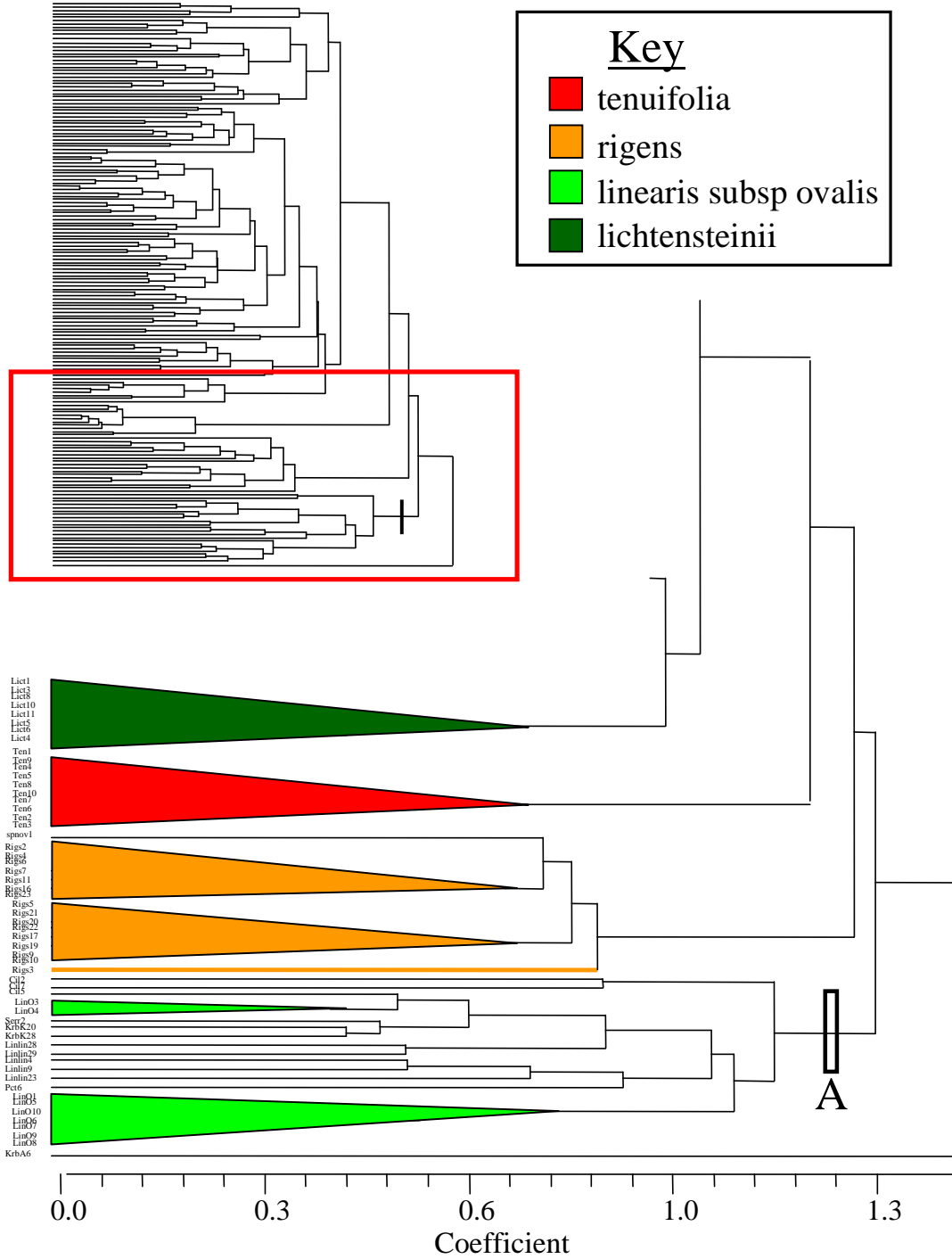


Figure 2.3.2: Lowest third of Cluster Analysis phenogram of RAW size data (full phenogram in Figure 2.3.1). Triangles indicate monospecific branches. “A” marks cluster discussed in detail in text.

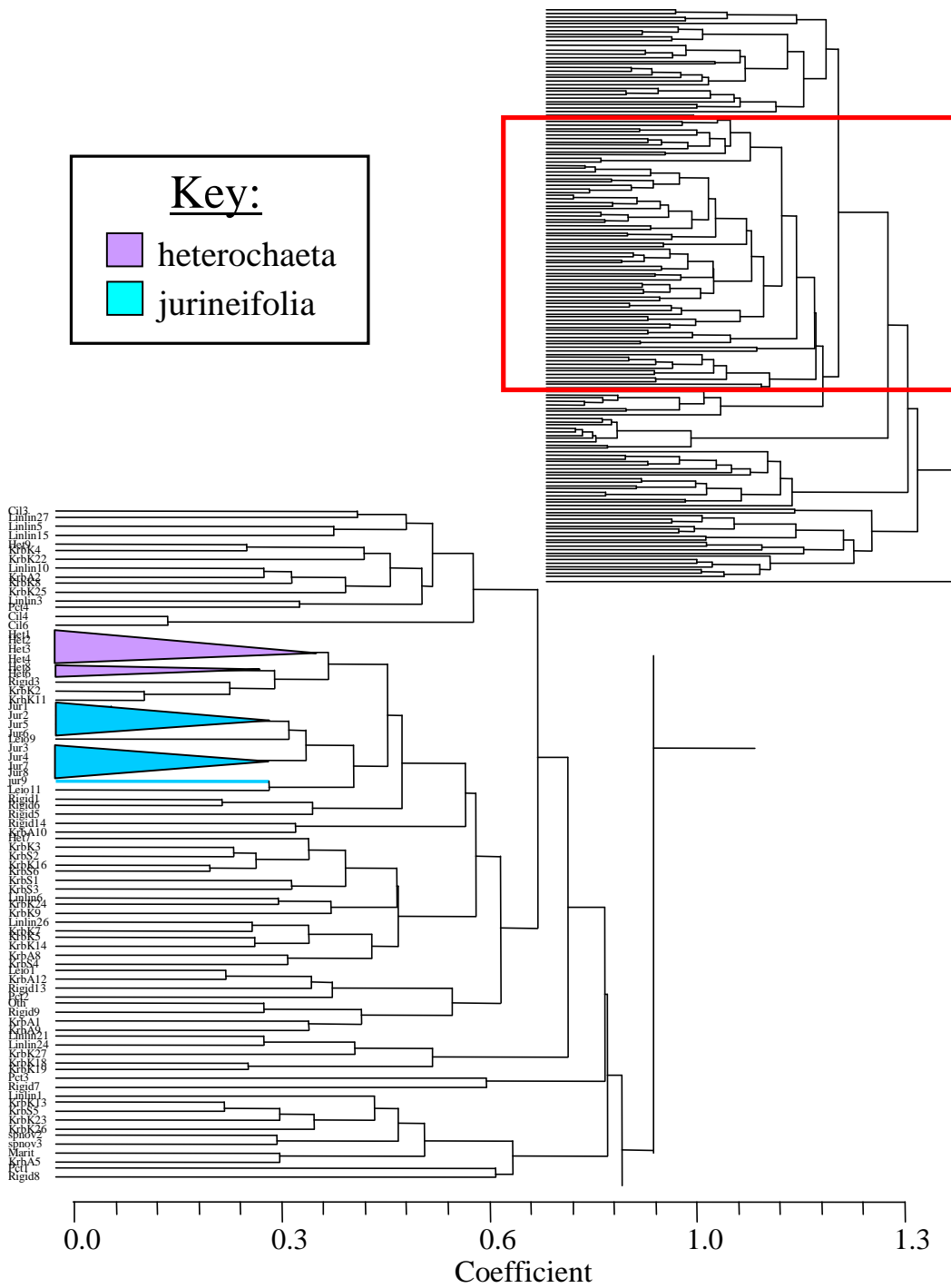


Figure 2.3.3: Middle third of Cluster Analysis phenogram of RAW size data (full phenogram in Figure 2.3.1). Triangles indicate monospecific branches.

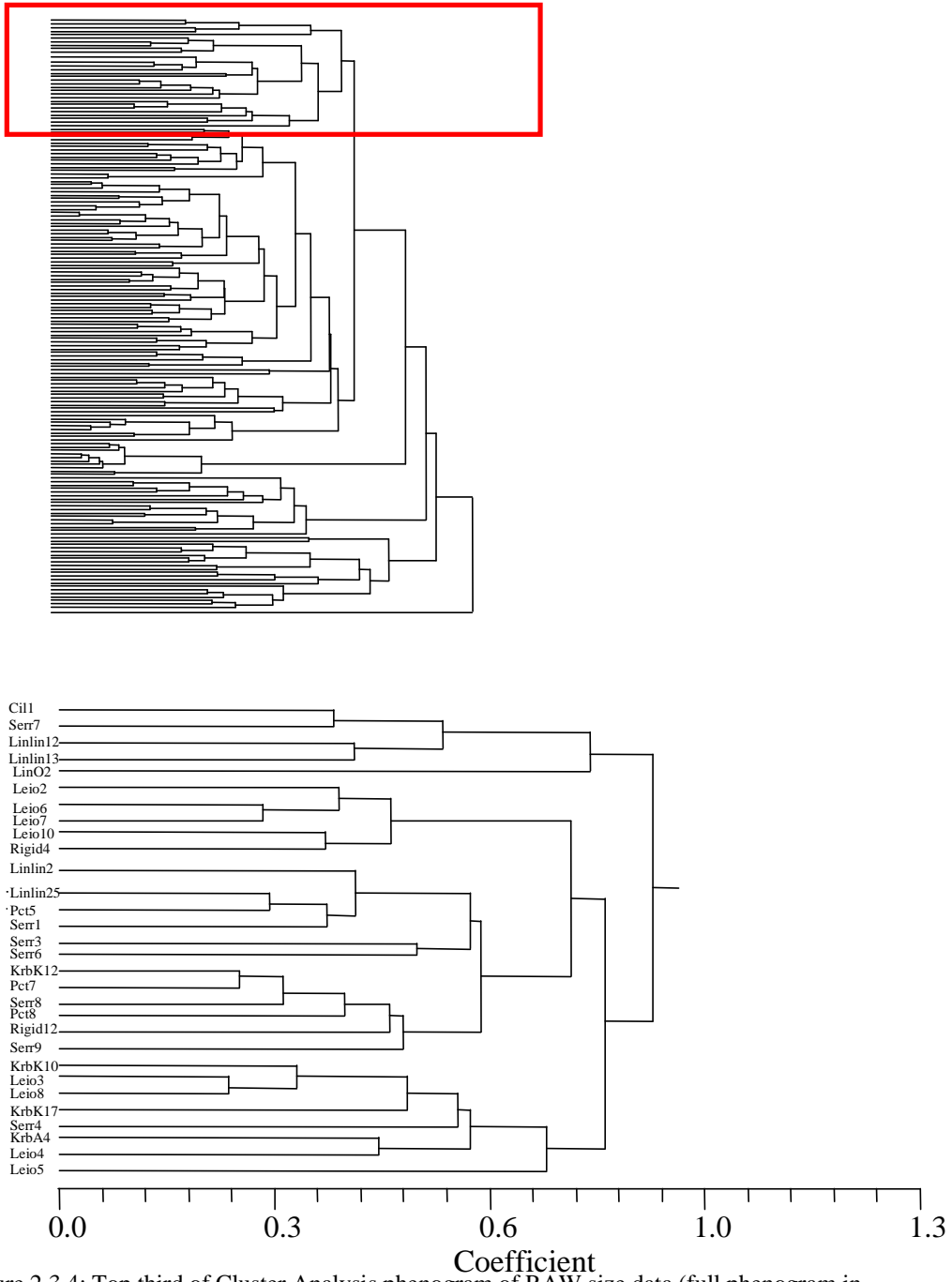


Figure 2.3.4: Top third of Cluster Analysis phenogram of RAW size data (full phenogram in Figure 2.3.1).

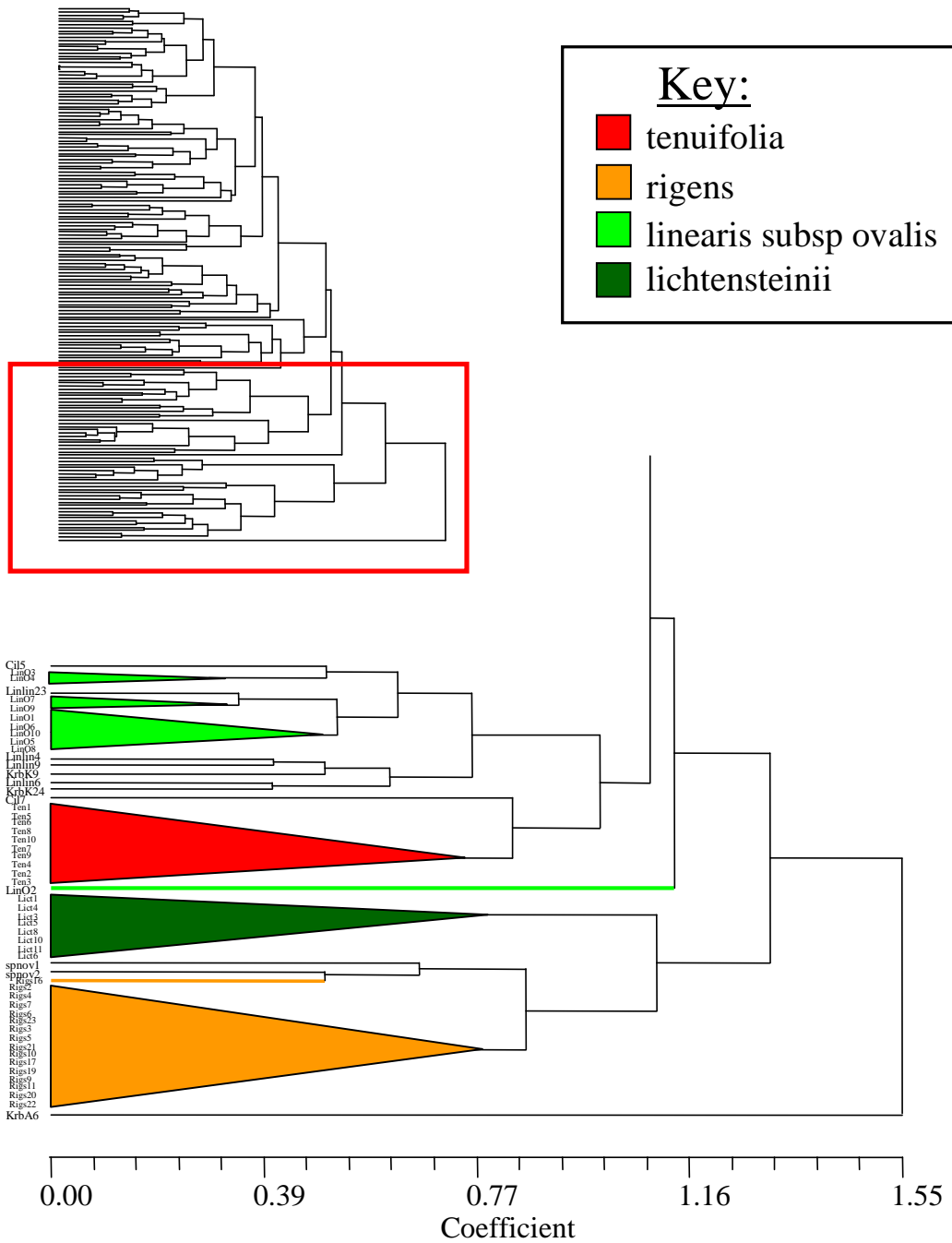


Figure 2.3.6: Lowest third of Cluster Analysis phenogram of RAT size data (full phenogram in Figure 2.3.5). Triangles indicate monospecific branches.

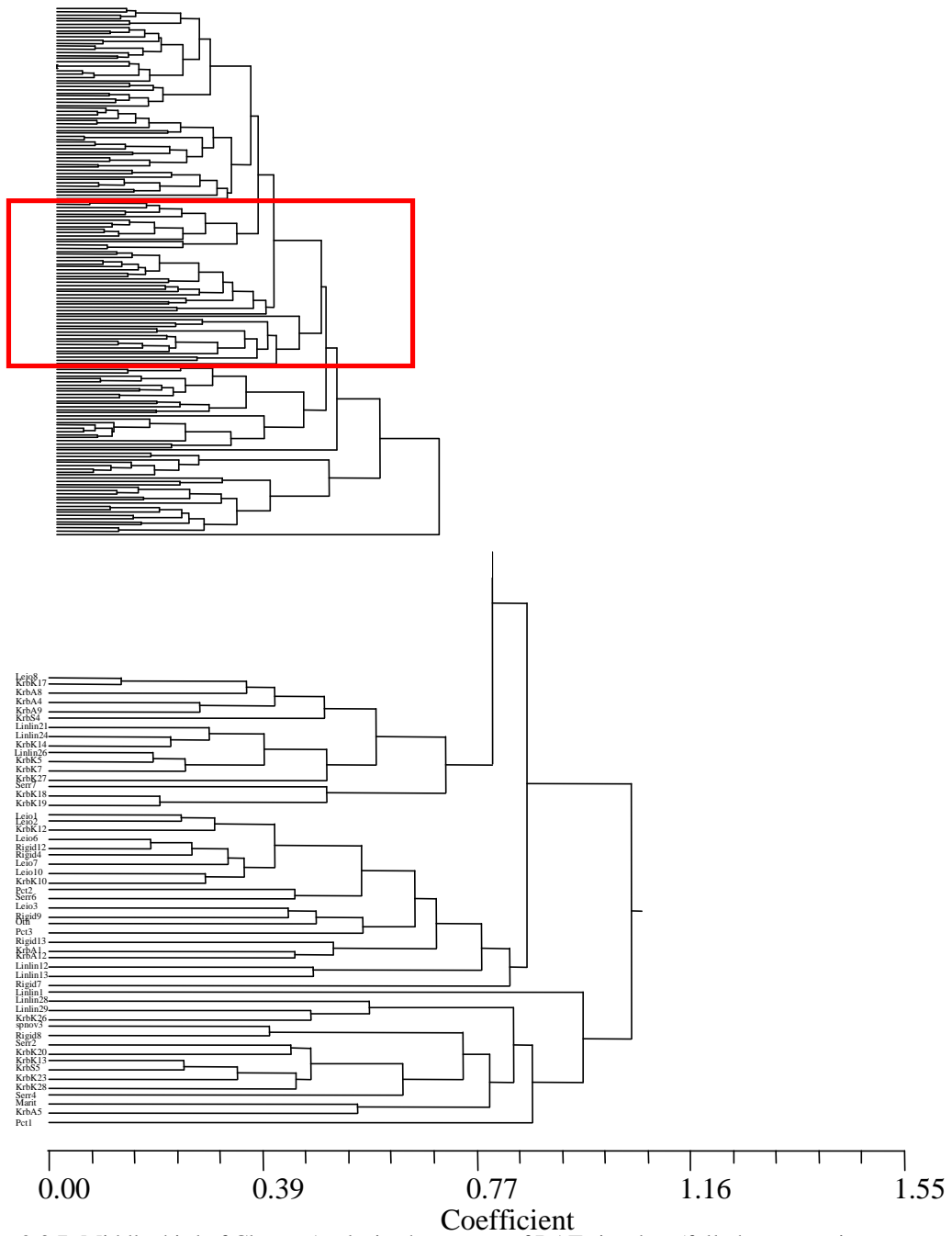


Figure 2.3.7: Middle third of Cluster Analysis phenogram of RAT size data (full phenogram in Figure 2.3.5).

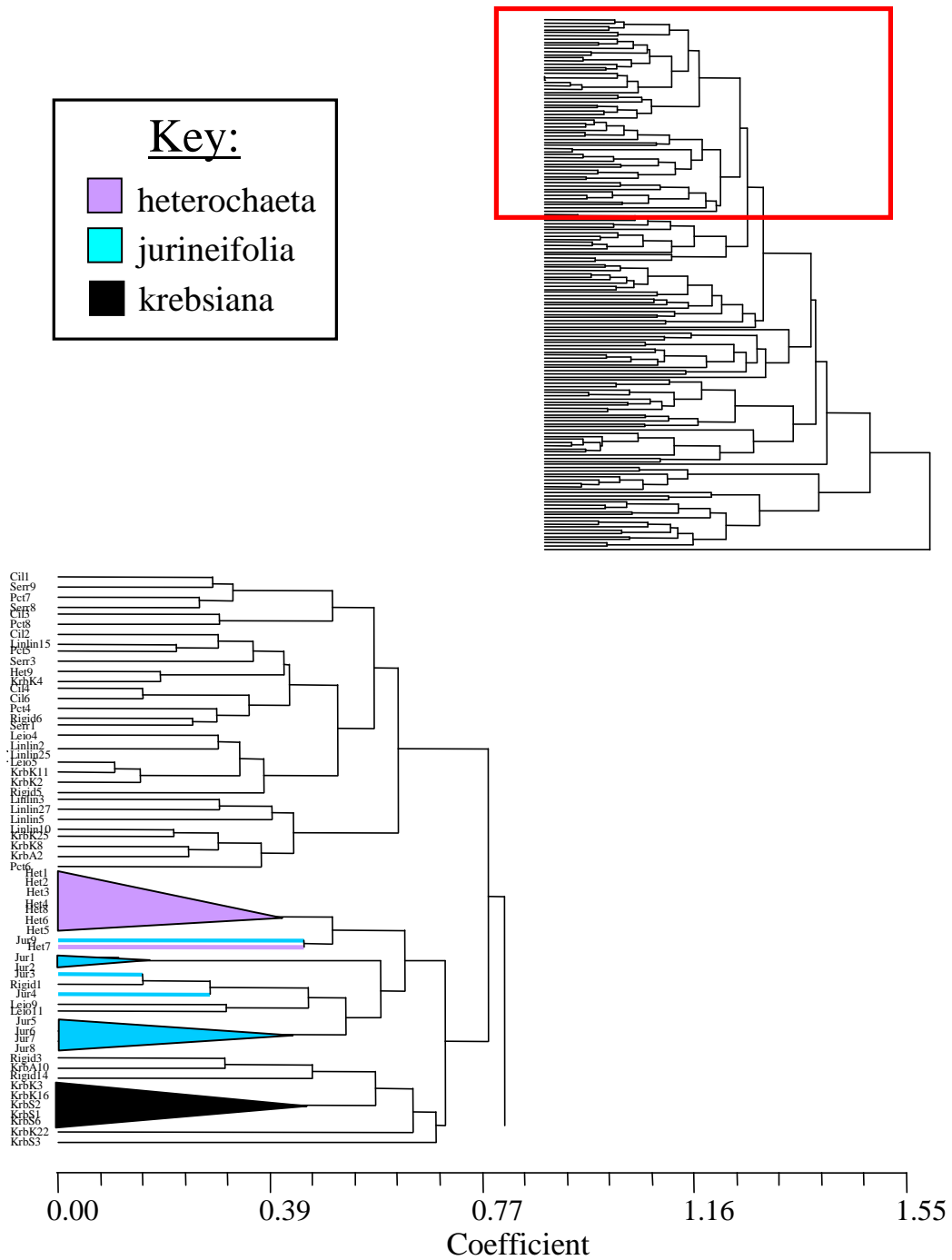


Figure 2.3.8: Top third of Cluster Analysis phenogram of RAT size data (full phenogram in Figure 2.3.5). Triangles indicate monospecific branches.

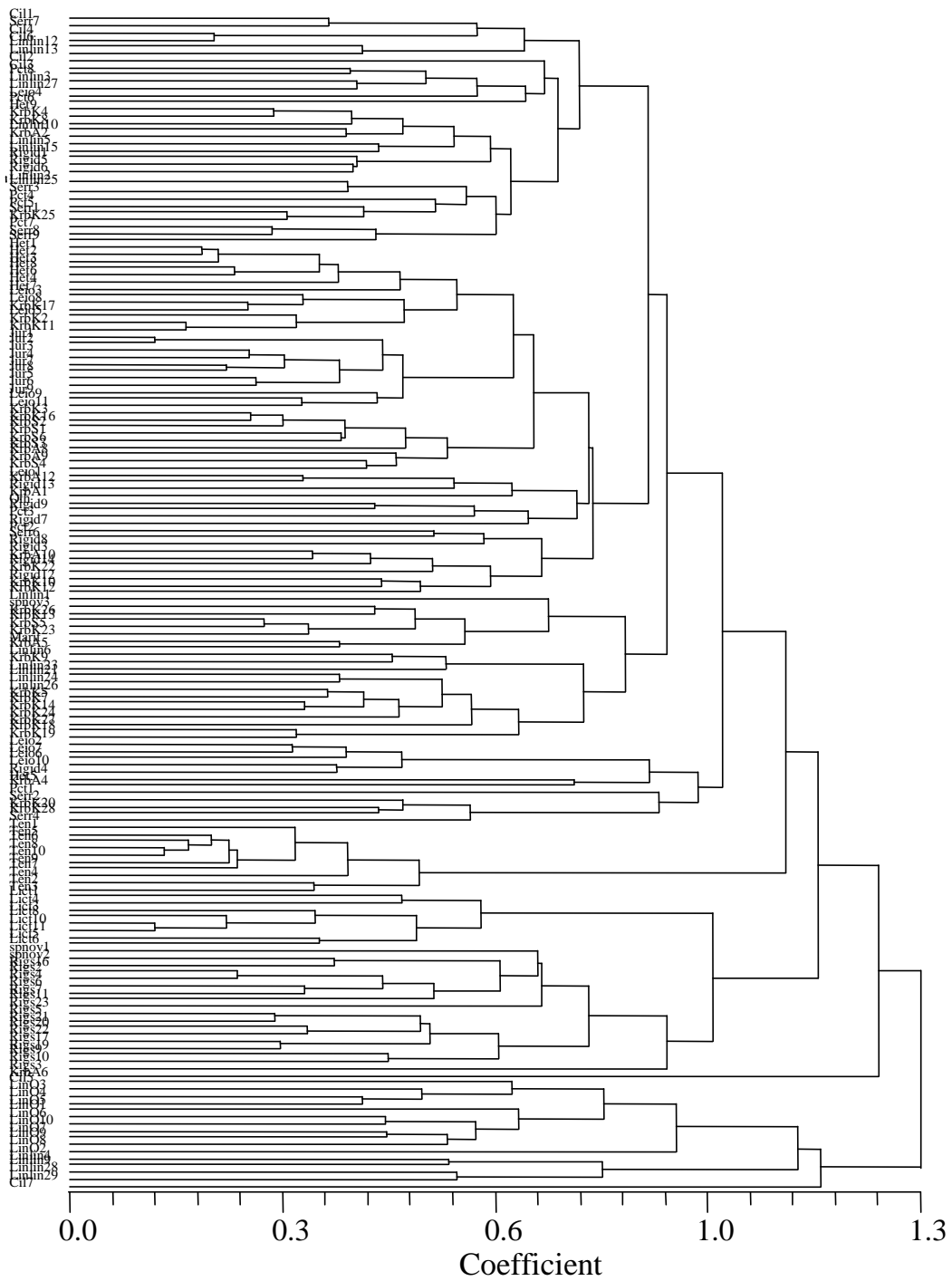


Figure 2.3.9: Cluster Analysis phenogram of TOTAL data (standardized, Manhattan distance, UPGMA, $r=0.68$). Detailed expansion of branches is provided in next three figures.

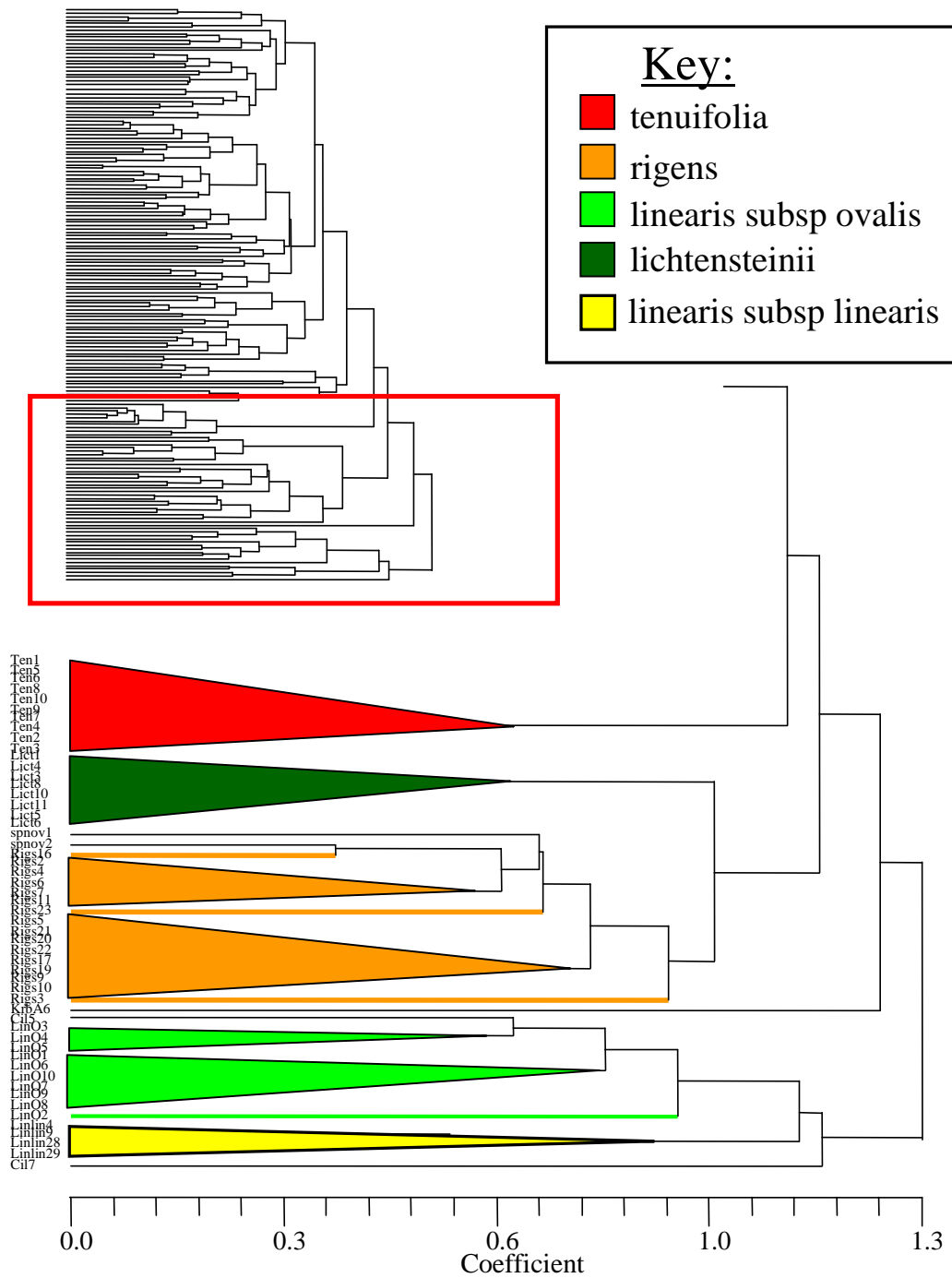


Figure 2.3.10: Lowest third of Cluster Analysis phenogram of TOTAL data (full phenogram in Figure 2.3.9). Triangles indicate monospecific branches.

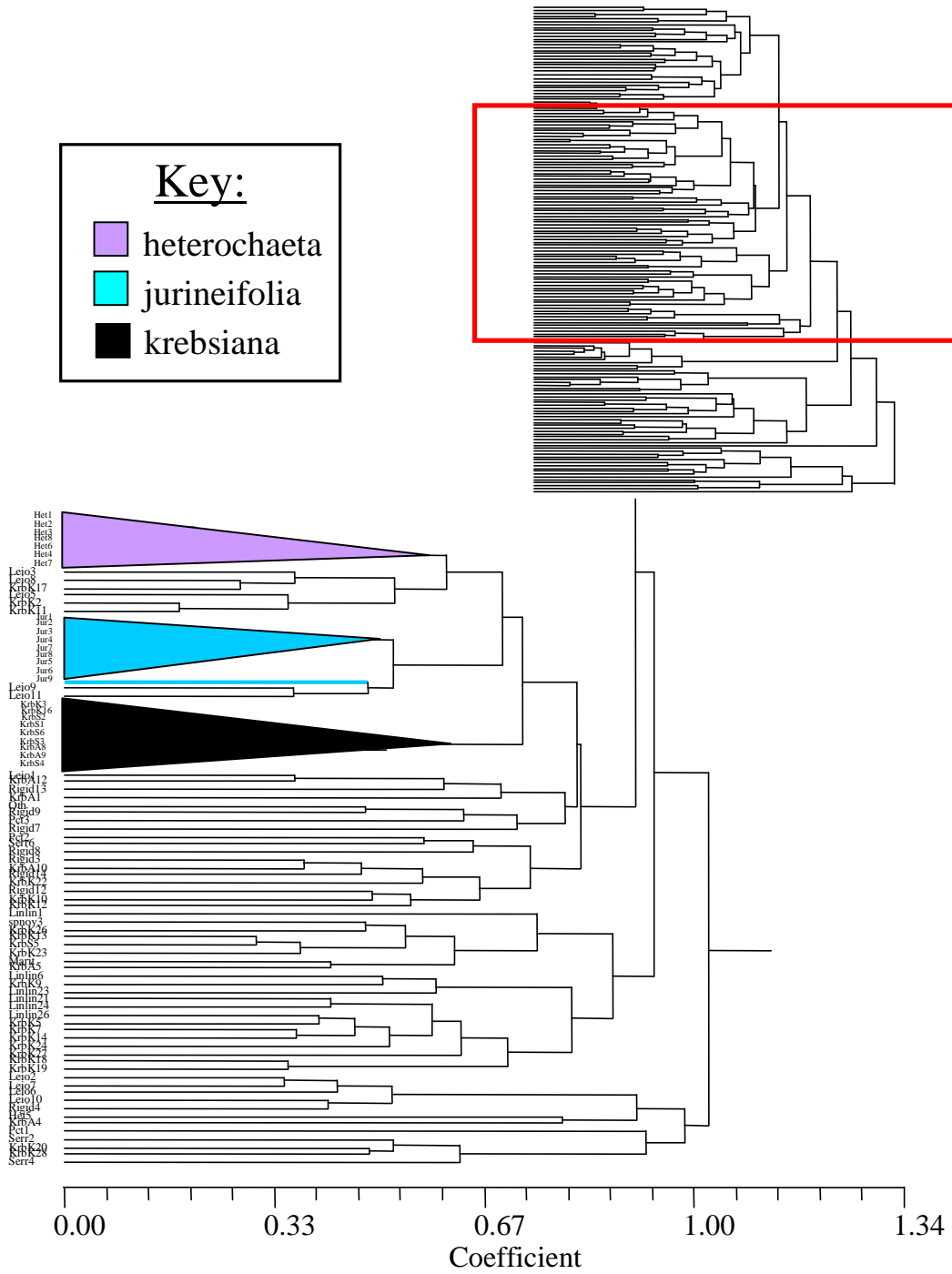


Figure 2.3.11: Middle third of Cluster Analysis phenogram of TOTAL data (full phenogram in Figure 2.3.9). Triangles indicate monospecific branches.

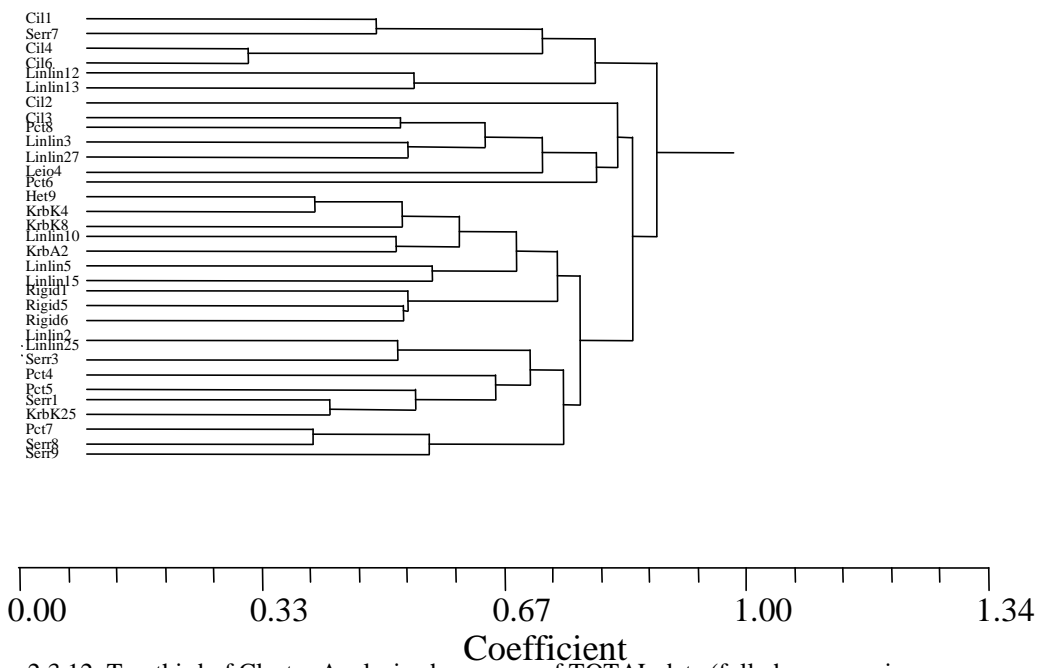
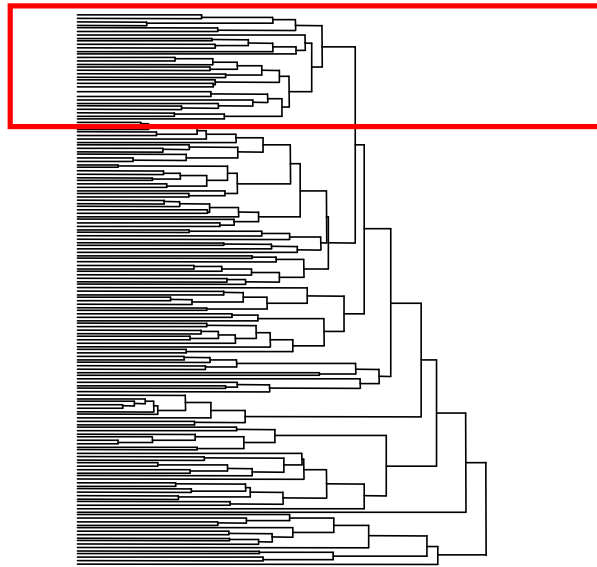


Figure 2.3.12: Top third of Cluster Analysis phenogram of TOTAL data (full phenogram in Figure 2.3.9).

The matrix goodness of fit test produced an $r = 0.67$ for the RAW data, 0.72 for the RAT data and 0.68 for the TOTAL data, all of which could be regarded as a “very poor” fit. The Mantel test resulted in $p = 1$ for all three data sets, likewise indicating a poor fit.

Despite the poor fit to the data, samples of six taxa are consistently clustered together. These six are:

- 1) *G. jurineifolia*,
- 2) *G. lichtensteinii*,
- 3) *G. linearis* subsp *ovalis*,
- 4) *G. rigens*,
- 5) *G. heterochaeta*, and
- 6) *G. tenuifolia*.

The samples of the remaining 10 species do not show any grouping.

Principle Component Analysis

Figures 2.3.13 to 2.3.15 are the scatter plots of the first three PCA axes of the RAW data set. The relative impact of each variable on each axis is presented in Tables 2.3.2 to 2.3.7, along with the percentage variability each axis accounts for. For the RAW data set, the first axis accounts for only 26% of the variability observed (and the next two axes both for significantly less than that).

The first and second axes (Figure 2.3.13) show one clearly discrete plot of *G. tenuifolia* samples (labeled “1”), along with two less clearly separate clusters (“2” and “3”). Cluster 2 consists of all the samples of *G. rigens*, *G. lichtensteinii*, as well as one sample each of *G. maritima*, *G. sp. nov.* and *G. krebsiana*. Cluster 3 consists of the remainder of all other samples.

The first and third axes (Figure 2.3.14) show no clearly discrete clusters. The second and third axes (Figure 2.3.15) show three small clusters that are separate from the rest of the samples. However, these are not single-species specific clusters. Cluster 1 consists of some samples of *G. lichtensteinii*, *G. rigens*, *G. sp. nov.*, and *G. krebsiana*, while Cluster 2 consists of samples of *G. rigens*, *G. maritima* and *G. krebsiana*. Cluster 3 consists of samples of *G. tenuifolia*, *G. linearis* subsp *linearis*, *G. ciliaris* and *G. krebsiana*.

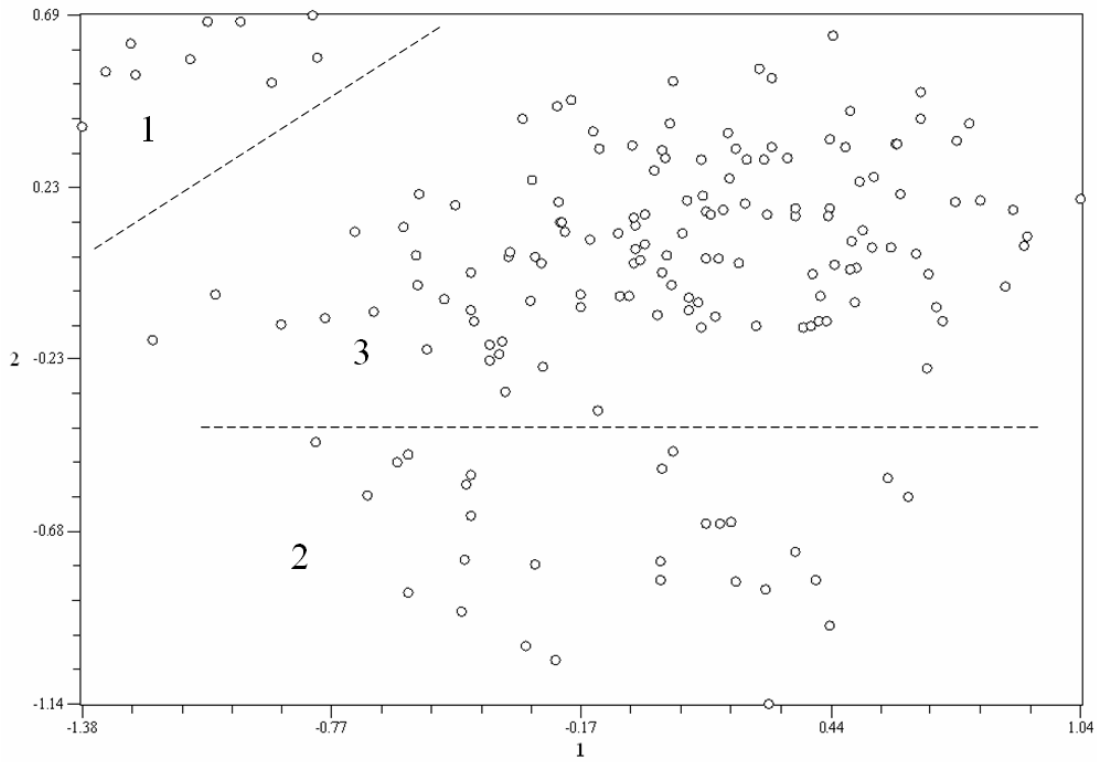


Figure 2.3.13: Scatterplot of first and second PCA axes of RAW data set. Dashed lines separate numbered clusters (details of cluster composition discussed in text).

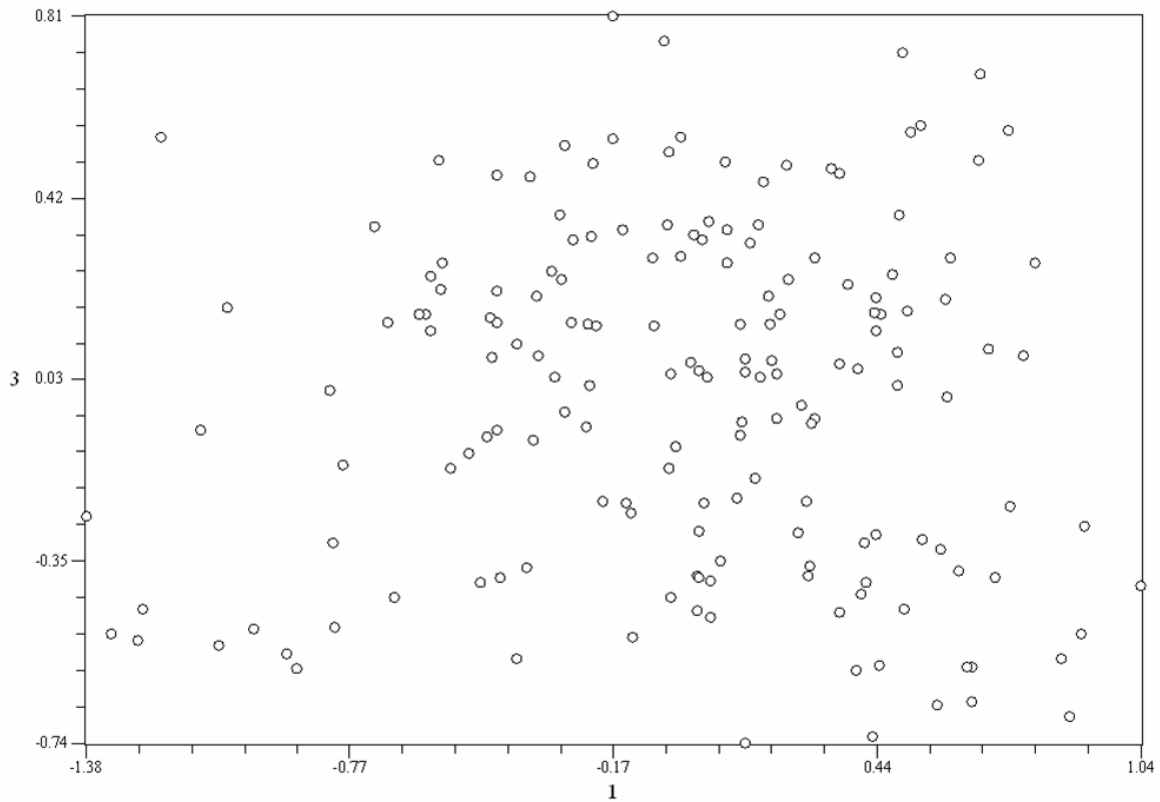


Figure 2.3.14: Scatterplot of first and third PCA axes of RAW data set. No clearly separate clusters are visible.

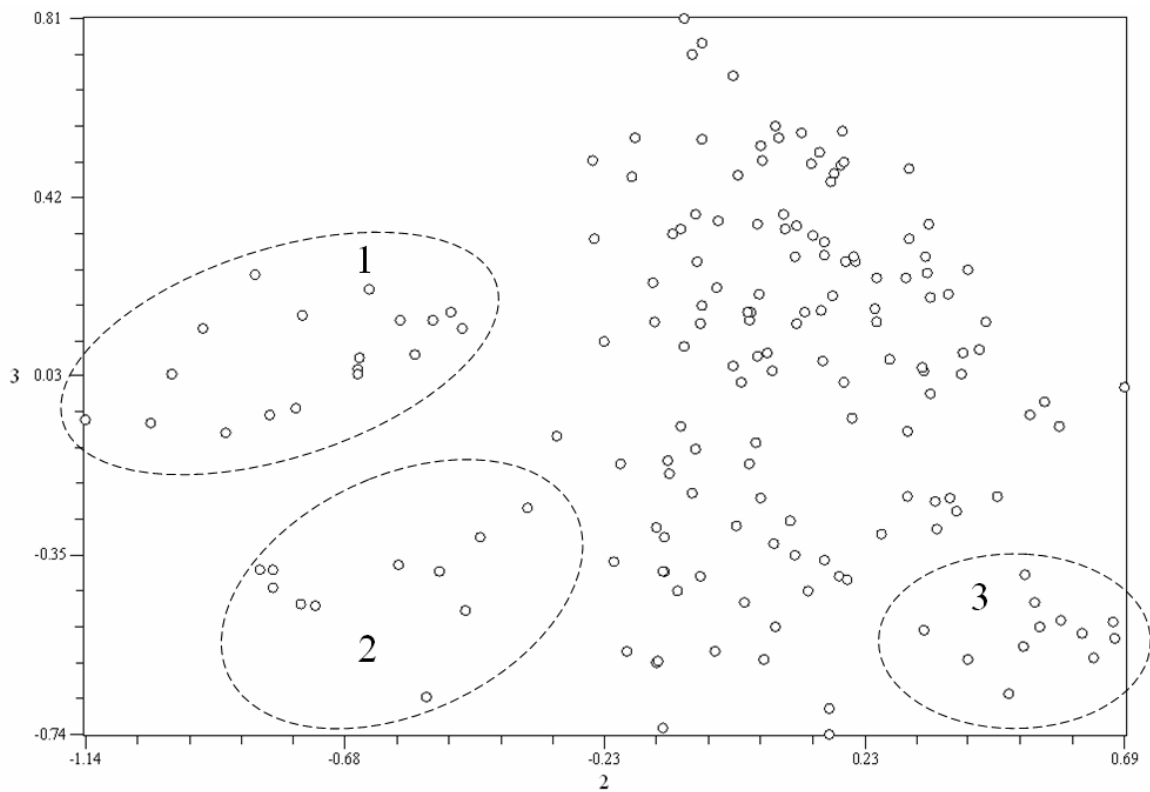


Figure 2.3.15: Scatterplot of second and third PCA axes of RAW data set. Circled and numbered clusters are discussed in detail in text.

Table 2.3.2: RAW data: Impact of each character on each PCA axis (most significant contributors highlighted in bold red) and total % variability accounted for by each PCA axis.

Character	Axis1	Axis2	Axis3
Habit	0.0484	0.7862	0.1503
InvSet	0.0559	-0.1737	0.3564
ParScl	-0.0776	0.3901	-0.4069
InvBase	-0.3034	0.3611	-0.3851
LfIndu	0.0894	0.2801	0.7703
LfMarg	-0.0021	0.5406	0.5412
LfDiss	-0.0826	0.4662	0.4411
OIL	0.723	0.3033	-0.3302
OIW	0.624	-0.4496	0.1656
IIL	0.6337	0.2582	-0.4154
IIW	0.5377	-0.1221	0.2743
InvL	0.7602	-0.163	0.2537
InvW	0.7935	0.0077	0.1636
LfLgth	0.6817	0.278	-0.1579
LfWdth	0.5469	-0.4753	-0.0412
StmLgth	0.6661	0.4168	-0.2225
% Variab.	25.8	15	13

Figures 2.3.16 to 2.3.18 are the scatter plots of the first three PCA axes of the RAT data set. As for the RAW data set, there are no discrete separate clusters apparent in the scatterplots. The first two axes accounts for only 21% and 18% of the observed variability.

Figures 2.3.19 to 2.3.21 are the scatter plots of the first three PCA axes of the TOTAL data set. Figure 2.3.19 shows some separation of the *G. tenuifolia* samples (above the dashed line), but little other cluster separation is visible. Figure 2.3.20 shows no clear cluster separation. Figure 2.3.21 shows three clusters. Cluster 1 consists of all the samples of *G. lichtensteinii*, *G. linearis* subsp *ovalis* and *G. rigens*, as well as some samples of *G. heterochaeta* and *G. sp. nov.*. Cluster 3 consists of *G. tenuifolia* samples, and Cluster 2 consists of the remaining samples. The first axis only accounts for just 22% of the variability observed in the data.

All three data sets achieve much the same level of results, indicating that, in *Gazania* at least, neither shape ratios nor actual size data can provide a better method for the separation of morphologically overlapping species.

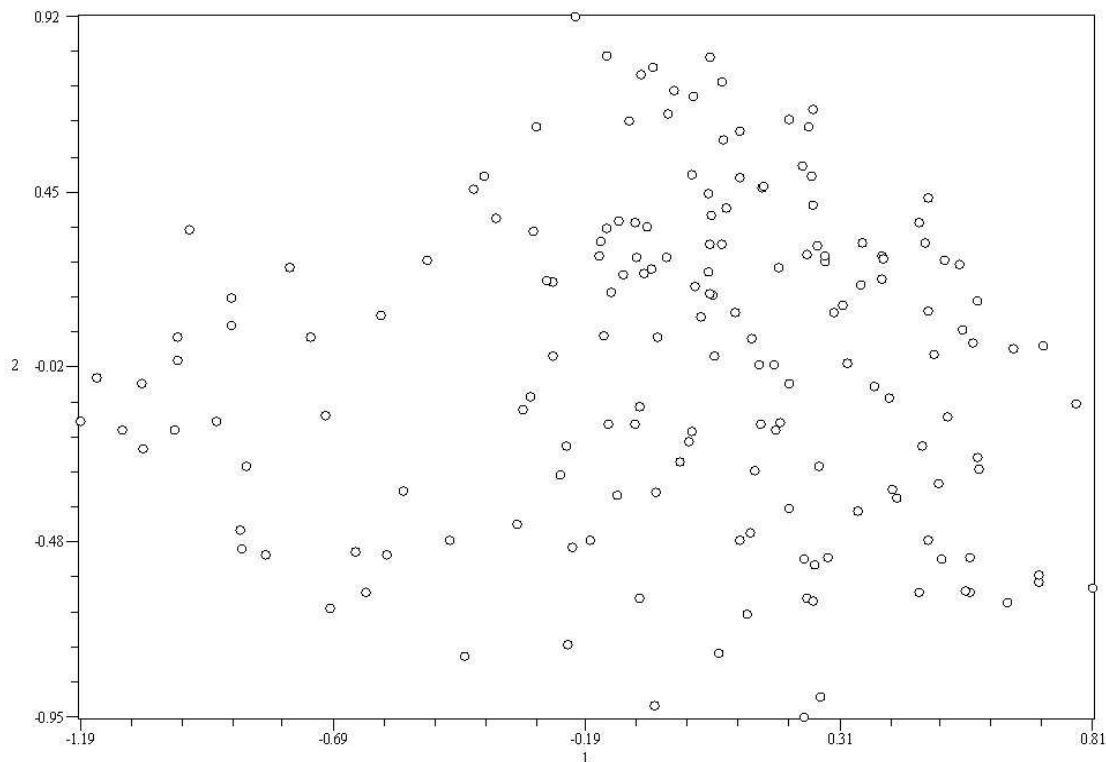


Figure 2.3.16: Scatterplot of first and second PCA axes of RAT data set. No clearly separate clusters are visible.

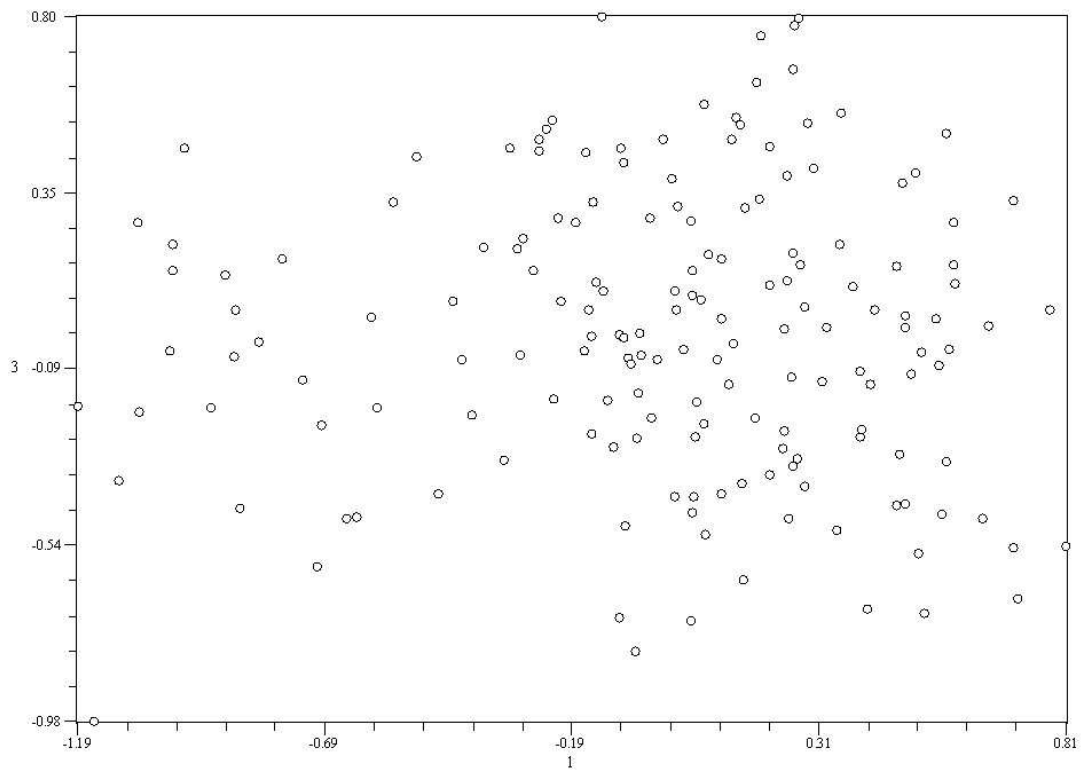


Figure 2.3.17: Scatterplot of first and third PCA axes of RAT data set. No clearly separate clusters are visible.

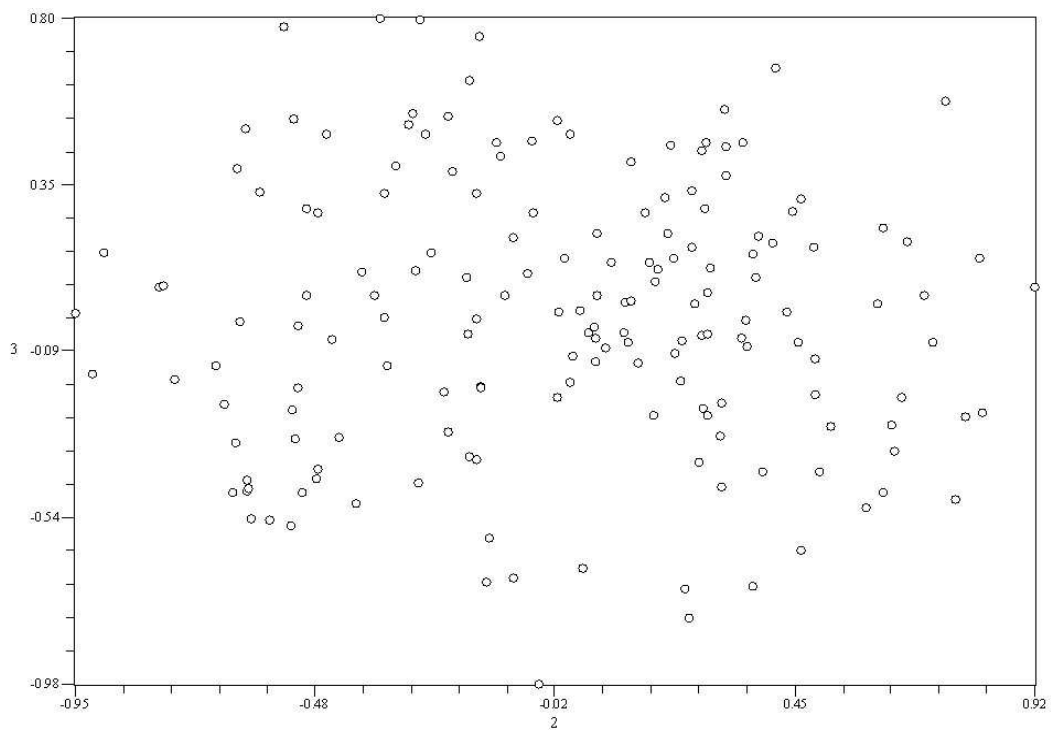


Figure 2.3.18: Scatterplot of second and third PCA axes of RAT data set. No clearly separate clusters are visible.

Table 2.3.3: RAT data: Impact of each character on each PCA axis (most significant contributors highlighted in bold red) and total % variability accounted for by each PCA axis.

Character	Axis1	Axis2	Axis3
Habit	0.7708	0.2323	0.1274
InvSet	-0.1604	0.2931	-0.3743
ParScl	0.3935	-0.4465	-0.5607
InvBase	0.341	-0.3343	-0.1013
LfIndu	0.2314	0.761	-0.0978
LfMarg	0.4706	0.5571	0.0362
LfDiss	0.394	0.4224	-0.5357
LogOIRAT	0.7135	-0.374	0.2858
LogIRAT	0.3954	-0.653	-0.0433
LogOI/II	0.2692	0.1959	0.5228
LogInvRAT	-0.2254	0.0632	0.6252
LogLFRAT	0.6175	0.0639	0.2055
% Variab.	20.8	17.8	13

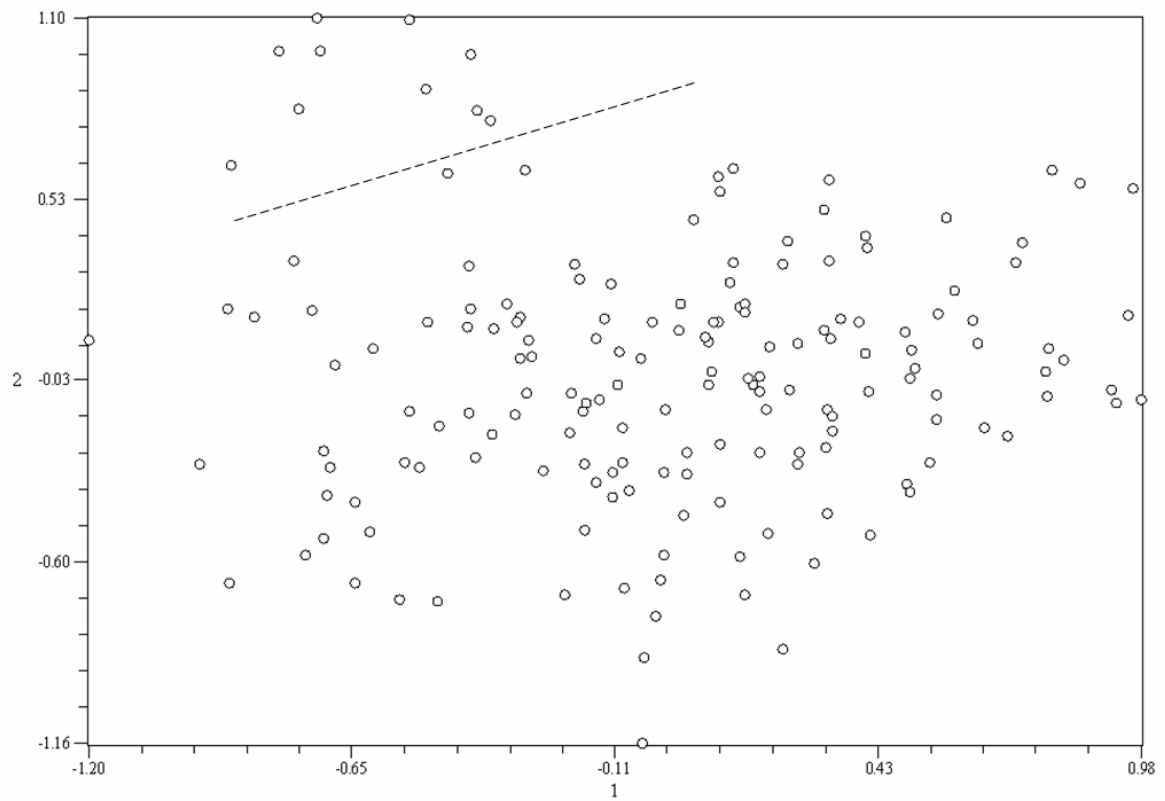


Figure 2.3.19: Scatterplot of first and second PCA axes of TOTAL data set. Dashed line separates *G. tenuifolia* samples (above line) from remaining samples.

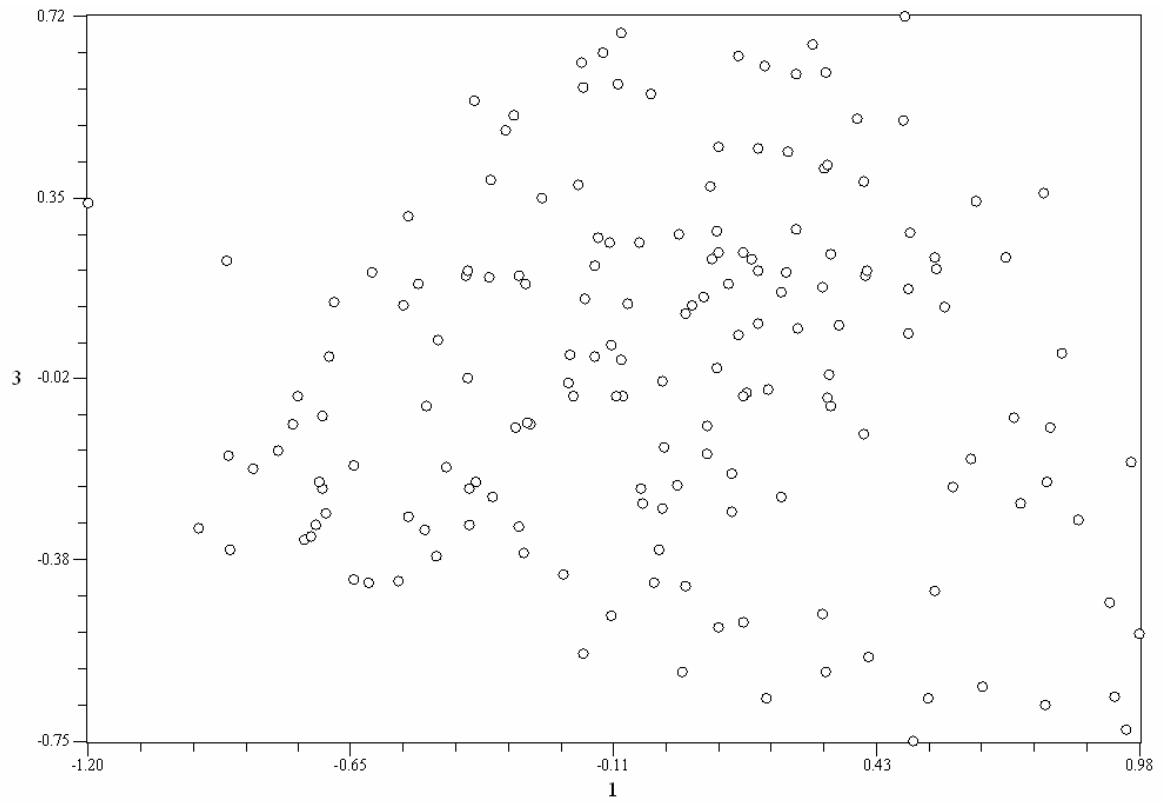


Figure 2.3.20: Scatterplot of first and third PCA axes of TOTAL data set. No clearly separate clusters are visible.

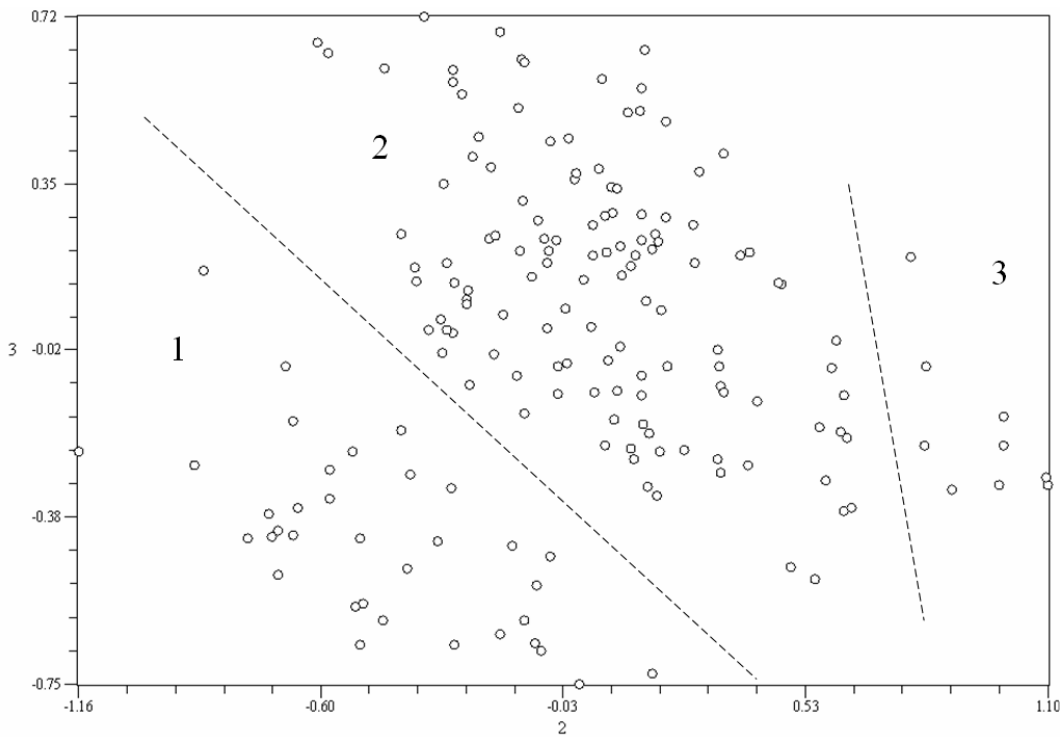


Figure 2.3.21: Scatterplot of second and third PCA axes of TOTAL data set. Dashed line separate three numbered clusters (details of cluster composition discussed in text).

Table 2.3.4: TOTAL data: Impact of each character on each PCA axis (most significant contributors highlighted in bold red) and total % variability accounted for by each PCA axis.

Character	Axis1	Axis2	Axis3
Habit	0.2476	0.5537	0.4819
InvSet	-0.0336	-0.2496	0.2514
ParScl	0.1323	0.4197	-0.264
InvBase	-0.123	0.4623	-0.1491
LfIndu	0.025	-0.1005	0.6925
LfMarg	0.0498	0.1964	0.5316
LfDiss	-0.02	0.1608	0.488
OIL	0.8761	0.1627	-0.1119
OIW	0.3808	-0.7232	0.0329
IIL	0.7527	0.1267	-0.419
IIW	0.3539	-0.492	0.2553
InvL	0.5816	-0.4781	0.1743
InvW	0.7254	-0.4114	0.158
LfLgth	0.7376	0.0877	0.2005
LfWdth	0.3503	-0.6457	-0.3568
StmLgth	0.7564	0.1791	0.0879
LogOIRAT	0.5318	0.6648	-0.1261
LogIIRAT	0.4781	0.45	-0.5691
LogOI/II	0.2955	0.0713	0.3688
LogInvRAT	-0.4184	0.1064	-0.0492
LogLFRAT	0.191	0.6326	0.453
% Variab.	22	17	12

Six species data set

In an effort to investigate the six most commonly clustered species retrieved in the CA dendrograms, the TOTAL data set was subdivided, and a smaller data set was constructed, consisting of only the six most commonly retrieved species clusters from the CA. A PCA was conducted on this smaller data set to see if the six CA species clusters could be distinguished by PCA.

Figures 2.3.22 to 2.3.24 are the scatterplots for the first three PCA axes for the TOTAL data set, containing only the six most commonly retrieved CA species. With the first two axes (Figure 2.3.22) the only species that shows true separation from all the others is *G. tenuifolia*. With the first and third axes (Figure 2.3.23), three separate clusters can be seen, one composed of *G. tenuifolia* samples, one composed of a mix of *G. lichtensteinii*, *G. jurineifolia* and *G. heterochaeta* samples and a third cluster composed of *G. linearis* subsp *ovalis* and *G. rigens* samples.

With the second and third axes (Figure 2.3.24), *G. lichtensteinii* becomes a distinct cluster. The cluster to the bottom right of the plot contains all the *G. tenuifolia*, *G. rigens* and *G. linearis* subsp

ovalis samples, and the cluster at the top again shows no separation between *G. heterochaeta* and *G. jurineifolia* is seen.

Ray colour was added as a 22nd character (in binary format: 1 = white, 0 = not white) to investigate if this could separate *G. jurineifolia* from *G. heterochaeta* (*G. jurineifolia* has white rays, while all the other species of *Gazania* have yellow, orange or red rays). Figures 2.3.25 to 2.3.27 are the scatterplots of the TOTAL data set, now including the additional ray colour character. Figure 2.3.25 now shows species clustering of *G. tenuifolia*, *G. linearis* subsp *ovalis* and *G. jurineifolia*. Figure 2.3.26 of the first and third axes shows an almost clear separation of all six species, although there is some slight overlap between some of the clusters it is only a narrow margin, rather than a more pronounced intermingling of samples.

Overall, while not all of the species produce clearly separate clusters on the scatterplots, there are definite trends visible. Certain species tend towards a certain region of the scatterplots, but there is too much overlap in morphological character variation to permit full separation of these species clusters from other similar species clusters. In the remaining species (those that showed no clear clustering on the CA dendrograms) the situation is even worse.

PCA of remaining species

Figures 3.2.28 to 3.2.30 illustrate the PCA analyses of the TOTAL data set containing those samples that showed no clustering in the CA dendrograms. No distinct clusters are visible.

Eigen values

None of the axes from any of the analyses containing all species was found to quantify more than 25% of the variability between the groups. The highest eigen values were found in the PCA of the six species data set, where the first axis quantified 31% of the variability (still a very low percentage).

Uninformative characters

The only characters that were never significant contributors to eigenvectors were “inner involucre scale width” and “outer involucre scale length/inner involucre scale length”. All other characters were significant contributors to at least one analysis’ first three axes.

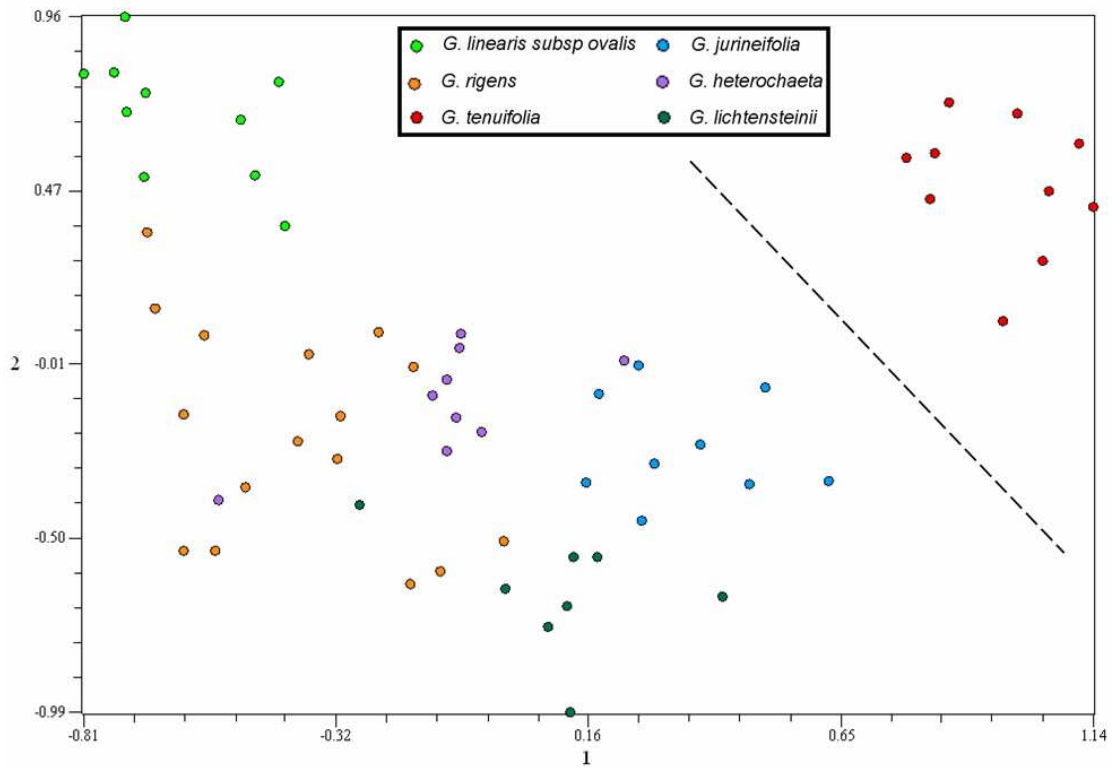


Figure 2.3.22: Scatterplot of first and second PCA axes of TOTAL data set, only containing six species that showed best clustering in CA analysis. Dashed line indicates clearly distinct cluster separation.

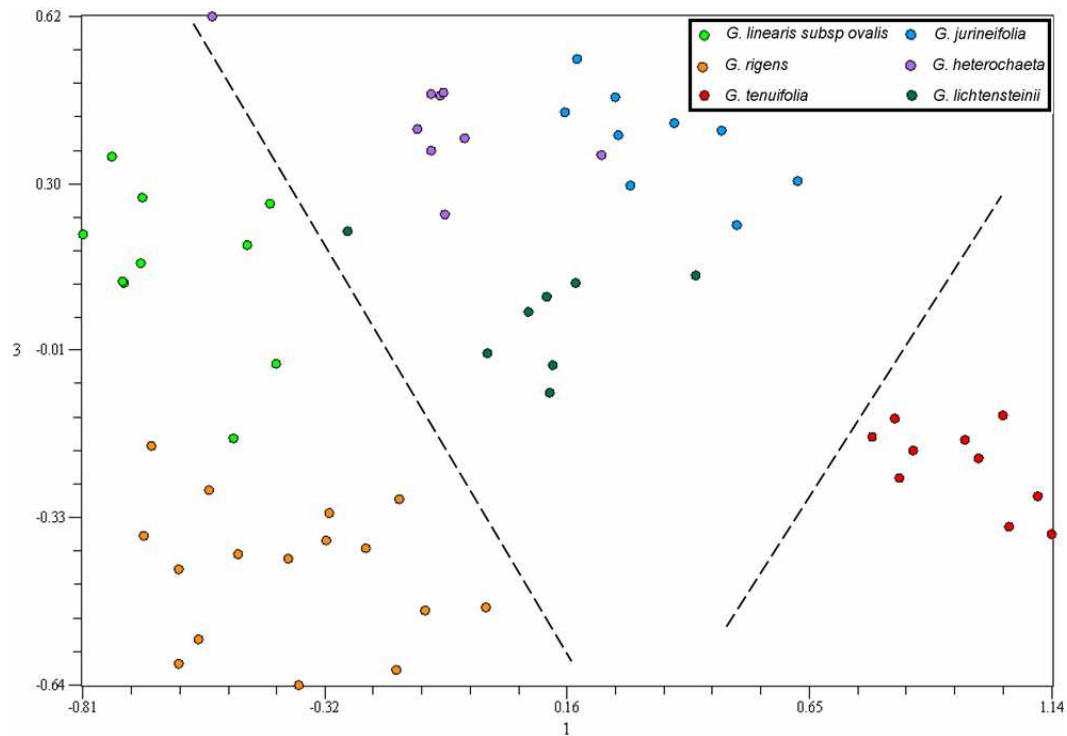


Figure 2.3.23: Scatterplot of first and third PCA axes of TOTAL data set, only containing six species that showed best clustering in CA analysis. Dashed lines indicate clearly distinct cluster separation.

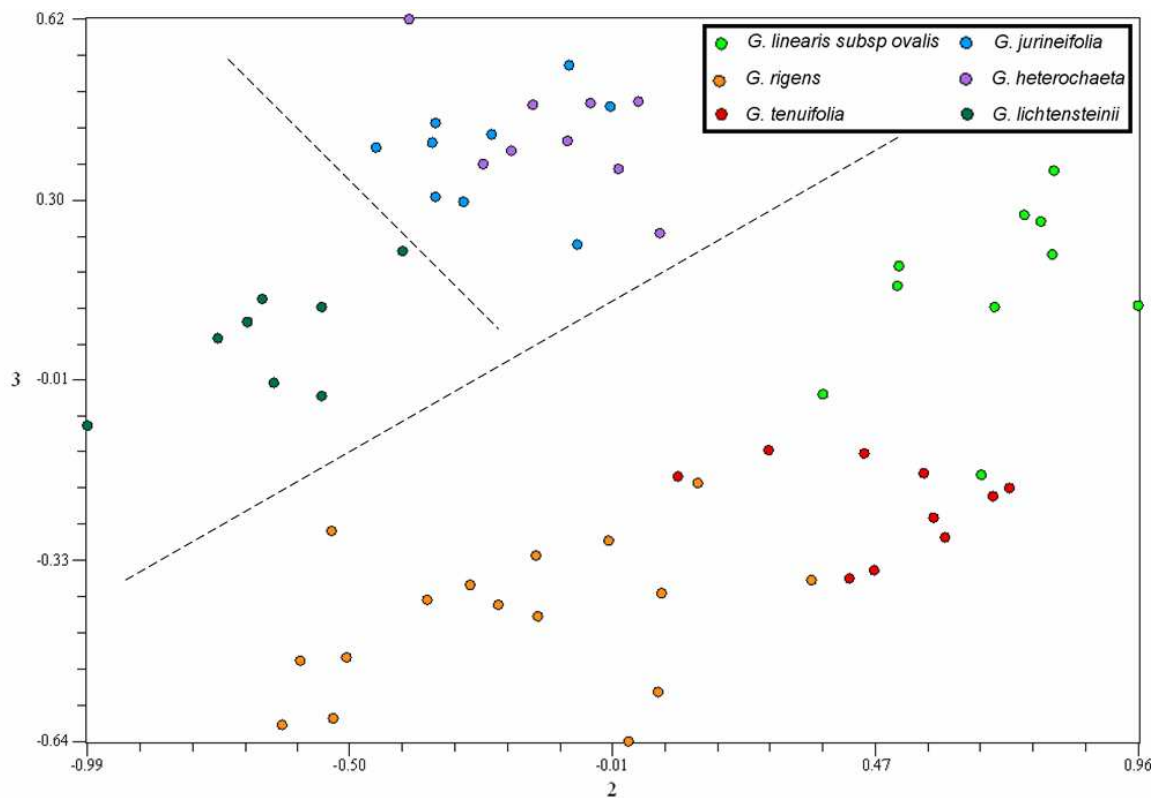


Figure 2.3.24: Scatterplot of second and third PCA axes of TOTAL data set, only containing six species that showed best clustering in CA analysis. Dashed line separates species clusters.

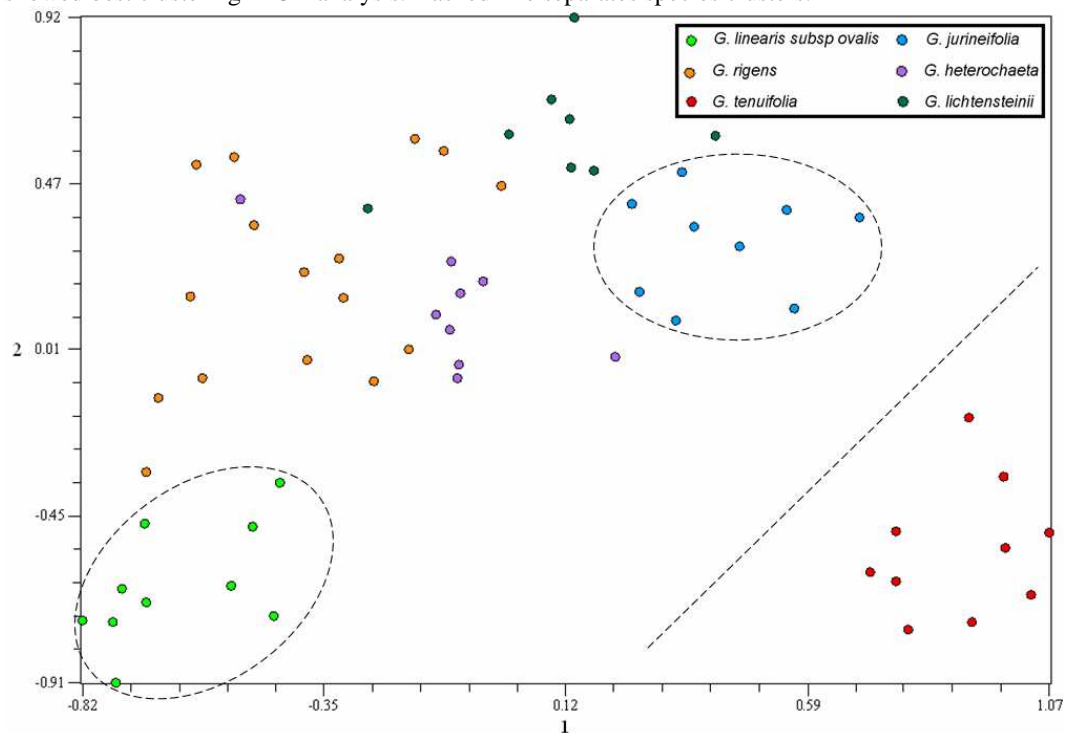


Figure 2.3.25: Scatterplot of first and second PCA axes of TOTAL data set (now including Ray Colour as an additional binary character), only containing six species that showed best clustering in CA analysis. Dashed lines and ovals indicates species clusters.

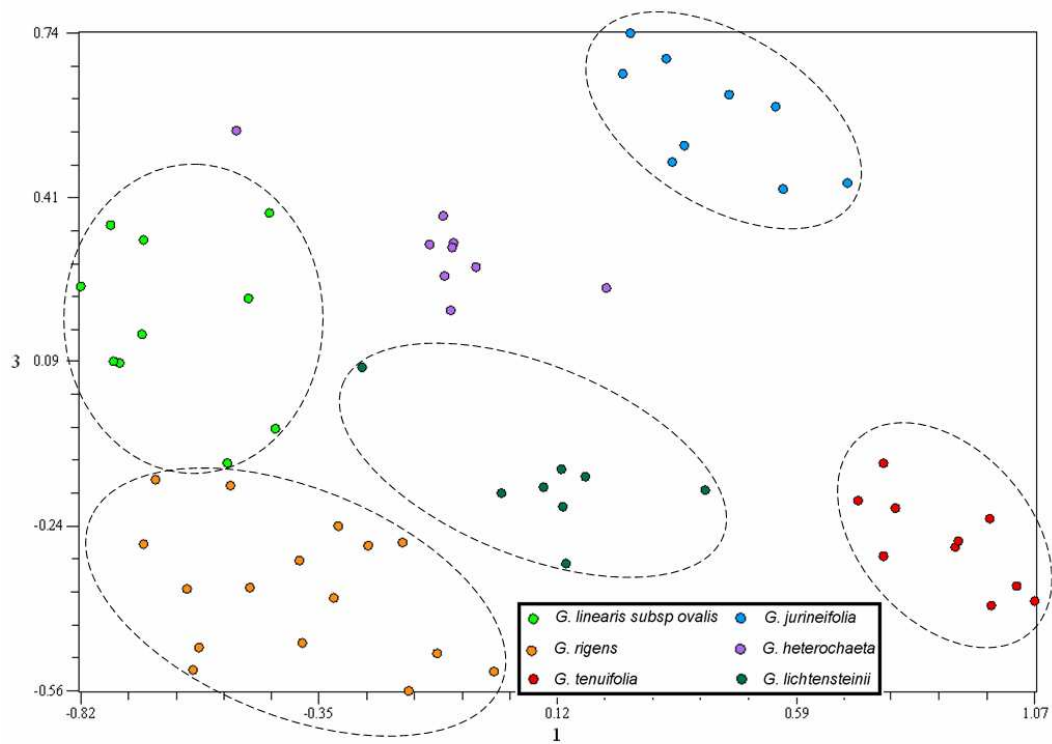


Figure 2.3.26: Scatterplot of first and third PCA axes of TOTAL data set (now including Ray Colour as an additional binary character), only containing six species that showed best clustering in CA analysis. Dashed ovals indicate species clusters.

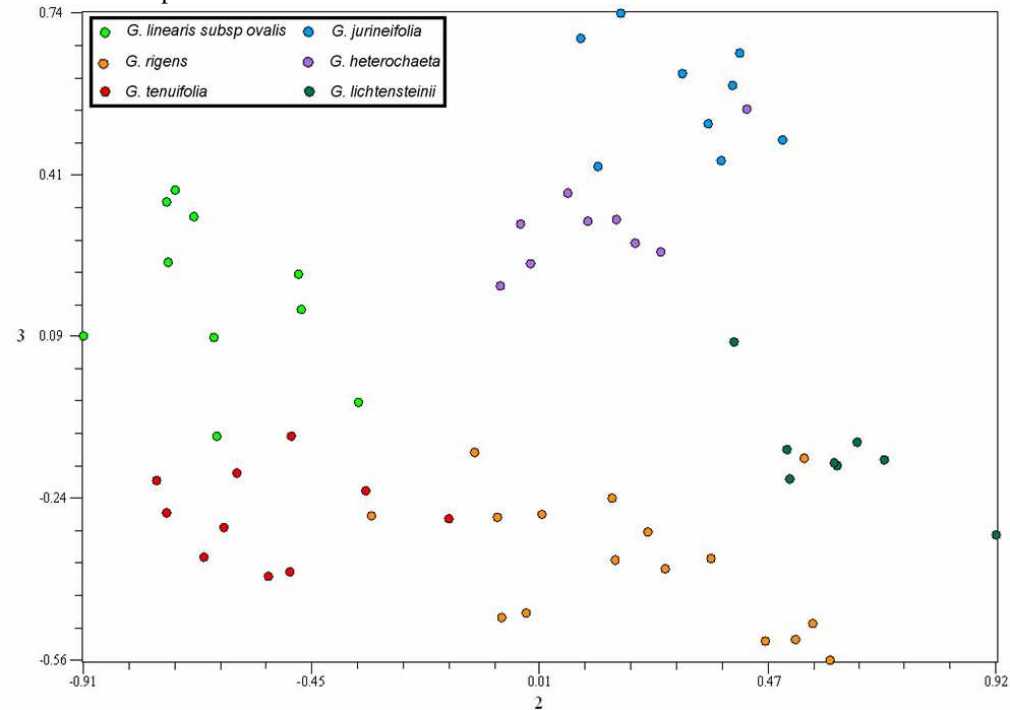


Figure 2.3.27: Scatterplot of second and third PCA axes of TOTAL data set (now including Ray Colour as an additional binary character), only containing six species that showed best clustering in CA analysis.

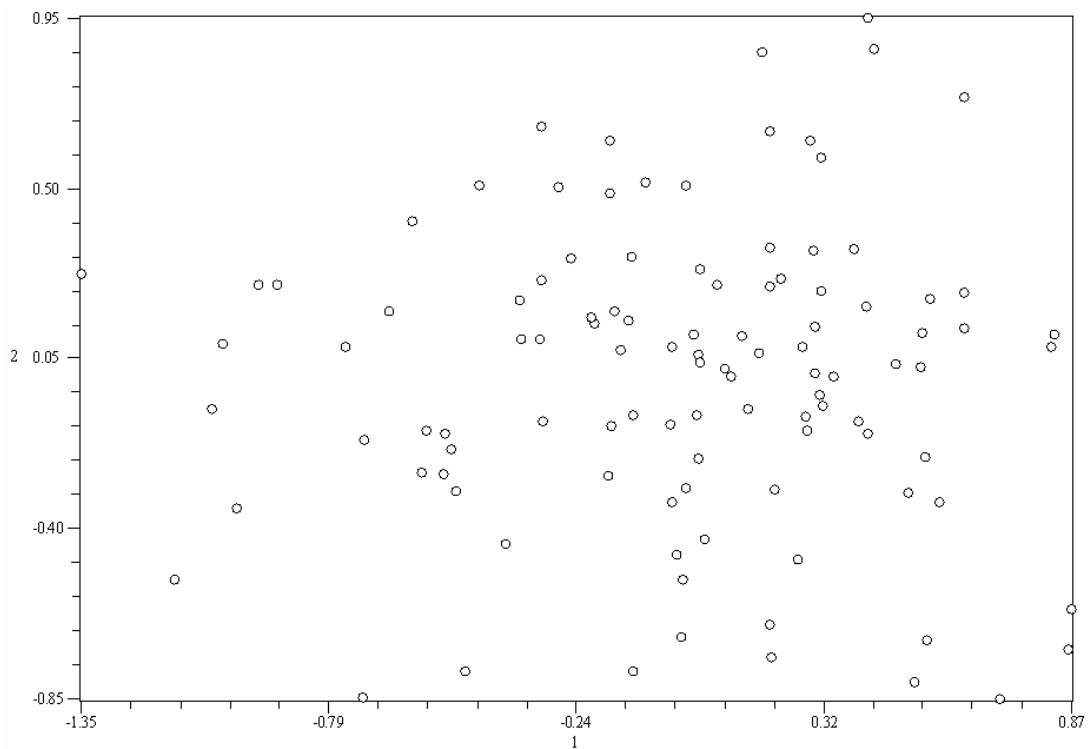


Figure 2.3.28: Scatterplot of first and second PCA axes of TOTAL data set, excluding six species that showed best clustering in CA analysis. No clearly separate clusters are visible.

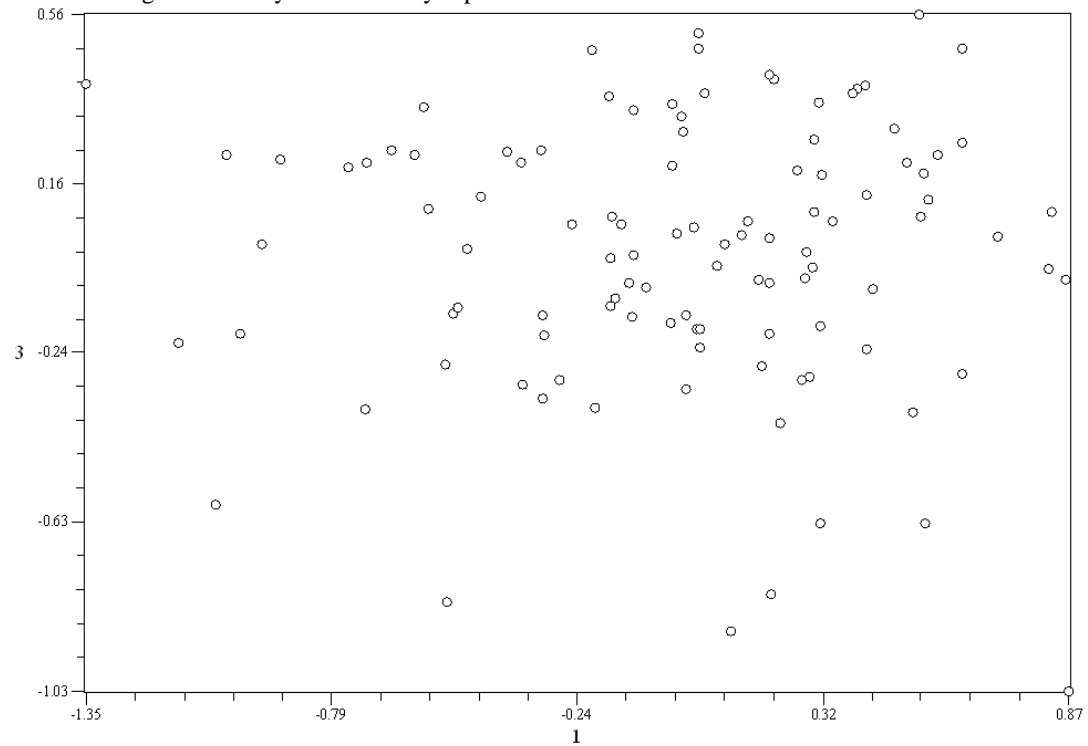


Figure 2.3.29: Scatterplot of first and third PCA axes of TOTAL data set, excluding six species that showed best clustering in CA analysis. No clearly separate clusters are visible.

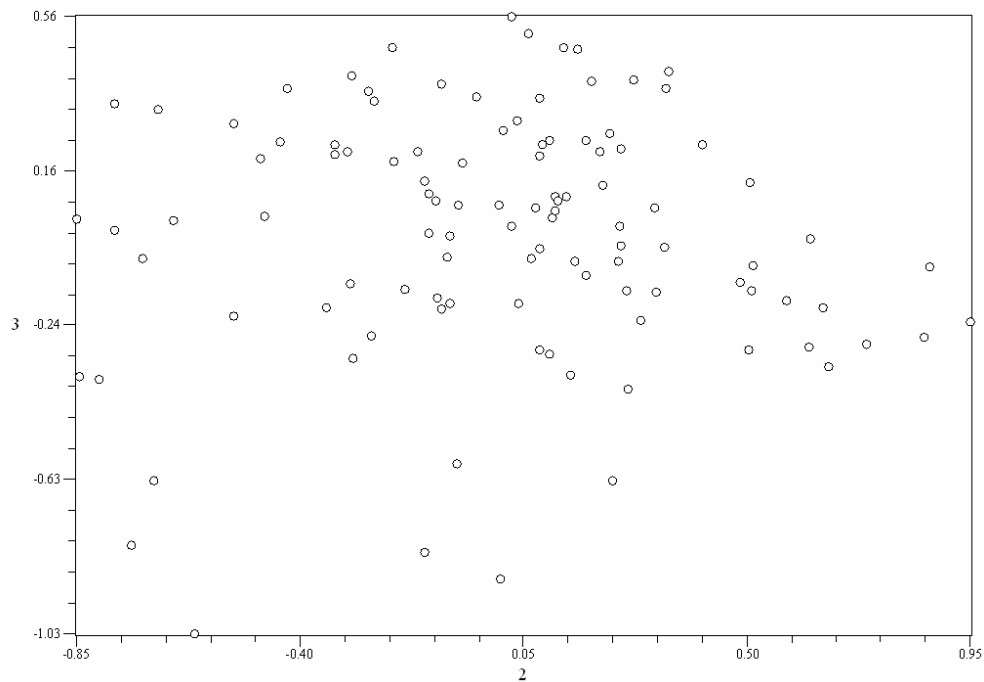


Figure 2.3.30: Scatterplot of second and third PCA axes of TOTAL data set, excluding six species that showed best clustering in CA analysis. No clearly separate clusters are visible.

Table 2.3.5: TOTAL data (selected six species from CA): Impact of each character on each PCA axis (most significant contributors highlighted in bold red) and total % variability accounted for by each PCA axis.

Character	Axis1	Axis2	Axis3
Habit	0.3334	0.5869	0.614
Invset	-0.1266	-0.133	-0.5247
ParScl	0.3662	0.6692	-0.4762
InvBase	0.527	0.4949	-0.1024
LfSet	0.243	-0.3389	0.6742
LfMarg	0.4323	0.0052	0.7941
LfDiss	0.6025	0.2017	0.359
OIL	-0.6994	0.5643	-0.0062
OIW	-0.8031	-0.3647	0.0701
IIL	-0.5762	0.6702	0.2941
IIW	-0.5107	-0.466	0.2862
InvL	-0.88	-0.1179	0.1877
InvW	-0.794	0.1763	0.1712
LfLgth	-0.6439	0.5276	-0.028
LfWdth	-0.9511	-0.0536	0.073
StmLgth	-0.4876	0.6566	0.0815
LogOIRAT	0.0366	0.8585	-0.0674
LogIIRAT	-0.2205	0.8753	0.0977
LogOI/II	-0.2506	-0.0712	-0.4007
LogInvRAT	0.1411	-0.3688	-0.0326
LogLFRAT	0.6871	0.4818	-0.1136
% Variab.	31	24	12

Table 2.3.6: TOTAL data (selected six species from CA, now including Ray Colour as additional binary character): Impact of each character on each PCA axis (most significant contributors highlighted in bold red) and total % variability accounted for by each PCA axis.

Character	Axis1	Axis2	Axis3
PetCol	0.3274	0.2603	0.6581
Habit	0.3354	-0.5648	0.6444
InvSet	-0.1351	0.1201	-0.4194
ParScl	0.3221	-0.7024	-0.3835
InvBase	0.4875	-0.5372	-0.1692
LfIndu	0.2892	0.3667	0.6696
LfMarg	0.4532	0.0039	0.6675
LfDiss	0.6154	-0.2006	0.4232
OIL	-0.7199	-0.5262	0.0865
OIW	-0.7719	0.417	0.162
IIL	-0.5938	-0.6275	0.3268
IIW	-0.474	0.5074	0.2964
InvL	-0.8751	0.1576	0.1354
InvW	-0.7782	-0.1119	0.3417
LfLgth	-0.6629	-0.4926	0.0573
LfWdth	-0.9512	0.0939	0.0553
StmLgth	-0.5232	-0.6394	0.0652
LogOIRAT	-0.0103	-0.868	-0.0595
LogIIRAT	-0.2579	-0.861	0.1212
LogOI/II	-0.2569	0.0698	-0.3094
LogInvRAT	0.1247	0.3233	-0.3229
LogLFRAT	0.6722	-0.5047	-0.0244
% Variab.	30	23	13

Table 2.3.7: TOTAL data (excluding six species from CA): Impact of each character on each PCA axis (most significant contributors highlighted in bold red) and total % variability accounted for by each PCA axis.

Character	Axis1	Axis2	Axis3
Habit	0.2353	0.1312	0.0664
InvSet	-0.0225	0.5224	-0.0839
ParScl	0.4246	-0.0542	0.1035
InvBase	-0.0846	-0.2	-0.2284
LfIndu	0.2435	0.4599	0.2993
LfMarg	0.2599	0.2847	0.5984
LfDiss	0.277	0.4832	0.0672
OIL	0.7844	-0.4406	0.2032
OIW	0.3686	0.4299	-0.4296
IIL	0.7192	-0.4549	-0.052
IIW	0.5071	0.4017	-0.1126
InvL	0.5153	0.3959	0.1335
InvW	0.7668	0.4458	-0.1389
LfLgth	0.6419	-0.0417	-0.1609
LfWdth	0.1705	0.3105	0.5687
StmLgth	0.7249	-0.1059	-0.1879
LogOIRAT	0.4672	-0.6756	0.4617
LogIIRAT	0.338	-0.7479	0.0318
LogOI/II	0.2355	-0.0548	0.4237
LogInvRAT	-0.603	-0.2825	0.2696
LogLFRAT	0.3481	-0.3058	-0.6256
% Variab.	22	16	8

Discussion

Rieseberg *et al.* (1991) note that the number of morphological characters suitable for phylogenetic and systematic analyses is often very low, that morphological characters are often functionally or developmentally correlated, that much morphological variation is nonheritable (environmental), and that morphological characters often converge when exposed to similar selective pressures. Schilling & Panero (1996) also note that the potential for homoplasy in such analyses is enhanced by the fact that groups close enough genetically to produce hybrids when crossed will necessarily tend to have similar morphological potentials. Roessler (1959) considered hybridization to be one of the problems that confused the taxonomy of the genus *Gazania*. The presence of hybrid herbaria collections that display novel combinations of characters that point to obvious incidences of hybridization also add weight to this possibility (Roessler, 1959; pers. obsv.). The actual extent of hybridization that occurs naturally within *Gazania* has, however, not been investigated here, and this must render all discussion of such processes as speculative.

The Morphological Species Concept relies on species being recognizable by discontinuities in morphological characters. The results of these analyses bear out Roessler's comment that there are a few well-delimited, easily recognisable species. His list included *G. rigens*, *G. othonnites*, *G. lichtensteinii* and *G. tenuifolia*. The CA highlighted *G. rigens*, *G. lichtensteinii*, *G. tenuifolia*, *G. jurineifolia*, *G. heterochaeta*, and *G. linearis* subsp *ovalis* as distinct species. However, it should be noted that not all the *G. heterochaeta* samples grouped together in the CA results.

PCA analysis of all the samples in each data set resulted in no clear clusters being visible on scatterplots of the first three axes of each analysis. Some researchers indicate that PCA should not be used for "multiple sample" situations where there are several groups, due to a tendency to confound within- and between-group sources of variation (James & McCulloch, 1990).

The PCA of a smaller subset of six taxa, as highlighted by CA, revealed that *G. tenuifolia* is a morphometrically distinct species, clustering tightly and separately from other samples. For the other five taxa, there were rarely entirely discrete clusters, but rather general trends of certain species occurring in certain areas of the scatterplots, but with insufficient morphological discontinuity to make clusters properly distinct from each other. It is only with the addition of flower colour as an extra character to aid in the separation of *G. heterochaeta* and *G. jurineifolia* that species clusters become more distinct. Figure 2.3.26 is the only PCA figure to illustrate six separate species clusters, although there is still some marginal overlap between *G. rigens* and *G. linearis* subsp *ovalis*.

Non-distinct taxa

The remaining species, when subjected to PCA, show no pattern of separation or clustering at all. Roessler (1959) stated that amongst the remaining taxa that are not distinctly different, relationships are so close and characteristics overlap to such a degree that a clear separation becomes impossible. The lack of clear signal in the morphometric analyses bears out his observation. Although the extremes of two or more taxa may be distinct when they are compared with each other, there may be so many intermediates that obvious lines of demarcation between states are unclear (Stevens, 1991).

This is a typical problem faced by systematists: the need to determine where, if at all, groups occur within a more or less continuous range of variation (Kores *et al.*, 1993). The problems seen in *Gazania* are quite common in plant systematics. A similar example exists in the *Viola alba* complex (Violaceae), where the taxa express high variability on the regional, local, and the individual scale (Marcussen, 2003). As with *Gazania*, this variation has brought about the description of large numbers of taxa of various taxonomic rank and distribution (Marcussen, 2003).

Another example exists in the *Euphorbia esula* group (Crompton *et al.*, 1990) where, again, several taxa were so similar that no clear separation into species groups could be accomplished. *Quercus* is notorious for interspecific hybridization, such that species tend to form a morphological continuum instead of separate or clear clustering (Borazan & Babac, 2003). In Borazan & Babac's (2003) study, PCA analyses could not clearly separate the four taxa belonging to the subgenus under scrutiny. *Lupinus nanus* (Leguminosae) offers another similar result, where no groups corresponding to infraspecific taxa could be distinguished by any single character or by a combination of characters (Riggins *et al.*, 1977). Specimens of any sample could not be identified with certainty and the range of variation in each sample is so extreme that consistent assignment is virtually impossible (Riggins *et al.*, 1977).

Apart from natural variation in *Gazania*, the possibility of contamination from "naturalized" garden escapes cannot be discounted. The presence of large (apparently naturally occurring) populations of anomalous large pink-flowered *Gazania* (possessing character combinations that do not naturally appear in any wild type species) on the south western coast (R. McKenzie, pers. comm.) highlights this issue.

Comparative data signal between ratios and size data

The raw size data and the ratio shape data both generated similar results, and inclusion of both ratio and size data in the same data set did produce better groupings. Ratio data appears to cause more scattering of samples and less separation between some groupings than raw size data. The tightest species clusters in CA were produced by the TOTAL data set.

Comparative analysis methods for morphometric analysis

Henderson (2006) notes that some authors (such as James & McCulloch, 1990) consider that PCA should not be used for multiple samples (a restriction which would entirely eliminate its usefulness in systematics); but he also notes that this opinion is not shared by others (e.g. Humphries *et al.*, 1981; Boyd, 2002; Chandler & Crisp, 1998). Chandler & Crisp (1998) successfully used PCA on a large data set of 150 samples which contained both quantitative and qualitative characters.

CA and PCA are exploratory methods, in that they require no *a priori* knowledge of species groupings, but rather search for groupings within a collection of samples (Henderson, 2006). These most commonly utilized morphometric data analysis methods have produced the same result: some few species (and one subspecies) are distinct, the remaining species overlap in morphological traits to such an extent that no clear disjunction exists. Although some authors indicate that PCA's method of reexpressing a large number of original variables into two or three new uncorrelated variables (such that they retain most of the original variation) can be used to uncover unexpected relationships (Ackerfield & Wen, 2002), there is little difference from the species cohesion achieved with CA.

Conclusion

Under the MSC, there are six distinct taxa within *Gazania* that correlate with Roessler's (1959) taxa.

These are:

- 1) *G. jurineifolia*,
- 2) *G. lichtensteinii*,
- 3) *G. linearis* subsp *ovalis*,
- 4) *G. rigens*,
- 5) *G. heterochaeta*, and
- 6) *G. tenuifolia*.

The remaining species show no clear morphological separation. While morphometrics is recognized as a valuable component of what systematists do (Jensen, 2003), there are other sources of data to investigate phylogeny. To this end, a DNA phylogeny is necessary to investigate the status of Roessler's species.

Chapter 3.

Molecular systematics of *Gazania* at the species level

“The genus ... comprises a number of well-delimited and recognisable species. Between the remaining taxa, such close relationships and overlaps of characteristics exist that a clear separation becomes impossible.” (Roessler, 1959, pp 100, translated from the original German).

Aim: To use DNA sequence data to determine the status and relationships of the taxonomic entities (“species”) as delimited by Roessler and the morphometric analysis conducted in Chapter 2.

Introduction

There are a number of different species concepts in used in biology today (22 at last count by Mayden, 1997). The different ways species arise and are described is crucially linked to the comprehension of biodiversity and evolution (de Meeus, 2003). For systematists, the question of “by what criteria shall species taxa be identified” lies at the heart of the species concept debate (Hey *et al.*, 2003).

Historically, and until the recent development of molecular tools, taxonomic groups (species) have been identified using morphological criteria alone (“morphospecies”). This has left uncertainty in some cases as to the validity, and support, of groups delineated using these criteria (Hendry *et al.*, 2000).

While morphological data has traditionally been used to delimit species and continues to be widely used today, recent studies have used DNA sequence data to test these morphology-based taxonomies (Wiens *et al.*, 2002). One of the species concepts that has come into use with DNA sequence data is that of the Phylogenetic Species concept (PSC). While various formulations of the PSC have been advanced (e.g. Wheeler & Platnick, 2000; Mishler & Theriot, 2000), all agree that species recognition should emphasize criteria of phylogenetic relationship (descent) and not reproductive relationships (as endorsed by the Biological Species Concept; Avise, 2000).

The PSC defines a species as “... the smallest aggregation of populations (sexual) or lineages (asexual) diagnosable by a unique combination of character states in comparable individuals” (Nixon & Wheeler, 1990). The question of the demarcation used to define an entity as a species or a subspecies (i.e. how much genetic divergence defines a species) based on the PSC is difficult to answer (Wheeler & Platnick, 2000). Hey *et al.* (2003) note that whatever the decision taken regarding

demarcations, one must also recognize that the decision may be an oversimplification demanded by the practical concerns of the research.

DNA sequence data as a tool for reviewing existing taxonomy

With the advent of DNA sequencing technology came access to additional sources of data for testing and revising the taxonomy of existing systematic and species delimitations. For plants, these sources are the three genomes present in the plant cell: nuclear, chloroplast and mitochondrial. Traditional morphometric analysis can only generate and use a relatively small set of characters, whilst DNA sequence data can generate thousands of potentially informative characters. When hundreds (or even thousands) of molecular characteristics are assayed among various organisms, any widespread and intricate similarities present in these macromolecules are highly unlikely to have arisen by convergent evolution and thus must reflect true phylogenetic descent (Avisé, 2004).

The proven track record of DNA sequence data as a valuable tool for phylogeny reconstruction and species delimitation (e.g. studies by Bayer *et al.*, 1996; Jeandroz *et al.*, 1997; Manos *et al.*, 1999; Peterson *et al.*, 2004) makes it an ideal alternative means to explore the validity of the six discrete morphological entities uncovered using “traditional” morphological methods in Chapter 2, as well as Roessler’s (1959) 16 species. It is, likewise, a means to investigate further the other less discrete, overlapping taxa that were unable to be satisfactorily separated by means of morphometric analysis.

When choosing loci for phylogenetic inference, the first step is to determine sequence variability over a small sample of taxa; as a matter of practicality, regions that present difficulty in either amplification or sequencing are often eliminated in this preliminary step (Mort *et al.*, 2007). There are many genes in several different regions of the plant genome that can be used, but for the purposes of this project, the nuclear ITS and ETS regions, and several chloroplast regions were selected following preliminary screening trials of multiple noncoding regions. Because ITS and ETS mutates faster than chloroplast DNA (Albach & Chase, 2004), at low level taxonomic studies, where the level of divergence between target taxa may be very low, a fast-changing set of characters would provide more information than a slower or invariant character set. The ITS and ETS have proven useful at low taxonomic levels, as their rapid evolution makes them useful in phylogenetic studies where little or no variation in chloroplast genes is found (Jeandroz *et al.*, 1997).

The choice of chloroplast regions may be made either on length or number of parsimony informative characters. Mort *et al.* (2007) note, however, that the absolute number of parsimony informative

characters is not entirely predictive of ability to resolve nodes with support, and that there may be no significant correlation between the number of aligned characters and the number of parsimony informative characters. Phylogenetic utility of any particular region may vary significantly among lineages, and two important measures of utility are resolution (loci that resolve many relationships but exhibit homoplasy are more useful than those that provide neither resolution nor conflict) and the degree to which data provide support for resolved clades (Mort *et al.*, 2007). It should also be noted that a region that provides the most characters (and the most parsimony informative characters in some groups) may not be especially useful in supporting nodes in general (Mort *et al.*, 2007).

The nuclear genome: Multicopy nuclear markers (ITS and ETS)

Eukaryote nuclear ribosomal DNA (nrDNA) is commonly utilized and consists of tandem repeat units, with each unit containing 18S, 5.8S and 26S nrDNA (Hung *et al.*, 2004). The 18S and 26S nrDNA code for the small and large ribosomal subunits respectively (Soltis & Soltis, 1998). These repeat units are organized into arrays, with each array containing hundreds to thousands of identical to near-identical repeats (Wendel *et al.*, 1995). These nrDNA arrays are typically located in the nucleolar organizing region (NOR), of which there may be several present on several different chromosomes (Soltis & Soltis, 1998; Muir *et al.*, 2001). Intragenomic nrDNA diversity is generally low (Buckler *et al.*, 1997), these repeats having become homogenised by evolutionary forces (e.g. unequal crossing-over, gene conversion) that are collectively referred to as concerted evolution (Wendel *et al.*, 1995). Regardless of small differences being reported between nrDNA families located in different chromosomal positions, in a phylogenetic context the nrDNA has been treated as a single-copy gene (Muir *et al.*, 2001).

The Internal Transcribed Spacers (ITS) and the External Transcribed Spacers (ETS) are part of this nrDNA. Figure 3.1.1 illustrates their proximity to each other and the other portions of the nrDNA tandem repeats. The ITS1 region lies between the 18S and 5.8S genes while the ITS2 region lies between the 5.8S and 26S genes. The ETS and the Nontranscribed Spacer (NTS) make up the Intergenic Spacer (IGS) that joins the repeats of 26S and 18S.

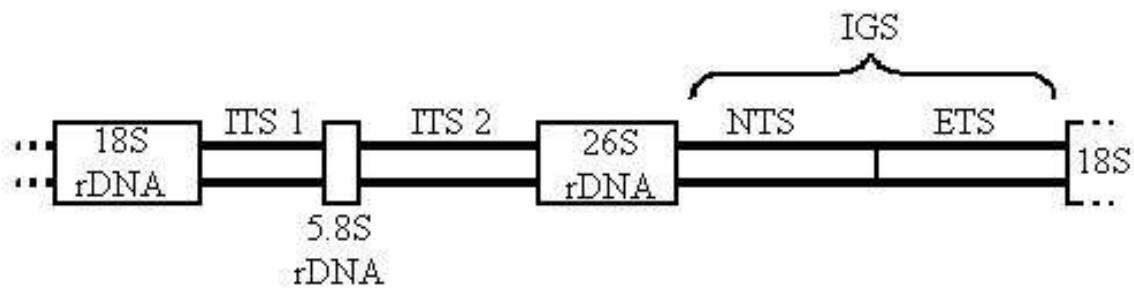


Figure 3.1.1: Diagrammatic representation of the nrDNA regions. ITS = Internal Transcribed Spacer, ETS = External Transcribed Spacer, NTS = Nontranscribed Spacer, IGS = Intergenic Spacer. Boxes indicate functional rDNA genes.

It should be noted that because the ETS is part of the same transcription unit as the ITS region, it cannot be regarded as an independent line of phylogenetic evidence for comparison with ITS results (e.g. for identifying factors such as lineage sorting or hybridization that may have led to deviation between rDNA tree and species tree; Baldwin & Markos, 1998). There are some instances where ITS alone has been used for phylogenetic reconstruction, or biogeographic studies (e.g. the Bellarosa *et al.* (2005) study on *Quercus* spp. did not use any other gene region than ITS), and although mention is made of ETS, this is not generally considered a separate gene system for these purposes.

The effectiveness of concerted evolution on the ITS region in most plants makes it the primary choice for phylogenetic reconstruction at lower taxonomic levels (Campbell *et al.*, 2005). However, this process of homogenization proceeds faster within chromosomes than it does among chromosomes, leading to the possibility of differing copies being located on different chromosomes (O’Kane *et al.*, 1996). If concerted evolution is slower than speciation, then a single individual will contain divergent paralogues (Buckler *et al.*, 1997). Intra- and inter-individual variation for nrDNA types has been found in several plant species, with up to five copies found among and within individuals of two species of *Picea* (O’Kane *et al.*, 1996). Unidentified paralogous relationships and infrequent recombination between paralogues can result in erroneous species phylogenies (Buckler *et al.*, 1997).

There is also some ambiguity as to how concerted evolution generally operates in the ETS (Linder *et al.*, 2000). Because the ETS is part of the 18S-26S nrDNA repeat, it is often assumed that concerted evolution will homogenize it in the same way that it does the ITS, but the presence of a small number of large (130 bp) tandem repeats at the 5’ end of the ETS may hinder or alter the rate of concerted evolution as the repeats in the NTS appear to do (Linder *et al.*, 2000).

The ITS region in angiosperms can range in size from 565 to 700 bp (Liston *et al.*, 1996). The IGS varies considerably in length, from 1 to 8 kb (Soltis & Soltis, 1998), but the entire IGS in *Gazania* is recorded as having a length of 1.3 kb (Linder *et al.*, 2000). Usually, rather than amplifying the entire IGS or ETS, a highly variable region of around 600-700 bp near the 18S end is utilized (e.g. Bena *et al.*, 1998; Clevinger & Panero, 2000; Linder *et al.*, 2000).

The use of the ITS region is not without its critics. Alvarez & Wendel (2003) firmly recommend that ITS should not be routinely used phylogenetic analyses, and recommend using single-copy nuclear loci instead. They cite several genetic processes that can confound accurate phylogenetic reconstruction, including: array duplication events, pseudogenes, and incomplete homogenization of sequences in different arrays (Alvarez & Wendel, 2003). The ITS region is also accused of being prone to high levels of homoplasy (possibly due to fast evolution of the ITS region), and this can mask the phylogenetic signal (Alvarez & Wendel, 2003). Additionally the presence of reticulation may obscure the phylogenetic signal (Alvarez & Wendel, 2003).

The chloroplast genome

Organelle genomes provide ideal markers for phylogeny reconstruction because their sequences record the history of a lineage uncomplicated by recombination (Harrison, 1991). The chloroplast (cp) genome offers many advantages for phylogenetic reconstruction, including the fact that the genome is small (Soltis & Soltis, 1998). Further advantages include the fact that the cpDNA genes are all linked with each other, and thus the plastid genome behaves as a single recombination unit; all the parts of the genome should have the same pedigree within species (and the same phylogenetic history among species) and should therefore contain the same phylogenetic signal in all DNA regions (Graham *et al.*, 1998; Albach & Chase, 2004).

There are three functional categories of DNA in the cp genome: (i) non-coding regions that do not code for transfer RNA, ribosomal RNA or proteins; (ii) coding genes (rRNA and proteins); and (iii) chloroplast introns (Clegg *et al.*, 1995). The cpDNA genome is extremely condensed compared to nrDNA and most of the noncoding DNA in the chloroplast genome is found in very short segments separating functional genes (Clegg *et al.*, 1995). It also accumulates nucleotide substitutions relatively slowly (Palmer, 1987) and has a lower rate of intraspecific mutation than nuclear DNA (Palmer & Zamir, 1982; Clegg *et al.*, 1984a; Clegg *et al.*, 1984b; Perl-Treves & Galun, 1985) which has made the chloroplast genome an ideal focus for studies of plant evolutionary history (Clegg *et al.*, 1995).

Because the cp genome is free from recombination, and inherited as a single unit, cpDNA sequences from different regions can readily be combined (Soltis & Soltis, 1998). The presence of different genealogical histories can be ruled out if there is any incongruence between cpDNA data sets, so any incongruence can be ascribed to differing functional constraints, as rates and modes of evolution are known to differ substantially in different parts of the cp genome (Graham *et al.*, 1998; Albach & Chase, 2004). If these processes are sufficiently strong, they may be a source of any tangible differences in trees that are inferred from separate parts of the cp genome (Graham *et al.*, 1998). Sequencing a second plastid marker is thus necessary to support the hypothesis that the results from the first plastid marker represent the phylogenetic signal of the plastic genome, despite relatively few potentially informative characters (Albach & Chase, 2004).

Different portions of the cp genome evolve at different rates, and at different rates across different lineages (Small *et al.*, 2005). A direct consequence of this is that the phylogenetic utility of different noncoding cpDNA regions within a given taxonomic group can vary tremendously (Shaw *et al.*, 2005). In principle, cpDNA sequencing should involve the selection of a sequence whose substitution rate is appropriate to the phylogenetic problem at hand (Olmstead & Palmer, 1994). To this end, a number of regions were screened to determine if they could provide the necessary intrageneric, specific and intraspecific variability among the species of *Gazania*.

Shaw *et al.* (2005) compiled a list of 21 variable and informative noncoding cpDNA regions sampled across all of the major lineages of flowering plants. From this, a selection of primers could be chosen for trial. Of all the lineages amplified, the clade that *Gazania* falls into had a very low level of cpDNA variability across all the regions tested. The region with the highest percentage variability for the Eupatorium clade (which *Gazania* falls into) was the *psbA-trnH* region (also referred to by some authors as the *trnH-psbA* region, and titled in full *trnH^{GUG}-psbA* by Shaw *et al.*, 2005). The next highest variable region for the Eupatorium clade was the *trnC^{GCA}-ycf6-psbM* region, and the other most variable regions across all angiosperms were *trnS-trnfM*, *trnT-trnL*, *rpS16* and *trnL-trnL-trnF*. These six regions were therefore investigated for potential utility in a subset of *Gazania* samples, and a subset of three of these regions was selected (Appendix 3 for details of screening procedure). The final choice of cpDNA data sets was composed of sequences from the *psbA-trnH*, *rpS16* and *trnLF* regions.

The *psbA-trnH* region has been used in phylogenetic studies at the intrageneric level (Olmstead & Palmer, 1994; Gielly *et al.*, 1996; Sang *et al.*, 1997; Kim *et al.*, 1999; Chandler *et al.*, 2001) as well as at the intraspecific level (Hamilton, 1999; Holdregger and Abbott, 2003).

The *rpS16* is not as widely used as other cpDNA regions, but is typically more informative than the *trnLF* region (Shaw *et al.*, 2005). It has proven useful at the genus level, in *Gunnera* (Wanntorp *et al.*, 2001; Wanntorp & Wanntorp, 2003), *Cymopterus* (Downie *et al.*, 2002) and *Alectryon* (Edwards & Gadek, 2001) and has also been used successfully at species level in *Silene aegaea* (Popp & Oxelman, 2001).

The *trnLF* region is comprised of the Group I intron that interrupts the *trnL* gene, and the intergenic spacer between the *trnL* and *trnF* genes (Shaw *et al.*, 2005). This region one of the most commonly used non-coding regions of cpDNA in phylogenetic studies (Sang *et al.*, 1997; and papers listed therein). The *trnL* intron and *trnL-trnF* spacer regions are easily co-amplified together using the “c” and “f” primers of Taberlet *et al.* (1991) and are often used as a single region (Shaw *et al.*, 2005). Due to the near-universal nature of the primers and their early publication, these regions have become the most widely used noncoding cpDNA sequences in plant systematics (Shaw *et al.*, 2005). The *trnLF* region has been used at many levels of phylogenetic study, including the intrageneric and species level (Olmstead & Palmer, 1994; Mes and t’Hart, 1994; Gielly *et al.*, 1996; Sang *et al.*, 1997; Chandler *et al.*, 2001).

Methods

Study samples

43 samples were collected from all 16 species and ten subspecies of *Gazania*, details of which are presented in Table 3.2.1. Two samples per taxa were used to investigate the monophyly of each taxon. All specimens were identified by using Roessler's key to *Gazania* (Roessler, 1959), to enable the testing of the validity of the current species recognized by Roessler. Three outgroup samples, one each from close sister genera *Berkheya*, *Hirpicium* and *Gorteria*, were also included. One sample of a putative new species (*G. sp. nov.*) is also included. This specimen was collected by L. Mucina (Univ. Stellenbosch) and is considered by him to be a new species (this is not a final designation, pending the collection of further samples and further investigation). Both the *G. othonnites* and the *G. sp. nov.* samples have grey (glaucous) leaves with a certain amount of fleshy succulence, although they show very different leaf morphology in other aspects (the *G. othonnites* sample has equal numbers of entire and pinnate leaves that are glabrous, while the *G. sp. nov.* sample has entire, roughly hispid leaves). Both samples come from the same geographical area (around Springbok in the Northern Cape).

DNA was extracted from all samples using a CTAB DNA extraction protocol (Doyle & Doyle, 1987). Multiple samples of each species and subspecies were used where possible to test for species monophyly. Although cloning of nrDNA samples would counteract the possible effects of multiple ITS/ETS paralogues, the budget required for cloning of all sequences is beyond the reach of this research project.

PCR amplification and sequencing

The PCR reagents and their volumes are presented in Table 3.2.2. Primers, annealing temperatures and number of cycles necessary to ensure clean product for each region are presented in Table 3.2.3.

Table 3.2.2: Table of PCR reagents, all units in microlitres.

	10x buffer	dNTPs	Primer1	Primer2	DNA	MgCl ₂	BioTaq	H ₂ O
nrDNA	5	2	2	2	2	1	0.25	34
cpDNA	"	"	"	"	"	4	"	31

10x = 10x Bioline NH₄ Dilution Buffer (MgCl₂ free); BioTaq = Bioline Taq Polymerase;
DNA = DNA template; H₂O = distilled PCR-quality water

MgCl₂ = 50 mM solution of MgCl₂ provided with enzyme and 10x buffer.

For some samples a DNA dilution of 1:20 or 1:100 in dH₂O was necessary to counteract the effects of putative contaminants that prevented successful PCR amplification at full DNA concentration. PCR

amplifications were conducted either on a ThermoHybaid PCR Sprint Temperature Cycling System or a Corbett Research PC-960G Microplate Gradient Thermal Cycler. The following standard conditions were used (although annealing temperature varied as per Table 3.2.3): 95°C for 1 min, 52°C for 1 min and 72°C for 3 minutes, repeated between 30 and 40 cycles, with a 10 minute 72°C extension period at the end of the PCR program.

PCR product was run on 1% agarose gels, which consisted of 0.5g agarose in 50ml TBE buffer (10.8g Tris(hydroxymethyl)aminomethane, 5.5g Boric acid and 0.93g EDTA made up to 1L with distilled water). Each gel contained 20µl ethidium bromide (0.5µg/ml) and the PCR products bands were visualised using a UV transilluminator. A clean clear bright band was taken as a positive result. Any smearing indicated an unsatisfactory PCR result, and PCR conditions were altered as necessary to reduce smearing (e.g. a reduction in number of cycles; a reduction in quantity of primers used in the PCR reaction).

The PCR product was cleaned using the PROMEGA Wizard SV Gel and PCR purification kit and resuspended in 30µl of dH₂O. The final product was checked for purity and concentration by running 1µl of the product, with 5µl water and 5µl of a loading buffer (Bromophenol blue and xylene cyanol in glycerol) on a 1% Agarose gel that contained 15µl of ethidium bromide (0.5µg/ml) and visualised by means of a UV transilluminator. Cleaned PCR product was sequenced using ABI prism BigDye Terminator v3.1 Ready Reaction Cycle sequencing kit (Applied Biosystematics) according to manufacturer's instructions with the primers listed as sequencing primers in Table 3.2.3.

Primer development for ITS and ETS amplification and sequencing

Figure 3.2.1 illustrates the starting positions and directionality of primers used to amplify and sequence in the ITS region. Boundaries of ITS1, ITS2 and the 5.8S regions were determined by comparison with published sequences of Asteraceae ITS (Goertzen *et al.*, 2003).

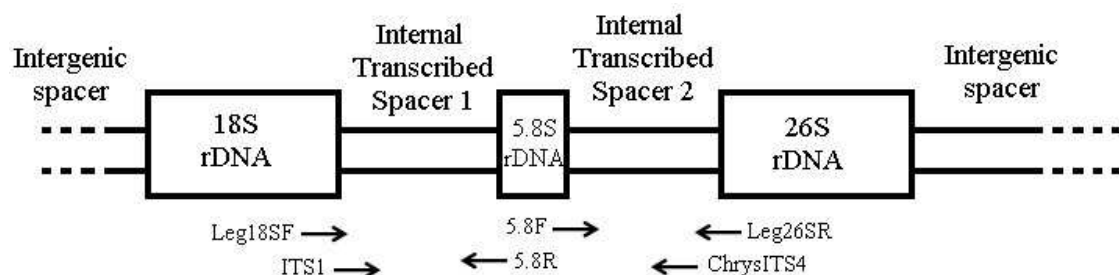


Figure 3.2.1: Diagrammatic representation of the ITS regions with primer start points and directionality. Boxes indicate functional rDNA genes.

Table 3.2.1: List of all samples used in DNA species-level phylogeny, including collection locality data.

Species	subsp	Sample(s)	Locality	South	East
caespitosa		RVC307	<u>South Africa. Graaff-Reinet</u> : Koudeveldberge, summit	32° 7' 30"	24° 7' 30"
		RVC_SR448	<u>South Africa. Somerset East</u> : Koudeberg, summit, Groot Vallei Farm.	32° 19' 50"	25° 00' 23"
ciliaris		RM1230	<u>South Africa. Cape Town</u> : Paarlberg.	33° 45' 8"	18° 57' 5"
		RM1382	<u>South Africa. Clan William</u> : Piketberg plateau	32° 48' 41"	18° 42' 40"
heterochaeta		RM1429_1	<u>South Africa. Steytlerville</u> : T2 road Steytlerville - Grootrivierpoort; 5km N Rietfontein turn	33° 22' 30"	24° 22' 30"
		RM1451	<u>South Africa. Springbok</u> : 5km N Steinkopf, beside N7 highway	39° 14' 4"	17° 45' 20"
jurineifolia	jurineifolia	RM1518	<u>South Africa. Steynsburg</u> : Eastern Cape: Conway, Alberta Farm.	31° 40'	25° 15'
		SR682	<u>South Africa. Gamoep</u> : 18km W of Aggeney's (between Springbok & Pofadder)	29° 22' 46"	18° 38' 53"
	scabra	CAM1604	<u>Namibia. Witputz</u> : Karas	27° 22' 30"	16° 07' 30"
		CAM2652	<u>Namibia. Aus</u> : In road verge on road between Aus and Rosh Pinah, in red sand	26° 45' 41"	16° 17' 21"
krebsiana	krebsiana	RM1114	<u>South Africa. Fort Beaufort</u> : Road to Bedford, R350.	32° 41'	26° 05'
		RM1136	<u>South Africa. Colesberg</u> : W of Venterstad, R58, 2km E of Gelykfontein farmstand.	30° 47'	25° 47'
	arctotoides	RM868	<u>South Africa. Kenhardt</u> : Rooipan, southeast of Lime Acres.	29° 47'	21° 56'
		RM876	<u>South Africa. Aliwal North</u> : Bloemfontein	30° 19'	26° 48'
	serrulata	RM965	<u>South Africa. Lady Frere</u> : 13km SW Elliot on R56 road.	31° 19'	27° 57'
		RM863	<u>South Africa. Olifantshoek</u> : southeast of Beeshoek	27° 45'	22° 37'
leiopoda		RM1309	<u>South Africa. Kamiesberg</u> : Roadside.	30° 24' 38"	18° 03' 09"
		M240901	<u>South Africa. Calvinia</u> : Nieuwoudtville, near turnoff to Rondekop.	31° 23' 23"	19° 11' 00"
lichtensteinii		CAM1916	<u>Namibia. Luderitz</u> : Gleckonberg West.	26° 22' 30"	15° 52' 30"
		RM1249	<u>South Africa. Wuppertal</u> : beside R355 road near Tankwa Karoo National Park.	32° 10' 30"	19° 42' 47"
linearis	linearis	RM1010	<u>South Africa. Stanger</u> : Mzimpunzi river mouth, Pondoland.	29° 13' 28"	31° 29' 51"
		SH113	<u>South Africa. Stutterheim</u> : 10km out of Stutterheim	32° 34'	27° 25'
	ovalis	RM854	<u>South Africa. Grahamstown</u> : north of Bathurst	33° 30' 18"	26° 49' 53"
		ND_Havens	<u>South Africa. Butterworth</u> : The haven, Transkei	32° 14' 50"	28° 54' 17"
maritima		M290606_6	<u>South Africa. Simonstown</u> : Table Mountain National Park, Diaz beach	34° 21' 12"	18° 25' 54"
		RM1038	<u>South Africa. Bredasdorp</u> : Cape Agulhas, about 2km E of actual cape, on shoreline.	34° 48' 48"	20° 02' 48"
othonnites		RM1306	<u>South Africa. Springbok</u> : Kleinzee, Molyneuz trail	29° 41' 27"	17° 05' 40"
pectinata		M120903_5	<u>South Africa. Clanwilliam</u> : Western Cape Province, Piketberg, Sauer, Uitvlug turnoff.	32° 50' 17"	18° 33' 14"
		RM1044_3	<u>South Africa. Caledon</u> : Agulhas peninsula, Bredasdorpberge.	34° 29' 47"	19° 53' 39"
rigens	rigens	RM763	<u>South Africa. Grahamstown</u> : Kasouga Beach.	33° 39'	26° 22'

		SR463	<u>South Africa. Stanger</u> : Tugela River mouth	29° 13'	31° 30'
	leucolaena	RM773	<u>South Africa. Knysna</u> : Plettenberg Bay	34° 02'	23° 22'
		RM952_1	<u>South Africa. Humansdorp</u> : Cape St Francis, in sand on rocky shoreline	34° 12'	24° 50'
	uniflora	RM920	<u>South Africa. Grahamstown</u> : SE of Cannon Rocks.	33° 44'	26° 33'
		JC201205	<u>South Africa. Port St Johns</u> : Lapatana, Pondoland, dunes between rocks and bush.	31° 25' 20"	29° 51' 15"
rigida		RM840	<u>South Africa. Caledon</u> : south of Caledon.	34° 16'	19° 26'
		M280902	<u>South Africa. Oudtshoorn</u> : Oudtshoorn, turn off to Zebra	33° 45' 45"	22° 20' 07"
schneckii		CAM2727	<u>Namibia. Luderitz</u> : Griffith bay area, in kloofs between rocky gneiss ridges	26° 40' 12"	15° 08' 00"
serrata		RM898	<u>South Africa. Worcester</u> : Robertson on R60 road.	33° 48'	19° 53'
		M250904_15	<u>South Africa. Simonstown</u> : Helderberg strand, R44 between Nautilus & Octopus streets	34° 08' 31"	18° 51' 06"
tenuifolia		CAM1601	<u>Namibia. Witputz</u> : Arras	27° 22' 30"	16° 07' 30"
		M7230	<u>South Africa. Springbok</u> : Goegap Nat Res, Bleshoek	29° 41' 31"	17° 58' 46"
sp. nov.		M040906_33	<u>South Africa. Hondeklipbaai</u> : Hondeklipbaai, coast at police station	30° 19' 22"	17° 16' 21"
Collector abbreviations: RM = Robert McKenzie, M = Laco Mucina, CAM = Colleen Mannheimer, SR = Syd Ramdhani, JC = Jessica Cockburn, RVC = Ralph Clark, ND = Nico Devos.					

Table 3.2.3: Primer names, uses, authors, sequences, PCR annealing temperature and number of cycles.

Name	Use	Reference	Sequence	Anneal Temp	No. Cycles
ITS					
Leg18SF	Amplification		GTC CAC TGA ACC TTA TCA TTT AGA GG	52°C	30-40
Leg26SR	Amplification		GCC GTT ACT AAG GGA ATC CTT GTT AG		
ITS1	Sequencing	White <i>et al.</i> , 1990	TCC GTA GGT GAA CCT GCG G		
ChrysITS4	Sequencing		TCC TCC GCT TAT GGA TAT GC		
Chrys5.8F	Sequencing		GAC TCT CGG CAA CGG ATA TC		
Chromo5.8R	Sequencing	Barker <i>et al.</i> , 2003	GAT TCT GCA ATT CAC ACC		

ETS					
ETS 18S	Amplif/Seq	Linder <i>et al.</i> , 2000	ACT TAC ACA TGC ATG GCT TAA TCT	51°C	35
ETS 1F	Amplification	Linder <i>et al.</i> , 2000	CTT TTT GTG CAT AAT TGA TAT ATA GGG G		
ETS IntF	Sequencing		ACC AGC TGA TGG ACA AG		
ETS IntR	Amplif/Seq		ACC ACC CGA CTA GTA GCC		

psbA-trnH					
psbA	Amplif/Seq	Sang <i>et al.</i> , 1997	GTT ATG CAT GAA CGT AAT GCT C	53°C	30
trnH	Amplif/Seq	Sang <i>et al.</i> , 1997	CGC GCA TGG TGG ATT CAC AAA TC		

rpS16					
Rps16F	Amplif/Seq	Oxelman <i>et al.</i> , 1997	GTG GTA GAA AGC AAC GTG CGA CTT	52°C	30
Rps16R2	Amplif/Seq	Oxelman <i>et al.</i> , 1997	TCG GGA TCG AAC ATC AAT TGC AAC		

trnLF					
tab c	Amplif/Seq	Taberlet <i>et al.</i> , 1991	CGA AAT CGG TAG ACG CTA CG	53-55°C	30-35
tab d	Amplif/Seq	Taberlet <i>et al.</i> , 1991	GGG GAT AGA GGG ACT TGA AC		
tab e	Amplif/Seq	Taberlet <i>et al.</i> , 1991	GGT TCA AGT CCC TCT ATC CC		
tab f	Amplif/Seq	Taberlet <i>et al.</i> , 1991	ATT TGA ACT GGT GAC ACG AG		

Initial ETS amplification of ± 10 samples using the “ETS18S” and “ETS1F” primers of Linder *et al.* (2000) (Table 3.2.3) showed intermittent success. Addition of Bovine Serum Albumen (BSA, 10 μ g/ml) and dilution of DNA template (1:100 dH₂O) was sometimes necessary to amplify the entire 1.3 kbp of the ETS region. Even so, amplification success was limited and sequencing using the “ETS1F” primer was never successful. Additionally, there were multiple amplification products in several samples (as seen by the presence of up to three clear different sized bands on agarose gels).

Using sequences obtained with the “ETS18S” primer, two stable invariable regions were found (located approximately 460 bp and 760 bp from the 18S end of ETS) and used for the design of internal primers (see Table 3.2.3 for details, Figure 3.2.2). The use of the “ETS IntF” primer in conjunction with the “ETS18S” for PCR amplification significantly increased the success rate. 763 bp of the 18S end of the ETS region were amplified for the remaining samples. A second internal primer

“ETS IntR”, located approx 460 bp from the 18S end, was utilized as an internal reverse sequencing primer. Extremely troublesome samples could be amplified successfully with the addition of a 1:1000 dilution of the “ETS IntR” primer to stimulate elongation of the ETS region.

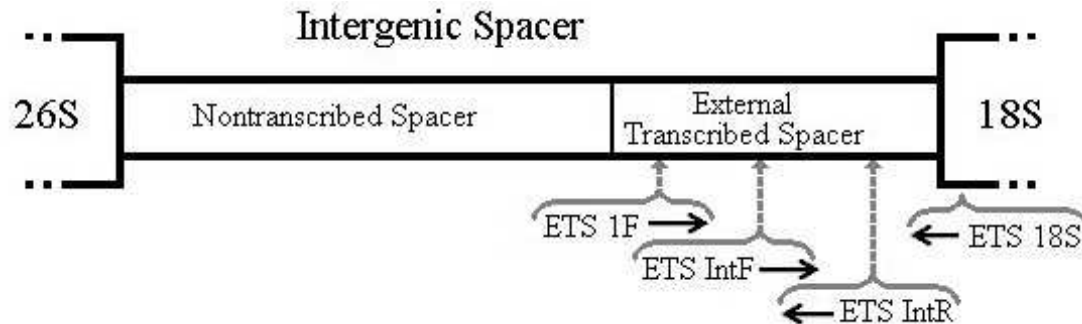


Figure 3.2.2: Diagrammatic representation of the IGS regions with primer start points and directionality. Boxes indicate functional rDNA genes.

The *trnL* intron and *trnL-trnF* spacer were co-amplified in most cases, with the primer pair of “tab c” and “tab f”. If amplification of this region in one segment was not successful, “tab c” and “tab d” were used to amplify the *trnL* intron and “tab e” and “tab f” were used to amplify the *trnL-trnF* spacer separately.

Sequence checking and alignment

Sequence data was checked and edited using SEQUENCHER (Version 3.1.1; Gene Code Corporation). Assembled sequences were exported from Sequencher, and imported into MACLADE (Version 4.06; Sinauer Associates, Inc.) and aligned manually by eye.

As the nuclear genome is biparentally inherited, two or more divergent copies of the ITS and ETS regions may be present in one organism. When the pool of divergent paralogous copies is sequenced, ambiguous bases (where two peaks of equal height occur at the same point in the electropherograms) are found. The presence of these ambiguous base calls (nucleotide additivity) has been considered evidence of the presence of multiple copies (Noyes, 2006; Dobeš *et al.*, 2004). For this reason, the IUPAC (international) ambiguity coding was utilized for the nuclear data where clear multiple paralogous copies were sequenced. The IILD test as implemented in PAUP* (as the Partition Homogeneity Test) was used to investigate possible incongruence between the various data sets, using simple addition and TBR branch swapping, for 100 replicates, saving the 500 most parsimonious trees per replicate.

Treatment of gaps

Different methods of treating gaps in analyses can influence the resulting phylogenetic hypothesis (Simmons & Ochoterena, 2000, and papers listed therein). Treatment of gaps can vary widely, from secondarily mapping gaps onto the tree inferred from base characters alone, to treating all gaps as separate characters or character states (Simmons & Ochoterena, 2000). Gaps are often not included in phylogenetic analyses, because presumed identical gaps may in fact have multiple origins in unrelated taxa (Johnson & Soltis, 1995; Simmons & Ochoterena, 2000). For *Gazania*, gaps are omitted from the analyses, but mapped onto the branches of the final phylogenetic tree. Exclusion of gaps allowed for a conservative approach to analysis of the data, and inclusion of the gaps did not influence the final phylogenies or significantly alter the support for clades and thus were not given additional consideration.

Testing for incongruence

Advocates of conditional combination have argued that testing for incongruence between data partitions is an important step in data exploration (Cunningham, 1997). If two data sets are congruent (i.e. they track the same underlying history) then it should not matter which characters are assigned to which data set, the resulting trees should remain the same (Kellogg *et al.*, 1994). The higher the incongruence between data partitions, the larger the homoplasy that arises when the partitions are combined (Ramirez, 2006). Some authors note that data partitions should be considered to be combinable if and only if they are not strongly incongruent with one another (Hipp *et al.*, 2004). Siddall (1997) cautions, however, that incongruence and combinability are different things.

Dowton & Austin (2002) comment that the most generally used assessment of congruence is the Incongruence Length Difference (ILD; Mickevich & Farris, 1981; Farris *et al.*, 1994), also known as the partition homogeneity test (Swofford, 2001). Although the ILD test was intended to detect the presence of strongly supported character conflict (“hard” incongruence) among individual data sets within a combined analysis, the test has gained wide usage in parsimony analyses as a general test of combinability (Barker & Lutzoni, 2002). The reason for this is that evidence for phylogenetic incongruence can be interpreted as being indicative that data partitions have different evolutionary histories (Ramirez, 2006).

There are several versions of the ILD (summarised in detail by Dowton & Austin, 2002). The ILD test with multiple randomizations as described by Farris *et al.* (1994) is the most commonly used, and is the one implemented in the PAUP* software package used for phylogenetic analysis of the *Gazania*

data sets. Barker & Lutzoni (2002) describe the ILD (as based on the ILD index of Mickevich & Johnson, 1976), which measures the proportion of inferred homoplasy attributable to the combination of individual data sets or partitions, which may each require conflicting minimal-length topologies. The ILD test first calculates the sum of the lengths of the two original trees, then all the characters are randomly partitioned into two new data sets (of the same size as the original two), and the two most parsimonious trees are computed and their lengths summed (Kellogg *et al.*, 1994). This is repeated to generate a distribution of the sums of tree lengths, and if the total length of the observed data falls within the distribution of the random data sets, then the division of the two data sets is inferred to be arbitrary, and there is no significant difference (incongruence) between them (Kellogg *et al.*, 1994). Otherwise, if the total length of the observed data sets falls outside of 95% of the randomly partitioned data, the data sets are considered to be significantly incongruent.

Despite some criticism (Albach & Chase, 2004; Barker & Lutzoni, 2002; Ramirez, 2006), the ILD has become a standard procedure in phylogenetic analyses involving more than one data set (Ramirez, 2006). Simulation studies have demonstrated that significant ILD test P values (i.e. $p < 0.05$, which is the original cut-off point suggested by Farris) even down to as low as $p < 0.001$ should not preclude data set combination (Yoder *et al.*, 2001), and should not be taken as a conclusive demonstration that analyzing independent data partitions in combination will produce misleading phylogenies (Hipp *et al.* 2004).

The interpretation of the significance of the p value from the ILD test as an indicator of combinability is subject to some debate (i.e. what value of p should be a cut-off mark). Clevinger & Panero (2000) considered a value of $p = 0.09$ as being positive support for combining their ITS and ETS data sets, but their cpDNA and nrDNA data sets were not considered combinable with $p = 0.026$. Chan *et al.* (2001) considered a value of $p = 0.07$ as being low enough to call into question whether data sets should be combined. Lee *et al.* (2002), however, considered a value of $p = 0.07$ to show that data sets were not significantly heterogeneous, and thus combined them with no further comments.

Ramirez (2006) notes that the results of the ILD test should be interpreted with caution, as common evolutionary conditions like heterogeneous rates of change between partitions may cause the test to report higher significance of incongruence than expected. Despite ITS and ETS being part of the same repeat array, the two data sets are not always congruent, and this apparent incongruence may be due to the faster rate of evolution in the ETS region. Okuyama *et al.* (2005) attribute significant incongruence between ITS and ETS to frequent hybridization, rather than rate heterogeneity.

In light of the controversy surrounding the ILD, while it is utilized for testing for the presence of incongruence between the various *Gazania* data sets, some advisable caution will be applied to the interpretation of the results.

Phylogenetic analyses

Several approaches can be used as an aid to phylogeny reconstruction and these generally fall into three classes: parsimony, distance methods and maximum likelihood methods (Olmstead & Palmer 1994). A fourth method, Bayesian analysis has become very popular in recent years. The methods used in this chapter are Parsimony and Bayesian analysis. *Berkheya*, *Hirpicium* and *Gorteria* samples were used as the outgroup rooting point for phylograms. Maximum likelihood was not chosen for use as it is computationally demanding, and would require a long time to run the analyses (especially on data sets of this size).

Parsimony analysis

As noted by Maddison (1991), in a set of most-parsimonious trees for a data matrix, there may be several distinct classes (islands) of trees. An island consists of interconnected parsimonious trees (all less than a certain length), with each tree within an island differing from each other by only a single rearrangement of branches (Maddison, 1991). Trees in different islands may have different implications for character evolution and each run of a random input heuristic search will typically find only one island (Maddison, 1991).

PAUP* (Swofford, 2001) was used for all parsimony analyses. A random input analysis was performed, to ensure all islands of equally most parsimonious trees were found. A brief HEURISTIC search was conducted to find the length of the shortest tree (MAXTREES was set to 100000). A second HEURISTIC search was conducted, of 1000 replicates, at each replicate saving 1 tree (TSAVE=1) no longer than the shortest tree length, with start trees RANDOM, and the MULTREES and STEEPEST ASCENT options in effect, and TBR branch-swapping in effect. Once these trees had been generated, a final HEURISTIC search was conducted on the trees found by this method, using all trees in memory. All trees were allowed to swap to completion. A strict consensus tree was produced from the set of equally most parsimonious trees obtained. Bootstrap support values were calculated for 1000 replicates with (MAXTREES = 1000). PAUP* allows for the use of ambiguous base-calls in sequence analysis and this facility was used for nrDNA data sets. Gaps were coded as missing data.

Bayesian analysis

As Bayesian analysis is based on explicit models of DNA evolution, the MrModelTest (Nylander, 2004) software package was used to identify the model of DNA substitution that best fit the data. The Bayesian analysis was run using MrBayes v3.1.2 (Huelsenbeck & Ronquist, 2001) as follows: four Markov chains, three heated and one cold, were run simultaneously for 5,000,000 generations and trees were saved every 100 generations. The starting tree was random, the branch lengths were saved and the first 4000 trees were discarded as burnin. The sumt function was used to generate a consensus tree. A majority-rule consensus calculated in PAUP* was then used to determine the posterior probabilities.

Results and Discussion

Choice of data sets

The suitability of a region for use in a phylogenetic study is dependant on two factors: the rate of change, which determines the taxonomic level at which a particular genome (or partial DNA sequence thereof) is most informative (Palmer, 1987); and sufficient length of sequence to provide enough phylogenetically informative nucleotide positions (Olmstead & Palmer, 1994). Both the ITS and ETS regions proved to be sufficiently variable and informative in the initial screening to advocate further use of both regions for a more detailed study.

Combining data sets

Character sampling for phylogenetic analysis involves two important elements: whether characters are independent, and whether there are enough of them (Olmstead & Palmer, 1994). Sufficient character sampling is necessary not only to achieve resolution, but also to have enough characters for synapomorphies to outweigh the inevitable randomly occurring homoplasies (Olmstead & Palmer, 1994). Increasing the number of characters can reveal a consistent phylogenetic signal that maybe hidden by the noise in each individual data set (Santiago-Valentin & Olmstead, 2003).

Researchers note that many recent studies have indicated that combined molecular data sets using regions with different levels of variation has provided resolution at different areas of cladograms, and phylogenetic resolution and levels of support are improved by directly combining independent molecular data sets (Chase & Cox, 1998; Soltis *et al.*, 1998; Whitten *et al.*, 2000). As noted previously, the combination of nuclear and cpDNA sequences also increases the likelihood of inferring a species tree instead of just a gene tree, which would allow any possible assessment of the role of hybridization in the evolution of a species or genus (Soliva *et al.*, 2001). Genealogy, it is thought, will most accurately be recovered if data are collected from character sets that have been under different selective pressures (Dowton & Austin, 2002). However, the analysis of large, heterogeneous data sets is not straightforward.

Although the acquisition of large and diverse molecular data sets is undoubtedly beneficial to phylogenetic reconstruction, exactly how to analyze the data remains an ongoing debate (Creer *et al.*, 2003). A number of methods have been proposed for addressing how to optimize the analysis of multiple data sets from diverse gene partitions in the pursuit of robust organismal phylogenies (Creer *et al.*, 2003). There are two major opposing approaches to the utilization of multiple data sets in

phylogenetic analysis: (i) Total evidence; and (ii) Congruence. 'Total evidence' requires that all the data be pooled into one large data set and analysed as one; and has been defined as the analysis of an unpartitioned body of evidence, ideally all the data available for a group of terminal taxa, that is characterised as seeking a single, best-fitting hypothesis, which in cladistics involves maximizing character congruence (Williams, 1994). The competing approach is 'taxonomic congruence' (also referred to as 'consensus'), which holds that trees derived from each separate data set should be compared to determine congruence, and seeks a consensus of hypotheses obtained from different data sets (Williams, 1994).

The advantages and disadvantages of each approach can depend on the heterogeneity of the data across multiple data sets. If data heterogeneity is rare, then the total evidence approach can lead to the best results, and if data heterogeneity is common, then combining all the data sets can lead to an erroneous answer that can obscure phylogenetic signal (Huelsenbeck, *et al.*, 1996). Proponents of total evidence hold that all of the independent characters available to the systematists should be combined and then analysed using parsimony. An extension of that argument says that all of the available taxa should be combined (both living and fossil) in a phylogenetic analysis (Huelsenbeck, *et al.*, 1996). Siddall (1997) opines that keeping data sets separate is anathema to explaining all of the data.

Instead of choosing between the two approaches, Huelsenbeck *et al.* (1996) advocate the idea of conditional combination. This is seen as sitting midway between the two extremes, as it prevents combination of heterogeneous data sets when partitions are clear, as well as allowing for interpretation of evolutionary processes when data sets are determined to be inappropriate for combination (Huelsenbeck *et al.*, 1996). Levasseur & Lapointe (2001) advocate another approach: using both combined and separate analyses jointly.

Testing for incongruence

The ILD test indicated that the ITS and ETS data sets were not significantly incongruent ($p=0.19$), and that all three cpDNA regions were highly congruent with each other ($p=0.79$). Based on these results, the ITS and ETS data sets were combined into the "nrDNA" data set, and the *psbA-trnH*, *rpS16* and *trnL-L-F* regions were combined into a "cpDNA" data set. The composite nrDNA and cpDNA data sets were, however, highly incongruent with each other ($p=0.01$) indicating that they should not be combined.

Final data set composition, variability and informativeness

Appendix 3 and 4 contain all sequence data for the nrDNA and cpDNA data sets. Table 3.3.1 lists the number of taxa, number of characters, variability, and informativeness of each nrDNA and cpDNA region, as well as the information for each compilation data set.

The presence of ambiguous base calls (indicated by two or more equally high signal peaks in otherwise clear electropherograms) is a sign that more than one paralogue of nrDNA is present in the plant genome of that particular sample. Out of 46 samples, 32 samples had at least one ambiguous base.

Table 3.3.1: Characteristics of each data set and DNA region, including number of samples, total number of characters, number and percentage of variable and parsimony informative characters, as well as data signal statistic.

	No. samp.	Tot. chars	Variable Characters		Parsimony Inform. Ch.	
			Number	%	Number	%
cpDNA	46	2367	204	8.6	84	3.5
<i>trnL-L-trnF</i>	46	901	60	6.7	16	1.8
<i>psbA-trnH</i>	46	600	73	12.2	46	7.7
<i>rpS16</i>	46	866	71	8.2	22	2.5
nrDNA	46	1441	439	30.5	232	16.1
ITS	46	678	176	26.0	92	13.6
ETS	46	763	263	34.5	140	18.3

Analyses results: nrDNA data set*Parsimony analysis*

Parsimony analysis found 100000+ trees (CI =0.709, RI =0.889) for the nrDNA data set. The strict consensus of these trees (Figure 3.3.1) shows several strongly supported clades. These include:

- 1) *G. jurineifolia* (although there is no clear separation of the two subspecies), with 100% Bootstrap support (BS);
- 2) *G. tenuifolia*, with 100% BS;
- 3) *G. heterochaeta*, with 100% BS;
- 4) *G. lichtensteinii*, with 100% BS;
- 5) *G. ciliaris*, with 100% BS; and
- 6) *G. caespitosa*, rendered paraphyletic by the *G. ciliaris* samples (with 100 % BS for the branch as a whole).

The remaining samples group together in a large well supported (100% BS) clade, named the “K-R clade” (due to the preponderance of *G. rigens* and *G. krebsiana* samples in the clade). There are two clades with significant support within this K-R clade:

7) a clade of all except two *G. rigens* specimens (with 94% BS); and

8) the grouping together of the *G. othonnites* sample and the sample of a putative new species (with 94% BS).

There is little other clear taxonomic pattern within this large group and no significant support exists for any other internal branches which includes a number of Roessler’s “species”.

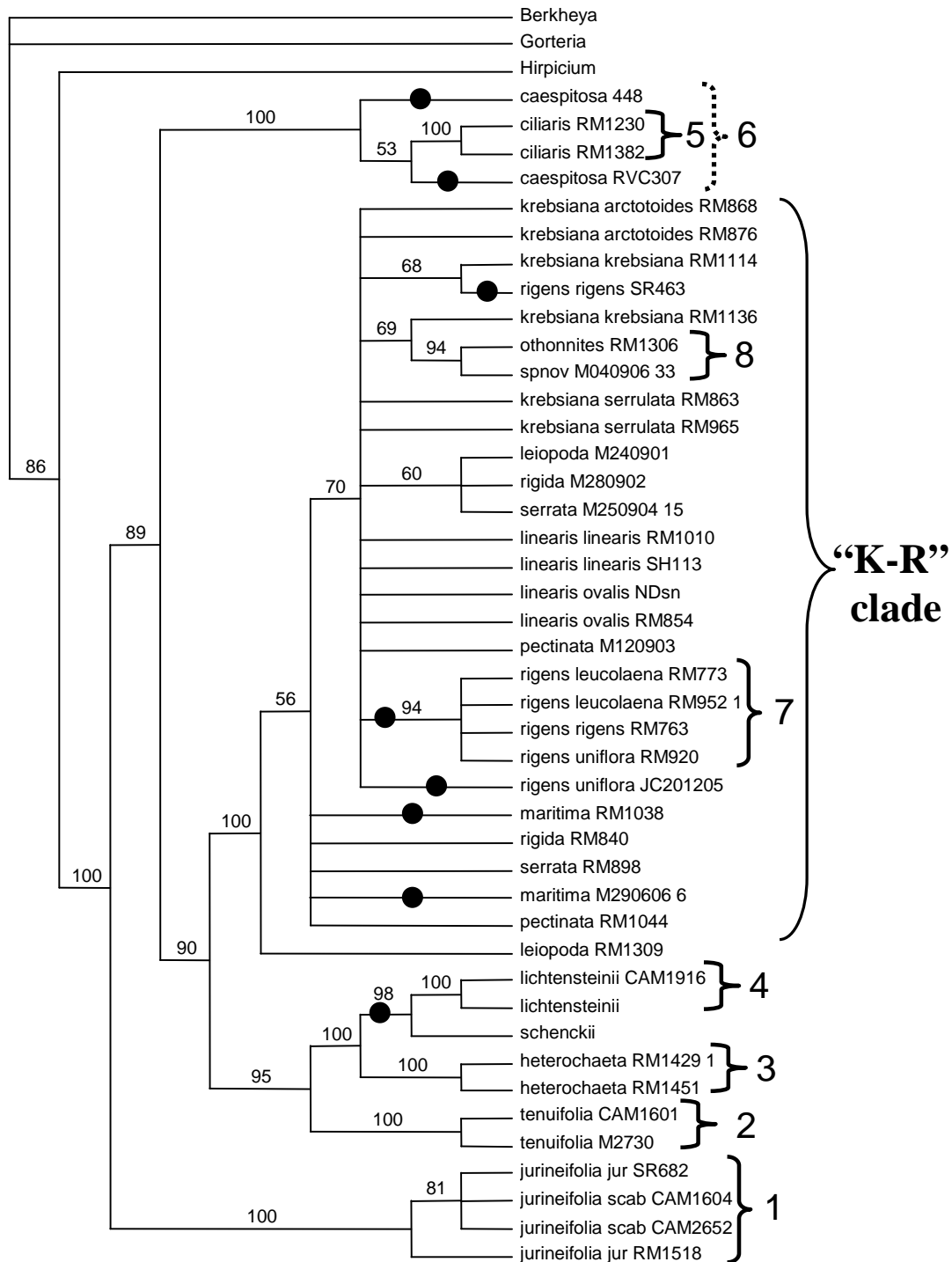


Figure 3.3.1: nrDNA strict consensus tree of 100000+ trees, L=508, CI=0.711, RI=0.896. Bootstrap support indicated above branches. Brackets highlight species clades discussed in the text. Black circles indicate the developed stem habit.

Bayesian analysis

For the nrDNA data set, MrModelTest identified the General Time Reversible model (GTR+G) (Tavaré, 1986) as the best fit (specific settings: Prset statefreqpr=dirichlet(1,1,1,1); Lset nst=6 rates=gamma). The Bayesian tree (Figure 3.3.2) shows exactly the same groupings as seen in the Parsimony results.

Correspondence between molecular phylogeny and taxonomy

Habits (rosette or developed stem) were mapped onto the phylogeny, with the presence of black circles indicating those samples with the developed habit. No particular pattern of growth habit in relation to phylogeny is apparent. This does not rule out the possibility that state reversals may have occurred (leafy stems may define Clade 6, with a subsequent reversal of state for Clade 5).

The nrDNA data set resolves seven taxa with high support (*G. lichtensteinii*, *G. heterochaeta*, *G. schenckii*, *G. tenuifolia*, *G. jurineifolia*, *G. ciliaris* and *G. caespitosa*). Four of these taxa (*G. jurineifolia*, *G. heterochaeta*, *G. tenuifolia* and *G. lichtensteinii*) also showed strong morphological distinction in the morphometric analyses (Chapter 2). This provides clear evidence (from the nuclear genome) of good species delimitations for at least some of the species of *Gazania*.

The remaining species samples form a large, poorly resolved clade composed of nine “species” that show little genetic grouping (the K-R clade). One nominal exception exists: an internal clade that groups most (but not all) of the *G. rigens* samples with strong support (94-100% BS). *G. rigens* was one of the other two morphologically defined clades from Chapter 2 (*G. rigens* and *G. linearis* subsp *ovalis*), but neither clade shows much genetic cohesion in the nrDNA analyses.

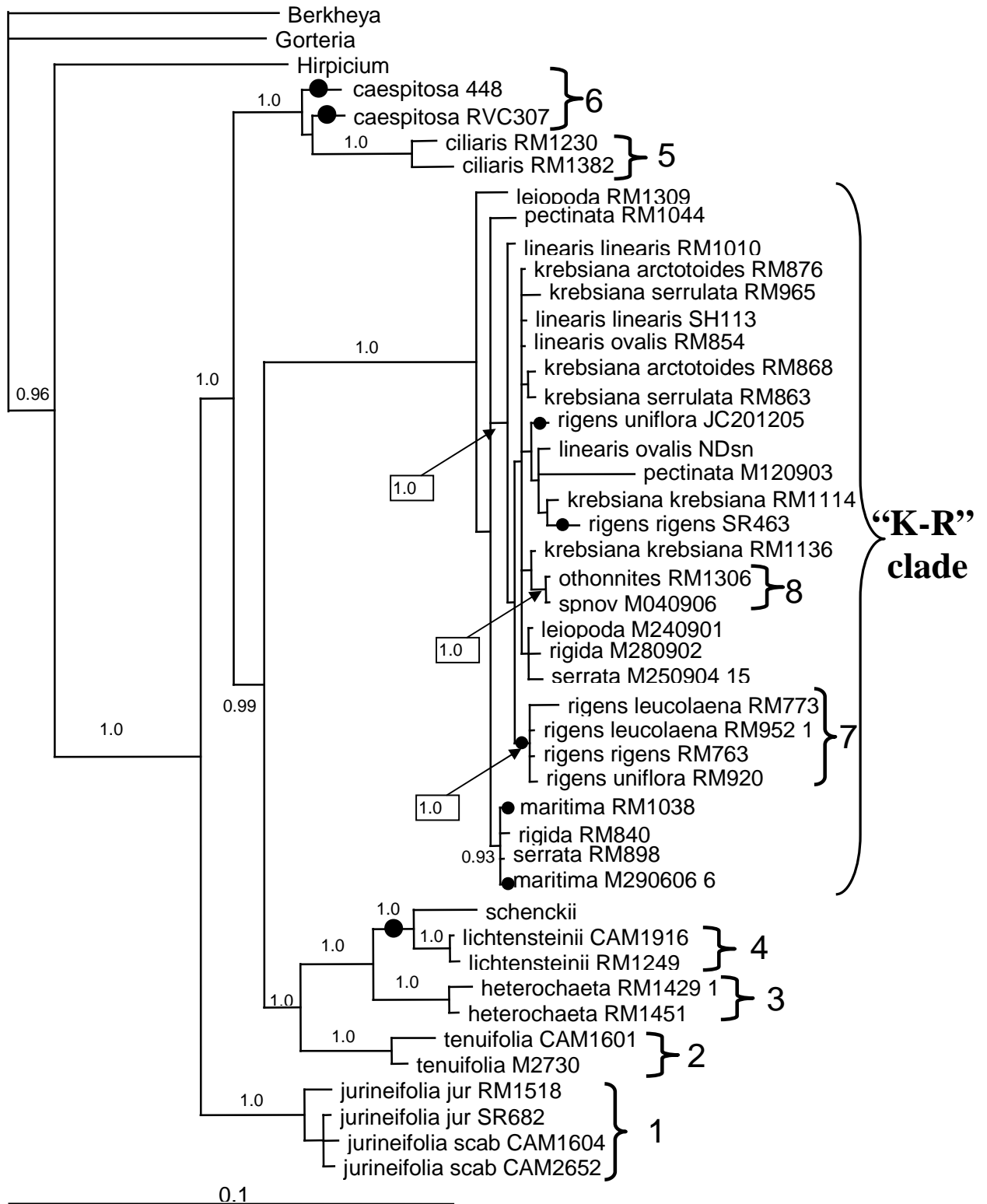


Figure 3.3.2: nrDNA Bayesian consensus tree. Posterior probabilities indicated on branches. Brackets highlight species clades discussed in the text. Black circles indicate the developed stem habit.

Analyses results: cpDNA data set

Parsimony analysis

Parsimony analysis found 100000+ trees (CI =0.785, RI =0.894) for the cpDNA data set. The Strict consensus of these trees (Figure 3.3.3) resolves only some of the same species groupings seen in the nrDNA trees. These include:

- 1) *G. jurineifolia*, with 100% BS;
- 2) *G. tenuifolia*, with 96% BS;
- 3) *G. ciliaris*, with 100% BS; and
- 4) *G. caespitosa*, with 77% BS.

The remaining samples show no clear species structure but are relatively strongly supported (80% BS) as a clade. The *G. rigens* clade seen in the nrDNA data is not retrieved in the cpDNA data.

Bayesian analysis

For the cpDNA data set, MrModelTest identified the General Time Reversible model (GTR+I+G) (Tavaré, 1986) as the best fit (specific settings: Prset statefreqpr=dirichlet(1,1,1,1); Lset nst=6 rates=invgamma). The Bayesian consensus tree (Figure 3.3.4) shows exactly the same groupings as the parsimony analysis. Some resolution is obtained inside the largest unresolved branch, although this shows little species coherency.

Correspondence between molecular phylogeny and taxonomy

Habits (rosette or developed stem) were mapped onto the phylogeny, with the presence of black circles indicating those samples with the developed habit. No particular pattern of growth habit in relation to phylogeny is apparent.

The cpDNA data set resolves only four taxa with high support (*G. jurineifolia*, *G. tenuifolia*, *G. ciliaris*, and *G. caespitosa*). These taxa were also well resolved in the nrDNA data set and two (*G. jurineifolia* and *G. tenuifolia*) were well resolved in the morphometric analysis in Chapter 2. This lends additional support to their status as distinct species.

As with the nrDNA data set, beyond the resolved clades, there remains a large unresolved clade consisting of multiple species samples.

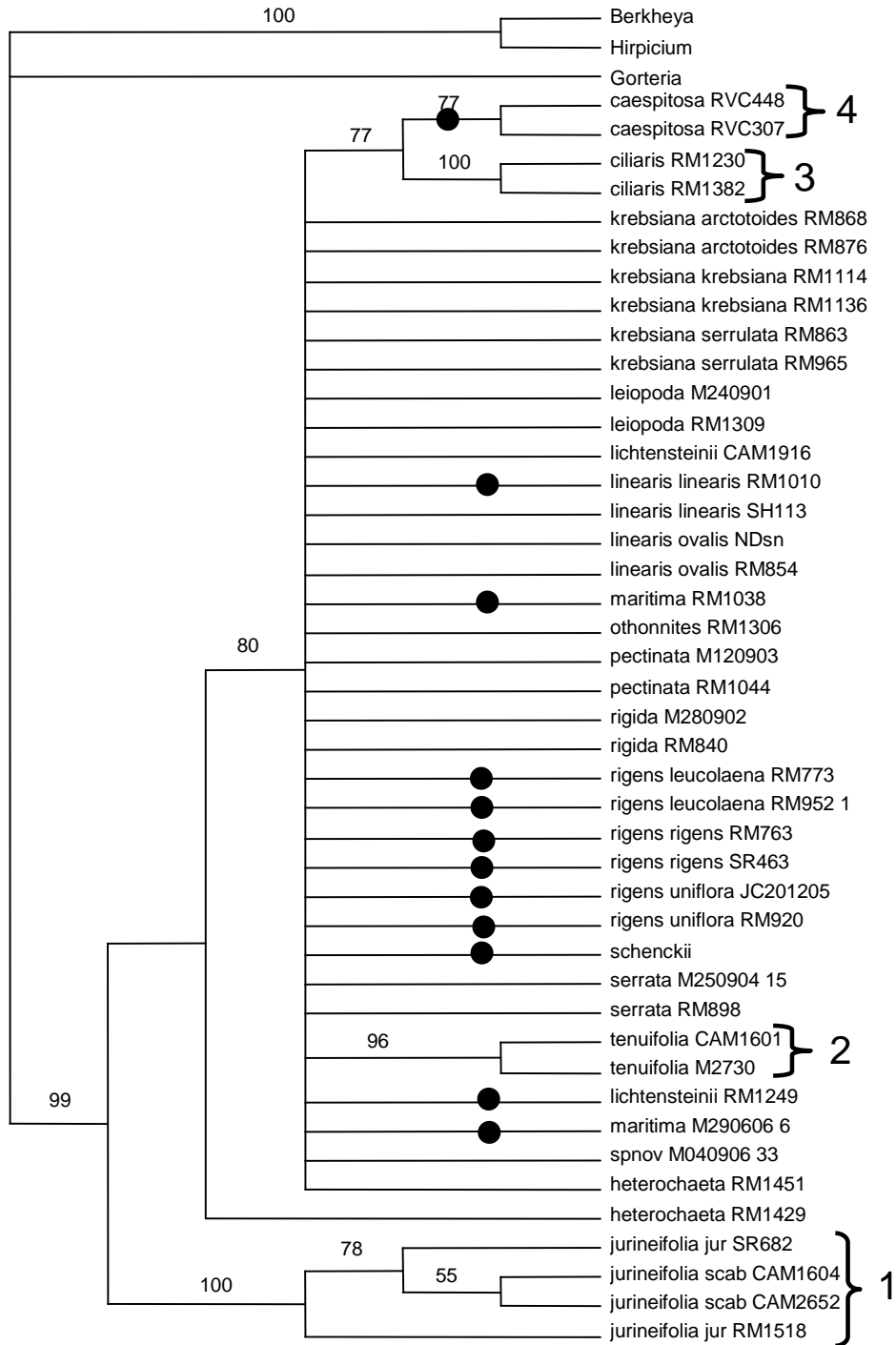
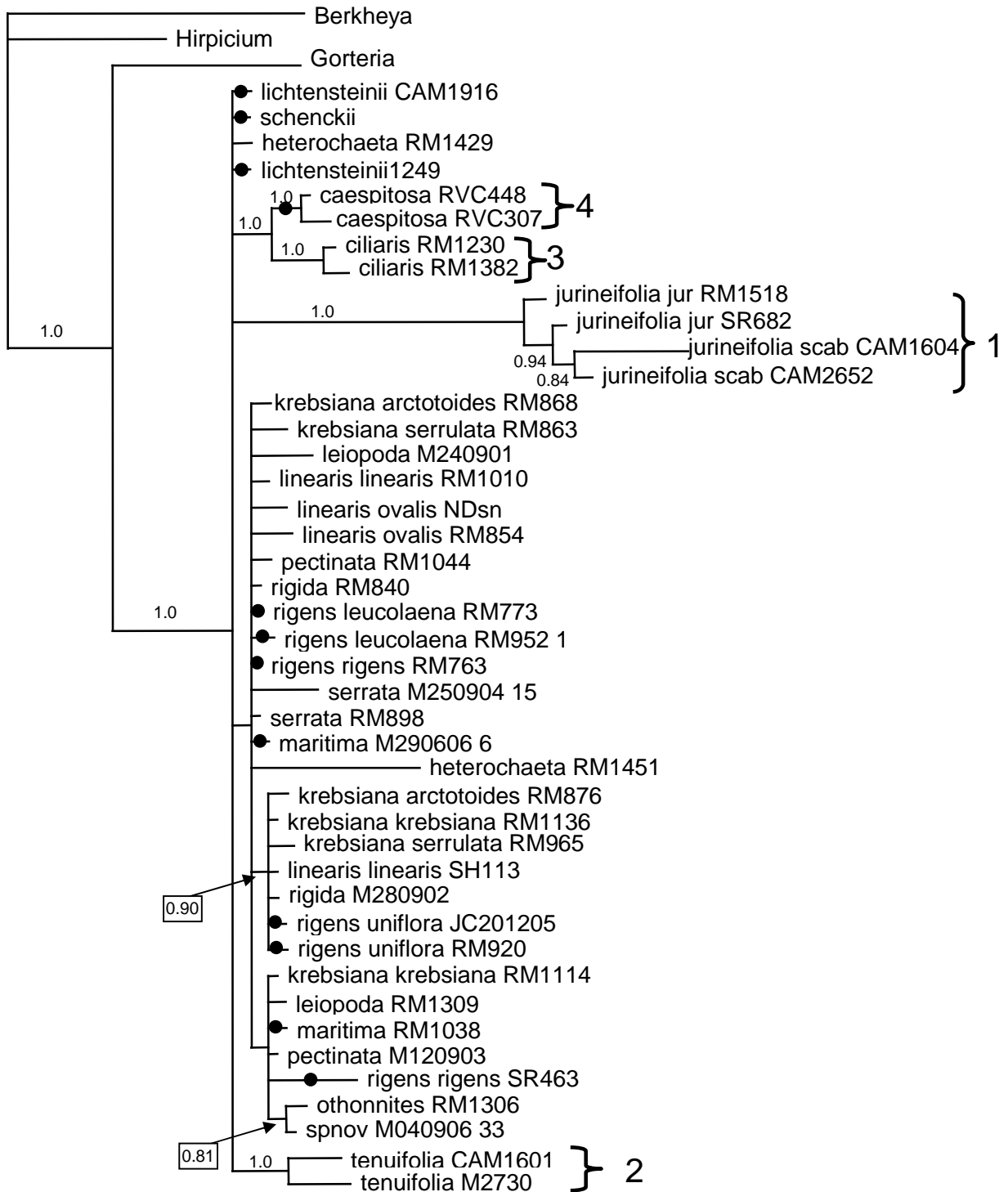


Figure 3.3.3: cpDNA strict consensus tree of 100000+ trees, L=112, CI =0.795, RI =0.894. Bootstrap support indicated above branches. Brackets highlight species clades discussed in the text. Black circles indicate the developed stem habit.



0.1

Figure 3.3.4: cpDNA Bayesian consensus tree. Posterior probabilities indicated above branches. Brackets highlight species clades discussed in the text. Black circles indicate the developed stem habit.

Composite combined evidence phylogeny

Despite the ILD test results, which indicate that the cpDNA and nrDNA data sets should not be combined, the two data sets repeatedly resolve the same genetically discrete basal species clades, suggesting that any incongruence present is more than likely due to the unresolved K-R clade, although it may also be due to rate heterogeneity. Sequential removal of taxa from the K-R clade resulted in improvements in the ILD test statistics. The initial test result was $p=0.01$ when all K-R clade taxa were present. Removal of all duplicate taxa in the K-R clade (i.e. so that there were only a single representative of each taxa present) resulted in $p=0.01$ again. Removing half of the species in the K-R clade (such that there were only eight taxa left) resulted in $p=0.1$. Halving this number again (such that there were only four taxa left) resulted in $p=0.27$. Total removal of the K-R clade taxa resulted in $p=0.36$. This indicates that the incongruence between the two data sets was due to the confounding effects of the K-R clade polytomy.

Disregarding the ILD test results, a composite data set (“combined”) was compiled from the cpDNA and nrDNA data, and subjected to parsimony analysis and Bayesian analysis (using the GTR+I+G model, with all other settings as for the cpDNA analysis).

The parsimony consensus tree (Figure 3.3.5) and the Bayesian consensus tree (Figure 3.3.6) once again retrieve the same basal well-resolved species clades. The Bayesian tree shows very strong support for all the basal clades (all with $pp=1.0$), while the support in the parsimony analysis remains much the same as the nrDNA analysis. *G. caespitosa* is no longer paraphyletic with respect to *G. ciliaris*, and there is still little species resolution in the well-supported K-R clade. The congruence between the combined DNA phylogeny and the nrDNA phylogeny supports the idea that the incongruence between the cpDNA and nrDNA data sets as indicated by the ILD test could be due to the confounding effects of the polytomy of the K-R clade.

Gaps in relation to species phylogeny

Gaps were mapped onto replicates of the combined DNA phylogeny. Gaps in both cpDNA (Figure 3.3.7) and nrDNA (Figure 3.3.8) were phylogenetically informative, although cpDNA showed some state reversals for these gaps. These apparent state reversals may be evidence of either hybridization events (with the dissimilar samples retaining cpDNA from maternal parents which lack the indels present in the majority of samples) or lineage sorting (with some few dissimilar samples retaining a less common ancestral cpDNA haplotype that lack the indels present in the majority of other samples).

Polytomies

There are polytomies present in results from both the nrDNA and cpDNA data sets. These may be a consequence of consensus methods (where conflicting relationships in different phylogenetic trees are summarised as a polytomy), or as the short branch lengths seen in the K-R clade in the Bayesian tree also indicate, a very low level of difference between the samples (i.e. lack of data). Although phylogenetic hypotheses can provide insights into mechanisms of evolution, their utility is limited by an inability to differentiate simultaneous speciation events (hard polytomies) from rapid cladogenesis (soft polytomies) (Walsh *et al.*, 1999). Phylogenetic analyses of molecular data often recover polytomies (multifurcating rather than bifurcating relationships) and most of these polytomies are assumed to be "soft" (i.e. they can be resolved by the addition of more data from more sources) (Walsh *et al.*, 1999). If, however, an ancestral lineage does generate three or more lineages at one time, the resulting multiple simultaneous speciation events are represented by a "hard" polytomy (i.e. no matter how many datasets are added, polytomies and uncertainties will remain) (Walsh *et al.*, 1999). These hard polytomies will remain even after analyses of very large data sets as they are genuine representations of multiple simultaneous branching events (Walsh *et al.*, 1999).

In the case of polytomies within *Gazania*, the low number of phylogenetically informative characters in the cpDNA data set does not resolve a soft polytomy that might be resolved with more informative data sources. However, the lack of resolution in the faster evolving nrDNA data set (with proportionally five times as many characters, 15% informative for nrDNA vs 3% informative for cpDNA) suggests a hard polytomy within the large, unresolved, nine-“species” K-R clade, due to a recent and rapid radiation event. Whether this was in fact a “speciation” event is open to interpretation, as this relies on the assumption that the morphologically based “species” that Roessler delimited are actually species in their own right.

Rapid cladogenesis and other such speciation events present serious difficulties for phylogeny reconstruction from molecular sequences as reconstruction of such recent radiations is hampered by insufficiently rapid sequence evolution and problems with incomplete lineage sorting and reticulate evolution (Fishbein & Soltis, 2004). Lee *et al.* (2005) noted that a lack of accumulated molecular sequence variation and the convergence of morphological traits limits one’s ability to make sense of evolutionary past of many plants, especially those suspected to be the products of radiations. This inadequacy is further confounded by the possibly misleading inferences that have been based on single-marker phylogenies (i.e. “gene trees” vs. “species tree” differences), as well as the poorly documented role of hybridization and introgression in radiations (Lee *et al.*, 2005).

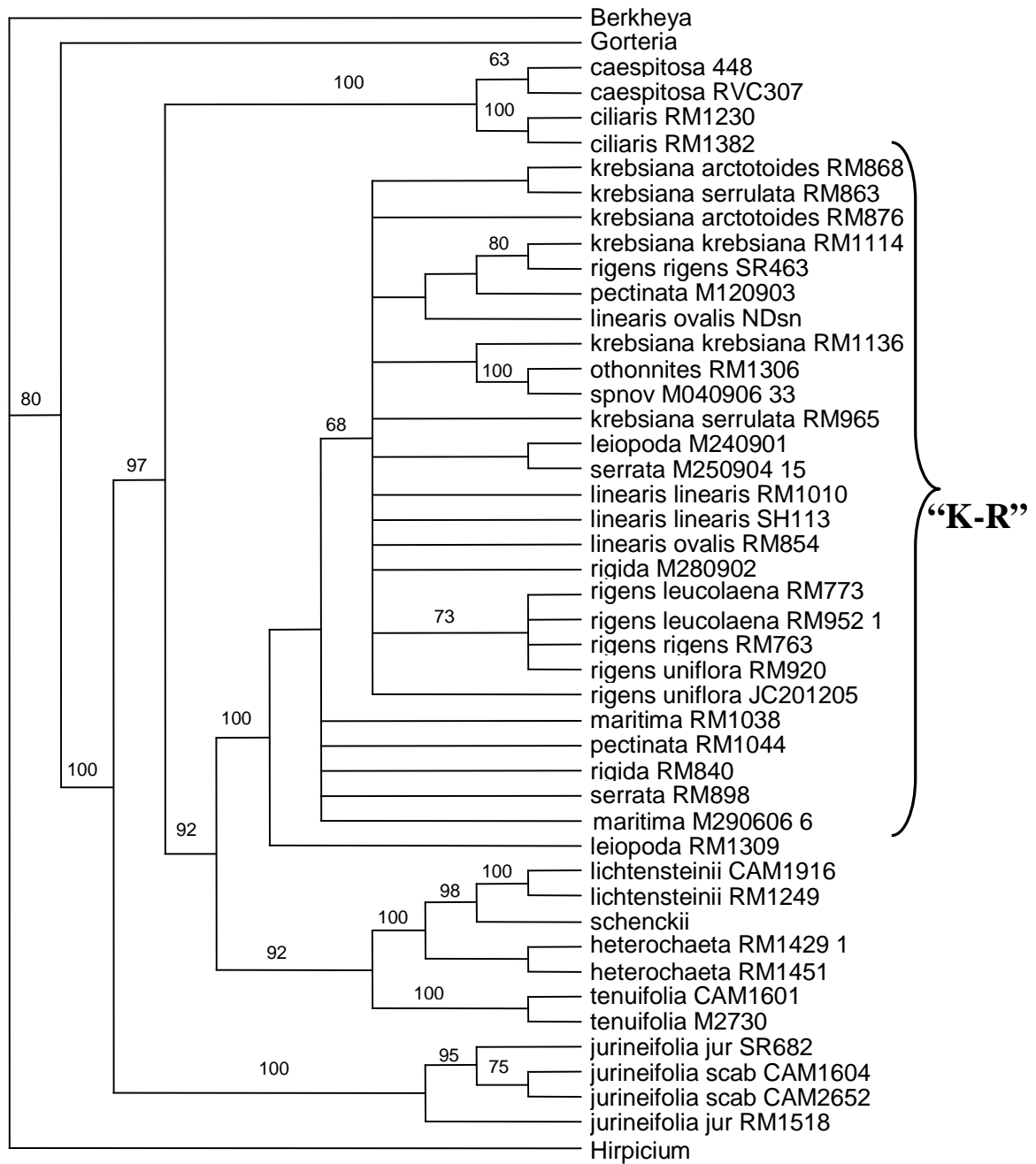


Figure 3.3.5: Combined DNA strict consensus tree of 100000+ trees, L=596, CI =0.678, RI =0.883. Bootstrap support indicated above branches.

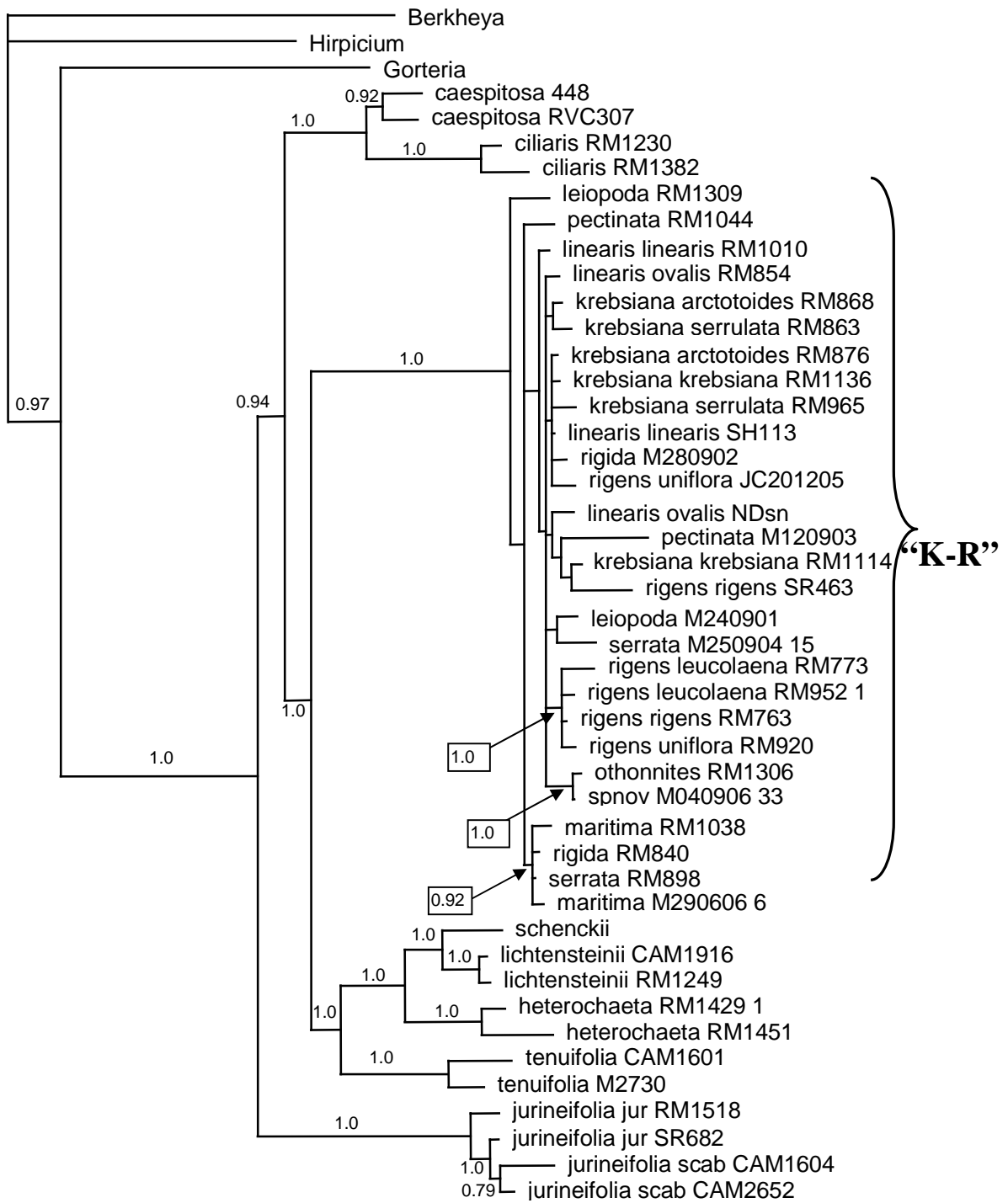


Figure 3.3.6: CombinedDNA Bayesian consensus tree. Posterior probabilities indicated on branches.

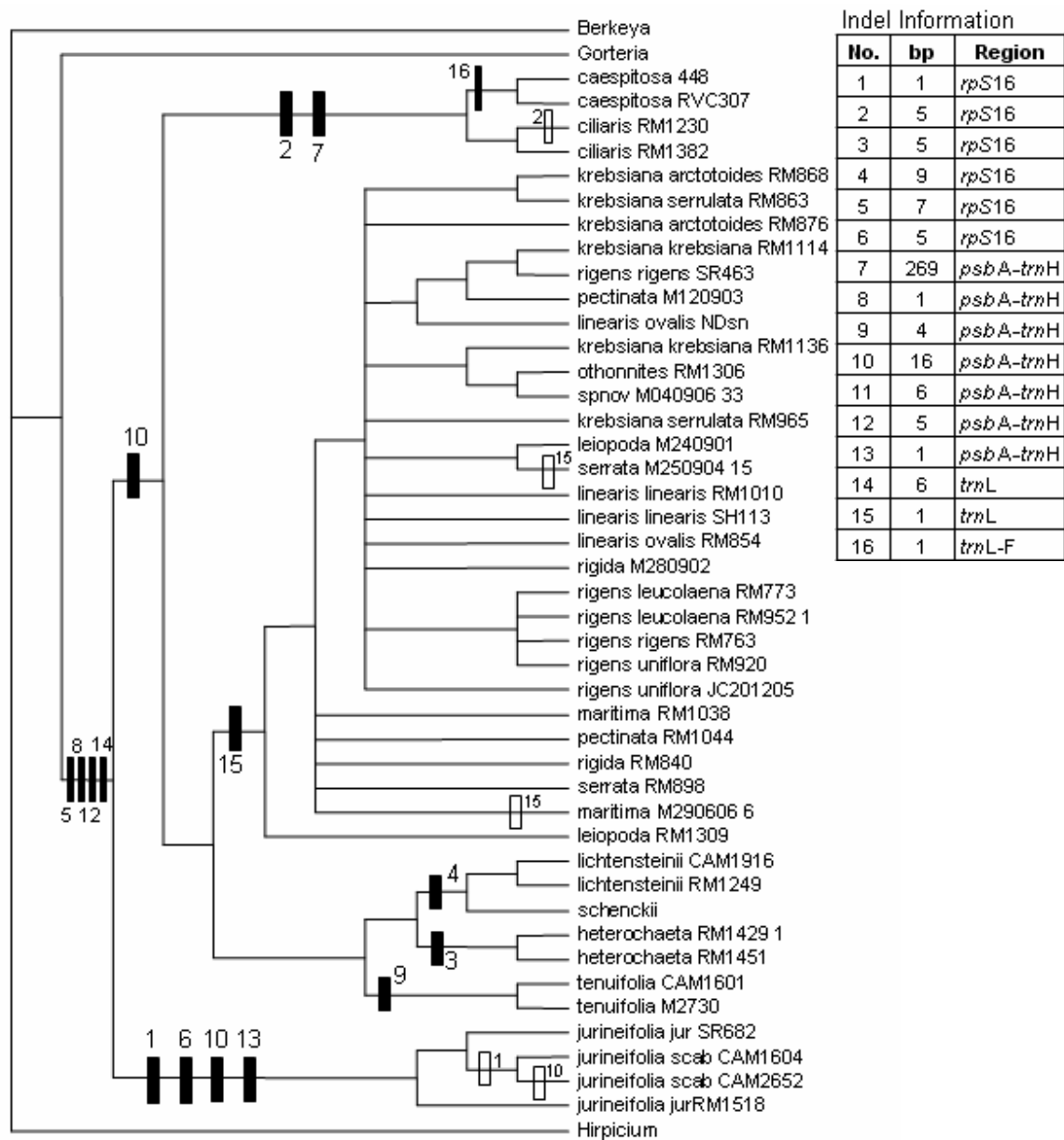


Figure 3.3.7: Combined DNA strict consensus tree. Black bars indicate synapomorphic gaps in cpDNA data, white bars indicate state reversals.

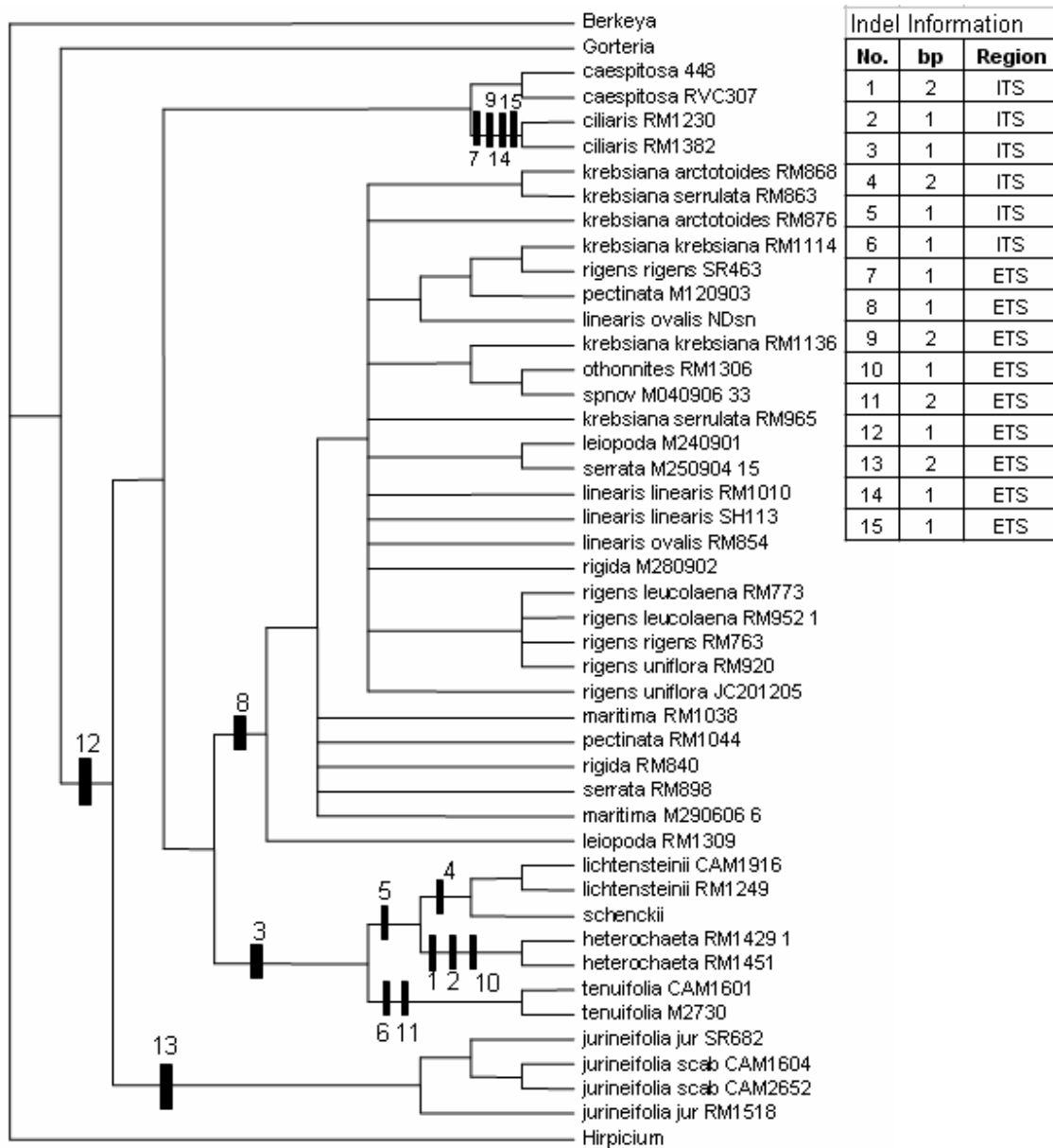


Figure 3.3.8: Combined DNA strict consensus tree. Black bars indicate synapomorphic gaps in nrDNA data.

Gene trees vs species trees

Doyle (1992) notes that while molecular phylogenies are now an accepted part of systematics, it often seems forgotten that the terminal taxa of a DNA phylogenetic reconstruction are genes, not necessarily species. No matter how well resolved and strongly supported a DNA phylogeny is, it can only be a hypothesis of relationships among the plants bearing these genes (Doyle, 1992). Wendel & Doyle

(1998) likewise note that with the proliferation of molecular tools has come a growing awareness that reliance on a single data set may often result in insufficient phylogenetic resolution, or misleading inferences. In accordance with this, they note, it has become increasingly widespread practice to apply multiple data sets to a common group of taxa.

One should exercise caution in estimation of species trees from gene trees, as while species trees may be “estimated” from gene trees, but the two are not synonymous (Doyle, 1992). Reliance on a single gene can result in a lack of resolution, misleading conclusions or both (Reeves *et al.*, 2001). Ideally, multiple regions from multiple genomes should be utilised. The three different genomes present in plants have different inheritance patterns. In angiosperms organellar markers are inherited maternally (usually) and transmitted by seed, while nuclear markers are inherited biparentally, through both pollen and seed (Albach & Chase, 2004). This differing pattern of inheritance allows for different aspects of the phylogenetic history of an organism to be investigated: the chloroplast genome tracks maternal inheritance patterns while the nuclear genome tracks population level processes of gene flow and hybridization.

The use of two different sources of sequence data lends stronger support to the species that are resolved. Likewise the presence of the same unresolved species in both phylogenies reaffirms the taxonomic uncertainty that surrounds these “species”.

Polyploidy

The possibility that polyploidy could have a confounding effect on phylogeny reconstruction (especially that of multicopy nrDNA) must also be considered. There is relatively little published information available on the chromosome numbers in *Gazania*. Mehra & Remananandan (1969) provide a count of $x=8$ for *Gazania krebsiana*, while Nordenstam (1967) provides $x=10$ for the same species. An initial attempt by the author to obtain a chromosome count for *Gazania rigens* resulted in a count of $x=9$. The Arctoteae are usually $x=9$ (Carr *et al.*, 1999), so this seems the most likely count for *Gazania* as well. While at least two species in the K-R complex do not show polyploidy, but this does not rule out polyploidy in other species of *Gazania*. Further research needs to be conducted in this regard.

Caveats

Given the possibility that ITS and ETS may suffer from reticulation (being a non-hierarchically inherited gene system, as opposed to maternally inherited cpDNA), the phylogeny presented here may

perhaps be interpreted with some caution. The presence of several instances of ambiguous base calls likewise suggests that reticulation and paralogy should be considered as having some effect on the phylogeny.

Conclusions

The nrDNA sequence data examined here reveals that there are seven clearly genetically distinct phylogenetic species in *Gazania*, some of which also show correlation with morphologically distinct species clades from Chapter 2. These are: *G. lichtensteinii*, *G. heterochaeta*, *G. schenckii*, *G. tenuifolia*, *G. jurineifolia*, *G. ciliaris* and *G. caespitosa*. There is some partial genetic cohesion for some *G. rigens* samples and none at all for *G. linearis* subsp *ovalis* (both of these showed strong morphometric distinction in Chapter 2). However, the cpDNA sequence data examined here only supports four of these distinct taxa (*G. jurineifolia*, *G. tenuifolia*, *G. ciliaris*, and *G. caespitosa*). This lack of support in the cpDNA does not, however, contradict the distinction of taxa in the nrDNA data set.

Despite the use of a substantial combined nuclear and chloroplast DNA data set, further resolution of species taxa could not be achieved. For the remaining nine unresolved “species” in the K-R clade, there is no clear correlation between morpho-species designation and phylogeny (or partial correlation as seen in *G. rigens*). The lack of genetic resolution for eight of the nine species (seven of which also showed an absence of morphometric separation in Chapter 2) casts further doubt on the validity of Roessler’s species delimitations for these taxonomic entities.

It should be noted that there are occasions where genetic data may not reflect clear morphological separations. In such cases, other methods (e.g. RFLP, microsatellites) can prove more informative (e.g. *Scalesia affinis*; Nielsen, 2004). This may certainly prove useful in *Gazania*, and is recommended as a future project.

As Roessler noted, for some species the geographical origin is important in species determination. The possibility that the groupings in the K-R clade may be dictated by geographical origin, rather than species designation, should be investigated. The use of phylogeographical methods is an appropriate tool for this, and may also elucidate the evolutionary history and origin and (potentially rapid and recent) diversification of the species within the genus *Gazania*.

Chapter 4. **Phylogeography of *Gazania***

“Between the remaining taxa, such close relationships and overlaps of characteristics exist that a clear separation becomes impossible. So only the observation that certain feature combinations arise especially frequently and are concentrated geographically in certain regions provides clues for a classification.” (Roessler, 1959, pp 100, translated from the original German).

Aim: To undertake a phylogeographic study of the genetic entities within *Gazania*.

Introduction

Apart from organisms with very short generation times, there is rarely an opportunity to observe the process of evolution directly, to track changes in diverging lineages as they become distinct (Harrison, 2001). To gain insights into change over time, evolutionary biologists attempt to infer historical events and processes from current patterns of genetic variation (Harrison, 2001). Phylogenies provide an estimate of the sequence of events leading to present-day patterns of species-richness and so provide indispensable information towards understanding the processes operating towards the evolution of diversity (Barracough *et al.*, 1998). Relatively new techniques (such as phylogeography) enable geography and biology to develop more synergistically, whereby patterns revealed by one discipline can be used as a hypothesis for testing by the other (Wallis & Trewick, 1998).

Phylogeography has a number of differently worded definitions, but all of them rely on two sources of data: a phylogeny and the geographical origins or distributions of the terminal taxa in that phylogeny. Phylogeography is defined by Bermingham & Moritz (1998) as an investigation of the fundamental links between population processes and regional patterns of diversity and biogeography. Avise (2000) defined phylogeography as being concerned with principles and processes governing the geographical distribution of genealogical lineages, but adds an additional note that this is especially true at the intraspecific level. This investigation into *Gazania* is not using phylogeography in the strictest sense of population level studies, but rather in the broader sense of correlation between phylogeny and geography.

Arbogast & Kenagy (2001) indicate that the goal of phylogeography renders it a subdiscipline of biogeography, in which the primary units of analysis are monophyletic groups that are inferred from phylogenetic analyses. Although this typically entails the use of one or more molecular markers when intraspecific population phylogeny is being examined, in principle, any set of phylogenetically informative characters could be used (Arbogast & Kenagy, 2001).

Phylogeography, as an analytical method, explicitly integrates micro-evolution and macro-evolution, relates ecology to evolution, current distributions to historical events, the physical environment to genetic structure, and patterns of variation within species to patterns of variation across species (Avice, 2000). This analysis relies on interpreting patterns of congruence (or lack of congruence) between the geographical distribution of haplotypes and their genealogical relationships (Schaal *et al.*, 1998).

Besides phylogeography's strength in testing for explicit evolutionary relationships between geographical areas occupied by phylogenetically related taxa, a phylogeographic approach traces the history of genealogic lineages (Dobeš *et al.*, 2004). Like Avice (2000), Dobeš *et al.* (2004) also emphasize a species level focus, noting that the advantage mentioned in the previous sentence may be of special importance at the junction of the intra- and interspecific level, where partially divergent lines may occur sympatrically. Phylogeography provides a framework to explain and integrate these patterns of biodiversity at infra- and supra-specific levels (Dawson, 2005), as well as investigating a wide range of other issues related to biogeography, including the relative roles of gene flow, bottlenecks, population expansion, and vicariant events in shaping geographical patterns of genetic variation (Arbogast & Kenagy, 2001).

In the last 20 years, phylogeographic research has added considerable insight into the effects of history on species distributions and diversification patterns (Ayoub & Riechert, 2004). Phylogeography has also been used to trace the origins and invasive histories of invasive species (Provan *et al.*, 2005; Shoemaker *et al.*, 2006). In many cases, phylogeographic analyses have revealed cryptic and deeply divergent evolutionary lineages that are not reflected in the current taxonomy, and nominal species have been found to be poly- or paraphyletic (see Arbogast & Kenagy, 2001, for list of examples).

Sources of genetic data

Geographical interpretation of current patterns of genetic variation can reveal the signature of historical events, but the ongoing influence of natural selection, gene flow, and genetic drift can erase those signatures, reflecting the current balance of evolutionary forces rather than the consequences of historical events (Harrison, 2001). While organellar DNA is theoretically ideal for studying phylogeographic patterns (Heuertz *et al.*, 2004), at very low levels of the taxonomic hierarchy, where insufficient time has elapsed for variation to accumulate in the slowly evolving chloroplast genome, a more rapidly evolving source of data must be utilized (with relevant caveats and cautions noted; Harrison, 2001).

Harrison (2001) notes some of the "biological hurdles" associated with using diploid nuclear markers, including the larger effective population size (four times that of organellar DNA). One can also expect random lineage extinction to be slower and ancestral polymorphisms to persist longer, meaning potentially less concordance among nuclear gene genealogies and less correspondence with the "real" population history (Harrison, 2001). Harrison (2001) also notes that nuclear gene genealogies will inevitably inform one's understanding of recent population history, as they trace independent pathways of descent for multiple gene regions (and any discordance between species or population designation and nuclear gene history will in itself tell the researcher something about the population history). Different regions of the genome will therefore provide different windows on recent evolutionary history (Harrison, 2001). Heuertz *et al.* (2004) claim that chloroplast DNA is a useful tool for the identification of recent post-glacial colonization routes, as colonization patterns which derive from seed dispersal are not blurred by pollen flow.

Application of phylogeographic methods to *Gazania*

The previous two chapters have shown that Roessler's species in *Gazania* can be divided into seven clades that show clear species groupings (some both morphologically and genetically) and nine that show little cohesion using either criterion. The phylogeography of both sets of species will be investigated, both as a means to investigate more recent and ongoing evolutionary, but also as a means to investigate the past evolutionary history of the group.

Phylogeographic analysis is an ideal tool to investigate the nine problematic *Gazania* species that fall into the K-R clade found in species-level analysis (Chapter 3). In *Gazania*, where little resolution exists in the slowly evolving cpDNA data, the faster evolving nrDNA data may provide clearer phylogenetic signal. A greater sampling of the nine species that fell into the large unresolved K-R clade collected from across South Africa is necessary to investigate any phylogeographical signal that may be present, and to infer possible evolutionary or ecological processes from the recent past. In addition, two samples from a potentially new species of *Gazania* (*G. sp. nov.*) are included in the analysis. The putative new species shares some characters (e.g. glaucous leaves, and a slight succulence to the leaves, stem and involucre) with a species recognised by Roessler: *G. othonnites*.

In Chapter 3 it became evident that cpDNA was not variable enough to provide much phylogenetic signal. For this reason, nrDNA sequence data (from both ITS and ETS) were utilized to assemble a much larger data set to better investigate the phylogeographic signal within the various taxonomic entities in *Gazania*.

Methods

Sampling

DNA was taken from 24 samples of the seven genetically discrete clades, and 145 samples of species that fall within the K-R clade, including those initially used for the species-level phylogeny (see Table 4.2.1 for details). These samples were selected not only to cover as wide a distribution range as possible, but also to investigate the validity of the morphologically delimited species of Roessler. Two datasets were defined: one of all the samples (using *Berkheya* and *Gorteria* samples as the rooting outgroup), and a second subset of the samples from the K-R clade (using *G. ciliaris* and *G. caespitosa* samples as the rooting outgroup). Additional sequences not already presented for the Chapter 3 phylogeny in Appendix 3 are presented in Appendix 6.

These samples were amplified and sequenced for both ITS and ETS, using the methods as outlined in Chapter 3. Due to the low resolution of the unresolved K-R clade taxa seen in the results obtained by Parsimony analysis, other methods have to be utilized. Therefore, Bayesian and Neighbor-Joining analysis are used, as well as additional Neighbor-Net analysis for the K-R clade. Neighbor-Joining was utilized in this study due to its sensitivity to low levels of nucleotide variation. The Neighbor-Net analysis produces a reticulating network, rather than a bifurcating tree. Unfortunately, many of the software packages developed for phylogeographic studies cannot handle data with ambiguity coding. Settings for Bayesian analysis are identical to those given in Chapter 3. Details of the Neighbor-Joining and Neighbor-Net methods are given below.

Neighbor-Joining

Neighbor-Joining (NJ) is a distance method, which converts the aligned sequences into a distance matrix of pairwise differences (distances) between the sequences. The Neighbor-Joining method is both fast and accurate (Bryant & Moulton, 2004). MrModelTest (Nylander, 2004) was used to identify the model of DNA substitution that best fit the data. PAUP* was used to conduct Neighbor-Joining analyses. Missing data was ignored for pairwise comparisons, and negative branch lengths were set to zero. Bootstrap support values were calculated from 1000 replicates, and shown on the NJ tree.

Neighbor-Net analysis

The ability to represent reticulating relationships (especially at the species-level) becomes a problem that requires methods other than bifurcating trees (Vriesendorp & Bakker, 2005). There are a range of methods and software for network estimation that can handle reticulations and multifurcations, but these methods have not been used frequently in published studies of angiosperm species phylogenies

(Vriesendorp & Bakker, 2005). These methods are often designed to be used with organellar data (e.g. the TCS software package), and thus cannot handle ambiguity coding (as utilised in the nrDNA data for this study). The use of networks, rather than simple branching trees, is necessary when the underlying evolutionary history is not treelike and confused by phenomena such as recombination, hybridization, gene conversion and gene transfer (Bryant & Moulton, 2004). Networks can uncover data ambiguity in a way that consensus trees cannot, providing new insights in the analysis of data structure (Vriesendorp & Bakker, 2005).

The Neighbor-Net algorithm is an extension of the Neighbor-Joining method, using similar selection and reduction formulae, but Neighbor-Net can additionally represent conflicting signals in the data, which NJ bifurcating trees cannot (Bryant & Moulton, 2004). These networks do not restrict the data to a rigid hierarchical single-line tree structure, but allow for the identification and visualisation of character conflicts within the data (Hollingsworth *et al.*, 1998), as contradictory signals are represented by box-like parts of the graph, whereas portions of the graph with little conflict appear more tree-like (Kennedy *et al.*, 2005). Neighbor-Nets are often more resolved than split-decomposition networks, especially when the number of taxa is large, as they do not show a tendency to become star-like as more taxa are added (Kennedy *et al.*, 2005). For this reason, a Neighbor-Net analysis was conducted on the unresolved K-R clade using the software SPLITSTREE v4 (Huson & Bryant, 2005), using the Neighbor-Net method (Bryant & Moulton, 2004). Outgroups were excluded from this analysis.

Distribution maps

The geographical origin of each clade (or subclade for the K-R clade) in the NJ and Bayesian trees were plotted onto maps of Southern Africa in an attempt to elucidate any phylogeographic patterns.

Morphometric comparison

A cluster analysis comprising samples of species occurring only in the K-R clade was undertaken. This was utilized to compare genetic clades with morphological clusters to determine if there is any correlation between morphometric characters and gene flow patterns. All CA settings are as per Chapter 2. The comparison between pairwise genetic distance and pairwise morphometric distance for all pairs of samples in each data set can illustrate the level of agreement between genetic signal and morphological signal. The genetic distances were taken from the uncorrected distances as output by PAUP*, the morphometric distances were taken from the distance matrix as output by the SIMINT function in NTSYS-pc. These were then plotted pair by pair on a scatterplot and the correlation between the two was analysed in STATISTICA 6.1 (StatSoft, Inc).

Table 4.2.1: List of all samples used in DNA species-level phylogeny, including collection locality data

Sample no	Spp	Subspp	Locality	South	East
Genetically discrete samples					
CAM1916	lichtensteinii		<u>Namibia. Lüderitz: Glockenberg West.</u>	26° 22' 30"	15° 52' 30"
RM1323	lichtensteinii		<u>South Africa. Kamiesberg: roadside, 40km northeast of Kamieskroon</u>	30° 07' 44"	18° 13' 40"
M050906_2	lichtensteinii		<u>South Africa. Vanrhynsdorp: Knersvlakte, Bitterfontein, road to Kilrand.</u>	31° 12' 55"	18° 32' 26"
RM1249	lichtensteinii		<u>South Africa. Wuppertal: beside R355 road near Tankwa Karoo National Park,</u>	32° 10' 30"	19° 42' 47"
CAM2727	schenckii		<u>Namibia. Luderitz: Griffith bay area, in kloofs between rocky gneiss ridges</u>	26° 40' 12"	15° 08' 00"
M160901_5g	heterochaeta		<u>South Africa. Gamoep: Springbok, Goegap Nat Res, 4x4 tracks N of reserve headquarters.</u>	29° 39' 33"	18° 00' 29"
RM1348	heterochaeta		<u>South Africa. Springbok: Roadside, 80km east of Port Nolloth</u>	29° 14' 57"	17° 40' 33"
RM1451	heterochaeta		<u>South Africa. Springbok: 5km N Steinkopf, beside N7 highway</u>	29° 14' 04"	17° 45' 20"
RM1429_1	heterochaeta		<u>South Africa. Steytlerville: T2 road from Steytlerville to Grootrivierpoort; 5km N of turnoff to Rietfontein;</u>	33° 22' 30"	24° 22' 30"
RM1255	heterochaeta		<u>South Africa. Worcester: beside R355, North of Karoopoort.</u>	33° 09' 41"	19° 45' 03"
CAM1601	tenuifolia		<u>Namibia. Witputz: Arras</u>	27° 22' 30"	16° 07' 30"
M7219_10	tenuifolia		<u>South Africa. Gamoep: Springbok, Goegap Nat. Res., SE of Carolusberg, 4x4 route N of reserve headquarters</u>	29° 39' 23"	18° 00' 32"
M7230_2	tenuifolia		<u>South Africa. Springbok: Goegap Nature Reserve, Bleshoek</u>	29° 41' 31"	17° 58' 46"
RM1352	tenuifolia		<u>South Africa. Springbok: 40km east of Port Nolloth</u>	29° 17' 56"	17° 12' 21"
RM1230	ciliaris		<u>South Africa. Cape Town: Paarlberg.</u>	33° 45' 08"	18° 57' 05"
RM1382	ciliaris		<u>South Africa. Clan William: Piketberg plateau</u>	32° 48' 41"	18° 42' 40"
SR705	ciliaris		<u>South Africa. Peddie: Fish River, near Port Alfred. Seven seas.</u>	33° 28' 58"	27° 04' 48"
RVC307	caespitosa		<u>South Africa. Graaff-Reinet: Koudeveldberge, summit</u>	32° 7' 30"	24° 07' 30"
RVC448	caespitosa		<u>South Africa. Somerset East: Koudeberg, summit, Groot Valle Farm.</u>	32° 19' 50"	25° 00' 23"
SR682	jurineifolia	jurineifolia	<u>South Africa. Gamoep: 18km W of Aggeneys (between Springbok & Pofadder)</u>	29° 22' 46"	18° 38' 53"
RM1518	jurineifolia	jurineifolia	<u>South Africa. Steynsburg: Eastern Cape: Conway, Alberta Farm.</u>	31° 40'	25° 15'
CAM2652	jurineifolia	scabra	<u>Namibia. Aus: In road verge on road between Aus and Rosh Pinah, in red sand</u>	26° 45' 41"	16° 17' 21"
CAM1604	jurineifolia	scabra	<u>Namibia. Witputz: Karas</u>	27° 22' 30"	16° 7' 30"
CAM1953	jurineifolia	scabra	<u>Namibia. Aus: Klein Aus Vista.</u>	26° 37'	16° 22'
K-R clade samples					
Boknes1	rigens	uniflora	<u>South Africa. Grahamstown: Boknes river mouth</u>	33° 43'	26° 35'
Boknes2	linearis	linearis	<u>South Africa. Grahamstown: Boknes river mouth</u>	33° 43'	26° 35'

JC201205	rigens	uniflora	<u>South Africa. Port St Johns:</u> Lupatana, Pondoland, dunes between rocks and bush.	31° 30'	29° 30'
M040906_33	sp nov?		<u>South Africa. Hondeklipbaai:</u> Namaqualand, Hondeklipbaai, coast at the police station.	30° 19' 22"	17° 16' 21"
M041001_2G	linearis	ovalis	<u>South Africa. Grahamstown:</u> Thornycroft at road between Alexandria and Port Elizabeth	33° 36' 42"	26° 01' 43"
M070704_1	rigens	leucolaena	<u>South Africa. Simonstown:</u> Miller's Point. 3m. granite (Cape Suite) coastal rocks; influence of salt spray	34° 13' 58"	18° 28' 32"
M071001_1g	krebsiana	krebsiana	<u>South Africa. Port Elizabeth:</u> Coega salt works, edge of succulent thicket, salty loamy soil.	33° 46' 35"	25° 40' 05"
M071001_3GL	krebsiana	krebsiana	<u>South Africa. Queenstown:</u> Stormberg Plateau, Penhoek Pass, rest place at road 3km North of the pass.	31° 25' 33"	26° 41' 29"
M071001_3GP	krebsiana	arctotoides	<u>South Africa. Queenstown:</u> Stormberg Plateau, Penhoek Pass, rest place at road 3km North of the pass.	31° 25' 33"	26° 41' 29"
M100903_4	rigida		<u>South Africa. Cape Town:</u> Darling, Tienie Versveld Flower Reserve.	33° 20' 07"	18° 16' 16"
M100904_4	rigida		<u>South Africa. Beaufort West:</u> Uniondale, bridge over Keurboomsrivier, gravel road bank.	33° 45' 39"	22° 57' 44"
M110805_10	rigida		<u>South Africa. Bredasdorp:</u> De Hoop Nature Reserve, Potberg, Melkosheuwel in the Poteberg River Valley.	34° 22' 50"	20° 29' 16"
M120805_80	rigida		<u>South Africa. Sutherland:</u> De Hoop Nature Reserve, Potberg, NE of the Potberg entrance.	34° 22' 10"	20° 31' 32"
M120903_5	pectinata		<u>South Africa. Clanwilliam:</u> Piketberg, Sauer, near turnoff to Uitvlug. Edge of salt pan.	32° 50' 17"	18° 33' 14"
M160704_5	leiopoda		<u>South Africa. Hondeklipbaai:</u> Namaqualand, Kamieskroon, on N7 40.1 km (near turnoff to Soebatsfontein).	30° 14' 15"	17° 53' 43"
M180904_5	pectinata		<u>South Africa. Bredasdorp:</u> De Hoop Nat Res., Kopie Alleen, disturbed edge of coastal sandy fynbos.	34° 28' 41"	20° 30' 39"
M210902_1	krebsiana	krebsiana	<u>South Africa. Fort Beaufort:</u> N of Fort Brown, road to Fort Beaufort, road verge.	32° 55' 43"	26° 37' 28"
M230803_8	krebsiana	krebsiana	<u>South Africa. Port Shepstone:</u> Umtamvuna Nature Reserve, Beacon hill. Sourveld grassland.	30° 48'	30° 11'
M230901_7G	serrata		<u>South Africa. Vanrhynsdorp:</u> Knersvlakte, Vanrhynsdorp, Quaggaskop Farm. Quartzite patch.	31° 24' 46"	18° 38' 33"
M250901_34	leiopoda		<u>South Africa. Vanrhynsdorp:</u> road from Vredendal to Strandfontein, near turnoff to Papendorp.	31° 42' 06"	18° 13' 32"
M250901_37	pectinata		<u>South Africa. Vanrhynsdorp:</u> Strandfontein, on road to Dooringbaai, 60m, disturbed road verge.	31° 45' 18"	18° 14' 02"
M250904_15	serrata		<u>South Africa. Simonstown:</u> Helderberg, strand, R44 btwn Nautilus and Octopus streets,	34° 08' 31"	18° 51' 06"
M260901_2G	pectinata		<u>South Africa. Clanwilliam:</u> Cederberg, Pakhuis pass, 720m.	32° 08' 11"	18° 58' 15"
M260901_5G	maritima		<u>South Africa. Simonstown:</u> Cape Peninsula, Cape of Good Hope.	34° 20' 46"	18° 27' 47"
M261001_2	krebsiana	krebsiana	<u>South Africa. Queenstown:</u> Stormberg, Penhoek Pass, road rest site.	31° 15' 34"	26° 44' 51"
M270901_5G	maritima		<u>South Africa. Simonstown:</u> Cape of Good Hope Nat Res. Neptune's Diary. Sandy beach.	34° 20' 46"	18° 27' 47"
M280902_9	rigida		<u>South Africa. Oudtshoorn:</u> Oudtshoorn, turn off to Zebra, succulent karoo, edge of dirt road.	33° 45' 45"	22° 20' 07"
M290606_6	maritima		<u>South Africa. Simonstown:</u> Cape peninsula, Simonstown, Table mountain national park, Diaz Beach.	34° 21' 12"	18° 28' 54"
M7293_1	rigens	rigens	<u>South Africa. Humansdorp:</u> Jeffereys Bay, beach south of Kabejows River mouth, coastal dune.	34° 00' 53"	24° 55' 42"
M7298_2	rigens	rigens	<u>South Africa. Humansdorp:</u> St Francis Bay, near bridge over Kromme river, middle tidal salt marsh.	34° 08' 15"	24° 48' 28"
M7527_2	rigens	rigens	<u>South Africa. Riversdale:</u> Gouritzmond, coast, near parking lot, leeward slope of coastal sandy dune.	34° 21' 01"	21° 53' 00"
MSG200901_22G	leiopoda		<u>South Africa. Hondeklipbaai:</u> Kamieskroon, Arakop Farm.	30° 05' 31"	17° 54' 33"
MSG240901_19	leiopoda		<u>South Africa. Calvinia:</u> Nieuwoudtville, near turnoff to Rondekop.	31° 23' 23"	19° 11' 00"

MSG7237_4	sp nov?		<u>South Africa. Port Nolloth</u> : South of McDougalls Bay.	29° 17' 39"	16° 52' 45"
NB_Hermanus	serrata		<u>South Africa. Caledon</u> : Hermanus, roadside grassland.	34° 25'	19° 08'
ND_Havens	linearis	ovalis	<u>South Africa. Butterworth</u> : The Haven, Transkei.	32° 14'	28° 54'
NPB 1465	krebsiana	krebsiana	<u>South Africa. Steytlerville</u> : Graaff Riet. Farm Welgemoed. Lower slopes of track to Nardousberg plateaux.	32° 47'	24° 32'
RM 1010	linearis	linearis	<u>South Africa. Calvinia</u> : Mzimponzi river mouth, Pondoland, grassland.	31° 19'	29° 56'
RM 1013	linearis	linearis	<u>South Africa. Port St Johns</u> : North of Mbotyi river mouth.	31° 26'	29° 43'
RM 1021	rigens	leucolaena	<u>South Africa. Bredasdorp</u> : Plettenberg Bay, Keurboomstrand. Seabeach rocks.	34° 00' 16"	20° 27' 19"
RM 1038	maritima		<u>South Africa. Bredasdorp</u> : Cape Agulhas, about 2km E of actual cape, in sand on shoreline.	34° 48' 48"	20° 02' 48"
RM 1044_1	pectinata		<u>South Africa. Caledon</u> : Agulhas peninsula, Bredasdorpberge. In young fynbos in ex pine plantation.	34° 29' 47"	19° 53' 39"
RM 1044_3	pectinata		<u>South Africa. Caledon</u> : Agulhas peninsula, Bredasdorpberge. In young fynbos in ex pine plantation.	34° 29' 47"	19° 53' 39"
RM 1061	garden hybrid?		<u>South Africa. Capetown</u> : Clanwilliam. Possible garden escape growing wild and profusely.	32° 11' 45"	18° 54' 32"
RM 1063	leiopoda		<u>South Africa. Vanrynsdorp</u> : SW of Lutzville on R362 road between Papendorp and Lutzville.	31° 33'	18° 21'
RM 1082	rigida		<u>South Africa. Tshane</u> : Karenterivierdam.	34° 00' 19"	21° 09' 30"
RM 1090	linearis	linearis	<u>South Africa. Port St Johns</u> : 25km W of Coffee Bay on road to village, roadside grassland.	31° 58'	29° 08'
RM 1092	linearis	linearis	<u>South Africa. Port St Johns</u> : Coffee Bay, Bumvu river mouth, grassland, E-facing slope.	31° 58'	29° 09'
RM 1094	linearis	linearis	<u>South Africa. Port St Johns</u> : W of Port St Johns, beside R61 road; at lookout point for Execution Rock.	31° 36'	29° 30'
RM 1103	linearis	linearis	<u>South Africa. Port Edward</u> : Mkambati Nature Reserve, N of the Msikaba River Mouth, grassland.	31° 01' 24"	30° 13' 48"
RM 1114	krebsiana	krebsiana	<u>South Africa. Fort Beaufort</u> : Road to Bedford, R350.	32° 41'	26° 05'
RM 1136	krebsiana	krebsiana	<u>South Africa. Colesberg</u> : W of Venterstad, 2km E of Gelykfontein stnd farm beside R58 road.	30° 47'	25° 47'
RM 1137	krebsiana	serrulata	<u>South Africa. Bloemfontein</u> : Bayswater area, junction of N1 + R400 roads.	29° 10'	26° 13'
RM 1182	linearis	linearis	<u>South Africa. Humansdorp</u> : on N2, Seekoei river.	34° 02'	24° 46'
RM 1210	rigida		<u>South Africa. Bredasdorp</u> : 14.5km North of Bredasdorp on R319 road.	34° 25' 50"	20° 07' 22"
RM 1216	serrata		<u>South Africa. Caledon</u> : 1km SW of Caledon on R320 road.	34° 16' 24"	19° 26' 09"
RM 1241	serrata		<u>South Africa. Worcester</u> : Du Toits Kloof Pass.	33° 41' 50"	19° 04' 06"
RM 1245	serrata		<u>South Africa. Worcester</u> : Skurweberg.	33° 14' 11"	19° 17' 42"
RM 1254	rigida		<u>South Africa. Wuppertal</u> : base of Katbakkies Pass, Swartuggens.	32° 52' 58"	19° 44' 27"
RM 1260	serrata		<u>South Africa. Worcester</u> : Calvinia.	33° 30' 21"	19° 44' 23"
RM 1270	rigida		<u>South Africa. Wuppertal</u> : North of base of Pakhuis Pass.	32° 3' 37"	19° 10' 10"
RM 1280	serrata		<u>South Africa. Calvinia</u> : 5km East of Nieuwoudtville.	31° 23'	19° 06'
RM 1291	leiopoda		<u>South Africa. Hondeklipbaai</u> : roadside.	30° 18' 37"	17° 53' 37"

RM 1306	othonnites		<u>South Africa. Springbok</u> : Kleinzee, Molyneux trail.	29° 42'	17° 04'
RM 1309	leiopoda		<u>South Africa. Kamiesberg</u> : roadside.	30° 24' 38"	18° 03' 09"
RM 1320	leiopoda		<u>South Africa. Hondeklipbaai</u> : Kamiesberg, 1070m	30° 11' 16"	17° 59' 21"
RM 1390	pectinata		<u>South Africa. Caledon</u> : Franschoek Pass, summit of pass.	33° 54' 27"	19° 09' 19"
RM 713	krebsiana	krebsiana	<u>South Africa. Port Elizabeth</u> : Coega.	33° 46'	25° 40'
RM 763	rigens	rigens	<u>South Africa. Grahamstown</u> : Kasouga Beach.	33° 39'	26° 22'
RM 770	krebsiana	arctotoides	<u>South Africa. Willowmore</u> : Prince Alfred's Pass.	33° 45'	23° 08'
RM 772	rigens	rigens	<u>South Africa. Knysna</u> : Plettenberg Bay.	34° 02'	23° 22'
RM 773	rigens	leucolaena	<u>South Africa. Knysna</u> : Plettenberg Bay.	34° 02'	23° 22'
RM 780	linearis	linearis	<u>South Africa. Fort Beaufort</u> : between East London and Cintsa turnoff on N2 highway.	32° 53'	28° 04'
RM 782	rigens	uniflora	<u>South Africa. Port St Johns</u> : Second Beach.	31° 37'	29° 32'
RM 783	rigens	uniflora	<u>South Africa. Port St Johns</u> : Third Beach.	31° 37'	29° 32'
RM 785	rigens	uniflora	<u>South Africa. Umtata</u> : Transkei, Misty Mount.	31° 34'	28° 55'
RM 787	linearis	linearis	<u>South Africa. Umtata</u> : between Umtata and Umlambo Mputi on N2 highway.	31° 59'	28° 40'
RM 789	linearis	linearis	<u>South Africa. Umtata</u> : between Umtata and Umlambo Mputi on N2 highway.	31° 35'	28° 47'
RM 794	linearis	linearis	<u>South Africa. Stutterheim</u> : south of King William's Town on N2 highway.	32° 52'	27° 23'
RM 804	krebsiana	krebsiana	<u>South Africa. Grahamstown</u> : Riebeeck East, 'Willowfontein' farm.	33° 12'	26° 09'
RM 812	serrata		<u>South Africa. Worcester</u> : Dassiehoek Nature Reserve.	33° 50'	19° 30'
RM 813	rigida		<u>South Africa. Worcester</u> : Dassiehoek Nature Reserve, track to Arangie's Kop.	33° 50'	19° 30'
RM 821	serrata		<u>South Africa. Worcester</u> : Robertson aerodrome.	33° 48'	19° 53'
RM 831	krebsiana	arctotoides	<u>South Africa. Oudtshoorn</u> : south of Oudtshoorn on N12 highway.	33° 35'	22° 11'
RM 840	rigida		<u>South Africa. Caledon</u> : south of Caledon.	34° 16'	19° 26'
RM 854	linearis	ovalis	<u>South Africa. Grahamstown</u> : north of Bathurst.	33° 29'	26° 49'
RM 856	krebsiana	krebsiana	<u>South Africa. Willowmore</u> : Bloukrans River.	33° 58'	23° 39'
RM 863	krebsiana	serrulata	<u>South Africa. Olifantshoek</u> : southeast of Beeshoek.	27° 45'	22° 37'
RM 868	krebsiana	arctotoides	<u>South Africa. Kenhardt</u> : Rooipan, southeast of Lime Acres.	29° 47'	21° 56'
RM 874	krebsiana	krebsiana	<u>South Africa. Kimberley</u> : SE of Kimberley on N8 highway.	28° 47'	24° 47'
RM 876	krebsiana	arctotoides	<u>South Africa. Aliwal North</u> : Bloemfontein.	30° 19'	26° 48'
RM 877	krebsiana	serrulata	<u>South Africa. Aliwal North</u> : north of Rouxville.	30° 25'	26° 49'
RM 884	linearis	linearis	<u>South Africa. Fort Beaufort</u> : Tor Doone, Hogsback.	32° 34'	26° 56'
RM 885	linearis	linearis	<u>South Africa. Fort Beaufort</u> : Tor Doone, Hogsback.	32° 34'	26° 56'
RM 888	krebsiana		<u>South Africa. Peddie</u> : north of Great Fish River, north of Kudu Lyndon Game Farm.	33° 29'	27° 07'

RM 898	serrata		<u>South Africa. Worcester</u> : Robertson on R60 road.	33° 48'	19° 53'
RM 900	rigida		<u>South Africa. Grahamstown</u> : between Uniondale and Willowmore	33° 14'	26° 37'
RM 903	krebsiana	arctotooides	<u>South Africa. Graaff-Rienet</u> : southwest of Aberdeen on N9 highway.	32° 31'	24° 00'
RM 904	krebsiana	arctotooides	<u>South Africa. Graaff-Rienet</u> : between Graaff-Reinet and Adendorp on R75 road.	32° 15'	24° 33'
RM 906	krebsiana	krebsiana	<u>South Africa. Fort Beaufort</u> : south of Bedford.	32° 41'	26° 05'
RM 919	rigens	leucolaena	<u>South Africa. Grahamstown</u> : SE of Cannon Rocks.	33° 44'	26° 33'
RM 920	rigens	uniflora	<u>South Africa. Grahamstown</u> : SE of Cannon Rocks.	33° 44'	26° 33'
RM 929	krebsiana	krebsiana	<u>South Africa. Witbank</u> : Middelburg, Agter-Renosterberg, between Uitsig hut and Welterede farmhouse in Transkaroo hiking trail.	25° 43'	29° 25'
RM 949	krebsiana	krebsiana	<u>South Africa. Humansdorp</u> : Eskom substation c. 500m north of N2 on R330 road to Hankey.	34° 08' 38"	24° 10' 41"
RM 950	krebsiana	krebsiana	<u>South Africa. Humansdorp</u> : NE of Humansdorp. 175m. on exposed ridge in Bobartia veld.	34° 01' 27"	24° 47' 24"
RM 951	linearis	linearis	<u>South Africa. Humansdorp</u> : St Francis bay beside R330 road, just before turnoff to St Francis Bay village.	34° 11'	24° 50'
RM 952	rigens	uniflora	<u>South Africa. Humansdorp</u> : Cape St Francis, in sandy and shelly substrate on rocky shoreline.	34° 11'	24° 50'
RM 960	krebsiana	krebsiana	<u>South Africa. Fort Beaufort</u> : SW of Seymour, junction of R67 and road to Katberg Pass.	32° 35'	26° 44'
RM 962	krebsiana	krebsiana	<u>South Africa. Queenstown</u> : NE of Queenstown on R359 road.	31° 49'	26° 55'
RM 965	krebsiana	serrulata	<u>South Africa. Lady Frere</u> : 13km SW Elliot on R56 road.	31° 19'	27° 57'
RM 966	krebsiana		<u>South Africa. Lady Grey</u> : Barkley Pass.	30° 57'	27° 36'
RM 968	krebsiana	krebsiana	<u>South Africa. Matatiele</u> : Carlisle's Hoek, beside road to Tiffindell Ski resort.	30° 40'	28° 03'
RM 992	krebsiana	krebsiana	<u>South Africa. Lady Frere</u> : Baster Voetpad. Near Elliot.	31° 19'	27° 57'
RM 996	krebsiana		<u>South Africa. Lady Grey</u> : W of Barkly East, top of road cutting on Wside of Kraairivier R58 road.	30° 57'	27° 35'
RM1403	krebsiana	krebsiana	<u>South Africa. Hanover</u> : Wapadsberg pass, at top of the pass beside R81 road.	31° 56'	24° 53'
RM1406_1	linearis	linearis	<u>South Africa. Hanover</u> : Compassberg, Compassberg farm, on flats at the base of the mountain.	31° 45'	24° 32'
RM1406_2	linearis	linearis	<u>South Africa. Hanover</u> : Compassberg, Compassberg farm, on flats at the base of the mountain.	31° 45'	24° 32'
RM1466	leiopoda		<u>South Africa. Hondeklipbaai</u> : Namakarroo National Park, W of Kamieskroon.	30° 05' 47"	17° 35' 03"
RMcolHerm	serrata		<u>South Africa. Caledon</u> : Hermanus.	34° 24'	19° 13'
RVC162	krebsiana		<u>South Africa. Graaff-Rienet</u> : Sneeuberg, 1800m+, mountain peak.	32° 09'	24° 32'
SH 110	krebsiana	krebsiana	<u>South Africa. Grahamstown</u> : 100m from Great Fish River Bridge.	33° 29'	26° 55'
SH 111/1	krebsiana	krebsiana	<u>South Africa. Peddie</u> : 10km East Peddie.	33° 12'	27° 07'
SH 111/2	krebsiana	krebsiana	<u>South Africa. Peddie</u> : 10km East Peddie.	33° 12'	27° 07'
SH 112	krebsiana	krebsiana	<u>South Africa. Stutterheim</u> : Road out of Kaiskammahoek.	32° 49'	27° 11'
SH 113	linearis	linearis	<u>South Africa. Stutterheim</u> : 10km out of Stutterheim.	32° 34'	27° 25'
SH 115	krebsiana		<u>South Africa. Somerset East</u> : S of Cradock beside N10.	32° 11'	25° 37'
SH 116	linearis	linearis	<u>Somerset East</u> : Daggaboersnek, 50 km SE from Cradock on N10 highway.	32° 11'	25° 37'

SH 117	linearis	linearis	<u>South Africa. Grahamstown</u> : W of Riebeck East, at N10/R400 road junction.	33° 12'	26° 09'
SH 118	krebsiana	krebsiana	<u>South Africa. Somerset East</u> : Daggaboersnek, 50 km SE from Cradock on N10 highway.	32° 11'	25° 37'
SH 131	linearis	linearis	<u>South Africa. Stutterheim</u> : Road between Hogsback and Cathcart, 7km out of Hogsback.	32° 33'	27° 04'
SH 132	linearis	linearis	<u>South Africa. Stutterheim</u> : Road between Hogsback and Cathcart, 14km out of Hogsback.	32° 22'	27° 07'
SH 133	krebsiana		<u>South Africa. Fort Beaufort</u> : Road from Hogsback to Committees, before Great Fish Nat. Res., after Alice.	32° 43'	26° 52'
SH135	krebsiana		<u>South Africa. Potchefstroom</u> : Road from Johannesburg to Potchefstroom.	26° 11'	27° 54'
SR 463	rigens	rigens	<u>South Africa. Stanger</u> : Tugela River mouth.	29° 13'	31° 30'
SR 480	krebsiana		<u>South Africa. Grahamstown</u> : Fort Brown, resolution hatchery.	33° 09' 53"	26° 37' 18"
SR 520	krebsiana		<u>South Africa. Underberg</u> : Estcourt.	29° 02' 35"	29° 52' 19"
SR 523	linearis	linearis	<u>South Africa. Humansdorp</u> : Maitlands, on road between Seaview and Maitlands River.	34° 00'	25° 41'
SR 564	krebsiana		<u>South Africa. Port Edward</u> : Umtamvuna nature reserve.	31° 04'	30° 11'
SR 571	linearis	linearis	<u>South Africa. Port Shepstone</u> : Port Shepstone.	30° 44'	30° 27'
SR 574	rigens	rigens	<u>South Africa. Port Shepstone</u> : Umkomaas, Warner Beach, Baggies Beach, 10km N Durban.	30° 04'	30° 52'
SR 575	rigens	rigens	<u>South Africa. Stanger</u> : Durban, Blue Lagoon.	29° 48'	31° 02'
SR 581	rigens		<u>South Africa. Grahamstown</u> : Kowie river.	33° 36'	26° 53'
SR 625	rigens	uniflora	<u>South Africa. Skoenmakerskop</u> : Cape Reciefe (Between PE and seaview).	34° 00'	25° 39'
SV GAZ HF1	krebsiana	krebsiana	<u>South Africa. Grahamstown</u> : Hownslow farm, edge of Grahamstown.	33° 17'	26° 31'
SV GAZ HF2	krebsiana	arctotoides	<u>South Africa. Grahamstown</u> : Hownslow farm, edge of Grahamstown.	33° 17'	26° 31'
Collector abbreviations: RM = Robert McKenzie, M = Laco Mucina, MSG= Mucina & Santos Guerra, CAM = Colleen Mannheimer, SR = Syd Ramdhani, JC = Jessica Cockburn, RVC = Ralph Clark, ND = Nico Devos, NPB = Nigel Barker, SV = Susi Vetter.					

Results and Discussion

MrModelTest identified the General Time Reversible (Tavaré, 1986) model of DNA sequence evolution as the best fit to the data set.

The length, variability and informativeness of the ITS and ETS regions are presented in Table 4.3.1 below. The ETS region is nearly twice as informative as the ITS region.

Table 4.3.1: Length, number of variable and parsimony informative characters, and g_1 statistics for ITS, ETS and combined nrDNA data set.

	No. samp.	Tot. chars	Variable Characters		Parsimony Inform. Ch.		g_1
			Number	%	Number	%	
nrDNA	171	1452	562	38.7	309	21.3	-0.93
ITS	171	696	212	30.5	108	15.5	-1.0
ETS	171	756	350	46.3	201	26.6	-0.9

Sample M7219_10 was found to have a deletion 244 bp in length.

Genetically discrete species

Neighbor-Joining analysis

The NJ tree of the seven genetically discrete (Figure 4.3.1) illustrates that increased sample number does not change the monophyly of the species clades, except for *G. caespitosa*, which is paraphyletic with respect to *G. ciliaris*, as it was in the original nrDNA phylogeny in Chapter 3 (only the addition of cpDNA data could render it monophyletic).

Figures 4.3.2 to 4.3.7 illustrate the distributions for samples of each of the genetically discrete species. *G. jurineifolia*, *G. tenuifolia* and *G. lichtensteinii* all have distributions that extend from south Namibia into western and central South Africa, while *G. schenckii* is limited to Namibia. *G. ciliaris* and *G. caespitosa* are found in the southern half of South Africa (Figure 4.3.7). The most basal of the *G. ciliaris* samples (SR705) is also the most easterly.

Bayesian analysis

Bayesian analysis (Figure 4.3.8) results in the same species clades as NJ, although the support for the internal nodes of the species clades is higher. There is also some difference in internal clade arrangement for *G. tenuifolia* and *G. jurineifolia*.

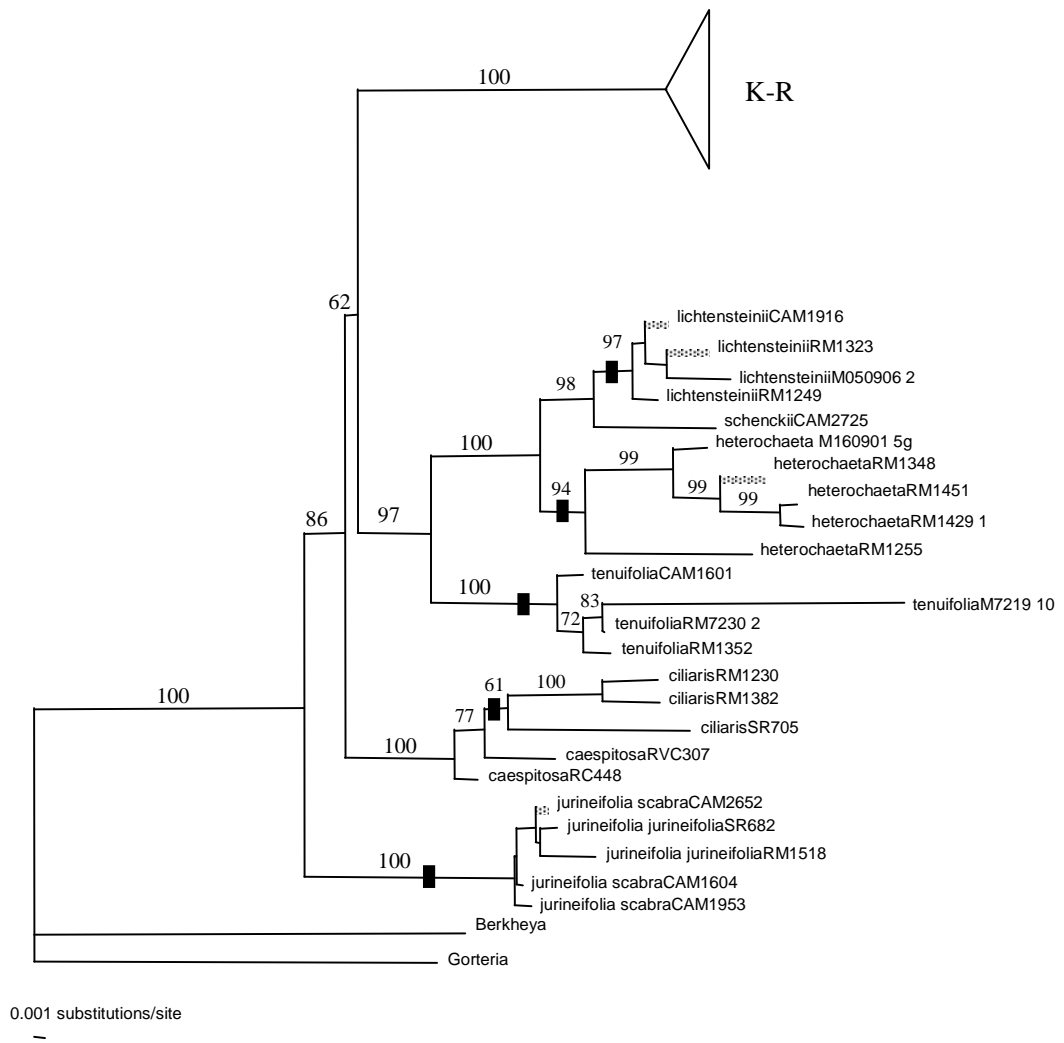


Figure 4.3.1: Neighbor-Joining tree of expanded nrDNA sample set of genetically discrete species. Bootstrap support above branches. Black bars indicate monophyletic species branches.

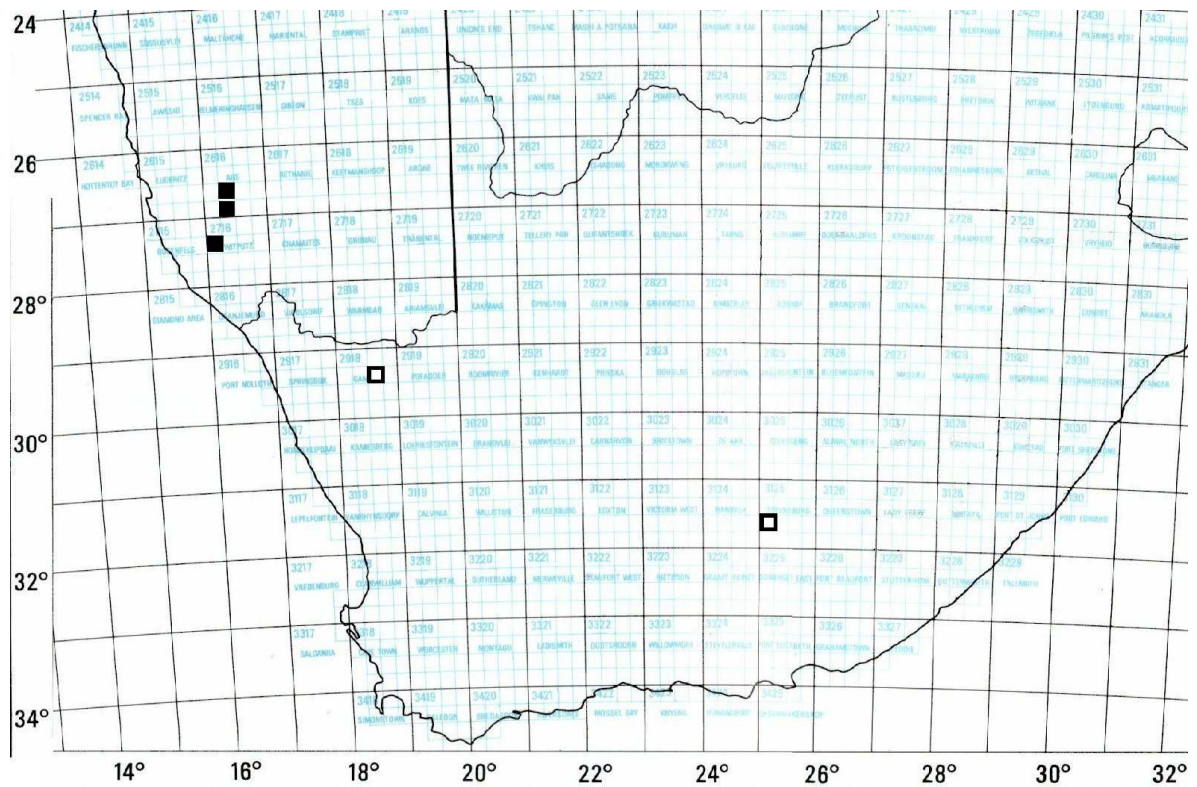


Figure 4.3.2: Distribution of samples for *G. jurineifolia*. Black squares indicate *G. jurineifolia* subsp *scabra* samples, hollow squares indicate *G. jurineifolia* subsp *jurineifolia* samples.

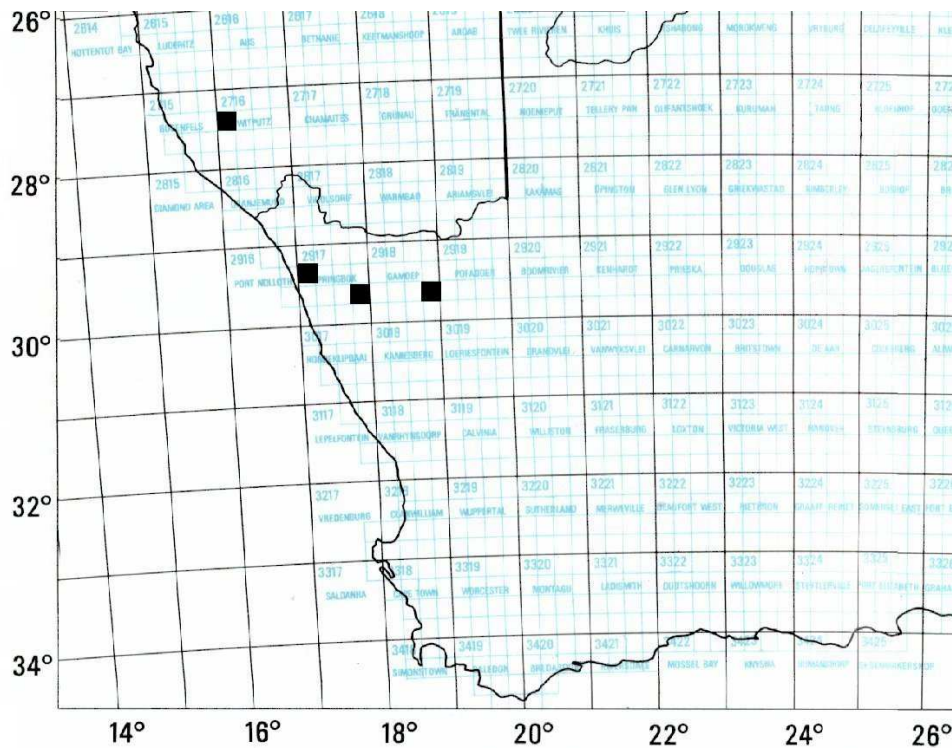


Figure 4.3.3: Distribution of samples for *G. tenuifolia*.

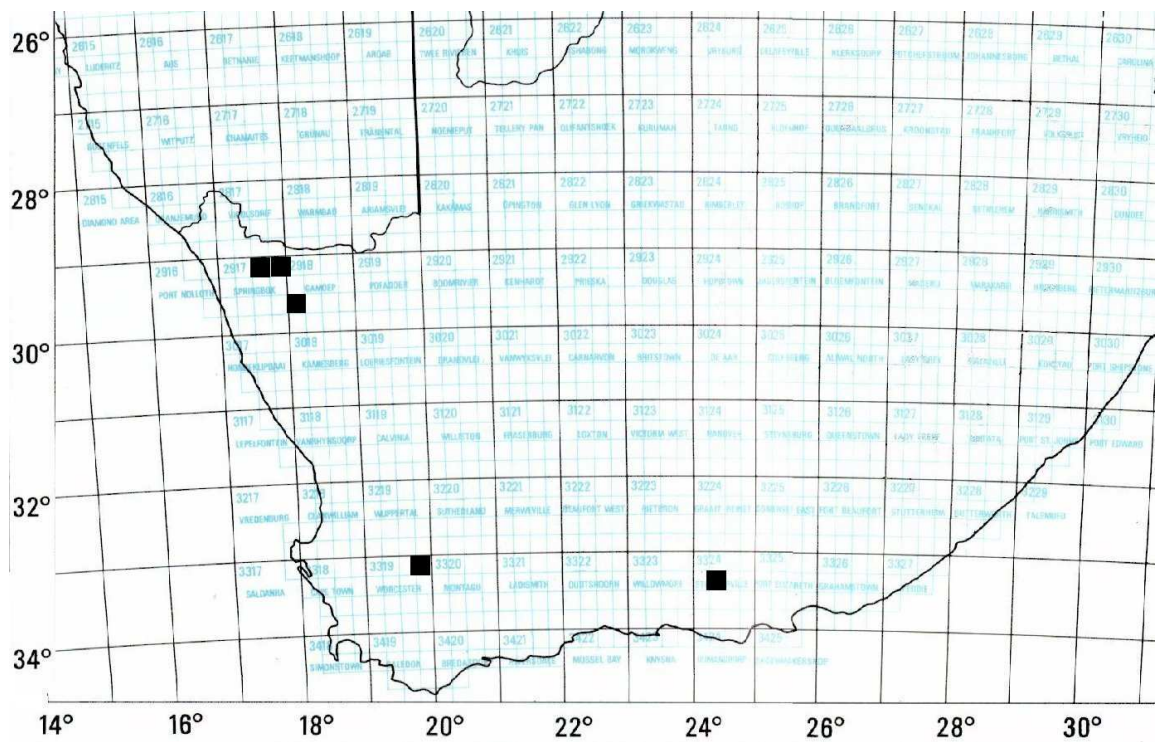


Figure 4.3.4: Distribution of samples for *G. heterochaeta*

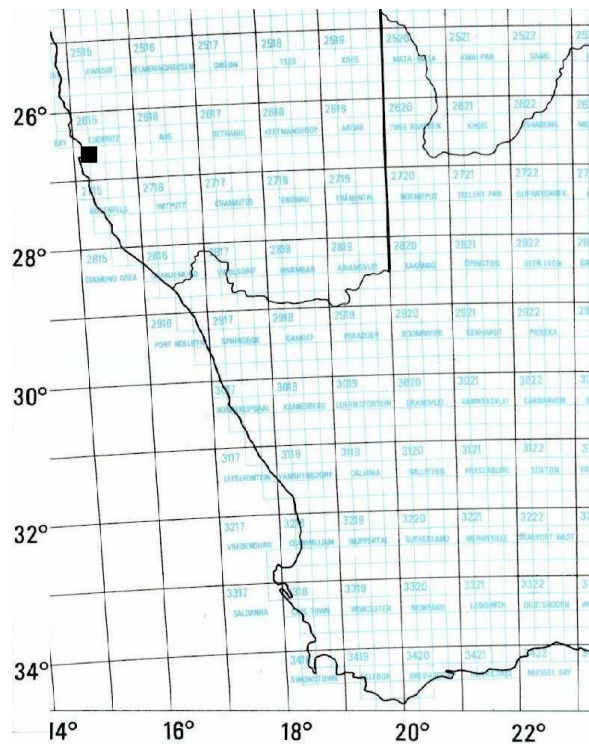


Figure 4.3.5: Distribution of samples for *G. schenckii*

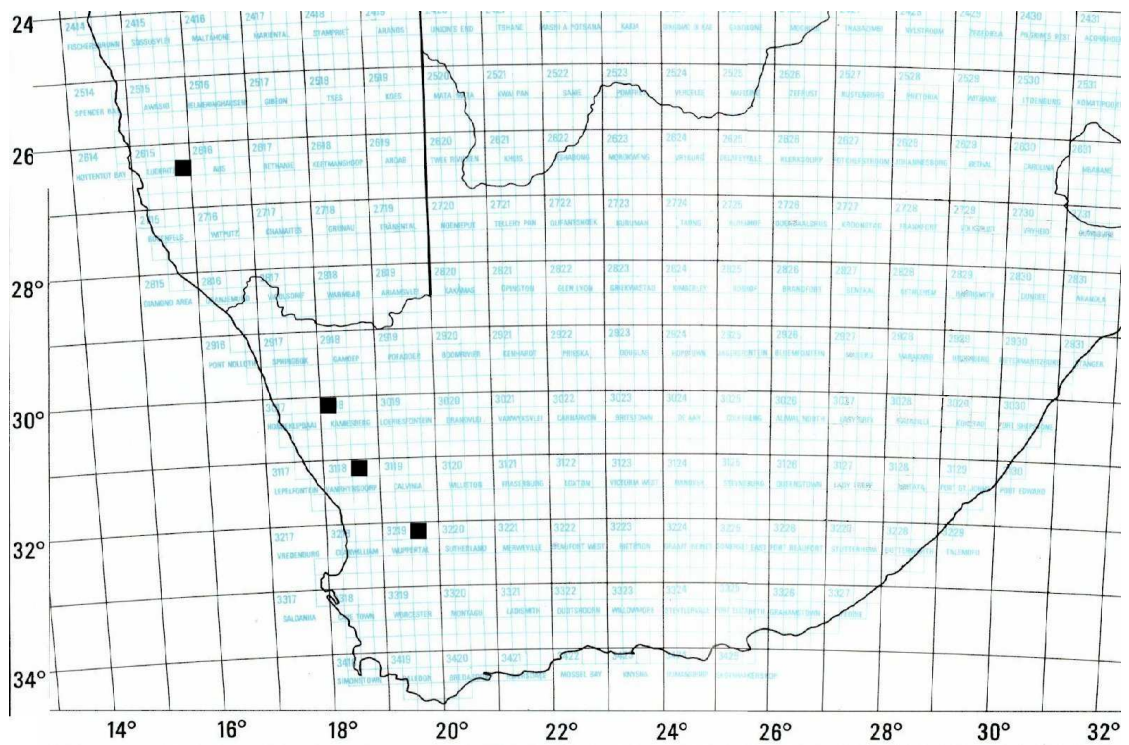


Figure 4.3.6: Distribution of samples for *G. lichtensteinii*

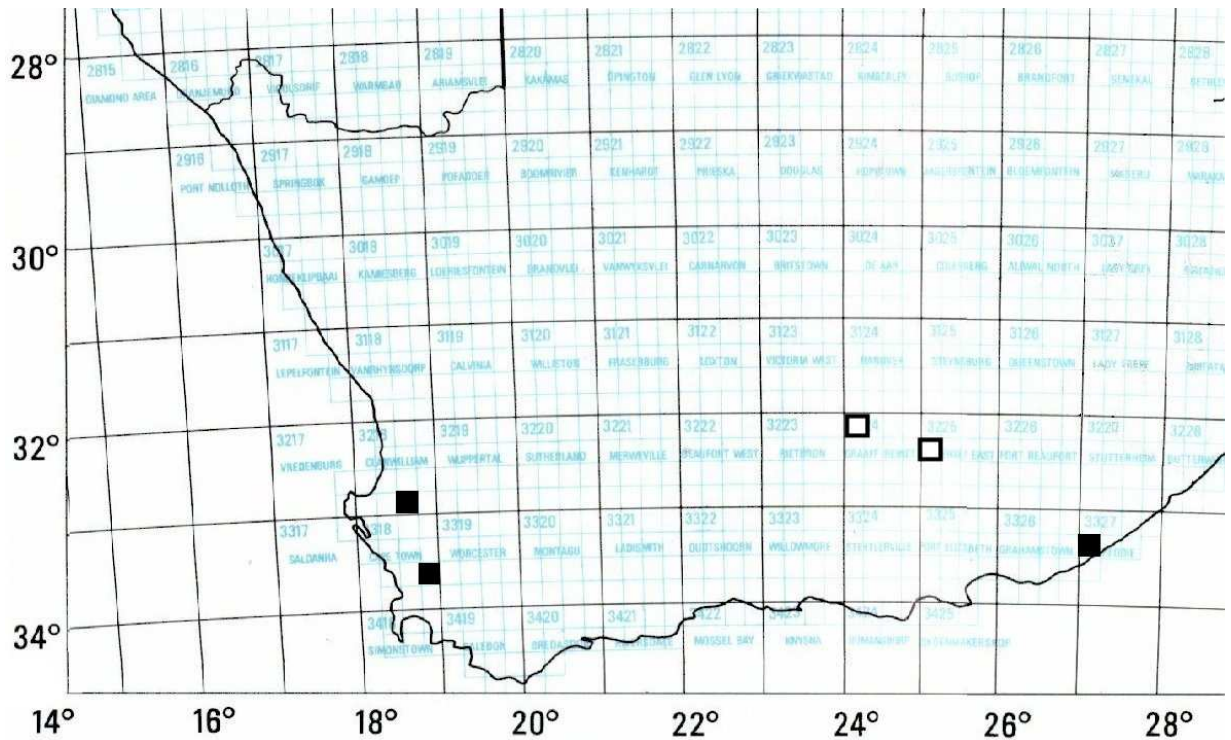


Figure 4.3.7: Distribution of samples for *G. ciliaris* (black squares) and *G. caespitosa* (hollow squares).

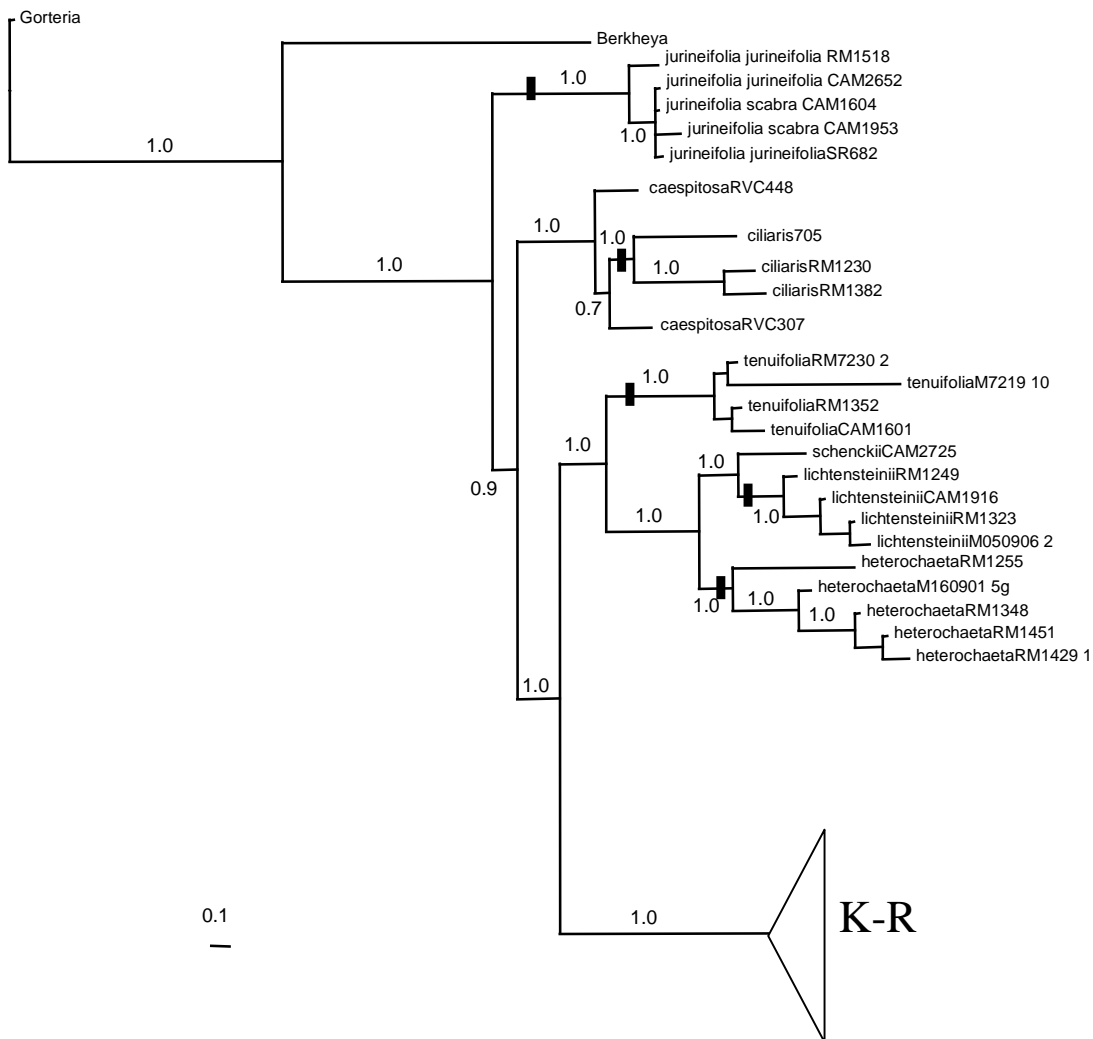


Figure 4.3.8: Bayesian consensus tree of expanded nrDNA sample set of genetically discrete species. Posterior probabilities indicated on branches. Black bars indicate monophyletic species branches.

K-R clade

Neighbor-Joining analysis

The Neighbor-Joining tree of the expanded K-R clade is presented in Figure 4.3.9, rooted using samples of *G. caespitosa* and *G. ciliaris*. 12 clades are obtained positioned along a poorly supported backbone, with a few samples placed between them. The localities of the samples of species are mapped, branch by branch, in Figures 4.3.10 to 4.3.21. No complete species cohesion is seen in this large clade as a whole, although two branches (Branch 1, which contains only *G. leiopoda* samples; and Branch 8, which contains only *G. rigens* samples) do show some species cohesion. However, these

branches do not contain all the samples of these species, as some samples are found in distant branches of the tree.

The K-R clade has some structure around the basal clades (Branches 1-4), but no bootstrap support for these branching patterns, and there is a large polychotomous backbone along which the majority of the terminal branches (5-12) are placed.

The first basal bifurcation results in Branch 1 (Figure 4.3.10), which contains only *G. leiopoda* samples (90% BS), and has some bootstrap support for its internal structure (a relative rarity in the rest of the K-R clade). The geographical origins of the samples in this clade fall into a small area around Hondeklipbaai (30° S 17° E) in the north Western Cape.

Branch 2 (Figure 4.3.11) shows little species cohesion and no bootstrap support, comprising a mix of *G. pectinata*, *G. serrata*, *G. rigida* and *G. maritima* samples. Despite the broad taxonomic mix, the geographical origins of these samples fall within a limited area of the Southern Cape, suggesting that geographical locality is superseding morphotaxonomic affinity (possibly due to recent hybridization or introgression, though neither of these can be conclusively proven by this dataset). Of course, the alternative explanation is that the species themselves may be badly delimited. If the localities of the samples are overlaid on the floristic regions (defined by Weimarck; Linder, 2003) the samples are not limited to only one region, but fall into the South Western centre, Peninsula, Agulhas and Langeberg regions.

Branches 3 (54% BS) and 4 (Figures 4.3.12 and 4.3.13) both show some internal bootstrap support. However, neither branch shows species coherency, both being composed of a mix of species. The geographical origins of the samples in each branch fall into two areas in the western and southern cape. Samples in Branch 3 occur in the South Western centre and Peninsula regions of the CFR, while samples in Branch 4 occur only in the North Western centre of the CFR.

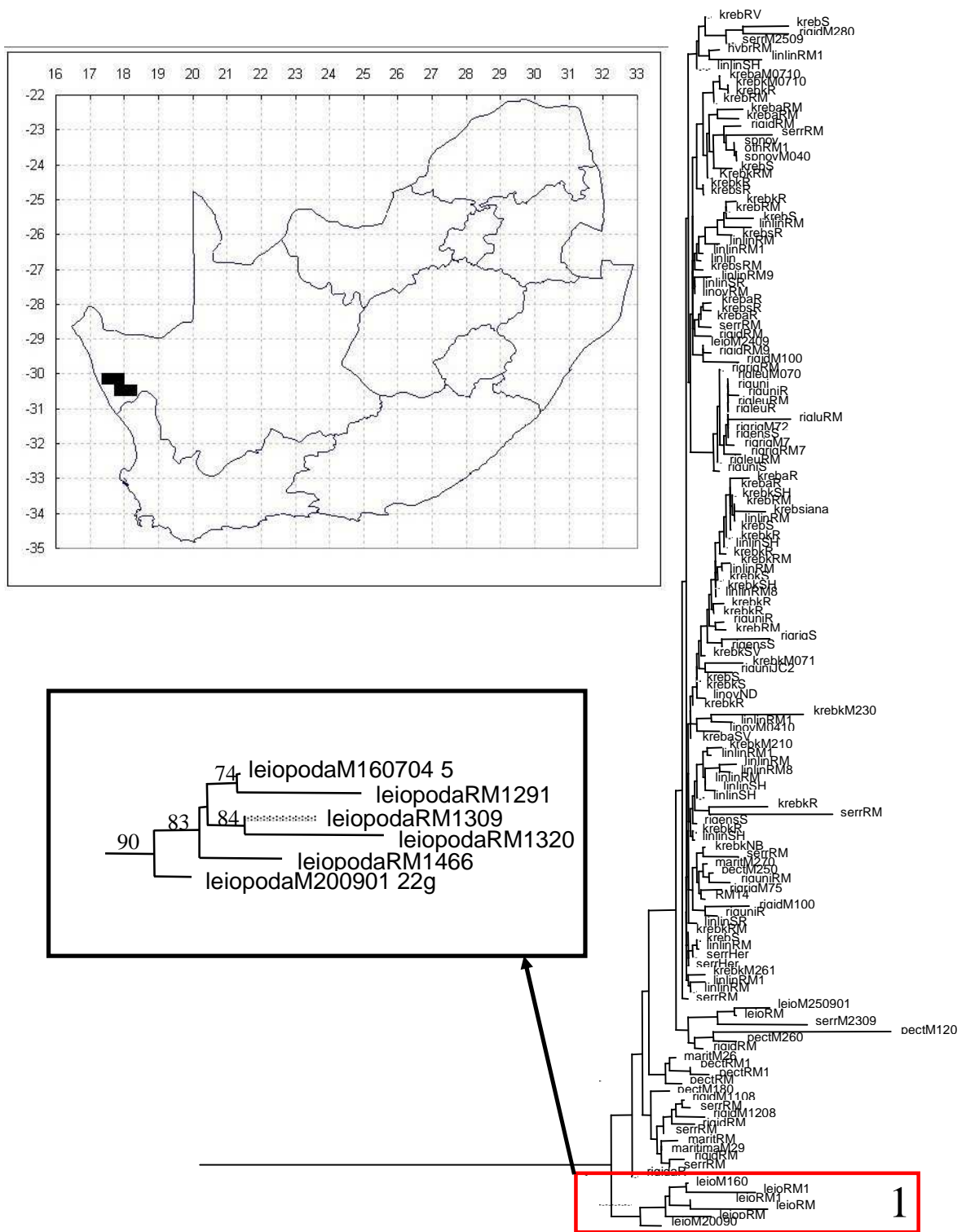


Figure 4.3.10: Branch 1 in detail with bootstrap support, the geographical origins of each sample and its position in the large unresolved clade

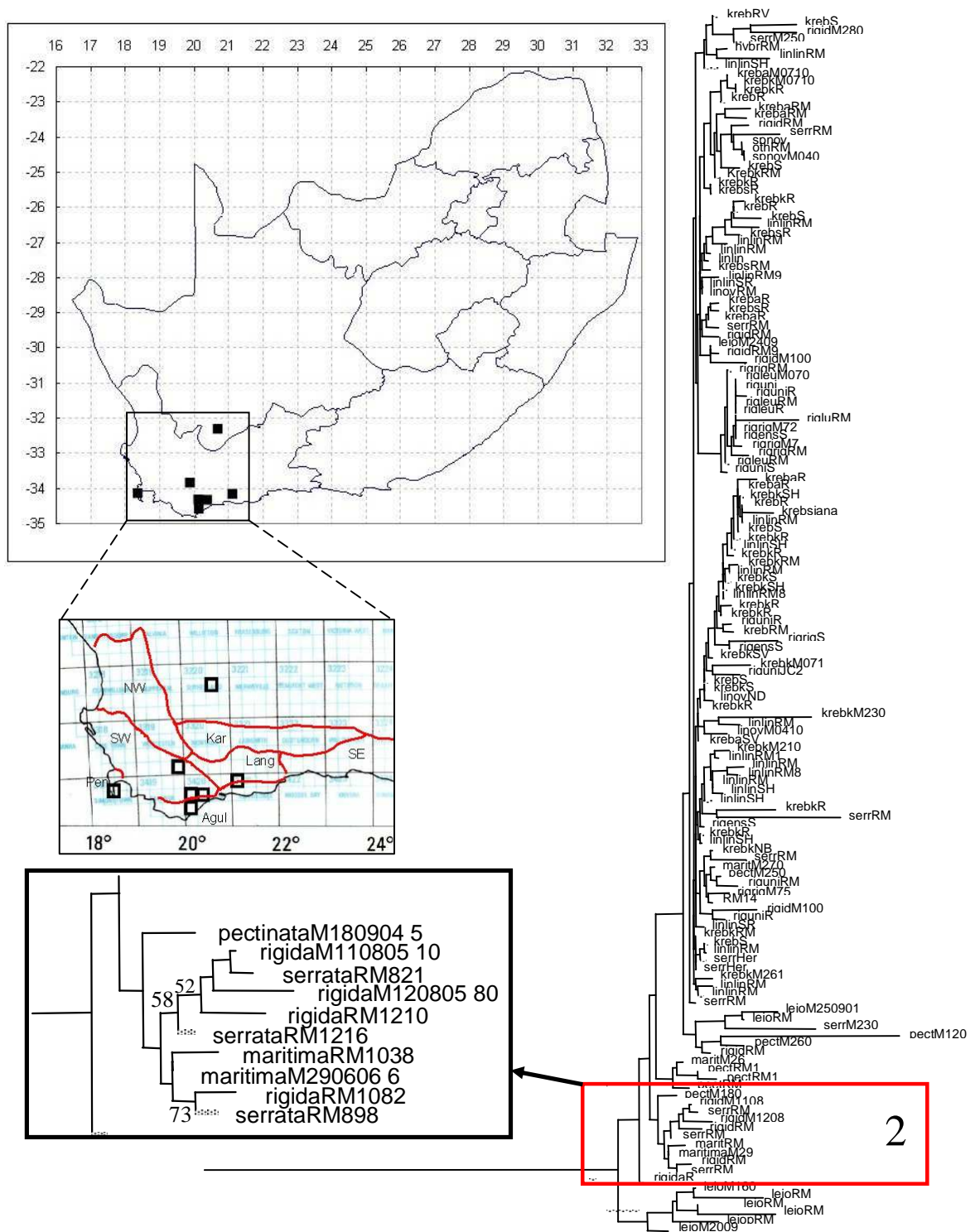


Figure 4.3.11: Branch 2 in detail with bootstrap support, the geographical origins of each sample and its position in the large unresolved clade. Red lines and letters on detailed map indicate Weimarck's floristic regions of CFR (Linder, 2003).

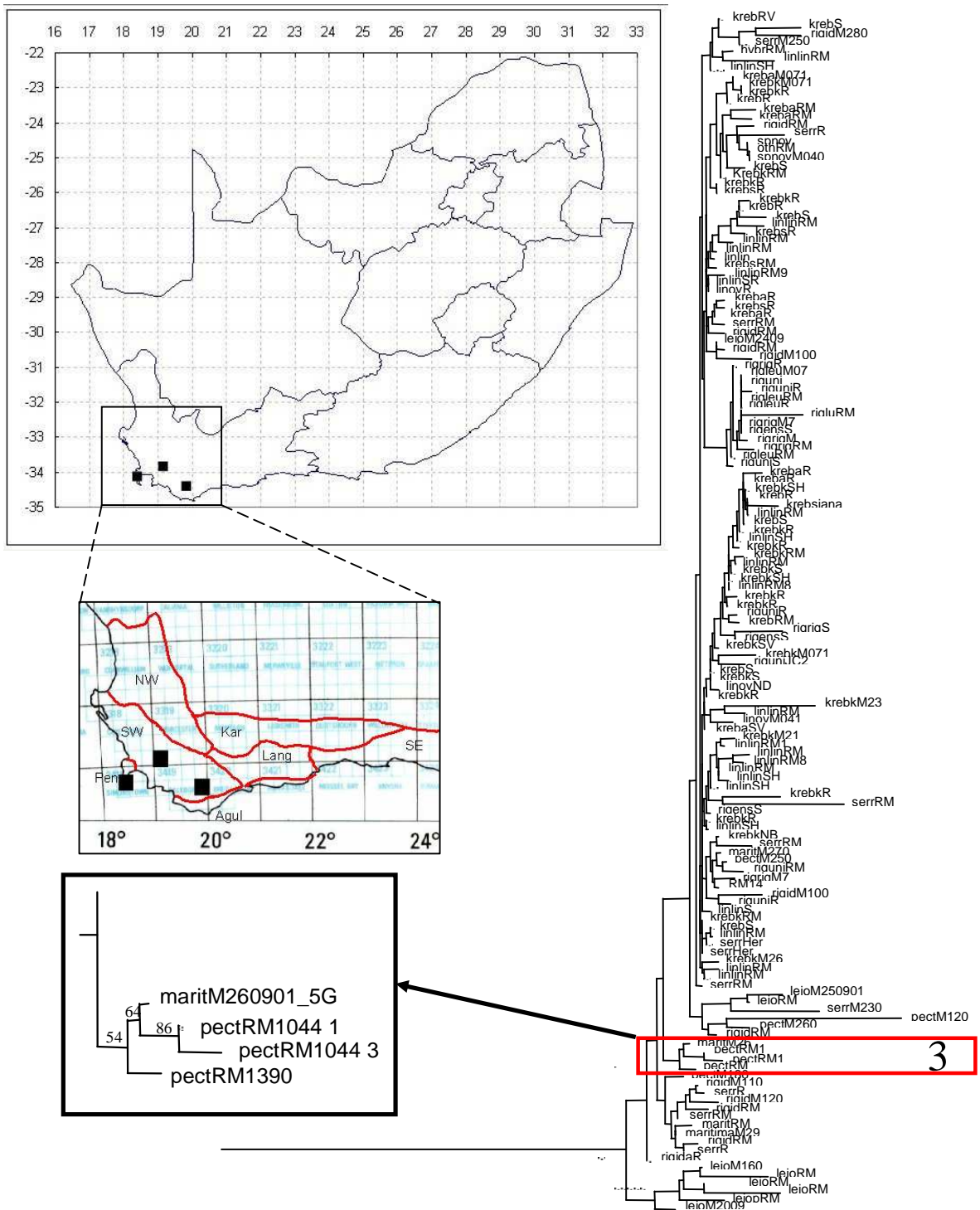


Figure 4.3.12: Branch 3 in detail with bootstrap support, the geographical origins of each sample and its position in the large unresolved clade. Red lines and letters on detailed map indicate Weimarck's floristic regions of CFR (Linder, 2003).

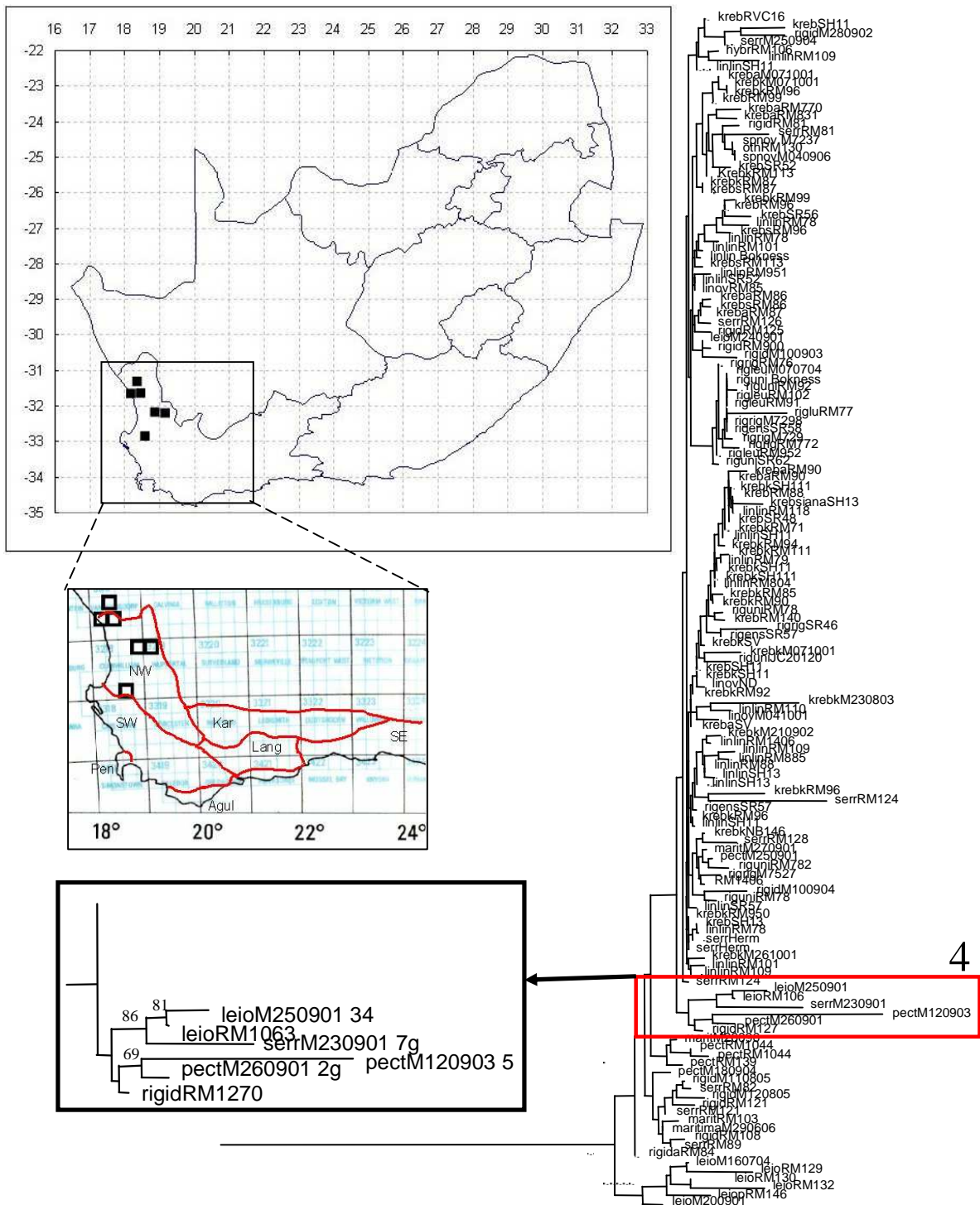


Figure 4.3.13: Branch 4 in detail with bootstrap support, the geographical origins of each sample and its position in the large unresolved clade. Red lines and letters on detailed map indicate Weimarck's floristic regions of CFR (Linder, 2003).

Branches 5 and 6 (Figures 4.3.14 and 4.3.15) show no bootstrap support, no species cohesion and no clear geographical signal, although samples in Branch 6 occur mostly in the Eastern Cape and Kwazulu-Natal.

Branch 7 (Figure 4.3.16) is a large branch composed of mostly (but not exclusively) *G. krebsiana* samples. It has no bootstrap support, but is composed of samples that fall only within the eastern half of South Africa.

Branch 8 (Figure 4.3.17) is composed of only *G. rigens* samples (with 66% BS). There are two samples (RM1021 and M070704_1) which occur in the Western Cape, and fall outside of Roessler's distribution limits for *G. rigens*. These may not be naturally occurring samples, and could have been transplanted for cultivation purposes, or may be hybrid garden escapes. Many cultivated *Gazania* specimens have a silvery-grey hirsute layer on the dorsal surface of their leaves and a decumbent habit, which is characteristic of *G. rigens* subsp. *leucolaena*, which is what the two outlier samples in the Western Cape are. As such, these two outliers should probably be disregarded from further consideration, due to their high potential to be horticultural hybrids. The *G. rigens* samples in Branch 8 that do occur in the Eastern Cape only occur in the southern half of the eastern coast. In contrast, the other samples of *G. rigens* that do not fall into Branch 8, occur (with two exceptions in the southern coast) in the northern half of the eastern coast of South Africa. The disjunction between the southern samples and the north-eastern samples may be due to a lack of suitable dune habitats along the rocky areas of the Wild Coast coastline that bisects the two distributions. However, a lack of intensive collection in this area may also account for this pattern.

Branch 9 (Figure 4.3.18) shows no species cohesion, bootstrap support or clear geographical signal, but could represent the poorly sampled semi-arid interior.

Branch 10 (Figure 4.3.19) with some internal support, is composed of samples that only occur in the eastern half of South Africa.

Branch 11 (Figure 4.3.20) shows some internal bootstrap support, but little species cohesion or geographical signal, except for the *G. othonnites*/*sp. nov.* clade (65% BS), suggesting a common link. Both possess mild succulence, and glaucous leaves, but some of the *G. sp. nov.* samples may have hispid leaves, which does not fit Roessler's description of *G. othonnites*. The hispid *G. sp. nov.*

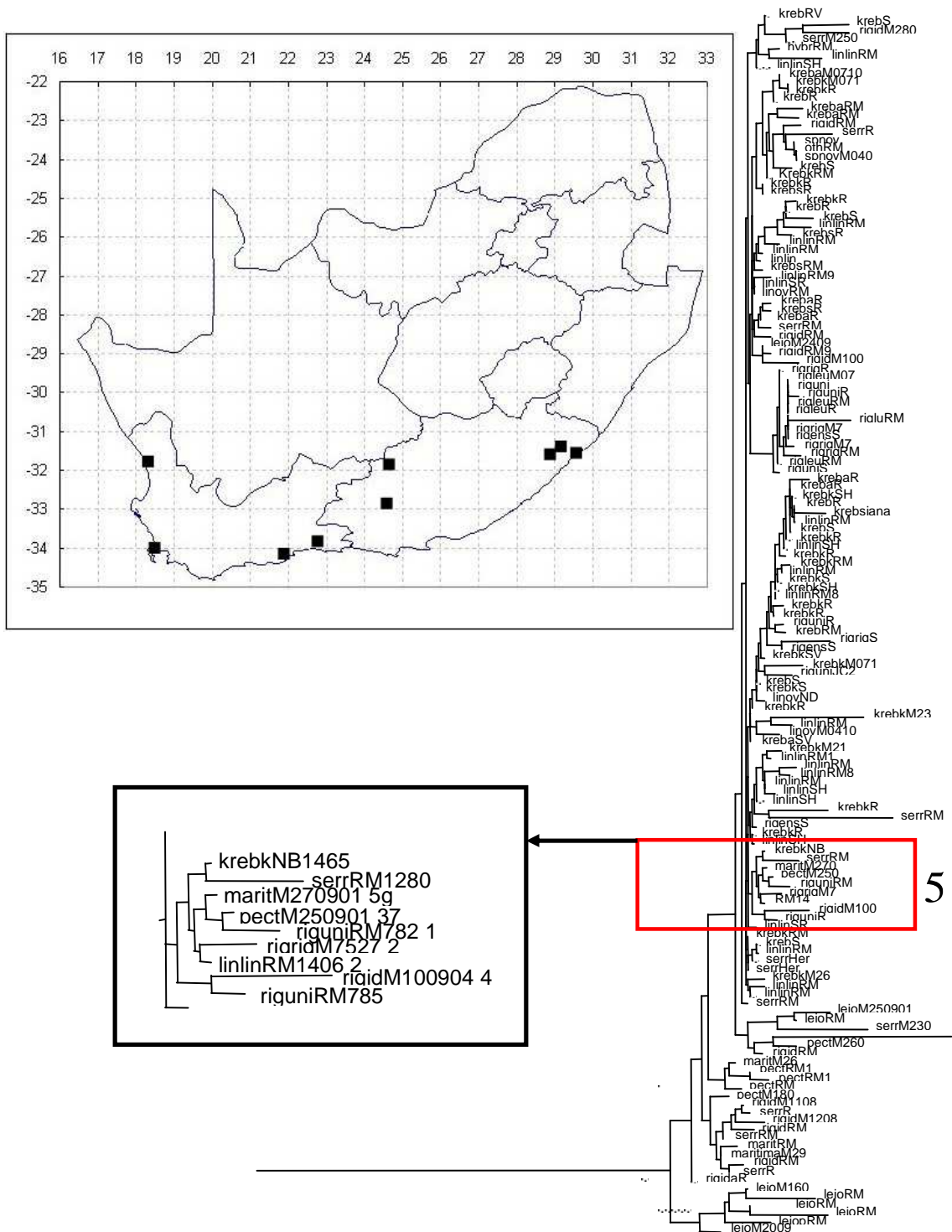


Figure 4.3.14: Branch 5 in detail, the geographical origins of each sample and its position in the large unresolved clade.

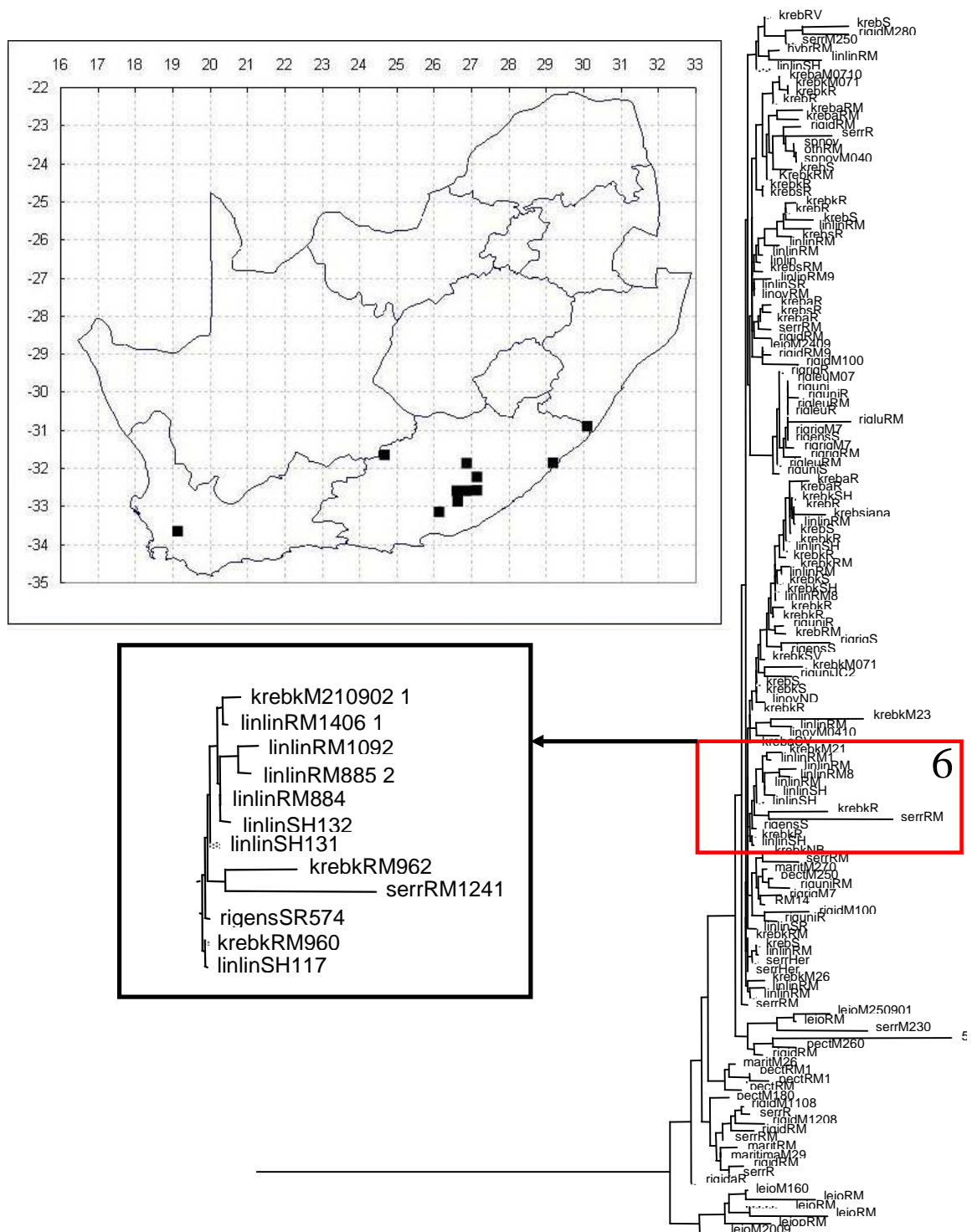


Figure 4.3.15: Branch 6 in detail, the geographical origins of each sample and its position in the large unresolved clade.

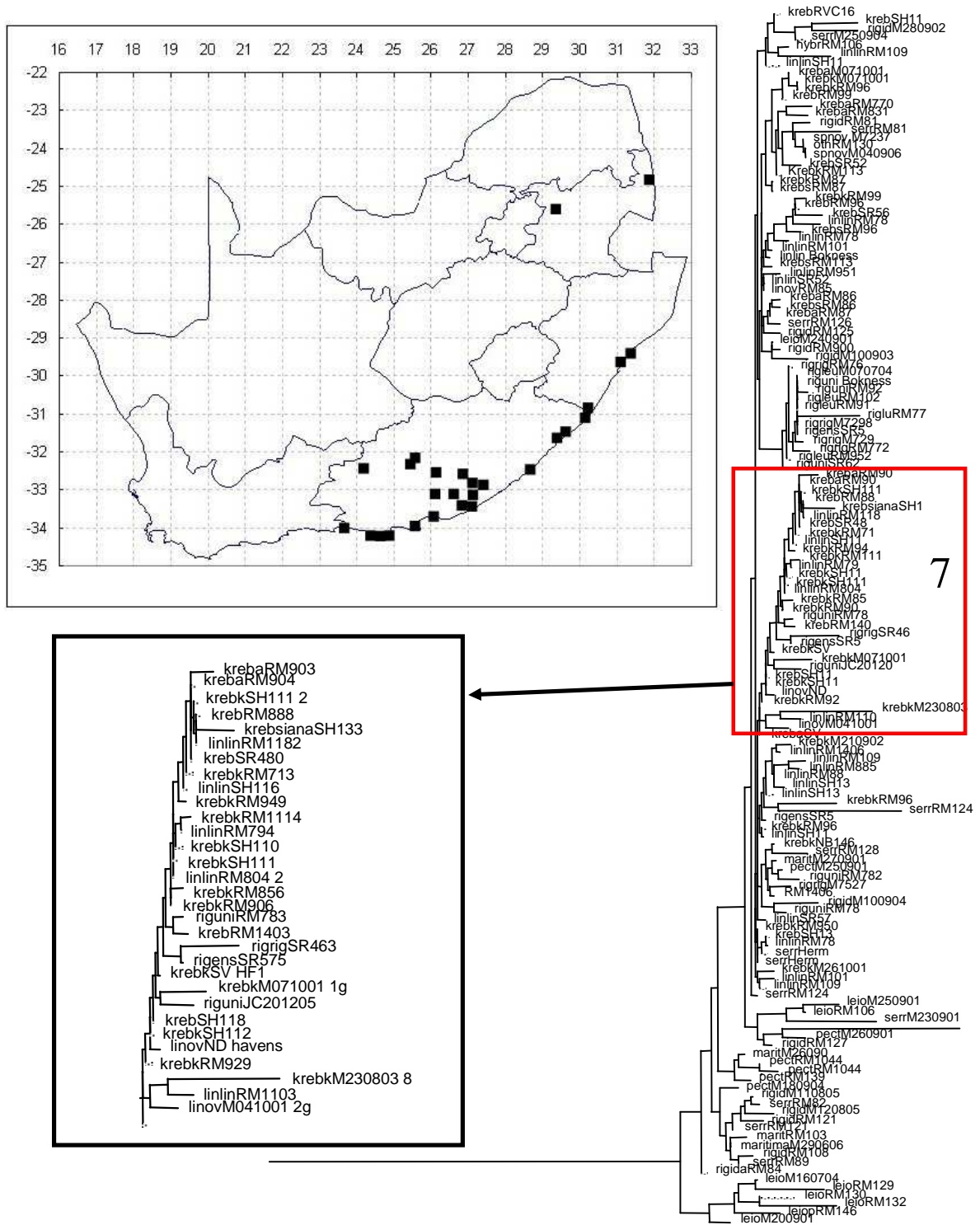


Figure 4.3.16: Branch 7 in detail, the geographical origins of each sample and its position in the large unresolved clade.

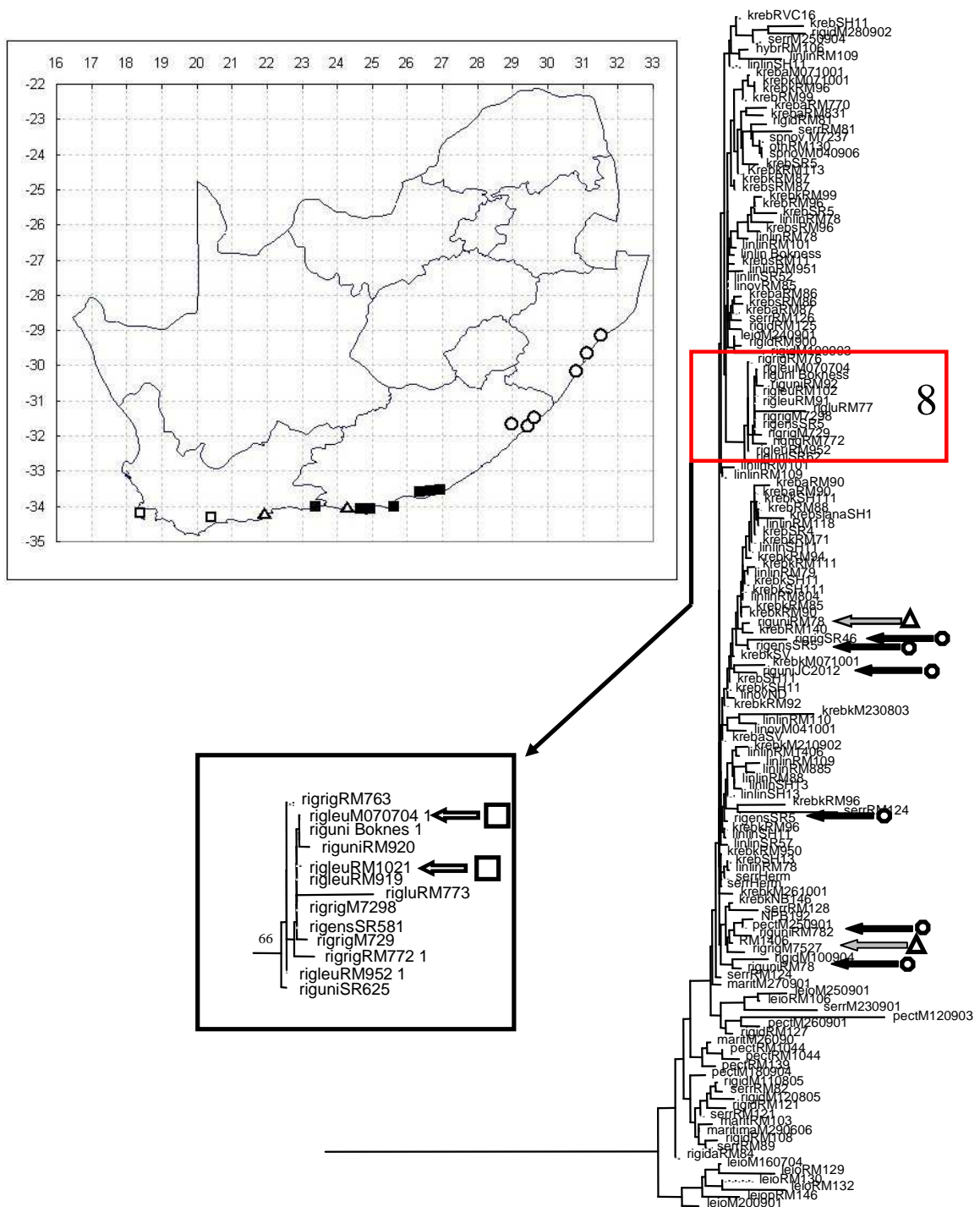


Figure 4.3.17: Branch 8 in detail with bootstrap support, and its position in the large unresolved clade, along with the geographical origins of each sample (black squares = samples that fall within Roessler’s distributional range for *G. rigens*, hollow squares = samples that fall outside of that range, hollow circles = *G. rigens* samples that fall outside of branch 7 and occur on the northern part of the eastern coastline, hollow triangles = *G. rigens* samples that fall outside of branch 7 and occur on the southern coast).

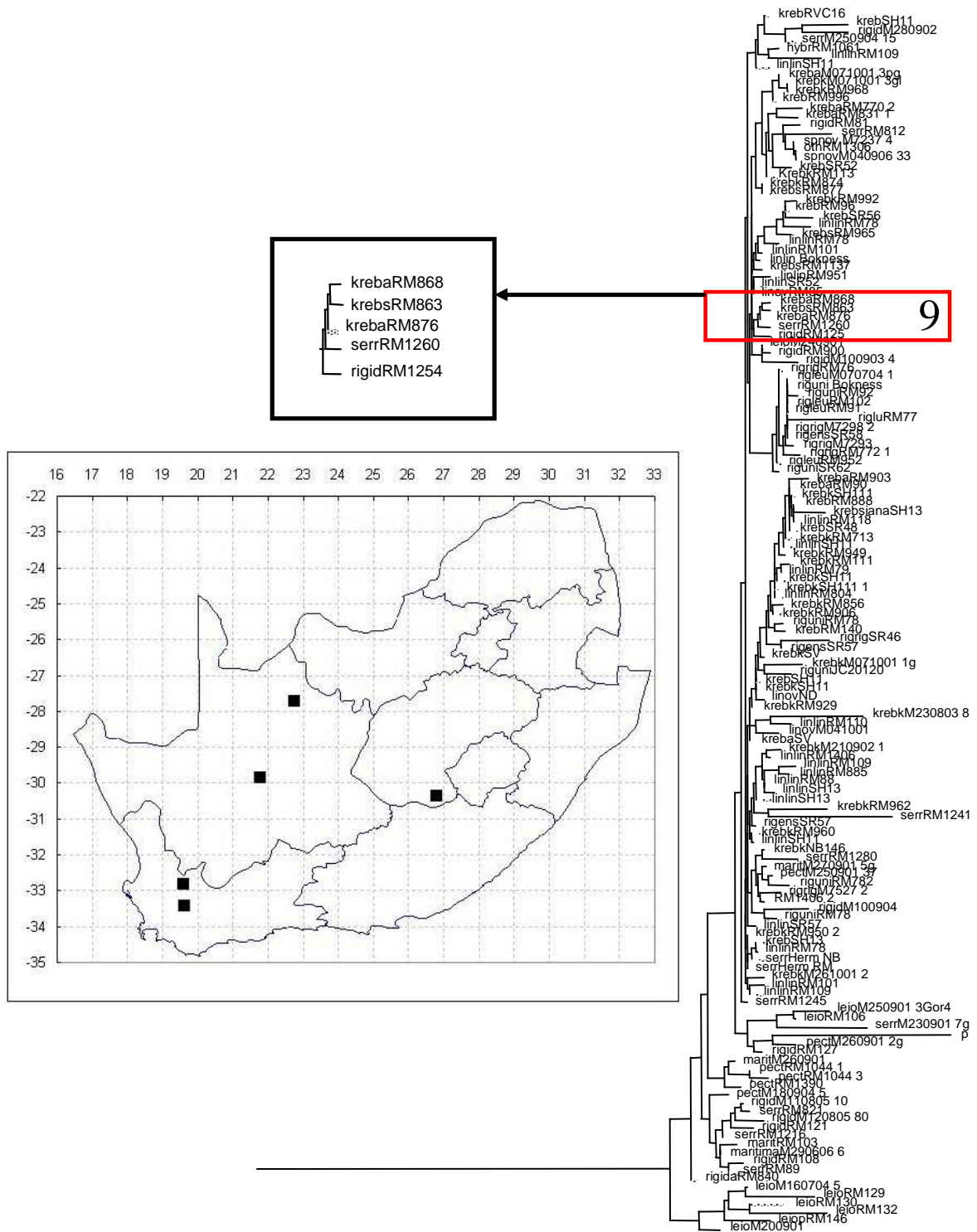


Figure 4.3.18: Branch 9 in detail, the geographical origins of each sample and its position in the large unresolved clade.

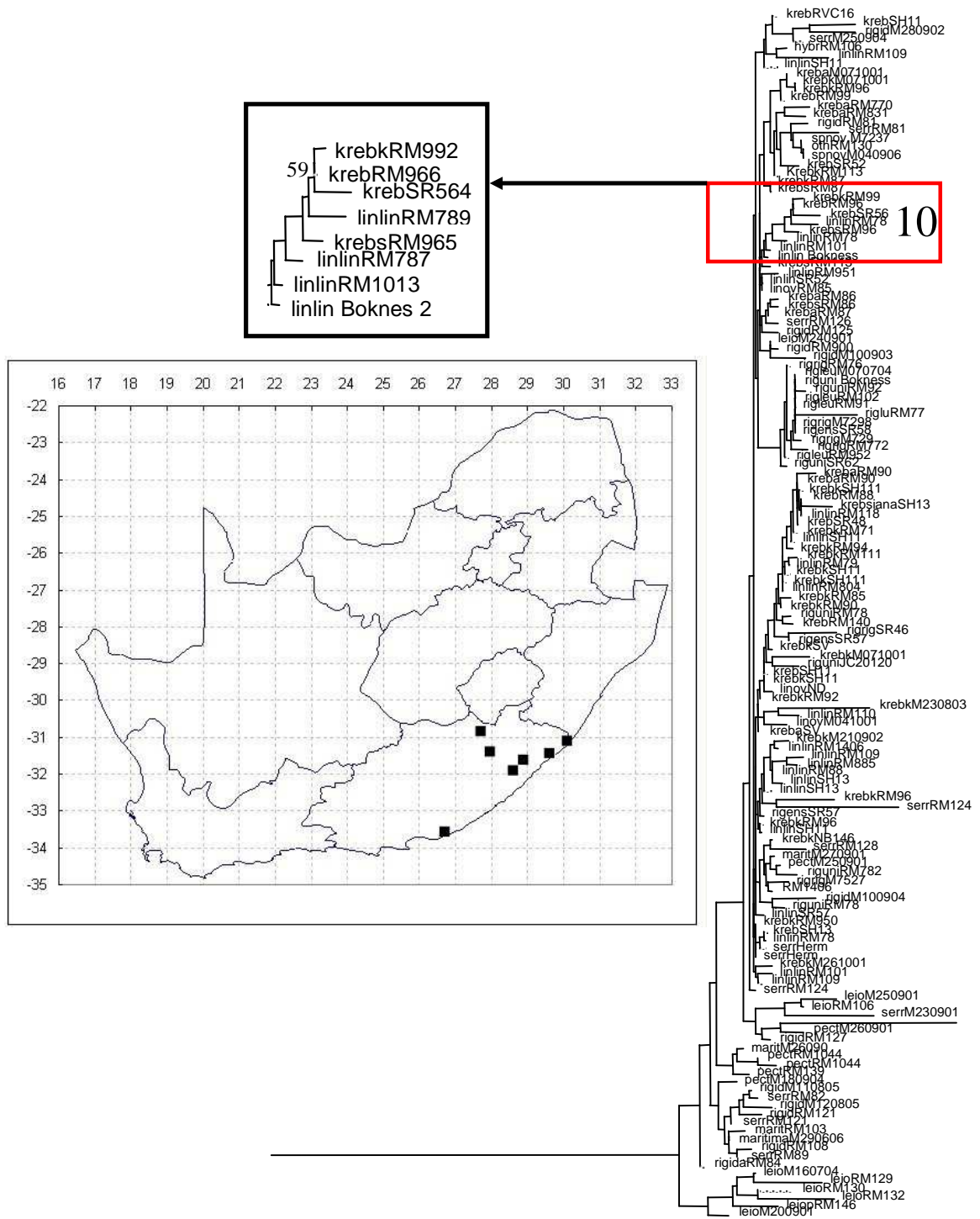


Figure 4.3.19: Branch 10 in detail with bootstrap support, the geographical origins of each sample and its position in the large unresolved clade.

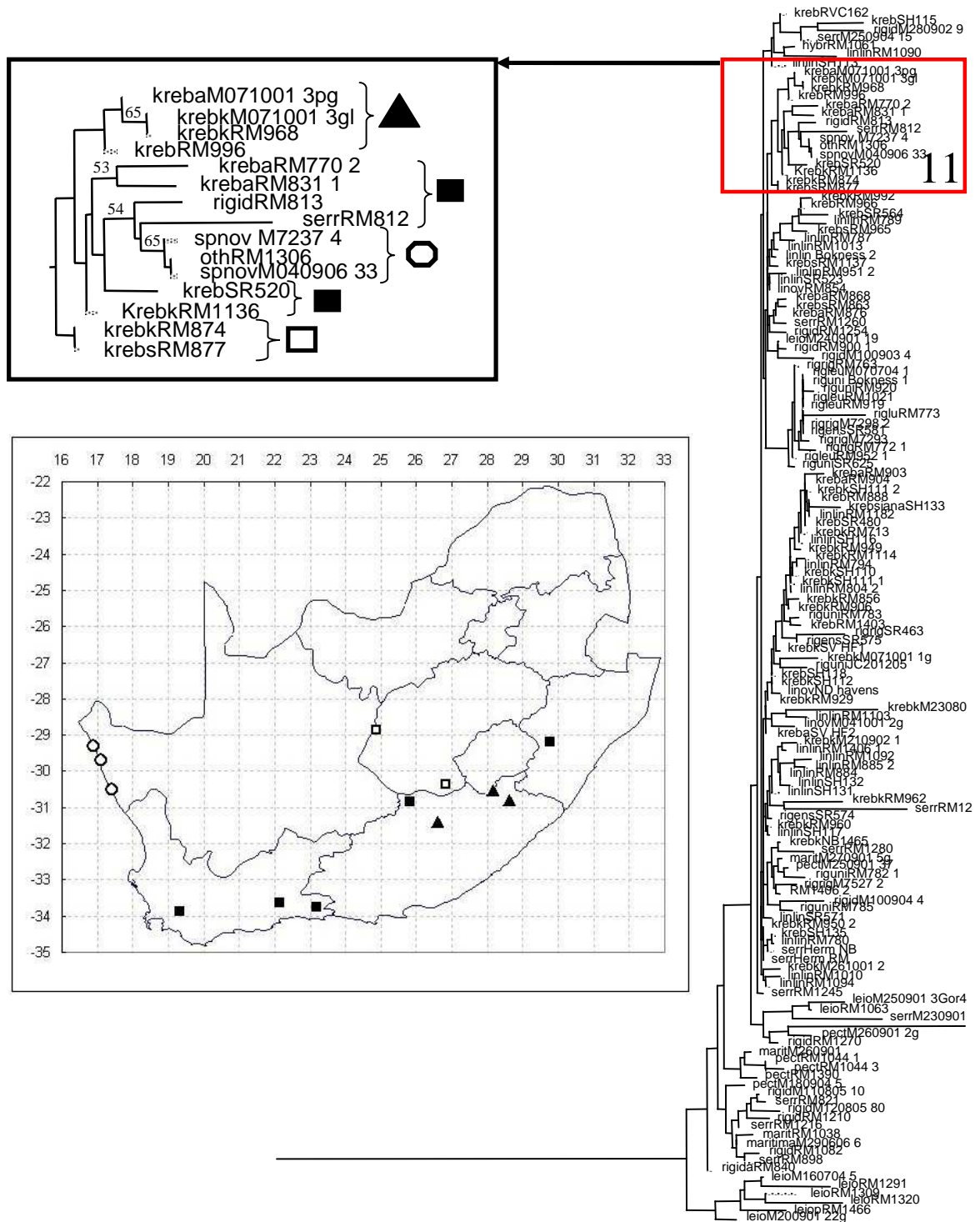


Figure 4.3.20: Branch 11 in detail with bootstrap support, the geographical origins of each sample and its position in the large unresolved clade.

samples may be examples of mixing between the glaucous *G. othonnites* morphotype and proximal hispid western cape *Gazanias*. This clade as a whole shows a strong geographical signal, and some moderate bootstrap support.

Branch 12 (Figure 4.3.21) shows no species cohesion, bootstrap support or clear geographical signal.

Although there are some trends of branches correlating to geographical areas, there is no overwhelming correlation between “species”, the clades they occur in and their geographical origins. As an example of this lack of clarity, it should be noted that two members of the same subspecies taken from the same area do not necessarily end up in the same branch (e.g. RM1406_1 and RM1406_2, are both *G. linearis* subsp *linearis*, and both are collected from the same area, yet one occurs in Branch 5 and the other in Branch 6). This may be a result of hybridization or simply a function of extremely low data signal.

Bayesian analysis

The Bayesian consensus tree (Figure 4.3.22) shows less resolution than the NJ tree, but retains the same basic branch structure. The branches along the polytomy in the Bayesian analysis tend to agree with the branches found in the NJ analysis, although some branches found in the NJ analysis have collapsed in the Bayesian analysis. There is some swapping of single samples between branches when the two analysis results are compared. This is not unexpected due to the very low level of informativeness in the data and the general lack of structure and support. A large number of samples do not show any clade groupings, but instead occur along the backbone.

Those branches that co-occur in both trees are as follows:

- Branch 4 remains the same in both analysis trees, although the version in the Bayesian tree has much higher support for internal nodes.
- Likewise, the *G. rigens* branch (Branch 8) remains the same in both trees.
- The Bayesian version of Branch 5 is missing three samples found in the NJ version of the same branch (see Figure 4.3.23 for detailed comparison).

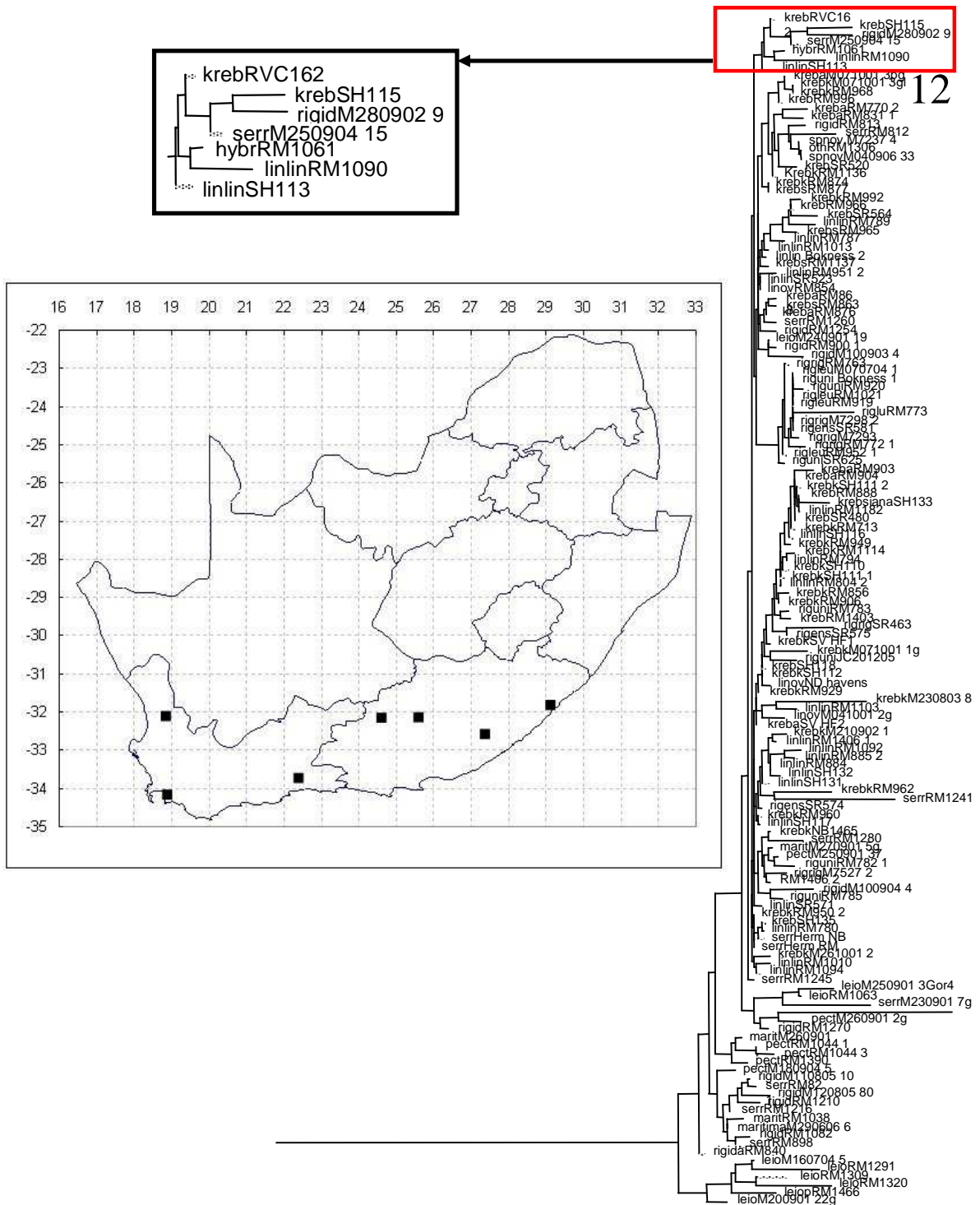


Figure 4.3.21: Branch 12 in detail with bootstrap support, the geographical origins of each sample and its position in the large unresolved clade.

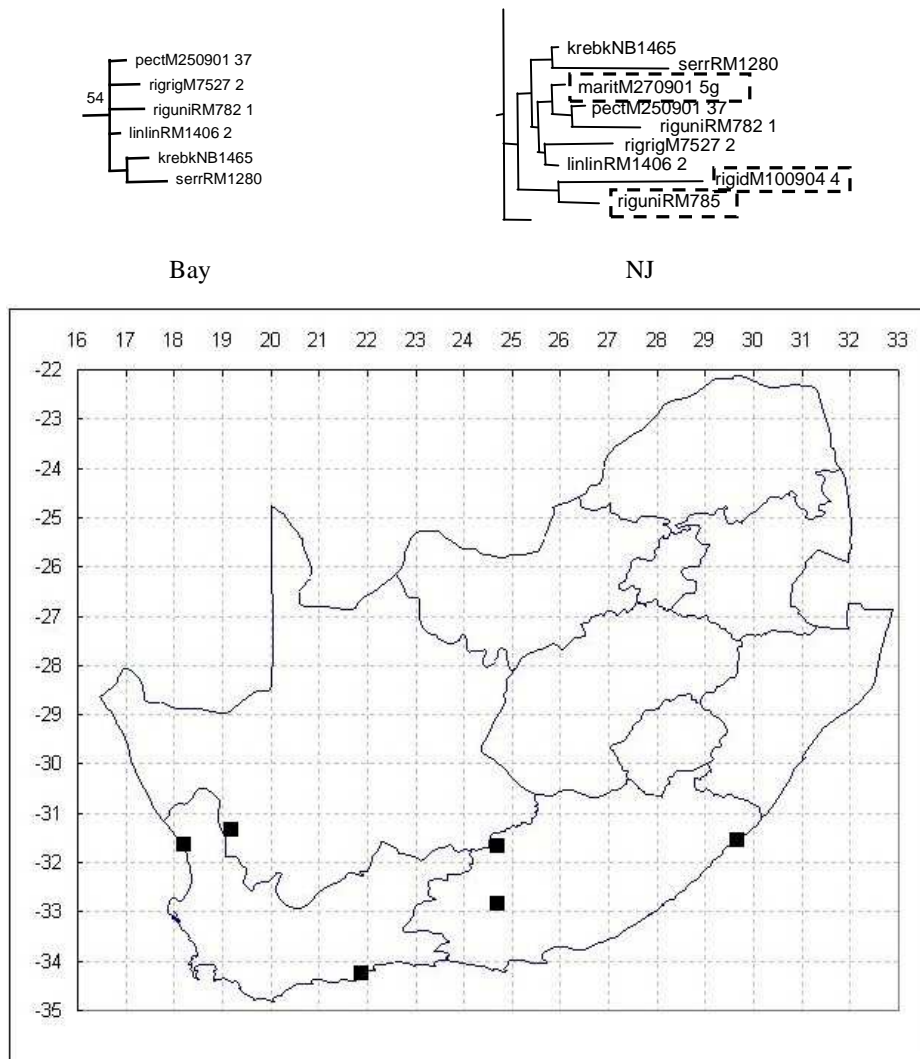


Figure 4.3.23: Partial Branch 5 from Bayesian tree in detail (on left), entire branch 6 from NJ tree on right. Dashed outlines indicate samples missing in the Bayesian branch. The map shows geographical origins of each sample in the Bayesian branch.

- The Bayesian version of Branch 6 is missing five samples found in the NJ version of the same branch (see Figure 4.3.24 for detailed comparison).
- The terminal section of the NJ Branch 7 retains its structure in the Bayesian analysis (with the addition of SH115, found in Branch 12 in the NJ analysis). The smaller partial Bayesian Branch 7 shows much tighter geographical grouping than the large NJ Branch 7 (Figure 4.3.25).
- The Bayesian version of Branch 10 has three samples found in the NJ version of the same branch, and has one additional sample included (see Figure 4.3.26 for detailed comparison).

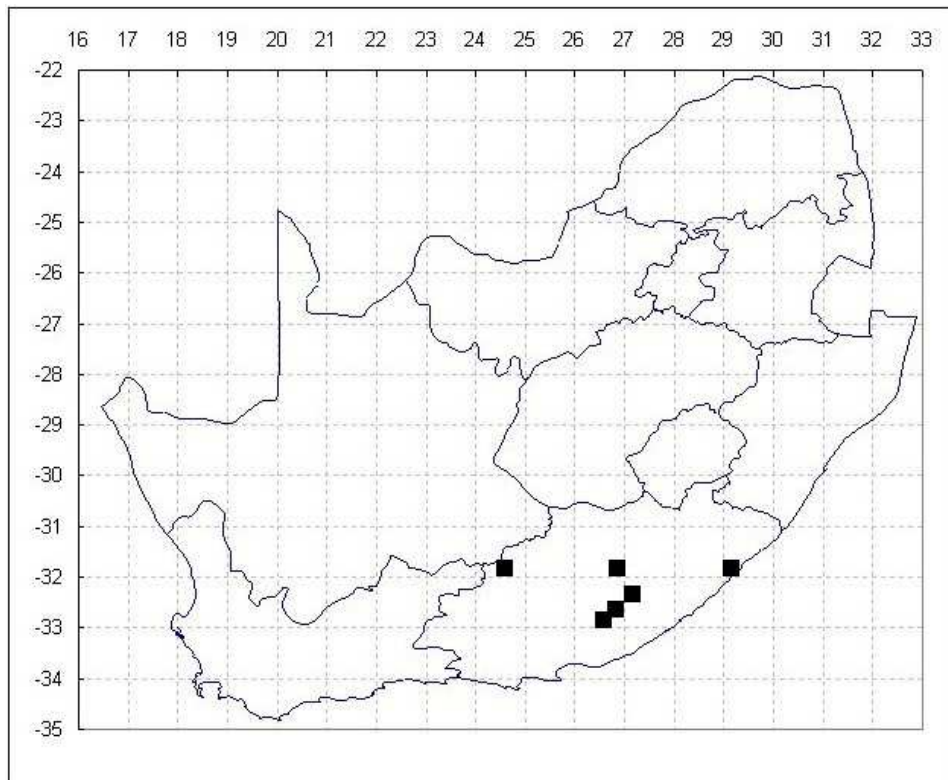


Figure 4.3.24: Partial Branch 6 from Bayesian tree in detail (on left), entire branch 6 from NJ tree on right. Dashed outlines indicate samples missing in the Bayesian branch. The map shows geographical origins of each sample in the Bayesian branch.

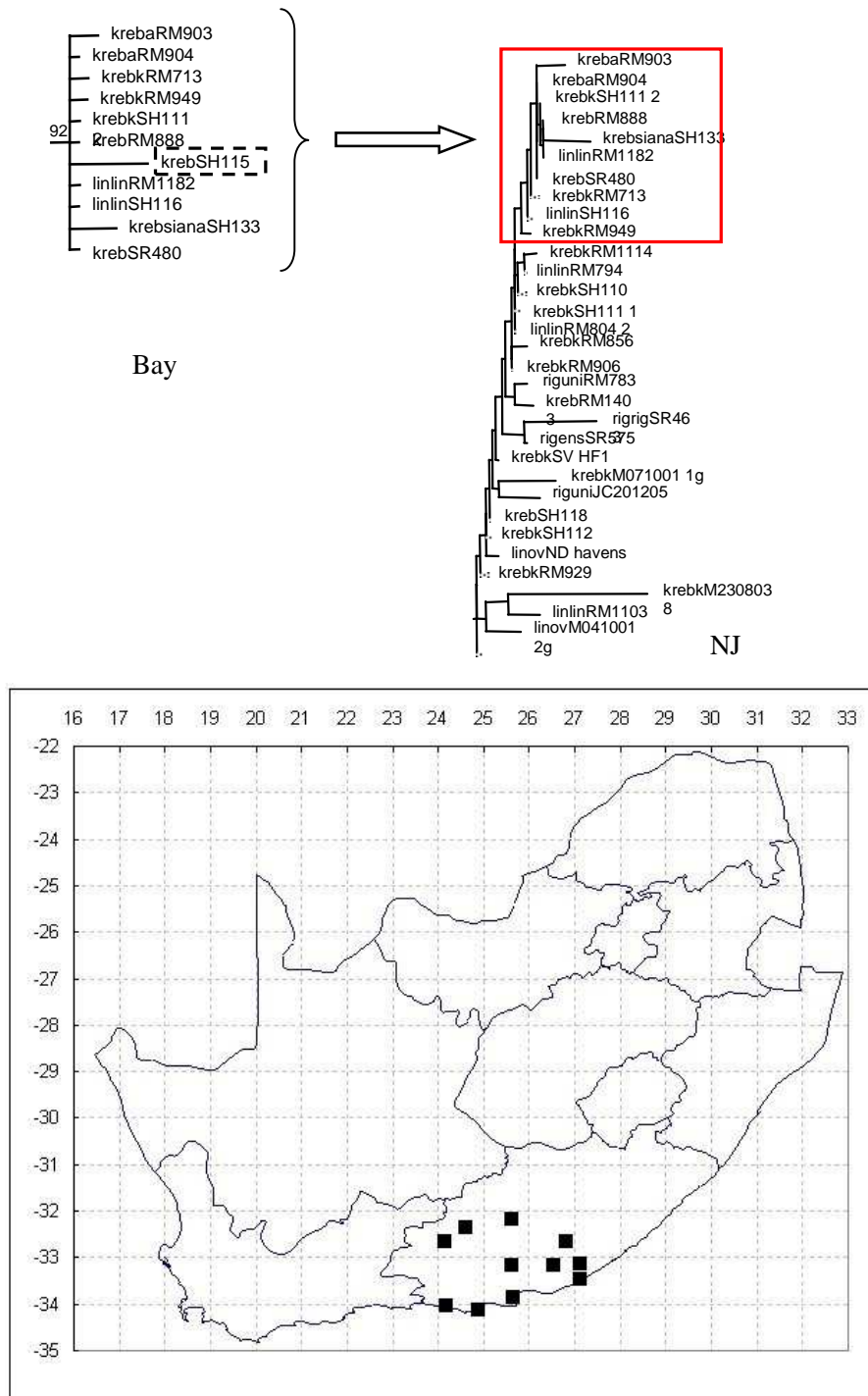


Figure 4.3.25: Partial Branch 7 from Bayesian tree in detail (on left), entire branch 7 from NJ tree on right. The map shows geographical origins of each sample in the Bayesian branch.

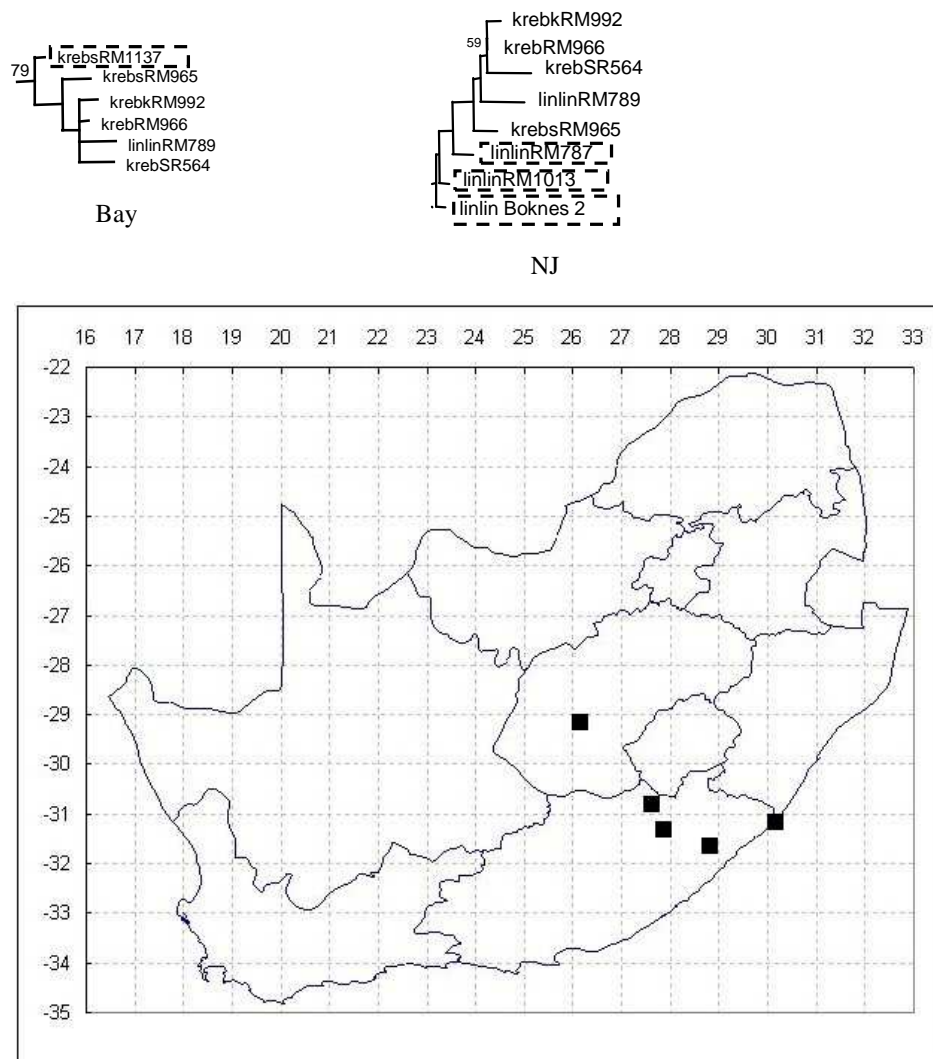


Figure 4.3.26: Partial Branch 10 from Bayesian tree in detail (on left), entire branch 10 from NJ tree on right. Dashed outlines indicate samples missing in the other branch. The map shows geographical origins of each sample in the Bayesian branch.

- The Bayesian version of Branch 11 (Figure 4.3.27) retains the same samples found in the NJ branch, although the Bayesian version of the branch is missing RM874 and now contains RVC162 (present in Branch 12 in the NJ analysis).

The Bayesian consensus tree also contains some branches that have no equivalent in the NJ tree. “Partial Branch A” (Figure 4.3.28) is made up of samples that fall into Branch 12 on the NJ tree, as well as some samples that are connected directly to the basal polytomy in the NJ tree.

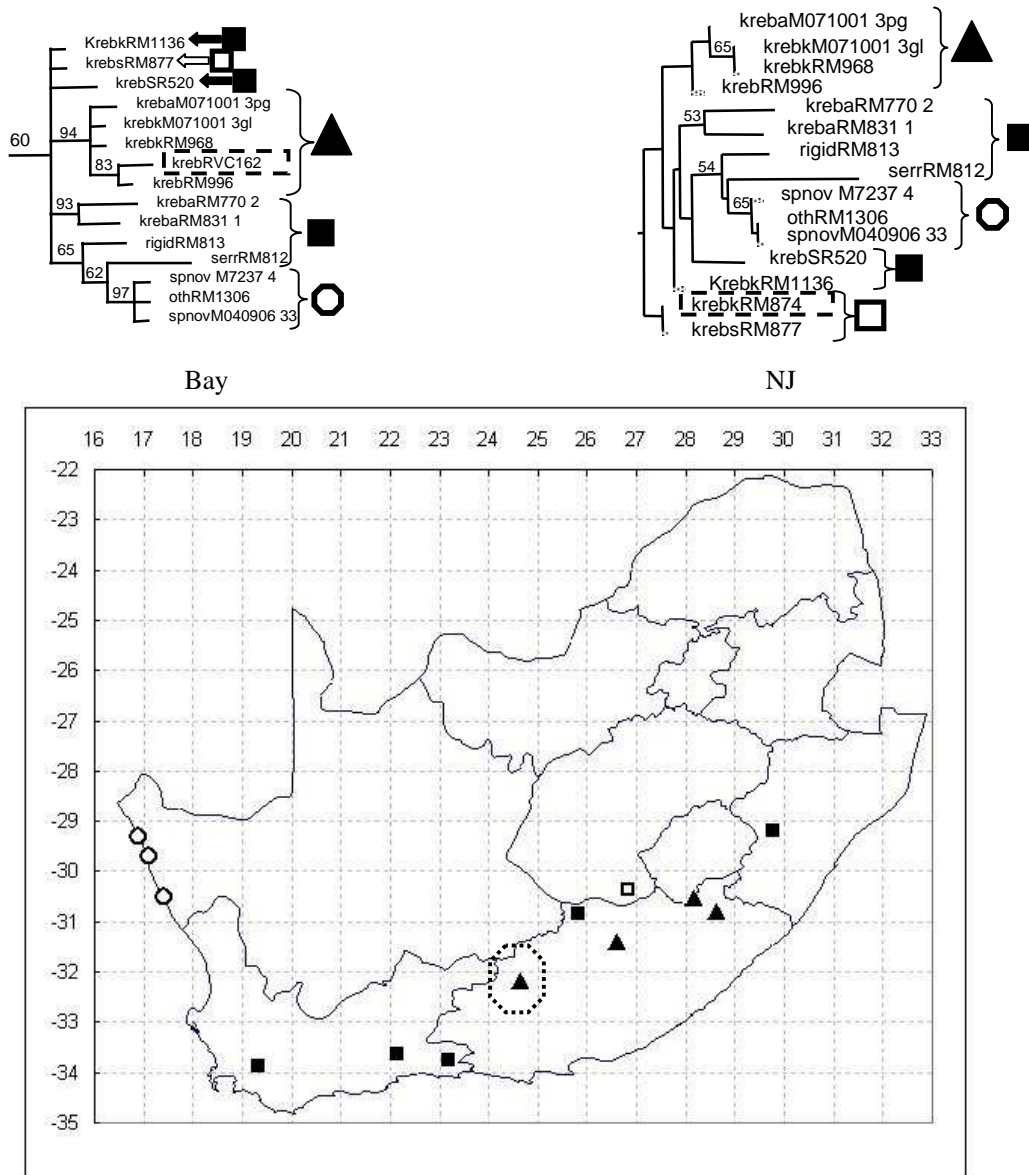


Figure 4.3.27: Branch 11 in detail with bootstrap support (Bayesian branch to left, NJ branch to right). Dashed outline indicates samples not found in the other analysis branch. The map shows the geographical origins of each sample, dotted line indicates locality for RVC162.

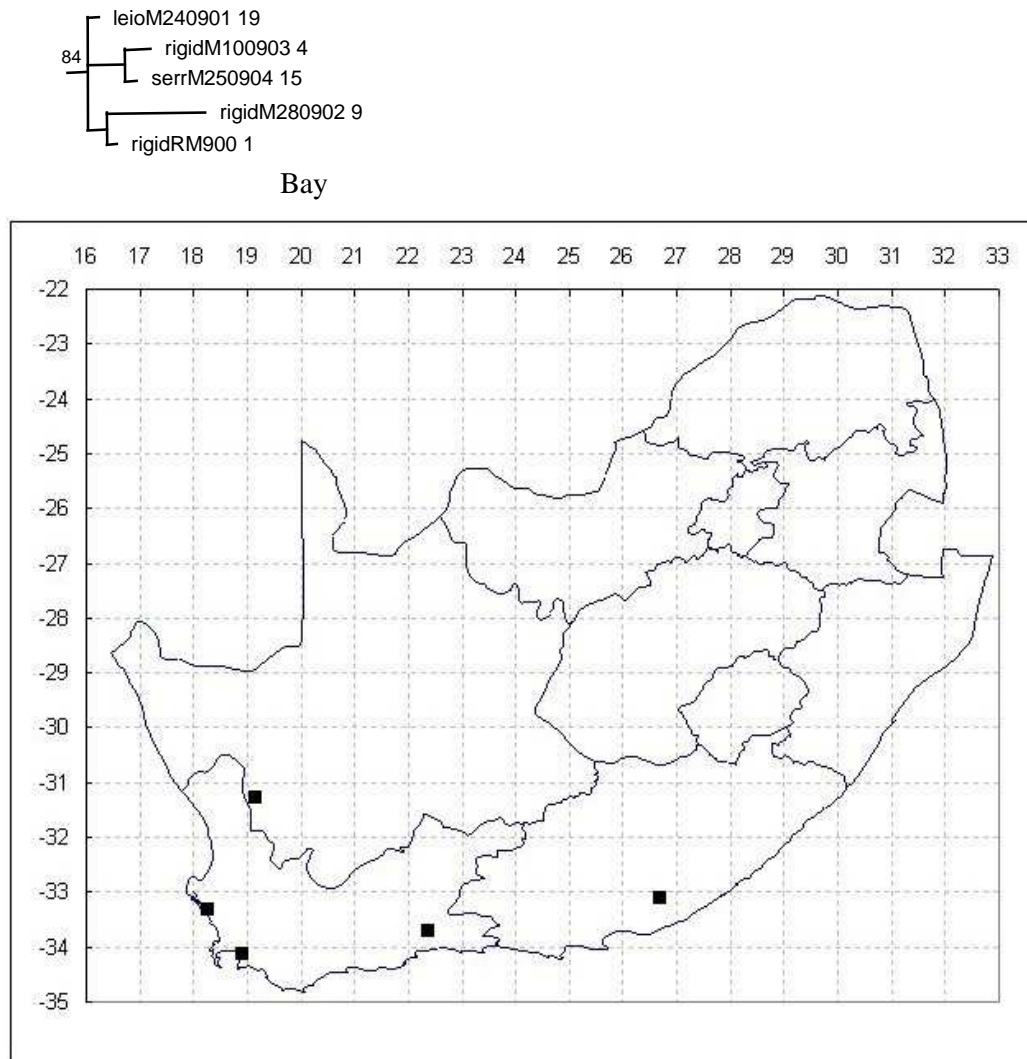


Figure 4.3.28: Partial Branch A from Bayesian tree in detail. The map shows geographical origins of each sample.

Neighbor-Net analysis

The Neighbor-Net analysis (Figure 4.3.29) shows a starlike topology. There is reticulation at the base of each branch (see the expanded centre in Figure 4.3.29.C), and a radiation of short branches from a central connection point. The branches (circled and numbered in Figure 4.3.29.B) correspond to the numbered branches in the NJ tree in Figure 4.3.9. There is no correlation between Neighbor-Net branch length and geographical origin of samples, other than that the two longest branches correspond to Western Cape samples. The Eastern Cape branches with clear geographical signal (7, 8 and 10) do not stand out among the other branches that show no geographic signal.

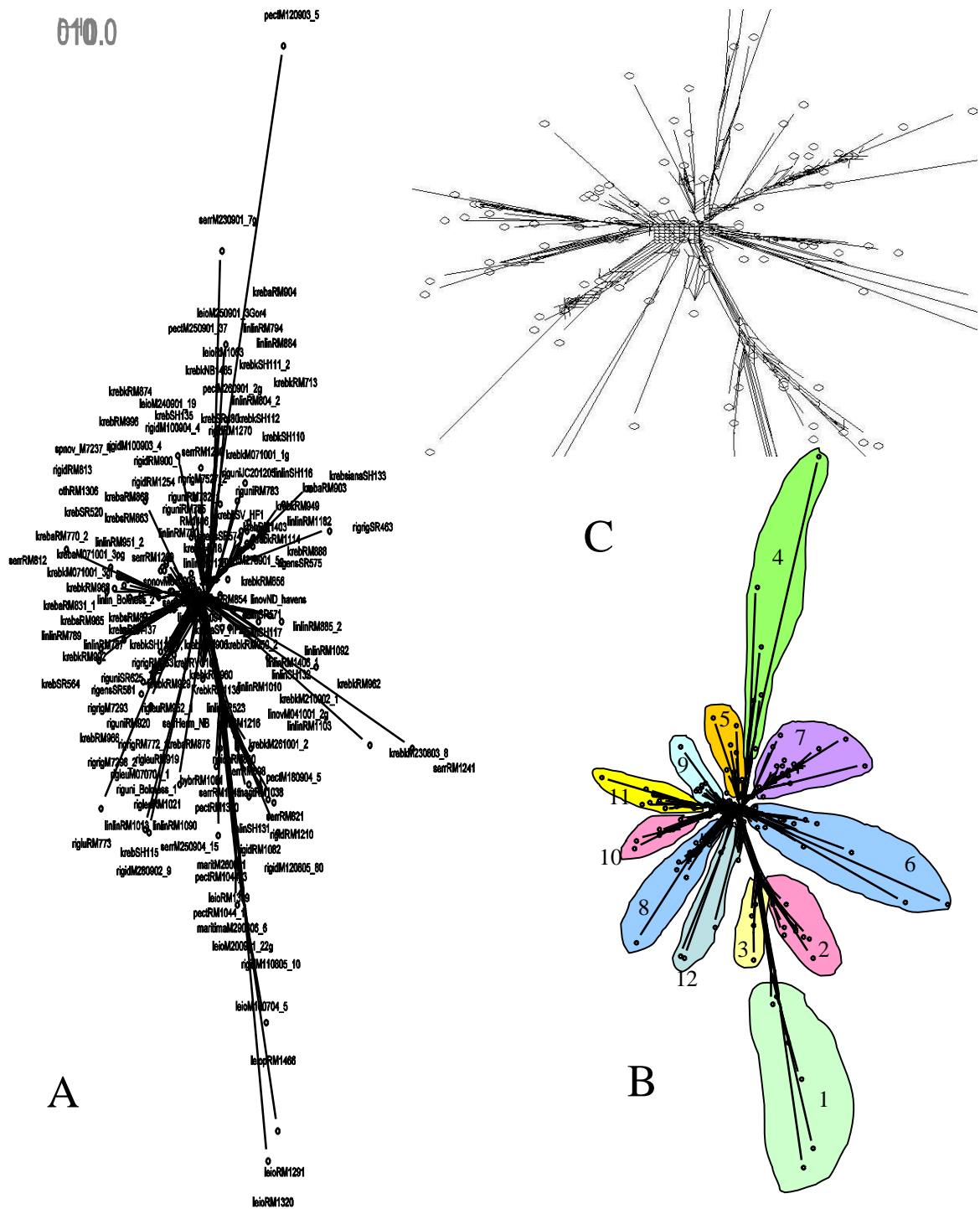


Figure 4.3.29: Neighbor-net network of KR clade, with labels (A) and without labels (B) Outlined areas with numbers indicate branches on NJ tree (B). C is an expansion of central core of network, showing reticulation.

Morphometric comparison

Figure 4.3.30 is a comparison between genetic distance and morphometric distance between each pair of samples. The correlation between the two is very poor ($r^2 = 0.0086$), indicating that there is little relationship between genetic distance and the morphological differences between pairs of samples.

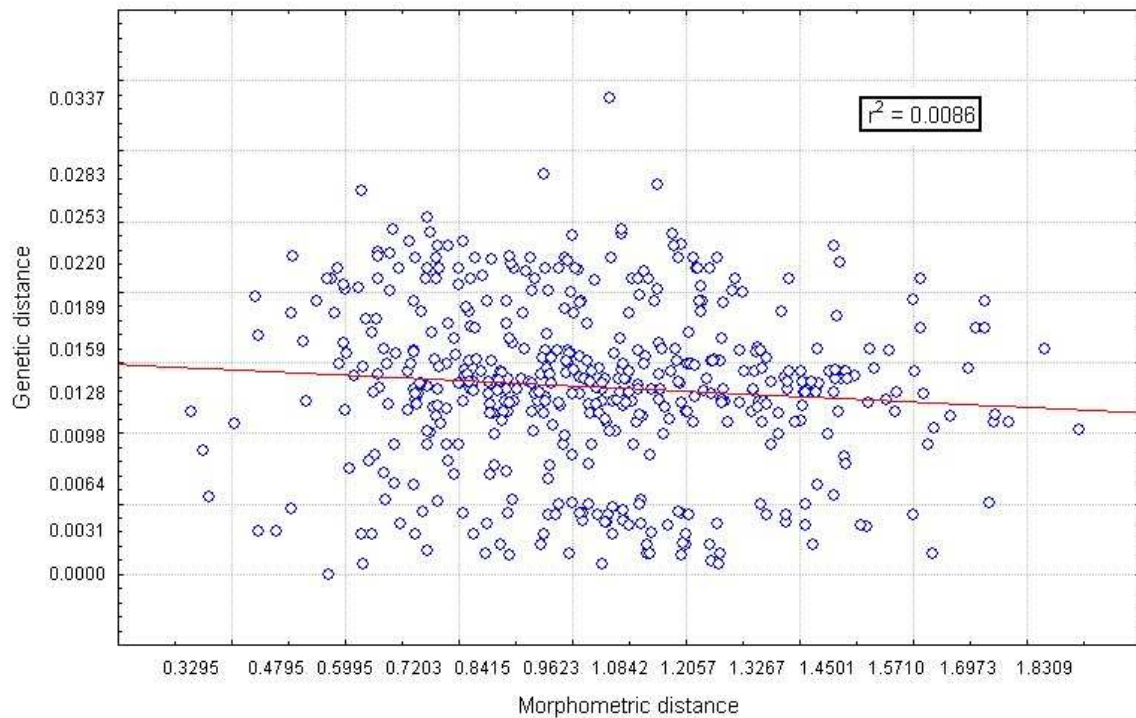


Figure 4.3.30: Scatterplot of genetic distance against morphometric distance between pairs of samples in K-R clade. Correlation r^2 value in box.

Figures 4.3.31 – 4.3.36 illustrate the comparison between NJ clades and morphometric clusters. The only two branches that show any sort of correlation between phylogenetic clade and morphometric clustering are Branch 1 (where four of six samples cluster together) and Branch 8 (where all the *G. rigens* samples cluster together).

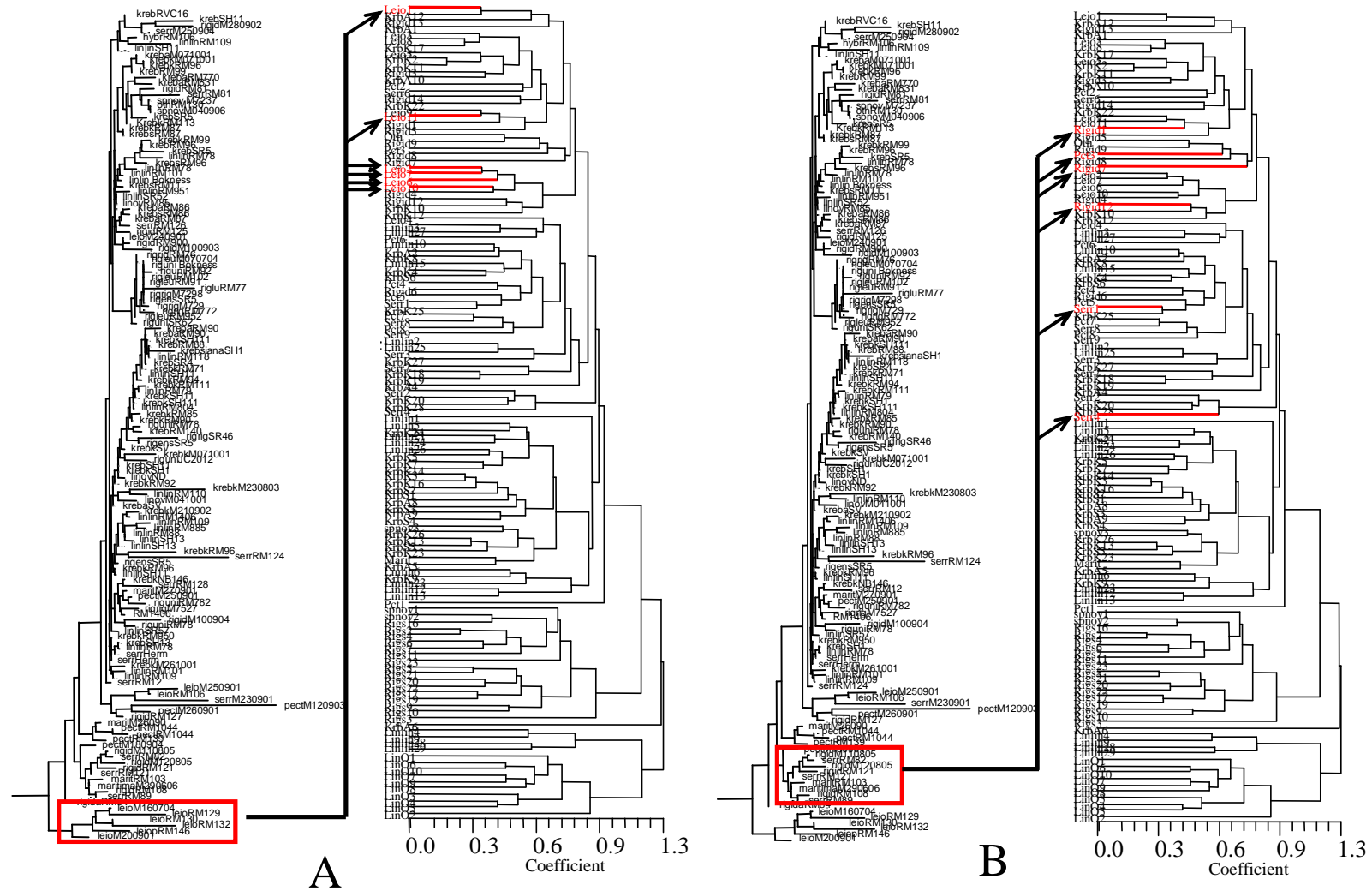


Figure 4.3.31: Comparisons between nrDNA phylogeny (left) and morphometric CA dendrogram (right). Arrows indicate positions of morphometric samples (in red) that correlate with genetic samples in Branch 1(A) and 2(B).

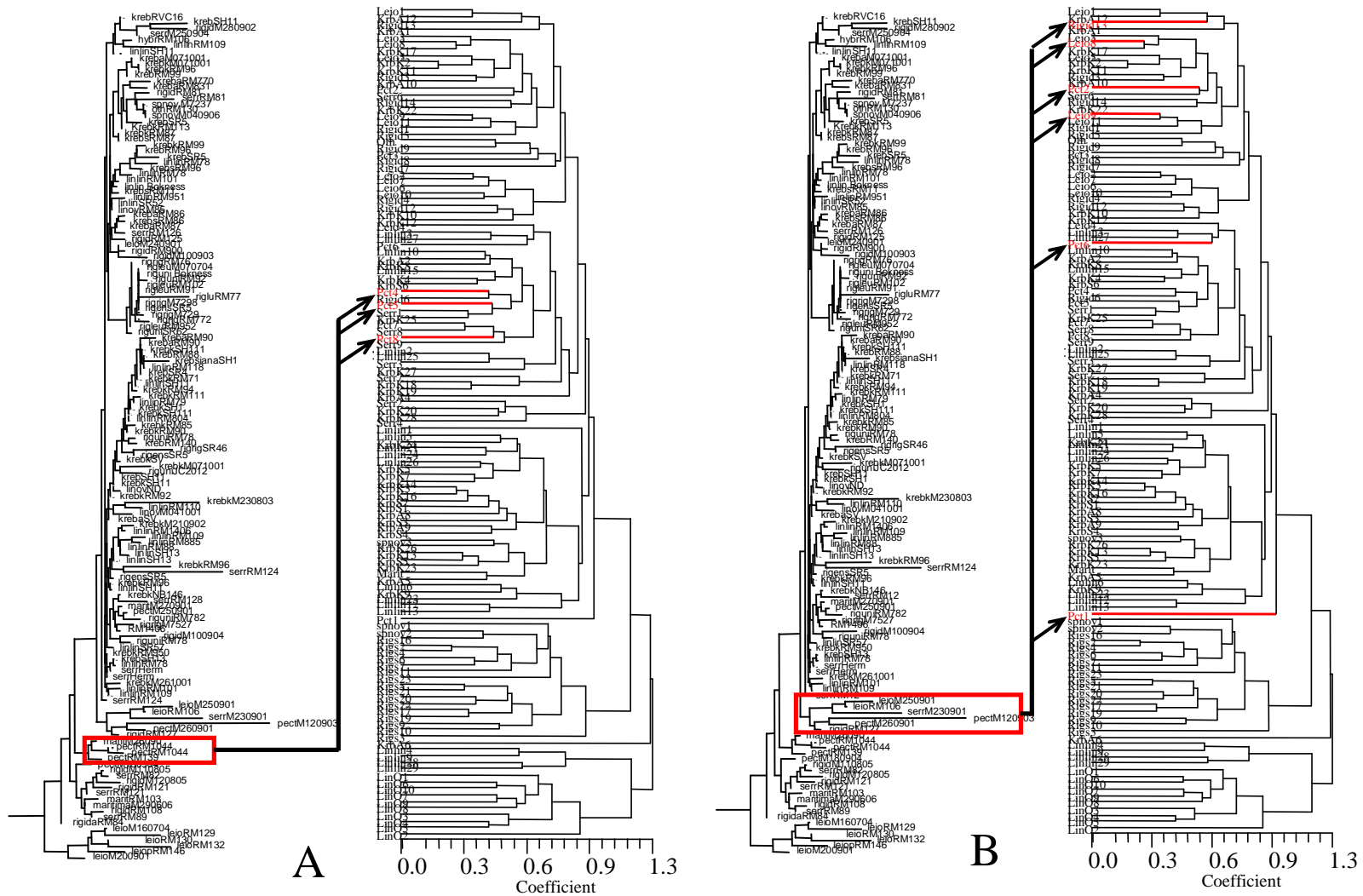


Figure 4.3.32: Comparisons between nrDNA phylogeny (left) and morphometric CA dendrogram (right). Arrows indicate positions of morphometric samples (in red) that correlate with genetic samples in Branch 3 (A) and 4 (B).

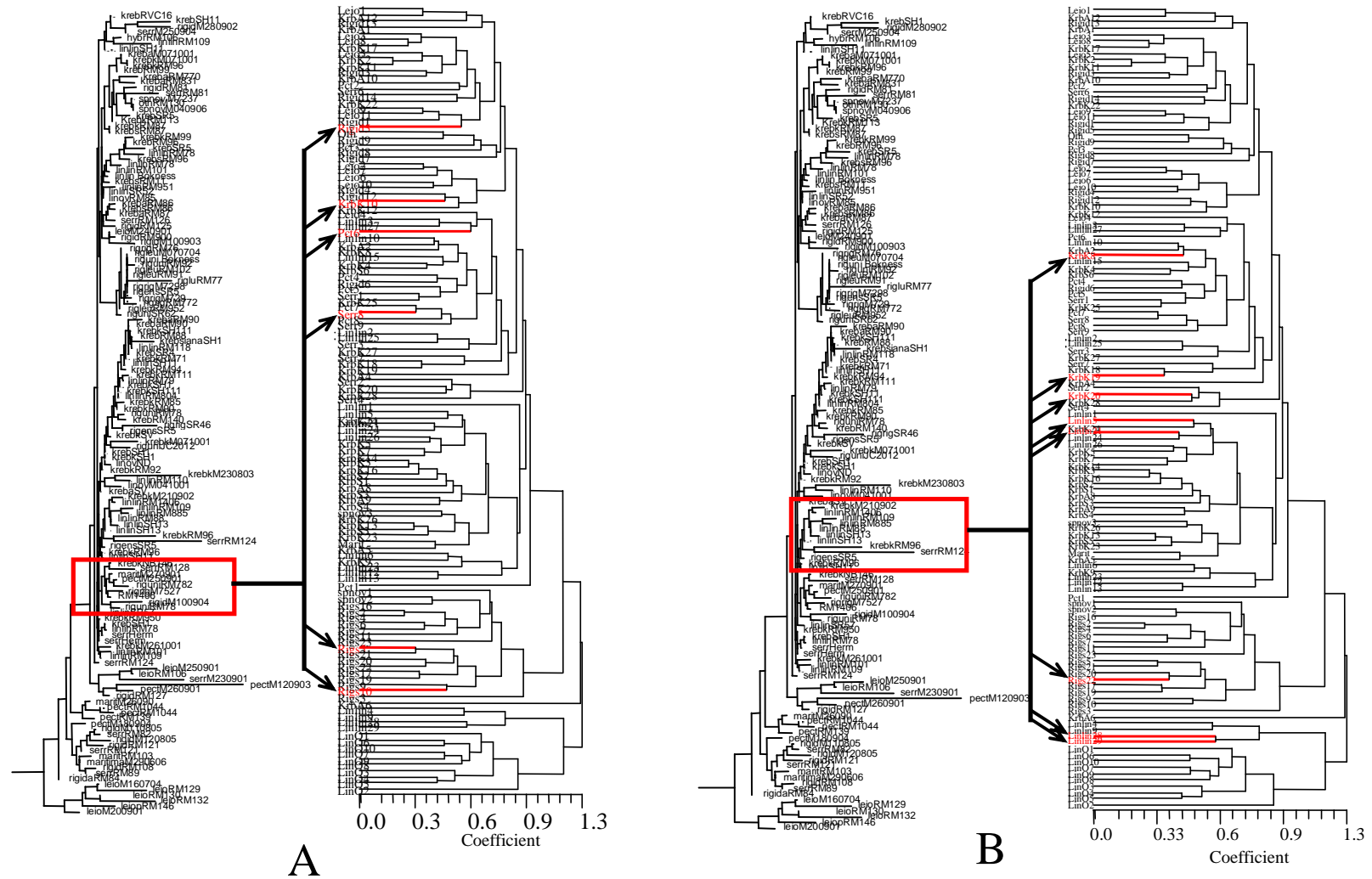


Figure 4.3.33: Comparisons between nrDNA phylogeny (left) and morphometric CA dendrogram (right). Arrows indicate positions of morphometric samples (in red) that correlate with genetic samples in Branch 5 (A) and 6 (B).

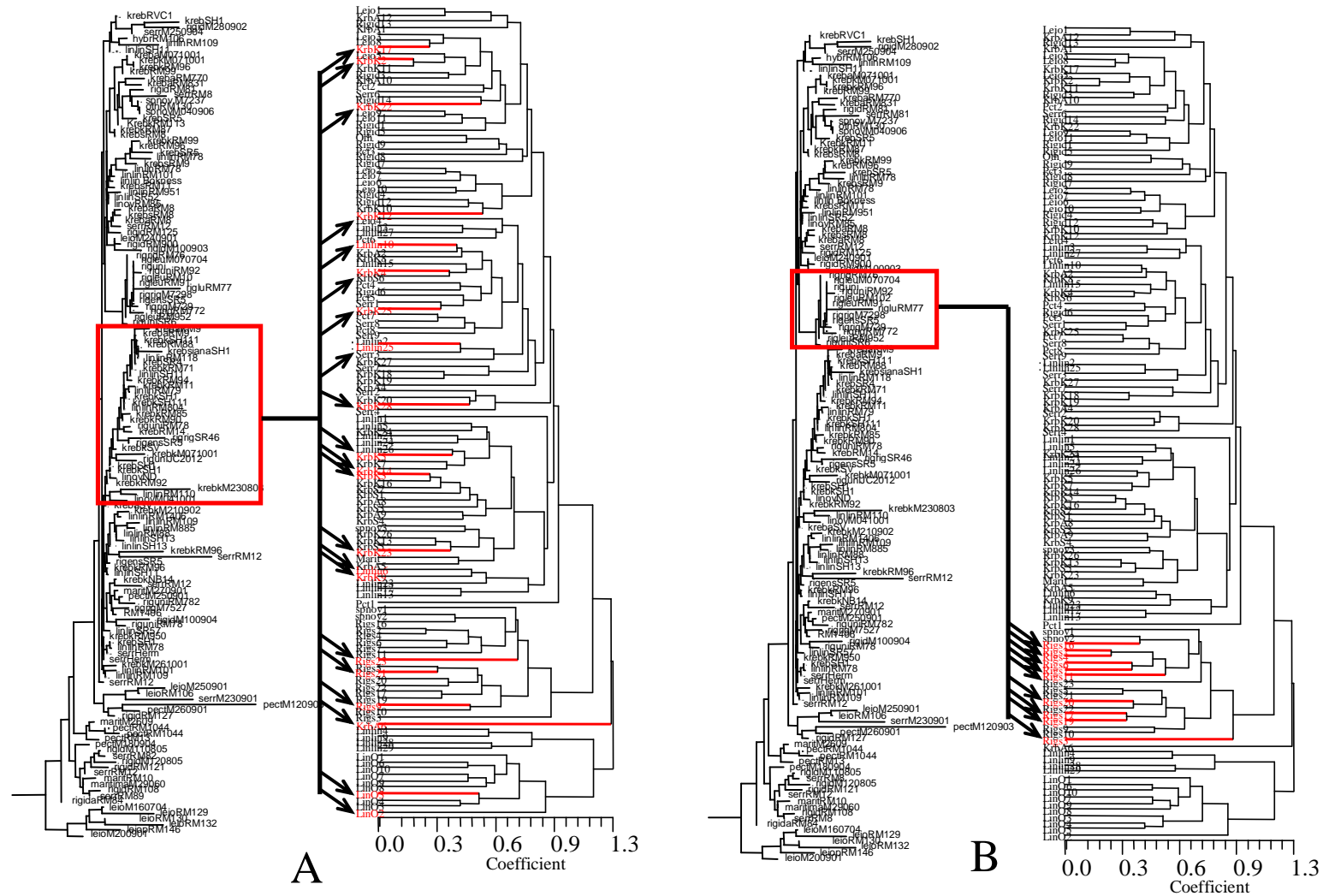


Figure 4.3.34: Comparisons between nrDNA phylogeny (left) and morphometric CA dendrogram (right). Arrows indicate positions of morphometric samples (in red) that correlate with genetic samples in Branch 7 (A) and 8 (B).

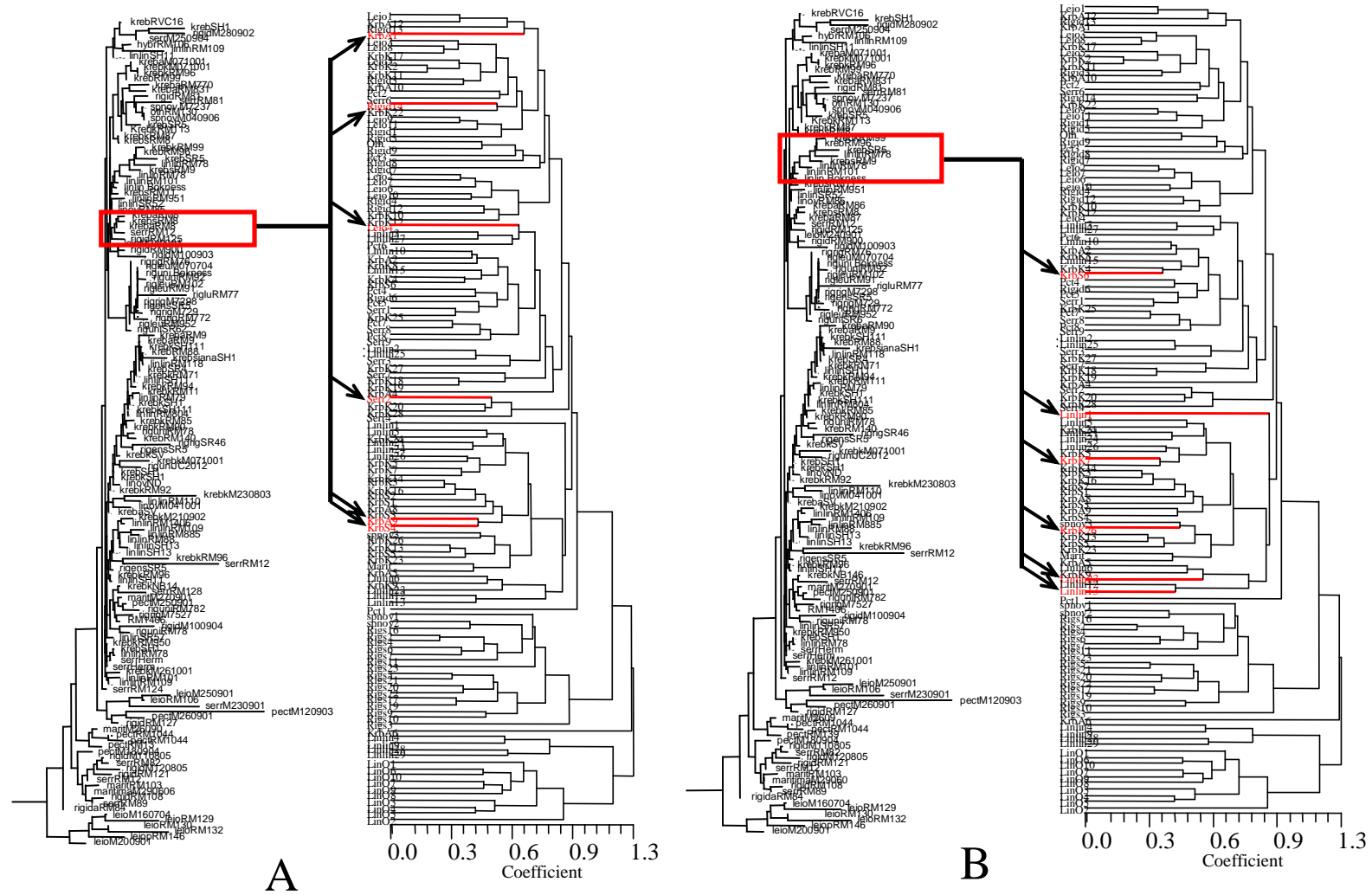


Figure 4.35: Comparisons between nrDNA phylogeny (left) and morphometric CA dendrogram (right). Arrows indicate positions of morphometric samples (in red) that correlate with genetic samples in Branch 9 (A) and 10 (B).

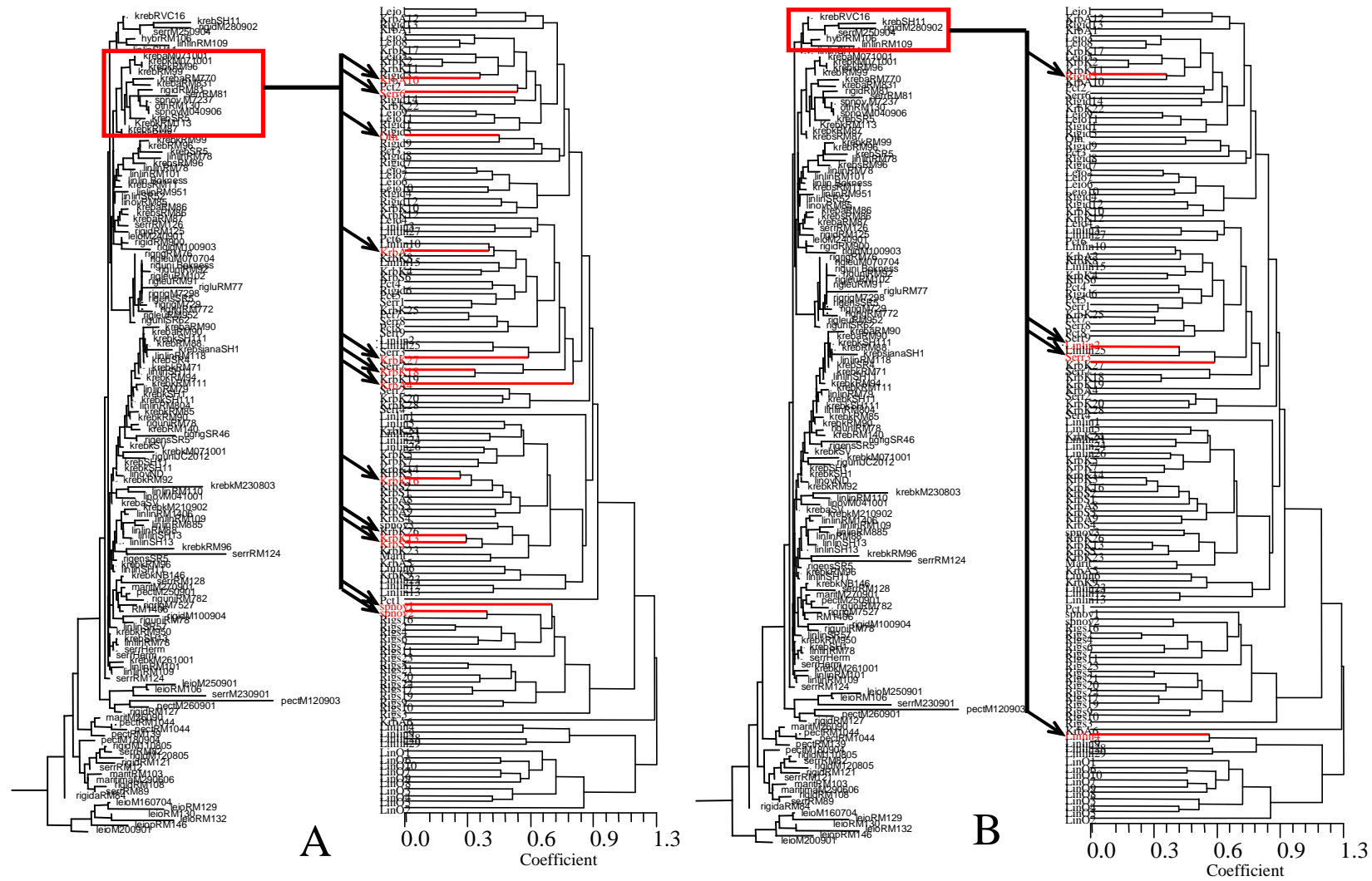


Figure 4.3.36: Comparisons between nrDNA phylogeny (left) and morphometric CA dendrogram (right). Arrows indicate positions of morphometric samples (in red) that correlate with genetic samples in Branch 11 (A) and 12 (B).

Caveats

The presence of reticulation in the Neighbor Net analysis, along with the presence of ambiguous base calls in the sequence data, suggest that some due caution must be applied to the assumption of accuracy of these nuclear phylogenies. Likewise, the lack of correlation between genetic and morphological data, and between genetic and geographical data, could also suggest that reticulation is affecting the retrieval of accurate phylogenies.

Conclusions

The presence in the K-R phylogeny of short terminal branches in a polytomy subtended by a much longer branch is a clear indication of a recent origin and a rapid radiation (Grant & Bowen, 1998). In combination with a star-shaped phylogeny and low levels of nucleotide diversity, this is evidence of recent expansion from a small number of ancestors (Grant & Bowen, 1998).

Within the K-R clade, there are three groups that show some species and phylogeographical cohesion:

- 1) *G. leiopoda*, (localised to the Namaqualand centre of endemism, around 30° S 18° E)
- 2) *G. rigens*, (localised to the south eastern cape coast), and
- 3) *G. othonnites*/*sp. nov.*, (localised to an area around Port Nolloth, this is a variable but distinctive group, showing mild succulence and pale grey leaves. The difference between *G. othonnites*, which is glabrous, and *G. sp. nov.*, which is occasionally hispid, may be a result of an initially poor description of morphological variation within *G. othonnites* by Roesler).

Two of these groups (*G. leiopoda* and *G. rigens*) also show some morphometric cohesion (*G. rigens* in particular). The rest of the samples in the K-R clade fall into a fourth paraphyletic group, with no species cohesion or clear phylogeographic signal.

In order for species to be useful units for evolutionary and ecological studies, they need to be recognizably identifiable as distinct entities (Riddle & Hafner, 1999). When biologists use species as a framework to study evolving entities in nature there may be uncertainty caused by the inherently ambiguous correspondence between a species and the entity or entities for which it is used as a hypothesis (Hey *et al.*, 2003).

Species taxa are devised by investigators and are partly a function of the investigator's tools, circumstances and inclinations, and for species that have distinguishing morphological characters, this subjective element will seem remote and biologists can agree on the organisms to be included in a

species (Hey *et al.*, 2003). For more problematic taxa, two investigators working with a common sample of organisms may disagree on the importance of a particular pattern of variation, and thus also on the designations and descriptions of these species, a type of uncertainty that can be difficult to mitigate (Hey *et al.*, 2003).

The three cohesive entities in the K-R clade may perhaps not be discrete enough to qualify as species. They are evolutionary lineages, and could perhaps be classified as Evolutionary Significant Units (ESU; Ryder, 1986), but their status as “species” is questionable, as is the status of all the K-R clade morphologically defined taxa. The cohesive lineages are perhaps best classified as distinct varieties. If the cohesive lineages were classified as species, they would render the remainder of the K-R clade paraphyletic. However, Goldstein & DeSalle (2000) note that the concepts of parapyly and monophyly (which rests on the identification of common ancestry) can become meaningless when applied to nonhierarchical systems where common ancestry is confounded by reticulating networks of interconnected parentage. Ultimately, ranking in this context (i.e. whether the cohesive lineages are species or varieties) may perhaps be arbitrary.

The reasons for this lack of taxonomic clarity and the historical and evolutionary causes that lead to this situation are investigated in Chapter 5.

Chapter 5.

Recent evolutionary history of *Gazania*

“The probability of a large amount of hybridization between the species and a resultant mixture of characters is very high... perhaps right here lies the actual difficulty of the taxonomic treatment of this genus.” (Roessler, 1959, pp 101, translated from the original German).

Aim: To explain the phylogenetic and phylogeographic distribution of the taxonomic entities within *Gazania*.

Geography and climate as driving factors in speciation

Ayoub & Riechert (2004) note that continental drift and mountain uplifting (and other such geological events) have predictable consequences for evolutionary lineages: they can create physical obstacles to gene flow. This leads to the formation of monophyletic groups on either side of the barrier (Ayoub & Riechert, 2004). A less understood but equally important type of historical event is climate change: generalization about the effects of climate change on evolutionary lineages is difficult as species may respond in different ways to changes in climate (Ayoub & Riechert, 2004). Ayoub & Riechert, (2004) cite examples where, since the last glacial maximum, range expansion or contraction of populations occurred at varying tempos and in different directions for individual species. Responses to climate change are species specific, which means that biogeographical studies searching for general patterns have focused on geological historical events, often ignoring the effects of climate change (Ayoub & Riechert, 2004).

Cheng *et al.* (2005) note that the present status of species distributions represents the effects of various geographical barriers, dispersal behaviours and abilities, and colonization competition with resultant nonsynchronous migration. Heuertz *et al.* (2004) likewise note that it is well established that species co-occurring today may have undergone very different responses to climate change and thus can show different evolutionary history patterns.

Population growth history

The analysis of variation in DNA sequences has the potential for providing insight into population genetic processes (Slatkin & Hudson, 1991). Episodes of population growth and decline leave characteristic signatures in the distribution of nucleotide site differences between pairs of individuals

(Rogers & Harpending, 1992), and the numbers of differences in sequences between all pairs of individuals can be used to summarise information in the data, while the shape of the graph can point to patterns of population growth and expansion (Slatkin & Hudson, 1991). A single (unimodal) distribution of pairwise distances (reflecting similarity in the amount of divergence among all pairs of haplotypes) can be indicative of populations which have gone through a period of rapid expansion or growth, while a multimodal distribution that has multiple peaks is indicative of populations which have been stable over time (Mahoney, 2004). In this type of distribution graph, an episode of growth generates a wave that travels from left to the right; the smaller the initial population, the steeper will be the leading face of the wave (Rogers & Harpending, 1992). If there have been any recent population expansions within *Gazania*, they should present as a star-like phylogeny associated with the unimodal mismatch distribution (Slatkin & Hudson, 1991; Mahoney, 2004).

In conjunction with information on the climatic history of Southern Africa, the data gathered in the previous chapters can now be utilised in unison to track the origin, and the evolutionary and biogeographical history of the various taxonomic entities within *Gazania*.

Methods

Geographical mapping

Each terminal node in the major branches of the genetically distinct clades in the phylogenetic trees generated in Chapter 3 was plotted onto maps of Southern Africa in an attempt to elucidate any biogeographical patterns that may exist. Likewise, the geographical origins of the terminal nodes in the expanded K-R clade from Chapter 4 are also mapped.

Maps of Roessler's original taxa collection sites and his species distributions, the collection locality data from the PRECIS database, and the locality data from the DNA samples collected for this project are also mapped out for comparative purposes. The possibility of erroneous species determinations or database entry errors with the PRECIS data suggests that reasonable caution should be exercised with any localities that appear to lie far outside the distributions for all other samples of each entity.

Divergence time estimation

A "molecular clock" model assumes that there is a global rate of mutation across all lineages in a phylogeny (Rutschmann, 2006). However, a clock is not always a good model for the process of molecular evolution, with variation in rates of nucleotide substitution pervasive, both along a lineage and between different lineages (Li, 1997).

To test if there is a constant mutational rate constant across all lineages, the Likelihood Ratio Test (Felsenstein, 1981) was conducted in PAUP*, comparing likelihoods obtained with and without an enforced molecular clock. The difference between the two likelihoods was doubled and then used in conjunction with Chi squared tables to determine if the difference between the two likelihoods was significant (degrees of freedom was calculated as Number of taxa – 2). A significant result ($p < 0.05$) would reject the molecular clock hypothesis for the data under investigation.

The dates of sequence divergence can be calculated manually. To obtain an approximate dating of branching events between species and species groups, the average sequence divergence values were calculated for highly supported sister groups. Only ITS sequence data was utilised for these calculations, as rates of change for other regions are not well studied or published. The uncorrected pairwise distances were determined using PAUP*. The pairwise sequence divergence values between two sister groups were determined as the average of all pairwise sequence divergence values between species from the two clades. These average sequence divergence values were calculated from the uncorrected pairwise distance to accommodate the divergence rates previously calibrated in other studies (Richardson *et al.*, 2001). Divergence time between a pair of species was calculated as half of

the divergence value divided by the rate of change in substitutions per site per year (Yuan *et al.*, 2005).

A variety of ITS rates of divergence are listed in Richardson *et al.* (2001). Rates for ITS divergence generally fall into a range from 1.72×10^{-9} substitutions per site per year (s/s/y) in the Saxifragaceae (Vargas *et al.*, 1998) to 7.83×10^{-9} s/s/y in the Compositae (Sang *et al.*, 1995). The mutation rates for annuals (1-2 years) are the fastest, and additionally the rates for the Asteraceae tend to be fairly high. Since *Gazania* is a small herbaceous perennial member of the Asteraceae that can go from seed to seed set in under a year, an average for the Asteraceae mutation rates can be calculated as 5.21×10^{-9} s/s/y, with a lower extreme of 3×10^{-9} s/s/y (from the Hawaiian Silverswords; Baldwin & Sanderson, 1988), and a higher extreme of 7.83×10^{-9} s/s/y (from *Robinsonia*; Sang *et al.*, 1995).

Apart from manual calculation, there are a number of software packages that can perform dating estimates, and some can employ both strict and relaxed molecular clocks (Drummond *et al.*, 2006). BEAST (Drummond *et al.*, 2003) implements a Bayesian Markov chain Monte Carlo method to estimate phylogenies and divergence times in the face of uncertainty in evolutionary rates and calibration times (Drummond *et al.*, 2006). The molecular clock assumption can either be enforced strictly, or relaxed by allowing the rate to vary throughout the tree in an autocorrelated manner (Ho *et al.*, 2005).

A relaxed clock can either use a lognormal distribution (with the variance scaled relative to the length of the branch in units of time, implying that the evolutionary rate changes continuously along the branch) or an exponential distribution (which implies that changes occurred at the nodes, with the size of the change being independent of the branch length) (Drummond *et al.*, 2006). The variable rate methods implemented in BEAST use Bayesian inference and the MCMC procedures to derive the posterior distribution of rates and times, and they do not require a starting tree topology (Rutschmann, 2006). Following a burn-in of 500,000 cycles, rates were sampled once every 1000 cycles from 5,000,000 Markov Chain Monte Carlo (MCMC) steps. Rates were estimated under a GTR model and the average mutation rate calculated above was utilised. Both the lognormal and the exponential relaxed clocks were used for comparative purposes.

Pairwise sequence divergences

Pairwise sequence divergences were tabulated using PAUP*. Frequencies of each pairwise sequence divergence distance were plotted against the number of differences between each pair of sequences.

Results

Maps of genetically cohesive species

Figures 5.3.1 to 5.3.8 are maps of the genetically discrete species found in Chapter 3. They layer three different sets of distribution data together: Roessler's original species distributions (represented by irregular shaped areas within solid outlines); the PRECIS database locality data (represented by squares); and the localities for samples collected for this study (represented by open circles).

In most cases, the species distributions mapped by Roessler do not map the true extent of the occurrences of these species across South Africa as indicated by the specimens in PRECIS. The addition of the locality data from the PRECIS database extends almost all of these species' distribution limits. The potential drawback with using PRECIS locality data is the danger of mistaken species determinations or erroneous database entries for locality data. A possible example of this is the presence of a *G. jurineifolia* subsp *scabra* sample at 3022AA (Figure 5.3.3), which lies well outside the subspecies's normal distribution, but lies well within the distribution of the other subspecies of *G. jurineifolia* (Figure 5.3.4).

There are two further major extensions of these species distributions. One occurred with the discovery of a *G. ciliaris* (Figure 5.3.7) population in the Eastern Cape at Seven Seas, near the Fish River (sampled as SR705). The other occurred with the discovery of extensive populations of the putatively rare *G. caespitosa* (Figure 5.3.8) on the high altitude areas of the Sneeuberg, Koudeveldberg, Meelberg and Toorberg mountain ranges (R. Clark, pers. comm., represented by RVC448 and RVC307). *G. caespitosa* was collected once in 1872 from the Sneeuberg and described from this exemplar. According to the PRECIS data base it was collected only twice more (in 1897 and 1976) from widely different localities (Garcia's Pass and Nuwerus) (although these may be erroneous species determinations or localities). The subsequent 2006 collections by Clark suggest that *G. caespitosa* is "very common" in the high altitude regions (around 2000 m) of the eastern and southern cape mountains (R. Clark, pers. comm.). But as this region is poorly collected, this is not entirely unexpected.

All but one of the genetically discrete species found in Chapter 3 occur in either the western half of South Africa (towards the more northern reaches of this area), or in the south-western regions of Namibia. The exception to this is *G. caespitosa*, which occurs in the high altitude regions of the mountain ranges in the eastern and southern cape. *G. ciliaris* usually occurs in the south-western cape (but a recent find has extended this range to the Eastern Cape; Figure 5.3.7).

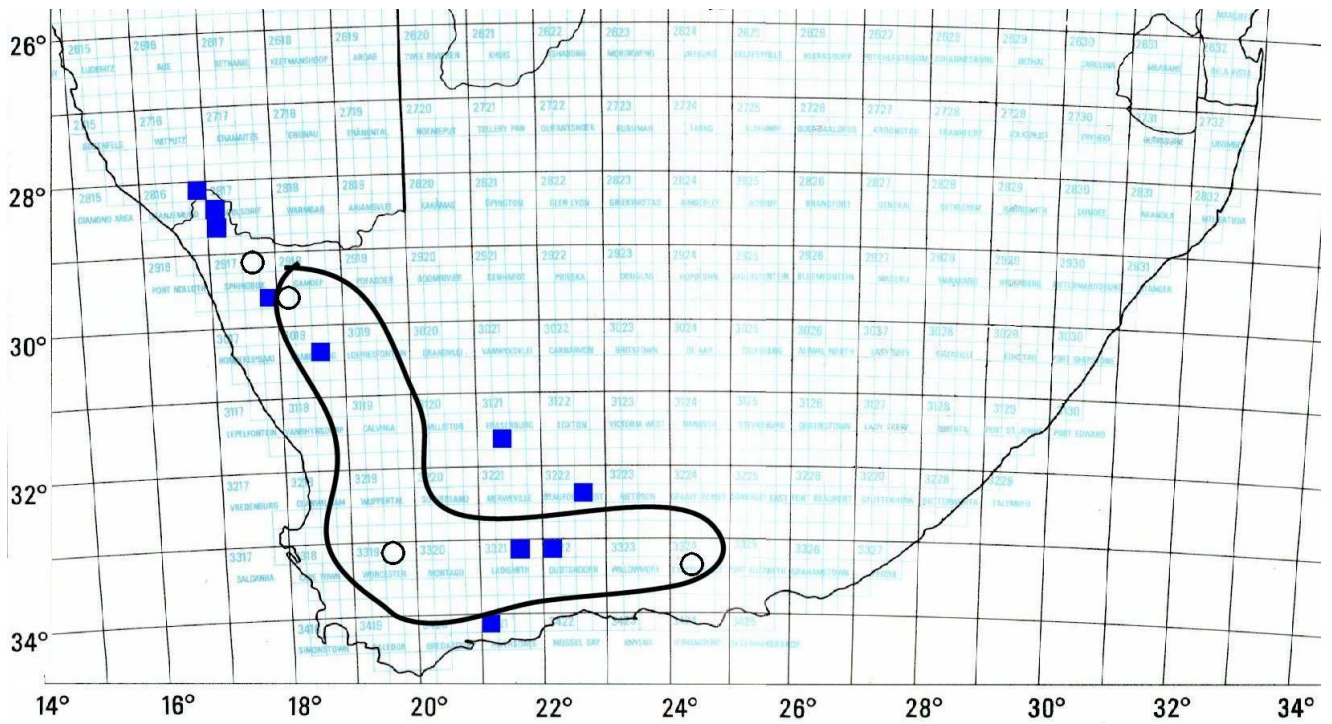


Figure 5.3.1: Distribution map for *G. heterochaeta*. Solid outline indicates Roessler's distribution, solid squares indicate PRECIS localities, and hollow circles indicate samples collected for this study.

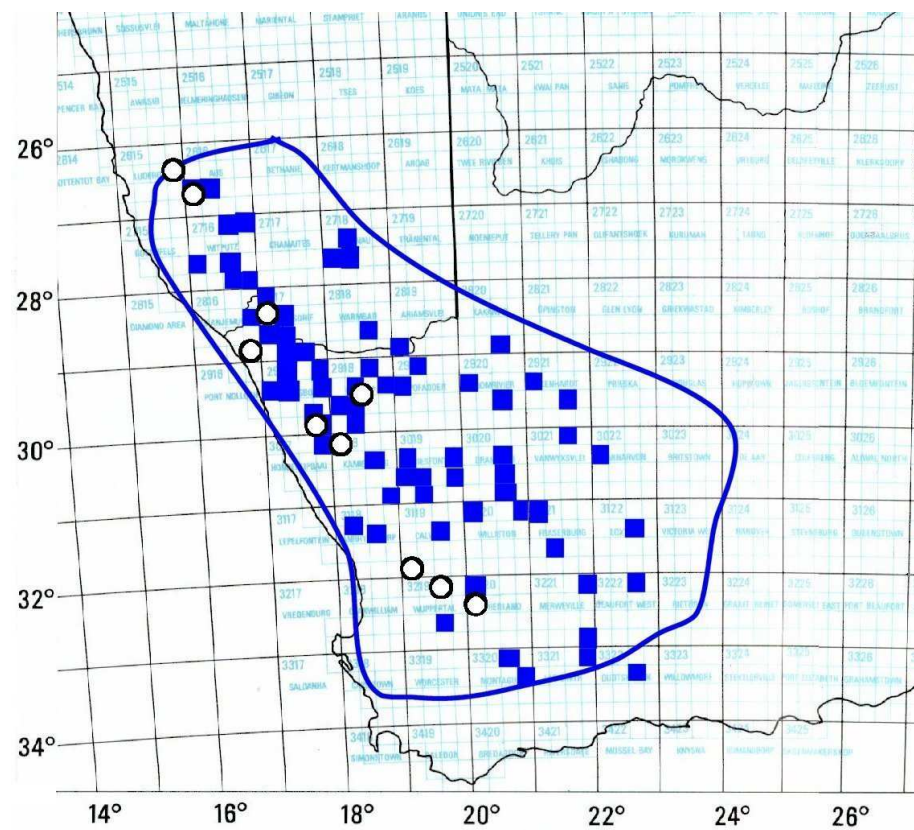


Figure 5.3.2: Distribution map for *G. lichtensteinii*. Solid outline indicates Roessler's distribution, solid squares indicate PRECIS localities, and hollow circles indicate samples collected for this study.

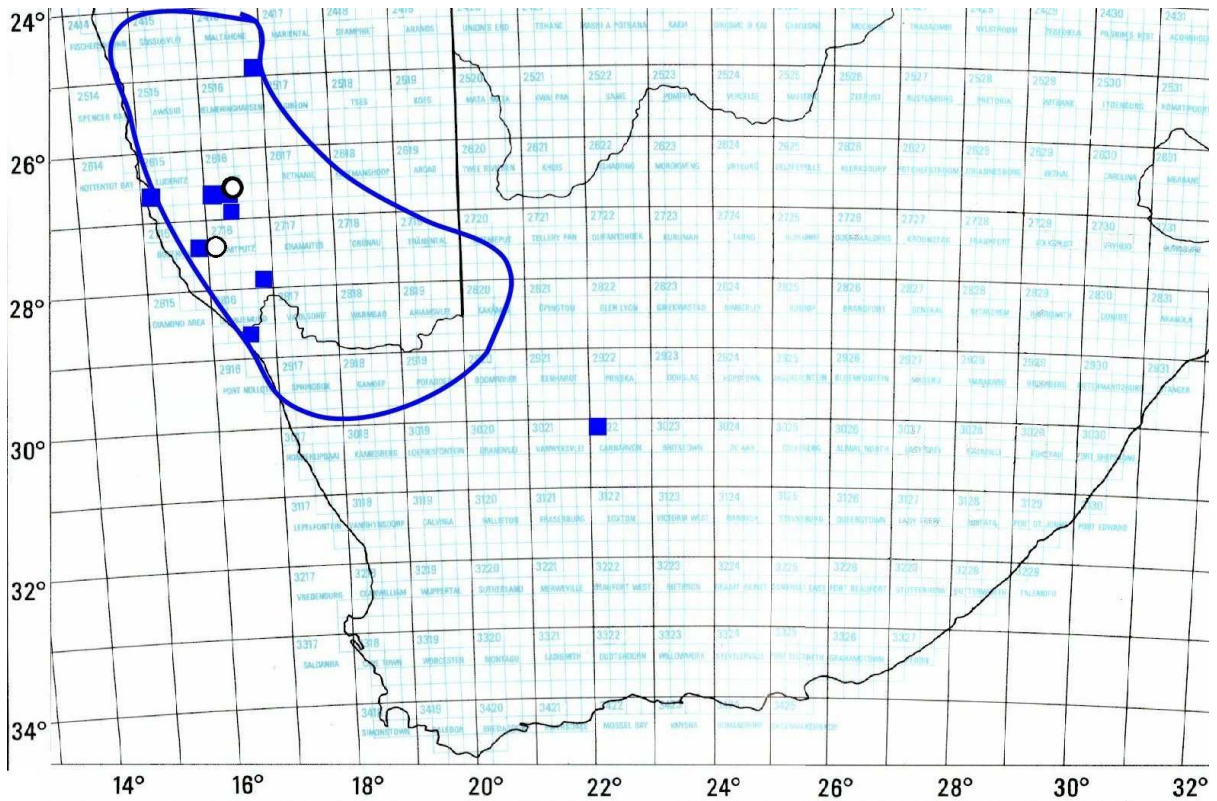


Figure 5.3.3: Distribution map for *G. jurineifolia* subsp. *scabra*. Solid outline indicates Roessler's distribution, solid squares indicate PRECIS localities, and hollow circles indicate samples collected for this study.

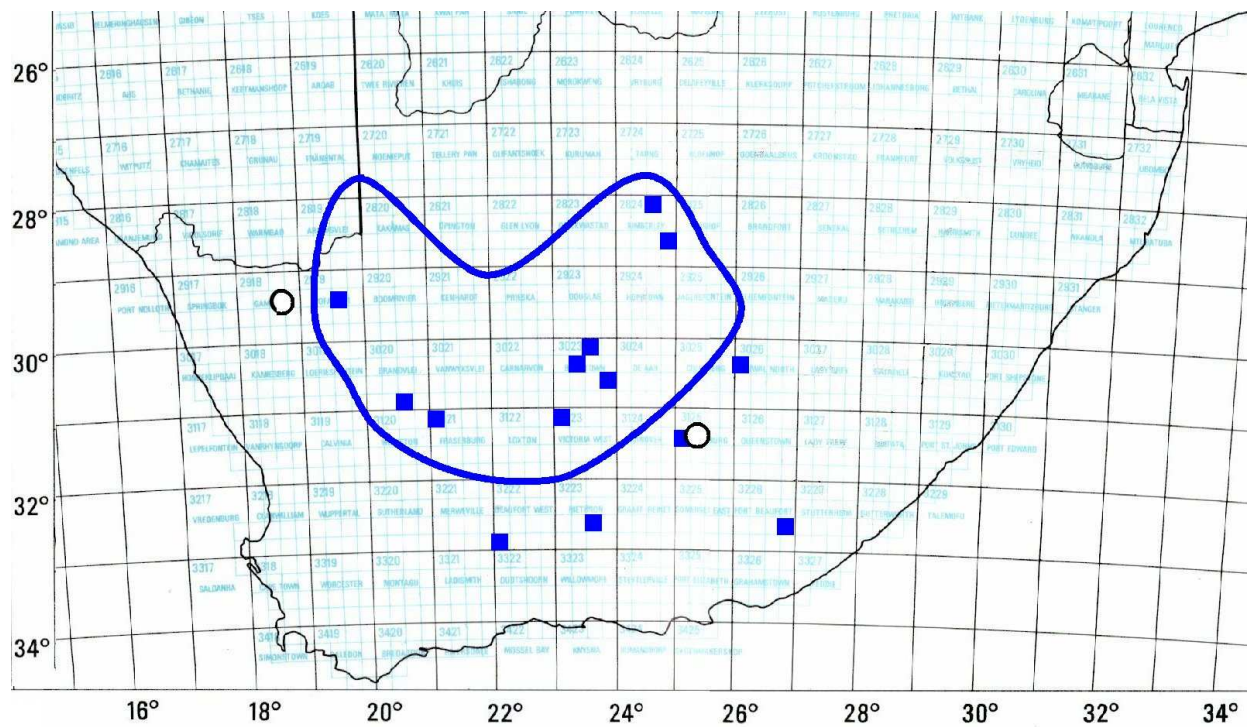


Figure 5.3.4: Distribution map for *G. jurineifolia* subsp. *jurineifolia*. Solid outline indicates Roessler's distribution, solid squares indicate PRECIS localities, and hollow circles indicate samples collected for this study.

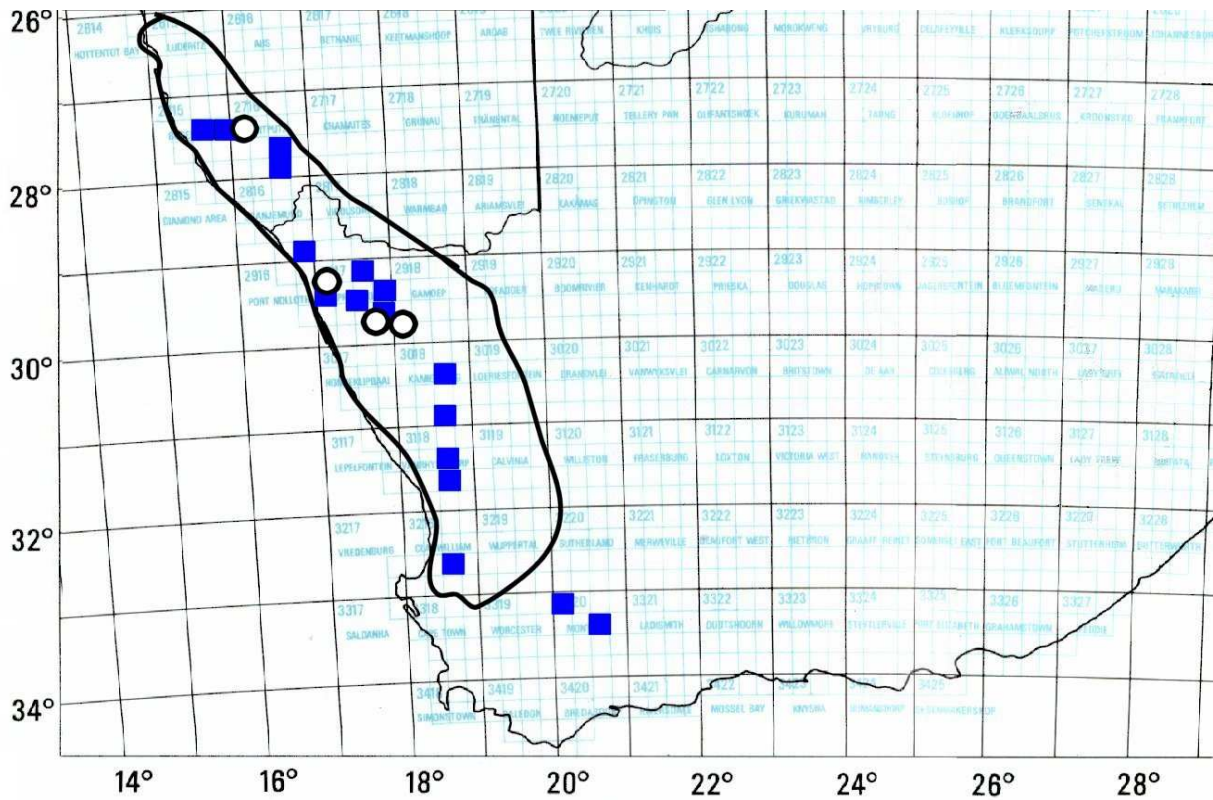


Figure 5.3.5: Distribution map for *G. tenuifolia*. Solid outline indicates Roessler's distribution, solid squares indicate PRECIS localities, and hollow circles indicate samples collected for this study.

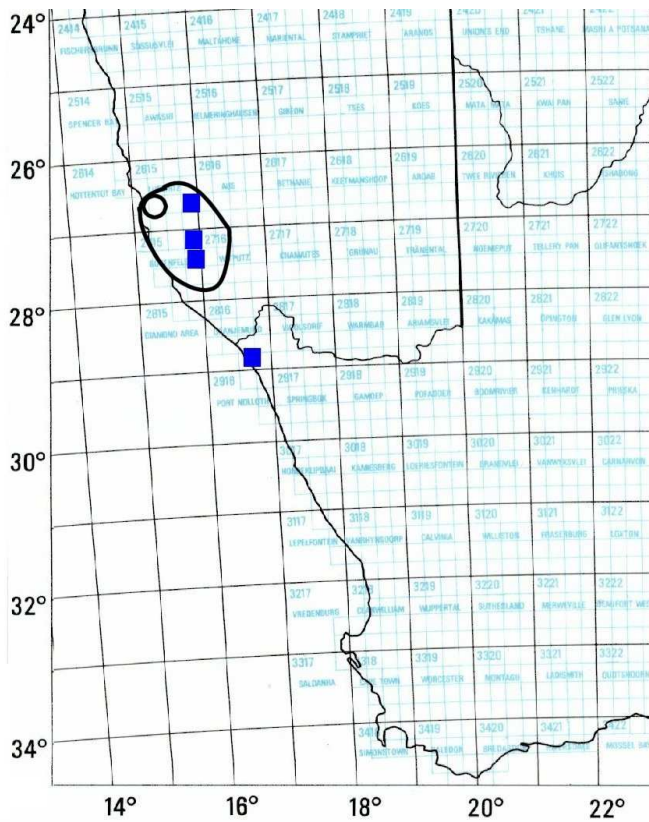


Figure 5.3.6: Distribution map for *G. schenckii*. Solid outline indicates Roessler's distribution, solid squares indicate PRECIS localities, and hollow circles indicate samples collected for this study.

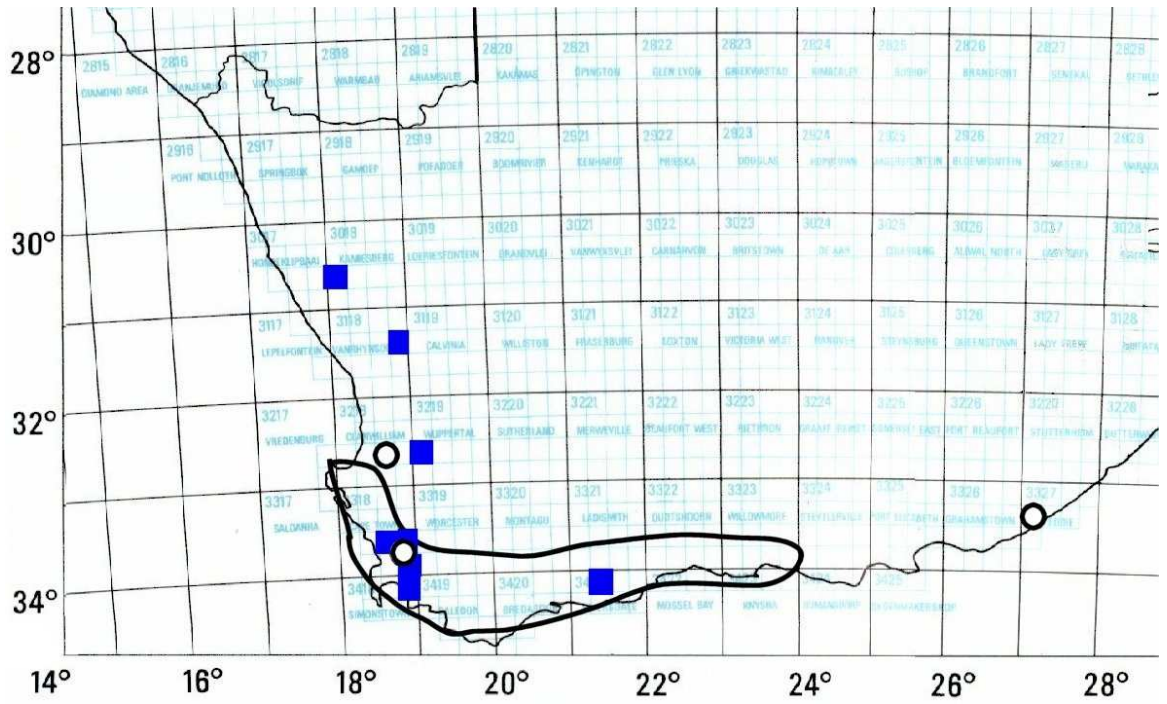


Figure 5.3.7: Distribution map for *G. ciliaris*. Solid outline indicates Roessler’s distribution, solid squares indicate PRECIS localities, and hollow circles indicate samples collected for this study.

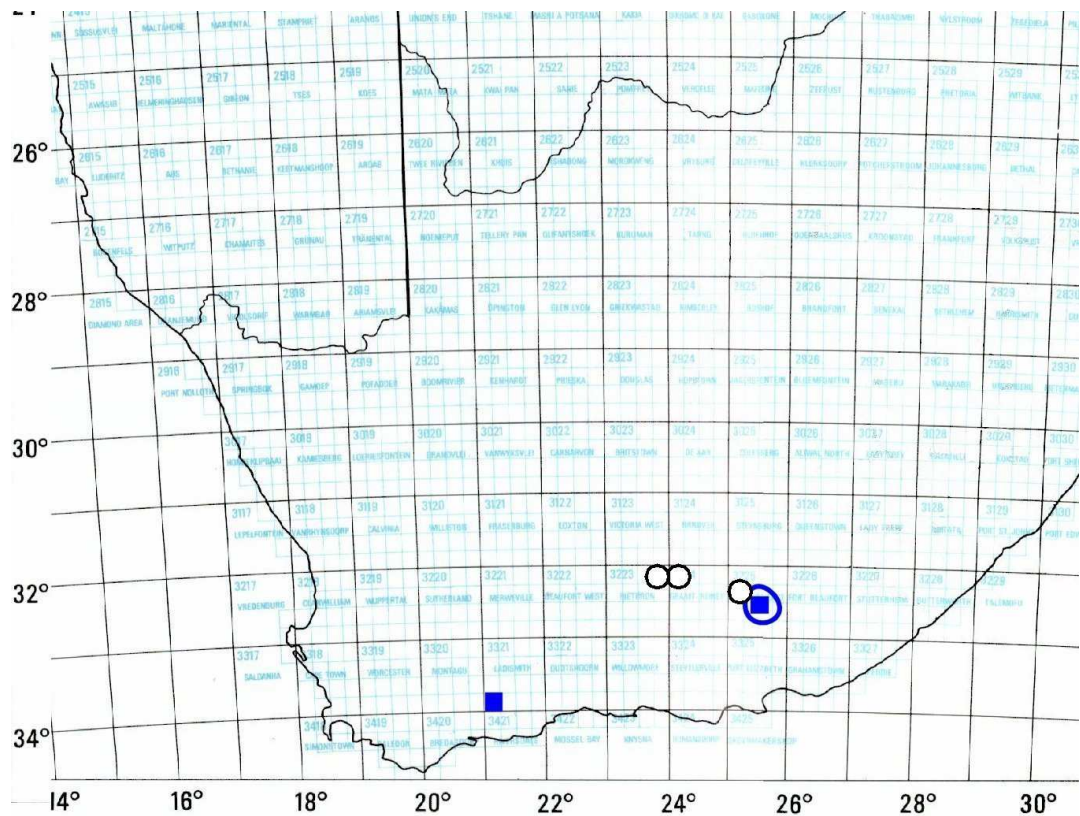


Figure 5.3.8: Distribution map for *G. caespitosa*. Solid outline indicates Roessler’s distribution, solid squares indicate PRECIS localities, and hollow circles indicate samples collected for this study.

Figure 5.3.9 illustrates the distributions for each major branch in the phylogeny of Chapter 3. *G. jurineifolia* (including both subspecies) has a distribution that extends from southern Namibia into northern central South Africa (Figure 5.3.9-A). Figure 5.3.9-B overlays the newly expanded species distributions for *G. lichtensteinii*, *G. schenckii*, *G. tenuifolia* and *G. heterochaeta* onto the same map. These species all group together with high support in the phylogenies of Chapter 3 (Figures 3.3.2 and 3.3.6), and are also sister to the K-R clade. Although these five genetically discrete species do not show any major geographical disjunctions, they nevertheless maintain their genetic separation.

The central area of overlap of these five species distributions is southern Namibia. This centre of diversity points to a possible refugial area, out of which *Gazania* radiated in the form of the K-R clade.

There is, however, a sharp disjunction with the high altitude mountainous *G. caespitosa* distribution, and a lesser disjunction with the south cape *G. ciliaris* distribution (Figure 5.3.9-A). Both these species occur together on the same branch, and share a unique 327 bp deletion in their *psbA-trnH* spacer. This suggests either dispersal to the mountain regions or a vicariance event.

K-R clade

Figure 5.3.9-C illustrates the distribution of the K-R clade as a whole, spread across much of South Africa, and showing no real pattern. When the clade is broken down into evolutionary lineages (Figures 5.3.10 and 5.3.11) (rather than “species” groupings) some patterns becomes apparent. Figure 5.3.10 overlays the widely distributed lineages that showed no clear geographic signal. Figure 5.3.11 overlays the geographical distributions for evolutionary lineages in the K-R clade that show some geographical localization, along with a summarised phylogeny of the K-R clade.

The most basal branch of the K-R clade (Branch 1) is strongly localised to the Namaqualand centre of endemism. The other basal branches (2, 3 and 4) are centred in the south western cape. The rest of the polychotomous branches either centre along the east coast or show generalised distributions that range across South Africa.

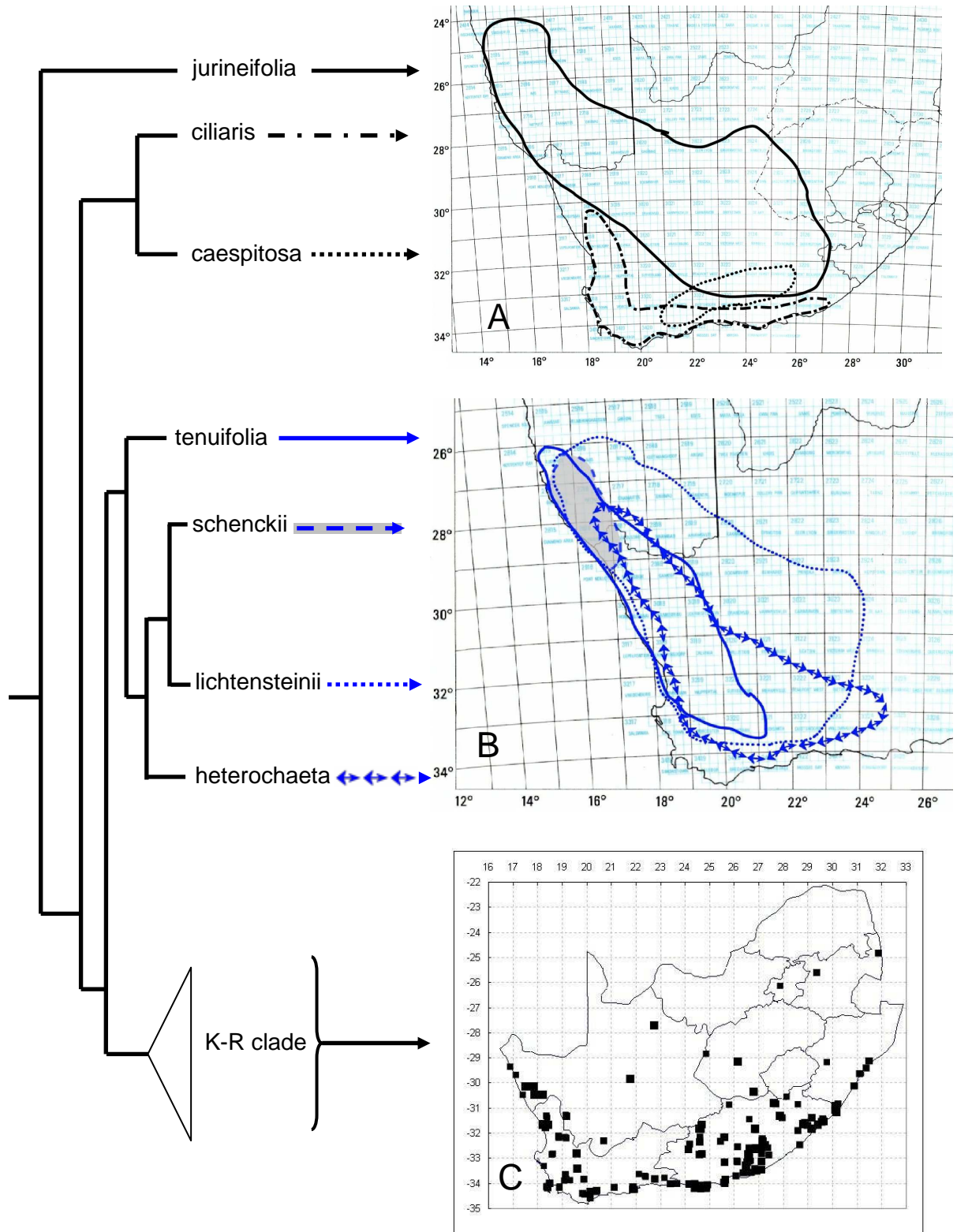


Figure 5.3.9: Summary tree of major branches in *Gazania* species-level phylogeny in conjunction with distributional overlays for each of the major branches in the phylogeny. Arrow line pattern indicates respective outline on accompanying map (*G. schenckii* is additionally shaded in grey in B to highlight distribution area).

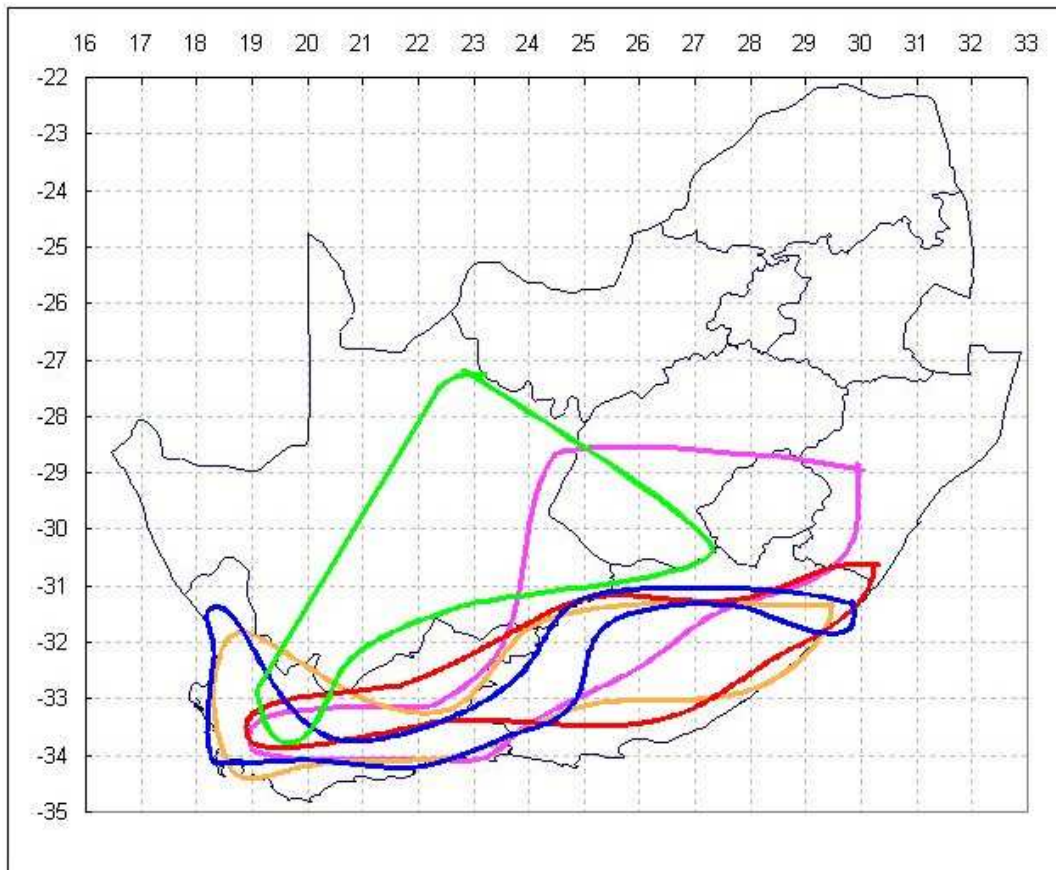


Figure 5.3.10: Overlays of distributions for geographically widespread clades in the K-R clade (outlines based on distributions mapped in Chapter 4 for branches 5, 6, 9, 11 and 12).

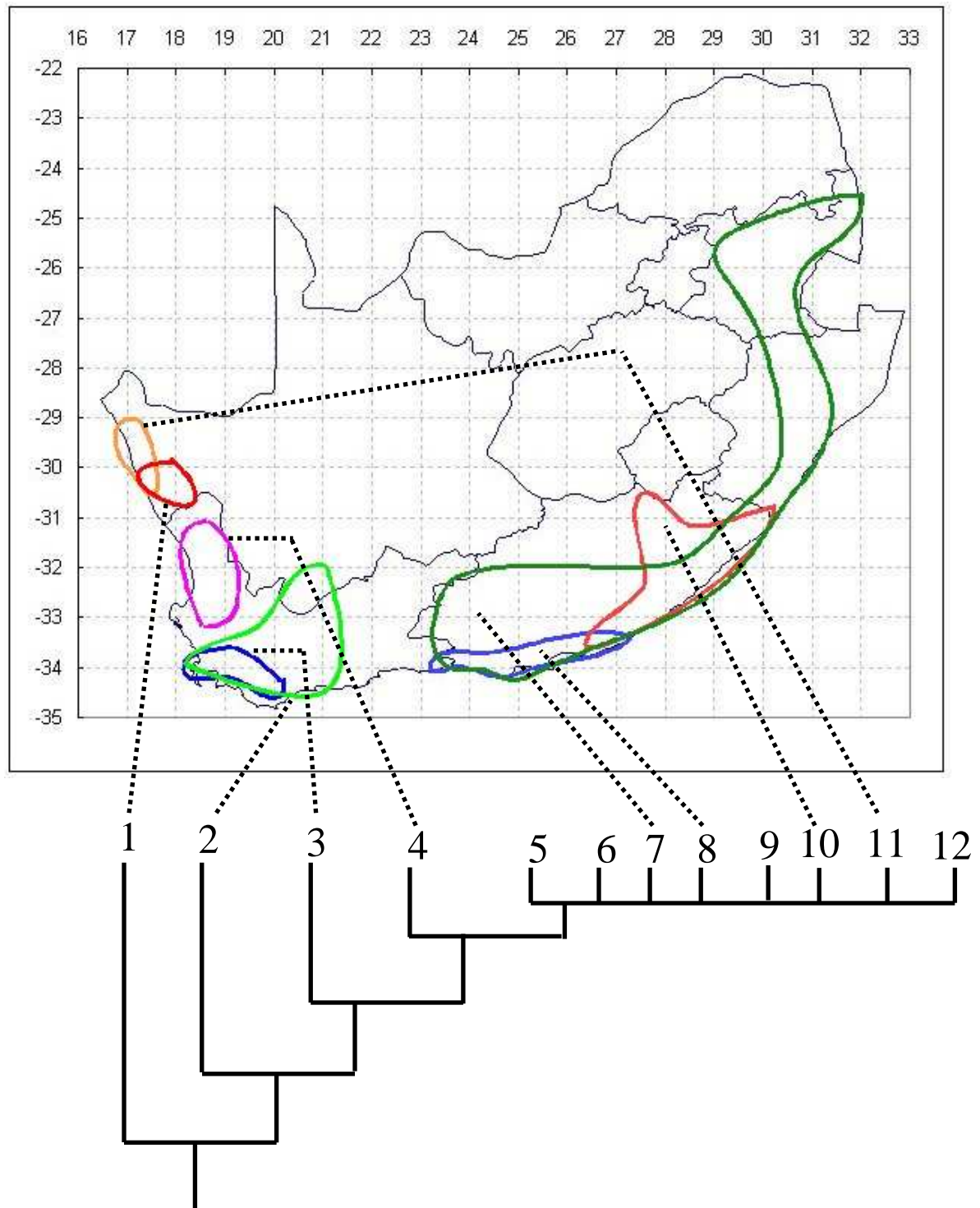


Figure 5.3.11: Overlays of distributions for geographically limited clades in the K-R clade (outlines based on distributions mapped in Chapter 4 for branches 1, 2, 3, 4, 7, 8, 10 and *G. othonnites*/sp. nov. clade), correlated with summary of branch positions in the K-R clade phylogeny.

Divergence date estimates

There are a number of important caveats and limitations to using mutation rates to estimate divergence dates, including substitution rate heterogeneity among lineages (which the LRT tests), uncertainties regarding clock calibration, and unknown but presumable large estimation errors

(Seelanan *et al.*, 1997). The molecular clock hypothesis was rejected by the Likelihood Ratio Test (2285.0211 vs 2250.2555, $p < 0.0084$). Therefore, any attempts at calculating dates from ITS mutation rates can only be regarded as estimates.

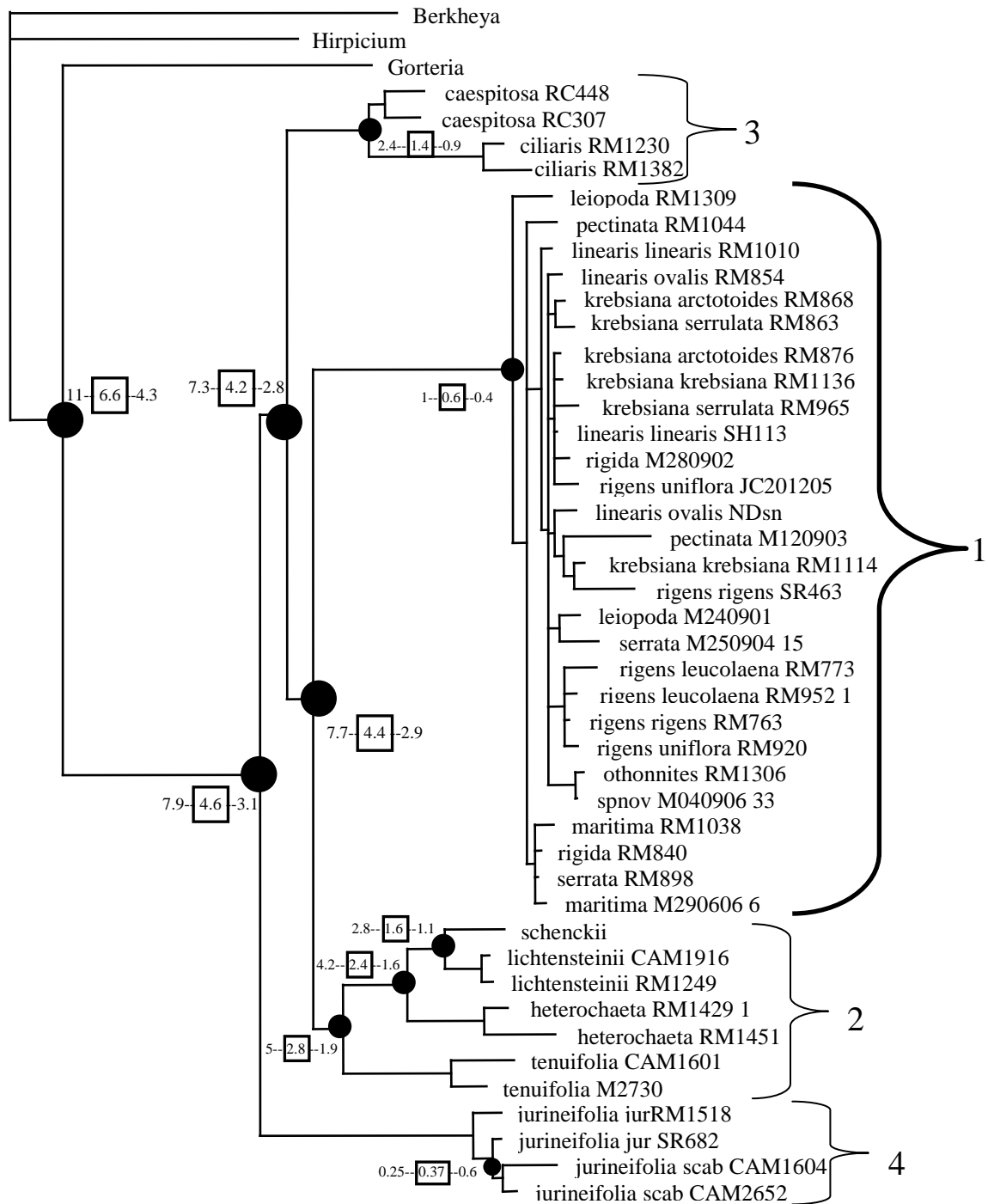
The date estimates for the lognormal relaxed clock model were the closest to the results of the manual calculations, with seven out of nine dates in close agreement (the dates estimated for the lognormal clock fell within the margin of standard deviation for seven of the results of the manual calculations). The exponential relaxed clock model dates were mostly in conflict with those calculated manually and using the lognormal relaxed clock model. For the purposes of further discussion below, the manual calculation dates are utilised.

Figure 5.3.12 is a replication of the totalDNA Bayesian tree from Chapter 3 (Figure 3.3.7), with the four major clades numbered for ease of reference in the following paragraphs. The average pairwise distances between and within sister clades are given in Table 4.3.1. The estimated time since divergence between each pair of lineages are also given in this table, with a possible lower and upper extreme. These estimates must, by necessity, be tentative at best, as comparative ITS mutation rates are not necessarily constant across the family or genus. Accurately estimating dates of divergence from molecular data is a challenging process (Arbogast & Slowsinski, 1998). It should be noted that a phylogeny based on ITS sequences only has a slight change in branching order (Clade 1 is sister to Clade 3, rather than to Clade 2) as compared to the branching order of the total DNA phylogeny. In addition, the divergence of populations from the ancestral population is necessarily defined by the cessation of gene flow, but whether this cessation coincides with particular geological events or occurs some time after such events is usually not known (Edwards & Beerli, 2000). None the less, these dates give a rough estimate to focus an investigation into the past factors that may have led to the current phylogeny of *Gazania*.

Gazania is estimated to have diverged from *Gorteria* and *Hirpicium* anywhere from 4.3 to 11.4 Mya, with an average estimate of 6.6 (± 0.5) Mya. The next divergence dates are 4.6 (± 0.5) Mya as an average estimate for the divergence of *G. jurineifolia*, and 4.4 (± 1) Mya as an average estimate for the divergence of Clades 1, 2 and 3. The average date for all three of these splits range around the start of a period of great climatic change that took place over the last several million years in southern Africa (and the rest of the world). The Miocene period extended from 50 Mya to the start of the Pliocene period at 5 Mya. This Miocene-Pliocene border correlates with the major estimated divergences of *Gazania* as a genus (6.6 Mya) and also of major lineages within *Gazania* (4.6 and 4.4 Mya).

Table 4.3.1: Divergence time estimates for each major split, including average, slowest and fastest rate of divergence for manual calculations, and comparative results for exponential and lognormal relaxed clock estimates from BEAST calculations.

Taxa splits	Clade splits	Manual calculations				Beast timing (Mya)	
		Average pairwise distance	Estimated average time of divergence	Estimate time of divergence at slowest rate	Estimate time of divergence at fastest rate	Relaxed clock (Exp)	Relaxed clock (Log)
<i>jur. scabra</i> - <i>jur. jurineifolia</i>	within 4	0.001928903	0.37 (± 0.4) Mya	0.6 Mya	0.25 Mya	0.99 (± 0.028)	0.7 (± 0.008)
divergence within K-R clade	within 1	0.002849533	0.6 (± 0.4) Mya	1 Mya	0.4 Mya		
	split of 1 + 2	0.023085066	4.4 (± 0.5) Mya	7.7 Mya	2.9 Mya	4.8 (± 0.05)	4.5 (± 0.02)
KR-clade - <i>ciliaris</i>	split of 1 + 3	0.021972915	4.2 (± 0.6) Mya	7.3 Mya	2.8 Mya	4.7 (± 0.05)	4.3 (± 0.02)
<i>tenuifolia</i> - (<i>lichensteinii</i> / <i>schlenckii</i> / <i>heterochaeta</i>)	Within 2	0.015022028	2.8 (± 0.6) Mya	5 Mya	1.9 Mya	3.7 (± 0.02)	3.0 (± 0.01)
<i>heterochaeta</i> - (<i>schlenckii</i> / <i>lichensteinii</i>)	Within 2	0.012662289	2.4 (± 0.5) Mya	4.2 Mya	1.6 Mya	2.9 (± 0.02)	2.0 (± 0.01)
<i>lichensteinii</i> - <i>schlenckii</i>	Within 2	0.008297585	1.6 (± 0.1) Mya	2.8 Mya	1.1 Mya	2.2 (± 0.01)	1.5 (± 0.007)
<i>ciliaris</i> - <i>caespitosa</i>	Within 3	0.007213994	1.4 (± 0.1) Mya	2.4 Mya	0.9 Mya	2.4 (± 0.04)	1.5 (± 0.01)
	(1+2+3) from 4	0.023954036	4.6 (± 0.5) Mya	7.9 Mya	3.1 Mya	5.1 (± 0.04)	5.1 (± 0.02)
<i>Gazania</i> - (<i>Gorteria</i> / <i>Hirpicium</i>)		0.034180443	6.6 (± 0.5) Mya	11.4 Mya	4.3 Mya	15.5 (± 0.1)	8.0 (± 0.02)



0.1
 Figure 5.3.12: Total DNA Bayesian consensus tree from Figure 3.3.7, numbered brackets indicate major clades for reference in divergence dating table. Numbers next to black circles and ellipses indicate proximate dates of divergence (maximum - average - minimum) in millions of years.

The Pliocene began at the peak in global cooling which occurred at approximately 5 Mya, in response to a pulse in Antarctic ice growth (Schnitker, 1980; Lindsay, 1998). Pickford (2004) notes that the early onset of arid biotopes in the Namib arose well before they occurred anywhere else in Africa, and this started a long period of adaptation to semi-arid conditions. The isolation of the Namib promoted a high degree of isolation of the Namibian gene pool, and once having adapted to conditions in the Namib arid areas, these lineages were pre-adapted to spread into neighbouring areas as they, in turn, became arid during climate change cycles (Pickford, 2004). The peak in global cooling at 5 Mya, and a consequential change in rainfall patterns, could have paved the way for the diversification of *Gazania* in Namibia and/or Namaqualand, and subsequent southerly and easterly spread out of this region.

Apart from the peak in cooling at 5 Mya, there were further cold peaks evident between 4.2 and 3.2 Mya, when Arctic ice sheets began to develop (Kennett, 1982; Lindsay, 1998). During glacial periods a substantial lowering in temperature, the influx of polar air and a change to winter rainfall caused major shifts in vegetation (van Zinderen Bakker, 1978). The first of these peaks coincides with the divergence estimates for the Clade 3 from Clade 1 at around 4.2 Mya.

The next divergence date at 2.8 (± 0.6) Mya is for the divergence of the *G. tenuifolia* from the three other species in Clade 2. There is evidence from faunal diversity studies that suggest that there was the first of three peaks of aridity and faunal speciation at 2.9-2.4 Mya concurrent with key junctures in hominid evolution (deMenocal, 2004). This shift in aridity at 2.8 Mya is the result of remote forcing by cold North Atlantic sea-surface temperatures associated with the onset of Northern Hemisphere glacial cycles (deMenocal, 1995). This date also coincides with a pulse of change in species composition in African fauna (with the emergence of more arid-adapted species) and a key juncture in hominid evolution (the first occurrence of *Paranthropus*) around 2.8 Mya (deMenocal, 2004).

Relatively close to this date is the estimate of 2.4 (± 0.5) Mya for the divergence of the *G. heterochaeta* from *G. lichtensteinii* and *G. schenckii*. There have been multiple instances of geographic uplift of the southern African continent, including a period of geographic uplift in the Miocene, ranging from 300 m on the east coast, to 150 m on the inland of the west coast (Partridge & Maud, 1987; Lindsay, 1998). There was a second, far greater geographic uplift at about 2.5 Mya, where the South-East region elevation increased by 600 – 900 m, the south rose by 200 m and the west by 100 m, which corresponded with a decline in temperatures in these newly elevated regions (Partridge & Maud, 1987; Lindsay, 1998).

Both sediment evidence and faunal species compositions point to wetter conditions in the mid-Pliocene (3.5 Mya) followed by increasingly episodic rainfall and drier conditions after 2.5 Mya when cooler conditions prevailed (Butzer, 1984; Vrba & Denton, 1995; Lindesay, 1998). This change from wet to dry conditions in the interior near 2.5 Mya has been considered to be of “remarkable magnitude” (Partridge & Maud, 1987; Lindesay, 1998). All of these dates of significant climate change towards a drier climate correlate with the estimated dates of divergence of several clades in the *Gazania* phylogeny, suggesting that the changes in conditions lead to the rapid divergence and emergence of new entities within *Gazania* (including the split of *G. heterochaeta* from *G. lichtensteinii* and *G. schenckii*, as well as the upper estimate for the divergence of *G. caespitosa* from *G. ciliaris*).

The remaining divergence events for genetically discrete species within clades 2 and 3 are at 1.6 (± 0.1) Mya, and 1.4 (± 0.1) Mya, both of which are in the Pleistocene. The divergence dated to 1.6 Mya also coincides with a second peak in climatic variability and increasing aridity that provoked faunal diversification (including a higher percentage of grazing animals) and also coincides with another juncture in hominid evolution (the extinction of *Homo habilis* and the first occurrence of *Homo erectus*) at around 1.8-1.6 Mya (deMenocal, 2004). The Pleistocene (which spans 1.8 Mya – 0.8 Mya) has been described as an important time for genetic diversification and speciation, based on the premise that climatic conditions in this period fostered the isolation of populations and, in some instances, allopatric speciation (Willis & Niklas, 2004).

The effects of Pleistocene climate change

During the last 2 Mya there have been periodic (or near periodic) alternations of glacial and interglacial conditions at approximately 100 000 year intervals, with each interglacial period lasted about 10 000 years (Jansson & Dynesius, 2002; Lindesay, 1998). These 100 000 year fluctuations are termed Milankovitch oscillations, which are caused by periodical changes in the orbit of the Earth, and are thought to contribute to large changes in the size and location of species' geographical distributions (Dynesius & Jansson, 2000).

The Pleistocene ice ages were environmentally distinctive and are presumed to have caused unusual patterns in organisms that many could consider are uncharacteristic of most of the Earth's history (Willis & Niklas, 2004). The repeated isolation and reexpansion of plants and animals in refugia (favorable locations with controlled microenvironments) during unfavourable conditions had important implications for evolutionary patterns (Willis & Niklas, 2004). An ideal refugium prevents extinction of genetic lineages and acts as a genetic reservoir by providing habitats for survival of plant populations during slow and abrupt climatic changes (Tribsch & Schönswetter, 2003). Besnard *et al.* (2002) note that during the Pleistocene ice ages, many species could survive only in favourable

refugia, and genetic patterns of differentiation among existing populations are often due to survival in different refugia, combined with genetic drift and founder effects during re-colonisation. Due to the periodic oscillations of the climate over the Pleistocene, resultant range contractions and expansions are believed to have played a central role in shaping the genetic and ecological diversity of many species (Excoffier, 2004).

Glacial cycles cause changes in distribution, and this can result in two different but typical genetic patterns emerging: a reduction in genetic diversity and/or genetic structuring on a regional basis (Ayoub & Riechert, 2004). This regional genetic structuring (ultimately leading to eventual monophyly) occurs when isolated populations in refugia arise during glacial maxima, and a reduction in genetic diversity is seen in populations that have expanded from glacial refugia into previously unoccupied areas (Ayoub & Riechert, 2004). Both of these phenomena are present in the K-R clade in *Gazania*: the K-R clade has a limited quantity of sequence diversity, and it also demonstrates regional genetic structuring in some lineages (i.e. the correlation between geographical locality and branches 1, 2, 3, 4, 6, 8, and 10 of the K-R phylogeny), most of which are confined to the south western cape.

Average speciation rate that can be calculated from the fossil record is roughly one new species every 10% of the average species lifetime (Niklas, 1997). Niklas (1997) calculates that if one assumes that the average generation time of an individual (from seed to sexual maturity) is about 5 years, a speciation event occurs roughly once in every 76000 generations, which is an ample number of sexual reproductive cycles for genetic divergence to have occurred in isolated plant populations during the Quaternary. There are herbaceous species where molecular and morphological evidence indicate genetic divergence leading to speciation in the last 100 kyrs (Willis & Niklas, 2004).

The divergence time for the various taxonomic entities sampled in the K-R clade can be estimated at 0.6 (± 0.4) Mya. This coincides with yet another pulse of change in species composition of certain African fauna at ± 0.7 Mya, suggesting widespread climatic change effects (deMenocal, 2004). The relatively large standard deviation in the dating estimate is due to the wide range of levels of divergence between samples in the unresolved branch. If one compares the distribution maps of the geographically limited evolutionary lineages in the unresolved K-R clade (Figure 5.3.13), one can see that only three lineages are endemic to the eastern cape, whereas six lineages are endemic to the western half of South Africa, and four of these six are confined to a southern area that corresponds with the Cape Floristic Region (CFR). These geographically limited clades could be evidence of refugia, out of which lineages have subsequently expanded and possibly hybridized to result in a mixture of characters (both morphological and genetic).

South Africa's CFR is very rich in plant species, most of which are the product of explosive speciation in the late Tertiary (Cowling & Lombard, 2002). The CFR has about 9000 species in an area of 90 000 km², of which 68.8% endemism at the species level (Linder & Hardy, 2004). The southern tip of Africa contains a number of plant lineages that are thought to have undergone recent and rapid speciation, and it could be argued that the whole flora might be the result of such a recent burst of speciation (Linder & Hardy, 2004). In southern Africa, there is an east–west gradient in the severity of the summer drought and for several groups, the greatest diversity, and apparently the most recent radiations, is situated in the more arid west; but there are no large recent radiations in the more mesic east (Linder, 2005).

Cowling & Lombard (2002) suggest that the disparity in taxa numbers between east and west (common to many lineages, and observed in the K-R clade lineages) is a consequence of higher speciation rates (promoted by enhanced opportunities for isolation of populations) and lower extinction rates (associated with more refugia) in the topographically complex montane regions of the west, which would explain the large number of rare species found there. Mountain areas in general are important refugial areas, as the high habitat diversity in mountain areas creates buffers, during not only alternations of cold and warm periods, but also of wetter and drier periods, which guarantees long-term ecological stability (Tribsh & Schönswetter, 2003). However, in the eastern mountains, differences in contemporary and historical climatic regimes reduced rates of speciation and elevated extinction rates, leading to lower steady state diversities, irrespective of landscape ruggedness (Cowling & Lombard, 2002).

Linder (2005), commenting on rapid radiations in the CFR, notes that for some lineages, the presence of a long basal branch in the phylogeny indicates that the group was present in the region for a longer period but that only one lineage from this period survives. This is likely to be the case for *Gazania* as well, with the long lineage of the K-R clade.

Population history

The graph of pairwise sequence divergence (Figure 5.3.13) shows that when the frequencies of all pairwise sequence divergences are plotted, there are two peaks. These can be correlated with two pulses of population expansion, the smaller shallower right peak correlating with an older expansion (the genetically discrete species) and the larger narrower left peak correlating with a much more recent expansion (the K-R clade). If the sequence divergence frequencies that make up the two peaks are plotted separately (Figures 5.3.14 and 5.3.15) then one can see that the K-R clade peak consists of only one peak with generally very low sequence divergence, while the genetically cohesive species peak consists of multiple peaks with a range of divergences (both low and high). A very recent

population expansion will result in a peak at the left side of the graph, comprising the comparisons among identical and highly similar sequences (Rogers & Harpending 1992), which is clearly seen for the K-R clade distribution in Figure 5.3.14. The fairly steep leading slope of the peak could also suggest an initially small founding population that lead to the K-R clade (Rogers & Harpending, 1992). The multimodal distribution for the genetically cohesive species clades seen in Figure 5.3.15 suggests long-term population stability resulting in substantial phylogenetic structure (Slatkin & Hudson, 1991).

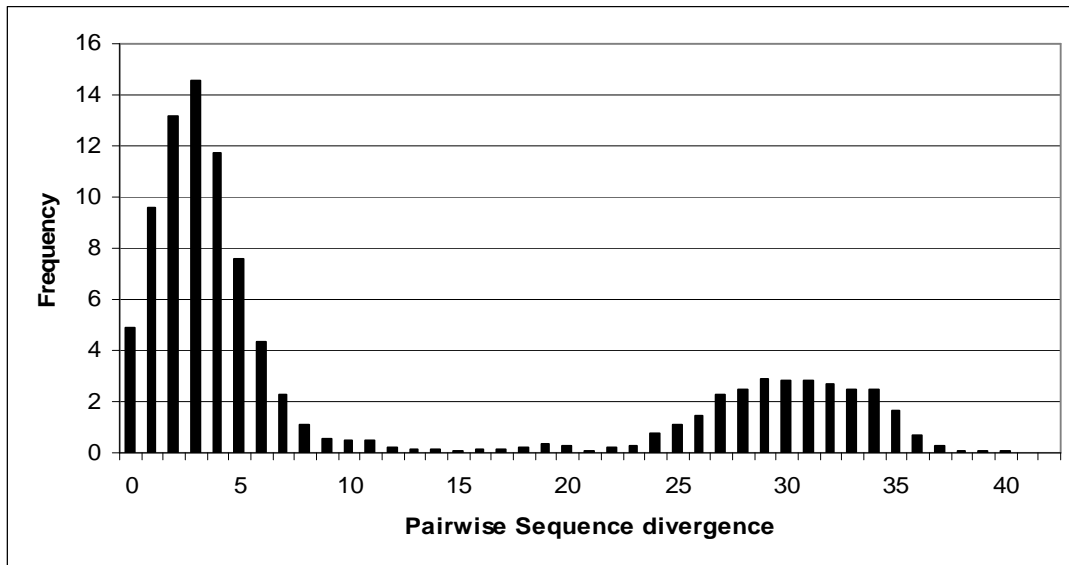


Figure 5.3.13: Frequency of pairwise sequence divergences for all samples.

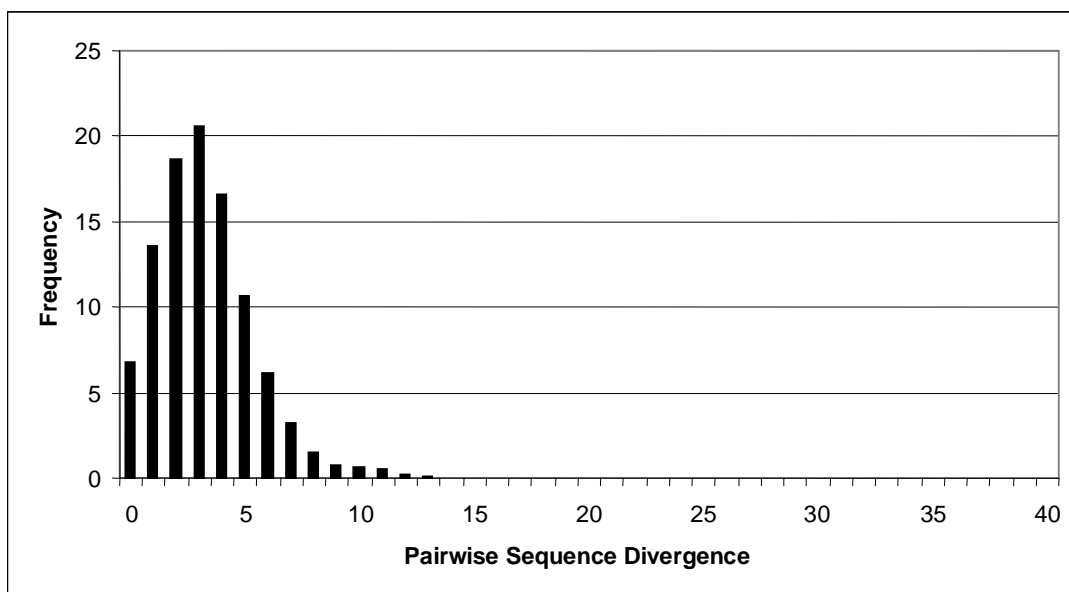


Figure 5.3.14: Frequency of pairwise sequence divergences for all samples from the K-R clade.

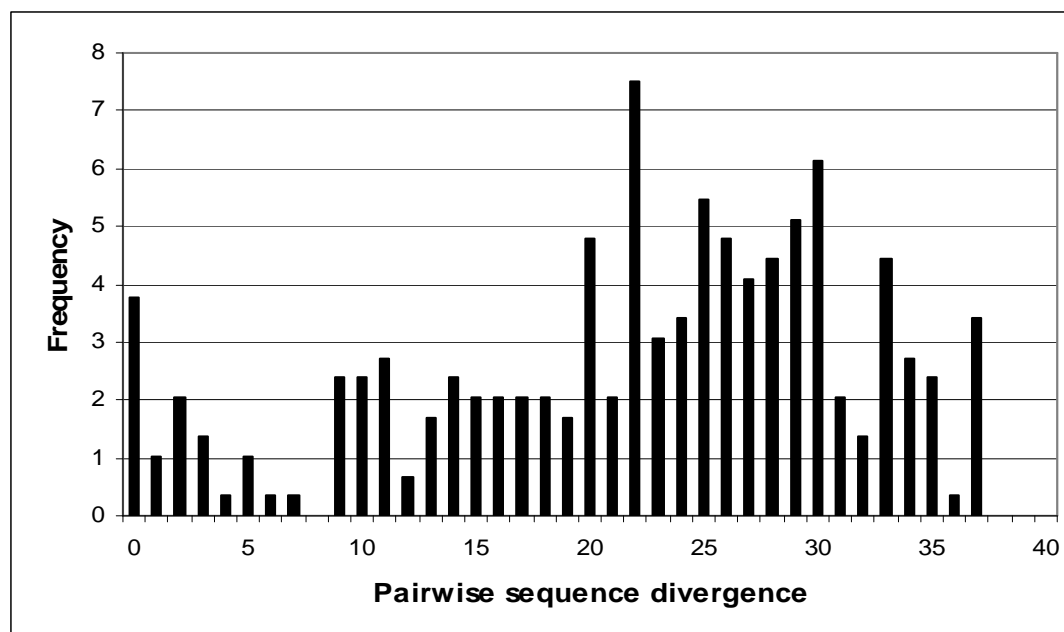


Figure 5.3.15: Frequency of pairwise sequence divergences for nrDNA data set for all samples from the six genetically cohesive species.

The Neighbor-Net analysis of the samples in the K-R branch has a starlike topology (Chapter 4, Figure 4.3.29), which is indicative of population expansion (Slatkin & Hudson, 1991). Mahoney (2004) observed a very similar pattern in *Plethodon*, noting that “in addition to poorly supported resolution among haplotypes, the similar length of the branches suggests descent from a single coalescent event at the base of the clade with subsequent divergence among lineages also proposed to correlate with rapid expansion”. The small short branches in Figure 4.3.29 that radiate out from the central area are most likely indicative of refugial evolutionary lineages from previous periods of climate change.

Congruent patterns in SA fauna/flora

Since the climatic changes that are hypothesised to have lead to the current phylogeographic patterns of *Gazania* taxa were of a large magnitude, it is reasonable to assume that other southern African endemic organisms (both plant and animal) may echo the geographical disjunctions and phylogenetic structure in *Gazania*. Unfortunately, there are relatively few such detailed phylogeographic studies of taxa in South Africa.

East-West split

Griffieon (1995), in an unpublished thesis on *Chrysanthemoides*, recognised 16 intraspecific taxonomic entities. Of these, 10 were found in the western half of South Africa (seven were confined to the south western cape, and three to the north-western and western cape, including one in the Namaqualand centre), while only five were confined to the eastern half of South Africa (three in the

south eastern and eastern half, and two in the north eastern half). A similar East-West split is found between distributions of varieties of *Cotyledon orbiculata* (Figure 5.3.16, Mort *et al.*, 2005)

Multiple papers have explored the regional plant diversity patterns in the Cape Floristic Region (e.g Cowling & Lombard, 2002; Linder & Hardy, 2004). Species-area analyses of the CFR by Cowling & Lombard (2002) have shown that the western winter-rainfall landscapes (east of “about 21°E”) have more than double the number of species than eastern nonseasonal-rainfall landscapes. Ritz *et al.* (2003) in a paper on Karoo *Euphorbia*, notice this same split, but consider the split between rainfall landscapes in South Africa to fall closer to 22.5°E, and attribute this split to western winter rainfall and eastern summer (rather than nonseasonal) rainfall landscapes. Regardless of the exact location of this rainfall zone of transition (Cowling & Lombard note that there is more likely a gradual transition over more than 100 km rather than a sharp disjunction anyway), there is a higher proportion of range-restricted, habitat-specialist species in the western floras, suggestive of a higher tempo of speciation in the west (Cowling & Lombard, 2002). *Gazania* clade distributions across the east/west divide appear to echo this pattern of speciation.

A similar pattern was found by Bakker *et al.* (2000), who investigated the phylogeny of *Pelargonium* species and found two major clades. One of these clades (comprising eight species, all of which were distinguished by small chromosomes) was confined to the south western cape, while the second clade (containing the remaining species with large chromosomes) was more widely spread across the Eastern Cape (and several other areas outside of South Africa). Bakker *et al.* (2000) credit the increase in the number of western cape clades as having been triggered by the late Pliocene aridification and the establishment of a winter rainfall climate in the Western Cape region.

Tolley *et al.* (2004) investigated the phylogeography of the southern African dwarf chameleons *Bradypodion*. They found two major clades, one of which was confined to the south western cape and southern cape, as well as a second larger more widespread clade that occurred mostly in the eastern half of South Africa (Figure 5.3.17). This second clade was a large well-supported clade with low sequence divergence, composed of several species, and they also found a strong correlation between the various clades in their phylogeny and the geographical origins of the samples in those clades. The authors suggest that repeated bouts of isolation and subsequent contact were responsible for promoting the phylogenetic diversity observed in these animals.

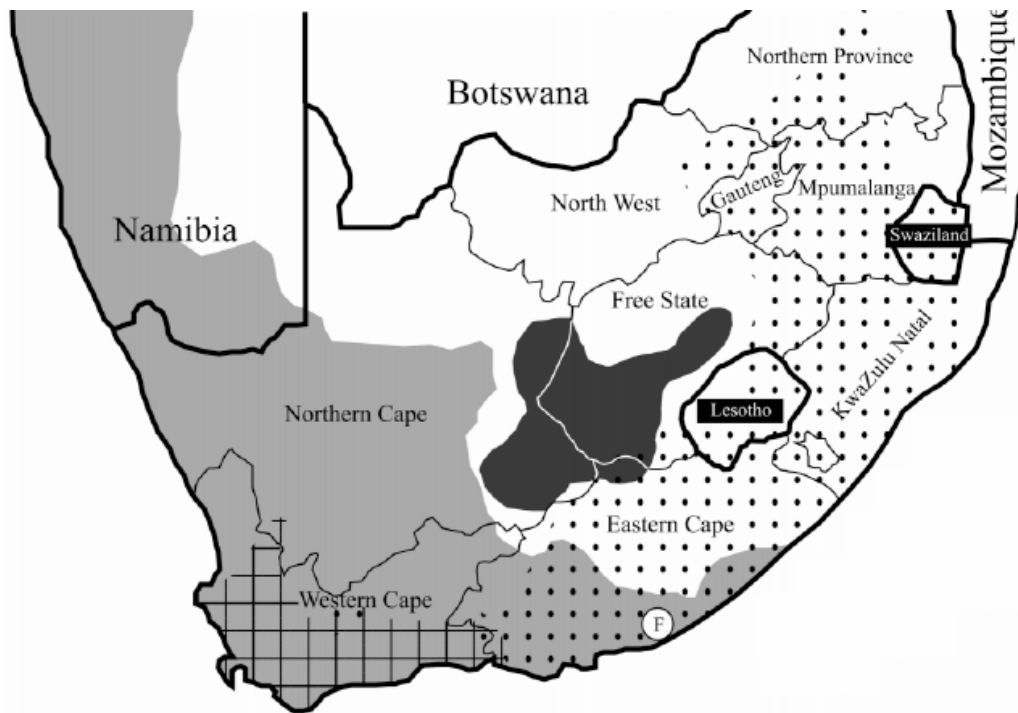


Figure 5.3.16: Distributions of five varieties of *Cotyledon orbiculata* (from Mort *et al.*, 2005: Figure 1).

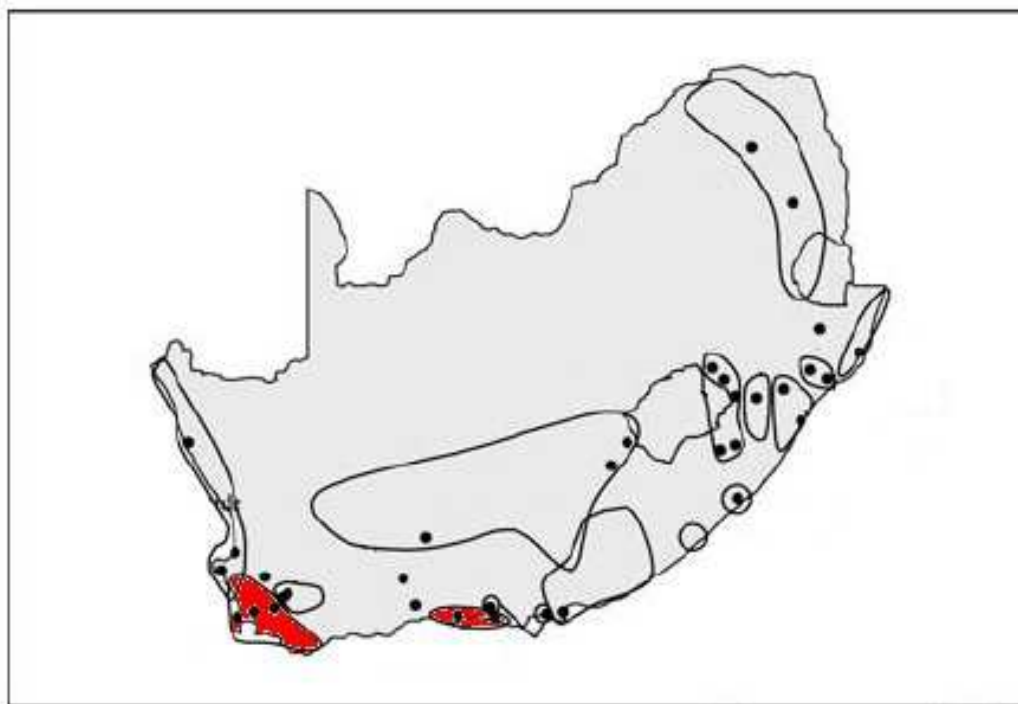


Figure 5.3.17: Distributions of two major *Bradypodium* genetic clades (from Tolley *et al.*, 2004). Areas in the south west shaded in red belong to one clade, all other unshaded areas belong to second clade.

North-South split

Matthee & Flemming (2002) investigated the population fragmentation in the rock agama (*Agama atra*) in southern Africa. They found three geographical disjunctions that correlated with three clades in their phylogeny (Figure 5.3.18). One of these clades occupies an area in southern Namibia that roughly correlates with the area that *G. schenckii* is restricted to, and *G. lichtensteinii*, *G. heterochaeta* and *G. jurineifolia* show distributional overlaps with. The other two clades are confined to South Africa, with a split between a northern central clade and a more southerly central clade that is spread countrywide. The geographical patterns observed in *A. atra* (congruent with the general patterns seen in *Gazania*) are attributed to vicariance caused by cyclical changes in temperature and rainfall over the last 3 million years (Matthee & Flemming, 2002).

A study of *Scarabaeus* dung beetles by Sole (2005) shows a similar three-part disjunction. The dung beetle phylogeny (Figure 5.3.19) shows three clades, the most basal being distributed in Namibia, and the other two derived sister clades being distributed in more southern areas. This pattern of disjunction between a north clade and a south clade is also seen (Figure 5.3.20) in the red rock rabbit (*Pronolagus rupestris*; Matthee & Robinson, 1996).

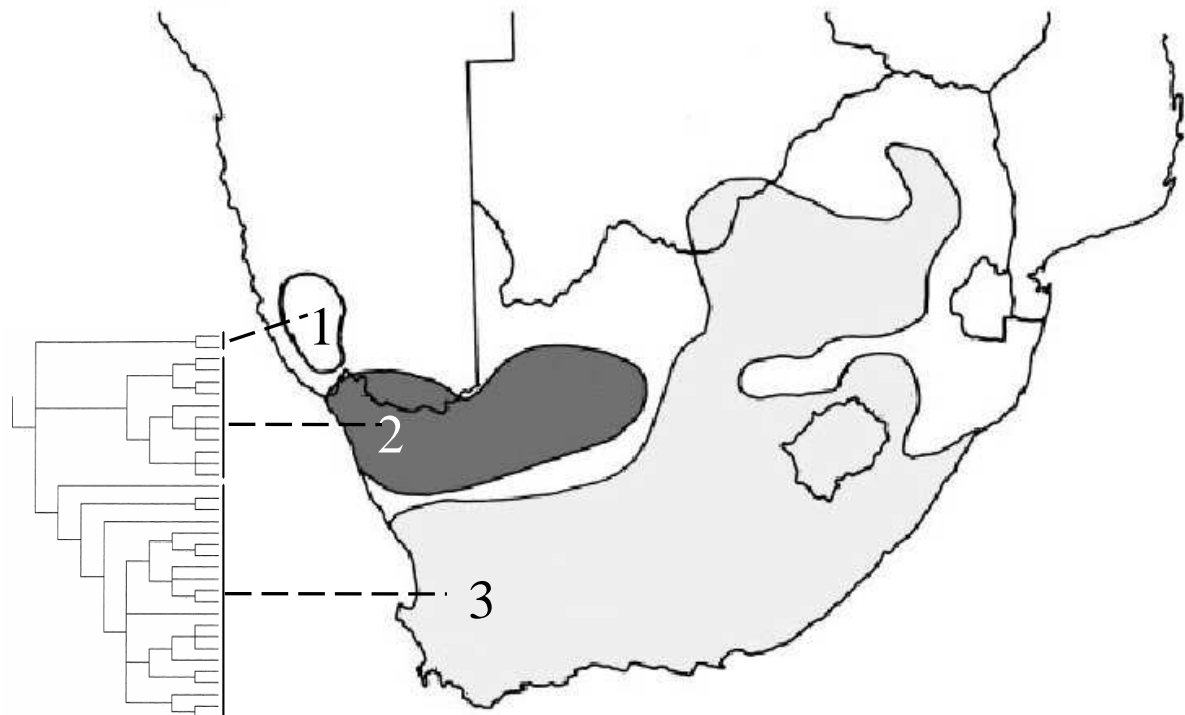


Figure 5.3.18 Distributions of three major *Agama atra* genetic clades (from Matthee & Flemming, 2002), 1- Namibian clade, 2 - northern central clade, 3 - eastern and central clade.

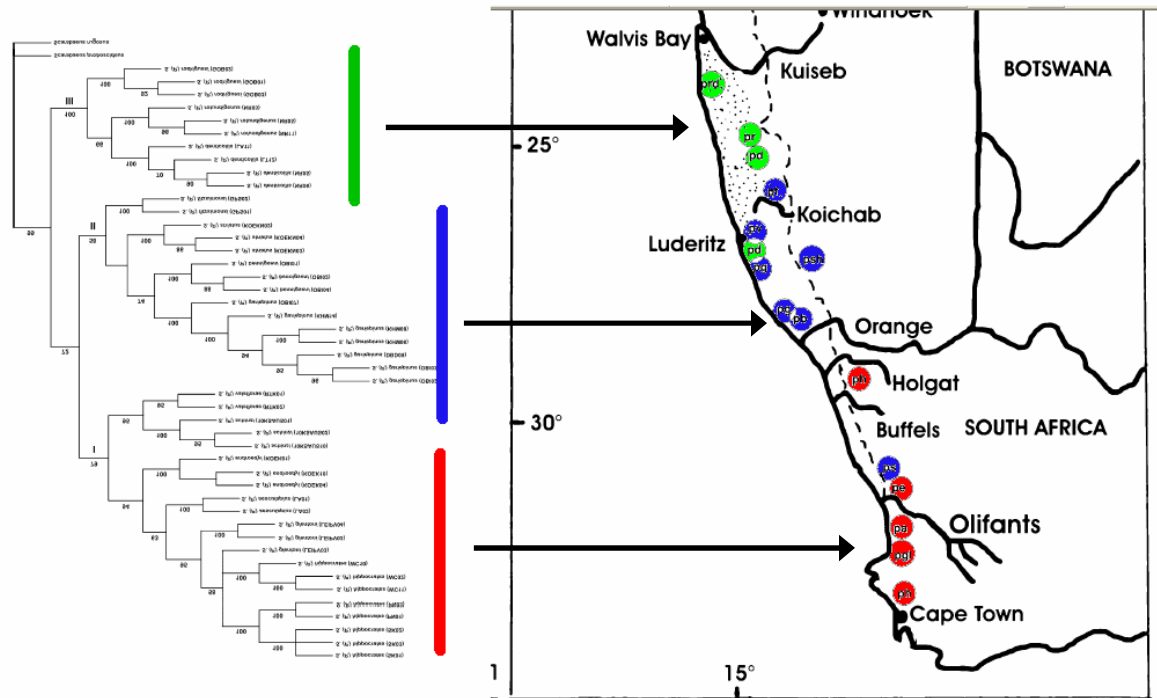


Figure 5.3.19: Distributions of three major *Scarabaeus* genetic clades (from Sole, 2005: Figure 1 and Figure 2).

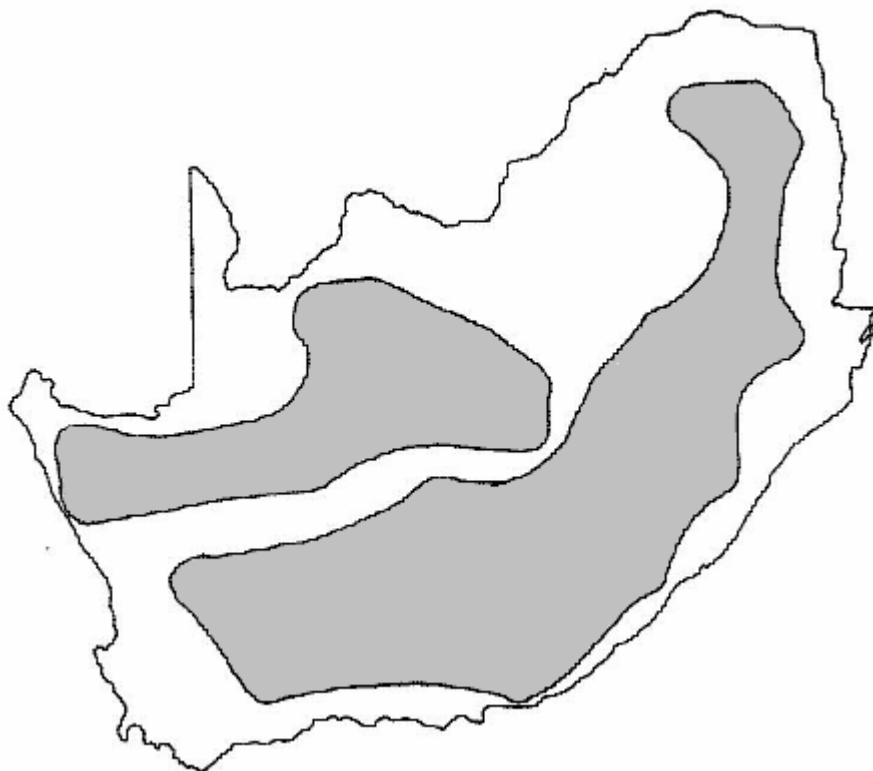


Figure 5.3.20: Distributions of two major *Pronolagus rupestris* genetic clades (from Mathee & Robinson, 1996).

Lamb & Bauer (2000) also found a similar pattern in *Pachydactylus* geckos. Here too is a north-south split between one basal taxon (located in Namibia) and the common ancestor for other more southerly located species. Like the other animal species mentioned above, the divergence between the two occurs around the Knersvlakte (Lamb & Bauer, 2000). Although the Namibian-centred *Gazania* species have spread out of their putative northern ancestral area (most likely due to their wind-dispersed seeds and ability to thrive on disturbed areas in poor soil), the historical split between the ancestors of the northern species and the ancestor of the more widely distributed eastern species remains detectable in the present day distributions of species.

Gazania is not unique in southern African plants, as these genetic disjunctions between Namibian and South African clades exist in other plant taxa. Touloumenidou *et al.* (2007) found geographic disjunctions between two sister clades of *Monsonia* (Geraniaceae), with one confined to Namibia and the other to South Africa. Jürgens (1997) summarised an overall similarity in North-South disjunction patterns that have been found in at least 15 plant taxa (Figure 5.3.21).

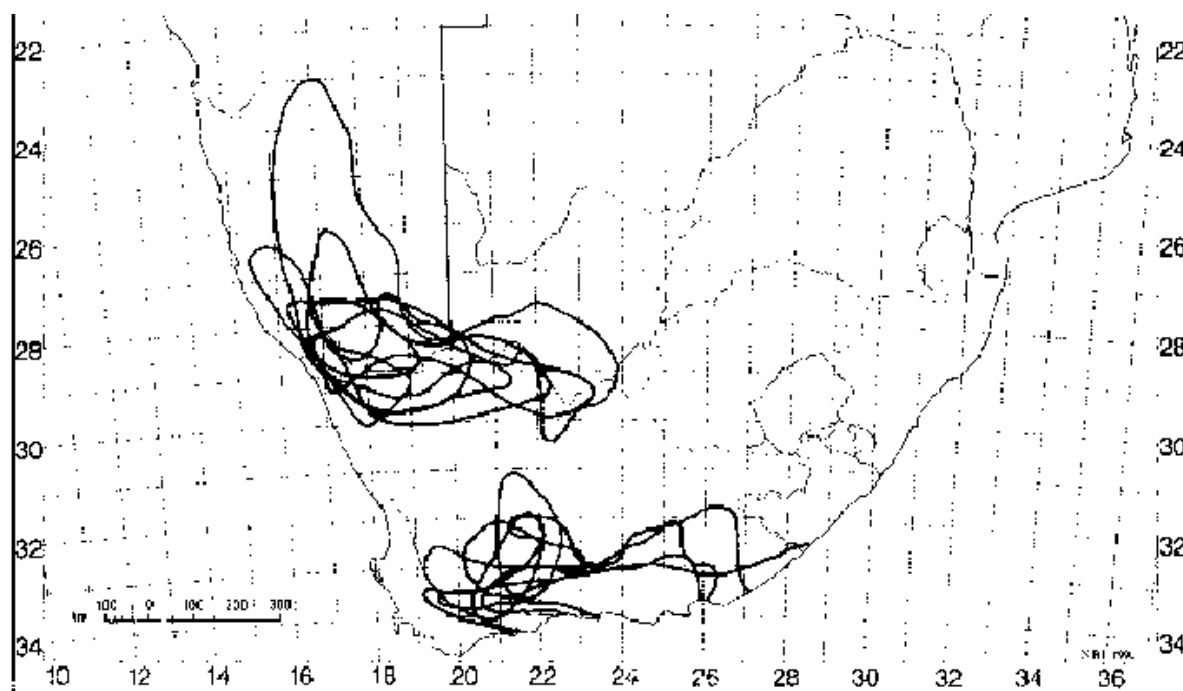


Figure 5.3.21: Summary of disjunct distributions of 15 plant taxa (from Jürgens, 1997: Figure 16).

Caveats

As mentioned in the previous chapters, some caution must be applied to these results. The choice of a bi-parentally inherited non-hierarchical nuclear marker for a phylogeographic study (in contrast to the usual choice of maternally inherited cpDNA markers) could invite some criticism as to the accuracy of the phylogeny used in this phylogeographic study. The effect that reticulation and paralogy could

have had on the phylogeny is not known, and is hard to quantify, without a comparative organellar phylogeny. The lack of sequence diversity found in the chloroplast markers used in Chapter 3 contraindicates the use of cpDNA spacer sequence data as a comparative measure of phylogeny retrieval. Further research could involve microsatellites or AFLP data as a means to test the nuclear phylogeny utilised in this study.

Conclusions

This phylogeographic investigation into *Gazania* suggests that there have been several instances of expansion and divergence within the genus. The older expansions and divergences have created the eight genetically cohesive taxa elucidated in Chapter 3. These species, even when occurring in sympatry, retain their genetic identity.

The most recent expansions and divergences in *Gazania* have led to the formation of a number of widely distributed morphotypes (each of which could be a result of isolation in refugia), which Roessler delimited and named as nine distinct species. However, the phylogeographic data collected here illustrates that there has been insufficient time since their divergence for species cohesion to have materialised, either through means of geographical or reproductive isolation. Reproductive isolation itself, between geographically isolated populations, evolves as an incidental outcome of genetic changes in the populations (Foster *et al.*, 1998) and insufficient time had elapsed within the isolation of refugia for enough of these incidental changes to either take place or become fixed across the population prior to re-expansion.

While some of Roessler's nine noncohesive species do show a certain amount of taxonomic cohesion and geographical localization (e.g. *G. rigens*, *G. leiopoda*), the fact that some individuals of these species may group with geographically co-occurring members of other species, rather than their more geographically distant conspecifics, suggests that their isolation or speciation is not yet complete. The identities of these troublesome samples (based on Roessler's key) have been rechecked and they are accurately identified according to Roessler's delimitations. The recent cycles of climate change that could have led to isolation and speciation within refugia, are just as responsible for subsequent geographical expansion out of these refugia.

The ability of an organism to survive climate change is dependant on several factors, most especially seed dispersal ability and ecological generalization (Dynesius & Jansson, 2000). For organisms to survive climate oscillation, they must have high enough seed dispersal ability to track their moving habitat, and a low enough level of ecological specialisation to not need to disperse rapidly to track their habitat and even to survive locally (Dynesius & Jansson, 2000). These factors would allow populations not only to survive climate change by moving with their shifting habitat, but also to

expand out of refugia when conditions altered. *Gazania*, with its generalist pollinators (pers. obsv.), wind dispersed seeds (pers. obsv.), ability to colonise disturbed areas, and short period between germination and seedset (under a year) possesses the characters necessary to shift with climate change and expand out of refugia.

This expansion could have lead to secondary contact between and melding of incipient species, breaking down species boundaries before they were completely formed. This would have resulted in the morass of types and varieties that now exist in the south-western cape, some of which Roessler named as species, despite their often dubious status. (Roessler himself was unsure about the status of *G. serrata* as a species, referring to it as “a not quite characteristic unit, that is at best regarded provisionally as a type” (Roessler, 1959: pp 400)). The possibility that pollinators may have played a part in the diversification in *Gazania* (especially within the CFR and Namaqualand) cannot be discounted, but this has not been investigated within the scope of this research project.

Apart from the south western cape refugia, a second potentially more recent refuge is centred along the southern coast. Evidence of the South Coast refugial lineage theory is found in the presence of two localised specializations of more widely distributed morphotypes: 1) The broad-leafed form *G. linearis* subsp *ovalis*, confined to a few small localities along the southern cape coast; and 2) the grey-leafed hirsute form *G. rigens* subsp *leucolaena*, also confined to the southern cape coast. Both of these morphotype ranges overlap with the area that the genetically cohesive clade of the *G. rigens* variety occupies. Figure 5.3.22 overlays all three distributions, pointing to a possible climatic refuge, out of which the current distributions have expanded. The lack of genetic cohesion for these distinct morphotypes suggests that the isolation and differentiation was very recent, and could point to a recent refugial area that fosters the diversification of endemic lineages.

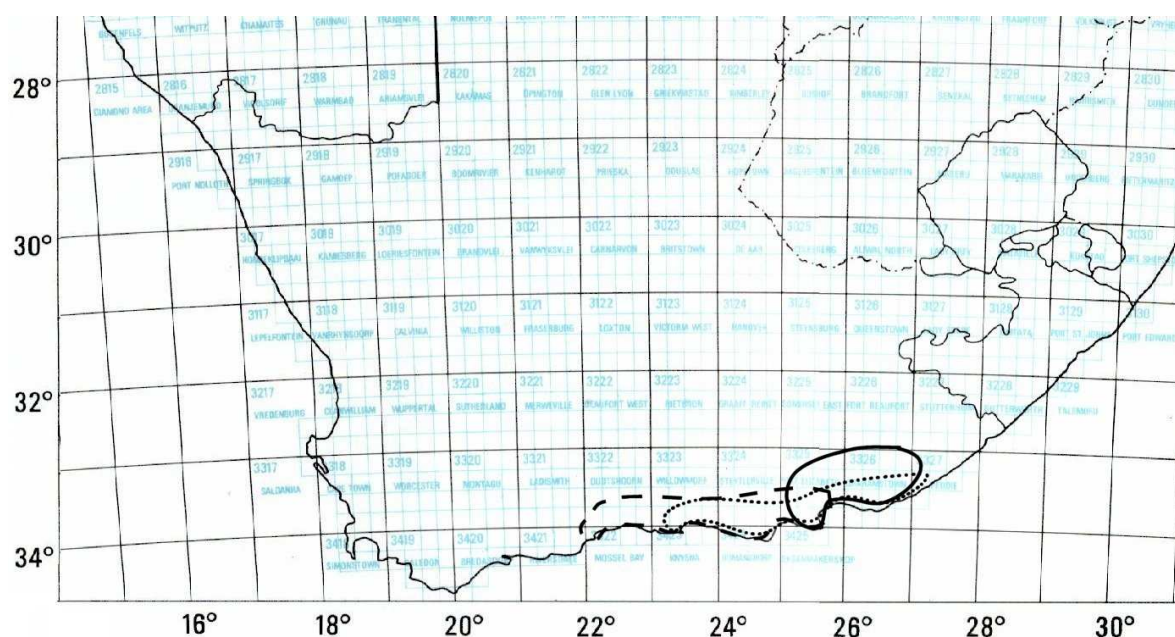


Figure 5.3.22: Distributions of two distinctive morphotypes and one genetically cohesive clade pointing to a possible Southern cape climatic refuge. Solid line = *G. linearis* subsp *ovalis*, dashed line = *G. rigens* subsp *leucolaena*, dotted line = genetically cohesive *G. rigens* clade in K-R clade.

Species

Just as there are multiple species concepts, so there are multiple ways to test species boundaries. Sites & Marshall (2003) list a number of these, both tree and non-tree based methods. Cladistic haplotype aggregation (CHA; Brower, 1999) is a tree based method that states that all members of a species form a contiguous section of an unrooted tree and are separated from all other populations by a branch along which character state change leading to a fixed character difference is inferred (Sites & Marshall, 2003). Under the CHA, genetic data defines eight species (*G. jurineifolia*, *G. tenuifolia*, *G. lichtensteinii*, *G. schenckii*, *G. caespitosa*, *G. ciliaris*, *G. heterochaeta* and the K-R clade). The exclusivity criterion (EXCL; Baum & Shaw, 1995) defines genealogical species by two criteria: species must be basal taxa (they must not themselves contain taxa), and unlinked genes should have concordant genealogical histories. Thus species are defined as exclusive groups; those in which all members are more closely related to each other than to any organism outside of the group (Sites & Marshall, 2003). The method requires the reconstruction of genealogies for unlinked loci collected from the same individuals, then a strict consensus of the trees is taken to define points of concordance (resolved nodes), and species are delimited by exclusive nodes (Sites & Marshall, 2003). This was accomplished in Chapter 3, and the same eight species are retrieved again.

What exist now in *Gazania* are seven distinct species, and an eighth entity, consisting of a collection of morphologically and geographically overlapping evolutionary lineages lacking any isolatory mechanisms. Three of these lineages could be genetically distinguished as named varieties, while the rest must be grouped under a fourth name. This fourth taxonomic entity is highly variable and

widespread, and while there are certain morphotypes or ecotypes present, these lack any genetic cohesion. These are probably the remnants of previously isolated refugial lineages that failed to achieve true disjunction from other similar entities during their periods of isolation. Subsequent post-refugial expansion has further sabotaged their chances of attaining recognisable status as species.

The Ochlopecies concept (White, 1998) describes a very variable (polymorphic) species with chaotic infraspecific variation (only partly correlated with ecology and geography) which is of such a complex pattern as to be intractable to formal taxonomic treatment (Cronk, 1998). Cronk (1998) lists 10 traits for the diagnosis of an ochlopecies (diagnosis as an ochlopecies requires only six), these include:

- 1) Non-hierarchical polymorphic variation;
- 2) Character-state distribution that is only partially correlated with geography and ecology;
- 3) Characters vary independently, and not in a correlated fashion;
- 4) Complexity of variation is not due to hybridization between currently recognisable species;
- 5) Geographically and ecologically widespread, occurring in several climatic zones;
- 6) At a particular locality two distinct and non-intergrading forms may be found, and other forms may be found at other localities, but taken together all the forms intergrade and the classification breaks down;
- 7) Have closely related, but morphologically distinct and monotypic satellite species;
- 8) Similar variants may occur in widely separate localities and appear to be polytypic in origin;
- 9) Often have long synonymies, the variation has driven a proliferation of names that eventually proves untenable.
- 10) They tend to occur in medium to large genera usually with more than 50 species.

The K-R clade of *Gazania* meets nine of those requirements (the tendency for ochlopecies to occur in large genera of 50 or more species does not fit *Gazania*, but seems a rather trivial character anyway).

One of the two proposed mechanisms that creates an ochlopecies is based on refugial isolation, re-expansion and subsequent hybridization after glacial-related climate change (the Prance hypothesis); the other proposed mechanism is based on the rapid population expansion of a colonising ecogeneralist, without any allopatric isolation stages (the rapid expansion hypothesis; Cronk, 1998). While *Gazania* is a colonising generalist (often found growing in disturbed areas in poor soil, and with wind dispersed seeds), the recent cycles of climate change in South Africa, and the concentration of localised genetic lineages in the western cape mountain areas, both suggest that the Prance hypothesis is more likely. Cronk (1998) considers the presence of clades that show more

geographical structuring of genetic haplotypes than morphotypes to be an indicator of the refugial hypothesis.

The situation in the K-R clade of *Gazania* is not that rare, with a number of recent phylogeographic studies having yielded data that are consistent with the hypothesis that many plant species may have fractured into isolated, independently evolving populations that then came back into contact during interglacial periods (Comes and Kadereit, 1998; Noyes, 2006.). The principal effects of global climate change may thus have been to increase genetic variance within plant species, with population subdivision during recent climactic events contributing to genetic diversity, but not to speciation. (Noyes, 2006).

In conclusion, recent climate-driven radiation within *Gazania* has given rise to eight genetically distinct species, seven of which (*G. jurineifolia*, *G. heterochaeta*, *G. tenuifolia*, *G. caespitosa*, *G. ciliaris*, *G. lichtensteinii* and *G. schenckii*) are diagnosable by both the Morphological and the Phylogenetic species concepts. The eighth entity (following repeated cycles of refugial isolation and possible range expansion hybridization) is an ochlopecies that is clearly genetically distinct from the other seven species. It also possesses some lineages within it that show some partial genetic, morphological and geographical cohesion, but not sufficient to warrant full species status. The general conclusions from this investigation, each of the previous chapters and the proposed changes in status of species in *Gazania* are discussed in further detail in the final Chapter.

Chapter 6.

General conclusions

This study of the systematics of *Gazania*, its recent evolutionary history, and the identification of refugia in the arid inland of southern Africa is novel research, and is in a field of plant species-level phylogeographic research that seems rarely attempted by other researchers who focus on the systematics of South Africa endemic genera. Given the difficulty in defining taxonomic entities within this genus, the possible reluctance of other researchers to approach the subject is understandable.

Recent evolutionary history

The genus *Gazania* is yet another example of a South African endemic clade that has undergone rapid and recent cladogenesis (see Linder, 2003, for other examples). This rapid cladogenesis in *Gazania* is hypothesised to be in response to fluctuating climatic conditions over the last few million years.

There are several other possible reasons for the diversification of the many lineages that comprise the CFR flora; among them, Linder (2003) lists:

- 1) adaptation to fire, (*Gazania* does not appear to show any specialised adaptations to the frequent fires that burn the fynbos of the CFR);
- 2) edaphic specialization, (edaphic specialization cannot be ruled out, but it was not investigated in this study. It should be noted that *Gazania* is a wide-spread colonising generalist that grows easily in a variety of soil types, so soil specialization may not be an important factor);
- 3) microhabitats in the mountainous regions, (*Gazania* may have diversified within the microhabitats of the mountainous regions of the CFR that could have acted as refugia in the past, but it is not localised or limited to them now);
- 4) pollinator selection, (the pollination of *Gazania* was not investigated in this study, but *Gazania* seems to attract generalist pollinators. However, regional variations in UV reflectance patterns could reveal further information and is suggested as a future avenue of research);
- 5) flowering seasonality, (flowering time in *Gazania* is not narrowly limited to a short period of the year);

6) and climatic specialization driven by steep gradients, (this cannot be ruled out without further detailed investigation into climatic data for *Gazania*).

However, it should be noted that unlike many other endemic CFR genera that have undergone rapid cladogenesis, *Gazania* does not contain hundreds of distinct localized species. This is most likely due to a lack of specialization (ecological, morphological or pollinator) in *Gazania* in combination with wind-dispersed seeds and a tendency to easily colonise disturbed sites with poor soil, leading to a wide distribution.

The taxonomic confusion that plagues this genus is most likely a result of alternating cycles of climate driven refugial isolation and subsequent expansion and hybridization events. Roessler's reservations about the status and validity of some of the taxonomic entities within this genus are proven well-founded by the results of the morphometric, phylogenetic and phylogeographic study of hundreds of samples from across southern Africa.

Caveats

Prior to a full reorganization of the genus *Gazania*, further research involving other genetic markers should be undertaken. Use of low copy nuclear markers, chloroplast microsatellites and AFLP could provide more clarity on the confusing taxonomic situation within *Gazania*. A much greater morphological sampling, including type specimens, is necessary before any meaningful nomenclatural analysis can be undertaken. As such, the taxonomic suggestions that follow are best regarded as preliminary until further more detailed research can be undertaken.

Morphological characters and species phylogeny

Figure 6.1 is a summary phylogeny of the species within *Gazania*, with various autapomorphic and synapomorphic morphological characters mapped onto the branches. Most of the characters (e.g. habit, obovate leaves) appear in multiple places in the phylogeny. The morphological characters are homoplasious when interpreted in context of the phylogeny.

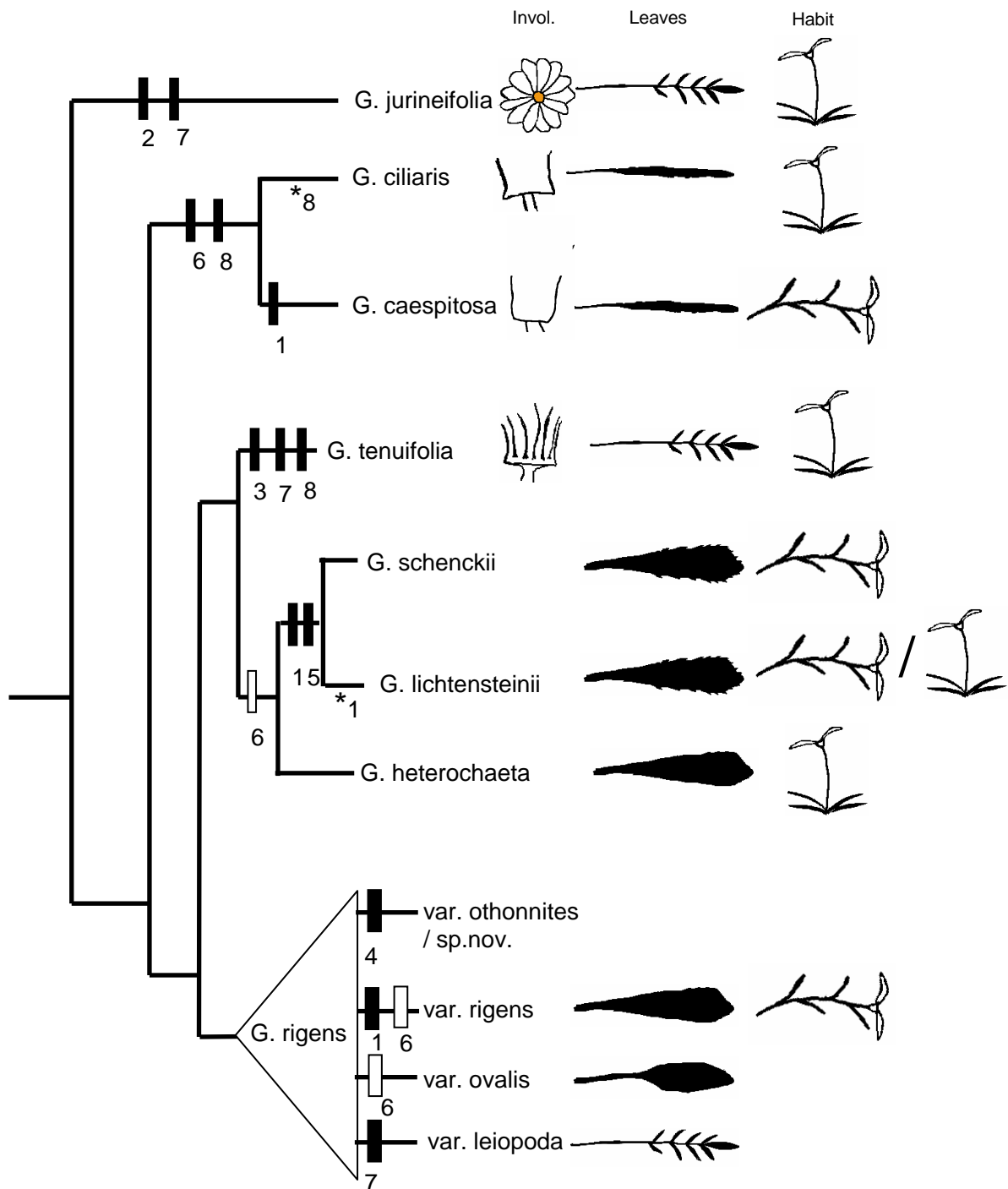


Figure 6.1: Summary DNA species phylogeny of *Gazania* with morphological character states mapped onto branches. 1 = Developed stem habit, 2 = White flowers, 3 = Multiple rows of involucre parietal scales, 4 = Mild succulence, 5 = Leaf margins dentate, 6: black bar = Linear leaf (< 4mm wide), 6: hollow bar = obovate leaf (>4 mm wide), 7 = All leaves dissected, 8 = involucre base truncate. Asterisks indicate partial presence of numbered character, i.e. some individuals may not show it.

Valid taxonomic entities with genetic and morphological distinction

The results of the investigations undertaken on *Gazania* in the previous chapters suggest that there are a number of genetically and morphologically distinct taxonomic entities that correlate with Roessler's species and that are without difficulty considered as valid taxa. Those considered valid under the Phylogenetic and Morphological species concepts are:

- 1) *G. jurineifolia*
- 2) *G. tenuifolia*
- 3) *G. heterochaeta*
- 4) *G. lichtensteinii*
- 5) *G. schenckii*
- 6) *G. caespitosa*
- 7) *G. ciliaris*

Problematic "species" lacking genetic and morphological distinction

The remaining nine species as delimited by Roessler are more challenging to assign taxonomic ranks to. One entity (*G. linearis* subspecies *ovalis*) has clear easily recognisable morphological distinction and geographic localization, yet does not show any evidence of genetic isolation. Another entity (*G. rigens*) shows clear morphological distinction, as well as geographical and ecological localization, but only incomplete evidence of genetic cohesion. Yet another (*G. leiopoda*) shows partial genetic cohesion and geographical localization, but little clear morphological distinction. A fourth entity (*G. othonnites*/*sp. nov.*) shows genetic cohesion, geographical localization and ecological specialization (by the presence of mild succulence).

For the rest of the taxonomic entities, as defined by Roessler, there are few informative morphological characters and those that do exist show large amounts of intra-specific variability. In conjunction with either recent or ongoing gene flow between these entities, there seems little chance of distinguishing discrete species within this impenetrable complex. The oldest species name for all nine of Roessler's species that fall within the K-R complex is that of *G. rigens* L. (1763), indicating that this should be the name of the ochlospecies.

It would seem more practical to define the entities within the "K-R" complex as members of a widely spread and highly variable ochlospecies. Within this ochlospecies are some consistently distinguishable varieties:

- 1) *G. rigens* var. *leiopoda* (formerly *G. leiopoda* under Roessler),
- 2) *G. rigens* var. *ovalis* (formerly *G. linearis* subspecies *ovalis* under Roessler),
- 3) *G. rigens* var. *rigens* (formerly *G. rigens* under Roessler),

4) *G. rigens* var *othonnites* (formerly *G. othonnites* under Roessler, and now including the putative new species *G. sp. nov.*).

However, the presence of these lineages within a larger clade will render that larger clade a paraphyletic or metaphyletic. Archibald (1994) illustrates the difference between paraphyletic and metaphyletic in Figure 6.2. The genetically distinct branches within the K-R clade (those numbered 1-12 in Chapter 4) are rendered paraphyletic, while the samples that cluster along the backbone of the clade are rendered metaphyletic. This distinction becomes important when attempting to apply the Metaspecies/Mixotaxic concepts to the K-R clade. A metaspecies is a previously named portion of a polytomy for which positive evidence of monophyly or paraphyly is lacking (Figure 6.2). A mixotaxon one is where some (but not all) constituent clades may possess autapomorphies (Figure 6.2), which describes the K-R clade.

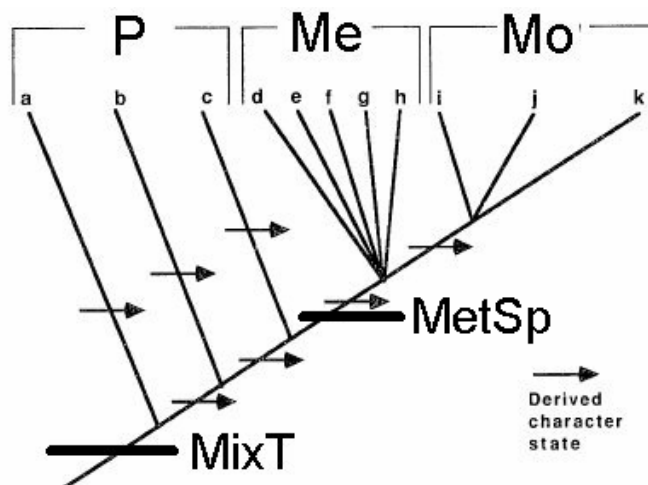


Figure 6.2: An illustration of the difference between paraphyletic taxa (P), metaphyletic taxa (Me) and monophyletic taxa (Mo), “MixT” marks the base of a mixotaxon, “MetSp” marks the base of a metaspecies. (Based on Archibald, 1995: Figure 1).

The remainder of the entities within the K-R complex (those not identified in the four varieties named above) lack sufficient genetic signal or morphological distinctiveness to warrant separate names. For just this situation, Olmstead (1995) proposes the concept of an apospecies which possesses a unique derived character, while an associated Plesiospecies lacks any uniquely derived character (Figure 6.3 illustrates the relationship between the two). In the K-R clade of *Gazania*, the four genetically recognisable lineages could be considered apospecies, whilst the remaining mixture of samples forms a plesiospecies. Despite describing extremely similar entities, the metaspecies concept is dismissed by Olmstead (1995) as "a conditional statement of lack of knowledge concerning relationships".

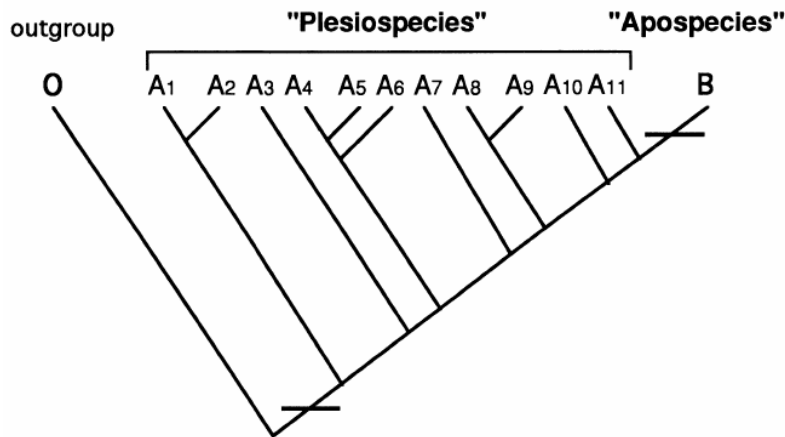


Figure 6.3: Diagrammatic illustration of the relationship between Plesiospecies and Apospecies (From Olmstead, 1995, Figure 2). Horizontal bars indicate unique characters that diagnose each clade.

Whether one chooses to define the greater unresolved portion of the K-R clade as a plesiospecies, or as para/metaphyletic members of a mixotaxon is a matter of personal taste. Species concepts are difficult to apply in a practical diagnostic sense in *Gazania*, as those based purely on morphology will conflict with those based purely on genes. Samples of *G. rigens* (*sensu* Roessler) diagnosed by morphology may or may not fall into the genetically monophyletic apospecies of *G. rigens* var. *rigens* diagnosed in this investigation. The contradiction between morphometric species designation and genetic species designation is yet another example of the problems incurred when investigating low-level phylogeny.

Sites & Marshall (2003) observe that speciation processes create fuzzy boundaries under which all methods of diagnosing species will occasionally fail or be discordant with each other (as clearly observed in *Gazania*, where application of the morphological and phylogenetic species concepts within the K-R clade are in conflict). It is these “problematic” taxa that should be of particular interest to evolutionary biologists, because these taxa are the most promising candidates for providing unique insights into the crucial early stages of the speciation process (Shoemaker *et al.*, 2006). Studies of differentiated populations have rarely been incorporated into research on speciation, even though population differentiation is envisioned as the first stage in speciation in the most widely favoured speciation models (Foster *et al.*, 1998).

The current taxonomic situation in *Gazania* is a complex mix of seven species that are distinct under the Morphological and Phylogenetic Species concepts, and an eighth ochlopecies mixotaxon, with four diagnosable apotaxa.

Morphological key to taxonomic entities within *Gazania*.

Below is the morphological key to those taxonomic entities within *Gazania* that show genetic and morphological distinction as species. *G. lichtensteinii* appears twice in the key due to the presence of both the developed and rosette stem habits. *G. rigens* appears in multiple places in the key due to the broad range of morphological variation that is found within this ochlopecies. Three of the four morphologically identifiable varieties within *G. rigens* are present in the key, except for *G. rigens* var *leiopoda*, which shows no clear morphological distinction, despite some geographical and genetic cohesion.

- 1) Stem developed with leaves spaced along entire length.
 - 2) Leaves linear (< 2 mm wide) *G. caespitosa*
 - 2) Leaves obovate/obovate-lanceolate/lanceolate (> 2 mm wide)
 - 3) All leaves deeply pinnatifid (1-5 lacinae) *G. rigens*
 - 3) Leaves entire or some few leaves pinnatifid (1-3 lacinae)
 - 4) Leaf margin entire *G. rigens* var. *rigens*
 - 4) Leaf margin dentate/denticulate
 - 5) Involucre tomentose, older stems woody *G. schenckii*
 - 5) Involucre glabrous, stem not woody *G. lichtensteinii*
- 1) Stem shortened with leaves crowded at base in rosette.
 - 6) Leaf abaxial surface glabrous, succulent glaucous leaves. *G. rigens* var *othonnites*/sp. nov.
 - 6) Abaxial surface tomentose.
 - 7) Leaf margins dentate/denticulate. *G. lichtensteinii*
 - 7) Leaf margins entire or ciliate
 - 8) Multiple rows of linear parietal scales upwards from truncate involucre base *G. tenuifolia*
 - 8) Most involucral scales terminal, some few single parietal.
 - 9) Inner involucre scales greatly and finely acuminate (> 8 mm long)
 - 10) Inner involucral scale margins entire
 - 11) Leaves lanceolate/elliptic, entire leaves > 10 mm wide, lacinae of pinnatifid leaves > 4 mm wide. *G. rigens* var. *ovalis*
 - 11) Leaves linear, lanceolate, entire leaves < 10mm wide, lacinae of pinnatifid leaves < 4 mm wide. *G. rigens*

- 10) Inner involucre scale margins ciliate. *G. ciliaris*
- 9) Inner involucre scales < 8 mm long.
- 12) Outer involucre scales < 4 mm long, inner > 4 mm long. Ray florets white. *G. jurineifolia*
- 12) Outer involucre scales > 4 mm long, inner < 4 mm long. Ray florets yellow / orange.
- 13) Leaf obovate *G. heterochaeta*
- 13) Leaf linear/lanceolate *G. rigens*

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Appendix 1: Morphological characters for each of Roessler's species

Appendix 1: Summary of morphological characters from Roessler's species descriptions.

	caespitosa	ciliaris	heterochaeta	jurineifolia	krebsiana	leiopoda
Annual or perennial	perennial	perennial	perennial	perennial	perennial	perennial
Habit	subshrub	herbaceous	herbaceous	herbaceous	herbaceous	herbaceous
Stem developed/rosette	developed	rosette	rosette	rosette	rosette	rosette
Leaves:						
whole/pinnate/both	whole	both	both	pinnate	both	pinnate
leaf shape	linear	linear/linear-lanceolate	obovate		linear/linear-lanceolate	
margins revolute	yes	yes	somewhat	yes	yes	yes
width (whole leaf, mm)	1-1.5 mm	1 -4 mm	30-60 mm		(1-)2-6(-8) mm	
length (whole leaf, mm)	20 - 30 mm	40-80 (-150) mm	(5-)8-15(-25)mm	10-50(-70) mm	(30-)60-180(-250) mm	(30-)40-80 mm
Laciniae:						
number of pairs		1-4	1-3	2-5	1-4	(4-)5-7
opposite/alternate		opp/alt		opposite	opposite	opposite
width of laciniae		1-2 mm			1-3(-4) mm	2-3.5 mm
length of laciniae		2-10 mm		2-5(-8) mm	3-10(-15) mm	3-7(-10) mm
width of middle stem		1-2 mm		1-2(-3) mm	1-2 mm	1 mm
notes on laciniae			apex rounded			apex acute/obtuse
terminal : side laciniae (longer/shorter/same)						similar
apex in spinule excurrent	yes	yes	yes	yes	yes	yes
other notes	edges ciliate with 1mm long spinules	setae all the way up to 2-3 mm long ciliate				
Top surface:	smooth/glabrous	setose (rough)	densely setose	rough/densely setose	smooth/rough	hispid
Lower surface:	tomentose	tomentose	tomentose	tomentose	tomentose	tomentose

Appendix 1: Morphological characters for each of Roessler's species

Capitula:						
on peduncles/scapes	peduncles	scapes	scapes	scapes	scapes	scapes
peduncle/scape length	30-50 mm	40-100(-140)mm	30-80(-120) mm	5-40(-80) mm	(30)-50-120(-150) mm	(30-)60-100(-120) mm
with ligules expanded (mm)	30-40 mm	40-70 mm	(30-)40-70 mm	25-50 (-70) mm	30-60 mm	(50-)60-80 mm
glabrous/tomentose	glabrous	setose	glabrous	glabrous	glabrous	
Involucre:						
glabrous/tomentose/ciliate	glabrous	glabrous	glabrous/partially setose	glabrous	glabrous	setose
fused part shape	subcampanulate	subcylindrical	campanulate	campanulate	campanulate	broadly cupuliform
base shape	obtuse	truncate, pleated annulus	obtuse	obtuse	obtuse	obtuse
base intrusa/subintruse	intrusa	margin in annulus	subintrusa		subintrusa	
height	7-8 mm	8-10(-12) mm	8-10 mm	6-8(-10) mm	7-10 mm	10-15 mm
width	4 mm	7-9 mm	(5-)7-9 mm	4-7(-8) mm	(4-)5-8 mm	10-15 mm
scales seriate number	2-3	2-3	2-3	3	2-3	2-3
parietal scales	no	few	few	few	few	few
scales inserted where	margin of fused part	margin of fused part	margin of fused part	margin of fused part	margin of fused part	
Outer involucreal scales:						
shape	linear-triangulate	linear/linear-triangulate	linear-lanceolate/triangulate	linear/triangulate-lanceolate	linear	oblong-linear/triangulate
length	5 mm	6-10 mm	2-4 mm	1-3 mm		2-5 mm
width	1-2 mm	1 mm	1 mm	1 mm	1 mm	1-1.5 mm
tip shape	acute	acute	short setae excurrent		acute	acute
margin description	shortly denticulate	ciliate with setae 1mm long	with setulae excurrent	densely ciliate with 0.2mm spinules	shortly ciliate	most shortly ciliate

Appendix 1: Morphological characters for each of Roessler's species

Inner involucre scale:						
shape	ovate-triangulate	narrowly triangulate	narrowly/ovate triangulate	ovate/narrow triangulate	narrowly/ovate triangulate	ovate/narrowly triangulate
length	7-8 mm	7-12(-20) mm	4-8 mm	(3-)4-6(-8) mm	See Note 1	4-7 mm
width	2-3 mm	2-3 mm	2-3 mm	1.5-2.5 (-3) mm	See Note 1	2-4 mm
tip shape	acuminate	acuminate			acuminate/acute/obtuse	obtuse/acute
margin description	membranous/entire	membranous, minutely ciliate	membranous, minutely ciliate/entire	membranous, scarcely ciliate/entire	membranous/entire	membranous, entire
Ligules:						
Colour	yellow	yellow	yellow/orange	white		orange
Eye spots		black/bicoloured	sometimes black/bicoloured			black/bicoloured
Other notes				disc florets sparsely hairy		

Ctd...

Appendix 1: Morphological characters for each of Roessler's species

	lichtensteinii	linearis linearis	linearis ovalis	maritima	othonnites	pectinata
Annual or perennial	annual/perennial	perennial	perennial	perennial	perennial	annual?
Habit	herbaceous	herbaceous	herbaceous	herbaceous	herbaceous	herbaceous
Stem developed/rosette	rosette/developed	rosette	rosette	developed	rosette	rosette
Leaves:						
whole/pinnate/both	entire	both	both	both	both	both
leaf shape	obovate	linear	linear	linear-lanceolate	linear/ linear-oblong	linear/linear-lanceolate
margins revolute	denticulate	yes	yes	yes	fleshy	yes
width (whole leaf, mm)	(3-)5-10 (-20) mm	1-5(-10) mm	1-25 mm		1-3 mm	1-3(-6) mm
length (whole leaf, mm)	(15-)20-40(-70) mm	(80-)100-300 mm	(80-)100-300 mm	20-60(-110)mm	20-50(-70) mm	(80-)100-250 mm
Laciniae:						
number of pairs		1-6	1-6	1-5	1-3	(1-)2-8
opposite/alternate		opposite	opposite	opposite	opposite	opposite
width of laciniae		1-4(-7) mm	1-10 mm	1-4 mm		1-2(-4) mm
length of laciniae		5-15(-25) mm	5-15(-25) mm	4-15(-20) mm	1-5 mm	5-15(-25) mm
width of middle stem		1-2 mm	1-2 mm			1-2 mm
notes on laciniae						apex acute
terminal : side laciniae (longer/shorter/same)				wider(6mm wide)		
apex in spinule excurrent	obtuse	yes	yes	yes	yes	yes
other notes	white ciliate spinules at edges			margin covered in tiny spinules		
Top surface:	tomentose (glabrous)	smooth/ciliate/ rough	smooth/ciliate/ rough	glabrous	glabrous, glaucous	smooth

Appendix 1: Morphological characters for each of Roessler's species

Lower surface:	tomentose	tomentose	tomentose	tomentose	glabrous, glaucous	tomentose
Capitula:						
on peduncles/scapes	peduncles	scapes	scapes	peduncles	scapes	scapes
peduncle/scape length	(10-)20-60(-120) mm	100-350 mm	100-350 mm	20-100 mm	20-100(-130) mm	(80-)150-300 mm
with ligules expanded (mm)	20-40 mm	40-70 mm	40-70 mm	30-40 mm	20-35 mm	45-70(-90) mm
glabrous/tomentose	glabrous	glabrous/setose	glabrous/setose	tomentose/ glabrous	glabrous	glabrous/setose
Involucre:						
glabrous/tomentose/ciliate	glabrous	glabrous/setose	glabrous/setose	glabrous	glabrous	glabrous/setose
fused part shape	cylindrical	campanulate/ subcupuliform	campanulate/ subcupuliform	campanulate	turbinate	campanulate
base shape		obtuse	obtuse	obtuse		obtuse
base intrusa/subintruse	intrusa	subintrusa	subintrusa	subintrusa (slight)	intrusa	subintrusa
height	7-10 mm	8-12 mm	8-12 mm	8-10 mm	6-9 mm	8-11 mm
width	3-5 mm	6-12(15) mm	6-12(15) mm	5-8 mm	3-6 mm	6-10(-15) mm
scales seriate number	2	2-3	2-3	2	2-3	2-3
parietal scales	none	few	few	few	few	few
scales inserted where	margin of fused part	margin of fused part	margin of fused part	margin of fused part	margin of fused part	margin of fused part
Outer involucre scales:						
shape	linear/ triangulate	linear	linear			linear
length	1-2 mm				1.5-2 mm	7-10(-20) mm
width	1-1.5 mm				1.5-2 mm	1mm

Appendix 1: Morphological characters for each of Roessler's species

tip shape						acute
margin description	minutely ciliate	ciliate setose	ciliate setose	with spinules ciliate		ciliate setose
Inner involucre scale:						
shape	ovate-triangulate					
length	4-7 mm	(8-)10-15(18) mm	(8-)10-15(18) mm		4-6 mm	8-15 mm
width	2-3 mm	1.5-2 mm	1.5-2 mm		1.5-3 mm	2 mm
tip shape		finely acuminate	finely acuminate			finely acuminate
margin description	membranous, entire	membranous, entire	membranous, entire	membranous, entire		membranous, entire
Ligules:						
Colour	yellow/orange	yellow/orange	yellow/orange	yellow/orange	yellow	yellow/orange
Eye spots	bicoloured	black/bicoloured	black/bicoloured			black/greybrown
Other notes	some green stripes					

Ctd...

Appendix 1: Morphological characters for each of Roessler's species

	rigens	rigida	schenckii	serrata	tenuifolia
Annual or perennial	perennial	perennial	perennial	perennial	annual
Habit	herbaceous	herbaceous	subshrub	herbaceous	herbaceous
Stem developed/rosette	developed	rosette	developed	rosette	rosette
Leaves:					
whole/pinnate/both	both	both	whole	both	both
leaf shape	lanceolate/ obovate-lanceolate	linear- lanceolate	obovate- spathulate	lanceolate	linear
margins revolute	somewhat	yes	dentate	yes	
width (whole leaf, mm)	(4-)5-10(-23) mm	2-5 mm	5-10(-15) mm	(3-)5-9 mm	1 mm
length (whole leaf, mm)	(30-)40-80(-110) mm	40-100(-150) mm	15-30(-35) mm	(40-)60-150 mm	(20-)30-60(-80) mm
Laciniae:					
number of pairs	1-2	1-2(-5)		(1-)2-4	1-5
opposite/alternate	opposite	opposite		opposite	opposite
width of laciniae		1-3 mm		2-5(-7) mm	1mm
length of laciniae		5-15(-20) mm		5-15 mm	2-8(-12) mm
width of middle stem		1 mm		1-2 mm	1 mm
notes on laciniae					
terminal : side laciniae (longer/shorter/same)	all same	same		2x wider/longer	
apex in spinule excurrent	no	yes	yes	yes	
other notes					
Top surface:	glabrous/tomentose	smooth/setose (rough)	tomentose	rough, setose	roughly setose
Lower surface:	tomentose	tomentose	tomentose	tomentose	tomentose
Capitula:					

Appendix 1: Morphological characters for each of Roessler's species

on peduncles/scapes	peduncles	scapes	peduncles	scapes	peduncles
peduncle/scape length	40-100(-150) mm	40-150 mm	20-60 mm	50-150 mm	20-80(-140) mm
with ligules expanded (mm)	25-80 mm	40-60 mm	20-30(-35) mm	45-75 mm	10-15 mm
glabrous/tomentose	glabrous/tomentose	setose	tomentose	setose	glabrous/cobwebby
Involucre:					
glabrous/tomentose/ciliate	glabrous/tomentose	setose	tomentose	setose	
fused part shape	campanulate	campanulate	cylindrical	campanulate	cylindrical
base shape	obtuse	obtuse	obtuse	obtuse	truncate
base intrusa/subintruse	subintrusa	subintrusa	little intrusa	subintrusa	pleated annulus
height	8-10 mm	9-11 mm	6-9 mm	8-12 mm	4-5 mm
width	7-15 mm	(6-)8-12(-15) mm	3-5 mm	7-10 mm	3-5 mm
scales seriate number	2-3	2-3	2	2-3	
parietal scales	few	few	few/no	few	many rows
scales inserted where	margin of fused part	margin of fused part	margin of fused part	margin of fused part	all over
Outer involucre scales:					
shape	triangulate-lanceolate	linear	same as inner, but smaller	linear	(parietal)subulate
length	4-7 mm	5-8 mm		5-12 mm	1-2 mm
width		1 mm		1 mm	
tip shape		acute		acute	acute
margin description	tomentose on outside	setose ciliate		setose	ciliate/entire

Appendix 1: Morphological characters for each of Roessler's species

Inner involucre scale:					
shape	narrowly triangulate	triangulate	narrowly triangulate	narrowly triangulate	(terminal) triangulate-subulate
length	5-10 mm	4-6 mm	6-9 mm	8-10 mm	5-6 mm
width		2 mm	2-3 mm	2-2.5 mm	1(-1.5) mm
tip shape	acuminate	obtuse/acute		acuminate	
margin description	glabrous	membranous, entire	entire	membranous, entire	membranous, entire
Ligules:					
Colour	yellow	yellow/orange	yellow	yellow/orange	yellow/orange
Eye spots	sometimes black spots	often black/grown	rarely black spot	sometimes black/bicoloured	black/bicoloured
Other notes					disc florets sparsely hairy

Morphometric characters and abbreviations used in data table.

Character	Abbrev
Habit	Habit
Involucre setose	InvSet
Parietal scales	ParScl
Involucre base	InvBase
Adaxial leaf indumentum	LfIndu
Leaf margin	LfMarg
Leaf dissectedness	LfDiss
Outer involcral scale length	OIL
Outer involcral scale width	OIW
Inner involcral scale length	IIL
Inner involcral scale width	IIW
Involucre length	InvL
Involucre width	InvW
Leaf length	LfLgth
Leaf width	LfWdth
Stem length	StmLgth
Log(Outer involcral scale length)	LogOIL
Log(Outer involcral scale width)	LogOIW
Log(Inner involcral scale length)	LogIIL
Log(Inner involcral scale width)	LogIIW
Log(Involucre length)	LogInvL
Log(Involucre width)	LogInvW
Log(Leaf length)	LogLfLgth
Log(Leaf width)	LogLfWdth
Log(Stem length)	LogStmLgth
Log(Outer Involucral scale length/width)	LogOIRAT
Log(Inner Involucral scale length/width)	LogIIRAT
Log(Outer/Inner Involucral scale length)	LogOI/II
Log(Involucral length/width)	LogInvRAT
Log(Leaf length/width)	LogLFRAT

Appendix 2: Morphometric data set for Chapter 2.

	Cil1	Cil2	Cil3	Cil4	Cil5	Cil6	Cil7	Het1	Het2	Het3	Het4	Het5	Het6
Habit	1	1	1	1	1	1	1	1	1	1	1	1	1
InvSet	1	0	0	0	0	0	0	0	0	0	0	0	0
ParScl	1	1	1	1	1	1	1	0	0	0	0	0	0
InvBase	2	1	0	3	3	3	3	2	2	2	2	1	1
LfIndu	2	2	2	2	0	2	0	2	2	2	2	2	2
LfMarg	3	3	3	3	0	3	2	3	3	3	3	3	3
LfDiss	5	5	5	5	1	5	5	4	4	4	4	4	5
OIL	7.67	11.4	8.59	10.16	6.2	8.38	10.56	4.4	4.47	3.44	3.72	4.13	3.82
OIW	1.57	2.18	1.82	2.67	1.74	2.23	2.3	2.12	2.05	2.3	1.37	2.97	1.53
IIL	10.13	10.55	12.37	9.37	14.99	10.31	22.32	5.53	6.74	5.78	7.16	7.65	6.68
IIW	3.74	4.32	2.97	2.68	1.93	2.56	3.33	2.1	1.77	1.5	1.47	3.56	2.06
InvL	7.48	7.31	8.59	7.34	8.4	7.55	4.74	9.53	8.73	9.89	7.02	11.36	8.95
InvW	8.32	10.96	9.96	9.34	8.62	8.04	12.12	9.1	10.14	9.65	7.25	14.25	9.72
LfLgth	72.75	147.3	67.53	58.9	89.28	45.94	150.31	48.03	47.53	51.1	41.94	59.69	61.44
LfWdth	3.13	5.06	4.9	2.85	1.09	2.38	0.84	9.28	10.83	8.58	5.59	17.92	9.26
StmLgth	64.59	200	100.99	49.68	105	38.38	160	55.17	54.9	49.72	34.41	83.43	101.7
LogOIL	0.88480	1.05690	0.93399	1.00689	0.79239	0.92324	1.02366	0.64345	0.65031	0.53656	0.57054	0.61595	0.58206
LogOIW	0.19590	0.33846	0.26007	0.42651	0.24055	0.34830	0.36173	0.32634	0.31175	0.36173	0.13672	0.47276	0.18469
LogIIL	1.00561	1.02325	1.09237	0.97174	1.17580	1.01326	1.34869	0.74273	0.82866	0.76193	0.85491	0.88366	0.82478
LogIIW	0.57287	0.63548	0.47276	0.42813	0.28556	0.40824	0.52244	0.32222	0.24797	0.17609	0.16732	0.55145	0.31387
LogInvL	0.87390	0.86392	0.93399	0.86570	0.92428	0.87795	0.67578	0.97909	0.94101	0.99520	0.84634	1.05538	0.95182
LogInvW	0.92012	1.03981	0.99826	0.97035	0.93551	0.90526	1.08350	0.95904	1.00604	0.98453	0.86034	1.15381	0.98767
LogLfLgth	1.86183	2.16820	1.82950	1.77012	1.95075	1.66219	2.17699	1.68151	1.67697	1.70842	1.62263	1.77590	1.78845
LogLfWdth	0.49554	0.70415	0.69020	0.45484	0.03743	0.37658	-0.07572	0.96755	1.03463	0.93349	0.74741	1.25334	0.96661
LogStmLgth	1.81017	2.30103	2.00428	1.69618	2.02119	1.58410	2.20412	1.74170	1.73957	1.69653	1.53668	1.92132	2.00732
LogOIRAT	0.68890	0.71845	0.67392	0.58038	0.55184	0.57494	0.66194	0.31712	0.33855	0.17483	0.43382	0.14319	0.39737
LogIIRAT	0.43274	0.38777	0.61961	0.54360	0.89024	0.60502	0.82625	0.42051	0.58069	0.58584	0.68760	0.33221	0.51091
LogOI/II	-0.12081	0.03365	-0.15838	0.03515	-0.38341	-0.09001	-0.32503	-0.09927	-0.17835	-0.22537	-0.28437	-0.26771	-0.24271
LogInvRAT	-0.04622	-0.17589	-0.06427	-0.10465	-0.01123	-0.02731	-0.40772	0.02005	-0.06502	0.01067	-0.01400	-0.09844	-0.03584
LogLFRAT	1.36629	1.46405	1.13930	1.31527	1.91333	1.28561	2.25271	0.71396	0.64234	0.77493	0.87522	0.52256	0.82184

Appendix 2: Morphometric data set for Chapter 2.

	Het7	Het8	Het9	Jur1	Jur2	Jur3	Jur4	Jur5	Jur6	Jur7	Jur8	Jur9	KrbA1
Habit	1	1	1	1	1	1	1	1	1	1	1	1	1
InvSet	0	0	0	0	0	0	0	0	0	0	0	0	1
ParScl	0	0	1	1	1	1	1	0	0	0	0	0	0
InvBase	2	1	2	0	0	2	2	0	0	2	2	0	1
LfIndu	2	2	2	2	2	2	2	2	2	2	2	2	1
LfMarg	3	3	3	3	3	3	3	3	3	3	3	3	3
LfDiss	2	5	5	6	6	6	6	6	6	6	6	3	5
OIL	3.97	3.68	6.84	3.11	2.94	3.51	2.84	3.11	3.5	2.62	2.99	1.93	1.67
OIW	1.93	1.23	1.58	2	2.06	1.34	1.75	1.72	2.17	1.3	1.74	1.72	0.77
IIL	10.25	6.55	6.09	8.83	9.84	5.15	5.85	3.79	5.65	4.9	5.94	4.94	2.11
IIW	2.23	2.2	2.94	2	2.39	1.99	2.33	2.06	2.56	2.6	1.98	1.72	1.28
InvL	7.74	8.79	8.15	5.52	5.51	5.63	5.59	5.66	5.41	5.34	6.17	7.22	6.67
InvW	6.5	7.94	7.8	9.13	8.92	7.84	6.06	7.82	8.74	9.58	10.15	6.91	3.56
LfLgth	62.73	55.44	64.51	39.69	37.03	38.97	21.59	65.21	48.04	30.18	40.91	42.86	32.03
LfWdth	6.84	15.71	8.04	2.74	3.82	2.84	1.85	2.93	3.68	2.74	3.03	3.62	2.68
StmLgth	118.15	67.93	102.61	44.19	45.9	22.27	16.29	65.88	39.4	21.43	15	51.67	17.22
LogOIL	0.59879	0.56585	0.83506	0.49276	0.46835	0.54531	0.45332	0.49276	0.54407	0.41830	0.47567	0.28556	0.22272
LogOIW	0.28556	0.08991	0.19866	0.30103	0.31387	0.12710	0.24304	0.23553	0.33646	0.11394	0.24055	0.23553	-0.11351
LogIIL	1.01072	0.81624	0.78462	0.94596	0.99300	0.71181	0.76716	0.57864	0.75205	0.69020	0.77379	0.69373	0.32428
LogIIW	0.34830	0.34242	0.46835	0.30103	0.37840	0.29885	0.36736	0.31387	0.40824	0.41497	0.29667	0.23553	0.10721
LogInvL	0.88874	0.94399	0.91116	0.74194	0.74115	0.75051	0.74741	0.75282	0.73320	0.72754	0.79029	0.85854	0.82413
LogInvW	0.81291	0.89982	0.89209	0.96047	0.95036	0.89432	0.78247	0.89321	0.94151	0.98137	1.00647	0.83948	0.55145
LogLfLgth	1.79748	1.74382	1.80963	1.59868	1.56855	1.59073	1.33425	1.81431	1.68160	1.47972	1.61183	1.63205	1.50556
LogLfWdth	0.83506	1.19618	0.90526	0.43775	0.58206	0.45332	0.26717	0.46687	0.56585	0.43775	0.48144	0.55871	0.42813
LogStmLgth	2.07243	1.83206	2.01119	1.64532	1.66181	1.34772	1.21192	1.81875	1.59550	1.33102	1.17609	1.71324	1.23603
LogOIRAT	0.31323	0.47594	0.63640	0.19173	0.15448	0.41820	0.21028	0.25723	0.20761	0.30436	0.23512	0.05003	0.33623
LogIIRAT	0.66242	0.47382	0.31627	0.64493	0.61460	0.41295	0.39980	0.26477	0.34381	0.27522	0.47712	0.45820	0.21707
LogOI/II	-0.41193	-0.25039	0.05044	-0.45320	-0.52465	-0.16650	-0.31384	-0.08588	-0.20798	-0.27189	-0.29812	-0.40817	-0.10157
LogInvRAT	0.07583	0.04417	0.01906	-0.21853	-0.20921	-0.14381	-0.03506	-0.14039	-0.20831	-0.25382	-0.21618	0.01906	0.27268
LogLFRAT	0.96242	0.54765	0.90437	1.16093	0.98649	1.13741	1.06708	1.34745	1.11576	1.04197	1.13039	1.07334	1.07742

Appendix 2: Morphometric data set for Chapter 2.

	KrbA2	KrbA4	KrbA5	KrbA6	KrbA8	KrbA9	KrbA10	KrbA12	KrbK2	KrbK3	KrbK4	KrbK5	KrbK7
Habit	1	1	1	1	1	1	1	1	1	1	1	1	1
InvSet	0	0	0	0	0	0	0	1	0	0	0	0	0
ParScl	1	0	0	0	0	0	0	0	0	0	1	0	0
InvBase	2	1	1	8	1	2	2	0	1	2	2	2	2
LfIndu	0	0	0	0	0	0	3	3	2	1	2	0	0
LfMarg	3	3	0	0	3	3	3	3	3	3	3	3	3
LfDiss	5	5	5	1	1	5	5	5	5	1	4	1	1
OIL	4.44	7.79	2.14	2.31	2.5	2.52	3.4	3.4	4.48	3.5	5.62	4.94	7.43
OIW	1.26	2.32	0.87	1.91	0.82	0.93	2.05	1.9	1.8	1.83	1.34	1.3	1.33
IIL	5.47	6.82	4.1	3.07	4.28	2.53	3.85	5	6.3	3.84	4.33	5.53	6.9
IIW	2.64	2.89	1.37	1.75	2.01	1.65	2.7	2.3	1.91	1.86	1.67	1.5	2.2
InvL	8.84	10.98	7.74	6.42	5.68	5.53	7.62	8.66	7.71	7.04	8.33	5.68	7.81
InvW	9.31	10.96	3.19	4.81	4.17	5.05	7.07	5.44	6.33	5.82	7.59	6.56	7.56
LfLgth	137.14	165	62.14	48.75	91.95	33.28	139.45	49.66	77.71	48.15	100.23	52.53	75.08
LfWdth	3.46	14.76	1.91	2.49	6.05	2.3	4.31	2.68	3.45	5.16	7.47	5.29	3.54
StmLgth	113.71	82.7	58.66	33	83.65	17.21	141.22	47.54	103.96	35.75	107.71	13.03	77.58
LogOIL	0.64738	0.89154	0.33041	0.36361	0.39794	0.40140	0.53148	0.53148	0.65128	0.54407	0.74974	0.69373	0.87099
LogOIW	0.10037	0.36549	-0.06048	0.28103	-0.08619	-0.03152	0.31175	0.27875	0.25527	0.26245	0.12710	0.11394	0.12385
LogIIL	0.73799	0.83378	0.61278	0.48714	0.63144	0.40312	0.58546	0.69897	0.79934	0.58433	0.63649	0.74273	0.83885
LogIIW	0.42160	0.46090	0.13672	0.24304	0.30320	0.21748	0.43136	0.36173	0.28103	0.26951	0.22272	0.17609	0.34242
LogInvL	0.94645	1.04060	0.88874	0.80754	0.75435	0.74273	0.88195	0.93752	0.88705	0.84757	0.92065	0.75435	0.89265
LogInvW	0.96895	1.03981	0.50379	0.68215	0.62014	0.70329	0.84942	0.73560	0.80140	0.76492	0.88024	0.81690	0.87852
LogLfLgth	2.13716	2.21748	1.79337	1.68797	1.96355	1.52218	2.14442	1.69601	1.89048	1.68260	2.00100	1.72041	1.87552
LogLfWdth	0.53908	1.16909	0.28103	0.39620	0.78176	0.36173	0.63448	0.42813	0.53782	0.71265	0.87332	0.72346	0.54900
LogStmLgth	2.05580	1.91751	1.76834	1.51851	1.92247	1.23578	2.14990	1.67706	2.01687	1.55328	2.03226	1.11494	1.88975
LogOIRAT	0.54701	0.52605	0.39089	0.08258	0.48413	0.43292	0.21973	0.25273	0.39601	0.28162	0.62263	0.57978	0.74714
LogIIRAT	0.31638	0.37289	0.47606	0.24410	0.32825	0.18564	0.15410	0.33724	0.51831	0.31482	0.41377	0.56663	0.49643
LogOI/II	-0.09060	0.05775	-0.28237	-0.12353	-0.23350	-0.00172	-0.05398	-0.16749	-0.14806	-0.04026	0.11325	-0.04900	0.03214
LogInvRAT	-0.02250	0.00079	0.38495	0.12539	0.13421	0.03943	0.03254	0.20192	0.08565	0.08265	0.04040	-0.06256	0.01413
LogLFRAT	1.59809	1.04840	1.51234	1.29178	1.18180	1.16046	1.50994	1.26787	1.35266	0.96995	1.12768	0.99695	1.32652

Appendix 2: Morphometric data set for Chapter 2.

	KrbK8	KrbK9	KrbK10	KrbK11	KrbK12	KrbK13	KrbK14	KrbK16	KrbK17	KrbK18	KrbK19	KrbK20	KrbK22
Habit	1	1	1	1	1	1	1	1	1	1	1	1	1
InvSet	0	0	1	0	1	0	0	0	0	0	0	0	0
ParScl	1	1	1	0	0	0	0	0	0	0	0	1	1
InvBase	2	2	2	1	1	1	1	2	1	1	1	2	2
LfIndu	0	2	3	2	2	0	0	2	0	3	3	0	2
LfMarg	3	3	3	3	3	0	3	3	3	3	3	1	1
LfDiss	5	1	5	5	5	1	1	1	5	1	1	1	5
OIL	8.24	6.96	3.54	5.72	2.99	4.57	6.63	4.27	3.82	7.24	9.68	4.93	4.07
OIW	1.8	0.98	1.66	2.11	1.79	1.66	1.3	1.66	2.44	1.28	1.48	1.76	1.86
IIL	7.11	9.78	5.55	6.08	5.28	3.96	5.09	5.21	6.11	6.43	7.76	6.82	5.76
IIW	2.84	1.38	2.87	2.07	2.24	1.54	1.2	2.23	2.29	2.64	2.45	3.39	1.86
InvL	7.03	8.41	8.61	8.66	11.76	8.01	8.4	7.57	9.11	8.73	7.75	7.82	8.45
InvW	7.6	5.92	10.82	7.2	12.92	8.71	7.54	6.09	6.72	7.86	9.43	11.45	6.65
LfLgth	105.78	70.05	200	80.85	200	90.49	37.49	85.15	75.74	200	140.11	149.64	162
LfWdth	5.41	2.56	4.77	2.91	4.44	3.25	1.43	6.16	6.79	6.43	5.82	6	4.75
StmLgth	152.27	79.24	125.68	108.88	230	51.56	23.62	59.04	74.71	138.43	93.75	130.45	149
LogOIL	0.91593	0.84261	0.54900	0.75740	0.47567	0.65992	0.82151	0.63043	0.58206	0.85974	0.98588	0.69285	0.60959
LogOIW	0.25527	-0.00877	0.22011	0.32428	0.25285	0.22011	0.11394	0.22011	0.38739	0.10721	0.17026	0.24551	0.26951
LogIIL	0.85187	0.99034	0.74429	0.78390	0.72263	0.59770	0.70672	0.71684	0.78604	0.80821	0.88986	0.83378	0.76042
LogIIW	0.45332	0.13988	0.45788	0.31597	0.35025	0.18752	0.07918	0.34830	0.35984	0.42160	0.38917	0.53020	0.26951
LogInvL	0.84696	0.92480	0.93500	0.93752	1.07041	0.90363	0.92428	0.87910	0.95952	0.94101	0.88930	0.89321	0.92686
LogInvW	0.88081	0.77232	1.03423	0.85733	1.11126	0.94002	0.87737	0.78462	0.82737	0.89542	0.97451	1.05881	0.82282
LogLfLgth	2.02440	1.84541	2.30103	1.90768	2.30103	1.95660	1.57392	1.93018	1.87933	2.30103	2.14647	2.17505	2.20952
LogLfWdth	0.73320	0.40824	0.67852	0.46389	0.64738	0.51188	0.15534	0.78958	0.83187	0.80821	0.76492	0.77815	0.67669
LogStmLgth	2.18261	1.89894	2.09927	2.03695	2.36173	1.71231	1.37328	1.77115	1.87338	2.14123	1.97197	2.11544	2.17319
LogOIRAT	0.66065	0.85138	0.32890	0.43311	0.22282	0.43981	0.70757	0.41032	0.19467	0.75253	0.81561	0.44733	0.34008
LogIIRAT	0.39855	0.85046	0.28641	0.46793	0.37239	0.41017	0.62754	0.36853	0.42621	0.38661	0.50070	0.30358	0.49091
LogOI/II	0.06406	-0.14773	-0.19529	-0.02651	-0.24696	0.06222	0.11480	-0.08641	-0.20398	0.05153	0.09601	-0.14094	-0.15083
LogInvRAT	-0.03386	0.15247	-0.09922	0.08019	-0.04086	-0.03639	0.04691	0.09448	0.13215	0.04559	-0.08521	-0.16560	0.10404
LogLFRAT	1.29121	1.43717	1.62251	1.44379	1.65365	1.44472	1.41858	1.14060	1.04746	1.49282	1.38155	1.39690	1.53282

Appendix 2: Morphometric data set for Chapter 2.

	KrbK23	KrbK24	KrbK25	KrbK26	KrbK27	KrbK28	KrbS1	KrbS2	KrbS3	KrbS4	KrbS5	KrbS6	Leio1
Habit	1	1	1	1	1	1	1	1	1	1	1	1	1
InvSet	0	0	0	0	0	0	0	0	0	0	0	0	1
ParScl	1	1	1	0	0	0	1	0	1	0	0	1	0
InvBase	2	1	2	0	0	2	2	2	0	0	2	2	0
LfIndu	0	0	0	0	0	0	2	2	2	0	0	2	2
LfMarg	0	3	3	0	3	0	3	3	3	3	0	3	3
LfDiss	1	1	5	1	1	1	1	1	1	1	1	1	6
OIL	3.88	5.43	6.68	3.81	4.79	4.59	2.57	2.19	2.1	2.81	3.32	5.1	3.32
OIW	1.63	1.56	0.99	0.91	1.69	2.23	1.18	0.93	1.68	1.98	1.17	1.42	1.55
IIL	4.35	6.42	7.36	5.44	4.56	5.29	3.04	3.45	3.51	3.05	4.01	4.69	4.73
IIW	1.5	1.7	1.74	1.35	1.18	2.99	1.46	1.74	1.76	1.71	1.67	2.03	2.34
InvL	5.63	8.89	6.36	5.48	7.2	8.08	7.14	7.58	9.12	5.39	7.08	7.58	8.38
InvW	4.83	5.42	6.51	3.13	9.25	11.32	8.05	5.25	5.81	4.95	6.13	6.56	10.94
LfLgth	101.99	83.93	181	89.25	135	114.85	116.28	70.12	95.62	54.07	87.19	79.99	60.22
LfWdth	5.32	6.43	5.37	1.03	1.54	1.24	6.66	4.01	6.76	5.9	2.95	2.03	2.77
StmLgth	64.06	100.85	200	74.36	137	176	57.98	48.57	31.85	20.24	81.05	56.37	42.82
LogOIL	0.58883	0.73480	0.82478	0.58092	0.68034	0.66181	0.40993	0.34044	0.32222	0.44871	0.52114	0.70757	0.52114
LogOIW	0.21219	0.19312	-0.00436	-0.04096	0.22789	0.34830	0.07188	-0.03152	0.22531	0.29667	0.06819	0.15229	0.19033
LogIIL	0.63849	0.80754	0.86688	0.73560	0.65896	0.72346	0.48287	0.53782	0.54531	0.48430	0.60314	0.67117	0.67486
LogIIW	0.17609	0.23045	0.24055	0.13033	0.07188	0.47567	0.16435	0.24055	0.24551	0.23300	0.22272	0.30750	0.36922
LogInvL	0.75051	0.94890	0.80346	0.73878	0.85733	0.90741	0.85370	0.87967	0.95999	0.73159	0.85003	0.87967	0.92324
LogInvW	0.68395	0.73400	0.81358	0.49554	0.96614	1.05385	0.90580	0.72016	0.76418	0.69461	0.78746	0.81690	1.03902
LogLfLgth	2.00856	1.92392	2.25768	1.95061	2.13033	2.06013	2.06551	1.84584	1.98055	1.73296	1.94047	1.90304	1.77974
LogLfWdth	0.72591	0.80821	0.72997	0.01284	0.18752	0.09342	0.82347	0.60314	0.82995	0.77085	0.46982	0.30750	0.44248
LogStmLgth	1.80659	2.00368	2.30103	1.87134	2.13672	2.24551	1.76328	1.68637	1.50311	1.30621	1.90875	1.75105	1.63165
LogOIRAT	0.37664	0.54168	0.82914	0.62188	0.45245	0.31351	0.33805	0.37196	0.09691	0.15204	0.45295	0.55528	0.33081
LogIIRAT	0.46240	0.57709	0.62633	0.60527	0.58708	0.24778	0.31852	0.29727	0.29979	0.25130	0.38043	0.36368	0.30565
LogOI/II	-0.04966	-0.07274	-0.04210	-0.15467	0.02137	-0.06164	-0.07294	-0.19737	-0.22309	-0.03559	-0.08201	0.03640	-0.15372
LogInvRAT	0.06656	0.21490	-0.01012	0.24324	-0.10881	-0.14644	-0.05210	0.15951	0.19582	0.03698	0.06257	0.06277	-0.11577
LogLFRAT	1.28265	1.11571	1.52770	1.93777	1.94281	1.96671	1.24203	1.24270	1.15060	0.96210	1.47064	1.59554	1.33726

Appendix 2: Morphometric data set for Chapter 2.

	Leio2	Leio3	Leio4	Leio5	Leio6	Leio7	Leio8	Leio9	Leio10	Leio11	Lict1	Lict3	Lict4
Habit	1	1	1	1	1	1	1	1	1	1	0	0	0
InvSet	1	1	0	0	1	1	0	0	1	0	0	0	0
ParScl	0	0	0	0	1	1	0	1	1	1	0	0	0
InvBase	1	1	1	1	1	0	1	1	2	0	1	1	1
LfIndu	2	0	2	2	2	2	0	2	2	1	0	1	0
LfMarg	3	3	3	3	3	3	3	3	3	3	1	3	3
LfDiss	6	4	5	5	6	6	5	4	6	3	3	1	2
OIL	4.29	3.83	8.54	6.37	5.41	4.09	4.8	3.36	3.57	2.68	1.95	1.43	2.57
OIW	3.51	2.58	2.18	2.92	2.83	3.17	2.49	2.03	2.03	1.76	1.91	1.06	1.51
IIL	5.95	5.55	9.43	6.93	6.22	6.01	7.25	5.6	5.9	4.23	6.11	5.64	8.28
IIW	3.04	2.35	2.28	2.41	3.32	3.62	2.68	2.15	2.44	1.84	2.74	2.13	3.1
InvL	11.46	9.35	12.53	10.49	13.17	11.92	8.48	7.71	10.25	6.21	7.89	8.48	9.82
InvW	12.43	9.22	14.76	10.49	15.87	14.04	7.59	9.14	13.93	8.07	6.44	4.2	10.32
LfLgth	73.41	102.17	80.97	90.02	129.43	110.43	108.51	67.29	74.01	50.49	23.22	28.05	46.78
LfWdth	3.09	6.14	6.24	3.5	2.62	4	7.11	2.62	3.2	2.57	4.34	2.66	9.98
StmLgth	93.17	175	240	116.71	150.26	111.39	170	54.08	84.82	110	80.44	39.53	55.44
LogOIL	0.63246	0.58320	0.93146	0.80414	0.73320	0.61172	0.68124	0.52634	0.55267	0.42813	0.29003	0.15534	0.40993
LogOIW	0.54531	0.41162	0.33846	0.46538	0.45179	0.50106	0.39620	0.30750	0.30750	0.24551	0.28103	0.02531	0.17898
LogIIL	0.77452	0.74429	0.97451	0.84073	0.79379	0.77887	0.86034	0.74819	0.77085	0.62634	0.78604	0.75128	0.91803
LogIIW	0.48287	0.37107	0.35793	0.38202	0.52114	0.55871	0.42813	0.33244	0.38739	0.26482	0.43775	0.32838	0.49136
LogInvL	1.05918	0.97081	1.09795	1.02078	1.11959	1.07628	0.92840	0.88705	1.01072	0.79309	0.89708	0.92840	0.99211
LogInvW	1.09447	0.96473	1.16909	1.02078	1.20058	1.14737	0.88024	0.96095	1.14395	0.90687	0.80889	0.62325	1.01368
LogLfLgth	1.86576	2.00932	1.90832	1.95434	2.11203	2.04309	2.03547	1.82795	1.86929	1.70321	1.36586	1.44793	1.67006
LogLfWdth	0.48996	0.78817	0.79518	0.54407	0.41830	0.60206	0.85187	0.41830	0.50515	0.40993	0.63749	0.42488	0.99913
LogStmLgth	1.96928	2.24304	2.38021	2.06711	2.17684	2.04685	2.23045	1.73304	1.92850	2.04139	1.90547	1.59693	1.74382
LogOIRAT	0.08715	0.17158	0.59300	0.33876	0.28141	0.11066	0.28504	0.21884	0.24517	0.18262	0.00900	0.13003	0.23096
LogIIRAT	0.29164	0.37323	0.61658	0.45872	0.27265	0.22017	0.43220	0.41575	0.38346	0.36152	0.34829	0.42290	0.42667
LogOI/II	-0.14206	-0.16109	-0.04305	-0.03659	-0.06059	-0.16715	-0.17910	-0.22185	-0.21818	-0.19821	-0.49601	-0.59594	-0.50810
LogInvRAT	-0.03529	0.00608	-0.07114	0.00000	-0.08099	-0.07109	0.04815	-0.07389	-0.13323	-0.11378	0.08819	0.30515	-0.02157
LogLFRAT	1.37580	1.22116	1.11314	1.41027	1.69373	1.44103	1.18360	1.40965	1.36414	1.29327	0.72837	1.02305	0.67093

Appendix 2: Morphometric data set for Chapter 2.

	Lict5	Lict6	Lict8	Lict10	Lict11	Linlin1	Linlin2	Linlin3	Linlin4	Linlin5	Linlin6	Linlin9	Linlin10
Habit	0	0	0	0	0	1	1	1	1	1	1	1	1
InvSet	0	0	0	0	0	1	0	0	0	0	0	0	0
ParScl	0	0	0	0	0	1	0	1	1	1	1	1	1
InvBase	1	1	1	1	1	2	1	2	2	1	1	1	2
LfIndu	1	1	1	1	1	0	2	0	0	0	0	0	0
LfMarg	3	3	3	3	3	0	3	3	3	1	3	3	3
LfDiss	4	3	3	3	1	1	5	4	1	5	1	1	5
OIL	3.37	3.54	2.13	2.57	2.5	1.87	5.6	9.33	13.47	7.79	4.53	12.53	5.95
OIW	2.44	2.29	1.3	1.41	1.58	1.4	1.49	2.01	1.66	1.77	1.17	1.36	0.55
IIL	4.34	3.55	5.18	4.92	5.21	5.31	4.82	10.56	12.24	8.92	8.88	17.44	7.23
IIW	1.76	2.28	1.92	2.37	2.26	1.42	1.03	1.93	1.86	1.8	1.4	2.2	2.52
InvL	5.04	6.61	8.39	7.82	8	6.2	10.24	9.91	7.3	5.91	7.01	9.29	7.69
InvW	3.37	3.22	4.5	4.99	5.09	6.11	10.24	10.88	10.25	5.07	3.34	7.26	7.38
LfLgth	57.28	29.48	32.97	29.12	25.86	108.39	151.02	121.66	230	85.81	57.96	210	82.59
LfWdth	10.24	11.91	6.55	7.93	7.19	2.05	2.32	6.73	3.81	4.21	1.57	3.33	3.15
StmLgth	52.94	13.97	70.33	33.97	26.35	111.98	230	125.46	380	91.92	70.5	235	74.11
LogOIL	0.52763	0.54900	0.32838	0.40993	0.39794	0.27184	0.74819	0.96988	1.12937	0.89154	0.65610	1.09795	0.77452
LogOIW	0.38739	0.35984	0.11394	0.14922	0.19866	0.14613	0.17319	0.30320	0.22011	0.24797	0.06819	0.13354	-0.25964
LogIIL	0.63749	0.55023	0.71433	0.69197	0.71684	0.72509	0.68305	1.02366	1.08778	0.95036	0.94841	1.24155	0.85914
LogIIW	0.24551	0.35793	0.28330	0.37475	0.35411	0.15229	0.01284	0.28556	0.26951	0.25527	0.14613	0.34242	0.40140
LogInvL	0.70243	0.82020	0.92376	0.89321	0.90309	0.79239	1.01030	0.99607	0.86332	0.77159	0.84572	0.96802	0.88593
LogInvW	0.52763	0.50786	0.65321	0.69810	0.70672	0.78604	1.01030	1.03663	1.01072	0.70501	0.52375	0.86094	0.86806
LogLfLgth	1.75800	1.46953	1.51812	1.46419	1.41263	2.03499	2.17903	2.08515	2.36173	1.93354	1.76313	2.32222	1.91693
LogLfWdth	1.01030	1.07591	0.81624	0.89927	0.85673	0.31175	0.36549	0.82802	0.58092	0.62428	0.19590	0.52244	0.49831
LogStmLgth	1.72378	1.14520	1.84714	1.53110	1.42078	2.04914	2.36173	2.09851	2.57978	1.96341	1.84819	2.37107	1.86988
LogOIRAT	0.14024	0.18917	0.21444	0.26071	0.19928	0.12571	0.57500	0.66669	0.90926	0.64356	0.58791	0.96441	1.03415
LogIIRAT	0.39198	0.19229	0.43103	0.31722	0.36273	0.57281	0.67021	0.73811	0.81827	0.69509	0.80228	0.89912	0.45774
LogOI/II	-0.10986	-0.00123	-0.38595	-0.28203	-0.31890	-0.45325	0.06514	-0.05378	0.04159	-0.05883	-0.29231	-0.14360	-0.08462
LogInvRAT	0.17480	0.31235	0.27055	0.19511	0.19637	0.00635	0.00000	-0.04056	-0.14740	0.06658	0.32197	0.10708	0.01787
LogLFRAT	0.74770	0.39362	0.70188	0.56492	0.55590	1.72324	1.81355	1.25713	1.78080	1.30926	1.56723	1.79978	1.41862

Appendix 2: Morphometric data set for Chapter 2.

	Linlin12	Linlin13	Linlin15	Linlin21	Linlin23	Linlin24	Linlin25	Linlin26	Linlin27	Linlin28	Linlin29	LinO1	LinO2
Habit	1	1	1	1	1	1	1	1	1	1	1	1	1
InvSet	1	1	0	0	0	0	0	0	0	0	0	0	1
ParScl	1	1	1	0	1	0	0	0	1	0	0	1	1
InvBase	1	1	1	1	2	1	1	2	1	0	2	1	2
LfIndu	2	2	2	0	0	0	2	0	0	1	0	0	2
LfMarg	1	3	3	3	3	3	3	3	3	0	0	3	3
LfDiss	5	1	5	1	1	1	5	1	5	1	1	1	5
OIL	7.42	5.03	9.24	8.27	7.99	6.36	5.6	5.48	8.89	11.7	12.85	9.33	10.41
OIW	1.71	1.6	1.34	1.55	1.05	1.06	1.49	2.42	1.54	1.94	2.39	2.35	1.8
IIL	13.16	11.26	7.62	9.1	13.07	8.39	4.82	6.32	12.69	12.9	12.5	16.2	16.38
IIW	2.61	2.28	2.14	1.55	2.04	1.71	1.03	1.78	2.19	1.26	2.52	1.51	1.81
InvL	9.2	9.5	6.85	8.27	7.83	6.39	10.24	7.31	7.43	8.08	10.32	9.35	6.92
InvW	7.21	9.01	5.93	5.7	5	5.98	10.24	7.06	9.59	9.76	8.32	13.76	14.63
LfLgth	81.71	73.34	101.94	210	19.5	141.44	151.02	87.49	83.07	170	180	122.13	88.16
LfWdth	3.23	3.53	3.61	3.68	2.06	7.28	2.32	5.43	5.97	2.02	1.22	24.67	13.27
StmLgth	94.25	49.97	74.36	153.28	240	139.13	230	120	210	150	170	290	124.48
LogOIL	0.87040	0.70157	0.96567	0.91751	0.90255	0.80346	0.74819	0.73878	0.94890	1.06819	1.10890	0.96988	1.01745
LogOIW	0.23300	0.20412	0.12710	0.19033	0.02119	0.02531	0.17319	0.38382	0.18752	0.28780	0.37840	0.37107	0.25527
LogIIL	1.11926	1.05154	0.88195	0.95904	1.11628	0.92376	0.68305	0.80072	1.10346	1.11059	1.09691	1.20952	1.21431
LogIIW	0.41664	0.35793	0.33041	0.19033	0.30963	0.23300	0.01284	0.25042	0.34044	0.10037	0.40140	0.17898	0.25768
LogInvL	0.96379	0.97772	0.83569	0.91751	0.89376	0.80550	1.01030	0.86392	0.87099	0.90741	1.01368	0.97081	0.84011
LogInvW	0.85794	0.95472	0.77305	0.75587	0.69897	0.77670	1.01030	0.84880	0.98182	0.98945	0.92012	1.13862	1.16524
LogLfLgth	1.91228	1.86534	2.00834	2.32222	1.29003	2.15057	2.17903	1.94196	1.91944	2.23045	2.25527	2.08682	1.94527
LogLfWdth	0.50920	0.54777	0.55751	0.56585	0.31387	0.86213	0.36549	0.73480	0.77597	0.30535	0.08636	1.39217	1.12287
LogStmLgth	1.97428	1.69871	1.87134	2.18549	2.38021	2.14342	2.36173	2.07918	2.32222	2.17609	2.23045	2.46240	2.09510
LogOIRAT	0.63741	0.49745	0.83857	0.72717	0.88136	0.77815	0.57500	0.35497	0.76138	0.78038	0.73051	0.59881	0.76218
LogIIRAT	0.70262	0.69360	0.55154	0.76871	0.80665	0.69077	0.67021	0.55030	0.76302	1.01022	0.69551	1.03054	0.95664
LogOI/II	-0.24885	-0.34997	0.08372	-0.04154	-0.21373	-0.12030	0.06514	-0.06194	-0.15456	-0.04240	0.01199	-0.23963	-0.19686
LogInvRAT	0.10585	0.02300	0.06264	0.16163	0.19479	0.02880	0.00000	0.01511	-0.11083	-0.08204	0.09356	-0.16781	-0.32514
LogLFRAT	1.40307	1.31757	1.45084	1.75637	0.97617	1.28844	1.81355	1.20716	1.14347	1.92510	2.16891	0.69465	0.82240

Appendix 2: Morphometric data set for Chapter 2.

	LinO3	LinO4	LinO5	LinO6	LinO7	LinO8	LinO9	LinO10	Marit	Oth	Pct1	Pct2	Pct3
Habit	1	1	1	1	1	1	1	1	0	1	1	1	1
InvSet	0	0	0	0	0	0	0	0	0	1	0	1	1
ParScl	1	1	1	1	1	1	1	1	0	0	1	0	1
InvBase	2	2	2	0	2	2	2	0	2	2	1	1	1
LfIndu	0	0	0	0	0	0	0	0	0	1	0	2	0
LfMarg	0	0	2	2	2	2	2	2	0	3	0	3	3
LfDiss	1	1	5	5	1	5	1	1	5	5	6	5	5
OIL	4.89	6.22	7.02	10.53	8.34	9.55	11.25	7.63	2.95	3.34	7.26	4.68	3.94
OIW	1.45	2.08	2.52	2.1	2.15	1.77	1.43	1.68	1.06	1.27	1.88	1.78	1.21
IIL	11.83	10.83	12.91	20.09	16.54	22.76	20.06	15.1	3.9	5.11	4.03	3.53	5.77
IIW	2.69	1.18	1.94	2.07	1.74	2.88	1.92	1.95	1.18	0.85	2	1.34	0.9
InvL	8.57	8.27	8.98	11.34	12.55	12.21	11.53	10.68	6.86	6.67	10.42	7.58	10.32
InvW	10.16	11.48	12.07	14.16	10.71	14.05	10.46	12.08	3.9	5.76	7.2	7.58	12.15
LfLgth	76.55	120.13	93.97	110.44	212	155.09	155.47	81.02	50.17	48.05	68.73	99.45	69.25
LfWdth	10.65	14.81	15.17	11.04	25.28	22.1	19.98	17.32	2.18	2.91	1.21	1.52	7.56
StmLgth	142.86	150.56	114.56	124.57	103.93	153.93	220	130.4	52.4	63.46	75.02	70.91	73.67
LogOIL	0.68931	0.79379	0.84634	1.02243	0.92117	0.98000	1.05115	0.88252	0.46982	0.52375	0.86094	0.67025	0.59550
LogOIW	0.16137	0.31806	0.40140	0.32222	0.33244	0.24797	0.15534	0.22531	0.02531	0.10380	0.27416	0.25042	0.08279
LogIIL	1.07298	1.03463	1.11093	1.30298	1.21854	1.35717	1.30233	1.17898	0.59106	0.70842	0.60531	0.54777	0.76118
LogIIW	0.42975	0.07188	0.28780	0.31597	0.24055	0.45939	0.28330	0.29003	0.07188	-0.07058	0.30103	0.12710	-0.04576
LogInvL	0.93298	0.91751	0.95328	1.05461	1.09864	1.08672	1.06183	1.02857	0.83632	0.82413	1.01787	0.87967	1.01368
LogInvW	1.00689	1.05994	1.08171	1.15106	1.02979	1.14768	1.01953	1.08207	0.59106	0.76042	0.85733	0.87967	1.08458
LogLfLgth	1.88395	2.07965	1.97299	2.04313	2.32634	2.19058	2.19165	1.90859	1.70044	1.68169	1.83715	1.99760	1.84042
LogLfWdth	1.02735	1.17056	1.18099	1.04297	1.40278	1.34439	1.30060	1.23855	0.33846	0.46389	0.08279	0.18184	0.87852
LogStmLgth	2.15491	2.17771	2.05903	2.09541	2.01674	2.18732	2.34242	2.11528	1.71933	1.80250	1.87518	1.85071	1.86729
LogOIRAT	0.52794	0.47573	0.44494	0.70021	0.58873	0.73203	0.89582	0.65722	0.44452	0.41994	0.58678	0.41983	0.51271
LogIIRAT	0.64323	0.96275	0.82312	0.98701	0.97799	0.89778	1.01903	0.88894	0.51918	0.77900	0.30428	0.42067	0.80693
LogOI/II	-0.38368	-0.24084	-0.26459	-0.28055	-0.29737	-0.37717	-0.25118	-0.29645	-0.12124	-0.18467	0.25563	0.12247	-0.16568
LogInvRAT	-0.07391	-0.14244	-0.12843	-0.09645	0.06885	-0.06096	0.04230	-0.05350	0.24526	0.06370	0.16054	0.00000	-0.07090
LogLFRAT	0.85660	0.90910	0.79200	1.00016	0.92356	0.84619	0.89105	0.67004	1.36199	1.21780	1.75436	1.81576	0.96190

Appendix 2: Morphometric data set for Chapter 2.

	Pct4	Pct5	Pct6	Pct7	Pct8	Rigid1	Rigid3	Rigid4	Rigid5	Rigid6	Rigid7	Rigid8	Rigid9
Habit	1	1	1	1	1	1	1	1	1	1	1	1	1
InvSet	0	0	0	1	1	0	0	1	0	0	2	1	1
ParScl	1	1	1	1	1	1	0	1	1	1	1	0	0
InvBase	2	1	2	1	0	2	1	1	1	2	2	2	2
LfIndu	2	2	0	2	2	2	2	2	2	2	0	0	0
LfMarg	3	3	3	3	3	3	3	3	3	3	3	0	3
LfDiss	4	5	5	5	5	6	6	5	6	6	5	5	5
OIL	8.9	6.2	7.44	7.08	6.97	2.96	2.79	3.72	5.09	6.29	2.52	5.88	3.33
OIW	1.03	0.87	1.85	1.13	1.96	1.1	1.6	2.08	1.74	0.82	1.66	1.72	1.44
IIL	9.32	6.84	8.95	4.89	9.94	4.33	3.64	4.59	6.29	6.82	4.11	5.89	5.85
IIW	1.89	2.13	2.39	2.15	2.25	1.61	2.22	2.52	1.47	1.63	2.41	1.33	2
InvL	9.23	10.48	8.79	8.92	8.99	8.31	8.58	12.36	12.03	9.34	7.26	9.31	6.48
InvW	12.45	11.43	17.49	10.26	10.49	9.72	8.69	19.81	11.85	9.34	10.13	8.87	8.71
LfLgth	114.81	165	200	140	150	68.57	98.5	110	39.76	47.13	65.66	146.55	77.87
LfWdth	3.04	10.5	8.45	5.08	6.35	1.9	2.86	4.84	1.44	2.58	2.47	4.99	2.17
StmLgth	98.42	230	240	150	140	83.91	117.68	120	80.6	42.12	35.27	91.45	83.04
LogOIL	0.94939	0.79239	0.87157	0.85003	0.84323	0.47129	0.44560	0.57054	0.70672	0.79865	0.40140	0.76938	0.52244
LogOIW	0.01284	-0.06048	0.26717	0.05308	0.29226	0.04139	0.20412	0.31806	0.24055	-0.08619	0.22011	0.23553	0.15836
LogIIL	0.96942	0.83506	0.95182	0.68931	0.99739	0.63649	0.56110	0.66181	0.79865	0.83378	0.61384	0.77012	0.76716
LogIIW	0.27646	0.32838	0.37840	0.33244	0.35218	0.20683	0.34635	0.40140	0.16732	0.21219	0.38202	0.12385	0.30103
LogInvL	0.96520	1.02036	0.94399	0.95036	0.95376	0.91960	0.93349	1.09202	1.08027	0.97035	0.86094	0.96895	0.81158
LogInvW	1.09517	1.05805	1.24279	1.01115	1.02078	0.98767	0.93902	1.29688	1.07372	0.97035	1.00561	0.94792	0.94002
LogLfLgth	2.05998	2.21748	2.30103	2.14613	2.17609	1.83613	1.99344	2.04139	1.59945	1.67330	1.81730	2.16599	1.89137
LogLfWdth	0.48287	1.02119	0.92686	0.70586	0.80277	0.27875	0.45637	0.68485	0.15836	0.41162	0.39270	0.69810	0.33646
LogStmLgth	1.99308	2.36173	2.38021	2.17609	2.14613	1.92381	2.07070	2.07918	1.90634	1.62449	1.54741	1.96118	1.91929
LogOIRAT	0.93655	0.85287	0.60440	0.79695	0.55098	0.42990	0.24148	0.25248	0.46617	0.88484	0.18129	0.53385	0.36408
LogIIRAT	0.69295	0.50668	0.57343	0.35687	0.64520	0.42966	0.21475	0.26041	0.63133	0.62160	0.23182	0.64626	0.46613
LogOI/II	-0.02003	-0.04266	-0.08025	0.16072	-0.15415	-0.16520	-0.11550	-0.09127	-0.09193	-0.03513	-0.21244	-0.00074	-0.24471
LogInvRAT	-0.12997	-0.03768	-0.29880	-0.06078	-0.06702	-0.06807	-0.00553	-0.20487	0.00655	0.00000	-0.14467	0.02103	-0.12844
LogLFRAT	1.57711	1.19629	1.37417	1.44026	1.37332	1.55738	1.53707	1.35655	1.44108	1.26168	1.42460	1.46789	1.55491

Appendix 2: Morphometric data set for Chapter 2.

	Rigid12	Rigid13	Rigid14	Rigs2	Rigs3	Rigs4	Rigs5	Rigs6	Rigs7	Rigs9	Rigs10	Rigs11	Rigs16
Habit	1	1	1	0	0	0	0	0	0	0	0	0	0
InvSet	1	1	0	1	1	1	0	1	1	0	0	0	1
ParScl	1	0	0	1	1	1	1	1	1	1	1	1	0
InvBase	1	0	2	0	0	0	1	0	0	0	1	0	2
LfIndu	2	2	2	1	0	1	0	0	1	0	0	0	1
LfMarg	3	3	3	0	0	0	0	0	0	0	0	0	0
LfDiss	5	5	3	5	5	1	1	1	1	5	1	1	1
OIL	3.33	5.18	2.12	3.71	2.43	3.59	5.2	3.63	2.33	7.44	9.55	4.47	3.12
OIW	1.28	1.06	1.05	1.67	3.26	1.99	2.92	2.16	1.67	2.35	1.8	1.64	1.82
IIL	4.71	4.26	3.74	6.48	5.45	6.34	5.32	4.71	4.14	10.46	10.52	6.81	4.66
IIW	2.33	2.2	2.04	1.89	2.68	1.91	1.88	2.4	1.56	2.36	2.48	2.78	1.64
InvL	7.15	10.24	7.6	9.97	10.03	9.48	9.66	7.78	8.39	9.6	8.23	7.38	6.53
InvW	7.99	5	6.12	11.87	17.05	13.33	11.76	8.23	8.77	9.49	10.53	6.88	6.03
LfLgth	109.65	102.25	150.42	70.13	60.8	58.67	76.76	26.91	37.29	113.59	114.04	63.2	35.06
LfWdth	1.99	3.63	2.08	8.82	13.31	6.23	14.35	4.71	8.76	18.37	12.97	9.65	6.53
StmLgth	180	88.97	142	56.33	77.16	61.02	100	23.94	28.59	93.13	114.02	41.94	33.23
LogOIL	0.52244	0.71433	0.32634	0.56937	0.38561	0.55509	0.71600	0.55991	0.36736	0.87157	0.98000	0.65031	0.49415
LogOIW	0.10721	0.02531	0.02119	0.22272	0.51322	0.29885	0.46538	0.33445	0.22272	0.37107	0.25527	0.21484	0.26007
LogIIL	0.67302	0.62941	0.57287	0.81158	0.73640	0.80209	0.72591	0.67302	0.61700	1.01953	1.02202	0.83315	0.66839
LogIIW	0.36736	0.34242	0.30963	0.27646	0.42813	0.28103	0.27416	0.38021	0.19312	0.37291	0.39445	0.44404	0.21484
LogInvL	0.85431	1.01030	0.88081	0.99870	1.00130	0.97681	0.98498	0.89098	0.92376	0.98227	0.91540	0.86806	0.81491
LogInvW	0.90255	0.69897	0.78675	1.07445	1.23172	1.12483	1.07041	0.91540	0.94300	0.97727	1.02243	0.83759	0.78032
LogLfLgth	2.04001	2.00966	2.17731	1.84590	1.78390	1.76842	1.88513	1.42991	1.57159	2.05534	2.05706	1.80072	1.54481
LogLfWdth	0.29885	0.55991	0.31806	0.94547	1.12418	0.79449	1.15685	0.67302	0.94250	1.26411	1.11294	0.98453	0.81491
LogStmLgth	2.25527	1.94924	2.15229	1.75074	1.88739	1.78547	2.00000	1.37912	1.45621	1.96909	2.05698	1.62263	1.52153
LogOIRAT	0.41523	0.68902	0.30515	0.34666	-0.12761	0.25624	0.25062	0.22545	0.14464	0.50051	0.72473	0.43546	0.23408
LogIIRAT	0.30566	0.28699	0.26324	0.53511	0.30826	0.52106	0.45175	0.29281	0.42388	0.64662	0.62756	0.38910	0.45354
LogOI/II	-0.15058	0.08492	-0.24654	-0.24220	-0.35079	-0.24699	-0.00991	-0.11311	-0.24964	-0.14796	-0.04201	-0.18284	-0.17423
LogInvRAT	-0.04824	0.31133	0.09406	-0.07576	-0.23042	-0.14802	-0.08543	-0.02442	-0.01924	0.00501	-0.10703	0.03047	0.03460
LogLFRAT	1.74116	1.44976	1.85924	0.90044	0.65973	0.97393	0.72828	0.75689	0.62909	0.79123	0.94412	0.81619	0.72990

Appendix 2: Morphometric data set for Chapter 2.

	Rigs17	Rigs19	Rigs20	Rigs21	Rigs22	Rigs23	Serr1	Serr2	Serr3	Serr4	Serr6	Serr7	Serr8
Habit	0	0	0	0	0	0	1	1	1	1	1	1	1
InvSet	0	0	1	0	1	1	0	0	0	0	1	1	1
ParScl	1	1	1	1	1	0	1	1	1	0	0	0	1
InvBase	2	2	2	2	2	0	2	2	0	1	1	2	0
LfIndu	0	0	0	0	0	0	2	0	2	0	3	2	2
LfMarg	0	0	0	0	0	0	3	0	3	1	3	3	3
LfDiss	5	5	1	1	1	1	5	4	5	6	4	1	5
OIL	5.51	3.36	5.97	4.58	6.26	6.42	5.68	5.44	6.48	5.02	5	9.81	5.04
OIW	2.44	2.26	2.38	2.74	2.15	3.54	1.14	3.11	1.61	2.56	2.24	1.54	1.07
IIL	6.12	6.09	6.93	5.23	8.14	4.75	7.36	4.95	5.56	7.6	6.59	10.51	4.78
IIW	2.05	1.72	1.83	2.96	1.93	2.15	1.84	2.64	2.02	2.99	1.64	3.92	2.04
InvL	5.5	7.76	5.64	9.06	9.23	8.67	8.47	8.38	10.7	9.74	9.03	8	9.83
InvW	8.91	9.01	11.1	10.56	10.37	8.19	9.21	10.1	11.46	12.54	8.12	8.18	10.81
LfLgth	86.74	82.37	66.73	69.86	77.33	76.03	160	151.3	180	90.17	135.1	117.74	94.53
LfWdth	9.98	9.18	10.38	12.99	15.27	11.76	4.67	5.51	3.08	1.9	3.84	5.81	5.04
StmLgth	81.94	88.18	35.53	54.87	70.03	36.89	230	135.83	160	194	210	53.23	95.09
LogOIL	0.74115	0.52634	0.77597	0.66087	0.79657	0.80754	0.75435	0.73560	0.81158	0.70070	0.69897	0.99167	0.70243
LogOIW	0.38739	0.35411	0.37658	0.43775	0.33244	0.54900	0.05690	0.49276	0.20683	0.40824	0.35025	0.18752	0.02938
LogIIL	0.78675	0.78462	0.84073	0.71850	0.91062	0.67669	0.86688	0.69461	0.74507	0.88081	0.81889	1.02160	0.67943
LogIIW	0.31175	0.23553	0.26245	0.47129	0.28556	0.33244	0.26482	0.42160	0.30535	0.47567	0.21484	0.59329	0.30963
LogInvL	0.74036	0.88986	0.75128	0.95713	0.96520	0.93802	0.92788	0.92324	1.02938	0.98856	0.95569	0.90309	0.99255
LogInvW	0.94988	0.95472	1.04532	1.02366	1.01578	0.91328	0.96426	1.00432	1.05918	1.09830	0.90956	0.91275	1.03383
LogLfLgth	1.93822	1.91577	1.82432	1.84423	1.88835	1.88098	2.20412	2.17984	2.25527	1.95506	2.13066	2.07092	1.97557
LogLfWdth	0.99913	0.96284	1.01620	1.11361	1.18384	1.07041	0.66932	0.74115	0.48855	0.27875	0.58433	0.76418	0.70243
LogStmLgth	1.91350	1.94537	1.55060	1.73933	1.84528	1.56691	2.36173	2.13300	2.20412	2.28780	2.32222	1.72616	1.97813
LogOIRAT	0.35376	0.17223	0.39940	0.22311	0.46414	0.25853	0.69744	0.24284	0.60475	0.29246	0.34872	0.80415	0.67305
LogIIRAT	0.47500	0.54909	0.57828	0.24721	0.62507	0.34426	0.60206	0.27300	0.43972	0.40514	0.60404	0.42832	0.36980
LogOI/II	-0.04560	-0.25828	-0.06476	-0.05764	-0.11405	0.13084	-0.11253	0.04099	0.06650	-0.18011	-0.11992	-0.02993	0.02300
LogInvRAT	-0.20952	-0.06486	-0.29404	-0.06654	-0.05058	0.02474	-0.03638	-0.08108	-0.02980	-0.10974	0.04613	-0.00966	-0.04127
LogLFRAT	0.93909	0.95293	0.80812	0.73062	0.70451	0.81058	1.53480	1.43869	1.76672	1.67631	1.54632	1.30675	1.27314

Appendix 2: Morphometric data set for Chapter 2.

	Serr9	spnov1	spnov2	spnov3	Ten1	Ten2	Ten3	Ten4	Ten5	Ten6	Ten7	Ten8	Ten9	Ten10
Habit	1	1	1	1	1	1	1	1	1	1	1	1	1	1
InvSet	1	1	1	1	0	1	1	0	0	0	0	0	0	0
ParScl	1	0	0	0	2	2	2	2	2	2	2	2	2	2
InvBase	2	0	1	0	3	3	3	3	3	3	3	3	3	3
LfIndu	2	0	1	0	0	2	2	0	0	0	0	0	0	0
LfMarg	3	0	0	0	3	2	3	3	2	2	2	2	2	2
LfDiss	5	1	3	3	6	6	6	6	6	5	5	6	6	6
OIL	10.56	3.8	2.44	3.8	3.72	2.43	3.78	3.34	2.85	2.67	2.22	2.2	3.25	2.74
OIW	1.45	2.46	1.53	1.2	0.9	0.63	0.68	0.79	0.64	0.89	0.73	0.56	0.99	0.49
IIL	7.81	5.61	3.58	4.96	5.95	6.72	5.5	4.6	4.48	5.87	4.19	5.12	6.68	6.46
IIW	2.54	3.19	1.27	1.4	0.92	1.85	1.79	1.33	1.08	1.1	1.22	0.97	1.55	1.34
InvL	11.43	6.53	7.42	6.5	3.88	3.96	4.19	4.16	4.37	4.57	3.25	4.13	4.29	4.33
InvW	11.15	10.2	5.71	5.67	5.4	3.17	5.75	4.88	4.17	4.49	3.77	3.87	5.12	4.53
LfLgth	122.96	57.3	32.4	81.46	34.35	37.63	44.11	4.98	38.27	71.59	52.14	55.34	45.72	52.1
LfWdth	6.54	6.5	4.4	3.23	1.35	1.3	1.45	1.42	1.14	1.62	0.88	1.2	1.18	1.16
StmLgth	131.16	59.58	32.55	57.84	84.86	49.77	70.33	38.3	37.84	63.72	51.18	52.8	89.92	60.74
LogOIL	1.02366	0.57978	0.38739	0.57978	0.57054	0.38561	0.57749	0.52375	0.45484	0.42651	0.34635	0.34242	0.51188	0.43775
LogOIW	0.16137	0.39094	0.18469	0.07918	-0.04576	-0.20066	-0.16749	-0.10237	-0.19382	-0.05061	-0.13668	-0.25181	-0.00436	-0.30980
LogIIL	0.89265	0.74896	0.55388	0.69548	0.77452	0.82737	0.74036	0.66276	0.65128	0.76864	0.62221	0.70927	0.82478	0.81023
LogIIW	0.40483	0.50379	0.10380	0.14613	-0.03621	0.26717	0.25285	0.12385	0.03342	0.04139	0.08636	-0.01323	0.19033	0.12710
LogInvL	1.05805	0.81491	0.87040	0.81291	0.58883	0.59770	0.62221	0.61909	0.64048	0.65992	0.51188	0.61595	0.63246	0.63649
LogInvW	1.04727	1.00860	0.75664	0.75358	0.73239	0.50106	0.75967	0.68842	0.62014	0.65225	0.57634	0.58771	0.70927	0.65610
LogLfLgth	2.08976	1.75815	1.51055	1.91094	1.53593	1.57553	1.64454	0.69723	1.58286	1.85485	1.71717	1.74304	1.66011	1.71684
LogLfWdth	0.81558	0.81291	0.64345	0.50920	0.13033	0.11394	0.16137	0.15229	0.05690	0.20952	-0.05552	0.07918	0.07188	0.06446
LogStmLgth	2.11780	1.77510	1.51255	1.76223	1.92870	1.69697	1.84714	1.58320	1.57795	1.80428	1.70910	1.72263	1.95386	1.78347
LogOIRAT	0.86230	0.18885	0.20270	0.50060	0.61630	0.58627	0.74498	0.62612	0.64866	0.47712	0.48303	0.59423	0.51625	0.74755
LogIIRAT	0.48782	0.24517	0.45008	0.54935	0.81073	0.56020	0.48751	0.53891	0.61785	0.72725	0.53585	0.72250	0.63444	0.68313
LogOI/II	0.13101	-0.16918	-0.16649	-0.11570	-0.20397	-0.44176	-0.16287	-0.13901	-0.19643	-0.34213	-0.27586	-0.36685	-0.31289	-0.37248
LogInvRAT	0.01077	-0.19369	0.11377	0.05933	-0.14356	0.09664	-0.13745	-0.06933	0.02035	0.00767	-0.06446	0.02824	-0.07681	-0.01961
LogLFRAT	1.27419	0.94524	0.86709	1.40174	1.40559	1.46159	1.48317	0.54494	1.52595	1.64534	1.77269	1.66386	1.58822	1.65238

cpDNA primer screening and selection for Chapter 3

For the six cpDNA regions initial screened, nine samples were selected to determine if any inter- and intraspecific variability could be distinguished in each region (see Table A3.1 for sample details).

Table A3.2 lists the primers details for the regions not detailed in Chapter 3, Table 3.2.3.

Table A3.1: Nine samples used for primer screening (full details in Table 3.2.1).

Species	subsp	Sample
leiopoda		M240901
linearis	linearis	RM1010
	ovalis	RM854
rigida		M280902
tenuifolia		CAM1601
jurineifolia	scabra	CAM1604
lichtensteinii		CAM1916
rigens	leucolaena	RM952_1
krebsiana	serrulata	RM965

Table A3.2: Rejected cpDNA regions primer names, uses, authors, sequences, PCR annealing temperature and number of cycles.

Name	Use	Reference	Sequence	Anneal Temp	No. Cycles
<i>trnC-psbM</i>					
<i>trnCF</i>	Amplif/Seq	Shaw et al., 2005	CCA GTT CRA ATC YGG GTG	52°C	30
<i>psbMR</i>	Amplif/Seq	Shaw et al., 2005	ATG GAA GTA AAT ATT CTY GCA TTT ATT GC		
<i>trnS-trnM</i>					
<i>trnS</i>	Amplif/Seq	Demesure et al., 1995	GAG AGA GAG GGA TTC GAA CC	52°C	30
<i>trnM</i>	Amplif/Seq	Demesure et al., 1995	CAT AAC CTT GAG GTC ACG GG		
<i>trnT-trnL</i>					
Tab a	Amplif/Seq	Taberlet et al., 1991	CAT TAC AAA TGC GAT GCT CT	53-55°C	30-35
tab b	Amplif/Seq	Taberlet et al., 1991	TCT ACC GAT TTC GCC ATA TC		

Table A3.3 presents a list of comparative information of each region's length, variability, informativeness and data signal strength. Initial investigations into relative variability and information content indicated that although the *trnC-psbM* and *trnT-trnL* regions proved to be the most variable and informative of all the cpDNA regions, there were significant amplification and sequencing problems with both. In the *trnC-psbM* region, one sample (even when PCR amplification produced a clean clear band on an agarose gel) could not be successfully sequenced in either direction, and another sample could not be successfully sequenced with the reverse primer. Table A3.4 lists the indel information for each region. In the *trnT-trnL* region, the presence of multiple poly-A/T strings (up to

Appendix 2: Morphometric data set for Chapter 2.

17 bp in length) in almost all samples made amplification and bidirectional sequencing problematic. The *psbA-trnH* region can be seen to be highly prone to multibase repeat insertions, while the *trnS-fM* region is prone to single base pair repeat strings.

Table A3.3: Characteristics of each cpDNA region, including number of samples, total number of characters, number and percentage of variable and parsimony informative characters, as well as data signal statistic.

	No. samp.	Tot. chars	Variable Characters		Parsimony Inform. Ch.		g ₁
			Number	%	Number	%	
<i>trnS-trnM</i>	9	1021	14	1.4	0	0	
<i>trnL-F</i>	9	858	23	2.7	0	0	
<i>trnC-psbM</i>	8	541	20	3.7	5	0.9	-0.77
<i>psbA-trnH</i>	9	533	34	6.4	1	0.2	-2.823
<i>rpS16</i>	9	827	15	1.8	2	0.3	-0.588
<i>trnT-trnL</i>	9	545	22	4	3	0.6	-0.491

The *psbA-trnH* and *rpS16* regions were thus the next most profitable cpDNA regions to pursue for potential phylogenetic signal content. The *trnL-F* regions (jointly amplified by the “tab c” and “tab f” primers) had the next highest number of variable characters, and this region was tentatively pursued in the hopes that a greater sample size would render more phylogenetically informative sites.

Table A3.4: Indel information for each cpDNA region.

Region	Indels	Poly-N repeat strings	Other
<i>rpS16</i>	2 x 1 bp	poly-G (6-8 bp)	1 x 5 bp repeat insertion
	1 x 9 bp	poly-A (9-13 bp)	
<i>trnL-F</i>	1 x 1 bp		
<i>trnS-fM</i>	1 x 2 bp	poly-A (3-4 bp)	
		poly-T (9-13 bp)	
		poly-C (3-4 bp)	
		poly-T (7-8 bp)	
<i>trnT-L</i>	1 x 1 bp	poly-T (11-17 bp)	1 x 4 bp repeat insertion
	1 x 5 bp	poly-A string (8-10 bp, some with T inserts)	
<i>psbA-trnH</i>	4 x 1 bp 1 x 6 bp 1 x 11 bp 1 x 19 bp 1 x 269 bp	poly-A (7-9 bp)	1 x 5 bp repeat insertion
			2 x 6 bp repeat insertion
			1 x 5 bp repeat insertion (imperfect)
			1x (3xTTAAA) repeat insertion (3rd repeat imperfect)
			1 x 4 bp repeat insertion (imperfect)
			1 x (2x5 bp) repeat insertion
			1 x 11bp inversion (inside larger matchpaired region)
<i>trnC-psbM</i>	1 x 1bp 1 x 5bp	poly-A (7-13 bp)	
		poly-T (8-9 bp)	
		poly-T (5-6 bp)	

Appendix 4: nrDNA sequence data for Chapter 3.

	10	20	30	40	50	60	70	80	90	100	110]	
Berkheya	T	C	G	A	A	C	C	T	G	C	A	T
Gorteria	T	C	G	A	A	C	C	T	G	C	A	T
Hirpicium	T	C	G	A	A	C	C	T	G	C	A	T
caespitosa_RC448	T	C	G	A	A	C	C	T	G	C	A	T
caespitosa_RVC307	T	C	G	A	A	C	C	T	G	C	A	T
ciliaris_RM1230	T	C	G	A	A	C	C	T	G	C	A	T
ciliaris_RM1382	T	C	G	A	A	C	C	T	G	C	A	T
heterochaeta_RM1429_1	T	C	G	A	A	C	C	T	G	C	A	T
heterochaeta_RM1451	T	C	G	A	A	C	C	T	G	C	A	T
jurineifolia_jur_SR682	T	C	G	A	A	C	C	T	G	C	A	T
jurineifolia_jur_RM1518	T	C	G	A	A	C	C	T	G	C	A	T
jurineifolia_scab_CAM1604	T	C	G	A	A	C	C	T	G	C	A	T
jurineifolia_scab_CAM2652	T	C	G	A	A	C	C	T	G	C	A	T
krebsiana_arctotoides_RM868	T	C	G	A	A	C	C	T	G	C	A	T
krebsiana_arctotoides_RM876	T	C	G	A	A	C	C	T	G	C	A	T
krebsiana_krebsiana_RM1114	T	C	G	A	A	C	C	T	G	C	A	T
krebsiana_krebsiana_RM1136	T	C	G	A	A	C	C	T	G	C	A	T
krebsiana_serrulata_RM863	T	C	G	A	A	C	C	T	G	C	A	T
krebsiana_serrulata_RM965	T	C	G	A	A	C	C	T	G	C	A	T
leiopoda_M240901	T	C	G	A	A	C	C	T	G	C	A	T
leiopoda_RM1309	T	C	G	A	A	C	C	T	G	C	A	T
lichtensteinii_CAM1916	T	C	G	A	A	C	C	T	G	C	A	T
lichtensteinii_RM1249	T	C	G	A	A	C	C	T	G	C	A	T
linearis_linearis_RM1010	?	?	?	?	?	?	?	?	?	?	?	?
linearis_linearis_SH113	T	C	G	A	A	C	C	T	G	C	A	T
linearis_ovalis_NDsn	T	C	G	A	A	C	C	T	G	C	A	T
linearis_ovalis_RM854	T	C	G	A	A	C	C	T	G	C	A	T
maritima_RM1038	T	C	G	A	A	C	C	T	G	C	A	T
maritima_M290606_6	T	C	G	A	A	C	C	T	G	C	A	T
othonnites_RM1306	T	C	G	A	A	C	C	T	G	C	A	T
pectinata_M120903	T	C	G	A	A	C	C	T	G	C	A	T
pectinata_RM1044	T	C	G	A	A	C	C	T	G	C	A	T
rigida_M280902	?	?	?	?	?	?	?	?	?	?	?	?
rigida_RM840	T	C	G	A	A	C	C	T	G	C	A	T
rigens_leucolaena_RM773	T	C	G	A	A	C	C	T	G	C	A	T
rigens_leucolaena_RM952_1	T	C	G	A	A	C	C	T	G	C	A	T
rigens_rigens_RM763	T	C	G	A	A	C	C	T	G	C	A	T
rigens_rigens_SR463	T	C	G	A	A	C	C	T	G	C	A	T
rigens_uniflora_JC201205	T	C	G	A	A	C	C	T	G	C	A	T
rigens_uniflora_RM920	T	C	G	A	A	C	C	T	G	C	A	T
schenckii	?	?	?	?	?	?	?	?	?	?	?	?
serrata_M250904_15	T	C	G	A	A	C	C	T	G	C	A	T
serrata_RM898	T	C	G	A	A	C	C	T	G	C	A	T
tenuifolia_CAM1601	?	?	?	?	?	?	?	?	?	?	?	?
tenuifolia_M2730	T	C	G	A	A	C	C	T	G	C	A	T
spnov_M040906_33	T	C	G	A	A	C	C	T	G	C	A	T

Appendix 4: nrDNA sequence data for Chapter 3.

	120	130	140	150	160	170	180	190	200	210	220]
Berkheya	TGCC	TCGT	TYGG	GGGCT	CATG	AAC--	GTC	AC	WT	AGGC	ATCA
Gorteria	TGCC	CTAT	AGGG	-CTC	ATG	AAC--	GTC	AT	GT	CGGC	ATCA
Hirpicium	TG	CCCC	TTTT	GGGG	CTCG	TGAAC--	GTC	AT	GTT	TGGC	ATYA
caespitosa_RC448	AG	CCCT	TTTT	TGGG	GCTSG	TGAAC--	GT	AG	TGT	TGGC	ATCA
caespitosa_RVC307	AG	CCCT	TTTT	TGGG	GCTSG	TGAAC--	GT	AG	N	TGGC	ATCA
ciliaris_RM1230	TG	CCCC	TTTT	GGGG	CTCG	TGAAC--	GT	AG	TGT	TGGC	ATCA
ciliaris_RM1382	GG	CCCT	TTTT	TGGG	GCTCG	TGAAC--	GT	AG	TGT	TGGC	ATCA
heterochaeta_RM1429_1	AG	CC	-TTT	CYGG	-CTC	GTAAC--	GT	AG	TGT	CGGC	ATCA
heterochaeta_RM1451	AG	CC	-TTT	CYGG	-CTC	GTAAC--	GT	AG	TGT	CGGC	ATCA
jurineifolia_jur_SR682	AG	CCCT	TTTT	TGGG	GCTCT	TGAAC--	GTT	AT	GT	AGGC	ATCA
jurineifolia_jur_RM1518	AG	CCCT	TTTT	TGGG	GCTCT	TGAAC--	GTT	AT	GT	AGGC	ATCA
jurineifolia_scab_CAM1604	AG	CCCT	TTTT	TGGG	GCTCT	TGAAC--	GTT	AT	GT	AGGC	ATCA
jurineifolia_scab_CAM2652	AG	CCCT	TTTT	TGGG	GCTCT	TGAAC--	GTT	AT	GT	AGGC	ATCA
krebsiana_arctotoides_RM868	AG	CCCT	TTTT	TGGG	GCTCG	TGAAC--	TT	AG	TGT	TGGC	ATCT
krebsiana_arctotoides_RM876	AG	CCCT	TTTT	TGGG	GCTCG	TGAAC--	TT	AG	TGT	TGGC	ATCT
krebsiana_krebsiana_RM1114	AG	CCCT	TTTT	TGGG	GCTCG	TGAAC--	TT	AG	TGT	TGGC	ATCT
krebsiana_krebsiana_RM1136	AG	CCCT	TTTT	TGGG	GCTCG	TGAAC--	TT	AG	TGT	TGGC	ATCT
krebsiana_serrulata_RM863	AG	CCCT	TTTT	TGGG	GCTCG	TGAAC--	TT	AG	TGT	TGGC	ATCT
krebsiana_serrulata_RM965	AG	CCCT	TTTT	TGGG	GCTCG	TGAAC--	TT	AG	TGT	TGGC	ATCT
leiopoda_M240901	AG	CCCT	TTTT	TGGG	GCTCG	TGAAC--	TT	AG	TGT	TGGC	ATCT
leiopoda_RM1309	GG	CCCT	TTT	CTGG	-CTC	GTAAC	GT	AG	TGT	TGGC	ATCA
lichtensteinii_CAM1916	GG	CCCT	TTT	CTGG	-CTC	GTAAC	GT	AG	TGT	TGGC	ATCA
lichtensteinii_RM1249	GG	CCCT	TTT	CTGG	-CTC	GTAAC	GT	AG	TGT	TGGC	ATCA
linearis_linearis_RM1010	AG	CCCT	TTTT	TGGG	CTCG	TGAAC--	TT	AG	TGT	TGGC	ATCT
linearis_linearis_SH113	AG	CCCT	TTTT	TGGG	CTCG	TGAAC--	TT	AG	TGT	TGGC	ATCT
linearis_ovalis_NDsn	AG	CCCT	TTTT	TGGG	CTCG	TGAAC--	TT	AG	TGT	TGGC	ATCT
linearis_ovalis_RM854	AG	CCCT	TTTT	TGGG	CTCG	TGAAC--	TT	AG	TGT	TGGC	ATCT
maritima_RM1038	AG	CCCT	TTTT	TGGG	CTCG	TGAAC--	TT	AG	TGT	TGGC	ATCT
maritima_M290606_6	AG	CCCT	TTTT	TGGG	CTCG	TGAAC--	TT	AG	TGT	TGGC	ATCT
othonnites_RM1306	AG	CCCT	TTTT	TGGG	CTCG	TGAAC--	TT	AG	TGT	TGGC	ATCT
pectinata_M120903	AG	CCCT	TTTT	TGGG	CTCG	TGAAC--	TT	AG	TGT	TGGC	ATCT
pectinata_RM1044	AG	CCCT	TTTT	TGGG	CTCG	TGAAC--	TT	AG	TGT	TGGC	ATCT
rigida_M280902	AG	CCCT	TTTT	TGGG	CTCG	TGAAC--	TT	AG	TGT	TGGC	ATCT
rigida_RM840	AG	CCCT	TTTT	TGGG	CTCG	TGAAC--	TT	AG	TGT	TGGC	ATCT
rigens_leucolaena_RM773	AG	CCCT	TTTT	TGGG	CTCG	TGAAC--	TT	AG	TGT	TGGC	ATCT
rigens_leucolaena_RM952_1	AG	CCCT	TTTT	TGGG	CTCG	TGAAC--	TT	AG	TGT	TGGC	ATCT
rigens_rigens_RM763	AG	CCCT	TTTT	TGGG	CTCG	TGAAC--	TT	AG	TGT	TGGC	ATCT
rigens_rigens_SR463	AG	CCCT	TTTT	TGGG	CTCG	TGAAC--	TT	AG	TGT	TGGC	ATCT
rigens_uniflora_JC201205	AG	CCCT	TTTT	TGGG	CTCG	TGAAC--	TT	AG	TGT	TGGC	ATCT
rigens_uniflora_RM920	AG	CCCT	TTTT	TGGG	CTCG	TGAAC--	TT	AG	TGT	TGGC	ATCT
schenckii	AG	CCCT	TTTT	TGGG	CTCG	TGAAC--	TT	AG	TGT	TGGC	ATCT
serrata_M250904_15	AG	CCCT	TTTT	TGGG	CTCG	TGAAC--	TT	AG	TGT	TGGC	ATCT
serrata_RM898	AG	CCCT	TTTT	TGGG	CTCG	TGAAC--	TT	AG	TGT	TGGC	ATCT
tenuifolia_CAM1601	AG	CCCT	TTTT	TGGG	-CTC	GTAAC	GT	AG	TGT	TGGC	ATCA
tenuifolia_M2730	AG	CCCT	TTTT	TGGG	-CTC	GTAAC	GT	AG	TGT	TGGC	ATCA
spnov_M040906_33	AG	CCCT	TTTT	TGGG	CTCG	TGAAC--	TT	AG	TGT	TGGC	ATCT

Appendix 4: nrDNA sequence data for Chapter 3.

	340	350	360	370	380	390	400	410	420	430	440]
Berkheya	GAATTGCAGAATCCCGTGAACCATCGAGTTTTTTGAACGCAAGTTGCGCCCGAAACCATTTCGGTTCGAGGGC	ACGCTCTGCCTGGGCGT	CACGCATCGCGT	CGCCCC	-CACA						
Gorteria	GAATTGCAGAATCCCGTGAACCATCGAGTTTTTTGAACGCAAGTTGCGCCCGAAACCATTTCGGTTCGAGGGC	ACGCTCTGCCTGGGCGT	CACGCATCGCGT	CGCCCC	CCCCCACA						
Hirpicium	GAATTGCAGAATCCCGTGAACCATCGAGTTTTTTGAACGCAAGTTGCGCCCGAAACCATTTCGGTTCGAGGGC	ACGCTCTGCCTGGGCGT	CACGCATCGCGT	CGCCCC	-CACA						
caespitosa_RC448	GAATTGCAGAATCCCGTGAACCATCGAGTTTTTTGAACGCAAGTTGCGCCCGAAACCATTTCGGTTCGAGGGC	ACGCTCTGCCTGGGCGT	CACGCATCGCGT	CGCCCC	CCCCCACA						
caespitosa_RVC307	GAATTGCAGAATCCCGTGAACCATCGAGTTTTTTGAACGCAAGTTGCGCCCGAAACCATTTCGGTTCGAGGGC	ACGCTCTGCCTGGGCGT	CACGCATCGCGT	CGCCCC	CCCCCACA						
ciliaris_RM1230	GAATTGCAGAATCCCGTGAACCATCGAGTTTTTTGAACGCAAGTTGCGCCCGAAACCATTTCGGTTCGAGGGC	ACGCTCTGCCTGGGCGT	CACGCATCGCGT	CGCCCC	CCCCCACA						
ciliaris_RM1382	GAATTGCAGAATCCCGTGAACCATCGAGTTTTTTGAACGCAAGTTGCGCCCGAAACCATTTCGGTTCGAGGGC	ACGCTCTGCCTGGGCGT	CACGCATCGCGT	CGCCCC	CCCCCACA						
heterochaeta_RM1429_1	GAATTGCAGAATCCCGTGAACCATCGAGTTTTTTGAACGCAAGTTGCGCCCGAAACCATTTCGGTTCGAGGGC	ACGCTCTGCCTGGGCGT	CACGCATCGCGT	CGCCCC	CCCCCACA						
heterochaeta_RM1451	GAATTGCAGAATCCCGTGAACCATCGAGTTTTTTGAACGCAAGTTGCGCCCGAAACCATTTCGGTTCGAGGGC	ACGCTCTGCCTGGGCGT	CACGCATCGCGT	CGCCCC	CCCCCACA						
jurineifolia_jur_SR682	GAATTGCAGAATCCCGTGAACCATCGAGTTTTTTGAACGCAAGTTGCGCCCGAAACCATTTCGGTTCGAGGGC	ACGCTCTGCCTGGGCGT	CACGCATCGCGT	CGCCCC	CCCCCACA						
jurineifolia_jur_RM1518	GAATTGCAGAATCCCGTGAACCATCGAGTTTTTTGAACGCAAGTTGCGCCCGAAACCATTTCGGTTCGAGGGC	ACGCTCTGCCTGGGCGT	CACGCATCGCGT	CGCCCC	CCCCCACA						
jurineifolia_scab_CAM1604	GAATTGCAGAATCCCGTGAACCATCGAGTTTTTTGAACGCAAGTTGCGCCCGAAACCATTTCGGTTCGAGGGC	ACGCTCTGCCTGGGCGT	CACGCATCGCGT	CGCCCC	CCCCCACA						
jurineifolia_scab_CAM2652	GAATTGCAGAATCCCGTGAACCATCGAGTTTTTTGAACGCAAGTTGCGCCCGAAACCATTTCGGTTCGAGGGC	ACGCTCTGCCTGGGCGT	CACGCATCGCGT	CGCCCC	CCCCCACA						
krebsiana_arctotoides_RM868	GAATTGCAGAATCCCGTGAACCATCGAGTTTTTTGAACGCAAGTTGCGCCCGAAACCATTTCGGTTCGAGGGC	ACGCTCTGCCTGGGCGT	CACGCATCGCGT	CGCCCC	CCCCCACA						
krebsiana_arctotoides_RM876	GAATTGCAGAATCCCGTGAACCATCGAGTTTTTTGAACGCAAGTTGCGCCCGAAACCATTTCGGTTCGAGGGC	ACGCTCTGCCTGGGCGT	CACGCATCGCGT	CGCCCC	CCCCCACA						
krebsiana_krebsiana_RM1114	GAATTGCAGAATCCCGTGAACCATCGAGTTTTTTGAACGCAAGTTGCGCCCGAAACCATTTCGGTTCGAGGGC	ACGCTCTGCCTGGGCGT	CACGCATCGCGT	CGCCCC	CCCCCACA						
krebsiana_krebsiana_RM1136	GAATTGCAGAATCCCGTGAACCATCGAGTTTTTTGAACGCAAGTTGCGCCCGAAACCATTTCGGTTCGAGGGC	ACGCTCTGCCTGGGCGT	CACGCATCGCGT	CGCCCC	CCCCCACA						
krebsiana_serrulata_RM863	GAATTGCAGAATCCCGTGAACCATCGAGTTTTTTGAACGCAAGTTGCGCCCGAAACCATTTCGGTTCGAGGGC	ACGCTCTGCCTGGGCGT	CACGCATCGCGT	CGCCCC	CCCCCACA						
krebsiana_serrulata_RM965	GAATTGCAGAATCCCGTGAACCATCGAGTTTTTTGAACGCAAGTTGCGCCCGAAACCATTTCGGTTCGAGGGC	ACGCTCTGCCTGGGCGT	CACGCATCGCGT	CGCCCC	CCCCCACA						
leiopoda_M240901	GAATTGCAGAATCCCGTGAACCATCGAGTTTTTTGAACGCAAGTTGCGCCCGAAACCATTTCGGTTCGAGGGC	ACGCTCTGCCTGGGCGT	CACGCATCGCGT	CGCCCC	CCCCCACA						
leiopoda_RM1309	GAATTGCAGAATCCCGTGAACCATCGAGTTTTTTGAACGCAAGTTGCGCCCGAAACCATTTCGGTTCGAGGGC	ACGCTCTGCCTGGGCGT	CACGCATCGCGT	CGCCCC	CCCCCACA						
lichtensteinii_CAM1916	GAATTGCAGAATCCCGTGAACCATCGAGTTTTTTGAACGCAAGTTGCGCCCGAAACCATTTCGGTTCGAGGGC	ACGCTCTGCCTGGGCGT	CACGCATCGCGT	CGCCCC	CCCCCACA						
lichtensteinii_RM1249	GAATTGCAGAATCCCGTGAACCATCGAGTTTTTTGAACGCAAGTTGCGCCCGAAACCATTTCGGTTCGAGGGC	ACGCTCTGCCTGGGCGT	CACGCATCGCGT	CGCCCC	CCCCCACA						
linearis_linearis_RM1010	GAATTGCAGAATCCCGTGAACCATCGAGTTTTTTGAACGCAAGTTGCGCCCGAAACCATTTCGGTTCGAGGGC	ACGCTCTGCCTGGGCGT	CACGCATCGCGT	CGCCCC	CCCCCACA						
linearis_linearis_SH113	GAATTGCAGAATCCCGTGAACCATCGAGTTTTTTGAACGCAAGTTGCGCCCGAAACCATTTCGGTTCGAGGGC	ACGCTCTGCCTGGGCGT	CACGCATCGCGT	CGCCCC	CCCCCACA						
linearis_ovalis_NDsn	GAATTGCAGAATCCCGTGAACCATCGAGTTTTTTGAACGCAAGTTGCGCCCGAAACCATTTCGGTTCGAGGGC	ACGCTCTGCCTGGGCGT	CACGCATCGCGT	CGCCCC	CCCCCACA						
linearis_ovalis_RM854	GAATTGCAGAATCCCGTGAACCATCGAGTTTTTTGAACGCAAGTTGCGCCCGAAACCATTTCGGTTCGAGGGC	ACGCTCTGCCTGGGCGT	CACGCATCGCGT	CGCCCC	CCCCCACA						
maritima_RM1038	GAATTGCAGAATCCCGTGAACCATCGAGTTTTTTGAACGCAAGTTGCGCCCGAAACCATTTCGGTTCGAGGGC	ACGCTCTGCCTGGGCGT	CACGCATCGCGT	CGCCCC	CCCCCACA						
maritima_M290606_6	GAATTGCAGAATCCCGTGAACCATCGAGTTTTTTGAACGCAAGTTGCGCCCGAAACCATTTCGGTTCGAGGGC	ACGCTCTGCCTGGGCGT	CACGCATCGCGT	CGCCCC	CCCCCACA						
othonnites_RM1306	GAATTGCAGAATCCCGTGAACCATCGAGTTTTTTGAACGCAAGTTGCGCCCGAAACCATTTCGGTTCGAGGGC	ACGCTCTGCCTGGGCGT	CACGCATCGCGT	CGCCCC	CCCCCACA						
pectinata_M120903	GAATTGCAGAATCCCGTGAACCATCGAGTTTTTTGAACGCAAGTTGCGCCCGAAACCATTTCGGTTCGAGGGC	ACGCTCTGCCTGGGCGT	CACGCATCGCGT	CGCCCC	CCCCCACA						
pectinata_RM1044	GAATTGCAGAATCCCGTGAACCATCGAGTTTTTTGAACGCAAGTTGCGCCCGAAACCATTTCGGTTCGAGGGC	ACGCTCTGCCTGGGCGT	CACGCATCGCGT	CGCCCC	CCCCCACA						
rigida_M280902	GAATTGCAGAATCCCGTGAACCATCGAGTTTTTTGAACGCAAGTTGCGCCCGAAACCATTTCGGTTCGAGGGC	ACGCTCTGCCTGGGCGT	CACGCATCGCGT	CGCCCC	CCCCCACA						
rigida_RM840	GAATTGCAGAATCCCGYGAACCATCGAGTTTTTTGAACGCAAGTTGCGCCCGAAACCATTTCGGTTCGAGGGC	ACGCTCTGCCTGGGCGT	CACGCATCGCGT	CGCCCC	CCCCCACA						
rigens_leucolaena_RM773	GAATTGCAGAATCCCGTGAACCATCGAGTTTTTTGAACGCAAGTTGCGCCCGAAACCATTTCGGTTCGAGGGC	ACGCTCTGCCTGGGCGT	CACGCATCGCGT	CGCCCC	CCCCCACA						
rigens_leucolaena_RM952_1	GAATTGCAGAATCCCGTGAACCATCGAGTTTTTTGAACGCAAGTTGCGCCCGAAACCATTTCGGTTCGAGGGC	ACGCTCTGCCTGGGCGT	CACGCATCGCGT	CGCCCC	CCCCCACA						
rigens_rigens_RM763	GAATTGCAGAATCCCGTGAACCATCGAGTTTTTTGAACGCAAGTTGCGCCCGAAACCATTTCGGTTCGAGGGC	ACGCTCTGCCTGGGCGT	CACGCATCGCGT	CGCCCC	CCCCCACA						
rigens_rigens_SR463	GAATTGCAGAATCCCGTGAACCATCGAGTTTTTTGAACGCAAGTTGCGCCCGAAACCATTTCGGTTCGAGGGC	ACGCTCTGCCTGGGCGT	CACGCATCGCGT	CGCCCC	CCCCCACA						
rigens_uniflora_JC201205	GAATTGCAGAATCCCGTGAACCATCGAGTTTTTTGAACGCAAGTTGCGCCCGAAACCATTTCGGTTCGAGGGC	ACGCTCTGCCTGGGCGT	CACGCATCGCGT	CGCCCC	CCCCCACA						
rigens_uniflora_RM920	GAATTGCAGAATCCCGTGAACCATCGAGTTTTTTGAACGCAAGTTGCGCCCGAAACCATTTCGGTTCGAGGGC	ACGCTCTGCCTGGGCGT	CACGCATCGCGT	CGCCCC	CCCCCACA						
schenckii	GAATTGCAGAATCCCGTGAACCATCGAGTTTTTTGAACGCAAGTTGCGCCCGAAACCATTTCGGTTCGAGGGC	ACGCTCTGCCTGGGCGT	CACGCATCGCGT	CGCCCC	CCCCCACA						
serrata_M250904_15	GAATTGCAGAATCCCGTGAACCATCGAGTTTTTTGAACGCAAGTTGCGCCCGAAACCATTTCGGTTCGAGGGC	ACGCTCTGCCTGGGCGT	CACGCATCGCGT	CGCCCC	CCCCCACA						
serrata_RM898	GAATTGCAGAATCCCGTGAACCATCGAGTTTTTTGAACGCAAGTTGCGCCCGAAACCATTTCGGTTCGAGGGC	ACGCTCTGCCTGGGCGT	CACGCATCGCGT	CGCCCC	CCCCCACA						
tenuifolia_CAM1601	GAATTGCAGAATCCCGTGAACCATCGAGTTTTTTGAACGCAAGTTGCGCCCGAAACCATTTCGGTTCGAGGGC	ACGCTCTGCCTGGGCGT	CACGCATCGCGT	CGCCCC	CCCCCACA						
tenuifolia_M2730	GAATTGCAGAATCCCGTGAACCATCGAGTTTTTTGAACGCAAGTTGCGCCCGAAACCATTTCGGTTCGAGGGC	ACGCTCTGCCTGGGCGT	CACGCATCGCGT	CGCCCC	CCCCCACA						
spnov_M040906_33	GAATTGCAGAATCCCGTGAACCATCGAGTTTTTTGAACGCAAGTTGCGCCCGAAACCATTTCGGTTCGAGGGC	ACGCTCTGCCTGGGCGT	CACGCATCGCGT	CGCCCC	CCCCCACA						

Appendix 4: nrDNA sequence data for Chapter 3.

	450	460	470	480	490	500	510	520	530	540	550]									
Berkheya	ACACGTC	CCCTAA	ACKGGT	ACGYTT	GCCTT	-GGGGG	CGGATA	TGGTCT	CCCGTC	CCCTT	AGGGT	GTGGTT	TGGCCT	AAACTA	GAGTCC	CCCTCG	GTGGAC	GCACGG	CTAGTGG	
Gorteria	ACTCCT	CCCTA	TAGGT	ACGTG	TGTGTC	--GGGG	CGGAAA	TGGTCT	CCCGTC	CCCTT	-GGTGT	GGTTGG	CCTAA	ACCAGA	GTCCTC	CGGTGG	ACGCAC	GGCTAG	TGG	
Hirpicium	ACTCCT	CCCTA	TAGGT	ACGTG	TGTGTC	--GGGG	CGGATA	TGGTCT	CCCGTC	CCCTT	-GGTGT	GGTTGG	CCTAA	ACCAGA	GTCCTC	CGGTGG	ACGCAC	GGCTAG	TGG	
caespitosa_RC448	ACTCCT	CCCTT	TGGG	GACACG	TGTGTC	-GGGGG	CGGATA	TGGTCT	CCCGTC	CCCTT	-GGTGT	GGTTGG	CCTAA	ATCAGA	GTCCTC	CGGTGG	ACGCAC	GGCTAG	TGG	
caespitosa_RVC307	ACTCCT	CCCTT	TGGG	GACACG	TGTGTC	-GGGGG	CGGATA	TGGTCT	CCCGTC	CCCTT	-GGTGT	GGTTGG	CCTAA	AWCAGA	GTCCTC	CGGTGG	ACGCAC	GGCTAG	TGG	
ciliaris_RM1230	ACTCCT	CCCTT	TGGG	GAGA	ACGTTG	TGTC--	GGGGG	CGTATA	TGGTCT	CCCGTC	CCCTT	-GGTGT	GGTTGG	CCTAA	ATCAGA	GTCCTC	CGGTGG	ACGCAC	GGCTAG	TGG
ciliaris_RM1382	ACTSCT	CCCTT	TGGG	GAGA	ACGTTG	TGTC--	GGGGG	CGTATA	TGGTCT	CCCGTC	CCCTT	-GGTGT	GGTTGG	CCTAA	ATCAGA	GTCCTC	CGGTGG	ACGCAC	GGCTAG	TGG
heterochaeta_RM1429_1	AC-CCTT	CCCTGT	TGGG	AACACG	TGTGTC	GAGGGG	CGGATA	TGGTCT	CCCATG	CCCTT	-GGTGT	GGTTGG	CCTAA	ATCAGA	GTCCTC	CGGTGG	ACGCAC	GGCTAG	TGG	
heterochaeta_RM1451	AC-CCTT	CCCTGT	TGGG	AACACG	TGTGTC	GAGGGG	CGGATA	TGGTCT	CCCATG	CCCTT	-GGTGT	GGTTGG	CCTAA	ATCAGA	GTCCTC	CGGTGG	ACGCAC	GGCTAG	TGG	
jurineifolia_jur_SR682	ACTCCT	CCCTG	TGGG	ATCAG	TTGGG	TTC--	GGGGG	CGGATA	TGGCTC	CCATG	CCCTT	-GGTGT	GGTTGG	CCTAA	ATCAGA	GTCCTC	CGGTGG	ACGCAC	GGCTAG	TGG
jurineifolia_jur_RM1518	ACTCCT	CCCTG	TGGG	ATCAG	TTGGG	TTC--	GGGGG	CGGATR	TGGCTC	CCGTC	CCCTT	-GGTGT	GGTTGG	CCTAA	ATCAGA	GTCCTC	CGGTGG	ACGCAC	GGCTAG	TGG
jurineifolia_scab_CAM1604	ACTCCT	CCCTG	TGGG	ATCAG	TTGGG	TTC--	GGGGG	CGGATA	TGGCTC	CCATG	CCCTT	-GGTGT	GGTTGG	CCTAA	ATCAGA	GTCCTC	CGGTGG	ACGCAC	GGCTAG	TGG
jurineifolia_scab_CAM2652	ACTCCT	CCCTG	TGGG	ATCAG	TTGGG	TTC--	GGGGG	CGGATA	TGGCTC	CCATG	CCCTT	-GGTGT	GGTTGG	CCTAA	ATCAGA	GTCCTC	CGGTGG	ACGCAC	GGCTAG	TGG
krebsiana_arctotoides_RM868	ACTCCT	CCCTG	TGGG	AAAACG	TTGTG	TGTCGG	GGGGG	CGGATA	TGGCTC	CCATG	CCCTT	-GGTGT	GGTTGG	CCTAA	ATCTGA	GTCCTC	CGGTGG	ACGCAC	GGCTAG	TGG
krebsiana_arctotoides_RM876	ACTCCT	CCCTG	TGGG	AAAACG	TTGTG	TGTCGG	GGGGG	CGGATA	TGGCTC	CCATG	CCCTT	-GGTGT	GGTTGG	CCTAA	ATCTGA	GTCCTC	CGGTGG	ACGCAC	GGCTAG	TGG
krebsiana_krebsiana_RM1114	ACTCCT	CCCTA	TGGG	AAAACG	TTGTG	TGTCGG	GGGGG	CGGATA	TGGCTC	CCATG	CCCTT	-GGTGT	GGTTGG	CCTAA	ATCTGA	GTCCTC	CGGTGG	ACGCAC	GGCTAG	TGG
krebsiana_krebsiana_RM1136	ACTCCT	CCCTG	TGGG	AAAACG	TTGTG	TGTCGG	GGGGG	CGGATA	TGGCTC	CCATG	CCCTT	-GGTGT	GGTTGG	CCTAA	ATCTGA	GTCCTC	CGGTGG	ACGCAC	GGCTAG	TGG
krebsiana_serrulata_RM863	ACTCCT	CCCTG	TGGG	AAAACG	TTGTG	TGTCGG	GGGGG	CGGATA	TGGCTC	CCATG	CCCTT	-GGTGT	GGTTGG	CCTAA	ATCTGA	GTCCTC	CGGTGG	ACGCAC	GGCTAG	TGG
krebsiana_serrulata_RM965	ACTCCT	CCCTG	TGGG	AAAACG	TTGTG	TGTCGG	GGGGG	CGGATA	TGGCTC	CCATG	CCCTT	-GGTGT	GGTTGG	CCTAA	ATCTGA	GTCCTC	CGGTGG	ACGCAC	GGCTAG	TGG
leiopoda_M240901	ACTCCT	CCCTG	TGGG	AAAACG	TTGTG	TGTCGG	GGGGG	CGGATA	TGGCTC	CCATG	CCCTT	-GGTGT	GGTTGG	CCTAA	ATCTGA	GTCCTC	CGGTGG	ACGCAC	GGCTAG	TGG
leiopoda_RM1309	ACTCCT	CCCTG	TGGG	AAAACG	TTGTG	TGTCGG	GGGGG	CGGATA	TGGCTC	CCATG	CCCTT	-GGTGT	GGTTGG	CCTAA	ATCTGA	GTCCTC	CGGTGG	ACGCAC	GGCTAG	TGG
lichtensteinii_CAM1916	AC-CCTC	CCYTGT	TGGG	AACACG	TGTGTC	CAGGGG	CGGATA	TGGTCT	CCCATG	CCCTT	-GGTGT	GGTTGG	CCTAA	ATCAGA	GTCCTC	CGGTGG	ACGCAC	GGCTAG	TGG	
lichtensteinii_RM1249	AC-CCTC	CCYTGT	TGGG	AACACG	TGTGTC	CAGGGG	CGGATA	TGGTCT	CCCATG	CCCTT	-GGTGT	GGTTGG	CCTAA	ATCAGA	GTCCTC	CGGTGG	ACGCAC	GGCTAG	TGG	
linearis_linearis_RM1010	ACTCCT	CCCTG	TGGG	AAAACG	TTGTG	TGTCGG	GGGGG	CGGATA	TGGCTC	CCATG	CCCTT	-GGTGT	GGTTGG	CCTAA	ATCTGA	GTCCTC	CGGTGG	ACGCAC	GGCTAG	TGG
linearis_linearis_SH113	ACTCCT	CCCTG	TGGG	AAAACR	TTGTG	TGTCGG	GGGGG	CGGATA	TGGTCT	CCCAWG	CCCTT	-GGTGT	GGTTGG	CCTAA	ATCTGA	GTCCTC	CGGTGG	ACGCAC	GGCTAG	TGG
linearis_ovalis_NDsn	ACTCCT	CCCTR	TGGG	AAAACR	TTGTG	TGTCGG	GGGGG	CGGATA	TGGTCT	CCCATG	CCCTT	-GGTGT	GGTTGG	CCTAA	ATCTGA	GTCCTC	CGGTGG	ACGCAC	GGCTAG	TGG
linearis_ovalis_RM854	ACTCCT	CCCTG	TGGG	AAAACG	TTGTG	TGTCGG	GGGGG	CGGATA	TGGTCT	CCCATG	CCCTT	-GGTGT	GGTTGG	CCTAA	ATCTGA	GTCCTC	CGGTGG	ACGCAC	GGCTAG	TGG
maritima_RM1038	ACTCCT	CCCTG	TGGG	AAAACG	TTGTG	TGTCGG	GGGGG	CGGATA	TGGTCT	CCCATG	CCCTT	-GGTGT	GGTTGG	CCTAA	ATCTGA	GTCCTC	CGGTGG	ACGCAC	GGCTAG	TGG
maritima_M290606_6	ACTCCT	CCCTG	TGGG	AAAACG	TTGTG	TGTCGG	GGGGG	CGGATA	TGGTCT	CCCATG	CCCTT	-GGTGT	GGTTGG	CCTAA	ATCTGA	GTCCTC	CGGTGG	ACGCAC	GGCTAG	TGG
othonnites_RM1306	ACTCCT	CCCTG	TGGG	AAAACG	TTGTG	TGTCGG	GGGGG	CGGATA	TGGTCT	CCCATG	CCCTT	-GGTGT	GGTTGG	CCTAA	ATCTGA	GTCCTC	CGGTGG	ACGCAC	GGCTAG	TGG
pectinata_M120903	ACTCCT	CCCTG	TGGG	AAAACG	TTGTG	TGTC--	GGGGG	CGGATA	TGGTCT	CCCATG	CCCTT	-GGTGT	GGATGG	CCTAA	ATCTGA	GTCCTC	CGGTGG	ACGCAC	GGCTAG	TGG
pectinata_RM1044	ACTCCT	CCCTG	TGGG	AAAACG	TTGTG	TGTCGG	GGGGG	CGGATA	TGGTCT	CCCATG	CCCTT	-GGTGT	GGCTGG	CCTAA	ATCTGA	GTCCTC	CGGTGG	ACGCAC	GGCTAG	TGG
rigida_M280902	ACTCCT	CCCTG	TGGG	AAAACG	TTGTG	TGTCGG	GGGGG	CGGATA	TGGTCT	CCCATG	CCCTT	-GGTGT	GGTTGG	CCTAA	ATCTGA	GTCCTC	CGGTGG	ACGCAC	GGCTAG	TGG
rigida_RM840	ACTCCT	CCCTG	TGGG	AAAACG	TTGTG	TGTCGG	GGGGG	CGGATA	TGGTCT	CCCATG	CCCTT	-GGTGT	GGCTGG	CCTAA	ATCTGA	GTCCTC	CGGTGG	ACGCAC	GGCTAG	TGG
rigens_leucolaena_RM773	ACTCCT	CCCTG	TGGG	AAAACG	TTGTG	TGTCGG	GGGGG	CGGATA	TGGTCT	CCCATG	CCCTT	-GGTGT	GGTTGG	CCTAA	ATCTGA	GTCCTC	CGGTGG	ACGCAC	GGCTAG	TGG
rigens_leucolaena_RM952_1	ACTCCT	CCCTG	TGGG	AAAACG	TTGTG	TGTCGG	GGGGG	CGGATA	TGGTCT	CCCATG	CCCTT	-GGTGT	GGTTGG	CCTAA	ATCTGA	GTCCTC	CGGTGG	ACGCAC	GGCTAG	TGG
rigens_rigens_RM763	ACTCCT	CCCTG	TGGG	AAAACG	TTGTG	TGTCGG	GGGGG	CGGATA	TGGTCT	CCCATG	CCCTT	-GGTGT	GGTTGG	CCTAA	ATCTGA	GTCCTC	CGGTGG	ACGCAC	GGCTAG	TGG
rigens_rigens_SR463	ACTCCT	CCCTA	TGGG	AAAACG	TTGTG	TGTCGG	GGGGG	CGGATA	TGGTCT	CCCATG	CCCTT	-GGTGT	GGTTGG	CCTAA	ATCTGA	GTCCTC	CGGTGG	ACGCAC	GGCTAG	TGG
rigens_uniflora_JC201205	ACTCCT	CCCTA	TGGG	AAAACG	TTGTG	TGTCGG	GGGGG	CGGATA	TGGTCT	CCCATG	CCCTT	-GGTGT	GGTTGG	CCTAA	ATCTGA	GTCCTC	CGGTGG	ACGCAC	GGCTAG	TGG
rigens_uniflora_RM920	ACTCCT	CCCTG	TGGG	AAAACG	TTGTG	TGTCGG	GGGGG	MGGATA	TGGTCT	CCCATG	CCCTT	-GGTGT	GGTTGG	CCTAA	ATCTGA	GTCCTC	MGGTGG	ACGCAC	GGGYTAG	TGG
schenckii	GC-CCTC	CCCTG	TGGG	AACACG	TTGTG	TGTCAG	GGGGG	CGGATA	TGGTCT	CCCATG	CCCTT	-GGTGT	GGTTGG	CCTAA	ATCAGA	GTCCTC	CGGTGG	ACGCAC	GGCTAG	TGG
serrata_M250904_15	ACTCCT	CCCTG	TGGG	AAAACG	TTGTG	TGTCGG	GGGGG	CGGATA	TGGTCT	CCCATG	CCCTT	-GGTGT	GGTTGG	CCTAA	TTGAGT	CCCCTC	CGGTGG	ACGCAC	GGCTAG	TGG
serrata_RM898	ACTCCT	CCCTG	TGGG	AAAACG	TTGTG	TGTCGG	GGGGG	CGGATA	TGGTCT	CCCATG	CCCTT	-GGTGT	GGCTGG	CCTAA	ATCTGA	GTCCTC	CGGTGG	ACGCAC	GGCTAG	TGG
tenuifolia_CAM1601	ACTCCT	CCCTG	TGGG	AACACG	TTGTG	TGTC--	GGGGG	CGGATA	TGGTCT	CCCATG	CCCTT	-GGTGT	GGTTGG	CCTAA	ATCAGA	GTCCTC	CGGTGG	ACGCAC	GGCTAG	TGG
tenuifolia_M2730	ACTCCT	CCCTG	TGGG	AACACG	TTGTG	TGTC--	GGGGG	CGGATA	TGGTCT	CCCATG	CCCTT	-GGTGT	GGTTGG	CCTAA	ATCAGA	GTCCTC	CGGTGG	ACGCAC	GGCTAG	TGG
spnov_M040906_33	ACTCCT	CCCTG	TGGG	AAAACG	TTGTG	TGTCGG	GGGGG	CGGATA	TGGTCT	CCCATG	CCCTT	-GGTGT	GGTTGG	CCTAA	ATCTGA	GTCCTC	CGGTGG	ACGCAC	GGCTAG	TGG

Appendix 4: nrDNA sequence data for Chapter 3.

	560	570	580	590	600	610	620	630	640	650	660
Berkheya	TGGTTGATAAGACCCTCGTCTGTTGTCGTGCTAAGCTGTTTGGGAAGTACTCGTAAAAAGACCCCAACGCATTGTCTTGTGACCATGCTTCGACCCGACCCAGGTCAG										
Gorteria	TGGTTGACAAGACCCTCGTCTGTTGTCGTGCTAAGCTATTGGGAAGTACTCAAGAAAAGACCCCAACGCATTGTCTTGYGATGATGCTTCGACCCGACCCAGGTCAG										
Hirpicium	TGGTTGACAAGACCCTCGTCTGTTGTCGTGCTAAGCTGTACGGGAAGTACTCATGAAACGACCCCAACGCATTGTCTTGTGACCAATGCTTCGACCCGACCCAGGTCAG										
caespitosa_RC448	TGGTTGACAAGACCCTCGTCTGTTGTCGTGCTAAGCTRTAAGGGAAGTACTCTTAAAAAGACCCCAACGCATTGTCTTGTGACGATGCTTCGACCCGACCCAGGTCAG										
caespitosa_RVC307	TGGTTGACAAGACCCTCGTCTGTTGTCGTGCTAAGCTRTAAGGGAAGTACTCTTAAAAAGACCCCAACGCATTGTCTTGTGACGATGCTTCGACCCGACCCAGGTCAG										
ciliaris_RM1230	TGGTTGACAAGACCCTCGTCTGTTGTCGTGCTAAGCTGTAAGGGAAGTACTCTTAAAAAGATCCCAACGCATTGTCTTGTGACGATGCTTCGACCCGACCCAGGTCAG										
ciliaris_RM1382	TGGTTGACAAGACCCTCGTCTGTTGTCGTGCTAAGCTGTAAGGGAAGTACTCTTAAAAAGATCCCAACGCATTGTCTTGTGACGATGCTTCGACCCGACCCAGGTCAG										
heterochaeta_RM1429_1	TGGTTGACAAGACCCTCGTCTGTTGTCGTGCTAAGCTGTAAGGGAAGTACTCATTAAATGACCCCAACGCATTGTCTTGTGACGATGCTTCGACCCGACCCAGGTCAG										
heterochaeta_RM1451	TGGTTGACAAGACCCTCGTCTGTTGTCGTGCTAAGCTGTAAGGGAAGTACTCATTAAATGACCCCAACGCATTGTCTTGTGACGATGCTTCGACCCGACCCAGGTCAG										
jurineifolia_jur_SR682	TGGTTGACAAGACCCTCGTCTGTTGTCGTGCTAAGCTGTAAGGGAAGTACTCATGAAAGACCCCAACGCATTGTCTCGYACRATG????????????????										
jurineifolia_jur_RM1518	TGGTTGACAAGACCCTCGTCTGTTGTCGTGCTAAGCTGTAAGGGAAGTACTCATGAAAGACCCCAACGCATTGTCTCGCGACGATGTTTCGACCCGACCCAGGTCAG										
jurineifolia_scab_CAM1604	TGGTTGACAAGACCCTCGTCTGTTGTCGTGCTAAGCTGTAAGGGAAGTACTCATGAAAGACCCCAACGCATTGTCTCGGACAAATGTTTCGACCAATGTTTCGACCCGACCCAGGTCAG										
jurineifolia_scab_CAM2652	TGGTTGACAAGACCCTCGTCTGTTGTCGTGCTAAGCTGTAAGGGAAGTACTCATGAAAGACCCCAAYGCAATGTTTCGACCGACRATGTTTCGACCCGACCCAGGTCAG										
krebsiana_arctotoides_RM868	TGGTTGACAAGACCCTCGTCTGTTGTCGTGCTAAGCTGTAAGGGAAGTACTCATGAAAGACCCCAACGCATTGTCTTGTGACGATGCTTCGACCCGACCCAGGTCAG										
krebsiana_arctotoides_RM876	TGGTTGACAAGACCCTCGTCTGTTGTCGTGCTAAGCTGTAAGGGAAGTACTCATGAAAGACCCCAACGCATTGTCTTGTGACGATGCTTCGACCCGACCCAGGTCAG										
krebsiana_krebsiana_RM1114	TGGTTGACAAGACCCTCGTCTGTTGTCGTGCTAAGCTGTAAGGGAAGTACTCATTAAAGACCCCAACGCATTGTCTTGTGACGATGCTTCGACCCGACCCAGGTCAG										
krebsiana_krebsiana_RM1136	TGGTTGACAAGACCCTCGTCTGTTGTCGTGCTAAGCTGTAAGGGAAGTACTCATGAAAGACCCCAACGCATTGTCTTGTGACGATGCTTCGACCCGACCCAGGTCAG										
krebsiana_serrulata_RM863	TGGTTGACAAGACCCTCGTCTGTTGTCGTGCTAAGCTGTAAGGGAAGTACTCATGAAAGACCCCAACGCATTGTCTTGTGACGATGCTTCGACCCGACCCAGGTCAG										
krebsiana_serrulata_RM965	TGGTTGACAAGACCCTCGTCTGTTGTCGTGCTAAGCTGTAAGGGAAGTACTCATGAAAGACCCCAACGCATTGTCTTGTGACGATGCTTCGACCCGACCCAGGTCAG										
leiopoda_M240901	TGGTTGACAAGACCCTCGTCTGTTGTCGTGCTAAGCTGTAAGGGAAGTACTCATGAAAGACCCCAACGCATTGTCTTGTGACGATGCTTCGACCCGACCCAGGTCAG										
leiopoda_RM1309	TGGTTGACAAGACCCTCGTCTGTTGTCGTGCTAAGCTGTAAGGGAAGTACTCATGAAAGACCCCAACGCATTGTCTTGTGACGATGCTTCGACCCGACCCAGGTCAG										
lichtensteinii_CAM1916	TGGTTGACAAGACCCTCGTCTGTTGTCGTGCTAAGCTGTAAGGGAAGTACTCATTAAAGACCCCAACGCATTGTCTTGTGACGATGCTTCGACCCGACCCAGGTCAG										
lichtensteinii_RM1249	TGGTTGACAAGACCCTCGTCTGTTGTCGTGCTAAGCTGTAAGGGAAGTACTCATTAAAGACCCCAACGCATTGTCTTGTGACGATGCTTCGACCCGACCCAGGTCAG										
linearis_linearis_RM1010	TGGTTGACAAGACCCTCGTCTGTTGTCGTGCTAAGCTGTAAGGGAAGTACTCATGAAAGACCCCAACGCATTGTCTTGTGACGATGCTTCGACCCGACCCAGGTCAG										
linearis_linearis_SH113	TGGTTGACAAGACCCTCGTCTGTTGTCGTGCTAAGCTGTAAGGGAAGTACTCATGAAAGACCCCAACGCATTGTCTTGTGACGATGCTTCGACCCGACCCAGGTCAG										
linearis_ovalis_NDsn	TGGTTGACAAGACCCTCGTCTGTTGTCGTGCTAAGCTGTAAGGGAAGTACTCATGAAAGACCCCAACGCATTGTCTTGTGACGATGCTTCGACCCGACCCAGGTCAG										
linearis_ovalis_RM854	TGGTTGACAAGACCCTCGTCTGTTGTCGTGCTAAGCTGTAAGGGAAGTACTCATGAAAGACCCCAACGCATTGTCTTGTGACGATGCTTCGACCCGACCCAGGTCAG										
maritima_RM1038	TGGTTGACAAGACCCTCGTCTGTTGTCGTGCTAAGCTGTAAGGGAAGTACTCATGAAAGACCCCAACGCATTGTCTTGTGACGATGCTTCGACCCGACCCAGGTCAG										
maritima_M290606_6	TGGTTGACAAGACCCTCGTCTGTTGTCGTGCTAAGCTGTAAGGGAAGTACTCATGAAAGACCCCAACGCATTGTCTTGTGACGATGCTTCGACCCGACCCAGGTCAG										
othonnites_RM1306	TGGTTGACAAGACCCTCGTCTGTTGTCGTGCTAAGCTGTAAGGGAAGTACTCATGAAAGACCCCAACGCATTGTCTTGTGACGATGCTTCGACCCGACCCAGGTCAG										
pectinata_M120903	TGGTTGACAAGACCCTCGTCTGTTGTCGTGCTAAGCTGTAAGGGAAGTACTCATGAAAGACCCCAACGCATTGTCTTGTGACGATGCTTCGACCCGACCCAGGTCAG										
pectinata_RM1044	TGGTTGACAAGACCCTCGTCTGTTGTCGTGCTAAGCTGTAAGGGAAGTACTCATGAAAGACCCCAACGCATTGTCTTGTGACGATGCTTCGACCCGACCCAGGTCAG										
rigida_M280902	TGGTTGACAAGACCCTCGTCTGTTGTCGTGCTAAGCTGTAAGGGAAGTACTCATGAAAGACCCCAACGCATTGTCTTGTGACGATGCTTCGACCCGACCCAGGTCAG										
rigida_RM840	TGGTTGACAAGACCCTCGTCTGTTGTCGTGCTAAGCTGTAAGGGAAGTACTCATGAAAGACCCCAACGCATTGTCTTGTGACGATGCTTCGACCCGACCCAGGTCAG										
rigens_leucolaena_RM773	TGGTTGACAAGACCCTCGTCTGTTGTCGTGCTAAGCTGTAAGGGAAGTACTCATGAAAGACCCCAACGCATTGTCTTGTGACGATGCTTCGACCCGACCCAGGTCAG										
rigens_leucolaena_RM952_1	TGGTTGACAAGACCCTCGTCTGTTGTCGTGCTAAGCTGTAAGGGAAGTACTCATGAAAGACCCCAACGCATTGTCTTGTGACGATGCTTCGACCCGACCCAGGTCAG										
rigens_rigens_RM763	TGGTTGACAAGACCCTCGTCTGTTGTCGTGCTAAGCTGTAAGGGAAGTACTCATGAAAGACCCCAACGCATTGTCTTGTGACGATGCTTCGACCCGACCCAGGTCAG										
rigens_rigens_SR463	TGGTTGACAAGACCCTCGTCTGTTGTCGTGCTAAGCTGTAAGGGAAGTACTCATGAAAGACCCCAACGCATTGTCTTGTGACGATGCTTCGACCCGACCCAGGTCAG										
rigens_uniflora_JC201205	TGGTTGACAAGACCCTCGTCTGTTGTCGTGCTAAGCTGTAAGGGAAGTACTCATGAAAGACCCCAACGCATTGTCTTGTGACGATGCTTCGACCCGACCCAGGTCAG										
rigens_uniflora_RM920	TGGTTGACAAGACCCTCGTCTGTTGTCGTGCTAAGCTGTAAGGGAAGTACTCATGAAAGACCCCAACGCATTGTCTTGTGACGATGCTTCGACCCGACCCAGGTCAG										
schenckii	TGGTTGACAAGACCCTCGTCTGTTGTCGTGCTAAGCTGTAAGGGAAGTACTCATTAAAGACCCCAACGCATTGTCTTGTGACGATGCTTCGACCCGACCCAGGTCAG										
serrata_M250904_15	TGGTTGACAAGACCCTCGTCTGTTGTCGTGCTAAGCTGTAAGGGAAGTACTCATGAAAGACCCCAACGCATTGTCTTGTGACGATGCTTCGACCCGACCCAGGTCAG										
serrata_RM898	TGGTTGACAAGACCCTCGTCTGTTGTCGTGCTAAGCTGTAAGGGAAGTACTCATGAAAGACCCCAACGCATTGTCTTGTGACGATGCTTCGACCCGACCCAGGTCAG										
tenuifolia_CAM1601	TGGTTGACAAGACCCTCGTCTGTTGTCGTGCTAAGCTGTAAGGGAAGTACTCATTAAAGACCCCTGACGATTGTCTCGTGACGACGCTTCGACCCGACCCAGGTCAG										
tenuifolia_M2730	TGGTTGACAAGACCCTCGTCTGTTGTCGTGCTAAGCTGTAAGGGAAGTACTCATTAAAGACCCCTGATGATTGTCTCGTGACGACGCTTCGACCCGACCCAGGTCAG										
spnov_M040906_33	TGGTTGACAAGACCCTCGTCTGTTGTCGTGCTAAGCTGTAAGGGAAGTACTCATGAAAGACCCCAACGCATTGTCTTGTGACGATGCTTCGACCCGACCCAGGTCAG										

Appendix 4: nrDNA sequence data for Chapter 3.

	ITS <	>	ETS										
[670	680	690	700	710	720	730	740	750	760	770]		
Berkheya	GCGGGACTACCCGCTGAGGGTAGCATTCCTCTTCGATACAACCCGCTCTGCATGGACATGCCAACRCACGACGAGTG-ATCGTTTTAGAGAAGCGAGAACCGCTAAACGAG												
Gorteria	GCGGGACTACCCGCTGAG??TAGCATTCCTCTTCGACGCAACCCGCCACGCATGGACGAGCCAACGCACGACGAGTG-ATCGTTTTAGAGAAGCGAGAACCGCTAAACGAG												
Hirpicium	GCGGGACTACCCGCTGAGGGTAGCATTCCTCTTCGATGCAACCCACCACGCATGGACATGCCAACACATGACGAGTG-ATCGTTTTAGAGAAGCGAGAACCGCTAAACGAG												
caespitosa_RC448	GCGGGACTACCCGCTGAGGGTAGCATTCCTCTTCGATGCAACCCGCCATGCATGGACTGGCCAACGCACGACGAGTG-ATCGTTTTAGAGAAGCGAGAACCGCTRAACGAG												
caespitosa_RVC307	GCGGGACTACCCGCTGAGGGTAGCATTCCTCTTCGATGCAACCCGCCATGCATGGACTGGCCAACGCACGACGAGTG-ATCGTTTTAGAGAAGCGAGAACCGCTAAACGAG												
ciliaris_RM1230	GCGGGACTACCCGCTGAGGGTAGCATTCCTCTTCGATGCAACCCGCCATGCACGGACTTGCCAACGCACGACGAGTG-ATCGTTTTAGAGAAGCGAGAAYGYAACGAG												
ciliaris_RM1382	GCGGGACTACCCGCTGAGGGTAGCATTCCTCTTCGACGCAACCCAGCATGCACGGACTTGCCAACGCACGACGAGTG-ATCGTTTTAGAGAAGCGAGAACCGCTAAACGAG												
heterochaeta_RM1429_1	????????????????GGTAGCATTCCTCTTCGACGCAACCCGTCACACATGGACTAGCCAACACGCGACGAGTG-ATCGTTTTAGAGAAGCGAGAACCTAAACGAG												
heterochaeta_RM1451	GCG????????????GGTAGCATTCCTCTTCGACGCAACCCGTCACACATGGACTAGCCAACACGCGACGAGTG-ATCGTTTTAGAGAAGCGAGAACCTAAACGAG												
jurineifolia_jur_SR682	????????????????GGTAGCATTCCTCTTCGATGCAACCCGCCATGCATGGACTTGCCAACACACGACGAGTG-ATCGTTTTAGAGAAGCGAGAACCGCTAAACGAG												
jurineifolia_jur_RM1518	G????????????GGTAGCATTCCTCTTCGATGCAACCCGCCATGCATGGACTTGCCAACACACGACGAGTG-ATCGTTTTAGAGAAGCGAGAACCGCTAAACGAG												
jurineifolia_scab_CAM1604	GCGGGACTACCCGCTGAGGGTAGCATTCCTCTTCGATGCAACCCGCCATGCATGGACTTGCCAACACGCGACGAGTG-ATCGTTTTAGAGAAGCGAGAACCTAAACGAG												
jurineifolia_scab_CAM2652	GCGGGACTACCCGCTGAGGGTAGCATTCCTCTTCGATGCAACCCGCCATGCATGGACTTGCCAACACACGACGAGTG-ATCGTTTTAGAGAAGCGAGAACCGCTAAACGAG												
krebsiana_arctotoides_RM868	GCGGGACTACCCGCTGAG??TAGCATTCCTCTTCGACGCAACCCGCCACGCATGGACTAGCCAACACGCGACGAGTG-ATCGTTTTAGAGAAGCGAGAACCGCTAAACAAG												
krebsiana_arctotoides_RM876	GCGGGACTACCCGCTGAG?GTAGCATTCCTCTTCGACGCAACCCGCCACGCATGGACTAGSAAACACGCGACGAGTG-ATCGTTTTAGAGAAGCGAGAACCGCTAAACAAG												
krebsiana_krebsiana_RM1114	GCGGGACTACCCGCTGAGGGTAGCATTCCTCTTCGACGCaACCCGCCACGCATGGACTAGCcaAACACGCGACGAGTG-ATCGTTTTAGAGAAGCGAGAACCGCTAAACAAG												
krebsiana_krebsiana_RM1136	GCGGGACTACCCGCTGAGGGTAGCATTCCTCTTCGACGCAACCCGCCACGCATGGACTAGCCAACACGCGACGAGTG-ATCGTTTTAGAGAAGCGAGAACCGCTAAACAAG												
krebsiana_serrulata_RM863	GCTGGACTACC?????GTAGCATTCCTCTTCGACGCAACCCGCCACGCATGGACTAGCCAACACGCGACGAGTG-ATCGTTTTAGAGAAGCGAGAACCGCTAAACAAG												
krebsiana_serrulata_RM965	????????????GGTAGCATTCCTCTTCGACGCAACCCGCCACGCATGGACTAGCCAACACGCGACGAGTG-ATCGTTTTAGAGAAGCGAGAACCGCTAAACAAG												
leiopoda_M240901	GCGGGACTACCCGCTGAGGGTAGCATTCCTCTTCGACGCAACCCGCCACGCATGGACTAGCCAACACGCGACGAGTG-ATCGTTTTAGAGAAGCGAGAACCGCTAAACAAG												
leiopoda_RM1309	GCGGGACTACCCGCTGAGGGTAGCATTCCTCTTCGACGCAACCCGCCACGCATGGACTAGCCAACACGCGACGAGTG-ATCGTTTTAGAGAAGCGAGAACCGCTAAACAAG												
lichtensteinii_CAM1916	GCGGGACTA?????GGTAGCATTCCTCTTCGACGCAACCCGCCACACATGGACTAGCCAACACACGACGAGTG-ATCGTTTTAGAGAAGCGAGAACCTAAACGAG												
lichtensteinii_RM1249	GCGGGACTACCCGCTGAGGGTAGCATTCCTCTTCGACGCAACCCGCCACACATGGACTAGCCAACACACGACGAGTG-ATCGTTTTAGAGAAGCGAGAACCTAAACGAG												
linearis_linearis_RM1010	GCGGGACTACCCGCTGAGGGTAGCATTCCTCTTCGACGCAACCCGCCACGCATGGACTAGCCAACACGCGACGAGTG-ATCGTTTTAGAGAAGCGAGAACCGCTAAACAAG												
linearis_linearis_SH113	GCGGGACTACCCGCTGAGGGTAGCATTCCTCTTCGACGCAACCCGCCACGCATGGACTAGCCAACACGCGACGAGTG-ATCGTTTTAGAGAAGCGAGAACCGCTAAACAAG												
linearis_ovalis_NDsn	GCGGGACTACCCGCTGAGGGTAGCATTCCTCTTCGACGCAACCCGCCACGCATGGACTAGCCAACACGCGACGAGTG-ATCGTTTTAGAGAAGCGAGAACCGCTAAACAAG												
linearis_ovalis_RM854	GCGGGACTACCCGCTGAGGGTAGCATTCCTCTTCGACGCAACCCGCCACGCATGGACTAGCCAACACGCGACGAGTG-ATCGTTTTAGAGAAGCGAGAACCGCTAAACAAG												
maritima_RM1038	GCGGGACTACCCGCTGAGGGTAGCATTCCTCTTCGACGCAACCCGCCACGCATGGACTAGCCAACACGCGACGAGTG-ATCGTTTTAGAGAAGCGAGAACCGCTAAACAAG												
maritima_M290606_6	GCGG????????GGTAGCATTCCTCTTCGACGCAACCCGCCACGCATGGACTAGCCAACACGCGACGAGTG-ATCGTTTTAGAGAAGCGAGAACCGCTAAACAAG												
othonnites_RM1306	GCGGGACTACCCGCTGAGGGTAGCATTCCTCTTCGACGCAACCCGCCACGCATGGACTAGCCAACACGCGACGAGTG-ATCGTTTTAGAGAAGCGAGAACCGCTAAACAAG												
pectinata_M120903	GCGGGACTACCCGCTGAG?GTAGCATTCCTCTTCGACGCAACCCGTCACGCATGGACTAGCCAACACGCGACGAGTG-ATCGTTTTAGAGAAGCGAGAACCGCTAAACAAG												
pectinata_RM1044	GCGGGACTACCCGCTGAGGGTAGCATTCCTCTTCGACGCAACCCGCCACGCATGGACTAGCCAACACGCGACGAGTG-ATCGTTTTAGAGAAGCGAGAACCGCTAAACAAG												
rigida_M280902	GCGGGACTACCCGCTGAGGGTAGCATTCCTCTTCGACGCAACCCGCCACGCATGGACTAGCCAACACGCGACGAGTG-ATCGTTTTAGAGAAGCGAGAACCGCTAAACAAG												
rigida_RM840	GCGGGACTACCCGCTGAGGGTAGCATTCCTCTTCGACGCAACCCGCCAYGCATGGACTAGCCAACACGCGACGAGTG-ATCGTTTTAGAGAAGCGAGAACCGCTAAACAAG												
rigens_leucolaena_RM773	GCGGGACTACCCGCTGAGGGTAGCATTCCTCTTCGACGCAACCCGCCACGCATGGACTAGCCAACACGCGACGAGTG-ATCGTTTTAGAGAAGCGAGAACCGCTAAACAAG												
rigens_leucolaena_RM952_1	GCGGGACTACCCGCTGAGGGTAGCATTCCTCTTCGACGCAACCCGCCACGCATGGACTAGCCAACACGCGACGAGTG-ATCGTTTTAGAGAAGCGAGAACCGCTAAACAAG												
rigens_rigens_RM763	GCGGGACTACCCGCTGAGGGTAGCATTCCTCTTCGACGCAACCCGCCACGCATGGACTAGCCAACACGCGACGAGTG-ATCGTTTTAGAGAAGCGAGAACCGCTAAACAAG												
rigens_rigens_SR463	GCGGGACTACCCGCTGAG?GTAGCATTCCTCTTCGACGCAACCCGCCACGCATGGACTAGCCAACACGCGACGAGTG-ATCGTTTTAGAGAAGCGAGAACCGCTAAACAAG												
rigens_uniflora_JC201205	GCGGGACTACCCGCTGAG?GTAGCATTCCTCTTCGACGCAACCCGCCACGCATGGACTAGCCAACACGCGACGAGTG-ATCGTTTTAGAGAAGCGAGAACCGCTAAACAAG												
rigens_uniflora_RM920	????????????GGTAGCATTCCTCTTCGACGCAACCCGCCACGCATGGACTAGCCAACACGCGACGAGTG-ATCGTTTTAGAGAAGCGAGAACCGCTAAACAAG												
schenckii	GCGGGACTACCCGCTGAGGGTAGCATTCCTCTTCGACGCAACCCGCCACACATGGACTAGCCAACACGCGACGAGTG-ATCGTTTTAGAGAAGCGAGAACCTAAACGAG												
serrata_M250904_15	GCGGGACTACCCGCTGAG??ATTCCTCTTCGACGCAACCCGCCACGCATGGACTAGCCAACACGCGACGAGTG-ATCGTTTTAGAGAAGCGAGAACCGCTAAACAAG												
serrata_RM898	GCGGGACTACCCGCTGAGGGTAGCATTCCTCTTCGACGCAACCCGCCACGCATGGACTAGCCAACACGCGACGAGTG-ATCGTTTTAGAGAAGCGAGAACCGCTAAACAAG												
tenuifolia_CAM1601	GCGGGACTACCCGCTGAG??TG-ATCGTTTTAGAGAAGTGAGAACCTAAACGAG												
tenuifolia_M2730	GCGGGACTACCCGCTGAGGGTAGCATTCCTCTTCGACGCAACCCGCCACGCATGGACTAGCCAACACGCGACGAGTG-ATCGTTTTAGAGAAGTGAGAACCTAAACGAG												
spnov_M040906_33	GCGGGACTACCCGCTGAGGGTAGCATTCCTCTTCGACGCAACCCGCCACGCATGGACTAGCCAACACGCGACGAGTG-ATCGTTTTAGAGAAGCGAGAACCGCTAAACAAG												

Appendix 4: nrDNA sequence data for Chapter 3.

	780	790	800	810	820	830	840	850	860	870	880]
Berkheya	GGCAAAAAGGATCGTGT	-AAGACCCCATGCCACAT	CAGGTTCAATATCCAAGAGACCAAGCANA	ACTCAGCAAGCCACATCGTCAAT	--G-TTTT	TACAACGACGAG-					
Gorteria	GGCAAAAAGGATGTGATT	-AGATCCCATGCCACAT	CAGGTTTCAGTATCCAAGACACCAAGCAGAACT	CAGCAAGCCACATCGTCGAA	--G-TGATA	AACAAC-ACGAGA					
Hirpicium	GGCAAAAAGGATCATGT	-AAGACCCCATGCCACAT	TAGGTTCAATATCCAAGAATCCAAGTGA	AACTCAGCAAGCCACATCATCAA	--G-TGTTT	TACAATGACGAGA					
caespitosa_RC448	GACATAAAAAGGATCATTT	-AAGACCCCATGCCACAT	CAGGTTCCGTATCCAAGACACCAAGCGAAWCT	CATCAAGCCACATCGTCGAA	--G-TGTTT	TACAACGACAAGA					
caespitosa_RVC307	GACATAAAAAGGATCATTTT	-AAGACCCCATGCCACAT	CAGGTTCCGTATCCAAGACACCAAGCTAAT	CTCAGCAAGCCACATCGTCGAA	--G-TGATT	TACAACGACAAGA					
ciliaris_RM1230	GACRTAAAAGGATCATTTT	-AAGACCCCATGCCACAT	CAGGTTCCGTATCCAAGACACCAAGCGAA	ACTCAGCAAGCCACATCGTCGAA	--G-TGATT	TACAACGACAAGA					
ciliaris_RM1382	GACGTA AAAAGGATCATTTT	-AAGACCCCATGCCACAT	CAGGTTCCGTATCCAAGACACCAAGCGAA	ACTCAGCAAGCCACATCGTCGAA	--G-TGATT	TACAACGACAAGA					
heterochaeta_RM1429_1	GACATAAAAAGGATCATCT	-AAGACCCCATGCCACAT	CAGGTTCCGTATCCAAGACACCAAGCGAA	ACTCAGCAAGCCACATCAACGAA	--G-TGTTT	TACAACGACAAGA					
heterochaeta_RM1451	GACATAAAAAGGATCATCT	-AAGACCCCATGCCACAT	CAGGTTCCGTATCCAAGACACCAAGCGAA	ACTCAGCAAGCCACATCAACGAA	--G-TGTTT	TACAACGACAAGA					
jurineifolia_jur_SR682	GGCATAAAAAGGATCATGT	-AAGACCCCATGCCACAT	CAGGTTCCGTATCCAAGACACCAAGCGAA	ACTCAGCAAGCCATATCGTCGTA	--G-TGTTT	TACAACRACAAGA					
jurineifolia_jur_RM1518	GGCATAAAAAGGATCATGT	-AAGACCCCATGCCACAT	CAGGTTCCGTATCCAAGACACCAAGCGAA	ACTCAGCAAGCCATATCGTCGTA	--G-TGTTT	TACAACGACAAGA					
jurineifolia_scab_CAM1604	GGCATAAAAAGGATCATGT	-AAGACCCCATGCCACAT	CAGGTTCCGTATCCAAGACACCAAGCGAA	ACTCAGCAAGCCATATCGTCGTA	--G-TGTTT	TACAACGACAAGA					
jurineifolia_scab_CAM2652	GGCATAAAAAGGATCATGT	-AAGACCCCATGCCACAT	CAGGTTCCGTATCCAAGACACCAAGCGAA	ACTCAGCAAGCCATATCGTCGTA	--G-TGTTT	TACAACRACAAGA					
krebsiana_arctotoides_RM868	GACATAAAAAGGATCATTT	-AAGACCCCATGCCACAT	TAGGTTCCATATCCAAGACACCAAGCGAA	ACTCAGCAAGCCACATCGCCGAT	--G-TGTAC	ACAACGACAAGA					
krebsiana_arctotoides_RM876	GACATAAAAAGGATCATYT	-AAGACCCCATGCCACAT	TAGGTTCCATATCCAAGACACCAAGCGAA	ACTCAGCAAGCCACATCGCCGAT	--G-TGTAC	ACAACGACAAGA					
krebsiana_krebsiana_RM1114	GACATAAAAAGGATCATTT	-AAGACCCCATGCCACAT	TAGGTTCCATATCCAAGACACCAAGCGAA	ACTCAGCAAGCCACATCGCCGAT	--G-TGTAC	ACAACGACAAGA					
krebsiana_krebsiana_RM1136	GACATAAAAAGGATCATYT	-AAGACCCCATGCCACAT	TAGGTTCCATATCCAAGACACCAAGCGAA	ACTCAGCAAGCCACATCGCCGAT	--G-TGTAC	ACAACGACAAGA					
krebsiana_serrulata_RM863	GACATAAAAAGGATCATTT	-AAGACCCCATGCCACAT	TAGGTTCCATATCCAAGACACCAAGCGAA	ACTCAGCAAGCCACATCGCCGAT	--G-TGTAC	ACAACGACAAGA					
krebsiana_serrulata_RM965	GACATAAAAAGGATCATTT	-AAGACCCCATGCCACAT	TAGGTTCCATATCCAAGACACCAAGCGAA	ACTCAGCAAGCCACATCGCCGAT	--G-TGTAC	ACAACGACAAGA					
leiopoda_M240901	GACATAAAAAGGATCATTT	-AAGACCCCATGCCACAT	TAGGTTCCATATCCAAGACACCAAGCGAA	ACTCAGCAAGCCACATCGCCGAT	--G-TGTAC	ACAACGACAAGA					
leiopoda_RM1309	GACATAAAAAGGATCATTT	-AAGACCCCATGCCACAT	TAGGTTCCATATCCAAGACACCAAGCGAA	ACTCAGCAAGCCACATCGCCGAT	--G-TGTAC	ACAACGACAAGA					
lichtensteinii_CAM1916	GACATAAAAAGGATCATCT	-AAGACCCCATGCCACAT	CAGGTTCCGTATCCAAGACACCAAGCGAA	ACTCAGCAAGCCACATCGACGAA	--G-TGTTT	TACAACGACRAAA					
lichtensteinii_RM1249	GACATAAAAAGGATCATCT	-AAGACCCCATGCCACAT	CAGGTTCCGTATCCAAGACACCAAGCGAA	ACTCAGCAAGCCACATCGACGAA	--G-TGTTT	TACAACGACRAAA					
linearis_linearis_RM1010	GACATAAAAAGGATCATTT	-AAGACCCCATGCCACAT	TAGGTTCCATATCCAAGACACCAAGCGAA	ACTCAGCAAGCCACATCGCCGAT	--G-TGTAC	ACAACGACAAGA					
linearis_linearis_SH113	GACATAAAAAGGATCATTT	-AAGACCCCATGCCACAT	TAGGTTCCATATCCAAGACACCAAGCGAA	ACTCAGCAAGCCACATCGCCGAT	--G-TGTAC	ACAACGACAAGA					
linearis_ovalis_NDsn	GACATAAAAAGGATCATTT	-AAGACCCCATGCCACAT	TAGGTTCCATATCCAAGACACCAAGCGAA	ACTCAGCAAGCCACATCGCCGAT	--G-TGTAC	ACAACGACAAGA					
linearis_ovalis_RM854	GACATAAAAAGGATCATTT	-AAGACCCCATGCCACAT	TAGGTTCCATATCCAAGACACCAAGCGAA	ACTCAGCAAGCCACATCGCCGAT	--G-TGTAC	ACAACGACAAGA					
maritima_RM1038	GACATAAAAAGGATCATTT	-AAGACCCCATGCCACAT	TAGGTTCCATATCCAAGACACCAAGCGAA	ACTCAGCAAGCCACATCGCCGAT	--G-TGTAC	ACAACGACAAGA					
maritima_M290606_6	GACATAAAAAGGATCATTT	-AAGACCCCATGCCACAT	TAGGTTCCATATCCAAGACACCAAGCGAA	ACTCAGCAAGCCACATCGCCGAT	--G-TGTAC	ACAACGACAAGA					
othonnites_RM1306	GACATAAAAAGGATCATCT	-AAGACCCCATGCCACAT	TAGGTTCCATATCCAAGACACCAAGCGAA	ACTCAGCAAGCCACATCGCCGAT	--G-TGTAC	ACAACGACAAGA					
pectinata_M120903	GACATAAAAAGGATCATTT	-AAGACCCCATGCCACAT	TAGGTTCCATATCCAAGACACCAAGCGAA	ACTCAGCAAGCCACATCGCCGAT	--G-TGTAC	ACAACGACAAGA					
pectinata_RM1044	GACATAAAAAGGATCATTT	-AAGACCCCATGCCACAT	TAGGTTCCATATCCAAGACACCAAGCGAA	ACTCAGCAAGCCACATCGCCGAT	--G-TGTAC	ACAACGACAAGA					
rigida_M280902	GACATAAAAAGGATCATTT	-AAGACCCCATGCCACAT	TAGGTTCCATATCCAAGACACCAAGCGAA	ACTCAGCAAGCCACATCGCCGAT	--G-TGTAC	ACAACGACAAGA					
rigida_RM840	GACATAAAAAGGATCATTT	-AAGACCCCATGCCACAT	TAGGTTCCATATCCAAGACACCAAGCGAA	ACTCAGCAAGCCACATCGCCGAT	--G-TGTAC	ACAACGACAAGA					
rigens_leucolaena_RM773	GACATAAAAAGGATCATGT	-AAGACCCCATGCCACAT	TAGGTTCAATATCCAAGACACCAAGCGAA	ACTCAGCAAGCCACATCGCCGAA	TG-TATAC	ACAACAACAAGA					
rigens_leucolaena_RM952_1	GACATAAAAAGGATCATTT	-AAGACCCCATGCCACAT	TAGGTTCCATATCCAAGACACCAAGCGAA	ACTCAGCAAGCCACATCGCCGAT	--G-TGTAC	ACAACGACAAGA					
rigens_rigens_RM763	GACATAAAAAGGATCATTT	-AAGACCCCATGCCACAT	TAGGTTCCATATCCAAGACACCAAGCGAA	ACTCAGCAAGCCACATCGCCGAT	--G-TGTAC	ACAACGACAAGA					
rigens_rigens_SR463	GACATAAAAAGGATCATTT	-AAGACCCCATGCCACAT	TAGGTTCCATATCCAAGACACCAAGCGAA	ACTCAGCAAGCCACATCGCCGAT	--G-TGTAC	ACAACGACAAGA					
rigens_uniflora_JC201205	GACATAAAAAGGATCATCT	-AAGACCCCATGCCACAT	TAGGTTCCATATCCAAGACACCAAGCGAA	ACTCAGCAAGCCACATCGACGAT	--G-TGTAC	ACAACGACAAGA					
rigens_uniflora_RM920	GACATAAAAAGGATCATTT	-AAGACCCCATGCCACAT	TAGGTTCCATATCCAAGACACCAAGCGAA	ACTCAGCAAGCCACATCGCCGAT	--G-TGTAC	ACAACGACAAGA					
schenckii	GACATTTAAAGGATCATCT	-AAGACCCCATGCCACAT	CAGGTTCCGTATCCAAGACACCAAGCGAA	ACTCAGCAAGCCACATCGACGAA	--G-TGTTT	TACAACGACGAAA					
serrata_M250904_15	GACATAAAAAGGATCATTT	-AAGACCCCATGCCACAT	TAGGTTCCATATCCAAGACACCAAGCGAA	ACTCAGCAAGCCACATCGCCGAT	--G-TGTAC	ACAACGACAAGA					
serrata_RM898	GACATAAAAAGGATCATTT	-AAGACCCCATGCCACAT	TAGGTTCCATATCCAAGACACCAAGCGAA	ACTCAGCAAGCCACATCGCCGAT	--G-TGTAC	ACAACGACAAGA					
tenuifolia_CAM1601	GACATAAAAAGGATCATTT	-AAGACCCCATGCCACAT	CAGGTTCCATATCCRAGACACCAAGCGAA	ACTCAGCAAGCCACATCGCCGAA	--G-TGTTT	TACAAGGACGAGA					
tenuifolia_M2730	GACATAAAAAGGATCATTT	-AAGACCCCATGCCACAT	CAGGTTCCATATCCAAGACACCAAGCGAA	ACTCAGCAAGCCACATCGCCGAA	--G-TGTTT	TACAACGACAAGA					
spnov_M040906_33	GACATAAAAAGGATCATCT	-AAGACCCCATGCCACAT	TAGGTTCCATATCCAAGACACCAAGCGAA	ACTCAGCAAGCCACATCGCCGAT	--G-TGTAC	ACAACGACAAGA					

Appendix 4: nrDNA sequence data for Chapter 3.

	890	900	910	920	930	940	950	960	970	980	990]
Berkheya	TGGATTACAGAGACC	ACTTCTCGTTCG	TCCACACACC	ACAAGTGTG	ATGCACGACG	AAACTGGCTTC	CGATCGGTCC	AYGCAATGC	CTTCGATT	AGGTATG	CAACACAGGA
Gorteria	TGGATTACAAAGACC	ACTTCTAGTCC	GTCCACACACC	CACAATTGT	GATGCATGGC	AAAAACGGCTTC	CGATCGGTCC	AAAAAATGC	CTTCGATT	AGGTACG	CAACACAGGA
Hirpicium	TGGATTACAGAGAACT	TTTTCTGGTCC	GTCCACACACC	ACAAGTGG	CGATGCATG	ACGAAACAGCTT	ATATCGAT	CCATACAAT	GCCTTTG	TTAGGTAC	GCAACACAGGA
caespitosa_RC448	TGGATTACAGAGAAC	CGTTACTGGTCC	GTCCATGCACC	CACATGTG	CGATGCGTG	ACGGAACAGAT	TCAATCGGT	CCATACAAT	GCCTTCG	ATTASGTAC	GCAACACAGGA
caespitosa_RVC307	TGGATTACAGAGACC	CGTTACTGGTCC	GTCCATGCACC	CACATGTG	CGATGCGTG	ACGGAACAGAT	TCAATCGGT	CCATACAAT	GCCTTCG	ATTAGGTAC	GCAACACAGGA
ciliaris_RM1230	TGGATTACAGAGAAC	CGTTACTGGTCC	GTCCATGCACC	CACATGTG	CGATGCGTG	ACGGAACAGAT	TCAATCGGT	CCATACAAT	GCCTTCG	ATTAGGTAC	GCAACACAGGA
ciliaris_RM1382	TGGATTACAGAGAAC	CGTTACTGGTCC	GTCCATGCACC	AAAATGTG	CGATGCGTG	AAAGAAACAGAT	TCAATCGGT	CCATACAAT	GCCTTCG	ATTAGGTAC	GCAACACAGGA
heterochaeta_RM1429_1	TGGATTACAGAGACC	ACTTACTGGTCC	GTCCATGCACC	CACA-GT	GCGATGCGTG	ACAAAAACAGAT	TCAATCGGT	CCATACAAT	GCCTTTG	ATTAGGAA	CGCAACACAGGA
heterochaeta_RM1451	TGGCTTACAGAGACC	ACTTACTGGTCC	GTCCATGCACC	CACA-GT	GCGATGCGTG	ACAAAAACAGAT	TCAATCGGT	CCATACAAT	GCCTTTG	ATTAGGAA	CGCAACACAGGA
jurineifolia_jur_SR682	TGGATTACAGAGACC	ACTAGTGGTCC	GTCCATGCACC	CACAAGT	GCGATGCGTG	ACGGAACAGAT	TCAATCGGT	CCATACAAT	GCCTTCG	ATTAGGTAC	GCAACACAGAA
jurineifolia_jur_RM1518	TGGATTACAGAGACC	ACTTGTGGTCC	GTCCATGCACC	ACAAGT	GCGATGCGTG	ACGGAACAGAT	TCAATCGGT	CCATACAAT	GCCTTCG	ATTAGGTAC	GCAACACAGAA
jurineifolia_scab_CAM1604	TGGATTACAGAGACC	ACTTGTGGTCC	GTCCATGCACC	ACAAGT	GCGATGCGTG	ACGGAACARAT	TCAATCGGT	CCATACAAT	GCCTTCG	ATTAGGTAC	GCAACACAGAA
jurineifolia_scab_CAM2652	TGGATTACAGAGACC	ACTTGTGGTCC	GTCCATGCACC	ACAAGT	GCGATGCGTG	ACGGAACAGAT	TCAATCGGT	CCATACAAT	GCCTTCG	ATTAGGTAC	GCAACACAGAA
krebsiana_arctotoides_RM868	TGGATTACTAAGACC	ACTTACCGGTCC	ATCATGCACC	ACTTGTG	CGATGACG	GATACATAT	TTCATTCGGT	CCATACAAT	GCCTTCG	ATTAGGTAC	GCAACACAGTA
krebsiana_arctotoides_RM876	TGGATTACTAAGACC	ACTTACCGGKCC	ATCATGCACC	ACTTGTG	CGATGACG	GATACATAT	TTCATTCGGT	CCATACAAT	GCCTTCG	ATTAGGTAC	GCAACACAGTA
krebsiana_krebsiana_RM1114	TGGATTACTAAGA	ACTTACCGGTCC	ATCATGCACC	ACTTGTG	CGATGACG	GATACATAT	TTCATTCGGT	CCATACAAT	GCCTTCG	ATTAGGTAC	GCAACACAGTA
krebsiana_krebsiana_RM1136	TGGATTACTAAGACC	ACTTACCGGTCC	ATCATGCACC	ACTTGTG	CGATGACG	GATACATAT	TTCATTCGGT	CCATACAAT	GCCTTCG	ATTAGGTAC	GCAACACAGTA
krebsiana_serrulata_RM863	TGGATTACTAAGACC	ACTTACCGGTCC	ATCATGCACC	ACTTGTG	CGATGACG	GATACATAT	TTCATTCGGT	CCATACAAT	GCCTTCG	ATTAGGTAC	GCAACACAGTA
krebsiana_serrulata_RM965	TGGATTACTAAGACC	ACTTACCGGTCC	ATCATGCACC	ACTTGTG	YATGACG	GATACATAT	TTCATTCGGT	CCATACAAT	GCCTTCG	ATTAGGTAC	GCAACACAGTA
leiopoda_M240901	TGGATTACTAAGACC	ACTTACCGGTCC	ATCATGCACC	ACTTGTG	CGATGACG	GATACATAT	TTCATTCGGT	CCATACAAT	GCCTTCG	ATTAGGTAC	GCAACACAGTA
leiopoda_RM1309	TGGATTACTAAGACC	ACTTACCGGTCC	ATCATGCACC	ACTTGTG	CGATGACG	GATACATAT	TTCATTCGGT	CCATACAAT	GCCTTCG	ATTAGGTAC	GCAACACAGTA
lichtensteinii_CAM1916	TGGCTTACAGAGACC	ACTTACTGGTCC	GTCCATGCACC	ACAAGT	GCGATGCGTG	ACGGAACAGAT	TCAATCGGT	CCATACAAT	GCCTTTG	ATTAGGTAC	GCAACACAGGA
lichtensteinii_RM1249	TGGCTTACAGAGACC	ACTTACTGGTCC	GTCCATGCACC	ACAAGT	GCGATGCGTG	ACGGAACAGAT	TCAATCGGT	CCATACAAT	GCCTTTG	ATTAGGTAC	GCAACACAGGA
linearis_linearis_RM1010	TGGATTACTAAGACC	ACTTACCGGTCC	ATCATGCACC	ACTTGTG	CGATGACG	GATACATAT	TTCATTCGGT	CCATACAAT	GCCTTCG	ATTAGGTAC	GCAACACAGTA
linearis_linearis_SH113	TGGATTACTAAGACC	ACTTACCGGTCC	ATCATGCACC	ACTTGTG	CGATGACG	GATACATAT	TTCATTCGGT	CCATACAAT	GCCTTCG	ATTAGGTAC	GCAACACAGTA
linearis_ovalis_NDsn	TGGATTACTAAGACC	ACTTACCGGKCC	ATCATGCACC	ACTTGTG	CGATGACG	GATACATAT	TTCATTCGGT	CCATACAAT	GCCTTCG	ATTAGGTAC	GCAACACAGTA
linearis_ovalis_RM854	TGGATTACTAAGACC	ACTTACCGGTCC	ATCATGCACC	ACTTGTG	CGATGACG	GATACATAT	TTCATTCGGT	CCATACAAT	GCCTTCG	ATTAGGTAC	GCAACACAGTA
maritima_RM1038	TGGATTACTGAGACC	ACTTACCGGTCC	ATCATGCACC	ACTTGTG	CGATGACG	GATACATAT	TTCATTCGGT	CCATACAAT	GCCTTCG	ATTAGGTAC	GCAACACAGTA
maritima_M290606_6	TGGATTACTGAGACC	ACTTACCGGTCC	ATCATGCACC	ACTTGTG	CGATGACG	GATACATAT	TTCATTCGGT	CCATACAAT	GCCTTCG	ATTAGGTAC	GCAACACAGTA
othonnites_RM1306	TGGATTACTAAGACC	ACTTACCGGTCC	ATCATGCACC	ACTTGTG	CGATGACG	GATACATAT	TTCATTCGGT	CCATACAAT	GCCTTCG	ATTAGGTAC	GCAACACAGTA
pectinata_M120903	TGGATTACAGAGACC	ACTTACCGGTCC	WGCATGCACC	ACKTGTG	CGATGACG	GATACATAT	TTCATTCGGT	CCATACAAT	GCCTTCG	ATTAGGTACT	CAACACAGTA
pectinata_RM1044	TGGATTACTGAGACC	ACTTACCGGTCC	ATCATGCACC	ACTTGTG	CGATGACG	GATACATAT	TTCATTCGGT	CCATACAAT	GCCTTCG	ATTAGGTAC	GCAACACAGTA
rigida_M280902	TGGATTACTAAGACC	ACTTACCGGTCC	ATCATGCACC	ACTTGTG	CGATGACG	GATACATAT	TTCATTCGGT	CCATACAAT	GCCTTCG	ATTAGGTAC	GCAACACAGTA
rigida_RM840	TGGATTACTGAGACC	ACTTACCGGTCC	ATCATGCACC	ACTTGTG	CGATGACG	GATACATAT	TTCATTCGGT	CCATACAAT	GCCTTCG	ATTAGGTAC	GCAACACAGTA
rigens_leucolaena_RM773	TGGATTACTAAGACC	ACTTACCGGTCC	ATCATGCACC	ACTTGTG	CGATGACG	GATACATAT	TTCATTCGGT	CCATACAAT	GCCTTCG	ATTAGGTAC	GCAACACAGTA
rigens_leucolaena_RM952_1	TGGATTACTAAGACC	ACTTACCGGTCC	ATCATGCACC	ACTTGTG	CGATGACG	GATACATAT	TTCATTCGGT	CCATACAAT	GCCTTCG	ATTAGGTAC	GCAACACAGTA
rigens_rigens_RM763	TGGATTACTAAGACC	ACTTACCGGTCC	ATCATGCACC	ACTTGTG	CGATGACG	GATACATAT	TTCATTCGGT	CCATACAAT	GCCTTCG	ATTAGGTAC	GCAACACAGTA
rigens_rigens_SR463	TGGATTACTAAGACC	ACTTACCGGTCC	ATCATGCACC	ACTTGTG	CGATGACG	GATACATAT	TTCATTCGGT	CCATACAAT	GCCTTCG	ATTAGGTAC	GCAACACAGTA
rigens_uniflora_JC201205	TGGATTACTAAGACC	ACTTACCGGTCC	ATCATGCACC	ACTTGTG	CGATGACG	GATACATAT	TTCATTCGGT	CCATACAAT	GCCTTCG	ATTAGGTAC	GCAACACAGTA
rigens_uniflora_RM920	TGGATTACTAAGACC	ACTTACCGGTCC	ATCATGCACC	ACTTGTG	CGATGACG	GATACATAT	TTCATTCGGT	CCATACAAT	GCCTTCG	ATTAGGTAC	GCAACACAGTA
schenckii	TGGCTTACAGAGACC	ACTTACTGGTCC	GTCCATGCACC	ACAAGT	GCGATGCGTG	ACGGAACAGAT	TCAATCGGT	CCATACAAT	GCCTTTG	ATTAGGTAC	GCAACACAGGA
serrata_M250904_15	TGGATTACTAAGACC	ACTTACCGGTCC	ATCATGCACC	ACTTGTG	CGATGACG	GATACATAT	TTCATTCGGT	CCATACAAT	GCCTTCG	ATTAGGTAC	GCAACACAGTA
serrata_RM898	TGGATTACTGAGACC	ACTTACCGGTCC	ATCATGCACC	ACTTGTG	CGATGACG	GATACATAT	TTCATTCGGT	CCATACAAT	GCCTTCR	ATTAGGTAC	GCAACACAGTA
tenuifolia_CAM1601	TGGATTACGGAGACC	ACTTACTGGTCC	GTCTTGCACC	ACAAGT	GCGATGCGTG	ACGGAACAGAT	TCAATCAGT	-CATA	CAATGC	CTTCGATT	AGGTACGCAACACAGGA
tenuifolia_M2730	TGGATTACGGAGACC	ACTTACTGGTCC	GTCCATGCACC	ACAAGT	GCGATGCGTG	ACGGAACAGAT	TCAATCTGT	-CATA	CAATGC	CTTCGATT	AGGTACGCAACACAGGA
spnov_M040906_33	TGGATTACTAAGACC	ACTTACCGGTCC	ATCATGCACC	ACTTGTG	CGATGACG	GATACATAT	TTCATTCGGT	CCATACAAT	GCCTTCG	ATTAGGTAC	GCAACACAGTA

Appendix 4: nrDNA sequence data for Chapter 3.

	1000	1010	1020	1030	1040	1050	1060	1070	1080	1090	1100]
Berkheya	A	A	A	A	A	A	A	A	A	A	A
Gorteria	A	A	A	A	A	A	A	A	A	A	A
Hirpicium	A	A	A	A	A	A	A	A	A	A	A
caespitosa_RC448	A	A	A	A	A	A	A	A	A	A	A
caespitosa_RVC307	A	A	A	A	A	A	A	A	A	A	A
ciliaris_RM1230	A	A	A	A	A	A	A	A	A	A	A
ciliaris_RM1382	A	A	A	A	A	A	A	A	A	A	A
heterochaeta_RM1429_1	A	A	A	A	A	A	A	A	A	A	A
heterochaeta_RM1451	A	A	A	A	A	A	A	A	A	A	A
jurineifolia_jur_SR682	A	A	A	A	A	A	A	A	A	A	A
jurineifolia_jur_RM1518	A	A	A	A	A	A	A	A	A	A	A
jurineifolia_scab_CAM1604	A	A	A	A	A	A	A	A	A	A	A
jurineifolia_scab_CAM2652	A	A	A	A	A	A	A	A	A	A	A
krebsiana_arctotoides_RM868	A	A	A	A	A	A	A	A	A	A	A
krebsiana_arctotoides_RM876	A	A	A	A	A	A	A	A	A	A	A
krebsiana_krebsiana_RM1114	A	A	A	A	A	A	A	A	A	A	A
krebsiana_krebsiana_RM1136	A	A	A	A	A	A	A	A	A	A	A
krebsiana_serrulata_RM863	A	A	A	A	A	A	A	A	A	A	A
krebsiana_serrulata_RM965	A	A	A	A	A	A	A	A	A	A	A
leiopoda_M240901	A	A	A	A	A	A	A	A	A	A	A
leiopoda_RM1309	A	A	A	A	A	A	A	A	A	A	A
lichtensteinii_CAM1916	A	A	A	A	A	A	A	A	A	A	A
lichtensteinii_RM1249	A	A	A	A	A	A	A	A	A	A	A
linearis_linearis_RM1010	A	A	A	A	A	A	A	A	A	A	A
linearis_linearis_SH113	A	A	A	A	A	A	A	A	A	A	A
linearis_ovalis_NDsn	A	A	A	A	A	A	A	A	A	A	A
linearis_ovalis_RM854	A	A	A	A	A	A	A	A	A	A	A
maritima_RM1038	A	A	A	A	A	A	A	A	A	A	A
maritima_M290606_6	A	A	A	A	A	A	A	A	A	A	A
othonnites_RM1306	A	A	A	A	A	A	A	A	A	A	A
pectinata_M120903	A	A	A	A	A	A	A	A	A	A	A
pectinata_RM1044	A	A	A	A	A	A	A	A	A	A	A
rigida_M280902	A	A	A	A	A	A	A	A	A	A	A
rigida_RM840	A	A	A	A	A	A	A	A	A	A	A
rigens_leucolaena_RM773	A	A	A	A	A	A	A	A	A	A	A
rigens_leucolaena_RM952_1	A	A	A	A	A	A	A	A	A	A	A
rigens_rigens_RM763	A	A	A	A	A	A	A	A	A	A	A
rigens_rigens_SR463	A	A	A	A	A	A	A	A	A	A	A
rigens_uniflora_JC201205	A	A	A	A	A	A	A	A	A	A	A
rigens_uniflora_RM920	A	A	A	A	A	A	A	A	A	A	A
schenckii	A	A	A	A	A	A	A	A	A	A	A
serrata_M250904_15	A	A	A	A	A	A	A	A	A	A	A
serrata_RM898	A	A	A	A	A	A	A	A	A	A	A
tenuifolia_CAM1601	A	A	A	A	A	A	A	A	A	A	A
tenuifolia_M2730	A	A	A	A	A	A	A	A	A	A	A
spnov_M040906_33	A	A	A	A	A	A	A	A	A	A	A

Appendix 4: nrDNA sequence data for Chapter 3.

	1110	1120	1130	1140	1150	1160	1170	1180	1190	1200	1210]
Berkheya	C	A	C	A	C	C	A	C	A	C	A
Gorteria	C	A	C	A	C	C	A	C	A	C	A
Hirpicium	C	A	C	A	C	C	A	C	A	C	A
caespitosa_RC448	C	A	C	A	C	C	A	C	A	C	A
caespitosa_RVC307	C	A	C	A	C	C	A	C	A	C	A
ciliaris_RM1230	C	A	C	A	C	C	A	C	A	C	A
ciliaris_RM1382	C	A	C	A	C	C	A	C	A	C	A
heterochaeta_RM1429_1	C	A	C	A	C	C	A	C	A	C	A
heterochaeta_RM1451	C	A	C	A	C	C	A	C	A	C	A
jurineifolia_jur_SR682	C	A	C	A	C	C	A	C	A	C	A
jurineifolia_jur_RM1518	C	A	C	A	C	C	A	C	A	C	A
jurineifolia_scab_CAM1604	C	A	C	A	C	C	A	C	A	C	A
jurineifolia_scab_CAM2652	C	A	C	A	C	C	A	C	A	C	A
krebsiana_arctotoides_RM868	C	A	C	A	C	C	A	C	A	C	A
krebsiana_arctotoides_RM876	C	A	C	A	C	C	A	C	A	C	A
krebsiana_krebsiana_RM1114	C	A	C	A	C	C	A	C	A	C	A
krebsiana_krebsiana_RM1136	C	A	C	A	C	C	A	C	A	C	A
krebsiana_serrulata_RM863	C	A	C	A	C	C	A	C	A	C	A
krebsiana_serrulata_RM965	C	A	C	A	C	C	A	C	A	C	A
leiopoda_M240901	C	A	C	A	C	C	A	C	A	C	A
leiopoda_RM1309	C	A	C	A	C	C	A	C	A	C	A
lichtensteinii_CAM1916	C	A	C	A	C	C	A	C	A	C	A
lichtensteinii_RM1249	C	A	C	A	C	C	A	C	A	C	A
linearis_linearis_RM1010	C	A	C	A	C	C	A	C	A	C	A
linearis_linearis_SH113	C	A	C	A	C	C	A	C	A	C	A
linearis_ovalis_NDsn	C	A	C	A	C	C	A	C	A	C	A
linearis_ovalis_RM854	C	A	C	A	C	C	A	C	A	C	A
maritima_RM1038	C	A	C	A	C	C	A	C	A	C	A
maritima_M290606_6	C	A	C	A	C	C	A	C	A	C	A
othonnites_RM1306	C	A	C	A	C	C	A	C	A	C	A
pectinata_M120903	C	A	C	A	C	C	A	C	A	C	A
pectinata_RM1044	C	A	C	A	C	C	A	C	A	C	A
rigida_M280902	C	A	C	A	C	C	A	C	A	C	A
rigida_RM840	C	A	C	A	C	C	A	C	A	C	A
rigens_leucolaena_RM773	C	A	C	A	C	C	A	C	A	C	A
rigens_leucolaena_RM952_1	C	A	C	A	C	C	A	C	A	C	A
rigens_rigens_RM763	C	A	C	A	C	C	A	C	A	C	A
rigens_rigens_SR463	C	A	C	A	C	C	A	C	A	C	A
rigens_uniflora_JC201205	C	A	C	A	C	C	A	C	A	C	A
rigens_uniflora_RM920	C	A	C	A	C	C	A	C	A	C	A
schenckii	C	A	C	A	C	C	A	C	A	C	A
serrata_M250904_15	C	A	C	A	C	C	A	C	A	C	A
serrata_RM898	C	A	C	A	C	C	A	C	A	C	A
tenuifolia_CAM1601	C	A	C	A	C	C	A	C	A	C	A
tenuifolia_M2730	C	A	C	A	C	C	A	C	A	C	A
spnov_M040906_33	C	A	C	A	C	C	A	C	A	C	A

Appendix 4: nrDNA sequence data for Chapter 3.

	1220	1230	1240	1250	1260	1270	1280	1290	1300	1310	1320]
Berkheya	ATGCACCGAACGATGCGAGAAACAAT	-AAGCTACGAAACCAA-CATG	-ATTGCCTCATCAAGACGCTCGTTTCATTATTTTCT	-TCACACAACGCATCGCTAGCC-AGGC							
Gorteria	ATGAACCGCACGATGCGAGAAACACAAAAGCT	TACGAAACCAA-CATGATTGCTCATAAAAACGCTCGCTTCATGATATTCT	-ATGCACAACGCATCGCTAGCC-GGGC								
Hirpicium	ATGCACCGAACGATGCGAGAAACAATTAAGCT	TACGAAACCGA-CA--ATTGCTTCGTCAAAACGCTCGCATTATGGTTTTCT	-ACGCACAACGCATCGCTAGCC-GGGC								
caespitosa_RC448	ATGCACCGAACGATGCGAGAAAGAGTAAAGCT	TACGAAACCAA-CATG-ATCGCCTCATCAAAACGCTCGCTTCATGATTTTCTA	-ACA????????????????????								
caespitosa_RVC307	ATGCACCGAACGATGCGAGAAAYATAAAGCT	TACGAAACCGA-CATG-ATCGCCTCATCAAAACGCTCGCTTGATGATTTTCT	-AGACACGACGCATCGCTAGCC-AGGC								
ciliaris_RM1230	ATGCACCGAACGATGCGAGAAACCATAAAGCT	TACGAAACCGTTCGCGAATCGCCTCATCAAAACGCTCGCTTCATGATTTTCTTTAGACACCACGCATCGCTAGCC-GAGC									
ciliaris_RM1382	ATGCACCGAACGATGCGAGAAACAATAAAGCT	TACGAAACCGTTCACGAATCGCCTCATCAAAACGCTCGCTTCATGATTTTCTTTAGACACCACGCATCGCTAGCC-GAGC									
heterochaeta_RM1429_1	ATGCACCGAACGACGCGAGAAACAATAAAGCT	TACGAAACCGA-CACG-ATCGCCTCATCAAAACGCTCGCTTCATGATTTTCT	-ACACACAACGCATCGCTAGACTRGGC								
heterochaeta_RM1451	ATGCACCGAACGACGCGAGAAACAATAAAGCT	TACGAAACCGA-CACG-ATCGCCTCATCAAAACGCTCGCTTCATGATTTTCT	-ACACACAACGCATCGCTAGACTAGGC								
jurineifolia_jur_SR682	ATGCACCGAACGATGCGAGAAACAATAAAGCT	TACGAAACCAA-CATG-ATCGCCTCATTAATAACGCTCGCTTCATGATTTTCT	-ACGCACAACGTATCGCTAGCC-GGGC								
jurineifolia_jur_RM1518	ATGCACCGAACGATGCGAGAAACAATAAAGCT	TACGAAACCAA-CATG-ATCGCCTCATTAATAACGCTCGCTTCATGATTTTCT	-ACGCACAACGTAAACGCTAGCC-GGGC								
jurineifolia_scab_CAM1604	ATGCACCGAACGATGCGAGAAACAATAAAGCT	TACGAAACCAA-CATG-ATCGCCTCATTAATAACGCTCGCTTCATGATTTTCT	-ACGCACAACGTATCGCTAGCC-GGGC								
jurineifolia_scab_CAM2652	ATGCACCGAACGATGCGAGAAACAATAAAGCT	TACGAAACCAA-CATG-ATCGCCTCATTAATAACGCTCGCTTCATGATTTTCT	-ACGCACAACGTATCGCTAGCC-GGGC								
krebsiana_arctotoides_RM868	ATGTACCGAGCGATGCGAGAAACAGTAAAGCT	TACGAAACCAA-CAGG-ATCGCCTCATCAAAACGCTCGCTTCATTATTTTCCA	-ACACACAACGCATCGCTAGCA-AGGC								
krebsiana_arctotoides_RM876	ATGTACCGARCGATGCGAGAAACAGTAAAGCT	TACGAAACCAA-CAGG-ATCGCCTCATCAAAACGCTCGCTTCATTATTTTCCA	-ACACACAACGCATCGCTAGCA-AGGC								
krebsiana_krebsiana_RM1114	ATGTACCGAACGATGCGAGAAACAGTAAAGCT	TACGAAACCAA-CAGG-ATCGCCTCATCAAAACGCTCGCTTCATTATTTTCCA	-ACGCACAACGCATCGCTAGCA-AGGC								
krebsiana_krebsiana_RM1136	ATGTACCGAACGATGCGAGAAACAGTAAAGCT	TACGAAACCAA-CAGG-ATCGCCTCATCAAAACGCTCGCTTCATTATTTTCCA	-ACACACAACGCATCGCTAGCA-AGGC								
krebsiana_serrulata_RM863	ATGTACCGAGCGATGCGAGAAACAGTAAAGCT	TACGAAACCAA-CAGG-ATCGCCTCATCAAAACGCTCGCTTCATTATTTTCCA	-ACACACAACGCATCGCTAGCA-AGGC								
krebsiana_serrulata_RM965	ATGTACCGAACGATGCGAGAAACAGTAAAGCT	TACGAAACCAA-CAGG-ATCGCCTCATCAAAACGCTCGCTTCATTATTTTCCA	-ACACACAACGCATCGCTAGCA-AGGC								
leiopoda_M240901	ATGTACCGAACGATGCGAGAAACAGTAAAGCT	TACGAAACCAA-CAGG-ATCGCCTCATCAAAACGCTCGCTTCATTATTTTCCA	-ACACACAACGCATCGCTAGCA-AGGC								
leiopoda_RM1309	ATGCACCGAACGATGCGAGAAACAGTAAAGCT	TACGAAACCAA-CAGG-ATCGCCTCATCAAAACGCTCGCTTCATTATTTTCCA	-A????????????????????								
lichtensteinii_CAM1916	ATGAACCGAACGATGCGAGAAACAATAAAGCT	TACGAAACCGA-CACG-ATCGCCTCATCAAAACGCTCGCTTCATGCTTTTCT	-ACACACAACGCATCGCAAGACTAGGC								
lichtensteinii_RM1249	ATGAACCGAACGATGCGAGAAACAATAAAGCT	TACGAAACCGA-CACG-ATCGCCTCATCAAAACGCTCGCTTCATGCTTTTCT	-ACACACAACGCATCGCAAGACTAGGC								
linearis_linearis_RM1010	ATGTACCGAACGATGCGAGAAACAGTAAAGCT	TACGAAACCAA-CAGG-ATCGCCTCATCAAAACGCTCGCTTCATTATTTTCCA	-ACACACAACGCATCGCTAGCA-AGGC								
linearis_linearis_SH113	????????????????????????????????	????????????????????????????????	????????????????????????????????								
linearis_ovalis_NDsn	ATGTACCGAACGATGCGAGAAACAGTAAAGCT	TACGAAACCAA-CAGG-ATCGCCTCATCAAAACGCTCGCTTCATTATTTTCCA	-ACACACAACGCATCGCTAGCA-AGGC								
linearis_ovalis_RM854	ATGTACCGAACGATGCGAGAAACAGTAAAGCT	TACGAAACCAA-CAGG-ATCGCCTCATCAAAACGCTCGCTTCATTATTTTCCA	-ACACACAACGCATCGCTAGCA-AGGC								
maritima_RM1038	ATGCACCGAACGATGCGAGAAACAGAAAAGCT	TACGAAACCAA-CAGG-ATCGCCTCATCAAAACGCTCGCTTCATTATTTTCCA	-ACACACAACGCATCGCTAGCA-AGGC								
maritima_M290606_6	ATGCACCGAACGATGCGAGAAACAGTAAAGCT	TACGAAACCAA-CAGG-ATCGCCTCATCAAAACGCTCGCTTCATTATTTTCCA	-ACACACAACGCATCGCTAGCA-AGGC								
othonnites_RM1306	ATGTACCGAACGATGCGAGAAACAGTAAAGCT	TACGAAACCAA-CAGG-ATCGCCTCATCAAAACGCTCGCTTCATTATTTTCCA	-ACACACAACGCATCGCTAGCA-AGGC								
pectinata_M120903	ATGTACCGAACGATGCGAGAAACAGTAAAGCT	TACGAAACCAA-CAGG-ATCGCCTCATCAAAACGCTCGCTTCATTATTTTCCA	-ACACACAACGCATCGCTAGCA-AGGC								
pectinata_RM1044	ATGCACCGAACGATGCGAGAAACAGTAAAGCT	TACGAAACCAA-CAGG-ATCGCCTCATCAAAACGCTCGCTTCATTATTTTCCA	-ACACACAACGCATCGCTAGCA-AGGC								
rigida_M280902	ATGTACCGAACGATGCGAGAAACAGTAAAGCT	TACGAAACCAA-CAGG-ATCGCCTCATCAAAACGCTCGCTTCATTATTTTCCA	-ACACACAACGCATCGCTAGCA-AGGC								
rigida_RM840	????????????????????????????????	????????????????????????????????	????????????????????????????????								
rigens_leucolaena_RM773	ATGTACCGAACGATGCGAGAAACAGTAAAGCT	TACGAAACCAA-CAGG-ATCGCCTCATCAAAACGCTCGCTTCATTATTTTCCA	-ACACACAACGCATCGCTAGCA-AGGC								
rigens_leucolaena_RM952_1	????????????????????????????????	????????????????????????????????	????????????????????????????????								
rigens_rigens_RM763	????????????????????????????????	????????????????????????????????	????????????????????????????????								
rigens_rigens_SR463	ATGTACCGAACGATGCGAGAAACAGTAAAGCT	TACGAAACCAA-CAGG-ATCGCCTCATCAAAACGCTCGCTTCATTATTTTCCA	-ACACACAACGCATCGCTAGCA-AGGC								
rigens_uniflora_JC201205	ATGTACCGAACGATGCGAGAAACAGTAAAGCT	TACGAAACCAA-CAGG-ATCGCCTCATCAAAACGCTCGCTTCATTATTTTCCA	-ACACACAACGCATCGCTAGCA-AGGC								
rigens_uniflora_RM920	ATGTACCGAACGATGCGAGAAACAGTAAAGCT	TACGAAACCAA-CAGG-ATCGCCTCATCAAAACGCTCGCTTCATTATTTTCCA	-ACACACAACGCATCGCTAGCA-AGGC								
schenckii	ATGAACCGAACGATGCGAGAAACAATAAAGCT	TACGAAACCGA-CACG-ATCGCCTCATCAAAACGCTCGCTTCATGATTTTCT	-ACACACAACGCATCGCAAGACAAGGC								
serrata_M250904_15	????????????????????????????????	????????????????????????????????	????????????????????????????????								
serrata_RM898	ATGCACCGAACGATGCGAGAAACAGAAAAGCT	TACGAAACCAA-CAGG-ATCGCCTCATCAAAACGCTCGCTTCATTATTTTCCA	-ACACACAACGCATCGCTAGCA-AGGC								
tenuifolia_CAM1601	ATGCACCGAACGATGCGAGAAACAATAAAGCT	TACG????????????????????????????	????????????????????????????????								
tenuifolia_M2730	ATGCACCGAACGATGCGAGAAACAATAAAGCT	TACGAAACCGA-CACG-ATCGCCTCATCAAAACGCTCGCTTCATGGTTTTCC	-ACACACAACGCATCACAAGCC-AGGC								
spnov_M040906_33	ATGTACCGAACGATGCGAGAAACAGTAAAGCT	TACGAAACCAA-CAGG-ATCGCCTCATCAAAACGCTCGCTTCATTATTTTCCA	-ACACACAACGCATCGCTAGCA-AGGC								

Appendix 4: nrDNA sequence data for Chapter 3.

	1330	1340	1350	1360	1370	1380	1390	1400	1410	1420	1430
Berkheya	TTGTGCCAACACGTCGTTT	TAGAAAAA	-TCAACTT	TGCCACCC	TCCGTT	GGTGTG	TGCGAAG	CGACAAT	ACCACAT	CCTCGA	????????????????
Gorteria	TTGTGCCAACACGTCATG	CATCGAAAT	CAAATCAG	CTTGCCAC	CCCTCCG	TGGTGT	TGCGAAG	CAACAT	CACCACAT	CCTCGAG	TATGCACCGTT
Hirpicium	TTGTGCCAACACGTCATG	TTCAAAAA	CAAATCAG	CTTGCTAC	CCCTCCRT	GGAAAT	TGCGAAG	CTACAT	TWCCACAT	CCTCGG	TACACACCGTT
caespitosa_RC448	caespitosa_RVC307	ciliaris_RM1230	ciliaris_RM1382	heterochaeta_RM1429_1	heterochaeta_RM1451	jurineifolia_jur_SR682	jurineifolia_jur_RM1518	jurineifolia_scab_CAM1604	jurineifolia_scab_CAM2652	krebsiana_arctotoides_RM868	krebsiana_arctotoides_RM876
krebsiana_krebsiana_RM1114	krebsiana_krebsiana_RM1136	krebsiana_serrulata_RM863	krebsiana_serrulata_RM965	leiopoda_M240901	leiopoda_RM1309	lichtensteinii_CAM1916	lichtensteinii_RM1249	linearis_linearis_RM1010	linearis_linearis_SH113	linearis_ovalis_NDsn	linearis_ovalis_RM854
maritima_RM1038	maritima_M290606_6	othonnites_RM1306	pectinata_M120903	pectinata_RM1044	rigida_M280902	rigida_RM840	rigens_leucolaena_RM773	rigens_leucolaena_RM952_1	rigens_rigens_RM763	rigens_rigens_SR463	rigens_uniflora_JC201205
rigens_uniflora_RM920	schenckii	serrata_M250904_15	serrata_RM898	tenuifolia_CAM1601	tenuifolia_M2730	spnov_M040906_33					

Appendix 4: nrDNA sequence data for Chapter 3.

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[                               1440]

Berkheya                ????????????
Gorteria                ????????????
Hirpicium               CCATCAGCTGG
caespitosa_RC448       ????????????
caespitosa_RVC307     ????????????
ciliaris_RM1230       CCATCAGCTGG
ciliaris_RM1382       CCATCAGCTGG
heterochaeta_RM1429_1 CCATCAGCTGG
heterochaeta_RM1451   CCATCAGCTGG
jurineifolia_jur_SR682 ????????????
jurineifolia_jur_RM1518 ????????????
jurineifolia_scab_CAM1604 CCATCAGCTGG
jurineifolia_scab_CAM2652 ????????????
krebsiana_arctotoides_RM868 CCATCAGCTGG
krebsiana_arctotoides_RM876 CCATCAGCTGG
krebsiana_krebsiana_RM1114 CCATCAGCTGG
krebsiana_krebsiana_RM1136 ????????????
krebsiana_serrulata_RM863 CCATCAGCTGG
krebsiana_serrulata_RM965 CCATCAGCTGG
leiopoda_M240901      CCATCAGCTGG
leiopoda_RM1309       ????????????
lichtensteinii_CAM1916 ????????????
lichtensteinii_RM1249 ????????????
linearis_linearis_RM1010 CCATCAGCTGG
linearis_linearis_SH113 ????????????
linearis_ovalis_NDsn  CCATCAGCTGG
linearis_ovalis_RM854 CCATCAGCTGG
maritima_RM1038       CC???????????
maritima_M290606_6    CCATCAGCTGG
othonnites_RM1306    CCATCAGCTG?
pectinata_M120903     ????????????
pectinata_RM1044      CCATCAGCTGG
rigida_M280902        ????????????
rigida_RM840          ????????????
rigens_leucolaena_RM773 CCATCAGCTGG
rigens_leucolaena_RM952_1 ????????????
rigens_rigens_RM763   ????????????
rigens_rigens_SR463   ????????????
rigens_uniflora_JC201205 ????????????
rigens_uniflora_RM920 CCATCAGCTGG
schenckii             AAATCAGCTGT
serrata_M250904_15    ????????????
serrata_RM898         ????????????
tenuifolia_CAM1601    ????????????
tenuifolia_M2730      CCATCAGCTGG
spnov_M040906_33     CCATCAGCTGG

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Appendix 5: cpDNA sequence data for Chapter 3

[10	20	30	40	50	60	70	80	90	100	110]
Berkheya	ATTCTTACATCCACCATTTTATATAGGAATGAAGGTGCT-CTTGGCTCGACGTCGTTTGTCTATTCTACTAGAACCCCT-CTTTTTT-ATTAGGTTGTAATGT-----A										
Gorteria	ATTCTTAGATCCACCATTTTATATAGGAATGAAGGTGCT-CTTAGCTCGACGTCGTTTGTCTATTCTACTAGAACCCCT-CTTTTTTTTATTGGGTTGTAATGT-----A										
Hirpicium	ATTCTTACATCCACCATTTTATATAGGAATGAAGGTGCT-CTTGGCTCGACGTCGTTTGTCTATTCTACTAGAACCCCT-TTTTTTTT-ATTGGGTTGTAATGT-----A										
caespitosa_RVC448	???????ATCCACCATTTTATATAGGAATGAAGGTGCT-CTTGGCTCGACGTCGTTTGTCTATTCTACTAGAACCCCT-CTTTTTTTTATTGGGTTGTAATGTAATGTA										
caespitosa_RVC307	ATTCTTACATCCACCATTTTATATAGGAATGAAGGTGCT-CTTGGCTCGACGTCGTTTGTCTATTCTACTAGAACCCCT-CTTTTTTTTATTGGGTTGTAATGTAATGTA										
ciliaris_RM1230	ATTCTTACATCCACCATTTTATATAGGAATGAAGGTGCT-CTTGGCTCGACGTCGTTTGTCTATTCTACTAGAACCCCT-CTTTTTTTTATTGGGTTGTAATGT-----A										
ciliaris_RM1382	ATTCTTACATCCACCATTTTATATAGGAATGAAGGTGCT-CTTGGCTCGACGTCGTTTGTCTATTCTACTAGAACCCCT-CTTTTTTTTATTGGGTTGTAATGTAATGTA										
heterochaeta_RM1429	ATTCTTACATCCACCATTTTATATAGGAATGAAGGTGCT-CTTGGCTCGACGTCGTTTGTCTATTCTACTAGAACCCCT-CTTTTTTTTATTGGGTTGTAATGT-----A										
heterochaeta_RM1451	ATTCTTACATCCACCATTTTATATAGGAATGAAGGTGCT-CTTGGCTCGACGTCGTTTGTCTATTCTACTAGAACCCCT-CTTTTTTTTATTGGGTTGTAATGT-----A										
jurineifolia_jur_SR682	????????????????ATTTTATATAGGAATGAAGGTGCTCCTTGGCTCGACGTCGTTTGTCTATTCTACTAGAACCCCT-CTTTTTT-ATTGGGTTGTAATGT-----A										
jurineifoliajur_RM1518	????????????????ATTTTATATAGGAATGAAGGTGCTCCTTGGCTCGACGTCGTTTGTCTATTCTACTAGAACCCCT-CTTTTTTTTATTGGGTTGTAATGT-----A										
jurineifolia_scab_CAM1604	ATTCTTACATCCACCATTTTATATAGGAATGAAGGTGCT-CTTGGCTCGACGTCGTTTGTCTATTCTACTAGAACCCCT-CTTTTTTTTATTGGGTTGTAATGT-----A										
jurineifolia_scab_CAM2652	ATTCTTACATCCACCATTTTATATAGGAATGAAGGTGCT-CTTGGCTCGACGTCGTTTGTCTATTCTACTAGAACCCCT-CTTTTTTTTATTGGGTTGTAATGT-----A										
krebsiana_arctotoides_RM868	????????????????CATTTTATATAGGAATGAAGGTGCT-CTTGGCTCGACGTCGTTTGTCTATTCTACTAGAACCCCT-TTTTTTTT-ATTGGGTTGTAATGT-----A										
krebsiana_arctotoides_RM876	????????????????CATTTTATATAGGAATGAAGGTGCT-CTTGGCTCGACGTCGTTTGTCTATTCTACTAGAACCCCT-TTTTTTTTTATTGGGTTGTAATGT-----A										
krebsiana_krebsiana_RM1114	ATTCTTACATCCACCATTTTATATAGGAATGAAGGTGCT-CTTGGCTCGACGTCGTTTGTCTATTCTACTAGAACCCCT-TTTTTTTTTATTGGGTTGTAATGT-----A										
krebsiana_krebsiana_RM1136	ATTCTTACATCCACCATTTTATATAGGAATGAAGGTGCT-CTTGGCTCGACGTCGTTTGTCTATTCTACTAGAACCCCT-TTTTTTTTTATTGGGTTGTAATGT-----A										
krebsiana_krebsiana_RM863	ATTCTTACATCCACCATTTTATATAGGAATGAAGGTGCT-CTTGGCTCGACGTCGTTTGTCTATTCTACTAGAACCCCT-TTTTTTTTTATTGGGTTGTAATGT-----A										
krebsiana_serrulata_RM965	ATTCTTACATCCACCATTTTATATAGGAATGAAGGTGCT-CTTGGCTCGACGTCGTTTGTCTATTCTACTAGAACCCCT-TTTTTTTTTATTGGGTTGTAATGT-----A										
leiopoda_M240901	ATTCTTACATCCACCATTTTATATAGGAATGAAGGTGCT-CTTGGCTCGACGTCGTTTGTCTATTCTACTAGAACCCCT-TTTTTTTTTATTGGGTTGTAATGT-----A										
leiopoda_RM1309	ATTCTTACATCCACCATTTTATATAGGAATGAAGGTGCT-CTTGGCTCGACGTCGTTTGTCTATTCTACTAGAACCCCT-TTTTTTTTTATTGGGTTGTAATGT-----A										
lichtenstenii_CAM1916	ATTCTTACATCCACCATTTTATATAGGAATGAAGGTGCT-CTTGGCTCGACGTCGTTTGTCTATTCTACTAGAACCCCT-CTTTTTTTTATTGGGTTGTAATGT-----A										
lichtenstenii_RM1249	ATTCTTACATCCACCATTTTATATAGGAATGAAGGTGCT-CTTGGCTCGACGTCGTTTGTCTATTCTACTAGAACCCCT-CTTTTTTTTATTGGGTTGTAATGT-----A										
linearis_linearis_RM1010	ATTCTTACATCCACCATTTTATATAGGAATGAAGGTGCT-CTTGGCTCGACGTCGTTTGTCTATTCTACTAGAACCCCT-TTTTTTTTTATTGGGTTGTAATGT-----A										
linearis_linearis_SH113	ATTCTTACATCCACCATTTTATATAGGAATGAAGGTGCT-CTTGGCTCGACGTCGTTTGTCTATTCTACTAGAACCCCT-TTTTTTTTTATTGGGTTGTAATGT-----A										
linearis_ovalis_NDsn	ATTCTTACATCCACCATTTTATATAGGAATGAAGGTGCT-CTTGGCTCGACGTCGTTTGTCTATTCTACTAGAACCCCT-TTTTTTTTTATTGGGTTGTAATGT-----A										
linearis_ovalis_RM854	????????????????CATTTTATATAGGAATGAAGGTGCC-CTTGGCTCGACGTCGTTTGTCTATTCTACTAGAACCCCT-TTCTTTTTTATTGGGTTGTAATGT-----A										
maritima_RM1038	ATTCTTACATCCACCATTTTATATAGGAATGAAGGTGCT-CTTGGCTCGACGTCGTTTGTCTATTCTACTAGAACCCCT-TTTTTTTTTATTGGGTTGTAATGT-----A										
maritima_M290606_6	ATTCTTACATCCACCATTTTATATAGGAATGAAGGTGCT-CTTGGCTCGACGTCGTTTGTCTATTCTACTAGAACCCCT-TTTTTTTTTATTGGGTTGTAATGT-----A										
othonnites_RM1306	????????????CCACCATTTTATATAGGAATGAAGGTGCT-CTTGGCTCGACGTCGTTTGTCTATTCTACTAGAACCCCT-TTTTTTTTTATTGGGTTGTAATGT-----A										
pectinata_M120903	????????????TCCACCATTTTATATAGGAATGAAGGTGCT-CTTGGCTCGACGTCGTTTGTCTATTCTACTAGAACCCCT-TTTTTTTTTATTGGGTTGTAATGT-----A										
pectinata_RM1044	ATTCTTACATCCACCATTTTATATAGGAATGAAGGTGCT-CTTGGCTCGACGTCGTTTGTCTATTCTACTAGAACCCCT-TTTTTTTTTATTGGGTTGTAATGT-----A										
rigida_M280902	???CTTACATCCACCATTTTATATAGGAATGAAGGTGCT-CTTGGCTCGACGTCGTTTGTCTATTCTACTAGAACCCCT-TTTTTTTTTATTGGGTTGTAATGT-----A										
rigida_RM840	??										
rigens_leucolaena_RM773	??										
rigens_leucolaena_RM952_1	ATTCTTACATCCACCATTTTATATAGGAATGAAGGTGCT-CTTGGCTCGACGTCGTTTGTCTATTCTACTAGAACCCCT-TTTTTTTTTATTGGGTTGTAATGT-----A										
rigens_rigens_RM763	??										
rigens_rigens_SR463	???????TTCTCCACCATTTTATATAGGAATGAAGGTGCA-CATGGCTCGACGTCGTTTGTCTATTCTACTAGAACCCCT-TTTTTTTTTATTGGGTTGTAATGT-----A										
rigens_uniflora_JC201205	ATTCTTACATCCACCATTTTATATAGGAATGAAGGTGCT-CTTGGCTCGACGTCGTTTGTCTATTCTACTAGAACCCCT-TTTTTTTTTATTGGGTTGTAATGT-----A										
rigens_uniflora_RM920	?????????CTCCACCATTTTATATAGGAATGAAGGTGCT-CTTGGCTCGACGTCGTTTGTCTATTCTACTAGAACCCCT-TTTTTTTTTATTGGGTTGTAATGT-----A										
schenckii	ATTCTTACATCCACCATTTTATATAGGAATGAAGGTGCT-CTTGGCTCGACGTCGTTTGTCTATTCTACTAGAACCCCT-CTTTTTTTTATTGGGTTGTAATGT-----A										
serrata_M250904_15	ATTCTTACATCCACCATTTTATATAGGAATGAAGGTGCT-CTTGGCTCGACGTCGTTTGTCTATTCTACTAGAACCCCT-TTCTTTTTTATTGGGTTGTAATGT-----A										
serrata_RM898	ATTCTTACATCCACCATTTTATATAGGAATGAAGGTGCT-CTTGGCTCGACGTCGTTTGTCTATTCTACTAGAACCCCT-TTTTTTT-ATTGGGTTGTAATGT-----A										
tenuifolia_CAM1601	ATTCTTACATCCACCATTTTATATAGGAATGAAGGTGCT-CTTGGCTCGACGTCGTTTGTCTATTCTACTAGAACCCCT-CTTTTTTTTATTGGGTTGTAATGT-----A										
tenuifolia_M2730	ATTCTTACATCCACCATTTTATATAGGAATGAAGGTGCT-CTTGGCTCGACGTCGTTTGTCTATTCTACTAGAACCCCT-CTTTTTTTTATTGGGTTGTAATGT-----A										
spnov_M040906_33	ATTCTTACATCCACCATTTTATATAGGAATGAAGGTGCT-CTTGGCTCGACGTCGTTTGTCTATTCTACTAGAACCCCT-TTTTTTTTTATTGGGTTGTAATGT-----A										

Appendix 5: cpDNA sequence data for Chapter 3

	120	130	140	150	160	170	180	190	200	210	220
Berkheya	AATAGTTCATGATGGAGCTCGAGTAGAAAAGTATTGATTAATTTCTCAGGGGCAACGATCTAGGGTAAATGCCAATCAATAAAATTGGAACAACCTTCGTAAGTATATCTTCC										
Gorteria	AATAGTTCATGATGGAGCTCGAGTAGAAAAGTATTGATTAATTTCTCAGGGGCAACGATCTAGGGTAAATGCCAATCAATAAAATTGGAACAACCTTCGTAAGTATATCTTCC										
Hirpicium	AATAGTTCATGATGGAGCTCGAGTAGAAAAGTATTGATTAATTTCTCAGGGGCAACGATCTAGGGTAAATGCCAATCAATAAAATTGGAACAACCTTCGTAAGTATATCTTCC										
caespitosa_RVC448	AATAGTTCATGATGGAGCTCGAGTAGAAAAGTATTGATTAATTTCTCAGGGGCAACGATCTAGGGTAAATGCCAATCAATAAAATTGGAACAACCTTCGTAAGTATATCTTCC										
caespitosa_RVC307	AATAGTTCATGATGGAGCTCGAGTAGAAAAGTATTGATTAATTTCTCAGGGGCAACGATCTAGGGTAAATGCCAATCAATAAAATTGGAACAACCTTCGTAAGTATATCTTCC										
ciliaris_RM1230	AATAGTTCATGATGGAGCTCGAGTAGAAAAGTATTGATTAATTTCTCAGGGGCAACGATCTAGGGTAAATGCCAATCAATAAAATTGGAACAACCTTCGTAAGTATATCTTCC										
ciliaris_RM1382	AATAGTTCATGATGGAGCTCGAGTAGAAAAGTATTGATTAATTTCTCAGGGGCAACGATCTAGGGTAAATGCCAATCAATAAAATTGGAACAACCTTCGTAAGTATATCTTCC										
heterochaeta_RM1429	AATAGTTCATGATGGAGCTCGAGTAGAAAAGTATTGATTAATTTCTCAGGGGCAACGATCTAGGGTAAATGCCAATCAATAAAATTGGAACAACCTTCGTAAGTATATCTTCC										
heterochaeta_RM1451	AATAGTTCATGATGGAGCTCGAGTAGAAAAGTATTGATTAATTTCTCAGGGGCAACGATCTAGGGTAAATGCCAATCAATAAAATTGGAACAACCTTCGTAAGTATATCTTCC										
jurineifolia_jur_SR682	AATAGTTCATGATGGAGCTCGAGTAGAAAAGTATTGATTAATTTCTCAGGGGCAACGATCTAGGGTAAATGCCAATCAATAAAATTGGAACAACCTTCGTAAGTATATCTTCC										
jurineifoliajur_RM1518	AATAGTTCATGATGGAGCTCGAGTAGAAAAGTATTGATTAATTTCTCAGGGGCAACGATCTAGGGTAAATGCCAATCAATAAAATTGGAACAACCTTCGTAAGTATATCTTCC										
jurineifolia_scab_CAM1604	AATAGTTCATGATGGAGCTCGAGTAGAAAAGTATTGATTAATTTCTCAGGGGCAACGATCTAGGGTAAATGCCAATCAATAAAATTGGAACAACCTTCGTAAGTATATCTTCC										
jurineifolia_scab_CAM2652	AATAGTTCATGATGGAGCTCGAGTAGAAAAGTATTGATTAATTTCTCAGGGGCAACGATCTAGGGTAAATGCCAATCAATAAAATTGGAACAACCTTCGTAAGTATATCTTCC										
krebsiana_arctotoides_RM868	AATAGTTCATGATGGAGCTCGAGTAGAAAAGTATTGATTAATTTCTCAGGGGCAACGATCTAGGGTAAATGCCAATCAATAAAATTGGAACAACCTTCGTAAGTATATCTTCC										
krebsiana_arctotoides_RM876	AATAGTTCATGATGGAGCTCGAGTAGAAAAGTATTGATTAATTTCTCAGGGGCAACGATCTAGGGTAAATGCCAATCAATAAAATTGGAACAACCTTCGTAAGTATATCTTCC										
krebsiana_krebsiana_RM1114	AATAGTTCATGATGGAGCTCGAGTAGAAAAGTATTGATTAATTTCTCAGGGGCAACGATCTAGGGTAAATGCCAATCAATAAAATTGGAACAACCTTCGTAAGTATATCTTCC										
krebsiana_krebsiana_RM1136	AATAGTTCATGATGGAGCTCGAGTAGAAAAGTATTGATTAATTTCTCAGGGGCAACGATCTAGGGTAAATGCCAATCAATAAAATTGGAACAACCTTCGTAAGTATATCTTCC										
krebsiana_serrulata_RM863	AATAGTTCATGATGGAGCTCGAGTAGAAAAGTATTGATTAATTTCTCAGGGGCAACGATCTAGGGTAAATGCCAATCAATAAAATTGGAACAACCTTCGTAAGTATATCTTCC										
krebsiana_serrulata_RM965	AATAGTTCATGATGGAGCTCGAGTAGAAAAGTATTGATTAATTTCTCAGGGGCAACGATCTAGGGTAAATGCCAATCAATAAAATTGGAACAACCTTCGTAAGTATATCTTCC										
leiopoda_M240901	AATAGTTCATGANGGAGCTCGAGTAGAAAAGTATTGATTAATTTCTCAGGGGCAACGATCTAGGGTAAATGCCAATCAATAAAATTGGAACAACCTTCGTAAGTATATCTTCC										
leiopoda_RM1309	AATAGTTCATGATGGAGCTCGAGTAGAAAAGTATTGATTAATTTCTCAGGGGCAACGATCTAGGGTAAATGCCAATCAATAAAATTGGAACAACCTTCGTAAGTATATCTTCC										
lichtenstenii_CAM1916	AATAGTTCATGATGGAGCTCGAGTAGAAAAGTATTGATTAATTTCTCAGGGGCAACGATCTAGGGTAAATGCCAATCAATAAAATTGGAACAACCTTCGTAAGTATATCTTCC										
lichtensteinii_RM1249	AATAGTTCATGATGGAGCTCGAGTAGAAAAGTATTGATTAATTTCTCAGGGGCAACGATCTAGGGTAAATGCCAATCAATAAAATTGGAACAACCTTCGTAAGTATATCTTCC										
linearis_linearis_RM1010	AATAGTTCATGATGGAGCTCGAGTAGAAAAGTATTGATTAATTTCTCAGGGGCAACGATCTAGGGTAAATGCCAATCAATAAAATTGGAACAACCTTCGTAAGTATATCTTCC										
linearis_linearis_SH113	AATAGTTCATGATGGAGCTCGAGTAGAAAAGTATTGATTAATTTCTCAGGGGCAACGATCTAGGGTAAATGCCAATCAATAAAATTGGAACAACCTTCGTAAGTATATCTTCC										
linearis_ovalis_NDsn	AATAGTTCATGAKGGAGCTCGAGTAGAAAAGTATTGATTAATTTCTCAGGGGCAACGATCTAGGGTAAATGCCAATCAATAAAATTGGAACAACCTTCGTAAGTATATCTTCC										
linearis_ovalis_RM854	AATAGTTCATGATGGAGCTCGAGTAGAAAAGTATTGATTAATTTCTCAGGGGCAACGATCTAGGGTAAATGCCAATCAATAAAATTGGAACAACCTTCGTAAGTATATCTTCC										
maritima_RM1038	AATAGTTCATGATGGAGCTCGAGTAGAAAAGTATTGATTAATTTCTCAGGGGCAACGATCTAGGGTAAATGCCAATCAATAAAATTGGAACAACCTTCGTAAGTATATCTTCC										
maritima_M290606_6	AATAGTTCATGATGGAGCTCGAGTAGAAAAGTATTGATTAATTTCTCAGGGGCAACGATCTAGGGTAAATGCCAATCAATAAAATTGGAACAACCTTCGTAAGTATATCTTCC										
othonnites_RM1306	AATAGTTCATGATGGAGCTCGAGTAGAAAAGTATTGATTAATTTCTCAGGGGCAACGATCTAGGGTAAATGCCAATCAATAAAATTGGAACAACCTTCGTAAGTATATCTTCC										
pectinata_M120903	AATAGTTCATGATGGAGCTCGAGTAGAAAAGTATTGATTAATTTCTCAGGGGCAACGATCTAGGGTAAATGCCAATCAATAAAATTGGAACAACCTTCGTAAGTATATCTTCC										
pectinata_RM1044	AATAGTTCATGATGGAGCTCGAGTAGAAAAGTATTGATTAATTTCTCAGGGGCAACGATCTAGGGTAAATGCCAATCAATAAAATTGGAACAACCTTCGTAAGTATATCTTCC										
rigida_M280902	AATAGTTCATGATGGAGCTCGAGTAGAAAAGTATTGATTAATTTCTCAGGGGCAACGATCTAGGGTAAATGCCAATCAATAAAATTGGAACAACCTTCGTAAGTATATCTTCC										
rigida_RM840	??										
rigens_leucolaena_RM773	AATAGTTCATGATGGAGCTCGAGTAGAAAAGTATTGATTAATTTCTCAGGGGCAACGATCTAGGGTAAATGCCAATCAATAAAATTGGAACAACCTTCGTAAGTATATCTTCC										
rigens_leucolaena_RM952_1	AATAGTTCATGATGGAGCTCGAGTAGAAAAGTATTGATTAATTTCTCAGGGGCAACGATCTAGGGTAAATGCCAATCAATAAAATTGGAACAACCTTCGTAAGTATATCTTCC										
rigens_rigens_RM763	AATAGTTCATGATGGAGCTCGAGTAGAAAAGTATTGATTAATTTCTCAGGGGCAACGATCTAGGGTAAATGCCAATCAATAAAATTGGAACAACCTTCGTAAGTATATCTTCC										
rigens_rigens_SR463	AATAGTTCATGATGGAGCTCGAGTAGAAAAGTATTGATTAATTTCTCAGGGGCAACGATCTAGGGTAAATGCCAATCAATAAAATTGGAACAACCTTCGTAAGTATATCTTCC										
rigens_uniflora_JC201205	AATAGTTCATGATGGAGCTCGAGTAGAAAAGTATTGATTAATTTCTCAGGGGCAACGATCTAGGGTAAATGCCAATCAATAAAATTGGAACAACCTTCGTAAGTATATCTTCC										
rigens_uniflora_RM920	AATAGTTCATGATGGAGCTCGAGTAGAAAAGTATTGATTAATTTCTCAGGGGCAACGATCTAGGGTAAATGCCAATCAATAAAATTGGAACAACCTTCGTAAGTATATCTTCC										
schenckii	AATAGTTCATGATGGAGCTCGAGTAGAAAAGTATTGATTAATTTCTCAGGGGCAACGATCTAGGGTAAATGCCAATCAATAAAATTGGAACAACCTTCGTAAGTATATCTTCC										
serrata_M250904_15	AATAGTTCATGATGGAGCTCGAGTAGAAAAGTATTGATTAATTTCTCAGGGGCAACGATCTAGGGTAAATGCCAATCAATAAAATTGGAACAACCTTCGTAAGTATATCTTCC										
serrata_RM898	AATAGTTCATGATGGAGCTCGAGTAGAAAAGTATTGATTAATTTCTCAGGGGCAACGATCTAGGGTAAATGCCAATCAATAAAATTGGAACAACCTTCGTAAGTATATCTTCC										
tenuifolia_CAM1601	AATAGTTCATGATGGAGCTCGAGTAGAAAAGTATTGATTAATTTCTCAGGGGCAACGATCTAGGGTAAATGCCAATCAATAAAATTGGAACAACCTTCGTAAGTATATCTTCC										
tenuifolia_M2730	AATAGTTCATGATGGAGCTCGAGTAGAAAAGTATTGATTAATTTCTCAGGGGCAACGATCTAGGGTAAATGCCAATCAATAAAATTGGAACAACCTTCGTAAGTATATCTTCC										
spnov_M040906_33	AATAGTTCATGATGGAGCTCGAGTAGAAAAGTATTGATTAATTTCTCAGGGGCAACGATCTAGGGTAAATGCCAATCAATAAAATTGGAACAACCTTCGTAAGTATATCTTCC										

Appendix 5: cpDNA sequence data for Chapter 3

	230	240	250	260	270	280	290	300	310	320	330
Berkheya	ATATAGAAATCGAAAGGATCCGATT	CGAGCAAATTTAAACTCAAATAATTTGTTGGAACCGCTAAAAC	TTTTTCGATCCACAGTGTATCGCGTATGAATCAACCGTCCG								
Gorteria	ATATAGAAATCGAAAGGATCCGATT	CGAGCAAATTTCAACTCAAAAAAATTTGTTGGAACCGCGAAAAC	TTTTTCGATCCACAGTGTATCGCGTATGAATCAACCGTCCG								
Hirpicium	ATATAGAAATCGAAAGGATCCGATT	CGAGCAAATTTCAACTCAAAAAAATTTGTTGGAACCGCTAAAAC	TTTTTCGATCCACAGTGTATCGCGTATGAATCAACCGTCCG								
caespitosa_RVC448	ATATAGAAATCGAAAGGATCCGATT	CGAGCAAATTTCAACTCAAAAAAATTTGTTGGAACCGCTAAAAC	TTTTTCGATCCACAGTGTATCGCGTATGAATCAACCGTCCG								
caespitosa_RVC307	ATATAGAAATCGAAAGGATCCGATT	CGAGCAAATTTCAACTCAAAAAAATTTGTTGGAACCGCTAAAAC	TTTTTCGATCCACAGTGTATCGCGTATGAATCAACCGTCCG								
ciliaris_RM1230	ATATAGAAATCGAAAGGATCCGATT	CGAGCAAATTTCAACTCAAAAAAATTTGTTGGAACCGCTAAAAC	TTTTTCGATCCACAGTGTATCGCGTATGAATCAACCGTCCG								
ciliaris_RM1382	ATATAGAAATCGAAAGGATCCGATT	CGAGCAAATTTCAACTCAAAAAAATTTGTTGGAACCGCTAAAAC	TTTTTCGATCCACAGTGTATCGCGTATGAATCAACCGTCCG								
heterochaeta_RM1429	ATATAGAAA-----AGGATCCGATT	CGAGCAAATTTCAACTCAAAAAAATTTGTTGGAACCGCTAAAAC	TTTTTCGATCCACAGTGTATCGCGTATGAATCAACCGTCCG								
heterochaeta_RM1451	ATATAGAAA-----AGGATCCGATT	CGAGCAAATTTCAACTCAAAAAAATTTGTTGGAACCGCTAAAAC	TTTTTCGATCCACAGTGTATCGCGTATGAATCAACCGTCCG								
jurineifolia_jur_SR682	ATATAGAAATCGAAAGGATCCGATT	CGAGCAAATTTCAACTCAAAAAAATTTGTTGGAACCGCTAAAAC	TTTTTCGATCCACAGTGTATCCCCTATGAATTAACCGTCCG								
jurineifoliajur_RM1518	ATATAGAAATCGAAAGGATCCGATT	CGAGCAAATTTCAACTCAAAAAAATTTGTTGGAACCGCTAAAAC	TTTTTCGATCCACAGTGTATCCCCTATGAATTAACCGTCCG								
jurineifolia_scab_CAM1604	ATATAGAAATCGAAAGGATCCGATT	CGAGCAAATTTCAACTCAAAAAAATTTGTTGGAACCGCTAAAAC	TTTTTCGATCCACAGTGTATCCCCTATGAATTAACCGTCCG								
jurineifolia_scab_CAM2652	ATATAGAAATCGAAAGGATCCGATT	CGAGCAAATTTCAACTCAAAAAAATTTGTTGGAACCGCTAAAAC	TTTTTCGATCCACAGTGTATCCCCTATGAATTAACCGTCCG								
krebsiana_arctotoides_RM868	ATATAGAAATCGAAAGGATCCGATT	CGAGCAAATTTCAACTCAAAAAAATTTGTTGGAACCGCTAAAAC	TTTTTCGATCCACAGTGTATCGCGTATGAATCAACCGTCCG								
krebsiana_arctotoides_RM876	ATATAGAAATCGAAAGGATCCGATT	CGAGCAAATTTCAACTCAAAAAAATTTGTTGGAACCGCTAAAAC	TTTTTCGATCCACAGTGTATCGCGTATGAATCAACCGTCCG								
krebsiana_krebsiana_RM1114	ATATAGAAATCGAAAGGATCCGATT	CGAGCAAATTTCAACTCAAAAAAATTTGTTGGAACCGCTAAAAC	TTTTTCGATCCACAGTGTATCGCGTATGAATCAACCGTCCG								
krebsiana_krebsiana_RM1136	ATATAGAAATCGAAAGGATCCGATT	CGAGCAAATTTCAACTCAAAAAAATTTGTTGGAACCGCTAAAAC	TTTTTCGATCCACAGTGTATCGCGTATGAATCAACCGTCCG								
krebsiana_serrulata_RM863	ATATAGAAATCGAAAGGATCCGATT	CGAGCAAATTTCAACTCAAAAAAATTTGTTGGAACCGCTAAAAC	TTTTTCGATCCACAGTGTATCGCGTATGAATCAACCGTCCG								
krebsiana_serrulata_RM965	ATATAGAAATCGAAAGGATCCGATT	CGAGCAAATTTCAACTCAAAAAAATTTGTTGGAACCGCTAAAAC	TTTTTCGATCCACAGTGTATCGCGTATGAATCAACCGTCCG								
leiopoda_M240901	ATATAGAAATCGAAAGGATCCGATT	CGAGCAAATTTCAACTCAAAAAAATTTGTTGGAACCGCTAAAAC	TTTTTCGATCCACAGTGTATCGCGTATGAATCAACCGTCCG								
leiopoda_RM1309	ATATAGAAATCGAAAGGATCCGATT	CGAGCAAATTTCAACTCAAAAAAATTTGTTGGAACCGCTAAAAC	TTTTTCGATCCACAGTGTATCGCGTATGAATCAACCGTCCG								
lichtenstenii_CAM1916	ATATAGAAATCGAAAGGATCCGATT	CGAGCAAATTTCAACTCAAAAAAATTTGTTGGAACCGCTAAAAC	TTTTTCGATCCACAGTGTATCGCGTATGAATCAACCGTCCG								
lichtensteinii_RM1249	ATATAGAAATCGAAAGGATCCGATT	CGAGCAAATTTCAACTCAAAAAAATTTGTTGGAACCGCTAAAAC	TTTTTCGATCCACAGTGTATCGCGTATGAATCAACCGTCCG								
linearis_linearis_RM1010	ATATAGAAATCGAAAGGATCCGATT	CGAGCAAATTTCAACTCAAAAAAATTTGTTGGAACCGCTAAAAC	TTTTTCGATCCACAGTGTATCGCGTATGAATCAACCGTCCG								
linearis_linearis_SH113	ATATAGAAATCGAAAGGATCCGATT	CGAGCAAATTTCAACTCAAAAAAATTTGTTGGAACCGCTAAAAC	TTTTTCGATCCACAGTGTATCGCGTATGAATCAACCGTCCG								
linearis_ovalis_NDsn	ATATAGAAATCGAAAGGATCCGATT	CGAGCAAATTTCAACTCAAAAAAATTTGTTGGAACCGCTAAAAC	TTTTTCGATCCACAGTGTATCGCGTATGAATCAACCGTCCG								
linearis_ovalis_RM854	ATATAGAAATCGAAAGGATCCGATT	CGAGCAAATTTCAACTCAAAAAAATTTGTTGGAACCGCTAAAAC	TTTTTCGATCCACAGTGTATCGCGTATGAATCAACCGTCCG								
maritima_RM1038	ATATAGAAATCGAAAGGATCCGATT	CGAGCAAATTTCAACTCAAAAAAATTTGTTGGAACCGCTAAAAC	TTTTTCGATCCACAGTGTATCGCGTATGAATCAACCGTCCG								
maritima_M290606_6	ATATAGAAATCGAAAGGATCCGATT	CGAGCAAATTTCAACTCAAAAAAATTTGTTGGAACCGCTAAAAC	TTTTTCGATCCACAGTGTATCGCGTATGAATCAACCGTCCG								
othonites_RM1306	ATATAGAAATCGAAAGGATCCGATT	CGAGCAAATTTCAACTCAAAAAAATTTGTTGGAACCGCTAAAAC	TTTTTCGATCCACAGTGTATCGCGTATGAATCAACCGTCCG								
pectinata_M120903	ATATAGAAATCGAAAGGATCCGATT	CGAGCAAATTTCAACTCAAAAAAATTTGTTGGAACCGCTAAAAC	TTTTTCGATCCACAGTGTATCGCGTATGAATCAACCGTCCG								
pectinata_RM1044	ATATAGAAATCGAAAGGATCCGATT	CGAGCAAATTTCAACTCAAAAAAATTTGTTGGAACCGCTAAAAC	TTTTTCGATCCACAGTGTATCGCGTATGAATCAACCGTCCG								
rigida_M280902	ATATAGAAATCGAAAGGATCCGATT	CGAGCAAATTTCAACTCAAAAAAATTTGTTGGAACCGCTAAAAC	TTTTTCGATCCACAGTGTATCGCGTATGAATCAACCGTCCG								
rigida_RM840	??	ACTCAAAAAAATTTGTTGGAACCGCTAAAAC	TTTTTCGATCCACAGTGTATCGCGTATGAATCAACCGTCCG								
rigens_leucolaena_RM773	ATATAGAAATCGAAAGGATCCGATT	CGAGCAAATTTCAACTCAAAAAAATTTGTTGGAACCGCTAAAAC	TTTTTCGATCCACAGTGTATCGCGTATGAATCAACCGTCCG								
rigens_leucolaena_RM952_1	ATATAGAAATCGAAAGGATCCGATT	CGAGCAAATTTCAACTCAAAAAAATTTGTTGGAACCGCTAAAAC	TTTTTCGATCCACAGTGTATCGCGTATGAATCAACCGTCCG								
rigens_rigens_RM763	ATATAGAAATCGAAAGGATCCGATT	CGAGCAAATTTCAACTCAAAAAAATTTGTTGGAACCGCTAAAAC	TTTTTCGATCCACAGTGTATCGCGTATGAATCAACCGTCCG								
rigens_rigens_SR463	AAATAGAAATCGAAAGGATCCGATT	CGAGCAAATTTCAACTCAAAAAAATTTGTTGGAACCGCTAAAAC	TTTTTCGATCCACAGTGTATCGCGTATGAATCAACCGTCCG								
rigens_uniflora_JC201205	ATATAGAAATCGAAAGGATCCGATT	CGAGCAAATTTCAACTCAAAAAAATTTGTTGGAACCGCTAAAAC	TTTTTCGATCCACAGTGTATCGCGTATGAATCAACCGTCCG								
rigens_uniflora_RM920	ATATAGAAATCGAAAGGATCCGATT	CGAGCAAATTTCAACTCAAAAAAATTTGTTGGAACCGCTAAAAC	TTTTTCGATCCACAGTGTATCGCGTATGAATCAACCGTCCG								
schenckii	ATATAGAAATCGAAAGGATCCGATT	CGAGCAAATTTCAACTCAAAAAAATTTGTTGGAACCGCTAAAAC	TTTTTCGATCCACAGTGTATCGCGTATGAATCAACCGTCCG								
serrata_M250904_15	ATATAGAAATCGAAAGGATCCGATT	CGAGCAAATTTCAACTCAAAAAAATTTGTTGGAACCGCTAAAAC	TTTTTCGATCCACAGTGTATCGCGTATGAATCAACCGTCCG								
serrata_RM898	ATATAGAAATCGAAAGGATCCGATT	CGAGCAAATTTCAACTCAAAAAAATTTGTTGGAACCGCTAAAAC	TTTTTCGATCCACAGTGTATCGCGTATGAATCAACCGTCCG								
tenuifolia_CAM1601	ATATAGAAATCGAAAGGATCCGATT	CGAGCAAATTTGCAACTCAAAAAAATTTGTTGGAACCGCTAAAAC	TTTTTCGATCCACAGTGTATCGCGTATGAATCAACCGTCCG								
tenuifolia_M2730	ATATAGAAATCGAAAGGATCCGATT	CGAGCAAATTTGCAACTCAAAAAAATTTGTTGGAACCGCTAAAAC	TTTTTCGATCCACAGTGTATCGCGTATGAATCAACCGTCCG								
spnov_M040906_33	ATATAGAAATCGAAAGGATCCGATT	CGAGCAAATTTCAACTCAAAAAAATTTGTTGGAACCGCTAAAAC	TTTTTCGATCCACAGTGTATCGCGTATGAATCAACCGTCCG								

Appendix 5: cpDNA sequence data for Chapter 3

[340	350	360	370	380	390	400	410	420	430	440]
Berkheya	GTATGATTCTTTGATAGAAAGAAATCACAAAAGGGGTATGTTGCTACCATTTTGAAGGATTAAGAAGCACC										
Gorteria	GTATGATTCTTTGATAGAAAGAAATCACAAAAGGGGTATGTTGCTACCATTTTGAAGGATTAAGAAGCACC										
Hirpicium	GTATGATTCTTTGATAGAAAGAAATCACAAAAGGGGTATGTTGCTACCATTTTGAAGGATTAAGAAGCACC										
caespitosa_RVC448	GTATGATTCTTTGATAGAAAGAAATCACAAAAGGGGTATGTTGCTACCATTTTGAAGGATTAAGAAGCACC										
caespitosa_RVC307	GTATGATTCTTTGATAGAAAGAAATCACAAAAGGGGTATGTTGCTACCATTTTGAAGGATTAAGAAGCACC										
ciliaris_RM1230	GTATGATTCTTTGATAGAAAGAAATCACAAAAGGGGTATGTTGCTACCATTTTGAAGGATTAAGAAGCACC										
ciliaris_RM1382	GTATGATTCTTTGATAGAAAGAAATCACAAAAGGGGTATGTTGCTACCATTTTGAAGGATTAAGAAGCACC										
heterochaeta_RM1429	GTATGATTCTTTGATAGAAAGAAATCACAAAAGGGGTATGTTGCTACCATTTTGAAGGATTAAGAAGCACC										
heterochaeta_RM1451	GTATGATTCTTTGATAGAAAGAAATCACAAAAGGGGTATGTTGCTACCATTTTGAAGGATTAAGAAGCACC										
jurineifolia_jur_SR682	GTATGATTCTTTGATAGAAAGAAATCACAAAAGGGGTATGTTGCTACCATTTTGAAGGATTAAGAAGCACC										
jurineifoliajur_RM1518	GTATGATTCTTTGATAGAAAGAAATCACAAAAGGGGTATGTTGCTACCATTTTGAAGGATTAAGAAGCACC										
jurineifolia_scab_CAM1604	GTATGATTCTTTGATAGAAAGAAATCACAAAAGGGGTATGTTGCTACCATTTTGAAGGATTAAGAAGCACC										
jurineifolia_scab_CAM2652	GTATGATTCTTTGATAGAAAGAAATCACAAAAGGGGTATGTTGCTACCATTTTGAAGGATTAAGAAGCACC										
krebsiana_arctotoides_RM868	GTATGATTCTTTGATAGAAAGAAATCACAAAAGGGGTATGTTGCTACCATTTTGAAGGATTAAGAAGCACC										
krebsiana_arctotoides_RM876	GTATGATTCTTTGATAGAAAGAAATCACAAAAGGGGTATGTTGCTACCATTTTGAAGGATTAAGAAGCACC										
krebsiana_krebsiana_RM1114	GTATGATTCTTTGATAGAAAGAAATCACAAAAGGGGTATGTTGCTACCATTTTGAAGGATTAAGAAGCACC										
krebsiana_krebsiana_RM1136	GTATGATTCTTTGATAGAAAGAAATCACAAAAGGGGTATGTTGCTACCATTTTGAAGGATTAAGAAGCACC										
krebsiana_serrulata_RM863	GTATGATTCTTTGATAGAAAGAAATCACAAAAGGGGTATGTTGCTACCATTTTGAAGGATTAAGAAGCACC										
krebsiana_serrulata_RM965	GTATGATTCTTTGATAGAAAGAAATCACAAAAGGGGTATGTTGCTACCATTTTGAAGGATTAAGAAGCACC										
leiopoda_M240901	GTATGATTCTTTGATAGAAAGAAATCACAAAAGGGGTATGTTGCTACCATTTTGAAGGATTAAGAAGCACC										
leiopoda_RM1309	GTATGATTCTTTGATAGAAAGAAATCACAAAAGGGGTATGTTGCTACCATTTTGAAGGATTAAGAAGCACC										
lichtenstenii_CAM1916	GTATGATTCTTTGATAGAAAGAAATCACAAAAGGGGTATGTTGCTACCATTTTGAAGGATTAAGAAGCACC										
lichtensteinii_RM1249	GTATGATTCTTTGATAGAAAGAAATCACAAAAGGGGTATGTTGCTACCATTTTGAAGGATTAAGAAGCACC										
linearis_linearis_RM1010	GTATGATTCTTTGATAGAAAGAAATCACAAAAGGGGTATGTTGCTACCATTTTGAAGGATTAAGAAGCACC										
linearis_linearis_SH113	GTATGATTCTTTGATAGAAAGAAATCACAAAAGGGGTATGTTGCTACCATTTTGAAGGATTAAGAAGCACC										
linearis_ovalis_NDsn	GTATGATTCTTTGATAGAAAGAAATCACAAAAGGGGTATGTTGCTACCATTTTGAAGGATTAAGAAGCACC										
linearis_ovalis_RM854	GTATGATTCTTTGATAGAAAGAAATCACAAAAGGGGTATGTTGCTACCATTTTGAAGGATTAAGAAGCACC										
maritima_RM1038	GTATGATTCTTTGATAGAAAGAAATCACAAAAGGGGTATGTTGCTACCATTTTGAAGGATTAAGAAGCACC										
maritima_M290606_6	GTATGATTCTTTGATAGAAAGAAATCACAAAAGGGGTATGTTGCTACCATTTTGAAGGATTAAGAAGCACC										
othonnites_RM1306	GTATGATTCTTTGATAGAAAGAAATCACAAAAGGGGTATGTTGCTACCATTTTGAAGGATTAAGAAGCACC										
pectinata_M120903	GTATGATTCTTTGATAGAAAGAAATCACAAAAGGGGTATGTTGCTACCATTTTGAAGGATTAAGAAGCACC										
pectinata_RM1044	GTATGATTCTTTGATAGAAAGAAATCACAAAAGGGGTATGTTGCTACCATTTTGAAGGATTAAGAAGCACC										
rigida_M280902	GTATGATTCTTTGATAGAAAGAAATCACAAAAGGGGTATGTTGCTACCATTTTGAAGGATTAAGAAGCACC										
rigida_RM840	GTATGATTCTTTGATAGAAAGAAATCACAAAAGGGGTATGTTGCTACCATTTTGAAGGATTAAGAAGCACC										
rigens_leucolaena_RM773	GTATGATTCTTTGATAGAAAGAAATCACAAAAGGGGTATGTTGCTACCATTTTGAAGGATTAAGAAGCACC										
rigens_leucolaena_RM952_1	GTATGATTCTTTGATAGAAAGAAATCACAAAAGGGGTATGTTGCTACCATTTTGAAGGATTAAGAAGCACC										
rigens_rigens_RM763	GTATGATTCTTTGATAGAAAGAAATCACAAAAGGGGTATGTTGCTACCATTTTGAAGGATTAAGAAGCACC										
rigens_rigens_SR463	GTATGATTCTTTGATAGAAAGAAATCACAAAAGGGGTATGTTGCTACCATTTTGAAGGATTAAGAAGCACC										
rigens_uniflora_JC201205	GTATGATTCTTTGATAGAAAGAAATCACAAAAGGGGTATGTTGCTACCATTTTGAAGGATTAAGAAGCACC										
rigens_uniflora_RM920	GTATGATTCTTTGATAGAAAGAAATCACAAAAGGGGTATGTTGCTACCATTTTGAAGGATTAAGAAGCACC										
schenckii	GTATGATTCTTTGATAGAAAGAAATCACAAAAGGGGTATGTTGCTACCATTTTGAAGGATTAAGAAGCACC										
serrata_M250904_15	GTATGATTCTTTGATAGAAAGAAATCACAAAAGGGGTATGTTGCTACCATTTTGAAGGATTAAGAAGCACC										
serrata_RM898	GTATGATTCTTTGATAGAAAGAAATCACAAAAGGGGTATGTTGCTACCATTTTGAAGGATTAAGAAGCACC										
tenuifolia_CAM1601	GTATGATTCTTTGATAGAAAGAAATCACAAAAGGGGTATGTTGCTACCATTTTGAAGGATTAAGAAGCACC										
tenuifolia_M2730	GTATGATTCTTTGATAGAAAGAAATCACAAAAGGGGTATGTTGCTACCATTTTGAAGGATTAAGAAGCACC										
spnov_M040906_33	GTATGATTCTTTGATAGAAAGAAATCACAAAAGGGGTATGTTGCTACCATTTTGAAGGATTAAGAAGCACC										

Appendix 5: cpDNA sequence data for Chapter 3

[450	460	470	480	490	500	510	520	530	540	550]
Berkheya	AAGGATCCCAGAACCAAGGAAACACCCTTCAATTGTCTCACGGATCTGAATAAAGAATCCAAATAGATTTTAAACGAGACAAAAGGGGGGGTTAAAGACCCTCAAT										
Gorteria	AAGGATCCCAGAACCAAGGAAACACCCTTCAATTGTCTCACAGATCTGAATAAAGAATCCAAATAGATTTTAAACGAGACAAAAGGGGGGG---TTAAAGACCCTCAAT										
Hirpicium	AAGGATCCCAGAACCAAGGAAACACCCTTCAATTGTCTCACGGATCTGAATAAAGAATCCAAATAGATTTTAAACGAGACAAAAGGGGGGG---TTAAAGACCCTCAAT										
caespitosa_RVC448	AAGGATCCCAGAACCAAGGAAACACCCTTCAATTGTCTCACGGATCTGAATAAAGAATCCAAATAGATTTTAAACGAGACAAAAGGGGGGG---TTAAAGACCCTCAAA										
caespitosa_RVC307	AAGGATCCCAGAACCAAGGAAACACCCTTCAATTGTCTCACGGATCTGAATAAAGAATCCAAATAGATTTTAAACGAGACAAAAGGGGGGG---TTAAAGACCCTCAAA										
ciliaris_RM1230	AAGGATCCCAGAACCAAGGAAACACCCTTCAATTGTCTCACGGATCTGAATAAAGAATCCAAATAGATTTTAAACGAGACAAAAGGGGGGG---TTAAAGACCCTCAAA										
ciliaris_RM1382	AAGGATCCCAGAACCAAGGAAACACCCTTCAATTGTCTCACGGATCTGAATAAAGAATCCAAATAGATTTTAAACGAGACAAAAGGGGGGG---TTAAAGACCCTCAAA										
heterochaeta_RM1429	AAGGATCCCAGAACCAAGGAAACACCCTTCAATTGTCTCACGGATCTGAATAAAGAATCCAAATAGATTTTAAACGAGACAAAAGGGGGGG---TTAAAGACCCTCAAA										
heterochaeta_RM1451	AAGGATCCCAGAACCAAGGAAACACCCTTCAATTGTCTCACGGATCTGAATAAAGAATCCAAATAGATTTTAAACGAGACAAAAGGGGGGGGG---TTAAAGACCCTCAAA										
jurineifolia_jur_SR682	AAGGATCCCAGAACCAAGGAAACACCCTTCAATTGTCTCACGGATCTGAATAAAGAATCCAAATAGATTTTAAACGAGACAAAAGGGGGGG---TTAAAGACCCTCAAA										
jurineifoliajur_RM1518	AAGGATCCCAGAACCAAGGAAACACCCTTCAATTGTCTCACAGATCTGAATAAAGAATCCAAATAGATTTTAAACGAGACAAAAGGGGGGG---TTAAAGACCCTCAAA										
jurineifolia_scab_CAM1604	AAGGATCCCAGAACCAAGGAAACACCCTTCAATTGTCTCACGGATCTGAATAAAGAATCCAAATAGATTTTAAACGAGACAAAAGGGGGGG---TTAAAGACCCTCAAA										
jurineifolia_scab_CAM2652	AAGGATCCCAGAACCAAGGAAACACCCTTCAATTGTCTCACGGATCTGAATAAAGAATCCAAATAGATTTTAAACGAGACAAAAGGGGGGG---TTAAAGACCCTCAAA										
krebsiana_arctotoides_RM868	AAGGATCCCAGAACCAAGGAAACACCCTTCAATTGTCTCACGGATCTGAATAAAGAATCCAAATAGATTTTAAACGAGACAAAAGGGGGGG---TTAAAGACCCTCAAA										
krebsiana_arctotoides_RM876	AAGGATCCCAGAACCAAGGAAACACCCTTCAATTGTCTCACGGATCTGAATAAAGAATCCAAATAGATTTTAAACGAGACAAAAGGGGGGGGG---TTAAAGACCCTCAAA										
krebsiana_krebsiana_RM1114	AAGGATCCCAGAACCAAGGAAACACCCTTCAATTGTCTCACGGATCTGAATAAAGAATCCAAATAGATTTTAAACGAGACAAAAGGGGGGGGG---TTAAAGACCCTCAAA										
krebsiana_krebsiana_RM1136	AAGGATCCCAGAACCAAGGAAACACCCTTCAATTGTCTCACGGATCTGAATAAAGAATCCAAATAGATTTTAAACGAGACAAAAGGGGGGGGG---TTAAAGACCCTCAAA										
krebsiana_serrulata_RM863	AAGGATCCCAGAACCAAGGAAACACCCTTCAATTGTCTCACGGATCTGAATAAAGAATCCAAATAGATTTTAAACGAGACAAAAGGGGGGGGG---TTAAAGACCCTCAAA										
krebsiana_serrulata_RM965	AAGGATCCCAGAACCAAGGAAACACCCTTCAATTGTCTCACGGATCTGAATAAAGAATCCAAATAGATTTTAAACGAGACAAAAGGGGGGGGG---TTAAAGACCCTCAAA										
leiopoda_M240901	AAGGATCCCAGAACCAAGGAAACACCCTTCAATTGTCTCACGGATCTGAATAAAGAATCCAAATAGATTTTAAACGAGACAAAAGGGGGGGGG---TTAAAGACCCTCAAA										
leiopoda_RM1309	AAGGATCCCAGAACCAAGGAAACACCCTTCAATTGTCTCACGGATCTGAATAAAGAATCCAAATAGATTTTAAACGAGACAAAAGGGGGGGGG---TTAAAGACCCTCAAA										
lichtenstenii_CAM1916	AAGGATCCCAGAACCAAGGAAACACCCTTCAATTGTCTCACGGATCTGAATAAAGAATCCAAATAGATTTTAAACGAGACAAAAGGGGGGGGG---TTAAAGACCCTCAAA										
lichtensteinii_RM1249	AAGGATCCCAGAACCAAGGAAACACCCTTCAATTGTCTCACGGATCTGAATAAAGAATCCAAATAGATTTTAAACGAGACAAAAGGGGGGGGG---TTAAAGACCCTCAAA										
linearis_linearis_RM1010	AAGGATCCCAGAACCAAGGAAACACCCTTCAATTGTCTCACGGATCTGAATAAAGAATCCAAATAGATTTTAAACGAGACAAAAGGGGGGGGG---TTAAAGACCCTCAAA										
linearis_linearis_SH113	AAGGATCCCAGAACCAAGGAAACACCCTTCAATTGTCTCACGGATCTGAATAAAGAATCCAAATAGATTTTAAACGAGACAAAAGGGGGGGGG---TTAAAGACCCTCAAA										
linearis_ovalis_NDsn	AAGGATCCCAGAACCAAGGAAACACCCTTCAATTGTCTCACGGATCTGAATAAAGAATCCAAATAGATTTTAAACGAGACAAAAGGGGGGGGG---TTAAAGACCCTCAAA										
linearis_ovalis_RM854	AAGGATCCCAGAACCAAGGAAACACCCTTCAATTGTCTCACGGATCTGAATAAAGAATCCAAATAGATTTTAAACGAGACAAAAGGGGGGGGG---TTAAAGACCCTCAAA										
maritima_RM1038	AAGGATCCCAGAACCAAGGAAACACCCTTCAATTGTCTCACGGATCTGAATAAAGAATCCAAATAGATTTTAAACGAGACAAAAGGGGGGGGG---TTAAAGACCCTCAAA										
maritima_M290606_6	AAGGATCCCAGAACCAAGGAAACACCCTTCAATTGTCTCACGGATCTGAATAAAGAATCCAAATAGATTTTAAACGAGACAAAAGGGGGGGGG---TTAAAGACCCTCAAA										
othonnites_RM1306	AAGGATCCCAGAACCAAGGAAACACCCTTCAATTGTCTCACGGATCTGAATAAAGAATCCAAATAGATTTTAAACGAGACAAAAGGGGGGGGG---TTAAAGACCCTCAAA										
pectinata_M120903	AAGGATCCCAGAACCAAGGAAACACCCTTCAATTGTCTCACGGATCTGAATAAAGAATCCAAATAGATTTTAAACGAGACAAAAGGGGGGGGG---TTAAAGACCCTCAAA										
pectinata_RM1044	AAGGATCCCAGAACCAAGGAAACACCCTTCAATTGTCTCACGGATCTGAATAAAGAATCCAAATAGATTTTAAACGAGACAAAAGGGGGGGGG---TTAAAGACCCTCAAA										
rigida_M280902	AAGGATCCCAGAACCAAGGAAACACCCTTCAATTGTCTCACGGATCTGAATAAAGAATCCAAATAGATTTTAAACGAGACAAAAGGGGGGGGG---TTAAAGACCCTCAAA										
rigida_RM840	AAGGATCCCAGAACCAAGGAAACACCCTTCAATTGTCTCACGGATCTGAATAAAGAATCCAAATAGATTTTAAACGAGACAAAAGGGGGGGGG---TTAAAGACCCTCAAA										
rigens_leucolaena_RM773	AAGGATCCCAGAACCAAGGAAACACCCTTCAATTGTCTCACGGATCTGAATAAAGAATCCAAATAGATTTTAAACGAGACAAAAGGGGGGGGG---TTAAAGACCCTCAAA										
rigens_leucolaena_RM952_1	AAGGATCCCAGAACCAAGGAAACACCCTTCAATTGTCTCACGGATCTGAATAAAGAATCCAAATAGATTTTAAACGAGACAAAAGGGGGGGGGTTAAAGACCCTCAAA										
rigens_rigens_RM763	AAGGATCCCAGAACCAAGGAAACACCCTTCAATTGTCTCACGGATCTGAATAAAGAATCCAAATAGATTTTAAACGAGACAAAAGGGGGGGGG---TTAAAGACCCTCAAA										
rigens_rigens_SR463	AAGGATCCCAGAACCAAGGAAACACCCTTCAATTGTCTCACGGATCTGAATAAAGAATCCAAATAGATTTTAAACGAGACAAAAGGGGGGGGG---TTAAAGACCCTCAAA										
rigens_uniflora_JC201205	AAGGATCCCAGAACCAAGGAAACACCCTTCAATTGTCTCACGGATCTGAATAAAGAATCCAAATAGATTTTAAACGAGACAAAAGGGGGGGGG---TTAAAGACCCTCAAA										
rigens_uniflora_RM920	AAGGATCCCAGAACCAAGGAAACACCCTTCAATTGTCTCACGGATCTGAATAAAGAATCCAAATAGATTTTAAACGAGACAAAAGGGGGGGGG---TTAAAGACCCTCAAA										
schenckii	AAGGATCCCAGAACCAAGGAAACACCCTTCAATTGTCTCACGGATCTGAATAAAGAATCCAAATAGATTTTAAACGAGACAAAAGGGGGGGGG---TTAAAGACCCTCAAA										
serrata_M250904_15	AAGGATCCCAGAACCAAGGAAACACCCTTCAATTGTCTCACGGATCTGAATAAAGAATCCAAATAGATTTTAAACGAGACAAAAGGGGGGGGG---TTAAAGACCCTCAAA										
serrata_RM898	AAGGATCCCAGAACCAAGGAAACACCCTTCAATTGTCTCACGGATCTGAATAAAGAATCCAAATAGATTTTAAACGAGACAAAAGGGGGGGGG---TTAAAGACCCTCAAA										
tenuifolia_CAM1601	AAGGATCCCAGAACCAAGGAAACACCCTTCAATTGTCTCACGGATCTGAATAAAGAATCCAAATAGATTTTAAACGAGACAAAAGGGGGGGGG---TTAAAGACCCTCAAA										
tenuifolia_M2730	AAGGATCCCAGAACCAAGGAAACACCCTTCAATTGTCTCACGGATCTGAATAAAGAATCCAAATAGATTTTAAACGAGACAAAAGGGGGGGGG---TTAAAGACCCTCAAA										
spnov_M040906_33	AAGGATCCCAGAACCAAGGAAACACCCTTCAATTGTCTCACGGATCTGAATAAAGAATCCAAATAGATTTTAAACGAGACAAAAGGGGGGGGG---TTAAAGACCCTCAAA										

Appendix 5: cpDNA sequence data for Chapter 3

[560	570	580	590	600	610	620	630	640	650	660]
Berkheya	AAAAAAA-----GATTTTCTTTAATATTATTTAAGAATTATTGAACCTTGAGTTATGAGTACAAATGATTTTTCTTTTCAGGAAGGAAGCTAAA										
Gorteria	AAAAAAA-----TATCTTAAAGATTT--CTTTAATAT--AATTGAGAATTATTGAACATGAGTTATGAGTACAAATGATTTTTCTTTTCAGGAAGGAAGCTAAA										
Hirpicium	AAAAAAA-----TCTTAAAGGTTTTCTTTAATAT--AATTGAGAATTATTGAACCTTGAGTTATGAGTACAAATGATTTTTCTTTTCAGGAAGGAAGCTAAA										
caespitosa_RVC448	AAAAAAA---TAAAAATATCTTAAAGATTTTTGTTTAATAT--AATTGAGAATTATTGAACCTTGAGTTATGAGTACAAATGATTTTTCTTTTCAGGAAGGAAGCTAAA										
caespitosa_RVC307	AAAAAAA---TAAAAATATCTTAAAGATTTTTGTTTAATAT--AATTGAGAATTATTGAACCTTGAGTTATGAGTACAAATGATTTTTCTTTTCAGGAAGGAAGCTAAA										
ciliaris_RM1230	AAAAAAA---TAAAAATATCTTAAAGATTTTTCTTTAATAT--AATTGAGAATTATTGAACCTTGAGTTATGAGTACAAATGATTTTTCTTTTCAGGAAGGAAGCTAAA										
ciliaris_RM1382	AAAAAAA---TAAAAATATCTTAAAGATTTTTCTTTAATAT--AATTGAGAATTATTGAACCTTGAGTTATGAGTACAAATGATTTTTCTTTTCAGGAAGGAAGCTAAA										
heterochaeta_RM1429	AAAAAAA---TAAAAATATCTTAAAGATTTTTCTTTAATAT--AATTGAGAATTATTGAACCTTGAGTTATGAGTACAAATGATTTTTCTTTTCAGGAAGGAAGCTAAA										
heterochaeta_RM1451	AAAAAAA---TAAAAATATCTTAAAGATTTTTCTTTAATAT--AATTGAGAATTATTGAACCTTGAGTTATGAGTACAAATGATTTTTCTTTTCAGGAAGGAAGCTAAA										
jurineifolia_jur_SR682	AAAAAAA---TAAAAATATCTTAAAGATTTTTCTTTAATAT--AATTGAGAATTCTTGAACCTTGAGTTATGAGTACAAATGATTTTTCTTTTCAGGAAGGAAGCTAAA										
jurineifoliajur_RM1518	AAAAAAA---TAAAAATATCTTAAAGATTTTTCTTTAATAT--AATTGAGAATTCTTGAACCTTGAGTTATGAGTACAAATGATTTTTCTTTTCAGGAAGGAAGCTAAA										
jurineifolia_scab_CAM1604	AAAAAAA---TAAAAATATCTTAAAGATTTTTCTTTAATAT--AATTGAGAATTCTTGAACCTTGAGTTATGAGTACAAATGATTTTTCTTTTCAGGAAGGAAGCTAAA										
jurineifolia_scab_CAM2652	AAAAAAA---TAAAAATATCTTAAAGATTTTTCTTTAATAT--AATTGAGAATTCTTGAACCTTGAGTTATGAGTACAAATGATTTTTCTTTTCAGGAAGGAAGCTAAA										
krebsiana_arctotoides_RM868	AAAAAAA---TAAAAATATCTTAAAGATTTTTCTTTAATAT--AATTGAGAATTCTTGAACCTTGAGTTATGAGTACAAATGATTTTTCTTTTCAGGAAGGAAGCTAAA										
krebsiana_arctotoides_RM876	AAAAAAA---TAAAAATATCTTAAAGATTTTTCTTTAATAT--AATTGAGAATTCTTGAACCTTGAGTTATGAGTACAAATGATTTTTCTTTTCAGGAAGGAAGCTAAA										
krebsiana_krebsiana_RM1114	AAAAAAA---TAAAAATATCTTAAAGATTTTTCTTTAATAT--AATTGAGAATTATTGAACCTTGAGTTATGAGTACAAATGATTTTTCTTTTCAGGAAGGAAGCTAAA										
krebsiana_krebsiana_RM1136	AAAAAAA---TAAAAATATCTTAAAGATTTTTCTTTAATAT--AATTGAGAATTATTGAACCTTGAGTTATGAGTACAAATGATTTTTCTTTTCAGGAAGGAAGCTAAA										
krebsiana_serrulata_RM863	AAAAAAA---TAAAAATATCTTAAAGATTTTTCTTTAATAT--AATTGAGAATTATTGAACCTTGAGTTATGAGTACAAATGATTTTTCTTTTCAGGAAGGAAGCTAAA										
krebsiana_serrulata_RM965	AAAAAAA---TAAAAATATCTTAAAGATTTTTCTTTAATAT--AATTGAGAATTATTGAACCTTGAGTTATGAGTACAAATGATTTTTCTTTTCAGGAAGGAAGCTAAA										
leiopoda_M240901	AAAAAAA---TAAAAATATCTTAAAGATTTTTCTTTAATAT--AATTGAGAATTATTGAACCTTGAGTTATGAGTACAAATGATTTTTCTTTTCAGGAAGGAAGCTAAA										
leiopoda_RM1309	AAAAAAA---TAAAAATATCTTAAAGATTTTTCTTTAATAT--AATTGAGAATTATTGAACCTTGAGTTATGAGTACAAATGATTTTTCTTTTCAGGAAGGAAGCTAAA										
lichtenstenii_CAM1916	AAAAAAA---TAAAAATATCTTAAAGATTTTTCTTTAATAT--AATTGAGAATTATTGAACCTTGAGTTATGAGTACAAATGATTTTTCTTTTCAGGAAGGAAGCTAAA										
lichtensteinii_RM1249	AAAAAAA---TAAAAATATCTTAAAGATTTTTCTTTAATAT--AATTGAGAATTATTGAACCTTGAGTTATGAGTACAAATGATTTTTCTTTTCAGGAAGGAAGCTAAA										
linearis_linearis_RM1010	AAAAAAA---TAAAAATATCTTAAAGATTTTTCTTTAATAT--AATTGAGAATTATTGAACCTTGAGTTATGAGTACAAATGATTTTTCTTTTCAGGAAGGAAGCTAAA										
linearis_linearis_SH113	AAAAAAA---TAAAAATATCTTAAAGATTTTTCTTTAATAT--AATTGAGAATTATTGAACCTTGAGTTATGAGTACAAATGATTTTTCTTTTCAGGAAGGAAGCTAAA										
linearis_ovalis_NDsn	AAAAAAA---TAAAAATATCTTAAAGATTTTTCTTTAATAT--AATTGAGAATTATTGAACCTTGAGTTATGAGTACAAATGATTTTTCTTTTCAGGAAGGAAGCTAAA										
linearis_ovalis_RM854	AAAAAAA---TAAAAATATCTTAAAGATTTTTCTTTAATAT--AATTGAGAATTATTGAACCTTGAGTTATGAGTACAAATGATTTTTCTTTTCAGGAAGGAAGCTAAA										
maritima_RM1038	AAAAAAA---TAAAAATATCTTAAAGATTTTTCTTTAATAT--AATTGAGAATTATTGAACCTTGAGTTATGAGTACAAATGATTTTTCTTTTCAGGAAGGAAGCTAAA										
maritima_M290606_6	AAAAAAA---TAAAAATATCTTAAAGATTTTTCTTTAATAT--AATTGAGAATTATTGAACCTTGAGTTATGAGTACAAATGATTTTTCTTTTCAGGAAGGAAGCTAAA										
othonnites_RM1306	AAAAAAA---TAAAAATATCTTAAAGATTTTTCTTTAATAT--AATTGAGAATTATTGAACCTTGAGTTATGAGTACAAATGATTTTTCTTTTCAGGAAGGAAGCTAAA										
pectinata_M120903	AAAAAAA---TAAAAATATCTTAAAGATTTTTCTTTAATAT--AATTGAGAATTATTGAACCTTGAGTTATGAGTACAAATGATTTTTCTTTTCAGGAAGGAAGCTAAA										
pectinata_RM1044	AAAAAAA---TAAAAATATCTTAAAGATTTTTCTTTAATAT--AATTGAGAATTATTGAACCTTGAGTTATGAGTACAAATGATTTTTCTTTTCAGGAAGGAAGCTAAA										
rigida_M280902	AAAAAAA---TAAAAATATCTTAAAGATTTTTCTTTAATAT--AATTGAGAATTATTGAACCTTGAGTTATGAGTACAAATGATTTTTCTTTTCAGGAAGGAAGCTAAA										
rigida_RM840	AAAAAAA---TAAAAATATCTTAAAGATTTTTCTTTAATAT--AATTGAGAATTATTGAACCTTGAGTTATGAGTACAAATGATTTTTCTTTTCAGGAAGGAAGCTAAA										
rigens_leucolaena_RM773	AAAAAAA---TAAAAATATCTTAAAGATTTTTCTTTAATAT--AATTGAGAATTATTGAACCTTGAGTTATGAGTACAAATGATTTTTCTTTTCAGGAAGGAAGCTAAA										
rigens_leucolaena_RM952_1	AAAAAAA---TAAAAATATCTTAAAGATTTTTCTTTAATAT--AATTGAGAATTATTGAACCTTGAGTTATGAGTACAAATGATTTTTCTTTTCAGGAAGGAAGCTAAA										
rigens_rigens_RM763	AAAAAAA---TAAAAATATCTTAAAGATTTTTCTTTAATAT--AATTGAGAATTATTGAACCTTGAGTTATGAGTACAAATGATTTTTCTTTTCAGGAAGGAAGCTAAA										
rigens_rigens_SR463	AAAAAAA---TAAAAATATCTTAAAGATTTTTCTTTAATAT--AATTGAGAATTATTGAACCTTGAGTTATGAGTACAAATGATTTTTCTTTTCAGGAAGGAAGCTAAA										
rigens_uniflora_JC201205	AAAAAAA---TAAAAATATCTTAAAGATTTTTCTTTAATAT--AATTGAGAATTATTGAACCTTGAGTTATGAGTACAAATGATTTTTCTTTTCAGGAAGGAAGCTAAA										
rigens_uniflora_RM920	AAAAAAA---TAAAAATATCTTAAAGATTTTTCTTTAATAT--AATTGAGAATTATTGAACCTTGAGTTATGAGTACAAATGATTTTTCTTTTCAGGAAGGAAGCTAAA										
schenckii	AAAAAAA---TAAAAATATCTTAAAGATTTTTCTTTAATAT--AATTGAGAATTATTGAACCTTGAGTTATGAGTACAAATGATTTTTCTTTTCAGGAAGGAAGCTAAA										
serrata_M250904_15	AAAAAAA---TAAAAATATCTTAAAGATTTTTCTTTAATAT--AATTGAGAATTATTGAACCTTGAGTTATGAGTACAAATGATTTTTCTTTTCAGGAAGGAAGCTAAA										
serrata_RM898	AAAAAAA---TAAAAATATCTTAAAGATTTTTCTTTAATAT--AATTGAGAATTATTGAACCTTGAGTTATGAGTACAAATGATTTTTCTTTTCAGGAAGGAAGCTAAA										
tenuifolia_CAM1601	AAAAAAA---TAAAAATATCTTAAAGATTTTTCTTTAATAT--AATTGAGAATTATTGAACCTTGAGTTATGAGTACAAATGATTTTTCTTTTCAGGAAGGAAGCTAAA										
tenuifolia_M2730	AAAAAAA---TAAAAATATCTTAAAGATTTTTCTTTAATAT--AATTGAGAATTATTGAACCTTGAGTTATGAGTACAAATGATTTTTCTTTTCAGGAAGGAAGCTAAA										
spnov_M040906_33	AAAAAAA---TAAAAATATCTTAAAGATTTTTCTTTAATAT--AATTGAGAATTATTGAACCTTGAGTTATGAGTACAAATGATTTTTCTTTTCAGGAAGGAAGCTAAA										

Appendix 5: cpDNA sequence data for Chapter 3

	670	680	690	700	710	720	730	740	750	760	770]
Berkheya	TAAAAATGACTATGAGTAAAT	-----	ATAGGCTAATTCCTTTT	-----	ACGGATTCCTTTACTATTTATTAGAA	-----	TTTTATCCATATTATTAGAATTTTA				
Gorteria	TAAAAATGATTATGAGTAAAT	-----	ATAGGCTAATTCCTTTT	-----	ACGGATTCCTTTACTATTTAATTTATTATAA	-----	TTTTATCCATA				
Hirpicium	TAAAAA-----	GTTAAAT	-----	ATAGGCTAATTCCTTTT	-----	ACGGATTCCTTTACTATTTATTAGAA	-----	TTTTACTCCATA			
caespitosa_RVC448	AAAAAATGACTATGAGTAAAT	-----	ATAGGCTAATTCCTTTT	-----	ATTTACGGATTCCTTTACTATTTATTAGAA	-----	TTTTATCCATA				
caespitosa_RVC307	AAAAAATGACTATGAGTAAAT	-----	ATAGGCTAATTCCTTTT	-----	ATTTACGGATTCCTTTACTATTTATTAGAA	-----	TTTTATCCATA				
ciliaris_RM1230	AAAAAATGACTATGAGTAAAT	-----	ATAGGCTAATTCCTTTT	-----	ATTTACGGATTCCTTTACTATTTATTAGAA	-----	TTTTATCCATA				
ciliaris_RM1382	AAAAAATGACTATGAGTAAAT	-----	ATAGGCTAATTCCTTTT	-----	ATTTACGGATTCCTTTACTATTTATTAGAA	-----	TTTTATCCATA				
heterochaeta_RM1429	TAAAAATGACTATGAGTAAAT	-----	ATAGGCTAATTCCTTTT	-----	ATTTACGGATTCCTTTACTATTTATTAGAA	-----	TTTTATCCATA				
heterochaeta_RM1451	TAAAAATGACTATGAGTAAAT	-----	ATAGGCTAATTCCTTTT	-----	ATTTACGGATTCCTTTACTATTTATTAGAA	-----	TTTTATCCATA				
jurineifolia_jur_SR682	TAAAAATGACTATGAGTAAAT	-----	ATAGGCTAATTCCTTTT	-----	ATTTACGGATTCCTTTACTATTTATTAGAA	-----	TTTTATCCATA				
jurineifoliajur_RM1518	TAAAAATGACTATGAGTAAAT	-----	ATAGGCTAATTCCTTTT	-----	ATTTACGGATTCCTTTACTATTTATTAGAA	-----	TTTTATCCATA				
jurineifolia_scab_CAM1604	TAAAAATGACTATGAGTAAAT	-----	ATAGGCTAATTCCTTTT	-----	ATTTACGGATTCCTTTACTATTTATTAGAA	-----	TTTTATCCATA				
jurineifolia_scab_CAM2652	TAAAAATGACTATGAGTAAAT	-----	ATAGGCTAATTCCTTTT	-----	ATTTACGGATTCCTTTACTATTTATTAGAA	-----	TTTTATCCATA				
krebsiana_arctotoides_RM868	TAAAAATGACTATGAGTAAAT	-----	ATAGGCTAATTCCTTTT	-----	ATTTACGGATTCCTTTACTATTTATTAGAA	-----	TTTTATCCATA				
krebsiana_arctotoides_RM876	TAAAAATGACTATGAGTAAAT	-----	ATAGGCTAATTCCTTTT	-----	ATTTACGGATTCCTTTACTATTTATTAGAA	-----	TTTTATCCATA				
krebsiana_krebsiana_RM1114	TAAAAATGACTATGAGTAAAT	-----	ATAGGCTAATTCCTTTT	-----	ATTTACGGATTCCTTTACTATTTATTAGAA	-----	TTTTATCCATA				
krebsiana_krebsiana_RM1136	TAAAAATGACTATGAGTAAAT	-----	ATAGGCTAATTCCTTTT	-----	ATTTACGGATTCCTTTACTATTTATTAGAA	-----	TTTTATCCATA				
krebsiana_serrulata_RM863	TAAAAATGACTATGAGTAAAT	-----	ATAGGCTAATTCCTTTT	-----	ATTTACGGATTCCTTTACTATTTATTAGAA	-----	TTTTATCCATA				
krebsiana_serrulata_RM965	TAAAAATGACTATGAGTAAAT	-----	ATAGGCTAATTCCTTTT	-----	ATTTACGGATTCCTTTACTATTTATTAGAA	-----	TTTTATCCATA				
leiopoda_M240901	TAAAAATGACTATGAGTAAAT	-----	ATAGGCTAATTCCTTTT	-----	ATTTACGGATTCCTTTACTATTTATTAGAA	-----	TTTTATCCATA				
leiopoda_RM1309	TAAAAATGACTATGAGTAAAT	-----	ATAGGCTAATTCCTTTT	-----	ATTTACGGATTCCTTTACTATTTATTAGAA	-----	TTTTATCCATA				
lichtenstenii_CAM1916	TAAAAA-----	GTTAAAT	-----	ATAGGCTAATTCCTTTT	-----	ATTTACGGATTCCTTTACTATTTATTAGAA	-----	TTTTATCCATA			
lichtenstenii_RM1249	TAAAAA-----	GTTAAAT	-----	ATAGGCTAATTCCTTTT	-----	ATTTACGGATTCCTTTACTATTTATTAGAA	-----	TTTTATCCATA			
linearis_linearis_RM1010	TAAAAATGACTATGAGTAAAT	-----	ATAGGCTAATTCCTTTT	-----	ATTTACGGATTCCTTTACTATTTATTAGAA	-----	TTTTATCCATA				
linearis_linearis_SH113	TAAAAATGACTATGAGTAAAT	-----	ATAGGCTAATTCCTTTT	-----	ATTTACGGATTCCTTTACTATTTATTAGAA	-----	TTTTATCCATA				
linearis_ovalis_NDsn	TAAAAATGACTATGAGTAAAT	-----	ATAGGCTAATTCCTTTT	-----	ATTTACGGATTCCTTTACTATTTATTAGAA	-----	TTTTATCCATA				
linearis_ovalis_RM854	TAAAAATGACTATGAGTAAAT	-----	ATAGGCTAATTCCTTTT	-----	ATTTACGGATTCCTTTACTATTTATTAGAA	-----	TTTTATCCATA				
maritima_RM1038	TAAAAATGACTATGAGTAAAT	-----	ATAGGCTAATTCCTTTT	-----	ATTTACGGATTCCTTTACTATTTATTAGAA	-----	TTTTATCCATA				
maritima_M290606_6	TAAAAATGACTATGAGTAAAT	-----	ATAGGCTAATTCCTTTT	-----	ATTTACGGATTCCTTTACTATTTATTAGAA	-----	TTTTATCCATA				
othonnites_RM1306	TAAAAATGACTATGAGTAAAT	-----	ATAGGCTAATTCCTTTT	-----	ATTTACGGATTCCTTTACTATTTATTAGAA	-----	TTTTATCCATA				
pectinata_M120903	TAAAAATGACTATGAGTAAAT	-----	ATAGGCTAATTCCTTTT	-----	ATTTACGGATTCCTTTACTATTTATTAGAA	-----	TTTTATCCATA				
pectinata_RM1044	TAAAAATGACTATGAGTAAAT	-----	ATAGGCTAATTCCTTTT	-----	ATTTACGGATTCCTTTACTATTTATTAGAA	-----	TTTTATCCATA				
rigida_M280902	????????????????????										
rigida_RM840	TAAAAATGACTATGAGTAAAT	-----	ATAGGCTAATTCCTTTT	-----	ATTTACGGATTCCTTTACTATTTATTAGAA	-----	TTTTATCCATA				
rigens_leucolaena_RM773	TAAAAATGACTATGAGTAAAT	-----	ATAGGCTAATTCCTTTT	-----	ATTTACGGATTCCTTTACTATTTATTAGAA	-----	TTTTATCCATA				
rigens_leucolaena_RM952_1	TAAAAATGACTATGAGTAAAT	-----	ATAGGCTAATTCCTTTT	-----	ATTTACGGATTCCTTTACTATTTATTAGAA	-----	TTTTATCCATA				
rigens_rigens_RM763	TAAAAATGACTATGAGTAAAT	-----	ATAGGCTAATTCCTTTT	-----	ATTTACGGATTCCTTTACTATTTATTAGAA	-----	TTTTATCCATA				
rigens_rigens_SR463	TAAAAATGACTATGAGTAAAT	-----	ATAGGCTAATTCCTTTT	-----	ATTTACGGATTCCTTTACTATTTATTAGAA	-----	TTTTATCCATA				
rigens_uniflora_JC201205	TAAAAATGACTATGAGTAAAT	-----	ATAGGCTAATTCCTTTT	-----	ATTTACGGATTCCTTTACTATTTATTAGAA	-----	TTTTATCCATA				
rigens_uniflora_RM920	TAAAAATGACTATGAGTAAAT	-----	ATAGGCTAATTCCTTTT	-----	ATTTACGGATTCCTTTACTATTTATTAGAA	-----	TTTTATCCATA				
schenckii	TAAAAA-----	GTTAAAT	-----	ATAGGCTAATTCCTTTT	-----	ATTTACGGATTCCTTTACTATTTATTAGAA	-----	TTTTATCCATA			
serrata_M250904_15	TAAAAATGACTATGAGTAAAT	-----	ATAGGCTAATTCCTTTT	-----	ATTTACGGATTCCTTTACTATTTATTAGAA	-----	TTTTATCCATA				
serrata_RM898	TAAAAATGACTATGAGTAAAT	-----	ATAGGCTAATTCCTTTT	-----	ATTTACGGATTCCTTTACTATTTATTAGAA	-----	TTTTATCCATA				
tenuifolia_CAM1601	TAAAAATGACTATGAGTAAAT	-----	ATAGGCTAATTCCTTTT	-----	ATTTACGGATTCCTTTACTATTTATTAGAA	-----	TTTTATCCATA				
tenuifolia_M2730	TAAAAATGACTATGAGTAAAT	-----	ATAGGCTAATTCCTTTT	-----	ATTTACGGATTCCTTTACTATTTATTAGAA	-----	TTTTATCCATA				
spnov_M040906_33	TAAAAATGACTATGAGTAAAT	-----	ATAGGCTAATTCCTTTT	-----	ATTTACGGATTCCTTTACTATTTATTAGAA	-----	TTTTATCCATA				

Appendix 5: cpDNA sequence data for Chapter 3

	780	790	800	810	820	830	840	850	rpS16 860	< > 	psbA-trnH 870	880]	
Berkheya	TCCATAGACAAA	ACTTCAAATC	ATTTTTCT	TCGAGCCGT	ACGAGGAGAAA	ACTTCC	TATACGGTT	CTAGGGGGGG	-TTCTTTTT	CATCTAC	ATCTACA	AATCCACTG	CC
Gorteria	-----GACAAA	ACTTCAAATC	ATTTTTCT	TCGAGCCGT	ACGAGGAGAAA	ACTTCC	TATACGGTT	CTAGGGGGGG	--TTCTTTTT	CATCTAC	ATCT???	????????	???
Hirpicium	-----GACAAA	ACTTCAAATC	ATTTTTCT	TCGAGCCGT	ACGAGGAGAAA	ACTTCC	TATACGGTT	CTAGGGGGGG	--TTCTTTTT	CATCTAC	ATCT???	????????	???
caespitosa_RVC448	-----GACAAA	ACTTCAAATC	ATTTTTCT	TCGAGCCGT	ACGAGGAGAAA	ACTTCC	TATACGGTT	CTAGGGGGGG	--TTCTTTTT	CATCTAC	ATCTACA	AATCCACTG	CC
caespitosa_RVC307	-----GACAAA	ACTTCAAATC	ATTTTTCT	TCGAGCCGT	ACGAGGAGAAA	ACTTCC	TATACGGTT	CTAGGGGGGG	--TTCTTTTT	CATCTAC	ATCTACA	AATCCACTG	CC
ciliaris_RM1230	-----GACAAA	ACTTCAAATC	ATTTTTCT	TCGAGCCGT	ACGAGGAGAAA	ACTTCC	TATACGGTT	CTAGGGGGGG	--TTCTTTTT	CATCTAC	ATCTACA	AATCCACTG	CC
ciliaris_RM1382	-----GACAAA	ACTTCAAATC	ATTTTTCT	TCGAGCCGT	ACGAGGAGAAA	ACTTCC	TATACGGTT	CTAGGGGGGG	--TTC????	????????	????????	????	???
heterochaeta_RM1429	-----GACAAA	ACTTCAAATC	ATTTTTCT	TCGAGCCGT	ACGAGGAGAAA	ACTTCC	TATACGGTT	CTAGGGGGGG	--TTCTTTTT	CATCTAC	ATCTACA	AATCCACTG	CC
heterochaeta_RM1451	-----GACAAA	ACTTCAAATC	ATTTTTCT	TCGAGCCGT	ACGAGGAGAAA	ACTTCC	TATACGGTT	CTAGGGGGGG	--TTCTTTTT	CATCTAC	ATCT???	????????	???
jurineifolia_jur_SR682	-----GACAAA	ACTTCAAATC	ATTTTTCT	TCGAGCCGT	ACGAGGAGAAA	ACTTCC	TATACGGTT	CTAGGGGGGG	--TTCTTTTT	CATCTAC	ATCTACA	AATCCACTG	CC
jurineifolia_jur_RM1518	-----GACAAA	ACTTCAAATC	ATTTTTCT	TCGAGCCGT	ACGAGGAGAAA	ACTTCC	TATACGGTT	CTAGGGGGGG	--TTCTTTTT	CATCTAC	ATCTACA	AATCCACTG	CC
jurineifolia_scab_CAM1604	-----GACAAA	ACTTCAAATC	ATTTTTCT	TCGAGCCGT	ACGAGGAGAAA	ACTTCC	TATACGGTT	CTAGGGGGGG	--TTCTTTTT	CATCTAC	ATCTACA	AATCCACTG	CC
jurineifolia_scab_CAM2652	-----GACAAA	ACTTCAAATC	ATTTTTCT	TCGAGCCGT	ACGAGGAGAAA	ACTTCC	TATACGGTT	CTAGGGGGGG	--TTCTTTTT	CATCTAC	ATCTACA	AATCCACTG	CC
krebsiana_arctotoides_RM868	-----GACAAA	ACTTCAAATC	ATTTTTCT	TCGAGCCGT	ACGAGGAGAAA	ACTTCC	TATACGGTT	CTAGGGGGGG	????????	????????	????????	????	???
krebsiana_arctotoides_RM876	-----GACAAA	ACTTCAAATC	ATTTTTCT	TCGAGCCGT	ACGAGGAGAAA	ACTTCC	TATACGGTT	CTA????	????????	????????	????????	????	???
krebsiana_krebsiana_RM1114	-----GACAAA	ACTTCAAATC	ATTTTTCT	TCGAGCCGT	ACGAGGAGAAA	ACTTCC	TATACGGTT	CTAGGGGGGG	--TTCTTTTT	CATCTAC	ATCTACA	AATCCACTG	CC
krebsiana_krebsiana_RM1136	-----GACAAA	ACTTCAAATC	ATTTTTCT	TCGAGCCGT	ACGAGGAGAAA	ACTTCC	TATACGGTT	CTAGGGGGGG	????????	????????	????????	????	???
krebsiana_serrulata_RM863	-----GACAAA	ACTTCAAATC	ATTTTTCT	TCGAGCCGT	ACGAGGAGAAA	ACTTCC	TATACGGTT	CTAGGGGGGG	--TTCTTTTT	CATCTAC	ATCTACA	AATCCACTG	CC
krebsiana_serrulata_RM965	-----GACAAA	ACTTCAAATC	ATTTTTCT	TCGAGCCGT	ACGAGGAGAAA	ACTTCC	TATACGGTT	CTAGGGGGGG	--TTCTTTTT	CATCTAC	ATCT?	CAAATCC	ACTGCC
leiopoda_M240901	-----GACAAA	ACTTCAAATC	ATTTTTCT	TCGAGCCGT	ACGAGGAGAAA	ACTTCC	TATACGGTT	CTAGGGGGGG	--TTCTTTTT	CATCTAC	ATCTACA	AATCCACTG	CC
leiopoda_RM1309	-----GACAAA	ACTTCAAATC	ATTTTTCT	TCGAGCCGT	ACGAGGAGAAA	ACTTCC	TATACGGTT	CTAGGGGGGG	--TTCTTTTT	CATCTAC	ATCTACA	AATCCACTG	CC
lichtenstenii_CAM1916	-----GACAAA	ACTTCAAATC	ATTTTTCT	TCGAGCCGT	ACGAGGAGAAA	ACTTCC	TATACGGTT	CTAGGGGGGG	--TTCTTTTT	CATCTAC	ATCT???	????????	???
lichtensteini_RM1249	-----GACAAA	ACTTCAAATC	ATTTTTCT	TCGAGCCGT	ACGAGGAGAAA	ACTTCC	????	????	????	????	????	????	???
linearis_linearis_RM1010	-----GACAAA	ACTTCAAATC	ATTTTTCT	TCGAGCCGT	ACGAGGAGAAA	ACTTCC	TATACGGTT	CTAGGGGGGG	--TTCTTTTT	CATCTAC	ATCTACA	AATCCACTG	CC
linearis_linearis_SH113	-----GACAAA	ACTTCAAATC	ATTTTTCT	TCGAGCCGT	ACGAGGAGAAA	ACTTCC	TATACGGTT	CTAGGGGGGG	--TTCTTTTT	CATCTAC	ATCTACA	AATCCACTG	CC
linearis_ovalis_NDsn	-----GACAAA	ACTTCAAATC	ATTTTTCT	TCGAGCCGT	ACGAGGAGAAA	ACTTCC	TATACGGTT	CTAGGGGGGG	--TTCTTTTT	CATCTAC	ATCTACA	AATCCACTG	CC
linearis_ovalis_RM854	-----GACAAA	ACTTCAAATC	ATTTTTCT	TCGAGCCGT	ACGAGGAGAAA	ACTTCC	TATACGGTT	CTAGGGGGGG	--TTCTTTTT	CATCTAC	ATCTACA	AATCCACTG	CC
maritima_RM1038	-----GACAAA	ACTTCAAATC	ATTTTTCT	TCGAGCCGT	ACGAGGAGAAA	ACTTCC	TATACGGTT	CTAGGGGGGG	--TTCTTTTT	CATCTAC	???	CAAATCC	ACTGCC
maritima_M290606_6	-----GACAAA	ACTTCAAATC	ATTTTTCT	TCGAGCCGT	ACGAGGAGAAA	ACTTCC	TATACGGTT	CTAGGGGGGG	--TTCTTTTT	CATCTAC	ATCTACA	AATCCACTG	CC
othonnites_RM1306	-----GACAAA	ACTTCAAATC	ATTTTTCT	TCGAGCCGT	ACGAGGAGAAA	ACTTCC	????	????	????	????	????	????	???
pectinata_M120903	-----GACAAA	ACTTCAAATC	ATTTTTCT	TCGAGCCGT	ACGAGGAGAAA	ACTTCC	TATACGGTT	CTAGGGGGGG	--TTCTTTTT	CATCTAC	ATCTACA	AATCCACTG	CC
pectinata_RM1044	-----GACAAA	ACTTCAAATC	ATTTTTCT	TCGAGCCGT	ACGAGGAGAAA	ACTTCC	TATACGGTT	CTA????	????	????	????	????	???
rigida_M280902	??????	??????	??????	??????	??????	??????	??????	??????	??????	??????	??????	????	???
rigida_RM840	-----GACAAA	ACTTCAAATC	ATTTTTCT	TCGAGCCGT	ACGAGGAGAAA	ACTTCC	TATACGGTT	CTAGGGGGGG	--TTCTTTTT	CATCTAC	ATCTACA	AATCCACTG	CC
rigens_leucolaena_RM773	-----GACAAA	ACTTCAAATC	ATTTTTCT	TCGAGCCGT	ACGAGGAGAAA	ACTTCC	TATACGGTT	CTAGGGGGGG	--TTCTTTTT	CATCTAC	ATCTACA	AATCCACTG	CC
rigens_leucolaena_RM952_1	-----GACAAA	ACTTCAAATC	ATTTTTCT	TCGAGCCGT	ACGAGGAGAAA	ACTTCC	TATACGGTT	CTAGGGGGGG	--TTCTTTTT	CATCTAC	ATCTACA	AATCCACTG	CC
rigens_rigens_RM763	-----GACAAA	ACTTCAAATC	ATTTTTCT	TCGAGCCGT	ACGAGGAGAAA	ACTTCC	TATACGGTT	CTAGGGGGGG	--TTCTTTTT	CATCTAC	ATCTACA	AATCCACTG	CC
rigens_rigens_SR463	-----GACAAA	ACTTCAAATC	ATTTTTCT	TCGAGCCGT	ACGAGGAGAAA	ACTTCC	TATACGGTT	CTAGGGGGGG	--TTCTTTTT	CATCTAC	ATCTACA	AATCCACTG	CC
rigens_uniflora_JC201205	-----GACAAA	ACTTCAAATC	ATTTTTCT	TCGAGCCGT	ACGAGGAGAAA	ACTTCC	TATACGGTT	CTAGGGGGGG	--TTCTTTTT	CATCTA	????	CAAATCC	ACTGCC
rigens_uniflora_RM920	-----GACAAA	ACTTCAAATC	ATTTTTCT	TCGAGCCGT	ACGAGGAGAAA	ACTTCC	TATACGGTT	CTAGGGGGGG	--TTCTTTTT	CATCTAC	ATCTACA	AATCCACTG	CC
schenckii	-----GACAAA	ACTTCAAATC	ATTTTTCT	TCGAGCCGT	ACGAGGAGAAA	ACTTCC	TATACGGTT	CTAGGGGGGG	--TTCTTTTT	CATCTAC	ATCTACA	AATCCACTG	CC
serrata_M250904_15	-----GACAAA	ACTTCAAATC	ATTTTTCT	TCGAGCCGT	ACGAGGAGAAA	ACTTCC	TATACGGTT	CTAGGGGGGG	--TTCTTTTT	CATCTAC	ATCTACA	AATCCACTG	CC
serrata_RM898	-----GACAAA	ACTTCAAATC	ATTTTTCT	TCGAGCCGT	ACGAGGAGAAA	ACTTCC	TATACGGTT	CTAGGGGGGG	--TTCTTTTT	CATCTAC	ATCT?	CAAATCC	ACTGCC
tenuifolia_CAM1601	-----GACAAA	ACTTCAAATC	ATTTTTCT	TCGAGCCGT	ACGAGGAGAAA	ACTTCC	TATACGGTT	CTAGGGGGGG	--TTCTTTTT	CATCTAC	ATCT???	AATCC	ACTGCC
tenuifolia_M2730	-----GACAAA	ACTTCAAATC	ATTTTTCT	TCGAGCCGT	ACGAGGAGAAA	ACTTCC	TATACGGTT	CTAGGGGGGG	--TTCTTTTT	CATCTAC	ATCT???	????	???
spnov_M040906_33	-----GACAAA	ACTTCAAATC	ATTTTTCT	TCGAGCCGT	ACGAGGAGAAA	ACTTCC	TATACGGTT	CTAGGGGGGG	--TTCTTTT	-CATCTAC	ATCTACA	AATCCACTG	CC

Appendix 5: cpDNA sequence data for Chapter 3

[890	900	910	920	930	940	950	960	970	980	990]
Berkheya	TTGATCCACTGGGCTACATCCGCCCTCTACTATTAT	-----	CTAGTATTAGCTAGTATTACTATATTTT	-----	TTCCATTAACATGAAA						
Gorteria	?TGATCCACTTGGCTACATCCGCCCTTTACTATTAT	-----	CTAGTATTATCTAGTATTACTATATTTT	-----	GTAATACTATATTTTTCCATTAACAGAAA						
Hirpicium	TTGATCCACTTGGCTACATCCGCCCTCTACTATTAT	-----	CTAGTATTATCTAGTATTACTATATTTT	-----	TTCCATTAACATGAAA						
caespitosa_RVC448	TTGATCCACTTGGCTACATCCGCCCTCTACTATTAT	-----	-----	-----	-----						
caespitosa_RVC307	TTGATCCACTTGGCTACATCCGCCCTCTACTATTAT	-----	-----	-----	-----						
ciliaris_RM1230	TTGATCCACTTGGCTACATCCGCCCTCTACTATTAT	-----	-----	-----	-----						
ciliaris_RM1382	TTGATCCACTTGGCTACATCCGCCCTCTACTATTAT	-----	-----	-----	-----						
heterochaeta_RM1429	TTGATCCACTTGGCTACATCCGCCCTCTACTATTAT	-----	CTAGTATTAA	-----	TAGTATTACTATATTTTTTACA	-----					
heterochaeta_RM1451	????????TTGGCTACATCCGCCCTCTACTATTAT	-----	CTAGTATTAA	-----	TAGTATTACTATATTTTTTACA	-----					
jurineifolia_jur_SR682	TTGATCCACTTGGCTACATCCGCCCTCTACTATTAT	-----	CTAGTATTAA	-----	TAGTATTACTATATTTTTTACA	-----					
jurineifoliajur_RM1518	TTGATCCACTTGGCTACATCCGCCCTCTACTATTAT	-----	CTAGTATTAA	-----	TAGTATTACTATATTTTTTACA	-----					
jurineifolia_scab_CAM1604	TTGATCCACTTGGCTACATCCGCCCTCTACTATTAT	-----	CTAGTATTAA	-----	TAGTATTACTATATTTTTTACA	-----					
jurineifolia_scab_CAM2652	TTGATCCACTTGGCTACATCCGCCCTCTACTATTAT	-----	CTAGTATTAA	-----	TAGTATTACTATATTTTTTACA	-----					
krebsiana_arctotoides_RM868	TTGATCCACTTGGCTACATCCGCCCTCTACTATTAT	-----	CTAGTATTAA	-----	TAGTATTACTATATTTTTTACA	-----					
krebsiana_arctotoides_RM876	TTGATCCACTTGGCTACATCCGCCCTCTACTATTAT	-----	CTAGTATTAA	-----	TAGTATTACTATATTTTTTACA	-----					
krebsiana_krebsiana_RM1114	TTGATCCACTTGGCTACATCCGCCCTCTACTATTAT	-----	CTAGTATTAA	-----	TAGTATTACTATATTTTTTACA	-----					
krebsiana_krebsiana_RM1136	TTGATCCACTTGGCTACATCCGCCCTCTACTATTAT	-----	CTAGTATTAA	-----	TAGTATTACTATATTTTTTACA	-----					
krebsiana_serrulata_RM863	TTGATCCACTTGGCTACATCCGCCCTCTACTATTAT	-----	CTAGTATTAA	-----	TAGTATTACTATATTTTTTACA	-----					
krebsiana_serrulata_RM965	TTGATCCACTTGGCTACATCCGCCCTCTACTATTAT	-----	CTAGTATTAA	-----	TAGTATTACTATATTTTTTACA	-----					
leiopoda_M240901	TTGATCCACTTGGCTACATCCGCCCTCTACTATTAT	-----	CTAGTATTAA	-----	TAGTATTACTATATTTTTTACA	-----					
leiopoda_RM1309	TTGATCCACTTGGCTACATCCGCCCTCTACTATTAT	-----	CTAGTATTAA	-----	TAGTATTACTATATTTTTTACA	-----					
lichtenstenii_CAM1916	????????????????????CTATTAT	-----	CTAGTATTAA	-----	TAGTATTACTATATTTTTTACA	-----					
lichtensteini_RM1249	TTGATCCACTTGGCTACATCCGCCCTCTACTATTAT	-----	CTAGTATTAA	-----	TAGTATTACTATATTTTTTACA	-----					
linearis_linearis_RM1010	TTGATCCACTTGGCTACATCCGCCCTCTACTATTAT	-----	CTAGTATTAA	-----	TAGTATTACTATATTTTTTACA	-----					
linearis_linearis_SH113	TTGATCCACTTGGCTACATCCGCCCTCTACTATTAT	-----	CTAGTATTAA	-----	TAGTATTACTATATTTTTTACA	-----					
linearis_ovalis_NDsn	TTGATCCACTTGGCTACATCCGCCCTCTACTATTAT	-----	CTAGTATTAA	-----	TAGTATTACTATATTTTTTACA	-----					
linearis_ovalis_RM854	TTGATCCACTTGGCTACATCCGCCCTCTACTATTAT	-----	CTAGTATTAA	-----	TAGTATTACTATATTTTTTACA	-----					
maritima_RM1038	TTGATCCACTTGGCTACATCCGCCCTCTACTATTAT	-----	CTAGTATTAA	-----	TAGTATTACTATATTTTTTACA	-----					
maritima_M290606_6	TTGATCCACTTGGCTACATCCGCCCTCTACTATTAT	-----	CTAGTATTAA	-----	TAGTATTACTATATTTTTTACA	-----					
othonnites_RM1306	TTGATCCACTTGGCTACATCCGCCCTCTACTATTAT	-----	CTAGTATTGA	-----	TAGTATTACTATATTTTTTACA	-----					
pectinata_M120903	TTGATCCACTTGGCTACATCCGCCCTCTACTATTAT	-----	CTAGTATTAA	-----	TAGTATTACTATATTTTTTACA	-----					
pectinata_RM1044	TTGATCCACTTGGCTACATCCGCCCTCTACTATTAT	-----	CTAGTATTAA	-----	TAGTATTACTATATTTTTTACA	-----					
rigida_M280902	TTGATCCACTTGGCTACATCCGCCCTCTACTATTAT	-----	CTAGTATTAA	-----	TAGTATTACTATATTTTTTACA	-----					
rigida_RM840	TTGATCCACTTGGCTACATCCGCCCTCTACTATTAT	-----	CTAGTATTAA	-----	TAGTATTACTATATTTTTTACA	-----					
rigens_leucolaena_RM773	TTGATCCACTTGGCTACATCCGCCCTCTACTATTAT	-----	CTAGTATTAA	-----	TAGTATTACTATATTTTTTACA	-----					
rigens_leucolaena_RM952_1	TTGATCCACTTGGCTACATCCGCCCTCTACTATTAT	-----	CTAGTATTAA	-----	TAGTATTACTATATTTTTTACA	-----					
rigens_rigens_RM763	TTGATCCACTTGGCTACATCCGCCCTCTACTATTAT	-----	CTAGTATTAA	-----	TAGTATTACTATATTTTTTACA	-----					
rigens_rigens_SR463	TTGATCCACTTGGCTACATCCGCCCTCTACTATTAT	-----	CTAGTATTAA	-----	TAGTATTACTATATTTTTTACA	-----					
rigens_uniflora_JC201205	TTGATCCACTTGGCTACATCCGCCCTCTACTATTAT	-----	CTAGTATTAA	-----	TAGTATTACTATATTTTTTACA	-----					
rigens_uniflora_RM920	TTGATCCACTTGGCTACATCCGCCCTCTACTATTAT	-----	CTAGTATTAA	-----	TAGTATTACTATATTTTTTACA	-----					
schenckii	TTGATCCACTTGGCTACATCCGCCCTCTACTATTAT	-----	CTAGTATTAA	-----	TAGTATTACTATATTTTTTACA	-----					
serrata_M250904_15	TTGATCCACTTGGCTACATCCGCCCTCTACTATTAT	-----	CTAG	-----	TAA	-----	TAGTATTACTATATTTTTTACA	-----			
serrata_RM898	TTGATCCACTTGGCTACATCCGCCCTCTACTATTAT	-----	CTAGTATTAA	-----	TAGTATTACTATATTTTTTACA	-----					
tenuifolia_CAM1601	TTGATCCACTTGGCTACATCCGCCCTCTACTATTAT	-----	ATAGTATTAA	-----	TAGTATTACTATATTTTTTACA	-----					
tenuifolia_M2730	TTGATCCACTTGGCTACATCCGCCCTCTACTATTAT	-----	ATAGTATTAA	-----	TAGTATTACTATATTTTTTACA	-----					
spnov_M040906_33	TTGATCCACTTGGCTACATCCGCCCTCTACTATTAT	-----	CTAGTATTAA	-----	TAGTATTACTATATTTTTTACA	-----					

Appendix 5: cpDNA sequence data for Chapter 3

	1000	1010	1020	1030	1040	1050	1060	1070	1080	1090	1100]
Berkheya	AAAAA----	GATTCTATTTTCTTTCTTTTCTGAAATTAAGTAATAA-----	ATAAGCAAAATTATCATTTC	CAATCTAAAATAGATTGAAATTGAATTGTAATAA							
Gorteria	AAAAAAAAAGATCATATTTTCTTTCTTATTTCTGAAATAAAAGTAATAA-----	ATAAGCAAAATTATCATTTTTATCTATTTTAGATTGAAATTGAATTGGAATAA									
Hirpicium	AAA-----	TATTCTATTTTCTTTCTTATTTCTGAAATTAAGTAATAATAAAATAAGCAAAATTATCATTTC	CAATCTAAAATAGATTGAAATTGAATTATAATAA								
caespitosa_RVC448	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
caespitosa_RVC307	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
ciliaris_RM1230	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
ciliaris_RM1382	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
heterochaeta_RM1429	-----	-----	TTAAAAAGTAATAA-----	ATAAGCAAAATTATCATTTTTATCTATCTTAGATTGAAATTGAATTGGAATAA							
heterochaeta_RM1451	-----	-----	TTAAAAAGTAATAA-----	ATAAGCAAAATTATCATTTTTATCTATCTTAGATTGAAATTGAATTGGAATAA							
jurineifolia_jur_SR682	-----	-----	TTAAATTAATAATTAATAATTAATAA-----	ATAAGCAAAATTCTCATTTTTATCCATTTTAGATTGAAATTGAATTGGAATAA							
jurineifoliajur_RM1518	-----	-----	TTAAATTAATAATTAATAATTAATAA-----	ATAAGCAAAATTCTCATTTTTATCCATTTTAGATTGAAATTGAATTGGAATAA							
jurineifolia_scab_CAM1604	-----	-----	TTAAATTAATAATTAATAATTAATAA-----	ATAAGCAAAATTCTCATTTTTATCCATTTTAGATTGAAATTGAATTGGAATAA							
jurineifolia_scab_CAM2652	-----	-----	TTAAATTAATAATTAATAATTAATAA-----	ATAAGCAAAATTCTCATTTTTATCCATTTTAGATTGAAATTGAATTGGAATAA							
krebsiana_arctotoides_RM868	-----	-----	TTAAAAAGTAATAA-----	ATAAGCAAAATTATCATTTTTATCTATTTTAGATTGAAATTGAATTGGAATAA							
krebsiana_arctotoides_RM876	-----	-----	TTAAAAAGTAATAA-----	ATAAGCAAAATTCTAATTTTATCTATTTTAGATTGAAATTGAATTGGAATAA							
krebsiana_krebsiana_RM1114	-----	-----	TTAAAAAGTAATAA-----	ATAAGCAAAATTATCATTTTTATCTATTTTAGATTGAAATTGAATTGGAATAA							
krebsiana_krebsiana_RM1136	-----	-----	TTAAAAAGTAATAA-----	ATAAGCAAAATTATAATTTTATCTATTTTAGATTGAAATTGAATTGGAATAA							
krebsiana_serrulata_RM863	-----	-----	TTAAAAAGTAATAA-----	ATAAGCAAAATTATCATTTTTATCTATTTTAGATTGAAATTGAATTGGAATAA							
krebsiana_serrulata_RM965	-----	-----	TTAAAAAGTAATAA-----	ATAAGCAAAATTATAATTTTATCTATTTTAGATTGAAATTGAATTGGAATAA							
leiopoda_M240901	-----	TAGTATTACTATATTTTTATTAATAAGTAATAA-----	ATAAGCAAAATTATCATTTTTATCTATTTTAGATTGAAATTGAATTGGAATAA								
leiopoda_RM1309	-----	-----	TTAAAAAGTAATAA-----	ATAAGCAAAATTATCATTTTTATCTATTTTAGATTGAAATTGAATTGGAATAA							
lichtenstenii_CAM1916	-----	-----	TTAAAAAGTAATAA-----	ATAAGCAAAATTATCATTTTTATCTATTTTAGATTGAAATTGAATTGGAATAA							
lichtensteini_RM1249	-----	-----	TTAAAAAGTAATAA-----	ATAAGCAAAATTATCATTTTTATCTATTTTAGATTGAAATTGAATTGGAATAA							
linearis_linearis_RM1010	-----	-----	TTAAAAAGTAATAA-----	ATAAGCAAAATTATCATTTTTATCTATTTTAGATTGAAATTGAATTGGAATAA							
linearis_linearis_SH113	-----	-----	TTTTAATTAATAAGTAATAA-----	ATAAGCAAAATTATAATTTTATCTATTTTAGATTGAAATTGAATTGGAATAA							
linearis_ovalis_NDsn	-----	-----	TTAAAAAGTAATAA-----	ATAAGCAAAATTATCATTTTTATCTATTTTAGATTGACATTGAATTGGAATAA							
linearis_ovalis_RM854	-----	-----	TTAAAAAGTAATAA-----	ATAAGCAAAATTATCATTTTTATCTATTTTAGATTGAAATTGAATTGGAATAA							
maritima_RM1038	-----	-----	TTAAAAAGTAATAA-----	ATAAGCAAAATTATCATTTTTATCTATTTTAGATTGAAATTGAATTGGAATAA							
maritima_M290606_6	-----	-----	TTAAAAAGTAATAA-----	ATAAGCAAAATTATCATTTTTATCTATTTTAGATTGAAATTGAATTGGAATAA							
othonnites_RM1306	-----	-----	TTAAAAAGTAATAA-----	ATAAGCAAAATTATCATTTTTATCTATTTTAGATTGAAATTGAATTGGAATAA							
pectinata_M120903	-----	-----	TTAAAAAGTAATAA-----	ATAAGCAAAATTATCATTTTTATCTATTTTAGATTGAAATTGAATTGGAATAA							
pectinata_RM1044	-----	-----	TTAAAAAGTAATAA-----	ATAAGCAAAATTATCATTTTTATCTATTTTAGATTGAAATTGAATTGGAATAA							
rigida_M280902	-----	-----	TTAAAAAGTAATAA-----	ATAAGCAAAATTATAATTTTATCTATTTTAGATTGAAATTGAATTGGAATAA							
rigida_RM840	-----	-----	TTAAAAAGTAATAA-----	ATAAGCAAAATTATCATTTTTATCTATTTTAGATTGAAATTGAATTGGAATAA							
rigens_leucolaena_RM773	-----	-----	TTAAAAAGTAATAA-----	ATAAGCAAAATTATCATTTTTATCTATTTTAGATTGAAATTGAATTGGAATAA							
rigens_leucolaena_RM952_1	-----	-----	TTAAAAAGTAATAA-----	ATAAGCAAAATTATCATTTTTATCTATTTTAGATTGAAATTGAATTGGAATAA							
rigens_rigens_RM763	-----	-----	TTAAAAAGTAATAA-----	ATAAGCAAAATTATCATTTTTATCTATTTTAGATTGAAATTGAATTGGAATAA							
rigens_rigens_SR463	-----	-----	TTAAAAAGTAATAA-----	ATAAGCAAAATTATCATTTTTATCTATTTTAGATTGAAATTGAATTGGAATAA							
rigens_uniflora_JC201205	-----	-----	TTAAAAAGTAATAA-----	ATAAGCAAAATTATAATTTTATCTATTTTAGATTGAAATTGAATTGGAATAA							
rigens_uniflora_RM920	-----	-----	TTAAAAAGTAATAA-----	ATAAGCAAAATTATAATTTTATCTATTTTAGATTGAAATTGAATTGGAATAA							
schenckii	-----	-----	TTAAAAAGTAATAA-----	ATAAGCAAAATTATCATTTTTATCTATTTTAGATTGAAATTGAATTGGAATAA							
serrata_M250904_15	-----	-----	TTAAAAAGTAATAA-----	ATAAGCAAAATTATCATTTTTATCTATTTTAGATTGAAATTGAATTGGAATAA							
serrata_RM898	-----	-----	TTAAAAAGTAATAA-----	ATAAGCAAAATTATCATTTTTATCTATTTTAGATTGAAATTGAATTGGAATAA							
tenuifolia_CAM1601	-----	-----	TTAAATAAATAGTAATAA-----	ATAAGCAAAATTATCATTTTTATCTATTTTAGATTGAAATTGAATTGGAATAA							
tenuifolia_M2730	-----	-----	TTAAATAAATAGTAATAA-----	ATAAGCAAAATTATCATTTTTATCTATTTTAGATTGAAATTGAATTGGAATAA							
spnov_M040906_33	-----	-----	TTAAAAAGTAATAA-----	ATAAGCAAAATTATCATTTTTATCTATTTTAGATTGAAATTGAATTGGAATAA							

Appendix 5: cpDNA sequence data for Chapter 3

	1110	1120	1130	1140	1150	1160	1170	1180	1190	1200	1210]
Berkheya	AACTTCATAAAAGATTGGGAAAAGGATATATAAAA	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
Gorteria	AACTTCATAAAAGATTGGGAAAAGGATATATAAAA	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
Hirpicium	AACTTCATAAAAGATTGGGAAAAGGATATATAAAA	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
caespitosa_RVC448	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
caespitosa_RVC307	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
ciliaris_RM1230	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
ciliaris_RM1382	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
heterochaeta_RM1429	AACTTCATAAAAGATTGGGAAAAGGATATATAAAA	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
heterochaeta_RM1451	AACTTCATAAAAGATTGGGAAAAGGATATATAAAA	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
jurineifolia_jur_SR682	AACTTCATAAAAGATTGGGAAAAGG-TATATAAAATATAAAA	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
jurineifoliajur_RM1518	AACTTCATAAAAGATTGGGAAAAGG-TATATAAAATATAAAA	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
jurineifolia_scab_CAM1604	AACTTCATAAAAGATTGGGAAAAGG-TATATAAAATATAAAA	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
jurineifolia_scab_CAM2652	AACTTCATAAAAGATTGGGAAAAGG-TATATAAAATATAAAA	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
krebsiana_arctotoides_RM868	AACTTCATAAAAGATTGGGAAAAGGATATATAAAATATAAAA	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
krebsiana_arctotoides_RM876	AACTTCATAAAAGATTGGGAAAAGGATATATAAAATATAAAA	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
krebsiana_krebsiana_RM1114	AACTTCATAAAAGATTGGGAAAAGGATATATAAAATATAAAA	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
krebsiana_krebsiana_RM1136	AACTTCATAAAAGATTGGGAAAAGGATATATAAAATATAAAA	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
krebsiana_serrulata_RM863	AACTTCATAAAAGATTGGGAAAAGGATATATAAAATATAAAA	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
krebsiana_serrulata_RM965	AACTTCATAAAAGATTGGGAAAAGGATATATAAAATATAAAA	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
leiopoda_M240901	AACTTCATAAAAGATTGGGAAAAGGATATATAAAATATAAAA	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
leiopoda_RM1309	AACTTCATAAAAGATTGGGAAAAGGATATATAAAATATAAAA	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
lichtenstenii_CAM1916	AACTTCATAAAAGATTGGGAAAAGGATATATAAAATATAAAA	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
lichtensteini_RM1249	AACTTCATAAAAGATTGGGAAAAGGATATATAAAATATAAAA	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
linearis_linearis_RM1010	AACTTCATAAAAGATTGGGAAAAGGATATATAAAATATAAAA	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
linearis_linearis_SH113	AACTTCATAAAAGATTGGGAAAAGGATATATAAAATATAAAA	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
linearis_ovalis_NDsn	AACTTCATAAAAGATTGGGAAAAGGATATATAAAATATAAAA	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
linearis_ovalis_RM854	AACTTCATAAAAGATTGGGAAAAGGATATATAAAATATAAAA	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
maritima_RM1038	AACTTCATAAAAGATTGGGAAAAGGATATATAAAATATAAAA	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
maritima_M290606_6	AACTTCATAAAAGATTGGGAAAAGGATATATAAAATATAAAA	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
othonnites_RM1306	AACTTCATAAAAGATTGGGAAAAGGATATATAAAATATAAAA	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
pectinata_M120903	AACTTCATAAAAGATTGGGAAAAGGATATATAAAATATAAAA	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
pectinata_RM1044	AACTTCATAAAAGATTGGGAAAAGGATATATAAAATATAAAACCT-ATAATAT	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
rigida_M280902	AACTTCATAAAAGATTGGGAAAAGGATATATAAAATATAAAA	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
rigida_RM840	AACTTCATAAAAGATTGGGAAAAGGATATATAAAATATAAAA	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
rigens_leucolaena_RM773	AACTTCATAAAAGATTGGGAAAAGGATATATAAAATATAAAA	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
rigens_leucolaena_RM952_1	AACTTCATAAAAGATTGGGAAAAGGATATATAAAATATAAAA	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
rigens_rigens_RM763	AACTTCATAAAAGATTGGGAAAAGGATATATAAAATATAAAA	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
rigens_rigens_SR463	AACTTCATAAAAGATTGGGAAAAGGATATATAAAATATAAAA	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
rigens_uniflora_JC201205	AACTTCATAAAAGATTGGGAAAAGGATATATAAAATATAAAA	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
rigens_uniflora_RM920	AACTTCATAAAAGATTGGGAAAAGGATATATAAAATATAAAA	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
schenckii	AACTTCATAAAAGATTGGGAAAAGGATATATAAAATATAAAA	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
serrata_M250904_15	AACTTCATAAAAGATTGGGAAAAGGATATATAAAATATAAAA	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
serrata_RM898	AACTTCATAAAAGATTGGGAAAAGGATATATAAAATATAAAA	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
tenuifolia_CAM1601	AACTTCATAAAAGATTGGGAAAAGGATATATAAAATATAAT	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
tenuifolia_M2730	AACTTCATAAAAGATTGGGAAAAGGATATATAAAATATAAT	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
spnov_M040906_33	AACTTCATAAAAGATTGGGAAAAGGATATATAAAATATAAAA	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

Appendix 5: cpDNA sequence data for Chapter 3

	1220	1230	1240	1250	1260	1270	1280	1290	1300	1310	1320]
Berkheya	ACCACGCTAATCGAACCAAA	-----	CTATAAAAAGCCCTTGTATTTTTAAAGAAACTATGTAAGGCAAATA	-----	-----	-----	-----	-----	GTACTAAATAAAAAAAA	-----	GGAGC
Gorteria	-----	ATCGAACCAAA	-----	CTATAAAAAGCCCTTGTATTTTTAAAGAAACTATGTAAGTCAAATA	-----	-----	-----	-----	GTACTAAATAAAAAAAA	-----	GGAGC
Hirpicium	AACACGCTAATTGAACCAAA	-----	CTATAAAAAGCCCTTCTTATTTTTAAAGAAACTATGTAAGGAAAAGA	-----	-----	-----	-----	-----	GTACTAAATAAAAAAAA	-----	GGAGC
caespitosa_RVC448	-----	-----	-----	AAAGCCCTTGTATTTTTAAAGAAACTATGTAAGGCAAATAGTATA	-----	-----	-----	-----	GTACTAAATAAAAAAAA	-----	GGAGC
caespitosa_RVC307	-----	-----	-----	AAAGCCCTTGTATTTTTAAAGAAACTATGTAAGGCAAATAGTATA	-----	-----	-----	-----	GTACTAAATAAAAAAAA	-----	GGAGC
ciliaris_RM1230	-----	-----	-----	AAAGCCCTTGTATTTTTAAAGAAACTATGTAAGGCAAATAGTATA	-----	-----	-----	-----	GTACTAAATAAAAAAAA	-----	GGAGC
ciliaris_RM1382	-----	-----	-----	AAAGCCCTTGTATTTTTAAAGAAACTATGTAAGGCAAATAGTATA	-----	-----	-----	-----	GTACTAAATAAAAAAAA	-----	GGA??
heterochaeta_RM1429	AACACGCTAATCGAACCAAA	-----	CTATAAAAAGCCCTTGTATTTTTAAAGAAACTATGTAAGGCAAATAGTATA	-----	-----	-----	-----	-----	GTACTAAATAAAAAAAA	-----	GGAGC
heterochaeta_RM1451	AACACGCTAATCGAACCAAA	-----	CTATAAAAAGCCCTTGTATTTTTAAAGAAACTATGTAAGGCAAATAGTATA	-----	-----	-----	-----	-----	GTACTAAATAAAAAAAA	-----	GGAGC
jurineifolia_jur_SR682	AACACGCTAATCGAACCAAA	-----	CTATAAAGAGCCCTTGTATTTTTAAAGAAACTATGTAAGGCAAATAGTATA	-----	-----	-----	-----	-----	GTACTAAATAAAAAAAA	-----	GGAGC
jurineifoliajur_RM1518	AACACGCTAATCGAACCAAA	-----	CTATAAAGAGCCCTTGTATTTTTAAAGAAACTATGTAAGGCAAATAGTATA	-----	-----	-----	-----	-----	GTACTAAATAAAAAAAA	-----	GGAGC
jurineifolia_scab_CAM1604	AACACGCTAATCGAACCAAA	-----	CTATAAAGAGCCCTTGTATTTTTAAAGAAACTATGTAAGGCAAATAGTATA	-----	-----	-----	-----	-----	GTACTAAATAAAAAAAA	-----	GGAGC
jurineifolia_scab_CAM2652	AACACGCTAATCGAACCAAA	-----	CTATAAAGAGCCCTTGTATTTTTAAAGAAACTATGTAAGGCAAATAGTATA	-----	-----	-----	-----	-----	GTACTAAATAAAAAAAA	-----	GGAGC
krebsiana_arctotoides_RM868	AACACGCTAATCGAACCAAA	-----	CTATAAAAAGCCCTTGTATTTTTAAAGAAACTATGTAAGGCAAATAGTATA	-----	-----	-----	-----	-----	GTACTAAATAAAAAAAA	-----	GGAGC
krebsiana_arctotoides_RM876	AACACGCTAATCGAACCAAA	-----	CTATAAAAAGCCCTTGTATTTTTAAAGAAACTATGTAAGGCAAATAGTATA	-----	-----	-----	-----	-----	GTACTAAATAAAAAAAA	-----	GGAGC
krebsiana_krebsiana_RM1114	AACACGCTAATCGAACCAAA	-----	CTATAAAAAGCCCTTGTATTTTTAAAGAAACTATGTAAGGCAAATAGTATA	-----	-----	-----	-----	-----	GTACTAAATAAAAAAAA	-----	GGAGC
krebsiana_krebsiana_RM1136	AACACGCTAATCGAACCAAA	-----	CTATAAAAAGCCCTTGTATTTTTAAAGAAACTATGTAAGGCAAATAGTATA	-----	-----	-----	-----	-----	GTACTAAATAAAAAAAA	-----	GGAGC
krebsiana_serrulata_RM863	AACACGCTAATCGAACCAAA	-----	CTATAAAAAGCCCTTGTATTTTTAAAGAAACTATGTAAGGCAAATAGTATA	-----	-----	-----	-----	-----	GTACTAAATAAAAAAAA	-----	GGAGC
krebsiana_serrulata_RM965	AACACGCTAATCGAACCAAA	-----	CTATAAAAAGCCCTTGTATTTTTAAAGAAACTATGTAAGGCAAATAGTATA	-----	-----	-----	-----	-----	GTACTAAATAAAAAAAA	-----	GGAGC
leiopoda_M240901	AACACGCTAATCGAACCAAA	-----	CTATAAAAAGCCCTTGTATTTTTAAAAAAGCCCTTGTATTTTTAAAGAAACTATGTAAGGCAAATAGTATA	-----	-----	-----	-----	-----	GTACTAAATAAAAAAAA	-----	GGAGC
leiopoda_RM1309	AACACGCTAATCGAACCAAA	-----	CTATAAAAAGCCCTTGTATTTTTAAAGAAACTATGTAAGGCAAATAGTATA	-----	-----	-----	-----	-----	GTACTAAATAAAAAAAA	-----	GGAGC
lichtenstenii_CAM1916	AACACGCTAATCGAACCAAA	-----	CTATAAAAAGCCCTTGTATTTTTAAAGAAACTATGTAAGGCAAATAGTATA	-----	-----	-----	-----	-----	GTACTAAATAAAAAAAA	-----	GGAGC
lichtensteini_RM1249	AACACGCTAATCGAACCAAA	-----	CTATAAAAAGCCCTTGTATTTTTAAAGAAACTATGTAAGGCAAATAGTATA	-----	-----	-----	-----	-----	GTACTAAATAAAAAAAA	-----	GGAGC
linearis_linearis_RM1010	AACACGCTAATCGAACCAAA	-----	CTATAAAAAGCCCTTGTATTTTTAAAGAAACTATGTAAGGCAAATAGTATA	-----	-----	-----	-----	-----	GTACTAAATAAAAAAAA	-----	GGAGC
linearis_linearis_SH113	AACACGCTAATCGAACCAAA	-----	CTATAAAAAGCCCTTGTATTTTTAAAGAAACTATGTAAGGCAAATAGTATA	-----	-----	-----	-----	-----	GTACTAAATAAAAAAAA	-----	GGAGC
linearis_ovalis_NDsn	AACACGCTAATCGAACCAAA	-----	CTATAAAAAGCCCTTGTATTTTTAAAGAAACTATGTAAGGCAAATAGTATA	-----	-----	-----	-----	-----	GTACTAAATAAAAAAAA	-----	GGAGC
linearis_ovalis_RM854	AACACGCTAATCGAACCAAA	-----	CTATAAAAAGCCCTTGTATTTTTAAATAAAACTATGTAAGGCAAATAGTATA	-----	-----	-----	-----	-----	GTACTAAATAAAAAAAA	-----	GGAGC
maritima_RM1038	AACACGCTAATCGAACCAAA	-----	CTATAAAAAGCCCTTGTATTTTTAAAGAAACTATGTAAGGCAAATAGTATA	-----	-----	-----	-----	-----	GTACTAAATAAAAAAAA	-----	GGAGC
maritima_M290606_6	AACACGCTAATCGAACCAAA	-----	CTATAAAAAGCCCTTGTATTTTTAAAGAAACTATGTAAGGCAAATAGTATA	-----	-----	-----	-----	-----	GTACTAAATAAAAAAAA	-----	GGAGC
othonnites_RM1306	AACACGCTAATCGAACCAAA	-----	CTATAAAAAGCCCTTGTATTTTTAAAGAAACTATGTAAGGCAAATAGTATA	-----	-----	-----	-----	-----	GTACTAAATAAAAAAAA	-----	GGAGC
pectinata_M120903	AACACGCTAATCGAACCAAA	-----	CTATAAAAAGCCCTTGTATTTTTAAAGAAACTATGTAAGGCAAATAGTATA	-----	-----	-----	-----	-----	GTACTAAATAAAAAAAA	-----	GGAGC
pectinata_RM1044	AACACGCTAATCGAACCAAA	-----	CTATAAAAAGCCCTTGTATTTTTAAAGAAACTATGTAAGGCAAATAGTATA	-----	-----	-----	-----	-----	GTACTAAATAAAAAAAA	-----	GGAGC
rigida_M280902	AACACGCTAATCGAACCAAA	-----	CTATAAAAAGCCCTTGTATTTTTAAAGAAACTATGTAAGGCAAATAGTATA	-----	-----	-----	-----	-----	GTACTAAATAAAAAAAA	-----	GGAGC
rigida_RM840	AACACGCTAATCGAACCAAA	-----	CTATAAAAAGCCCTTGTATTTTTAAAGAAACTATGTAAGGCAAATAGTATA	-----	-----	-----	-----	-----	GTACTAAATAAAAAAAA	-----	GGAGC
rigens_leucolaena_RM773	AACACGCTAATCGAACCAAA	-----	CTATAAAAAGCCCTTGTATTTTTAAAGAAACTATGTAAGGCAAATAGTATA	-----	-----	-----	-----	-----	GTACTAAATAAAAAAAA	-----	GGAGC
rigens_leucolaena_RM952_1	AACACGCTAATCGAACCAAA	-----	CTATAAAAAGCCCTTGTATTTTTAAAGAAACTATGTAAGGCAAATAGTATA	-----	-----	-----	-----	-----	GTACTAAATAAAAAAAA	-----	GGAGC
rigens_rigens_RM763	AACACGCTAATCGAACCAAA	-----	CTATAAAAAGCCCTTGTATTTTTAAAGAAACTATGTAAGGCAAATAGTATA	-----	-----	-----	-----	-----	GTACTAAATAAAAAAAA	-----	GGAGC
rigens_rigens_SR463	AACACGCTAATCGAACCAAA	-----	CTATAAAAAGCCCTTGTATTTTTAAAGAAACTATGTAAGGCAAATAGTATA	-----	-----	-----	-----	-----	GTACTAAATAAAAAAAA	-----	GGAGC
rigens_uniflora_JC201205	AACACGCTAATCGAACCAAA	-----	CTATAAAAAGCCCTTGTATTTTTAAAGAAACTATGTAAGGCAAATAGTATA	-----	-----	-----	-----	-----	GTACTAAATAAAAAAAA	-----	GGAGC
rigens_uniflora_RM920	AACACGCTAATCGAACCAAA	-----	CTATAAAAAGCCCTTGTATTTTTAAAGAAACTATGTAAGGCAAATAGTATA	-----	-----	-----	-----	-----	GTACTAAATAAAAAAAA	-----	GGAGC
schenckii	AACACGCTAATCGAACCAAA	-----	CTATAAAAAGCCCTTGTATTTTTAAAGAAACTATGTAAGGCAAATAGTATA	-----	-----	-----	-----	-----	GTACTAAATAAAAAAAA	-----	GGAGC
serrata_M250904_15	AACACGCTAATCGAACCAAACTATAAAAGCCCTTGTATTTTTAAAGAAACTATGTAAGGCAAATAGTATA	-----	-----	-----	-----	-----	-----	-----	GTACTAAATAAAAAAAA	-----	GGAGC
serrata_RM898	AACACGCTAATCGAACCAAA	-----	CTATAAAAAGCCCTTGTATTTTTAAAGAAACTATGTAAGGCAAATAGTATA	-----	-----	-----	-----	-----	GTACTAAATAAAAAAAA	-----	GGAGC
tenuifolia_CAM1601	AACACGCTAATCGAACCAAA	-----	CTATAAAAAGCCCTTGTATTTTTAAAGAAACTATGTAAGGCAAATAGTATA	-----	-----	-----	-----	-----	GTACTAAATAAAAAAAA	-----	GGAGC
tenuifolia_M2730	AACACGCTAATCGAACCAAA	-----	CTATAAAAAGCCCTTGTATTTTTAAAGAAACTATGTAAGGCAAATAGTATA	-----	-----	-----	-----	-----	GTACTAAATAAAAAAAA	-----	GGAGC
spnov_M040906_33	AACACGCTAATCGAACCAAA	-----	CTATAAAAAGCCCTTGTATTTTTAAAGAAACTATGTAAGGCAAATAGTATA	-----	-----	-----	-----	-----	GTACTAAATAAAAAAAA	-----	GGAGC

Appendix 5: cpDNA sequence data for Chapter 3

	1330	1340	1350	1360	1370	1380	1390	1400	1410	1420	1430]
Berkheya	AATAGCTTCCCTCTTGT	TTTATC-----	AAGAGGG-CGTTATTGCTCCTTTTTAGTTCAAAAAC	TCGTATAACAATCAGACCAAAGTCTTATCCATTTGTAGATGGAGC							
Gorteria	AATA-ACGCCCTCTTG-----	ATAAAAC-AAGATGGAAGCTATTGCTCCTTTTTAGTTCAAAAAC	TCGTATAACAATCAGACCAAAGTCTTATCCATTTGTAGATGGAGC								
Hirpicium	AATA-ACGCCCTCTTG-----	ATAAAAC-AAGAGGGAAGCTATTGCTCCTTTTTAGTTCAAAAAC	TCGTATAACAATCAGACCAAAGTCTTATCCATTTGTAGATGGAGC								
caespitosa_RVC448	AATA-ACGCCCTCTTGATATGATAAAAC	-AAGAGGGAAGCTATTGCTCCTTTTTAGTTCAAAAAC	TCGTATAACAATCAGACCAAAGTCTTATCCATTTGTAGATGGAGC								
caespitosa_RVC307	AATA-ACGCCCTCTTGATATGATAAAAC	-AAGAGGGAAGCTATTGCTCCTTTTTAGTTCAAAAAC	TCGTATAACAATCAGACCAAAGTCTTATCCATTTGTAGATGGAGC								
ciliaris_RM1230	AATA-ACGCCCTCTTGATATGATAAAAC	-AAGAGGGAAGCTATTGCTCCTTTTTAGTTCAAAAAC	TCGTATAACAATCAGACCAAAGTCTTATCCATTTGTAGATGGAGC								
ciliaris_RM1382	????????????????	????????????????	????????????????	????????????????	????????????????	????????????????	????????????????	????????????????	????????????????	????????????????	????????????????
heterochaeta_RM1429	AATA-ACGCCCTCTTGATATAATAAAAC	-AAGAGGGAAGCTATTGCTCCTTTTTAGTTCAAAAAC	TCGTATAACAATCAGACCAAAGTCTTATCCATTTGTAGATGGAGC								
heterochaeta_RM1451	AATA-ACGCCCTCTTGATATGATAAAAC	-AAGAGGGAAGCTATTGCTCCTTTTTAGTTCAAAAAC	TCGTATAACAATCAGACCAAAGTCTTATCCATTTGTAGATGGAGC								
jurineifolia_jur_SR682	AATAGCTTCCCTCTTGT	TTTTATCATATC-AAGAGGG-CGTTATTGCTCCTTTTTAGTTCAAGA	ACTCGTATAACAATCAGACCAAAGTCTTATCCATTTGTAGATGGAGC								
jurineifolia_jur_RM1518	AATAGCTCCCTCTTGT	TTTTATCATATC-AAGAGGG-CGTTATTGCTCCTTTTTAGTTCAAGA	ACTCGTATAACAATCAGACCAAAGTCTTATCCATTTGTAGATGGAGC								
jurineifolia_scab_CAM1604	AATAGCTTCCCTCTTGT	TTTTATCATATC-AAGAGGG-CGTTATTGCTCCTTTTTAGTTCAAGA	ACTCGTATAACAATCAGACCAAAGTCTTATCCATTTGTAGATGGAGC								
jurineifolia_scab_CAM2652	AATAGCTTCCCTCTTGT	TTTTATCATATC-AAGAGGG-CGTTATTGCTCCTTTTTAGTTCAAGA	ACTCGTATAACAATCAGACCAAAGTCTTATCCATTTGTAGATGGAGC								
krebsiana_arctotoides_RM868	AATA-ACGCCCTCTTGATATGATAAAAC	-AAGAGGGAAGCTATTGCTCCTTTTTAGTTCAAAAAC	TCGTATAACAATCAGACCAAAGTCTTATCCATTTGTAGATGGAGC								
krebsiana_arctotoides_RM876	AATA-ACGCCCTCTTGATATGATAAAAC	-AAGAGGGAAGCTATTGCTCCTTTTTAGTTCAAAAAC	TCGTATAACAATCAGACCAAAGTCTTATCCATTTGTAGATGGAGC								
krebsiana_krebsiana_RM1114	AATA-ACGCCCTCTTGATATGATAAAAC	-AAGAGGGAAGCTATTGCTCCTTTTTAGTTCAAAAAC	TCGTATAACAATCAGACCAAAGTCTTATCCATTTGTAGATGGAGC								
krebsiana_krebsiana_RM1136	AATA-ACGCCCTCTTGATATGATAAAAC	-AAGAGGGAAGCTATTGCTCCTTTTTAGTTCAAAAAC	TCGTATAACAATCAGACCAAAGTCTTATCCATTTGTAGATGGAGC								
krebsiana_serrulata_RM863	AATA-ACGCCCTCTTGATATGATAAAAC	-AAGAGGGAAGCTATTGCTCCTTTTTAGTTCAAAAAC	TCGTATAACAATCAGACCAAAGTCTTATCCATTTGTAGATGGAGC								
krebsiana_serrulata_RM965	AATA-ACGCCCTCTTGATATGATAAAAC	-AAGAGGGAAGCTATTGCTCCTTTTTAGTTCAAAAAC	TCGTATAACAATCAGACCAAAGTCTTATCCATTTGTAGATGGAGC								
leiopoda_M240901	AATA-ACGCCCTCTTGATATGATAAAAC	-AAGAGGGAAGCTATTGCTCCTTTTTAGTTCAAAAAC	TCGTATAACAATCAGACCAAAGTCTTATCCATTTGTAGATGGAGC								
leiopoda_RM1309	AATA-ACGCCCTCTTGATATGATAAAAC	-AAGAGGGAAGCTATTGCTCCTTTTTAGTTCAAAAAC	TCGTATAACAATCAGACCAAAGTCTTATCCATTTGTAGATGGAGC								
lichtenstenii_CAM1916	AATA-ACGCCCTCTTGATATGATAAAAC	-AAGAGGGAAGCTATTGCTCCTTTTTAGTTCAAAAAC	TCGTATAACAATCAGACCAAAGTCTTATCCATTTGTAGATGGAGC								
lichtensteini_RM1249	AATA-ACGCCCTCTTGATATGATAAAAC	-AAGAGGGAAGCTATTGCTCCTTTTTAGTTCAAAAAC	TCGTATAACAATCAGACCAAAGTCTTATCCATTTGTAGATGGAGC								
linearis_linearis_RM1010	AATA-ACGCCCTCTTGATATGATAAAAC	-AAGAGGGAAGCTATTGCTCCTTTTTAGTTCAAAAAC	TCGTATAACAATCAGACCAAAGTCTTATCCATTTGTAGATGGAGC								
linearis_linearis_SH113	AATA-ACGCCCTCTTGATATGATAAAAC	-AAGAGGGAAGCTATTGCTCCTTTTTAGTTCAAAAAC	TCGTATAACAATCAGACCAAAGTCTTATCCATTTGTAGATGGAGC								
linearis_ovalis_NDsn	AATA-ACGCCCTCTTGATATGATAAAAC	-AAGAGGGAAGCTATTGCTCCTTTTTAGTTCAAAAAC	TCGTATAACAATCAGACCAAAGTCTTATCCATTTGTAGATGGAGC								
linearis_ovalis_RM854	AATA-ACGCCCTCTTGATATGATAAAAC	-AAGAGGGAAGCTATTGCTCCTTTTTAGTTCAAAAAC	TCGTATAACAATCAGACCAAAGTCTTATCCATTTGTAGATGGAGC								
maritima_RM1038	AATA-ACGCCCTCTTGATATGATAAAAC	-AAGAGGGAAGCTATTGCTCCTTTTTAGTTCAAAAAC	TCGTATAACAATCAGACCAAAGTCTTATCCATTTGTAGATGGAGC								
maritima_M290606_6	AATA-ACGCCCTCTTGATATGATAAAAC	-AAGAGGGAAGCTATTGCTCCTTTTTAGTTCAAAAAC	TCGTATAACAATCAGACCAAAGTCTTATCCATTTGTAGATGGAGC								
othonnites_RM1306	AATA-ACGCCCTCTTGATATGATAAAAC	-AAGAGGGAAGCTATTGCTCCTTTTTAGTTCAAAAAC	TCGTATAACAATCAGACCAAAGTCTTATCCATTTGTAGATGGAGC								
pectinata_M120903	AATA-ACGCCCTCTTGATATGATAAAAC	-AAGAGGGAAGCTATTGCTCCTTTTTAGTTCAAAAAC	TCGTATAACAATCAGACCAAAGTCTTATCCATTTGTAGATGGAGC								
pectinata_RM1044	AATA-ACGCCCTCTTGATATGATAAAAC	-AAGAGGGAAGCTATTGCTCCTTTTTAGTTCAAAAAC	TCGTATAACAATCAGACCAAAGTCTTATCCATTTGTAGATGGAGC								
rigida_M280902	AATA-ACGCCCTCTTGATATGATAAAAC	-AAGAGGGAAGCTATTGCTCCTTTTTAGTTCAAAAAC	TCGTATAACAATCAGACCAAAGTCTTATCCATTTGTAGATGGAGC								
rigida_RM840	AATA-ACGCCCTCTTGATATGATAAAAC	-AAGAGGGAAGCTATTGCTCCTTTTTAGTTCAAAAAC	TCGTATAACAATCAGACCAAAGTCTTATCCATTTGTAGATGGAGC								
rigens_leucolaena_RM773	AATA-ACGCCCTCTTGATATGATAAAAC	-AAGAGGGAAGCTATTGCTCCTTTTTAGTTCAAAAAC	TCGTATAACAATCAGACCAAAGTCTTATCCATTTGTAGATGGAGC								
rigens_leucolaena_RM952_1	AATA-ACGCCCTCTTGATATGATAAAAC	-AAGAGGGAAGCTATTGCTCCTTTTTAGTTCAAAAAC	TCGTATAACAATCAGACCAAAGTCTTATCCATTTGTAGATGGAGC								
rigens_rigens_RM763	AATA-ACGCCCTCTTGATATGATAAAAC	-AAGAGGGAAGCTATTGCTCCTTTTTAGTTCAAAAAC	TCGTATAACAATCAGACCAAAGTCTTATCCATTTGTAGATGGAGC								
rigens_rigens_SR463	AATA-ACGCCCTCTTGATATGATAAAAC	-AAGAGGGAAGCTATTGCTCCTTTTTAGTTCAAAAAC	TCGTATAACAATCAGACCAAAGTCTTATCCATTTGTAGATGGAGC								
rigens_uniflora_JC201205	AATA-ACGCCCTCTTGATATGATAAAAC	-AAGAGGGAAGCTATTGCTCCTTTTTAGTTCAAAAAC	TCGTATAACAATCAGACCAAAGTCTTATCCATTTGTAGATGGAGC								
rigens_uniflora_RM920	AATA-ACGCCCTCTTGATATGATAAAAC	-AAGAGGGAAGCTATTGCTCCTTTTTAGTTCAAAAAC	TCGTATAACAATCAGACCAAAGTCTTATCCATTTGTAGATGGAGC								
schenckii	AATA-ACGCCCTCTTGATATGATAAAAC	-AAGAGGGAAGCTATTGCTCCTTTTTAGTTCAAAAAC	TCGTATAACAATCAGACCAAAGTCTTATCCATTTGTAGATGGAGC								
serrata_M250904_15	AATA-ACGCCCTCTTGATATGATAAAAC	-AAGAGGGAAGCTATTGCTCCTTTTTAGTTCAAAAAC	TCGTATAACAATCAGACCAAAGTCTTATCCATTTGTAGATGGAGC								
serrata_RM898	AATA-ACGCCCTCTTGATATGATAAAAC	-AAGAGGGAAGCTATTGCTCCTTTTTAGTTCAAAAAC	TCGTATAACAATCAGACCAAAGTCTTATCCATTTGTAGATGGAGC								
tenuifolia_CAM1601	AATA-ACGCCCTCTTGATATGATAAAAC	-AAGAGGGAAGCTATTGCTCCTTTTTAGTTCAAAAAC	TCGTATAACAATCAGACCAAAGTCTTATCCATTTGTAGATGGAGC								
tenuifolia_M2730	AATA-ACGCCCTCTTGATATGATAAAAC	-AAGAGGGAAGCTATTGCTCCTTTTTAGTTCAAAAAC	TCGTATAACAATCAGACCAAAGTCTTATCCATTTGTAGATGGAGC								
spnov_M040906_33	AATA-ACGCCCTCTTGATATGATAAAAC	-AAGAGGGAAGCTATTGCTCCTTTTTAGTTCAAAAAC	TCGTATAACAATCAGACCAAAGTCTTATCCATTTGTAGATGGAGC								

Appendix 5: cpDNA sequence data for Chapter 3

	1440	1450	1460	1470	1480	1490	1500	1510	1520	1530	1540
			psbA-trnH	< >	trnL						
Berkheya	TTCGATAGCAGCTAAGTCTAGAGGGAAATTATGAGCACGGACTTAATTGGATTGAGCCTTGGTATGGAACTTACTAAGTGATAACTTTCAAATTCAGAGAAACCTGGA										
Gorteria	??CGGACTTAATTGGATTGAGCCTTGGTATGGAACTTACTAAGTGATAACTTTCAAATTCAGAGAAACCTGGA										
Hirpicium	TTCGATAGCAGCTAAGTCTAGAGGGAAATTATGAGCACGGACTTAATTGGATTGAGCCTTGGTATGGAACTTACTAAGTGATAACTTTCAAATTCAGAGAAACCTGGA										
caespitosa_RVC448	TTCGATAGCAGCTAAGTCTAGAGGGAAATTATGAGCACGGACTTAATTGGATTGAGCCTTGGTATGGAACTTACTAAGTGATAACTTTCAAATTCAGAGAAACCTGGA										
caespitosa_RVC307	TTCGATAGCAGCTAAGTCTAGAGGGAAATTATGAGCACGGACTTAATTGGATTGAGCCTTGGTATGGAACTTACTAAGTGATAACTTTCAAATTCAGAGAAACCTGGA										
ciliaris_RM1230	TTCGATAGCAGCTAAGTCTAGAGGGAAATTATGAGCACGGACTTAATTGGATTGAGCCTTGGTATGGAACTTACTAAGTGATAACTTTCAAATTCAGAGAAACCTGGA										
ciliaris_RM1382	??ACGGACTTAATTGGATTGAGCCTTGGTATGGAACTTACTAAGTGATAACTTTCAAATTCAGAGAAACCTGGA										
heterochaeta_RM1429	TTCGATAGCAGCTAAGTCTAGAGGGAAATTATGAGCACGGACTTAATTGGATTGAGCCTTGGTATGGAACTTACTAAGTGATAACTTTCAAATTCAGAGAAACCTGGA										
heterochaeta_RM1451	TTCGATAGCAGCTAAGTCTAGAGGGAAATTATGAGCACGGAAATTAATTGGATTGAGCCTTGGTATGGAACTTACTAAGTGATAACTTTCAAATTCAGAGAAACCTGGA										
jurineifolia_jur_SR682	TTCGATAGCAGCTAAGTCTAGAGGGAAATTATGAGC??										
jurineifoliajur_RM1518	TTCGATAGCAGCTAAGTCTAGAGGGAAATTATGAGC??										
jurineifolia_scab_CAM1604	TTCGATAGCAGCTAAGTCTAGAGGGAAATTATGAGC??										
jurineifolia_scab_CAM2652	TTCGATAGCAGCTAAGTCTAGAGGGAAATTATGAGCACGGACTTAATTGGATTGAGCCTTGGTATGGAACTTACTAAGTGATAACTTTCAAATTCAGAGAAACCTGGA										
krebsiana_arctotoides_RM868	TTCGATAGCAGCTAAGTCTAGAG??										
krebsiana_arctotoides_RM876	TTCGATAGCAGCTAAGTCTAGAGGGAAATTATGAGC??										
krebsiana_krebsiana_RM1114	TTCGATAGCAGCTAAGTCTAGAGGGAAATTATGAGC?GGACTTAATTGGATTGAGCCTTGGTATGGAACTTACTAAGTGATAACTTTCAAATTCAGAGAAACCTGGA										
krebsiana_krebsiana_RM1136	TTCGATAGCAGCTAAGTCTAGAGGGAAATTATGAGC?ACGGACTTAATTGGATTGAGCCTTGGTATGGAACTTACTAAGTGATAACTTTCAAATTCAGAGAAACCTGGA										
krebsiana_serrulata_RM863	TTCGATAGCAGCTAAGTCTAGAGGGAAATTATGAGCACGGACTTAATTGGATTGAGCCTTGGTATGGAACTTACTAAGTGATAACTTTCAAATTCAGAGAAACCTGGA										
krebsiana_serrulata_RM965	TTCGATAGCAGCTAAGTCTAGAGGGAAATTATGAGC??										
leiopoda_M240901	TTCGATAGCAGCTAAGTCTAGAGGGAAATTATGAGC??										
leiopoda_RM1309	TTCGATAGCAGCTAAGTCTAGAGGGAAATTATGAGCACGGACTTAATTGGATTGAGCCTTGGTATGGAACTTACTAAGTGATAACTTTCAAATTCAGAGAAACCTGGA										
lichtenstenii_CAM1916	TTCGATAGCAGCTAAGTCTAGAGGGAAATTATGAGC??										
lichtensteini_RM1249	TTCGATAGCAGCTAAGTCTAGAGGGAAATTATGAGCACGGACTTAATTGGATTGAGCCTTGGTATGGAACTTACTAAGTGATAACTTTCAAATTCAGAGAAACCTGGA										
linearis_linearis_RM1010	TTCGATAGCAGCTAAGTCTAGAGGGAAATTATGAG????GACTTAATTGGATTGAGCCTTGGTATGGAACTTACTAAGTGATAACTTTCAAATTCAGAGAAACCTGGA										
linearis_linearis_SH113	TTCGATAGCAGCTAAGTCTAGAGGGAAATTATGAGCACGGACTTAATTGGATTGAGCCTTGGTATGGAACTTACTAAGTGATAACTTTCAAATTCAGAGAAACCTGGA										
linearis_ovalis_NDsn	TTCGATAGCAGCTAAGTCTAGAGGGAAATTATGAGCACGGACTTAATTGGATTGAGCCTTGGTATGGAACTTACTAAGTGATAACTTTCAAATTCAGAGAAACCTGGA										
linearis_ovalis_RM854	TTCGATAGCAGCTAAGTCTAGAGGGAAATTATGAGC??										
maritima_RM1038	TTCGATAGCAGCTAAGTCTAGAGGGAAATTATGAGC??										
maritima_M290606_6	TTCGATAGCAGCTAAGTCTAGAGGGAAATTATGAGCACGGACTTAATTGGATTGAGCCTTGGTATGGAACTTACTAAGTGATAACTTTCAAATTCAGAGAAACCTGGA										
othonnites_RM1306	TTCGATAGCAGCTAAGTCTAGAGGGAAATTATGAGCACGGACTTAATTGGATTGAGCCTTGGTATGGAACTTACTAAGTGATAACTTTCAAATTCAGAGAAACCTGGA										
pectinata_M120903	TTCGATAGCAGCTAAGTCTAGAGGGAAATTATGAGCACGGACTTAATTGGATTGAGCCTTGGTATGGAACTTACTAAGTGATAACTTTCAAATTCAGAGAAACCTGGA										
pectinata_RM1044	??										
rigida_M280902	TTCGATAGCAGCTAAGTCTAGAGGGAAATTATGAGC??										
rigida_RM840	TTCGATAGCAGCTAAGTCTAGAGGGAAATTATGAGCACGGACTTAATTGGATTGAGCCTTGGTATGGAACTTACTAAGTGATAACTTTCAAATTCAGAGAAACCTGGA										
rigens_leucolaena_RM773	TTCGATAGCAGCTAAGTCTAGAGGGAAATTATGAGC????????TAATTGGATTGAGCCTTGGTATGGAACTTACTAAGTGATAACTTTCAAATTCAGAGAAACCTGGA										
rigens_leucolaena_RM952_1	TTCGATAGCAGCTAAGTCTAGAGGGAAATTATGAGC??										
rigens_rigens_RM763	TTCGATAGCAGCTAAGTCTAGAGGGAAATTATGAGC??										
rigens_rigens_SR463	TTCGATAGCAGCTAAGTCTAGAGGGAAATTATGAGC??										
rigens_uniflora_JC201205	TTCGATAGCAGCTAAGTCTAGAGGGAAATTATGAGCACGGACTTAATTGGATTGAGCCTTGGTATGGAACTTACTAAGTGATAACTTTCAAATTCAGAGAAACCTGGA										
rigens_uniflora_RM920	TTCGATAGCAGCTAAGTCTAGAGGGAAATTATGAGC??										
schenckii	TTCGATAGCAGCTAAGTCTAGAGGGAAATTATGAGCACGGACTTAATTGGATTGAGCCTTGGTATGGAACTTACTAAGTGATAACTTTCAAATTCAGAGAAACCTGGA										
serrata_M250904_15	TTCGATAGCAGCTAAGTCTAGAGGGAAATTATGAGC??										
serrata_RM898	TTCGATAGCAGCTAAGTCTAGAGGGAAATTATGAGCACGGACTTAATTGGATTGAGCCTTGGTATGGAACTTACTAAGTGATAACTTTCAAATTCAGAGAAACCTGGA										
tenuifolia_CAM1601	TTCGATAGCAGCTAAGTCTAGAGGGAAATTATGAG??										
tenuifolia_M2730	TCCGATAGCAGCTAAGTCTAGA??										
spnov_M040906_33	TTCGATAGCAGCTAAGTCTAGAGGGAAATTATGAGCACGGACTTAATTGGATTGAGCCTTGGTATGGAACTTACTAAGTGATAACTTTCAAATTCAGAGAAACCTGGA										

Appendix 5: cpDNA sequence data for Chapter 3

[1550	1560	1570	1580	1590	1600	1610	1620	1630	1640	1650]
Berkheya	ATTAATAAAAAATGGGCAATCCTGAGCCAAATCACGTTTTCCGAAAACAAACAAAGGTTTCAGAAAGCGAAAATCAAAAAGGATAGGTGCAGAGACTCGATGGAAGCTGTTT										
Gorteria	ATTAATAAAAAATGGGCAATCCTGAGCCAAATCACGTTTTCCGAAAACAAACAAAGGTTTCAGAAAGCGAAAATCAAAAAGGATAGGTGCAGAGACTCGATGGAAGCTGTTT										
Hirpicium	ATTAATAAAAAATGGGCGATCCTGAGCCAAATCACGTTTTCCGAAAACAAACAAAGGTTTCAGAAAGCGAAAAAAGGATAGGTGCAGAGACTCGATGGAAGCTGTTT										
caespitosa_RVC448	ATTAATAAAAAATGGGTAATCCTGAGCCAAATCACGTTTTCCGAAAACAAACAAAGGTTTCAGAAAGCGAAAATCAAAAAGGATAGGTGCAGAGACTCGATGGAAGCTGTTT										
caespitosa_RVC307	ATTAATAAAAAATGGGTAATCCTGAGCCAAATCACGTTTTCCGAAAACAAACAAAGGTTTCAGAAAGCGAAAATCAAAAAGGATAGGTGCAGAGACTCGATGGAAGCTGTTT										
ciliaris_RM1230	ATTAATAAAAAATGGGTAATCCTGAGCCAAATCACGTTTTCCGAAAACAAACAAAGGTTTCAGAAAGCGAAAATCAAAAAGGATAGGTGCAGAGACTCGATGGAAGCTGTTT										
ciliaris_RM1382	ATTAATAAAAAATGGGTAATCCTGAGCCAAATCACGTTTTCCGAAAACAAACAAAGGTTTCAGAAAGCGAAAATCAAAAAGGATAGGTGCAGAGACTCGATGGAAGCTGTTT										
heterochaeta_RM1429	ATTAATAAAAAATGGGCAATCCTGAGCCAAATCACGTTTTCCGAAAACAAACAAAGGTTTCAGAAAGCGAAAATCAAAAAGGATAGGTGCAGAGACTCGATGGAAGCTGTTT										
heterochaeta_RM1451	ATTAATAAAAAATGGGCAATCCTGAGCCAAATCACGTTTTCCGAAAACAAACAAAGGTTTCAGAAAGCGAAAATCAAAAAGGATAGGTGCAGAGACTCGATGGAAGCTGTTT										
jurineifolia_jur_SR682	ATTAATAAAAAATGGGCAATCCTGAGCCAAATCACGTTTTCCGAAAACAAACAAAGGTTTCAGAAAGCGAAAATCAAAAAGGATAGGTGCAGAGACTCGATGGAAGCTGTTT										
jurineifolia_jur_RM1518	ATTAATAAAAAATGGGCAATCCTGAGCCAAATCACGTTTTCCGAAAACAAACAAAGGTTTCAGAAAGCGAAAATCAAAAAGGATAGGTGCAGAGACTCGATGGAAGCTGTTT										
jurineifolia_scab_CAM1604	??										
jurineifolia_scab_CAM2652	ATTAATAAAAAATGGGCAATCCTGAGCCAAATCACGTTTTCCGAAAACAAACAAAGGTTTCAGAAAGCGAAAATCAAAAAGGATAGGTGCAGAGACTCGATGGAAGCTGTTT										
krebsiana_arctotoides_RM868	??										
krebsiana_arctotoides_RM876	??										
krebsiana_krebsiana_RM1114	ATTAATAAAAAATGGGCAATCCTGAGCCAAATCACGTTTTCCGAAAACAAACAAAGGTTTCAGAAAGCGAAAATCAAAAAGGATAGGTGCAGAGACTCGATGGAAGCTGTTT										
krebsiana_krebsiana_RM1136	ATTAATAAAAAATGGGCAATCCTGAGCCAAATCACGTTTTCCGAAAACAAACAAAGGTTTCAGAAAGCGAAAATCAAAAAGGATAGGTGCAGAGACTCGATGGAAGCTGTTT										
krebsiana_serrulata_RM863	ATTAATAAAAAATGGGCAATCCTGAGCCAAATCACGTTTTCCGAAAACAAACAAAGGTTTCAGAAAGCGAAAATCAAAAAGGATAGGTGCAGAGACTCGATGGAAGCTGTTT										
krebsiana_serrulata_RM965	ATTAATAAAAAATGGGCAATCCTGAGCCAAATCACGTTTTCCGAAAACAAACAAAGGTTTCAGAAAGCGAAAATCAAAAAGGATAGGTGCAGAGACTCGATGGAAGCTGTTT										
leiopoda_M240901	??AGCCAAATCACGTTTTCCGAAAACAAACAAAGGTTTCAGAAAGCGAAAATCAAAAAGGATAGGTGCAGAGACTCGATGGAAGCTGTTT										
leiopoda_RM1309	ATTAATAAAAAATGGGCAATCCTGAGCCAAATCACGTTTTCCGAAAACAAACAAAGGTTTCAGAAAGCGAAAATCAAAAAGGATAGGTGCAGAGACTCGATGGAAGCTGTTT										
lichtenstenii_CAM1916	ATT-ATAAAAATGGGCAATCCTGAGCCAAATCACGTTTTCCGAAAACAAACAAAGGTTTCAGAAAGCGAAAATCAAAAAGGATAGGTGCAGAGACTCGATGGAAGCTGTTT										
lichtensteini_RM1249	ATTAATAAAAAATGGGCAATCCTGAGCCAAATCACGTTTTCCGAAAACAAACAAAGGTTTCAGAAAGCGAAAATCAAAAAGGATAGGTGCAGAGACTCGATGGAAGCTGTTT										
linearis_linearis_RM1010	ATTAATAAAAAATGGGCAATCCTGAGCCAAATCACGTTTTCCGAAAACAAACAAAGGTTTCAGAAAGCGAAAATCAAAAAGGATAGGTGCAGAGACTCGATGGAAGCTGTTT										
linearis_linearis_SH113	ATTAATAAAAAATGGGCAATCCTGAGCCAAATCACGTTTTCCGAAAACAAACAAAGGTTTCAGAAAGCGAAAATCAAAAAGGATAGGTGCAGAGACTCGATGGAAGCTGTTT										
linearis_ovalis_NDsn	ATTAATAAAAAATGGGCAATCCTGAGCCAAATCACGTTTTCCGAAAACAAACAAAGGTTTCAGAAAGCGAAAATCAAAAAGGATAGGTGCAGAGACTCGATGGAAGCTGTTT										
linearis_ovalis_RM854	??										
maritima_RM1038	ATTAATAAAAAATGGGCAATCCTGAGCCAAATCACGTTTTCCGAAAACAAACAAAGGTTTCAGAAAGCGAAAATCAAAAAGGATAGGTGCAGAGACTCGATGGAAGCTGTTT										
maritima_M290606_6	ATTAATAAAAAATGGGCAATCCTGAGCCAAATCACGTTTTCCGAAAACAAACAAAGGTTTCAGAAAGCGAAAATCAAAAAGGATAGGTGCAGAGACTCGATGGAAGCTGTTT										
othonnites_RM1306	ATTAATAAAAAATGGGCAATCCTGAGCCAAATCACGTTTTCCGAAAACAAACAAAGGTTTCAGAAAGCGAAAATCAAAAAGGATAGGTGCAGAGACTCGATGGAAGCTGTTT										
pectinata_M120903	ATTAATAAAAAATGGGCAATCCTGAGCCAAATCACGTTTTCCGAAAACAAACAAAGGTTTCAGAAAGCGAAAATCAAAAAGGATAGGTGCAGAGACTCGATGGAAGCTGTTT										
pectinata_RM1044	??										
rigida_M280902	ATTAATAAAAAATGGGCAATCCTGAGCCAAATCACGTTTTCCGAAAACAAACAAAGGTTTCAGAAAGCGAAAATCAAAAAGGATAGGTGCAGAGACTCGATGGAAGCTGTTT										
rigida_RM840	ATTAATAAAAAATGGGCAATCCTGAGCCAAATCACGTTTTCCGAAAACAAACAAAGGTTTCAGAAAGCGAAAATCAAAAAGGATAGGTGCAGAGACTCGATGGAAGCTGTTT										
rigens_leucolaena_RM773	ATTAATAAAAAATGGGCAATCCTGAGCCAAATCACGTTTTCCGAAAACAAACAAAGGTTTCAGAAAGCGAAAATCAAAAAGGATAGGTGCAGAGACTCGATGGAAGCTGTTT										
rigens_leucolaena_RM952_1	ATTAATAAAAAATGGGCAATCCTGAGCCAAATCACGTTTTCCGAAAACAAACAAAGGTTTCAGAAAGCGAAAATCAAAAAGGATAGGTGCAGAGACTCGATGGAAGCTGTTT										
rigens_rigens_RM763	??										
rigens_rigens_SR463	ATTAATAAAAAATGGGCAATCCTGAGCCAAATCACGTTTTCCGAAAACAAACAAAGGTTTCAGAAAGCGAAAATCAAAAAGGATAGGTGCAGAGACTCGATGGAAGCTGTTT										
rigens_uniflora_JC201205	ATTAATAAAAAATGGGCAATCCTGAGCCAAATCACGTTTTCCGAAAACAAACAAAGGTTTCAGAAAGCGAAAATCAAAAAGGATAGGTGCAGAGACTCGATGGAAGCTGTTT										
rigens_uniflora_RM920	??										
schenckii	ATTAATAAAAAATGGGCAATCCTGAGCCAAATCACGTTTTCCGAAAACAAACAAAGGTTTCAGAAAGCGAAAATCAAAAAGGATAGGTGCAGAGACTCGATGGAAGCTGTTT										
serrata_M250904_15	??GGCAATCCTGAGCCAAATCACGTTTTCCGAAAACAAACAAAGGTTTCAGAAAGCGAAAATCAAAAAGGATAGGTGCAGAGACTCGATGGAAGCTGTTT										
serrata_RM898	ATTAATAAAAAATGGGCAATCCTGAGCCAAATCACGTTTTCCGAAAACAAACAAAGGTTTCAGAAAGCGAAAATCAAAAAGGATAGGTGCAGAGACTCGATGGAAGCTGTTT										
tenuifolia_CAM1601	ATTAATAAAAAATGGGCAATCCTGAGCCAAATCACGTTTTCCGAAAACAAACAAAGGTTTCAGAAAGCGAAAATCAAAAAGGATAGGTGCAGAGACTCGATGGAAGCTGTTT										
tenuifolia_M2730	ATT-ATAAAAATGGGCAATCCTGAGCCAAATCACGTTTTCCGTAACAAACAAAGGTTTCAGAAAGCGAAAATCAAAAAGGATAGGTGCAGAGACTCGATGGAAGCTGTTT										
spnov_M040906_33	ATTAATAAAAAATGGGCAATCCTGAGCCAAATCACGTTTTCCGAAAACAAACAAAGGTTTCAGAAAGCGAAAATCAAAAAGGATAGGTGCAGAGACTCGATGGAAGCTGTTT										

Appendix 5: cpDNA sequence data for Chapter 3

	1660	1670	1680	1690	1700	1710	1720	1730	1740	1750	1760]	
Berkheya	T	A	A	C	G	A	A	T	G	G	A	A
Gorteria	T	A	A	C	G	A	A	T	G	G	A	A
Hirpicium	T	A	A	C	G	A	A	T	G	G	A	A
caespitosa_RVC448	T	A	A	C	G	A	A	T	G	G	A	A
caespitosa_RVC307	T	A	A	C	G	A	A	T	G	G	A	A
ciliaris_RM1230	T	A	A	C	G	A	A	T	G	G	A	A
ciliaris_RM1382	T	A	A	C	G	A	A	T	G	G	A	A
heterochaeta_RM1429	T	A	A	C	G	A	A	T	G	G	A	A
heterochaeta_RM1451	T	A	A	C	G	A	A	T	G	G	A	A
jurineifolia_jur_SR682	T	A	A	C	G	A	A	T	G	G	A	A
jurineifolia_jur_RM1518	T	A	A	C	G	A	A	T	G	G	A	A
jurineifolia_scab_CAM1604	T	A	A	C	G	A	A	T	G	G	A	A
jurineifolia_scab_CAM2652	T	A	A	C	G	A	A	T	G	G	A	A
krebsiana_arctotoides_RM868	T	A	A	C	G	A	A	T	G	G	A	A
krebsiana_arctotoides_RM876	T	A	A	C	G	A	A	T	G	G	A	A
krebsiana_krebsiana_RM1114	T	A	A	C	G	A	A	T	G	G	A	A
krebsiana_krebsiana_RM1136	T	A	A	C	G	A	A	T	G	G	A	A
krebsiana_serrulata_RM863	T	A	A	C	G	A	A	T	G	G	A	A
krebsiana_serrulata_RM965	T	A	A	C	G	A	A	T	G	G	A	A
leiopoda_M240901	T	A	A	C	G	A	A	T	G	G	A	A
leiopoda_RM1309	T	A	A	C	G	A	A	T	G	G	A	A
lichtenstenii_CAM1916	T	A	A	C	G	A	A	T	G	G	A	A
lichtensteini_RM1249	T	A	A	C	G	A	A	T	G	G	A	A
linearis_linearis_RM1010	T	A	A	C	G	A	A	T	G	G	A	A
linearis_linearis_SH113	T	A	A	C	G	A	A	T	G	G	A	A
linearis_ovalis_NDsn	T	A	A	C	G	A	A	T	G	G	A	A
linearis_ovalis_RM854	T	A	A	C	G	A	A	T	G	G	A	A
maritima_RM1038	T	A	A	C	G	A	A	T	G	G	A	A
maritima_M290606_6	T	A	A	C	G	A	A	T	G	G	A	A
othonnites_RM1306	T	A	A	C	G	A	A	T	G	G	A	A
pectinata_M120903	T	A	A	C	G	A	A	T	G	G	A	A
pectinata_RM1044	T	A	A	C	G	A	A	T	G	G	A	A
rigida_M280902	T	A	A	C	G	A	A	T	G	G	A	A
rigida_RM840	T	A	A	C	G	A	A	T	G	G	A	A
rigens_leucolaena_RM773	T	A	A	C	G	A	A	T	G	G	A	A
rigens_leucolaena_RM952_1	T	A	A	C	G	A	A	T	G	G	A	A
rigens_rigens_RM763	T	A	A	C	G	A	A	T	G	G	A	A
rigens_rigens_SR463	T	A	A	C	G	A	A	T	G	G	A	A
rigens_uniflora_JC201205	T	A	A	C	G	A	A	T	G	G	A	A
rigens_uniflora_RM920	T	A	A	C	G	A	A	T	G	G	A	A
schenckii	T	A	A	C	G	A	A	T	G	G	A	A
serrata_M250904_15	T	A	A	C	G	A	A	T	G	G	A	A
serrata_RM898	T	A	A	C	G	A	A	T	G	G	A	A
tenuifolia_CAM1601	T	A	A	C	G	A	A	T	G	G	A	A
tenuifolia_M2730	T	A	A	C	G	A	A	T	G	G	A	A
spnov_M040906_33	T	A	A	C	G	A	A	T	G	G	A	A

Appendix 5: cpDNA sequence data for Chapter 3

[1770	1780	1790	1800	1810	1820	1830	1840	1850	1860	1870]
Berkheya	GATTTCCATATTGAAGAAAGAATCGAATATTCATTGATCAAACC-----ATTCCTCCATAATCTGATAGATCTTTTGAAGAACTGATTAATCGGACGAGAATAAAGAT										
Gorteria	GATTTCCATATTGAAGAAAGAATCGAATATTCATTGATCAAACC-----ATTCCTCCATAATCTGATAGATCTTTTGAAGAACTGATTAATCGGACGAGAATAAAGAT										
Hirpicium	GATTTCCATATTGAAGAAAGAATCGAATATTCATTGATCAAACC-----ATTCCTCCATAATCTGATAGATCTTTTGAAGAACTGATTAATCGGACGAGAATAAAGAT										
caespitosa_RVC448	GATTTCCATATTGAAGAAAGAATCGAATATTCATTGATCAAACC-----ATTCCTCCATAATCTGATAGATCTTTTGAAGAACTGATTAATCGGACGAGAATAAAGAT										
caespitosa_RVC307	GATTTCCATATTGAAGAAAGAATCGAATATTCATTGATCAAACC-----ATTCCTCCATAATCTGATAGATCTTTTGAAGAACTGATTAATCGGACGAGAATAAAGAT										
ciliaris_RM1230	GATTTCCATATTGAAGAAAGAATCGAATATTCATTGATCAAACC-----ATTCCTCCATAATCTGATAGATCTTTTGAAGAACTGATTAATCGGACGAGAATAAAGAT										
ciliaris_RM1382	GATTTCCATATTGAAGAAAGAATCGAATATTCATTGATCAAACC-----ATTCCTCCATAATCTGATAGATCTTTTGAAGAACTGATTAATCGGACGAGAATAAAGAT										
heterochaeta_RM1429	GATTTCCATATTGAAGAAAGAATCGAATATTCATTGATCAAACC-----ATTCCTCCATAATCTGATAGATCTTTTGAAGAACTGATTAATCGGACGAGAATAAAGAT										
heterochaeta_RM1451	GATTTCCATATTGAAGAAAGAATCGAATATTCATTGATCAAACC-----ATTCCTCCATAATCTGATAGATCTTTTGAAGAACTGATTAATCGGACGAGAATAAAGAT										
jurineifolia_jur_SR682	GATTTCCATATTGAAGAAAGAATCGAATATTCATTGATCAAACC-----ATTCCTCCATAATCTGATAGATCTTTTGAAGAACTGATTAATCGGACGAGAATAAAGAT										
jurineifoliajur_RM1518	GATTTCCATATTGAAGAAAGAATCGAATATTCATTGATCAAACC-----ATTCCTCCATAATCTGATAGATCTTTTGAAGAACTGATTAATCGGACGAGAATAAAGAT										
jurineifolia_scab_CAM1604	GATTTCCATATTGAAGAAAGAATCGAATATTCATTGATCAAACC-----ATTCCTCCATAATCTGATAGATCTTTTGAAGAACTGATTAATCGGACGAGAATAAAGAT										
jurineifolia_scab_CAM2652	GATTTCCATATTGAAGAAAGAATCGAATATTCATTGATCAAACC-----ATTCCTCCATAATCTGATAGATCTTTTGAAGAACTGATTAATCGGACGAGAATAAAGAT										
krebsiana_arctotoides_RM868	GATTTCCATATTGAAGAAAGAATCGAATATTCATTGATCAAACC-----ATTCCTCCATAATCTGATAGATCTTTTGAAGAACTGATTAATCGGACGAGAATAAAGAT										
krebsiana_arctotoides_RM876	GATTTCCATATTGAAGAAAGAATCGAATATTCATTGATCAAACC-----ATTCCTCCATAATCTGATAGATCTTTTGAAGAACTGATTAATCGGACGAGAATAAAGAT										
krebsiana_krebsiana_RM1114	GATTTCCATATTGAAGAAAGAATCGAATATTCATTGATCAAACC-----ATTCCTCCATAATCTGATAGATCTTTTGAAGAACTGATTAATCGGACGAGAATAAAGAT										
krebsiana_krebsiana_RM1136	GATTTCCATATTGAAGAAAGAATCGAATATTCATTGATCAAACC-----ATTCCTCCATAATCTGATAGATCTTTTGAAGAACTGATTAATCGGACGAGAATAAAGAT										
krebsiana_serrulata_RM863	GATTTCCATATTGAAGAAAGAATCGAATATTCATTGATCAAACC-----ATTCCTCCATAATCTGATAGATCTTTTGAAGAACTGATTAATCGGACGAGAATAAAGAT										
krebsiana_serrulata_RM965	GATTTCCATATTGAAGAAAGAATCGAATATTCATTGATCAAACC-----ATTCCTCCATAATCTGATAGATCTTTTGAAGAACTGATTAATCGGACGAGAATAAAGAT										
leiopoda_M240901	GATTTCCATATTGAAGAAAGAATCGAATATTCATTGATCAAACC-----ATTCCTCCATAATCTGATAGATCTTTTGAAGAACTGATTAATCGGACGAGAATAAAGAT										
leiopoda_RM1309	GATTTCCATATTGAAGAAAGAATCGAATATTCATTGATCAAACC-----ATTCCTCCATAATCTGATAGATCTTTTGAAGAACTGATTAATCGGACGAGAATAAAGAT										
lichtenstenii_CAM1916	GATTTCCATATTGAAGAAAGAATCGAATATTCATTGATCAAACC-----ATTCCTCCATAATCTGATAGATCTTTTGAAGAACTGATTAATCGGACGAGAATAAAGAT										
lichtensteini_RM1249	GATTTCCATATTGAAGAAAGAATCGAATATTCATTGATCAAACC-----ATTCCTCCATAATCTGATAGATCTTTTGAAGAACTGATTAATCGGACGAGAATAAAGAT										
linearis_linearis_RM1010	GATTTCCATATTGAAGAAAGAATCGAATATTCATTGATCAAACC-----ATTCCTCCATAATCTGATAGATCTTTTGAAGAACTGATTAATCGGACGAGAATAAAGAT										
linearis_linearis_SH113	GATTTCCATATTGAAGAAAGAATCGAATATTCATTGATCAAACC-----ATTCCTCCATAATCTGATAGATCTTTTGAAGAACTGATTAATCGGACGAGAATAAAGAT										
linearis_ovalis_NDsn	GATTTCCATATTGAAGAAAGAATCGAATATTCATTGATCAAACC-----ATTCCTCCATAATCTGATAGATCTTTTGAAGAACTGATTAATCGGACGAGAATAAAGAT										
linearis_ovalis_RM854	GATTTCCATATTGAAGAAAGAATCGAATATTCATTGATCAAACC-----ATTCCTCCATAATCTGATAGATCTTTTGAAGAACTGATTAATCGGACGAGAATAAAGAT										
maritima_RM1038	GATTTCCATATTGAAGAAAGAATCGAATATTCATTGATCAAACC-----ATTCCTCCATAATCTGATAGATCTTTTGAAGAACTGATTAATCGGACGAGAATAAAGAT										
maritima_M290606_6	GATTTCCATATTGAAGAAAGAATCGAATATTCATTGATCAAACC-----ATTCCTCCATAATCTGATAGATCTTTTGAAGAACTGATTAATCGGACGAGAATAAAGAT										
othonnites_RM1306	GATTTCCATATTGAAGAAAGAATCGAATATTCATTGATCAAACC-----ATTCCTCCATAATCTGATAGATCTTTTGAAGAACTGATTAATCGGACGAGAATAAAGAT										
pectinata_M120903	GATTTCCATATTGAAGAAAGAATCGAATATTCATTGATCAAACC-----ATTCCTCCATAATCTGATAGATCTTTTGAAGAACTGATTAATCGGACGAGAATAAAGAT										
pectinata_RM1044	GATTTCCATATTGAAGAAAGAATCGAATATTCATTGATCAAACC-----ATTCCTCCATAATCTGATAGATCTTTTGAAGAACTGATTAATCGGACGAGAATAAAGAT										
rigida_M280902	GATTTCCATATTGAAGAAAGAATCGAATATTCATTGATCAAACC-----ATTCCTCCATAATCTGATAGATCTTTTGAAGAACTGATTAATCGGACGAGAATAAAGAT										
rigida_RM840	GATTTCCATATTGAAGAAAGAATCGAATATTCATTGATCAAACC-----ATTCCTCCATAATCTGATAGATCTTTTGAAGAACTGATTAATCGGACGAGAATAAAGAT										
rigens_leucolaena_RM773	GATTTCCATATTGAAGAAAGAATCGAATATTCATTGATCAAACC-----ATTCCTCCATAATCTGATAGATCTTTTGAAGAACTGATTAATCGGACGAGAATAAAGAT										
rigens_leucolaena_RM952_1	GATTTCCATATTGAAGAAAGAATCGAATATTCATTGATCAAACC-----ATTCCTCCATAATCTGATAGATCTTTTGAAGAACTGATTAATCGGACGAGAATAAAGAT										
rigens_rigens_RM763	GATTTCCATATTGAAGAAAGAATCGAATATTCATTGATCAAACC-----ATTCCTCCATAATCTGATAGATCTTTTGAAGAACTGATTAATCGGACGAGAATAAAGAT										
rigens_rigens_SR463	GATTTCCATATTGAAGAAAGAATCGAATATTCATTGATCAAACC-----ATTCCTCCATAATCTGATAGATCTTTTGAAGAACTGATTAATCGGACGAGAATAAAGAT										
rigens_uniflora_JC201205	GATTTCCATATTGAAGAAAGAATCGAATATTCATTGATCAAACC-----ATTCCTCCATAATCTGATAGATCTTTTGAAGAACTGATTAATCGGACGAGAATAAAGAT										
rigens_uniflora_RM920	GATTTCCATATTGAAGAAAGAATCGAATATTCATTGATCAAACC-----ATTCCTCCATAATCTGATAGATCTTTTGAAGAACTGATTAATCGGACGAGAATAAAGAT										
schenckii	GATTTCCATATTGAAGAAAGAATCGAATATTCATTGATCAAACC-----ATTCCTCCATAATCTGATAGATCTTTTGAAGAACTGATTAATCGGACGAGAATAAAGAT										
serrata_M250904_15	GATTTCCATATTGAAGAAAGAATCGAATATTCATTGATCAAACC-----ATTCCTCCATAATCTGATAGATCTTTTGAAGAACTGATTAATCGGACGAGAATAAAGAT										
serrata_RM898	GATTTCCATATTGAAGAAAGAATCGAATATTCATTGATCAAACC-----ATTCCTCCATAATCTGATAGATCTTTTGAAGAACTGATTAATCGGACGAGAATAAAGAT										
tenuifolia_CAM1601	GATTTCCATATTGAAGAAAGAATCGAATATTCATTGATCAAACC-----ATTCCTCCATAATCTGATAGATCTTTTGAAGAACTGATTAATCGGACGAGAATAAAGAT										
tenuifolia_M2730	GATTTCCATATTGAAGAAAGAATCGAATATTCATTGATCAAACC-----ATTCCTCCATAATCTGATAGATCTTTTGAAGAACTGATTAATCGGACGAGAATAAAGAT										
spnov_M040906_33	GATTTCCATATTGAAGAAAGAATCGAATATTCATTGATCAAACC-----ATTCCTCCATAATCTGATAGATCTTTTGAAGAACTGATTAATCGGACGAGAATAAAGAT										

Appendix 5: cpDNA sequence data for Chapter 3

	1880	1890	1900	1910	1920	1930	1940	1950	trnL < >	trnL-F	1960	1970	1980
Berkheya	AGAGT	CCT	-GTTCTACATGTCAATACCGGCAACAATGAAATTTATAGTAAGAAGAAAATCCGTCGATTTCAAAAATCGTGAGGGTTCAAGTCCCTCTATCCCCAAAAAGA										
Gorteria	AGAGT	CCC	-GTTCTACATGTCAATACCGGCAACAATGAAATTTATAGTAAGAAGAAAATCCGTCGATTTCAAAAATCGGGAGGGTTCAAGTCCCTCTATCCCCAAAAAGA										
Hirpicium	AGAGT	CCT	-GTTCTACATGTCAATACCGGCAACAATGAAATTTATAGTAAGAAGAAAATCCGTCGATTTCAAAAATCGTGAGGGTTCAAGTCCCTCTATCCCCAAAAAGA										
caespitosa_RVC448	AGAGT	CCC	-GTTCTACATGTCAATACCGGCAACAATGAAATTTATAGTAAGAAGAAAATCCGTCGATTTCAAAAATCGTGAGGGTTCAAGTCCCTCTATCCCCAAAAAGA										
caespitosa_RVC307	AGAGT	CCC	-GTTCTACATGTCAATACCGGCAACAATGAAATTTATAGTAAGAAGAAAATCCGTCGATTTCAAAAATCGTGAGGGTTCAAGTCCCTCTATCCCCAAAAAGA										
ciliaris_RM1230	AGAGT	CCC	-GTTCTACATGTCAATACCGGCAACAATGAAATTTATAGTAAGAAGAAAATCCGTCGATTTCAAAAATCGTGAGGGTTCAAGTCCCTCTATCCCCAAAAAGA										
ciliaris_RM1382	AGAGT	CCC	-GTTCTACATGTCAATACCGGCAACAATGAAATTTATAGTAAGAAGAAAATCCGTCGATTTCAAAAATCGTGAGGGTTCAAGTCCCTCTATCCCCAAAAAGA										
heterochaeta_RM1429	AGAGT	CCC	-GTTCTACATGTCAATACCGGCAACAATGAAATTTATAGTAAGAAGAAAATCCGTCGATTTCAAAAATCGTGAGGGTTCAAGTCCCTCTATCCCCAAAAAGA										
heterochaeta_RM1451	AGAGT	CCC	-GTTCTACATGTCAATACCGGCAACAATGAAATTTATAGTAAGAAGAAAATCCGTCGATTTCAAAAATCGTGAGGGTTCAAGTCCCTCTATCCCCAAAAAGA										
jurineifolia_jur_SR682	AGAGT	CCC	-GTTCTACATGTCAATACCGGCAACAATGAAATTTATAGTAAGAAGAAAATCCGTCGATTTCAAAAATCGTGAGGGTTCAAGTCCCTCTATCCCCAAAAAGA										
jurineifoliajur_RM1518	AGAGT	CCC	-GTTCTACATGTCAATACCGGCAACAATGAAATTTATAGTAAGAAGAAAATCCGTCGATTTCAAAAATCGTGAGGGTTCAAGTCCCTCTATCCCCAAAAAGA										
jurineifolia_scab_CAM1604	AGAGT	CCC	-GTTCTACATGTCAATACCGGCAACAATGAAATTTATAGTAAGAAGAAAATCCGTCGATTTCAAAAATCGTGAGGGTTCAAGTCCCTCTATCCCCAAAAAGA										
jurineifolia_scab_CAM2652	AGAGT	CCC	-GTTCTACATGTCAATACCGGCAACAATGAAATTTATAGTAAGAAGAAAATCCGTCGATTTCAAAAATCGTGAGGGTTCAAGTCCCTCTATCCCCAAAAAGA										
krebsiana_arctotoides_RM868	AGAGT	CCC	-GTTCTACATGTCAATACCGGCAACAATGAAATTTATAGTAAGAAGAAAATCCGTCGATTTCAAAAATCGTGAGGGTTCAAGTCCCTCTATCCCCAAAAAGA										
krebsiana_arctotoides_RM876	AGAGT	CCC	-GTTCTACATGTCAATACCGGCAACAATGAAATTTATAGTAAGAAGAAAATCCGTCGATTTCAAAAATCGTGAGGGTTCAAGTCCCTCTATCCCCAAAAAGA										
krebsiana_krebsiana_RM1114	AGAGT	CCC	-GTTCTACATGTCAATACCGGCAACAATGAAATTTATAGTAAGAAGAAAATCCGTCGATTTCAAAAATCGTGAGGGTTCAAGTCCCTCTATCCCCAAAAAGA										
krebsiana_krebsiana_RM1136	AGAGT	CCC	-GTTCTACATGTCAATACCGGCAACAATGAAATTTATAGTAAGAAGAAAATCCGTCGATTTCAAAAATCGTGAGGGTTCAAGTCCCTCTATCCCCAAAAAGA										
krebsiana_serrulata_RM863	AGAGT	CCC	-GTTCTACATGTCAATACCGGCAACAATGAAATTTATAGTAAGAAGAAAATCCGTCGATTTCAAAAATCGTGAGGGTTCAAGTCCCTCTATCCCCAAAAAGA										
krebsiana_serrulata_RM965	AGAGT	CCC	-GTTCTACATGTCAATACCGGCAACAATGAAATTTATAGTAAGAAGAAAATCCGTCGATTTCAAAAATCGTGAGGGTTCAAGTCCCTCTATCCCCAAAAAGA										
leiopoda_M240901	AGAGT	CCC	-GTTCTACATGTCAATACCGGCAACAATGAAATTTATAGTAAGAAGAAAATCCGTCGATTTCAAAAATCGTGAGGGTTCAAGTCCCTCTATCCCCAAAAAGA										
leiopoda_RM1309	AGAGT	CCCCCGTT	CATGTCAATACCGGCAACAATGAAATTTATAGTAAGAAGAAAATCCGTCGATTTCAAAAATCGTGAGGGTTCAAGTCCCTCTATCCCCAAAAAGA										
lichtenstenii_CAM1916	AGAGT	CCC	-GTTCTACATGTCAATACCGGCAACAATGAAATTTATAGTAAGAAGAAAATCCGTCGATTTCAAAAATCGTGAGGGTTCAAGTCCCTCTATCCCCAAAAAGA										
lichtensteini_RM1249	AGAGT	CCC	-GTTCTACATGTCAATACCGGCAACAATGAAATTTATAGTAAGAAGAAAATCCGTCGATTTCAAAAATCGTGAGGGTTCAAGTCCCTCTATCCCCAAAAAGA										
linearis_linearis_RM1010	AGAGT	CCC	-GTTCTACATGTCAATACCGGCAACAATGAAATTTATAGTAAGAAGAAAATCCGTCGATTTCAAAAATCGTGAGGGTTCAAGTCCCTCTATCCCCAAAAAGA										
linearis_linearis_SH113	AGAGT	CCC	-GTTCTACATGTCAATACCGGCAACAATGAAATTTATAGTAAGAAGAAAATCCGTCGATTTCAAAAATCGTGAGGGTTCAAGTCCCTCTATCCCCAAAAAGA										
linearis_ovalis_NDsn	AGAGT	CCC	-GTTCTACATGTCAATACCGGCAACAATGAAATTTATAGTAAGAAGAAAATCCGTCGATTTCAAAAATCGGGAGGGTTCAAGTCCCTCTATCCCCAAAAAGA										
linearis_ovalis_RM854	AGAGT	CCC	-GTTCTACATGTCAATACCGGCAACAATGAAATTTATAGTAAGAAGAAAATCCGTCGATTTCAAAAATCGTGAGGGTTCAAGTCCCTCTATCCCCAAAAAGA										
maritima_RM1038	AGAGT	CCC	-GTTCTACATGTCAATACCGGCAACAATGAAATTTATAGTAAGAAGAAAATCCGTCGATTTCAAAAATCGTGAGGGTTCAAGTCCCTCTATCCCCAAAAAGA										
maritima_M290606_6	AGAGT	CCC	-GTTCTACATGTCAATACCGGCAACAATGAAATTTATAGTAAGAAGAAAATCCGTCGATTTCAAAAATCGTGAGGGTTCAAGTCCCTCTATCCCCAAAAAGA										
othonnites_RM1306	AGAGT	CCC	-GTTCTACATGTCAATACCGGCAACAATGAAATTTATAGTAAGAAGAAAATCCGTTGATTTCAAAAATCGTGAGGGTTCAAGTCCCTCTATCCCCAAAAAGA										
pectinata_M120903	AGAGT	CCC	-GTTCTACATGTCAATACCGGCAACAATGAAATTTATAGTAAGAAGAAAATCCGTCGATTTCAAAAATCGTGAGGGTTCAAGTCCCTCTATCCCCAAAAAGA										
pectinata_RM1044	AGAGT	CCC	-GTTCTACATGTCAATACCGGCAACAATGAAATTTATAGTAAGAAGAAAATCCGTCGATTTCAAAAATCGTGAGGGTTCAAGTCCCTCTATCCCCAAAAAGA										
rigida_M280902	AGAGT	CCC	-GTTCTACATGTCAATACCGGCAACAATGAAATTTATAGTAAGAAGAAAATCCGTCGATTTCAAAAATCGTGAGGGTTCAAGTCCCTCTATCCCCAAAAAGA										
rigida_RM840	AGAGT	CCC	-GTTCTACATGTCAATACCGGCAACAATGAAATTTATAGTAAGAAGAAAATCCGTCGATTTCAAAAATCGTGAGGGTTCAAGTCCCTCTATCCCCAAAAAGA										
rigens_leucolaena_RM773	AGAGT	CCC	-GTTCTACATGTCAATACCGGCAACAATGAAATTTATAGTAAGAAGAAAATCCGTCGATTTCAAAAATCGTGAGGGTTCAAGTCCCTCTATCCCCAAAAAGA										
rigens_leucolaena_RM952_1	AGAGT	CCC	-GTTCTACATGTCAATACCGGCAACAATGAAATTTATAGTAAGAAGAAAATCCGTCGATTTCAAAAATCGTGAGGGTTCAAGTCCCTCTATCCCCAAAAAGA										
rigens_rigens_RM763	AGAGT	CCC	-GTTCTACATGTCAATACCGGCAACAATGAAATTTATAGTAAGAAGAAAATCCGTCGATTTCAAAAATCGTGAGGGTTCAAGTCCCTCTATCCCCAAAAAGA										
rigens_rigens_SR463	AGAGT	CCC	-GTTCTACATGTCAATACCGGCAACAATGAAATTTATAGTAAGAAGAAAATCCGTCGATTTCAAAAATCGTGAGGGTTCAAGTCCCTCTATCCCCAAAAAGA										
rigens_uniflora_JC201205	AGAGT	CCC	-GTTCTACATGTCAATACCGGCAACAATGAAATTTATAGTAAGAAGAAAATCCGTCGATTTCAAAAATCGTGAGGGTTCAAGTCCCTCTATCCCCAAAAAGA										
rigens_uniflora_RM920	AGAGT	CCC	-GTTCTACATGTCAATACCGGCAACAATGAAATTTATAGTAAGAAGAAAATCCGTCGATTTCAAAAATCGTGAGGGTTCAAGTCCCTCTATCCCCAAAAAGA										
schenckii	AGAGT	CCC	-GTTCTACATGTCAATACCGGCAACAATGAAATTTATAGTAAGAAGAAAATCCGTCGATTTCAAAAATCGTGAGGGTTCAAGTCCCTCTATCCCCAAAAAGA										
serrata_M250904_15	AGAGT	CCC	-GTTCTACATGTCAATACCGGCAACAATGAAATTTATAGTAAGAAGAAAATCCGTCGATTTCAAAAATCGTGAGGGTTCAAGTCCCTCTATCCCCAAAAAGA										
serrata_RM898	AGAGT	CCC	-GTTCTACATGTCAATACCGGCAACAATGAAATTTATAGTAAGAAGAAAATCCGTCGATTTCAAAAATCGTGAGGGTTCAAGTCCCTCTATCCCCAAAAAGA										
tenuifolia_CAM1601	AGAGT	CCC	-GTTCTACATGTCAATACCGGCAACAATGAAATTTATAGTAAGAAGAAAATCCGTCGATTTCAAAAATCGTGAGGGTTCAAGTCCCTCTATCCCCAAAAAGA										
tenuifolia_M2730	AGAGT	CCC	-GTTCTACATGTCAATACCGGCAACAATGAAATTTATAGTAAGAAGAAAATCCGTCGATTTCAAAAATCGTGAGGGTTCAAGTCCCTCTATCCCCAAAAAGA										
spnov_M040906_33	AGAGT	CCC	-GTTCTACATGTCAATACCGGCAACAATGAAATTTATAGTAAGAAGAAAATCCGTTGATTTCAAAAATCGTGAGGGTTCAAGTCCCTCTATCCCCANNNNNN										

Appendix 5: cpDNA sequence data for Chapter 3

	1990	2000	2010	2020	2030	2040	2050	2060	2070	2080	2090
Berkheya	GCTTTCGGCTCCTTATCGTATCCTTTTT	-----	TCGTTAGCGGTTCAA	AAC	TCCTTATCTTTCTCATTCACTACTCTTTTATACAAATGAATCTGGGCGGAA						
Gorteria	GCTTTCGGCTCCTTATCGTATCCTTTTT	ATTTATCCTTTTT	TCGTTAGCGGTTCAA	AAC	TCCTTATCTTTCTCATTCACTACTCTTTTATACAAATGGATCTGAGCGGAA						
Hirpicium	GCTTTCGGCTCCTTATCGTATCCTTTTT	ATTTATCCTTTTT	CGTTAGCGGTTCAA	AAC	-----	TTCTCATTCACTACTCTTTTATACAAATGGATCTGAGCGGAA					
caespitosa_RVC448	GCTTTCGGCTCCTTATCGTATCCTTTTT	ATTTATCCTTTTT	TCGTTAGCGGTTCAA	AAC	TCCTTATCTTTCTCATTCACTACTCTTTTATACAAATGGATCTGAGCGGAA						
caespitosa_RVC307	GCTTTCGGCTCCTTATCGTATCCTTTTT	ATTTATCCTTTTT	TCGTTAGCGGTTCAA	AAC	TCCTTATCTTTCTCATTCACTACTCTTTTATACAAATGGATCTGAGCGGAA						
ciliaris_RM1230	???????????	TATCGTATCCTTTTT	ATTTATCCTTTTT	TCGTTAGCGGTTCAA	AAC	-----	CTCCTTATCTTTCTCATTCACTACTCTTTTATACAAATGGATCTGAGCGGAA				
ciliaris_RM1382	???????????	TTTCGGCTCCTTATCGTATCCTTTTT	ATTTATCCTTTTT	TCGTTAGCGGTTCAA	AAC	TCCTTATCTTTCTCATTCACTACTCTTTTATACAAATGGATCTGAGCGGAA					
heterochaeta_RM1429	GCTTTCGGCTCCTTATCGTATCCTTTTT	ATTTATCCTTTTT	TCGTTAGCGGTTCAA	AAC	TCCTTATCTTTCTCATTCACTACTCTTTTATACAAATGGATCTGAGCGGAA						
heterochaeta_RM1451	GCTTTCGGCTCCTTATCGTATCCTTTTT	ATTTATCCTTTTT	TCGTTAGCGGTTCAA	AAC	TCCTTATCTTTCTCATTCACTACTCTTTTATACAAATGGATCTGAGCGGAA						
jurineifolia_jur_SR682	GCTTTCGGCTCCTTATCGTATCCTTTTT	ATTTATCCTTTTT	TCGTTAGCGGTTCAA	AAC	TCCTTATCTTTCTCATTCACTACTCTTTTATACAAATGGATCTGAGCGGAA						
jurineifolia_jur_RM1518	GCTTTCGGCTCCTTATCGTATCCTTTTT	ATTTATCCTTTTT	TCGTTAGCGGTTCAA	AAC	TCCTTATCTTTCTCATTCACTACTCTTTTATACAAATGGATCTGAGCGGAA						
jurineifolia_scab_CAM1604	GCTTTCGGCTCCTTATCGTATCCTTTTT	ATTTATCCTTTTT	TCGTTAGCGGTTCAA	AAC	TCCTTATCTTTCTCATTCACTACTCTTTTATACAAATGGATCTGAGCGGAA						
jurineifolia_scab_CAM2652	GCTTTCGGCTCCTTATCGTATCCTTTTT	ATTTATCCTTTTT	TCGTTAGCGGTTCAA	AAC	TCCTTATCTTTCTCATTCACTACTCTTTTATACAAATGGATCTGAGCGGAA						
krebsiana_arctotoides_RM868	GCTTTCGGCTCCTTATCGTATCCTTTTT	ATTTATCCTTTTT	TCGTTAGCGGTTCAA	AAC	TCCTTATCTTTCTCATTCACTACTCTTTTATACAAATGGATCTGAGCGGAA						
krebsiana_arctotoides_RM876	GCTTTCGGCTCCTTATCGTATCCTTTTT	ATTTATCCTTTTT	TCGTTAGCGGTTCAA	AAC	TCCTTATCTTTCTCATTCACTACTCTTTTATACAAATGGATCTGAGCGGAA						
krebsiana_krebsiana_RM1114	GCTTTCGGCTCCTTATCGTATCCTTTTT	ATTTATCCTTTTT	TCGTTAGCGGTTCAA	AAC	TCCTTATCTTTCTCATTCACTACTCTTTTATACAAATGGATCTGAGCGGAA						
krebsiana_krebsiana_RM1136	GCTTTCGGCTCCTTATCGTATCCTTTTT	ATTTATCCTTTTT	TCGTTAGCGGTTCAA	AAC	TCCTTATCTTTCTCATTCACTACTCTTTTATACAAATGGATCTGAGCGGAA						
krebsiana_serrulata_RM863	GCTTTCGGCTCCTTATCGTATCCTTTTT	ATTTATCCTTTTT	TCGTTAGCGGTTCAA	AAC	TCCTTATCTTTCTCATTCACTACTCTTTTATACAAATGGATCTGAGCGGAA						
krebsiana_serrulata_RM965	GCTTTCGGCTCCTTATCGTATCCTTTTT	ATTTATCCTTTTT	TCGTTAGCGGTTCAA	AAC	TCCTTATCTTTCTCATTCACTACTCTTTTATACAAATGGATCTGAGCGGAA						
leiopoda_M240901	GCTTTCGGCTCCTTATCGTATCCTTTTT	ATTTATCCTTTTT	TCGTTAGCGGTTCAA	AAC	TCCTTATCTTTCTCATTCACTACTCTTTTATACAAATGGATCTGAGCGGAA						
leiopoda_RM1309	???????????	TATCGTATCCTTTTT	ATTTATCCTTTTT	TCGTTAGCGGTTCAA	AAC	-----	CTCCTTATCTTTCTCATTCACTACTCTTTTATACAAATGGATCTGAGCGGAA				
lichtenstenii_CAM1916	GCTTTCGGCTCCTTATCGTATCCTTTTT	ATTTATCCTTTTT	TCGTTAGCGGTTCAA	AAC	TCCTTATCTTTCTCATTCACTACTCTTTTATACAAATGGATCTGAGCGGAA						
lichtensteini_RM1249	GCTTTCGGCTCCTTATCGTATCCTTTTT	ATTTATCCTTTTT	TCGTTAGCGGTTCAA	AAC	TCCTTATCTTTCTCATTCACTACTCTTTTATACAAATGGATCTGAGCGGAA						
linearis_linearis_RM1010	GCTTTCGGCTCCTTATCGTATCCTTTTT	ATTTATCCTTTTT	TCGTTAGCGGTTCAA	AAC	TCCTTATCTTTCTCATTCACTACTCTTTTATACAAATGGATCTGAGCGGAA						
linearis_linearis_SH113	GCTTTCGGCTCCTTATCGTATCCTTTTT	ATTTATCCTTTTT	TCGTTAGCGGTTCAA	AAC	TCCTTATCTTTCTCATTCACTACTCTTTTATACAAATGGATCTGAGCGGAA						
linearis_ovalis_NDsn	GCTTTCGGCTCCTTATCGTATCCTTTTT	ATTTATCCTTTTT	TCGTTAGCGGTTCAA	AAC	TCCTTATCTTTCTCATTCACTACTCTTTTATACAAATGGATCTGAGCGGAA						
linearis_ovalis_RM854	GCTTTCGGCTCCTTATCGTATCCTTTTT	ATTTATCCTTTTT	TCGTTAGCGGTTCAA	AAC	TCCTTATCTTTCTCATTCACTACTCTTTTATACAAATGGATCTGAGCGGAA						
maritima_RM1038	GCTTTCGGCTCCTTATCGTATCCTTTTT	ATTTATCCTTTTT	TCGTTAGCGGTTCAA	AAC	TCCTTATCTTTCTCATTCACTACTCTTTTATACAAATGGATCTGAGCGGAA						
maritima_M290606_6	GCTTTCGGCTCCTTATCGTATCCTTTTT	ATTTATCCTTTTT	TCGTTAGCGGTTCAA	AAC	TCCTTATCTTTCTCATTCACTACTCTTTTATACAAATGGATCTGAGCGGAA						
othonnites_RM1306	GCTTTCGGCTCCTTATCGTATCCTTTTT	ATTTATCCTTTTT	TCGTTAGCGGTTCAA	AAC	TCCTTATCTTTCTCATTCACTACTCTTTTATACAAATGGATCTGAGCGGAA						
pectinata_M120903	GCTTTCGGCTCCTTATCGTATCCTTTTT	ATTTATCCTTTTT	TCGTTAGCGGTTCAA	AAC	TCCTTATCTTTCTCATTCACTACTCTTTTATACAAATGGATCTGAGCGGAA						
pectinata_RM1044	GCTTTCGGCTCCTTATCGTATCCTTTTT	ATTTATCCTTTTT	TCGTTAGCGGTTCAA	AAC	TCCTTATCTTTCTCATTCACTACTCTTTTATACAAATGGATCTGAGCGGAA						
rigida_M280902	GCTTTCGGCTCCTTATCGTATCCTTTTT	ATTTATCCTTTTT	TCGTTAGCGGTTCAA	AAC	TCCTTATCTTTCTCATTCACTACTCTTTTATACAAATGGATCTGAGCGGAA						
rigida_RM840	GCTTTCGGCTCCTTATCGTATCCTTTTT	ATTTATCCTTTTT	TCGTTAGCGGTTCAA	AAC	TCCTTATCTTTCTCATTCACTACTCTTTTATACAAATGGATCTGAGCGGAA						
rigens_leucolaena_RM773	GCTTTCGGCTCCTTATCGTATCCTTTTT	ATTTATCCTTTTT	TCGTTAGCGGTTCAA	AAC	TCCTTATCTTTCTCATTCACTACTCTTTTATACAAATGGATCTGAGCGGAA						
rigens_leucolaena_RM952_1	GCTTTCGGCTCCTTATCGTATCCTTTTT	ATTTATCCTTTTT	TCGTTAGCGGTTCAA	AAC	TCCTTATCTTTCTCATTCACTACTCTTTTATACAAATGGATCTGAGCGGAA						
rigens_rigens_RM763	GCTTTCGGCTCCTTATCGTATCCTTTTT	ATTTATCCTTTTT	TCGTTAGCGGTTCAA	AAC	TCCTTATCTTTCTCATTCACTACTCTTTTATACAAATGGATCTGAGCGGAA						
rigens_rigens_SR463	GCTTTCGGCTCCTTATCGTATCCTTTTT	ATTTATCCTTTTT	TCGTTAGCGGTTCAA	AAC	TCCTTATCTTTCTCATTCACTACTCTTTTATACAAATGGATCTGAGCGGAA						
rigens_uniflora_JC201205	GCTTTCGGCTCCTTATCGTATCCTTTTT	ATTTATCCTTTTT	TCGTTAGCGGTTCAA	AAC	TCCTTATCTTTCTCATTCACTACTCTTTTATACAAATGGATCTGAGCGGAA						
rigens_uniflora_RM920	GCTTTCGGCTCCTTATCGTATCCTTTTT	ATTTATCCTTTTT	TCGTTAGCGGTTCAA	AAC	TCCTTATCTTTCTCATTCACTACTCTTTTATACAAATGGATCTGAGCGGAA						
schenckii	GCTTTCGGCTCCTTATCGTATCCTTTTT	ATTTATCCTTTTT	TCGTTAGCGGTTCAA	AAC	TCCTTATCTTTCTCATTCACTACTCTTTTATACAAATGGATCTGAGCGGAA						
serrata_M250904_15	GCTTTCGGCTCCTTATCGTATCCTTTTT	ATTTATCCTTTTT	TCGTTAGCGGTTCAA	AAC	TCCTTATCTTTCTCATTCACTACTCTTTTATACAAATGGATCTGAGCGGAA						
serrata_RM898	GCTTTCGGCTCCTTATCGTATCCTTTTT	ATTTATCCTTTTT	TCGTTAGCGGTTCAA	AAC	TCCTTATCTTTCTCATTCACTACTCTTTTATACAAATGGATCTGAGCGGAA						
tenuifolia_CAM1601	GCTTTCGGCTCCTTATCGTATCCTTTTT	ATTTATCCTTTTT	TCGTTAGCGGTTCAA	AAC	TCCTTATCTTTCTCATTCACTACTCTTTTATACAAATGGATCTGAGCGGAA						
tenuifolia_M2730	GCTTTCGGCTCCTTATCGTATCCTTTTT	ATTTATCCTTTTT	TCGTTAGCGGTTCAA	AAC	TCCTTATCTTTCTCATTCACTACTCTTTTATACAAATGGATCTGAGCGGAA						
spnov_M040906_33	NNNNNNNNNNNNNNNN	CGTATCCTTTTT	ATTTATCCTTTTT	TCGTTAGCGGTTCAA	AAC	TCCTTATCTTTCTCATTCACTACTCTTTTATACAAATGGATCTGAGCGGAA					

Appendix 5: cpDNA sequence data for Chapter 3

	2100	2110	2120	2130	2140	2150	2160	2170	2180	2190	2200]
Berkheya	ATGCTGTTTTCTTATCACA	-GTGATATATATGATACAT	GTACAAATGAACATCTTTGAGGAAGGAATCCCC	-----	TGATTCCAGATCGATATTTTTATTTCATACTGA						
Gorteria	ATGCTGTTCTCTTATCACAT	GTGATATATATGATACAT	GTACAAATGAACATCTTTGAGGAAGGAATCCCC	ATTTGAATGATTCCAGATCGATATTTTTATTTCATACTGA							
Hirpicium	ATGCTGTTCTCTTATCACAC	GTGATATATATGATACAT	GTACAAATGAACATCTTTGAGGAAGGAATCCCC	ATTTGAATGATTCCAGATCGATATTTTTATTTCATACTGA							
caespitosa_RVC448	ATGCGGTTCTCTTATCACAT	GTGATATATA-GATACAT	GTACAAACGAACATCTTTGAGGAAGGAATCCCC	ATTTGAATGATTCCAGATCGATATTTTTATTTCATACTGA							
caespitosa_RVC307	ATGCGGTTCTCTTATCACAT	GTGATATATA-GATACAT	GTACAAACGAACATCTTTGAGGAAGGAATCCCC	ATTTGAATGATTCCAGATCGATATTTTTATTTCATACTGA							
ciliaris_RM1230	ATGCTGTTCTCTTATCACAT	GTGATATATATGATACAT	GTACAAACGAACATCTTTGAGGAAGGAATCCCC	ATTTGAATGATTCCAGATCGATATTTTTATTTCATACTGA							
ciliaris_RM1382	ATGCTGTTCTCTTATCACAT	GTGATATATATGATACAT	GTACAAACGAACATCTTTGAGGAAGGAATCCCC	ATTTGAATGATTCCAGATCGATATTTTTATTTCATACTGA							
heterochaeta_RM1429	ATGCTGTTCTCTTATCACAT	GTGATATATATGATACAT	GTACAAACGAACATCTTTGAGGAAGGAATCCCC	ATTTGAATGATTCCAGATCGATATTTTTATTTCATACTGA							
heterochaeta_RM1451	ATGCTGTTCTCTTATCACAT	GTGATATATATGATACAT	GTACAAACGAACATCTTTGAGGAAGGAATCCCC	ATTTGAATGATTCCAGATCGATATTTTTATTTCATACTGA							
jurineifolia_jur_SR682	ATGCTGTTCTCTTATCACAT	GTGATATATATGATACAT	GTACAAACGAACATCTTTGAGGAAGGAATCCCC	ATTTGAATGATTCCAGATCGATATTTTTATTTCATACTGA							
jurineifolia_jur_RM1518	ATGATGTTCTCTTATCACAT	GTGATATATATGATACAT	GTACAAACGAACATCTTTGAGGAAGGAATCCCC	ATTTGAATGATTCCAGATCGATATTTTTATTTCATACTGA							
jurineifolia_scab_CAM1604	ATGCTGTTCTCTTATCACAT	GTGATATATATGATACAT	GTACAAACGAACATCTTTGAGGAAGGAATCCCC	ATTTGAATGATTCCAGATCGATATTTTTATTTCATACTGA							
jurineifolia_scab_CAM2652	ATGCTGTTCTCTTATCACAT	GTGATATATATGATACAT	GTACAAACGAACATCTTTGAGGAAGGAATCCCC	ATTTGAATGATTCCAGATCGATATTTTTATTTCATACTGA							
krebsiana_arctotoides_RM868	ATGCTGTTCTCTTATCACAT	GTGATATATATGATACAT	GTACAAACGAACATCTTTGAGGAAGGAATCCCC	ATTTGAATGATTCCAGATCGATATTTTTATTTCATACTGA							
krebsiana_arctotoides_RM876	ATGCTGTTCTCTTATCACAT	GTGATATATATGATACAT	GTACAAACGAACATCTTTGAGGAAGGAATCCCC	ATTTGAATGATTCCAGATCGATATTTTTATTTCATACTGA							
krebsiana_krebsiana_RM1114	ATGCTGTTCTCTTATCACAT	GTGATATATATGATACAT	GTACAAACGAACATCTTTGAGGAAGGAATCCCC	ATTTGAATGATTCCAGATCGATATTTTTATTTCATACTGA							
krebsiana_krebsiana_RM1136	ATGCTGTTCTCTTATCACAT	GTGATATATATGATACAT	GTACAAACGAACATCTTTGAGGAAGGAATCCCC	ATTTGAATGATTCCAGATCGATATTTTTATTTCATACTGA							
krebsiana_serrulata_RM863	ATGCTGTTCTCTTATCACAT	GTGATATATATGATACAT	GTACAAACGAACATCTTTGAGGAAGGAATCCCC	ATTTGAATGATTCCAGATCGATATTTTTATTTCATACTGA							
krebsiana_serrulata_RM965	ATGCTGTTCTCTTATCACAT	GTGATATATATGATACAT	GTACAAACGAACATCTTTGAGGAAGGAATCCCC	ATTTGAATGATTCCAGATCGATATTTTTATTTCATACTGA							
leiopoda_M240901	ATGCGGTTCTCTTATCACAT	GTGATATATATGATACAT	GTACAAACGAACATCTTTGAGGAAGGAATCCCC	ATTTGAATGATTCCAGATCGATATTTTTATTTCATACTGA							
leiopoda_RM1309	ATGCTGTTCTCTTATCACAT	GTGATATATATGATACAT	GTACAAACGAACATCTTTGAGGAAGGAATCCCC	ATTTGAATGATTCCAGATCGATATTTTTATTTCATACTGA							
lichtenstenii_CAM1916	ATGCTGTTCTCTTATCACAT	GTGATATATATGATACAT	GTACAAACGAACATCTTTGAGGAAGGAATCCCC	ATTTGAATGATTCCAGATCGATATTTTTATTTCATACTGA							
lichtensteini_RM1249	ATGCTGTTCTCTTATCACAT	GTGATATATATGATACAT	GTACAAACGAACATCTTTGAGGAAGGAATCCCC	ATTTGAATGATTCCAGATCGATATTTTTATTTCATACTGA							
linearis_linearis_RM1010	ATGCTGTTCTCTTATCACAT	GTGATATATATGATACAT	GTACAAACGAACATCTTTGAGGAAGGAATCCCC	ATTTGAATGATTCCAGATCGATATTTTTATTTCATACTGA							
linearis_linearis_SH113	ATGCTGTTCTCTTATCACAT	GTGATATATATGATACAT	GTACAAACGAACATCTTTGAGGAAGGAATCCCC	ATTTGAATGATTCCAGATCGATATTTTTATTTCATACTGA							
linearis_ovalis_NDsn	ATGCTGTTCTCTTATCACAT	GTGATATATATGATACAT	GTACAAACGAACATCTTTGAGGAAGGAATCCCC	ATTTGAATGATTCCAGATCGATATTTTTATTTCATACTGA							
linearis_ovalis_RM854	ATGCTGTTCTCTTATCACAT	GTGATATATATGATACAT	GTACAAACGAACATCTTTGAGGAAGGAATCCCC	ATTTGAATGATTCCAGATCGATATTTTTATTTCATACTGA							
maritima_RM1038	ATGCTGTTCTCTTATCACAT	GTGATATATATGATACAT	GTACAAACGAACATCTTTGAGGAAGGAATCCCC	ATTTGAATGATTCCAGATCGATATTTTTATTTCATACTGA							
maritima_M290606_6	ATGCTGTTCTCTTATCACAT	GTGATATATATGATACAT	GTACAAACGAACATCTTTGAGGAAGGAATCCCC	ATTTGAATGATTCCAGATCGATATTTTTATTTCATACTGA							
othonnites_RM1306	ATGCTGTTCTCTTATCACAT	GTGATATATATGATACAT	GTACAAACGAACATCTTTGAGGAAGGAATCCCC	ATTTGAATGATTCCAGATCGATATTTTTATTTCATACTGA							
pectinata_M120903	ATGCTGTTCTCTTATCACAT	GTGATATATATGATACAT	GTACAAACGAACATCTTTGAGGAAGGAATCCCC	ATTTGAATGATTCCAGATCGATATTTTTATTTCATACTGA							
pectinata_RM1044	ATGCTGTTCTCTTATCACAT	GTGATATATATGATACAT	GTACAAACGAACATCTTTGAGGAAGGAATCCCC	ATTTGAATGATTCCAGATCGATATTTTTATTTCATACTGA							
rigida_M280902	ATGCTGTTCTCTTATCACAT	GTGATATATATGATACAT	GTACAAACGAACATCTTTGAGGAAGGAATCCCC	ATTTGAATGATTCCAGATCGATATTTTTATTTCATACTGA							
rigida_RM840	ATGCTGTTCTCTTATCACAT	GTGATATATATGATACAT	GTACAAACGAACATCTTTGAGGAAGGAATCCCC	ATTTGAATGATTCCAGATCGATATTTTTATTTCATACTGA							
rigens_leucolaena_RM773	ATGCTGTTCTCTTATCACAT	GTGATATATATGATACAT	GTACAAACGAACATCTTTGAGGAAGGAATCCCC	ATTTGAATGATTCCAGATCGATATTTTTATTTCATACTGA							
rigens_leucolaena_RM952_1	ATGCTGTTCTCTTATCACAT	GTGATATATATGATACAT	GTACAAACGAACATCTTTGAGGAAGGAATCCCC	ATTTGAATGATTCCAGATCGATATTTTTATTTCATACTGA							
rigens_rigens_RM763	ATGCTGTTCTCTTATCACAT	GTGATATATATGATACAT	GTACAAACGAACATCTTTGAGGAAGGAATCCCC	ATTTGAATGATTCCAGATCGATATTTTTATTTCATACTGA							
rigens_rigens_SR463	ATGCTGTTCTCTTATCACAT	GTGATATATATGATACAT	GTACAAACGAACATCTTTGAGGAAGGAATCCCC	ATTTGAATGATTCCAGATCGATATTTTTATTTCATACTGA							
rigens_uniflora_JC201205	ATGCTGTTCTCTTATCACAT	GTGATATATATGATACAT	GTACAAACGAACATCTTTGAGGAAGGAATCCCC	ATTTGAATGATTCCAGATCGATATTTTTATTTCATACTGA							
rigens_uniflora_RM920	ATGCTGTTCTCTTATCACAT	GTGATATATATGATACAT	GTACAAACGAACATCTTTGAGGAAGGAATCCCC	ATTTGAATGATTCCAGATCGATATTTTTATTTCATACTGA							
schenckii	ATGCTGTTCTCTTATCACAT	GTGATATATATGATACAT	GTACAAACGAACATCTTTGAGGAAGGAATCCCC	ATTTGAATGATTCCAGATCGATATTTTTATTTCATACTGA							
serrata_M250904_15	ATGCTGTTCTCTTATCACAT	GTGATATATATGATACAT	GTACAAACGAACATCTTTGAGGAAGGAATCCCC	ATTTGAATGATTCCAGATCGATATTTTTATTTCATACTGA							
serrata_RM898	ATGCTGTTCTCTTATCACAT	GTGATATATATGATACAT	GTACAAACGAACATCTTTGAGGAAGGAATCCCC	ATTTGAATGATTCCAGATCGATATTTTTATTTCATACTGA							
tenuifolia_CAM1601	ATGCTGTTCTCTTATCACAT	GTGATATATATGATACAT	GTACAAACGAACATCTTTGAGGAAGGAATCCCC	ATTTGAATGATTCCAGATCGATATTTTTATTTCATACTGA							
tenuifolia_M2730	ATGCTGTTCTCTTATCACAT	GTGATATATATGATACAT	GTACAAACGAACATCTTTGAGGAAGGAATCCCC	ATTTGAATGATTCCAGATCGATATTTTTATTTCATACTGA							
spnov_M040906_33	ATGCTGTTCTCTTATCACAT	GTGATATATATGATACAT	GTACAAACGAACATCTTTGAGGAAGGAATCCCC	ATTTGAATGATTCCAGATCGATATTTTTATTTCATACTGA							

Appendix 5: cpDNA sequence data for Chapter 3

	2210	2220	2230	2240	2250	2260	2270	2280	2290	2300	2310
Berkheya	AA-CTTACAAAGTTGTTCTTTTGACAAATTATAGGGCCTGGATGAGGCTTTGTAATACCCCTTCAATTGACATAGACCCAAGTTCTCTAGTAAAAATGAAAATGAGGATGA										
Gorteria	AA-CTTACAAAGTAGTTCTTTTGACAAATTATAGGGCCTGGATGAGGCTTTGTAATACCCCTTCAATTGACATAGACCCAAGTTCTCTAGTAAAAATGAAAATGAGGATGA										
Hirpicium	AA-CTTACAAAGTTGTTCTTTTGACAAATTATAGGGCCTGGATGAGGCTTTGTAATACCCCTTCAATTGACATAGACCCAAGTTCTCTAGTAAAAATGAAAATGAGGATGA										
caespitosa_RVC448	AA-CTTACAAAGTTGTTCTTTTGACAAATTATAGGGCCTGGATGAGGCTTTGTAATACCCCTTCAATTGACATAGACCCAAGTTCTCTAGTAAAAATGAAAATGAGGATGA										
caespitosa_RVC307	AA-CTTACAAAGTTGTTCTTTTGACAAATTATAGGGCCTGGATGAGGCTTTGTAATACCCCTTCAATTGACATAGACCCAAGTTCTCTAGTAAAAATGAAAATGAGGATGA										
ciliaris_RM1230	AA-CTTACAAAGTTGTTCTTTTGACAAATTATAGGGCCTGGATGAGGCTTTGTAATACCCCTTCAATTGACATAGACCCAAGTTCTCTAGTAAAAATGAAAATGAGGATGA										
ciliaris_RM1382	AA-CTTACAAAGTTGTTCTTTTGACAAATTATAGGGCCTGGATGAGGCTTTGTAATACCCCTTCAATTGACATAGACCCAAGTTCTCTAGTAAAAATGAAAATGAGGATGA										
heterochaeta_RM1429	AA-CTTACAAAGTTGTTCTTTTGACAAATTATAGGGCCTGGATGAGGCTTTGTAATACCCCTTCAATTGACATAGACCCAAGTTCTCTAGTAAAAATGAAAATGAGGATGA										
heterochaeta_RM1451	AA-CTTACAAAGTTGTTCTTTTGACAAATTATAGGGCCTGGATGAGGCTTTGTAATACCCCTTCAATTGACATAGACCCAAGTTCTCTAGTAAAAATGAAAATGAGGATGA										
jurineifolia_jur_SR682	AA-CTTACAAAGTTGTTCTTTTGACAAATTATAGGGCCTGGATGAGGCTTTGTAATACCCCTTCAATTGACATAGACCCAAGTTCTCTAGTAAAAATGAAAATGAGGATGA										
jurineifolia_jur_RM1518	AA-CTTACAAAGTTGTTCTTTTGACAAATTATAGGGCCTGGATGAGGCTTTGTAATACCCCTTCAATTGACATAGACCCAAGTTCTCTAGTAAAAATGAAAATGAGGATGA										
jurineifolia_scab_CAM1604	??										
jurineifolia_scab_CAM2652	AA-CTTACAAAGTTGTTCTTTTGACAAATTATAGGGCCTGGATGAGGCTTTGTAATACCCCTTCAATTGACATAGACCCAAGTTCTCTAGTAAAAATGAAAATGAGGATGA										
krebsiana_arctotoides_RM868	AA-CTTACAAAGTTGTTCTTTTGACAAATTATAGGGCCTGGATGAGGCTTTGTAATACCCCTTCAATTGACATAGACCCAAGTTCTCTAGTAAAAATGAAAATGAGGATGA										
krebsiana_arctotoides_RM876	AA-CTTACAAAGTTGTTCTTTTGACAAATTATAGGGCCTGGATGAGGCTTTGTAATACCCCTTCAATTGACATAGACCCAAGTTCTCTAGTAAAAATGAAAATGAGGATGA										
krebsiana_krebsiana_RM1114	AA-CTTACAAAGTTGTTCTTTTGACAAATTATAGGGCCTGGATGAGGCTTTGTAATACCCCTTCAATTGACATAGACCCAAGTTCTCTAGTAAAAATGAAAATGAGGATGA										
krebsiana_krebsiana_RM1136	AA-CTTACAAAGTTGTTCTTTTGACAAATTATAGGGCCTGGATGAGGCTTTGTAATACCCCTTCAATTGACATAGACCCAAGTTCTCTAGTAAAAATGAAAATGAGGATGA										
krebsiana_serrulata_RM863	AA-CTTACAAAGTTGTTCTTTTGACAAATTATAGGGCCTGGATGAGGCTTTGTAATACCCCTTCAATTGACATAGACCCAAGTTCTCTAGTAAAAATGAAAATGAGGATGA										
krebsiana_serrulata_RM965	AA-CTTACAAAGTTGTTCTTTTGACAAATTATAGGGCCTGGATGAGGCTTTGTAATACCCCTTCAATTGACATAGACCCAAGTTCTCTAGTAAAAATGAAAATGAGGATGA										
leiopoda_M240901	AA-CTTACAAAGTTGTTCTTTTGACAAATTATAGGGCCTGGATGAGGCTTTGTAATACCCCTTCAATTGACATAGACCCAAGTTCTCTAGTAAAAATGAAAATGAGGATGA										
leiopoda_RM1309	AA-CTTACAAAGTTGTTCTTTTGACAAATTATAGGGCCTGGATGAGGCTTTGTAATACCCCTTCAATTGACATAGACCCAAGTTCTCTAGTAAAAATGAAAATGAGGATGA										
lichtenstenii_CAM1916	AA-CTTACAAAGTTGTTCTTTTGACAAATTATAGGGCCTGGATGAGGCTTTGTAATACCCCTTCAATTGACATAGACCCAAGTTCTCTAGTAAAAATGAAAATGAGGATGA										
lichtensteini_RM1249	AA-CTTACAAAGTTGTTCTTTTGACAAATTATAGGGCCTGGATGAGGCTTTGTAATACCCCTTCAATTGACATAGACCCAAGTTCTCTAGTAAAAATGAAAATGAGGATGA										
linearis_linearis_RM1010	AA-CTTACAAAGTTGTTCTTTTGACAAATTATAGGGCCTGGATGAGGCTTTGTAATACCCCTTCAATTGACATAGACCCAAGTTCTCTAGTAAAAATGAAAATGAGGATGA										
linearis_linearis_SH113	AA-CTTACAAAGTTGTTCTTTTGACAAATTATAGGGCCTGGATGAGGCTTTGTAATACCCCTTCAATTGACATAGACCCAAGTTCTCTAGTAAAAATGAAAATGAGGATGA										
linearis_ovalis_NDsn	AA-CTTACAAAGTTGTTCTTTTGACAAATTATAGGGCCTGGATGAGGCTTTGTAATACCCCTTCAATTGACATAGACCCAAGTTCTCTAGTAAAAATGAAAATGAGGATGA										
linearis_ovalis_RM854	??										
maritima_RM1038	AA-CTTACAAAGTTGTTCTTTTGACAAATTATAGGGCCTGGATGAGGCTTTGTAATACCCCTTCAATTGACATAGACCCAAGTTCTCTAGTAAAAATGAAAATGAGGATGA										
maritima_M290606_6	AA-CTTACAAAGTTGTTCTTTTGACAAATTATAGGGCCTGGATGAGGCTTTGTAATACCCCTTCAATTGACATAGACCCAAGTTCTCTAGTAAAAATGAAAATGAGGATGA										
othonnites_RM1306	AA-CTTACAAAGTTGTTCTTTTGACAAATTATAGGGCCTGGATGAGGCTTTGTAATACCCCTTCAATTGACATAGACCCAAGTTCTCTAGTAAAAATGAAAATGAGGATGA										
pectinata_M120903	AA-CTTACAAAGTTGTTCTTTTGACAAATTATAGGGCCTGGATGAGGCTTTGTAATACCCCTTCAATTGACATAGACCCAAGTTCTCTAGTAAAAATGAAAATGAGGATGA										
pectinata_RM1044	AA-CTTACAAAGTTGTTCTTTTGACAAATTATAGGGCCTGGATGAGGCTTTGTAATACCCCTTCAATTGACATAGACCCAAGTTCTCTAGTAAAAATGAAAATGAGGATGA										
rigida_M280902	AA-CTTACAAAGTTGTTCTTTTGACAAATTATAGGGCCTGGATGAGGCTTTGTAATACCCCTTCAATTGACATAGACCCAAGTTCTCTAGTAAAAATGAAAATGAGGATGA										
rigida_RM840	AA-CTTACAAAGTTGTTCTTTTGACAAATTATAGGGCCTGGATGAGGCTTTGTAATACCCCTTCAATTGACATAGACCCAAGTTCTCTAGTAAAAATGAAAATGAGGATGA										
rigens_leucolaena_RM773	AA-CTTACAAAGTTGTTCTTTTGACAAATTATAGGGCCTGGATGAGGCTTTGTAATACCCCTTCAATTGACATAGACCCAAGTTCTCTAGTAAAAATGAAAATGAGGATGA										
rigens_leucolaena_RM952_1	AA-CTTACAAAGTTGTTCTTTTGACAAATTATAGGGCCTGGATGAGGCTTTGTAATACCCCTTCAATTGACATAGACCCAAGTTCTCTAGTAAAAATGAAAATGAGGATGA										
rigens_rigens_RM763	AA-CTTACAAAGTTGTTCTTTTGACAAATTATAGGGCCTGGATGAGGCTTTGTAATACCCCTTCAATTGACATAGACCCAAGTTCTCTAGTAAAAATGAAAATGAGGATGA										
rigens_rigens_SR463	AA-CTTACAAAGTTGTTCTTTTGACAAATTATAGGGCCTGGATGAGGCTTTGTAATACCCCTTCAATTGACATAGACCCAAGTTCTCTAGTAAAAATGAAAATGAGGATGA										
rigens_uniflora_JC201205	AA-CTTACAAAGTTGTTCTTTTGACAAATTATAGGGCCTGGATGAGGCTTTGTAATACCCCTTCAATTGACATAGACCCAAGTTCTCTAGTAAAAATGAAAATGAGGATGA										
rigens_uniflora_RM920	AA-CTTA??										
schenckii	AA-CTTACAAAGTTGTTCTTTTGACAAATTATAGGGCCTGGATGAGGCTTTGTAATACCCCTTCAATTGACATAGACCCAAGTTCTCTAGTAAAAATGAAAATGAGGATGA										
serrata_M250904_15	AA-CTTACAAAGTTGTTCTTTTGACAAATTATAGGGCCTGGATGAGGCTTTGTAATACCCCTTCAATTGACATAGACCCAAGTTCTCTAGTAAAAATGAAAATGAGGATGA										
serrata_RM898	AA-CTTACAAAGTTGTTCTTTTGACAAATTATAGGGCCTGGATGAGGCTTTGTAATACCCCTTCAATTGACATAGACCCAAGTTCTCTAGTAAAAATGAAAATGAGGATGA										
tenuifolia_CAM1601	AA-CTTACAAAGTTGTTCTTTTGACAAATTATAGGGCCTGGATGAGGCTTTGTAATACCCCTTCAATTGACATAGACCCAAGTTCTCTAGTAAAAATGAAAATGAGGATGA										
tenuifolia_M2730	AACTTACAAAGTTGTTCTTTTGACAAATTATAGGGCCTGGATGAGGCTTTGTAATACCCCTTCAATTGACATAGACCCAAGTTCTCTAGTAAAAATGAAAATGAGGATGA										
spnov_M040906_33	AA-CTTACAAAGTTGTTCTTTTGACAAATTATAGGGCCTGGATGAGGCTTTGTAATACCCCTTCAATTGACATAGACCCAAGTTCTCTAGTAAAAATGAAAATGAGGATGA										

Appendix 5: cpDNA sequence data for Chapter 3

	2320	2330	2340	2350	2360]
Berkheya	GACATCAGGAATAGTCGGGATAGCTCAGTTGGTAGAGCAGAGGACTGAAAAATCCTCG					
Gorteria	GACATCAGGAATAGTCGGGATAGCTCAGTTGGTAGAGCAGAGGACTGAAAAATCCTCG					
Hirpicium	GACATCAGGAATAGTCGGGATAGCTCAGTTGGTAGAGCAGAGGACTGAAAAATCCTCG					
caespitosa_RVC448	GACATCAGGAATAGTCGGGATAGCTCAGTTGGTAGAGCAGAGGACTGAAAAATCCTCG					
caespitosa_RVC307	GACATCAGGAATAGTCGGGATAGCTCAGTTGGTAGAGCAGAGGACTGAAAAATCCTCG					
ciliaris_RM1230	GACATCAGGAATAGTCGGGATAGCTCAGTTGGTAGAGCAGAGGACTGAAAAATCCTCG					
ciliaris_RM1382	GACATCAGGAATAGTCGGGATAGCTCAGTTGGTAGAGCAGAGGACTGAAAAATCCTCG					
heterochaeta_RM1429	GACATCAGGAATAGTCGGGATAGCTCAGTTGGTAGAGCAGAGGACTGAAAAATCCTCG					
heterochaeta_RM1451	GACATCAGGAATAGTCGGGATAGCTCAGTTGGTAGAGCAGAGGACTGAAAAATCCTCG					
jurineifolia_jur_SR682	GACATCAGGAATAGTCGGGATAGCTCAGTTGGTAGAGCAGAGGACTGAAAAATCCTCG					
jurineifoliajur_RM1518	GACATCAGGAATAGTCGGGATAGCTCAGTTGGTAGAGCAGAGGACTGAAAAATCCTCG					
jurineifolia_scab_CAM1604	??					
jurineifolia_scab_CAM2652	GACATCAGGAATAGTCGGGATAGCTCAGTTGGTAGAGCAGAGGACTGAAAAATCCTCG					
krebsiana_arctotoides_RM868	GACATCAGGAATAGTCGGGATAGCTCAGTTGGTAGAGCAGAGGACTGAAAAATCCTC?					
krebsiana_arctotoides_RM876	GACATCAGGAATAGTCGGGATAGCTCAGTTGGTAGAGCAGAGGACTGAAAAATCCTC?					
krebsiana_krebsiana_RM1114	GACATCAGGAATAGTCGGGATAGCTCAGTTGGTAGAGCAGAGGACTGAAAAATCCTCG					
krebsiana_krebsiana_RM1136	GACATCAGGAATAGTCGGGATAGCTCAGTTGGTAGAGCAGAGGACTGAAAAATCCTCG					
krebsiana_serrulata_RM863	GACATCAGGAATAGTCGGGATAGCTCAGTTGGTAGAGCAGAGGACTGAAAAATCCTCG					
krebsiana_serrulata_RM965	GACATCAGGAATAGTCGGGATAGCTCAGTA??????????????????????????					
leiopoda_M240901	??					
leiopoda_RM1309	GACATCAGGAATAGTCGGGATAGCTCAGTTGGTAGAGCAGAGGACTGAAAAATCCTCG					
lichtenstenii_CAM1916	GACATCAGGAATAGTC??					
lichtensteini_RM1249	GACATCAGGAATAGTCGGGATAGCTCAGTTGGTAGAGCAGAGGACTGAAAAATCCTCG					
linearis_linearis_RM1010	GACATCAGGAATAGTCGGGATAGCTCAGTTGGTAGAGCAGAGGACTGAAAAATCCTCG					
linearis_linearis_SH113	GACATCAGGAATAGTCGGGATAGCTCAGTTGGTAGAGCAGAGGACTGAAAAATCCTCG					
linearis_ovalis_NDsn	GACATCAGGAATAGTCGGGATAGCTCAGTTGGTAGAGCAGAGGACTGAAAAATCCTCG					
linearis_ovalis_RM854	??					
maritima_RM1038	GACATCAGGAATAGTCGGGATAGCTCAGTTGGTAGAGCAGAGGACTGAAAAATCCTCG					
maritima_M290606_6	GACATCAGGAATAGTCGGGATAGCTCAGTTGGTAGAGCAGAGGACTGAAAAATCCTCG					
othonnites_RM1306	GACATCAGGAATAGTCGGGATAGCTCAGTTGGTAGAGCAGAGGACTGAAAAATCCTCG					
pectinata_M120903	GACATCAGGAATAGTCGGGATAGCTCAGTTGGTAGAGCAGAGGACTGAAAAATCCTCG					
pectinata_RM1044	GACATCAGGAATAGTCGGGATAGCTCAGTTGGTAGAGCAGAGGACTGAAAAATCCTCG					
rigida_M280902	GACATCAGGAATAGTCGGGATAGCTCAGTTGGTAGAGCAGAGGACTGAAAAATCCTCG					
rigida_RM840	GACATCAGGAATAGTCGGGATAGCTCAGTTGGTAGAGCAGAGGACTGAAAAATCCTCG					
rigens_leucolaena_RM773	GACATCAGGAATAGTCGGGATAGCTCAGTTGGTAGAGCAGAGGACTGAAAAATCCTCG					
rigens_leucolaena_RM952_1	GACATCAGGAATAGTCGGGATA??????????????????????????????????					
rigens_rigens_RM763	??					
rigens_rigens_SR463	GACATCAGGAATAGTCGGGATAGCTCAGTTGGTAGAGCAGAGGACTGAAAAATCCTCG					
rigens_uniflora_JC201205	GACATCAGGAATAGTCGGGATAGCTCAGTTGGTAGAGCAGAGGACTGAAAAATCCTCG					
rigens_uniflora_RM920	??					
schenckii	GACATCAGGAATAGTCGGGATAGCTCAGTTGGTAGAGCAGAGGACTGAAAAATCCTCG					
serrata_M250904_15	??					
serrata_RM898	GACATCAGGAATAGTCGGGATAGCTCAGTTGGTAGAGCAGAGGACTGAAAAATCCTCG					
tenuifolia_CAM1601	GACATCAGGAATAGTC??					
tenuifolia_M2730	GACATCAGGAATAGTCGGGATAGCTCAGTTGGTAGAGCAGAGGACTGAAAAATCCTCG					
spnov_M040906_33	GACATCAGGAATAGTCGGGATAGCTCAGTTGGTAGAGCAGAGGACTGAAAAATCCTCG					

Appendix 6: Additional nrDNA sequence data for Chapter 4

[10	20	30	40	50	60	70	80	90	100	110]
lichtensteiniRM1323	TCGAACCCCTGCATAGCGGAACGACCCCGGAACACGTACATACAACCGGGTGTAAAGGGGGCAGG-CTCTAGCCGGCGACCCCTTGACGCCCTGCCTTCTGCGTACATGT										
lichtesteiniiM050906_2	TCGAACCCCTGCATAGCRGAACGACCCCGGAACACGTACATACAACCGGGTGTAAAGGGGGCAGG-CTCTAGCCGGCGACCCCTTGACGCCCTGCCTTCTGCGTACATGT										
heterochaetaM160901_5g	TCGAACCCCTGCATAGCAGAACGACCCCGGAACATGTACATACAACCGGGTGTAAAGGGG--CAGG-CTCTAGCCGGCGACCCCTTGACGCCCTGCCTTCTGCGTGCATGT										
heterochaetaRM1348	TCGAACCCCTGCATAGCAGAACGACCCCGGAACATGTACATACAACCGGGTGTAAAGGGG--CAGG-CTCTAGCCGGCGACCCCTTGACGCCCTGCCTTCTGCGTGCATGT										
heterochaetaRM1255	TCGAACCCCTGCATAGCAGAACGACCCCGGAACATGTACATACAACCGGGTGTAAAGGGGGCAGG-CTCTAGCCGGCGACCCCTTGATGCCCTGCCTTCTGCGTGCATGT										
tenuifoliaM7219_10	TCGAACCCCTGCATAGCAGAACGACCCCGGAACACGTACATACAACCGGGTGTAAAGGGGGACAGG-CTCTAGCCGGCGACCCCTTGATGCCCTGCCTACCTGCGTGCATGT										
tenuifoliaRM1352	TCGAACCCCTGCATAGCAGAACGACCCCGGAACACGTACATACAACCGGGTGTAAAGGGGGACAGG-CTCTAGCCGGCGACCCCTTGATGCCCTGCCTACCTGCGTGCATGT										
ciliarisSR705	TCGAACCCCTGCAAAAGCAGAACGACCCCGGAACACGTACATACAACCGGGTGTCAAGGGGGACAGG-CACTAGCCGGCGACCCCTTGATGCCCTGCCTACCTGCGTGCATGT										
jurineifolia_scabCAM1953	TCGAACCCCTGCATAGCAGAACGACCCCGGAACACGTACATACAACCGGGTGTAAAGGGGGACAGG-CTATAGCCGGCGACCCCTTGACGCCCTGCCTACCTGCGTGCATGT										
rigens_unifl_Boknes1	?????CCTGCATAGCAGAACGACCCCGGAACACGTACATACAACCGGGTGTCAAGGGGGACTGG-CTCTAGCCGGCGACCCCTTGATGCCCTGCCTACCTGCGTGCATGT										
linearis_linear_Boknes2	TCGAACCCCTGCATAGCAGAACGACCCCGGAACACGTACATACAACCGGGTGTCAAGGGGGACTGG-CTCTAGCCGGCGACCCCTTGATGCCCTGCCTACCTGCGTGCATGT										
linearis_ovalM041001_2g	?????CCCTGCATAGCAGAACGACCCCGGAACACGTACATACAACCGGGTGTCAAGGGGGACTGG-CTCTAGCCGGCGACCCCTTGATGCCCTGCCACCTGCGTGCATGT										
rigens_leuco_M070704_1	TCGAACCCCTGCATAGCAGAACGACCCCGGAACACGTACATACAACCGGGTGTCAAGGGGGACTGG-CTCTAGCCGGCGACCCCTTGATGCCCTGCCTACCTGCGTGCATGT										
krebsiana_krebM071001_1g	TCGAACCCCTGCATAGCAGAACGACCCCGGAACACGTACATACAACCGGGTGTCAAGGGGGACTGG-CTCTAGCCGGCGACCCCTTGATGCCCTGCCTACCTGCGTGCATGT										
krebsiana_krebM071001_3gl	TCGAACCCCTGCATAGCAGAACGACCCCGGAACACGTACATACAACCGGGTGTCAAGGGGGACTGG-CTCTAGCCGGCGACCCCTTGATGCCCTGCCTACCTGCGTGCATGT										
krebsiana_arctM071001_3pg	TCGAACCCCTGCATAGCAGAACGACCCCGGAACACGTACATACAACCGGGTGTCAAGGGGGACTGG-CTCTAGCCGGCGACCCCTTGATGCCCTGCCTACCTGCGTGCATGT										
rigidaM100903_4	TCGAACCCCTGCATAGCAGAACGACCCCGGAACACGTACATACAACCGGGTGTCAAGGGGGACTGG-CTCTAACC GGCGACCCCTTGATGCCCTGCCTACCTGCGTGCATGT										
rigidaM100904_4	TCGAACCCCTGCATAGCAGAACGACCCCGGAACACGTACATACAACCGGGTGTCAAGGGGGACTGG-CTCTAGCCGGCGACCCCTTGATGCCCTGCCTACCTGCGTGCATGT										
rigidM110805_10	TCGAACCCCTGCATAGCAGAACGACCCCGGAACACGTACATACAACCGGGTGTCAAGGGGGACTGG-CTCTAGCCGGCGACCCCTTGATGCCCTGCCTACCTGCGTGCATGT										
rigidaM120805_80	TCGAACCCCTGCATAGCAGAACGACCCCGGAACACGTACATACAACCGGGTGTCAAGGGGGACTGG-CTCTAGCCGGCGACCCCTTGATGCCCTGCCTACCTGCGTGCATGT										
leiopodaM160704_5	TCGAACCCCTGCATAGCAGAACGACCCCGGAACACGTACATACAACCGGGTGTCAAGGGGGACTGG-CTCTAGCCGGCGACCCCTTGATGCCCTGCCTACCTGCGTGCATGT										
pectinataM180904_5	TCGAACCCCTGCATAGCAGAACGACCCCGGAACACGTACATACAACCGGGTGTCAAGGGGGACTGG-CTCTAGCCGGCGACCCCTTGATGCCCTGCCTACCTGCGTGCATGT										
krebsiana_krebM210902_1	?????????ATAGCAGAACGACCCCGGAACACGTACATACAACCGGGTGTCAAGGGGGACTGG-CTCTAGCCGGCGACCCCTTGATGCCCTGCCTACCTGCGTGCATGT										
krebsiana_krebM230803_8	TCGAACCCCTGCATAGCAGAACGACCCCGGAACACGTACATACAACCGGGTGTCAAGGGGGACTGG-CTCTAGCCGGCGACCCCTTGATGCCCTGCCTACCTGCGTGCATGT										
serrM230901_7g	TCGAACCCCTGCATAGCAGAACGACCCCGGAACACGTACATACAACCGGGTGTCAAGGGGGACTGG-CTCTAGCCGGCGACCCCTTGATGCCCTGCCTACCTGCGTGCATGT										
leiopodaM250901_34	TCGAACCCCTGCATAGCAGAACGACCCCGGAACACGTACATACAACCGGGTGTCAAGGGGGACTGG-CTCTAGCCGGCGACCCCTTGATGCCCTGCCTACCTGCGTGCATGT										
pectinataM250901_37	TCGAACCCCTGCATAGCAGAACGACCCCGGAACACGTACATACAACCGGGTGTCAAGGGGGACTGG-CTCTAGCCGGCGACCCCTTGATGCCCTGCCTACCTGCGTGCATGT										
pectM260901_2g	TCGAACCCCTGCATAGCAGAACGACCCCGGAACACGTACATACAACCGGGTGTCAAGGGGGACTGG-CTCTAGCCGGCGACCCCTTGATGCCCTGCCTACCTGCGTGCATGT										
maritimaM260901	?????????????????????GCGAACACGTACATACAACCGGGTGTCAAGGGGGACTGG-CTCTAGCCGGCGACCCCTTGATGCCCTGCCTACCTGCGTGCATGT										
krebsiana_krebM261001_2	TCGAACCCCTGCATAGCAGAACGACCCCGGAACACGTACATACAACCGGGTGTCAAGGGGGACTGG-CTCTAGCCGGCGACCCCTTGATGCCCTGCCTACCTGCGTGCATGT										
maritimaM270901_5g	TCGAACCCCTGCATAGCAGAACGACCCCGGAACACGTACATACAACCGGGTGTCAAGGGGGACTGG-CTCTAGCCGGCGACCCCTTGATGCCCTGCCTACCTGCGTGCATGT										
rigens_rigensM7293	TCGAACCCCTGCATAGCAGAACGACCCCGGAACACGTACATACAACCGGGTGTCAAGGGGGACTGG-CTCTAGCCGGCGACCCCTTGATGCCCTGCCTACCTGCGTGCATGT										
rigens_rigensM7298_2	TCGAACCCCTGCATAGCAGAACGACCCCGGAACACGTACATACAACCGGGTGTCAAGGGGGACTGG-CTCTAGCCGGCGACCCCTTGATGCCCTGCCTACCTGCGTGCATGT										
rigens_rigensM7527_2	TCGAACCCCTGCATAGCAGAACGACCCCGGAACACGTACATACAACCGGGTGTCAAGGGGGACTGG-CTCTAGCCGGCGACCCCTTGATGCCCTGCCTACCTGCGTGCATGT										
leiopodaM200901_22g	TCGAACCCCTGCATAGCAGAACGACCCCGGAACACGTACATACAACCGGGTGTCAAGGGGGACTGG-CTCTAGCCGGCGACCCCTTGATGCCCTGCCTACCTGCGTGCATGT										
spnov_M7237_4	TCGAACCCCTGCATAGCAGAACGACCCCGGAACACGTACATACAACCGGGTGTCAAGGGGGACTGG-CTCTAGCCGGCGACCCCTTGATGCCCTGCCTACCTGCGTGCATGT										
serrataHerm_NB	TCGAACCCCTGCATAGCAGAACGACCCCGGAACACGTACATACAACCGGGTGTCAAGGGGGACTGG-CTCTAGCCGGCGACCCCTTGATGCCCTGCCTACCTGCGTGCATGT										
krebsiana_krebNB1465	TCGAACCCCTGCATAGCAGAACGACCCCGGAACACGTACATACAACCGGGTGTCAAGGGGGACTGG-CTCTAGCCGGCGACCCCTTGATGCCCTGCCTACCTGCGTGCATGT										
linearis_linearRM1013	TCGAACCCCTGCATAGCAGAACGACCCCGGAACACGTACATACAACCGGGTGTCAAGGGGGACTGG-CTCTAGCCGGCGACCCCTTGATGCCCTGCCTACCTGCGTGCATGT										
rigens_leucoRM1021	TCGAACCCCTGCATAGCAGAACGACCCCGGAACACGTACATACAACCGGGTGTCAAGGGGGACTGG-CTCTAGCCGGCGACCCCTTGATGCCCTGCCTACCTGCGTGCATGT										
pectinataRM1044_1	TCGAACCCCTGCATAGCAGAACGACCCCGGAACACGTACATACAACCGGGTGTCAAGGGGGACTGG-CTCTAGCCGGCGACCCCTTGATGCCCTGCCTACCTGCGTGCATGT										
hybrRM1061	TCGAACCCCTGCATAGCAGAACGACCCCGGAACACGTACATACAACCGGGTGTCAAGGGGGACTGG-CTCTAGCCGGCGACCCCTTGATGCCCTGCCTACCTGCGTGCATGT										
leiopodaRM1063	TCGAACCCCTGCATAGCAGAACGACCCCGGAACACGTACATACAACCGGGTGTCAAGGGGGACTGG-CTCTAGCCGGCGACCCCTTGATGCCCTGCCTACCTGCGTGCATGT										
rigidaRM1082	TCGAACCCCTGCATAGCAGAACGACCCCGGAACACGTACATACAACCGGGTGTCAAGGGGGACTGG-CTCTAGCCGGCGACCCCTTGATGCCCTGCCTACCTGCGTGCATGT										
linearis_linearRM1090	TCGAACCCCTGCATAGCAGAACGACCCCGGAACACGTACATACAACCGGGTGTCAAGGGGGACTGG-CTCTAGCCGGCGACCCCTTGATGCCCTGCCTACCTGCGTGCATGT										
linearis_linearRM1092	TCGAACCCCTGCATAGCAGAACGACCCCGGAACACGTACATACAACCGGGTGTCAAGGGGGACTGG-CTCTAGCCGGCGACCCCTTGATGCCCTGCCTACCTGCGTGCATGT										
linearis_linearRM1094	TCGAACCCCTGCATAGCAGAACGACCCCGGAACACGTACATACAACCGGGTGTCAAGGGGGACTGG--CTCTAGCCGGCGACCCCTTGATGCCCTGCCTACCTGCGTGCATGT										
linearis_linearRM1103	TCGAACCCCTGCATAGCAGAACGACCCCGGAACACGTACATACAACCGGGTGTCAAGGGGGACTGG-CTCTAGCCGGCGACCCCTTGATGCCCTGCCTACCTGCGTGCATGT										
krebsiana_serrRM1137	TCGAACCCCTGCATAGCAGAACGACCCCGGAACACGTACATACAACCGGGTGTCAAGGGGGACTGG-CTCTAGCCGGCGACCCCTTGATGCCCTGCCTACCTGCGTGCATGT										

Appendix 6: Additional nrDNA sequence data for Chapter 4

leiopodaRM1466	TCGAACCCCTGCATAGCAGAACGACCCCGGAACACGTACATACAACCGGGTGTCAAGGGGGACTGG-CTCTAGCCGGCGACCCCTTGATGCCCTGCCAACCTGCGTGCATGT
serrataHerm_RM	TCGAACCCCTGCATAGCAGAACGACCCCGGAACACGTACATACAACCGGGTGTCAAGGGGGACTGG-CTCTAGCCGGCGACCCCTTGATGCCCTGCCTACCTGCGTGCATGT
krebsiana_RVC162	TCGAACCCCTGCATAGCAGAACGACCCCGGAACACGTACATACAACCGGGTGTCAAGGGGGACTGG-CTCTAGCCGGCGACCCCTTGATGCCCTGCCTACCTGCGTKCATGT
krebsiana_krebSH110	TCGAACCCCTGCATAGCAGAACGACCCCGGAACACGTACATACAACCGGGTGTCAAGGGGGACTGG-CTCTAGCCGGCGACCCCTTGATGCCCTGCCTACCTGCGTGCATGT
krebsiana_krebSH111_1	TCGAACCCCTGCATAGCAGAACGACCCCGGAACACGTACATACAACCGGGTGTCAAGGGGGACTGG-CTCTAGCCGGCGACCCCTTGATGCCCTGCCTACCTGCGTGCATGT
krebsiana_krebSH111_2	TCGAACCCCTGCATAGCAGAACGACCCCGGAACACGTACATACAACCGGGTGTCAAGGGGGACTGG-CTCTAGCCGGCGACCCCTTGATGCCCTGCCTACCTGCGTGCATGT
krebsiana_krebSH112	TCGAACCCCTGCATAGCAGAACGACCCCGGAACACGTACATACAACCGGGTGTCAAGGGGGACTGG-CTCTAGCCGGCGACCCCTTGATGCCCTGCCTACCTGCGTGCATGT
krebsianaSH115	TCGAACCCCTGCATAGCAGAACGACCCCGGAACACGTACATACAACCGGGTGTCAAGGGGGACTGG-CTCTAGCCGGCGACCCCTTGATGCCCTGCCTACCTGCGTGCATGT
linearis_linearSH116	TCGAACCCCTGCATAGCAGAACGACCCCGGAACACGTACATACAACCGGGTGTCAAGGGGGACTGG-CTCTAGCCGGCGACCCCTTGATGCCCTGCCTACCTGCGTGCATGT
linearis_linearSH117	TCGAACCCCTGCATAGCAGAACGACCCCGGAACACGTACATACAACCGGGTGTCAAGGGGGACTGG-CTCTAGCCGGCGACCCCTTGATGCCCTGCCTACCTGCGTGCATGT
krebsianaSH118	TCGAACCCCTGCATAGCAGAACGACCCCGGAACACGTACATACAACCGGGTGTCAAGGGGGACTGG-CTCTAGCCGGCGACCCCTTGATGCCCTGCCTACCTGCGTGCATGT
linearis_linearSH131	TCGAACCCCTGCATAGCAGAACGACCCGYGAACACGTACATACAACCGGGTGTCAAGGGGGACTGG-CTCTAGCCGGCGACCCCTTGATGCCCTGCCTACCTGCGTGCATGT
linearis_linearSH132	TCGAACCCCTGCATAGCAGAACGACCCCGGAACACGTACATACAACCGGGTGTCAAGGGGGACTGG-CTCTAGCCGGCGACCCCTTGATGCCCTGCCTACCTGCGTGCATGT
krebsianaSH133	TCGAACCCCTGCATAGCAGAACGACCCCGGAACACGTACATACAACCGGGTGTCAAGGGGGACTGG-CTCTAGCCGGCGACCCCTTGATGCCCTGCCTACCTGCGTGCATGT
krebsianaSH135	TCGAACCCCTGCATAGCAGAACGACCCCGGAACACGTACATACAACCGGGTGTCAAGGGGGACTGG-CTCTAGCCGGCGACCCCTTGATGCCCTGCCTACCTGCGTGCATGT
krebsianaSR480	TCGAACCCCTGCATAGCAGAACGACCCCGGAACACGTACATACAACCGGGTGTCAAGGGGGACTGG-CTCTAGCCGGCGACCCCTTGATGCCCTGCCTACCTGCGTGCATGT
krebsianaSR520	TCGAACCCCTGCATAGCAGAACGACCCCGGAACACGTACATACAACCGGGTGTCAAGGGGGACTGG-CTCTAGCCGGCGACCCCTTGATGCCCTGCCTACCTGCGTGCATGT
linearis_linearSR523	TCGAACCCCTGCATAGCAGAACGACCCCGGAACACGTACATACAACCGGGTGTCAAGGGGGACTGG-CTCTAGCCGGCGACCCCTTGATGCCCTGCCTACCTGCGTGCATGT
krebsianaSR564	TCGAACCCCTGCATAGCAGAACGACCCCGGAACACGTACATACAACCGGGTGTCAAGGGGGACTGG-CTCTAGCCGGCGACCCCTTGATGCCCTGCCTACCTGCGTGCATGT
linearis_linearSR571	TCGAACCCCTGCATAGCAGAACGACCCCGGAACACGTACATACAACCGGGTGTCAAGGGGGACTGG-CTCTAGCCGGCGACCCCTTGATGCCCTGCCTACCTGCGTGCATGT
rigens_rigSR574	TCGAACCCCTGCATAGCAGAACGACCCCGGAACACGTACATACAACCGGGTGTCAAGGGGGACTGG-CTCTAGCCGGCGACCCCTTGATGCCCTGCCTACCTGCGTGCATGT
rigens_rigSR575	TCGAACCCCTGCATAGCAGAACGACCCCGGAACACGTACATACAACCGGGTGTCAAGGGGGACTGG-CTCTAGCCGGCGACCCCTTGATGCCCTGCCTACCTGCGTGCATGT
rigensSR581	TCGAACCCCTGCATAGCAGAACGACCCCGGAACACGTACATACAACCGGGTGTCAAGGGGGACTGG-CTCTAGCCGGCGACCCCTTGATGCCCTGCCTACCTGCGTGCATGT
rigens_uniflSR625	TCGAACCCCTGCATAGCAGAACGACCCCGGAACACGTACATACAACCGGGTGTCAAGGGGGACTGG-CTCTAGCCGGCGACCCCTTGATGCCCTGCCTACCTGCGTGCATGT
krebsiana_krebSVHF1	TCGAACCCCTGCATAGCAGAACGACCCCGGAACACGTACATACAACCGGGTGTCAAGGGGGACTGG-CTCTAGCCGGCGACCCCTTGATGCCCTGCCTACCTGCGTGCATGT
krebsiana_arctSV_HF2	TCGAACCCCTGCATAGCAGAACGACCCCGGAACACGTACATACAACCGGGTGTCAAGGGGGACTGG-CTCTAGCCGGCGACCCCTTGATGCCCTGCCTACCTGCGTGCATGT

[120	130	140	150	160	170	180	190	200	210	220]
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lichtensteiniRM1323	GGCCCTTTCTGGG-CTCGTGAACGTGTAGTGTGGCATCAAAAACAAA-CCCCGGCACGGCATGTGCCAAGGAAAACAAAACATAAGAAGGGCTCGTATCGTGTGTCGCCG
lichtesteniM050906_2	GGCCCTTTCTGGG-CTCGTGAACGTGTAGTGTGGCATCAAAAACAAA-CCCCGGCACGGCATGTGCCAAGGAAAACAAAACATAAGAAGGGCTCGTATCGTGTGTCGCCG
heterochaetaM160901_5g	AGCC-TTTCTGGG-CTCGTGAAC--GTAGTGTGGCATCAAAAACAAA-CCCCGGCACGGCATGTGCCAAGGAAAACAAAACAAAAGAAGGGCTCGTATCGTGTGTCGCCG
heterochaetaRM1348	AGCC-TTTCTGGG-CTCGTGAAC--GTAGTGTGGCATCAAAAACAAA-CCCCGGCACGGCATGTGCCAAGGAAAACAAAACAAAAGAAGGGCTCGTATCGTGTGTCGCCG
heterochaetaRM1255	AGCCCTTTCTGGG-CTCGTGAAC--GTAGTGTGGCATCAAAAACAAA-CCCCGGCACGGCATGTGCCAAGGAAAACAAAACATAAGAAGGGCTCGTATCGTGTGTCGCCG
tenuifoliaM7219_10	AGCCCTTTCTGGG-CTCGTGAAC--GTAGTGTGGCATCAAAAACAAA-CCCCGGCACGGCATGTGCCAAGGAAAAGAAAACATAAGAAGGGCTCGTATCGTGTGTCGCCG
tenuifoliaRM1352	AGCCCTTTCTGGG-CTCGTGAAC--GTAGTGTGGCATCAAAAACAAA-CCCCGGCACGGCATGTGCCAAGGAAAAGAAAACATAAGAAGGGCTCGTATCGTGTGTCGCCG
ciliarisSR705	AGCCCTTTCTGGGCTCGTGAAC--GCAGTGTGGCATCAAAAACAAA-CCCCGGCACGGCATGTGCCAAGGAAAACAAAATATAAGAAGGGCTCGCATCTTGTGTCGCCG
jurineifolia_scabCAM1953	AGCCCTTTCTGGGCTCGTGAAC--GTTA-TGTAGGCACAAAACAAA-CCCCGGCACGGCATGTGCCAAGGAAAACAAAACATAAGAAGGGCTCGTAYCGTGTGTCGCCG
rigens_unifl_Boknes1	AGCCCTTTCTGGGCTCGTGAAC--TTAGTGTGGCATCTAAACAAA-CCCCGGCACGGCATGTGCCAAGGAAAACAAAACATAGGAAGGGCTCGTACCCTGGCGTCCCG
linearis_linear_Boknes2	AGCCCTTTCTGGGCTCGTGAAC--TTAGTGTGGCATCTAAACAAA-CCCCGGCACGGCATGTGCCAAGGAAAACAAAACATAGGAAGGGCTCGTACCCTGGCGTCCCG
linearis_ovalM041001_2g	AGCCCTTTCTGGGCTCGTGAAC--TTAGTGTGGCATCTAAACAAA-CCCCGGCACGGCATGTGCCAAGGAAAACAAAACATAGGAAGGGCTCGTACCCTGGCGTCCCG
rigens_leuco_M070704_1	AGCCCTTTCTGGGCTCGTGAAC--TTAGTGTGGCATCTAAACAAA-CCCCGGCACGGCATGTGCCAAGGAAAACAAAACATAGGAAGGGCTCGTACCCTGGCGTCCCG
krebsiana_krebM071001_1g	AGCCCTTTCTGGGCTCGTGAAC--TTAGTGTGGCATCTAAACAAA-CCCCGGCACGGCATGTGCCAAGGAAAACAAAACATAGGAAGGGCTCGTACCCTGGCGTCCCG
krebsiana_krebM071001_3g1	AGCCCTTTCTGGGCTCGTGAAC--TTAGTGTGGCATCTAAACAAA-CCCCGGCACGGCATGTGCCAAGGAAAACAAAACATAGGAAGGGCTCGTACCCTGGCGTCCCG
krebsiana_arctM071001_3pg	AGCCCTTTCTGGGCTCGTGAAC--TTAGTGTGGCATCTAAACAAA-CCCCGGCACGGCATGTGCCAAGGAAAACAAAACATAGGAAGGGCTCGTACCCTGGCGTCCCG
rigidaM100903_4	AGCCCTTTCTGGGCTCGTGAAC--TTAGTGTGGCATCTAAACAAA-CCCCGGCACGGCATGTGCCAAGGAAAACAAAACATAGGAAGGGCTCGTACCCTGGCGTCCCG
rigidaM100904_4	AGCCCTTTCTGGGCTCGTGAAC--TTAGTGTGGCATCTAAACAAA-CCCCGGCACGGCATGTGCCAAGGAAAACAAAACATAGGAAGGGCTCGTACCCTGGCGTCCCG
rigidM110805_10	AGCCCTTTCTGGGCTCGTGAAC--TTAGTGTGGCATCTAAACAAA-CCCCGGCACGGCATGTGCCAAGGAAAACAAAACATAGGAAGGGCTCGTACCCTGGCGTCCCG
rigidaM120805_80	AGCCCTTTCTGGGCTCGTGAAC--TCAGTGTGGCATCTAAACAAA-CCCCGGCACGGCATGTGCCAAGGAAAACAAAACATAGGAAGGGCTCGTACCCTGGCGTCCCG
leiopodaM160704_5	AGCCCTTTCTGGGCTCGTGAAC--TTAGTGTGGCATCTAAACAAA-CCCCGGCACGGCATGTGCCAAGGAAAACAAAACATAGGAAGGGCTCGTACCCTGGCGTCCCG
pectinataM180904_5	AGCCCTTTCTGGGCTCGTGAAC--TCAGTGTGGCATCTAAACAAA-CCCCGGCACGGCATGTGCCAAGGAAAACAAAACATAGGAAGGGCTCGTACCCTGGCGTCCCG

Appendix 6: Additional nrDNA sequence data for Chapter 4

krebsiana_krebRM992	TTCGCGGTGTGCGCATGTGCGTGTCTCTTTTGTAAATCACAAACGACTCTCGGCAACGGATATCTCGGCTCACGCATCGATGAAGAACGTAGCAAAATGCGATACTTGGTG
krebsiana_RM996	TTCGCGGTGTGCGCATGTGCGTGTCTCTTTTGTAAATCACAAACGACTCTCGGCAACGGATATCTCGGCTCACGCATCGATGAAGAACGTAGCAAAATGCGATACTTGGTG
krebsiana_krebRM1403	TTCGCGGTGTGCGCATGTGCGTGTCTCTTTTGTAAATCACAAACGACTCTCGGCAACGGATATCTCGGCTCACGCATCGATGAAGAACGTAGCAAAATGCGATACTTGGTG
linearis_linearRM1406_1	TTCGCGGTGTGCGCATGTGCGTGTCTCTTTTGTAAATCACAAACGACTCTCGGCAACGGATATCTCGGCTCACGCATCGATGAAGAACGTAGCAAAATGCGATACTTGGTG
linearis_linearRM1406_2	TTCGCGGTGTGCGCATGTGCGTGTCTCTTTTGTAAATCACAAACGACTCTCGGCAACGGATATCTCGGCTCACGCATCGATGAAGAACGTAGCAAAATGCGATACTTGGTG
leiopodaRM1466	TTCGCGGTGTGCGCATGTGCGTGTCTCTTTTGTAAATCACAAACGACTCTCGGCAACGGATATCTCGGCTCACGCATCGATGAAGAACGTAGCAAAATGCGATACTTGGTG
serrataHerm_RM	TTCGCGGTGTGCGCATGTGCGTGTCTCTTTTGTAAATCACAAACGACTCTCGGCAACGGATATCTCGGCTCACGCATCGATGAAGAACGTAGCAAAATGCGATACTTGGTG
krebsiana_RVC162	TTCGCGGTGTGCGCATGTGCGTGTCTCTTTTGTAAATCACAAACGACTCTCGGCAACGGATATCTCGGCTCACGCATCGATGAAGAACGTAGCAAAATGCGATACTTGGTG
krebsiana_krebSH110	TTCGCGGTGTGCGCATGTGCGTGTCTCTTTTGTAAATCACAAACGACTCTCGGCAACGGATATCTCGGCTCACGCATCGATGAAGAACGTAGCAAAATGCGATACTTGGTG
krebsiana_krebSH111_1	TTCGCGGTGTGCGCATGTGCGTGTCTCTTTTGTAAATCACAAACGACTCTCGGCAACGGATATCTCGGCTCACGCATCGATGAAGAACGTAGCAAAATGCGATACTTGGTG
krebsiana_krebSH111_2	TTCGCGGTGTGCGCATGTGCGTGTCTCTTTTGTAAATCACAAACGACTCTCGGCAACGGATATCTCGGCTCACGCATCGATGAAGAACGTAGCAAAATGCGATACTTGGTG
krebsiana_krebSH112	TTCGCGGTGTGCGCATGTGCGTGTCTCTTTTGTAAATCACAAACGACTCTCGGCAACGGATATCTCGGCTCACGCATCGATGAAGAACGTAGCAAAATGCGATACTTGGTG
krebsianaSH115	TTCGCGGTGTGCGCATGTGCGTGTCTCTTTTGTAAATCACAAACGACTCTCGGCAACGGATATCTCGGCTCACGCATCGATGAAGAACGTAGCAAAATGCGATACTTGGTG
linearis_linearSH116	TTCGCGGTGTGCGCATGTGCGTGTCTCTTTTGTAAATCACAAACGACTCTCGGCAACGGATATCTCGGCTCACGCATCGATGAAGAACGTAGCAAAATGCGATACTTGGTG
linearis_linearSH117	TTCGCGGTGTGCGCATGTGCGTGTCTCTTTTGTAAATCACAAACGACTCTCGGCAACGGATATCTCGGCTCACGCATCGATGAAGAACGTAGCAAAATGCGATACTTGGTG
krebsianaSH118	TTCGCGGTGTGCGCATGTGCGTGTCTCTTTTGTAAATCACAAACGACTCTCGGCAACGGATATCTCGGCTCACGCATCGATGAAGAACGTAGCAAAATGCGATACTTGGTG
linearis_linearSH131	TTCGCGGTGTGCGCATGTGCGTGTCTCTTTTGTAAATCACAAACGACTCTCGGCAACGGATATCTCGGCTCACGCATCGATGAAGAACGTAGCAAAATGCGATACTTGGTG
linearis_linearSH132	TTCGCGGTGTGCGCATGTGCGTGTCTCTTTTGTAAATCACAAACGACTCTCGGCAACGGATATCTCGGCTCACGCATCGATGAAGAACGTAGCAAAATGCGATACTTGGTG
krebsianaSH133	TTCGCGGTGTGCGCATGTGCGTGTCTCTTTTGTAAACACAAACGACTCTCGGCAACGGATATCTCGGCTCACGCATCGATGAAGAACGTAGCAAAATGCGATACTTGGTG
krebsianaSH135	TTCGCGGTGTGCGCATGTGCGTGTCTCTTTTGTAAATCACAAACGACTCTCGGCAACGGATATCTCGGCTCACGCATCGATGAAGAACGTAGCAAAATGCGATACTTGGTG
krebsianaSR480	TTCGCGGTGTGCGCATGTGCGTGTCTCTTTTGTAAATCACAAACGACTCTCGGCAACGGATATCTCGGCTCACGCATCGATGAAGAACGTAGCAAAATGCGATACTTGGTG
krebsianaSR520	TTCGCGGTGTGCGCATGTGCGTGTCTCTTTTGTAAATCACAAACGACTCTCGGCAACGGATATCTCGGCTCACGCATCGATGAAGAACGTAGCAAAATGCGATACTTGGTG
linearis_linearSR523	TTCGCGGTGTGCGCATGTGCGTGTCTCTTTTGTAAATCACAAACGACTCTCGGCAACGGATATCTCGGCTCACGCATCGATGAAGAACGTAGCAAAATGCGATACTTGGTG
krebsianaSR564	TTCGCGGTGTGCGCATGTGCGTGTCTCTTTTGTAAATCACAAACGACTCTCGGCAACGGATATCTCGGCTCACGCATCGATGAAGAACGTAGCAAAATGCGATACTTGGTG
linearis_linearSR571	TTCGCGGTGTGCGCATGTGCGTGTCTCTTTTGTAAATCACAAACGACTCTCGGCAACGGATATCTCGGCTCACGCATCGATGAAGAACGTAGCAAAATGCGATACTTGGTG
rigens_rigSR574	TTCGCGGTGTGCGCATGTGCGTGTCTCTTTTGTAAATCACAAACGACTCTCGGCAACGGATATCTCGGCTCACGCATCGATGAAGAACGTAGCAAAATGCGATACTTGGTG
rigens_rigSR575	TTCGCGGTGTGCGCATGTGCGTGTCTCTTTTGTAAATCACAAACGACTCTCGGCAACGGATATCTCGGCTCACGCATCGATGAAGAACGTAGCAAAATGCGATACTTGGTG
rigensSR581	TTCGCGGTGTGCGCATGTGCGTGTCTCTTTTGTAAATCACAAACGACTCTCGGCAACGGATATCTCGGCTCACGCATCGATGAAGAACGTAGCAAAATGCGATACTTGGTG
rigens_uniflSR625	TTCGCGGTGTGCGCATGTGCGTGTCTCTTTTGTAAATCACAAACGACTCTCGGCAACGGATATCTCGGCTCACGCATCGATGAAGAACGTAGCAAAATGCGATACTTGGTG
krebsiana_krebSVHF1	TTCGCGGTGTGCGCATGTGCGTGTCTCTTTTGTAAATCACAAACGACTCTCGGCAACGGATATCTCGGCTCACGCATCGATGAAGAACGTAGCAAAATGCGATACTTGGTG
krebsiana_arctSV_HF2	TTCGCGGTGTGCGCATGTGCGTGTCTCTTTTGTAAATCACAAACGACTCTCGGCAACGGATATCTCGGCTCACGCATCGATGAAGAACGTAGCAAAATGCGATACTTGGTG
[340 350 360 370 380 390 400 410 420 430 440]
lichtensteiniRM1323	TGAATTGCAGAATCCCGTGAACCATCGAGTTTTTGAACGCAAGTTGCGCCCGAAACCATTTCGGTCGAGGGCACGTCTGCCTGGGCGTCACGCATCGCGTCGCCCCCTCAC
lichtesteniim050906_2	TGAATTGCAGAATCCCGTGAACCATCGAGTTTTTGAACGCAAGTTGCGCCCGAAACCATTTCGGTCGAGGGCACGTCTGCCTGGGCGTCACGCATCGCGTCGCCCCCTCAC
heterochaetaM160901_5g	TGAATTGCAGAATCCCGTGAACCATCGAGTTTTTGAACGCAAGTTGCGCCCGAAACCATTTCGGTCGAGGGCACGTCTGCCTGGGCGTCACGCATCGCGTCGCCCCCTCAC
heterochaetaRM1348	TGAATTGCAGAATCCCGTGAACCATCGAGTTTTTGAACGCAAGTTGCGCCCGAAACCATTTCGGTCGAGGGCACGTCTGCCTGGGCGTCACGCATCGCGTCGCCCCCTCAC
heterochaetaRM1255	TGAATTGCAGAATCCCGTGAACCATCGAGTTTTTGAACGCAAGTTGCGCCCGAAACCATTTCGGTCGAGGGCACGTCTGCCTGGGCGTCACGCATCGCGTCGCCCCCTCAC
tenuifoliaM7219_10	TGAATTGCAGAATCCCGTGAACCATCGAGTTTTTGAACGCAAGTTGCGCCCGAAACCATTTCGGTCGAGGGCACGTCTGCCTGGGCGTCACGCATCGCGTCGCCCCCTCAC
tenuifoliaRM1352	TGAATTGCAGAATCCCGTGAACCATCGAGTTTTTGAACGCAAGTTGCGCCCGAAACCATTTCGGTCGAGGGCACGTCTGCCTGGGCGTCACGCATCGCGTCGCCCCCTCAC
ciliarisSR705	TGAATTGCAGAATCCCGTGAACCATCGAGTTTTTGAACGCAAGTTGCGCCCGAAACCATTTCGGTCGAGGGCACGTCTGCCTGGGCGTCACGCATCGCGTCGCCCCCTCAC
jurineifolia_scabCAM1953	TGAATTGCAGAATCCCGTGAACCATCGAGTTTTTGAACGCAAGTTGCGCCCGAAACCATTTCGGTCGAGGGCACGTCTGCCTGGGCGTCACGCATCGCGTCGCCCCCTCAC
rigens_unifl_Boknes1	TGAATTGCAGAATCCCGTGAACCATCGAGTTTTTGAACGCAAGTTGCGCCCGAAACCATTTCGGTCGAGGGCACGTCTGCCTGGGCGTCACGCATCGCGTCGCCCCCTCAC
linearis_linear_Boknes2	TGAATTGCAGAATCCCGTGAACCATCGAGTTTTTGAACGCAAGTTGCGCCCGAAACCATTTCGGTCGAGGGCACGTCTGCCTGGGCGTCACGCATCGCGTCGCCCCCTCAC
linearis_ovalM041001_2g	TGAATTGCAGAATCCCGTGAACCATCGAGTTTTTGAACGCAAGTTGCGCCCGAAACCATTTCGGTCGAGGGCACGTCTGCCTGGGCGTCACGCATCGCGTCGCCCCCTCAC
rigens_leuco_M070704_1	TGAATTGCAGAATCCCGTGAACCATCGAGTTTTTGAACGCAAGTTGCGCCCGAAACCATTTCGGTCGAGGGCACGTCTGCCTGGGCGTCACGCATCGCGTCGCCCCCTCAC
krebsiana_krebM071001_1g	TGAATTGCAGAATCCCGTGAACCATCGAGTTTTTGAACGCAAGTTGCGCCCGAAACCATTTCGGTCGAGGGCACGTCTGCCTGGGCGTCACGCATCGCGTCGCCCCCTCAC
krebsiana_krebM071001_3g1	TGAATTGCAGAATCCCGTGAACCATCGAGTTTTTGAACGCAAGTTGCGCCCGAAACCATTTCGGTCGAGGGCACGTCTGCCTGGGCGTCACGCATCGCGTCGCCCCCTCAC
krebsiana_arctM071001_3pg	TGAATTGCAGAATCCCGTGAACCATCGAGTTTTTGAACGCAAGTTGCGCCCGAAACCATTTCGGTCGAGGGCACGTCTGCCTGGGCGTCACGCATCGCGTCGCCCCCTCAC
rigidaM100903_4	TGAATTGCAGAATCCCGTGAACCATCGAGTTTTTGAACGCAAGTTGCGCCCGAAACCATTTCGGTCGAGGGCACGTCTGCCTGGGCGTCACGCATCGCGTCGCCCCCTCAC

Appendix 6: Additional nrDNA sequence data for Chapter 4

linearis_linearSR571 TGAATTGCAGAATCCCCTGAACCATCGAGTTTTTGAACGCAAGTTGCGCCCGAAACCATTCCGGTCGAGGGCACGCTGCCTGGGCGTCACGCATCGCGTCGCCCCCTCAC
 rigens_rigSR574 TGAATTGCAGAATCCCCTGAACCATCGAGTTTTTGAACGCAAGTTGCGCCCGAAACCATTCCGGTCGAGGGCACGCTGCCTGGGCGTCACGCATCGCGTCGCCCCCTCAC
 rigens_rigSR575 TGAATTGCAGAATCCCCTGAACCATCGAGTTTTTGAACGCAAGTTGCGCCCGAAACCATTCCGGTCGAGGGCACGCTGCCTGGGCGTCACGCATCGCGTCGCCCCCTCAC
 rigensSR581 TGAATTGCAGAATCCCCTGAACCATCGAGTTTTTGAACGCAAGTTGCGCCCGAAACCATTCCGGTCGAGGGCACGCTGCCTGGGCGTCACGCATCGCGTCGCCCCCTCAC
 rigens_uniflSR625 TGAATTGCAGAATCCCCTGAACCATCGAGTTTTTGAACGCAAGTTGCGCCCGAAACCATTCCGGTCGAGGGCACGCTGCCTGGGCGTCACGCATCGCGTCGCCCCCTCAC
 krebsiana_krebSVHF1 TGAATTGCAGAATCCCCTGAACCATCGAGTTTTTGAACGCAAGTTGCGCCCGAAACCATTCCGGTCGAGGGCACGCTGCCTGGGCGTCACGCATCGCGTCGCCCCCTCAC
 krebsiana_arctSV_HF2 TGAATTGCAGAATCCCCTGAACCATCGAGTTTTTGAACGCAAGTTGCGCCCGAAACCATTCCGGTCGAGGGCACGCTGCCTGGGCGTCACGCATCGCGTCGCCCCCTCAC

[450 460 470 480 490 500 510 520 530 540 550]

lichtensteiniRM1323 AAC-CCTCCTGTTGGGAAACAGTTGTGTGTCAGGGGGCGGATATTGGTCTCCCATGCCTTTGGTGTGGTTGGCCTAAATCAGAGTCCCCTYGGTGGACGCACGGCTAGTGG
 lichtesteiniM050906_2 AAC-CCTCCTGTTGGGAAACAGTTGTGTGTCAGGGGGCGGATATTGGTCTCCCATGCCTTTGGTGTGGTTGGCCTAAATCAGAGTCCCCTYGGTGGACGCACGGCTAGTGG
 heterochaetaM160901_5g TAC-CCTTCCTGTTGGGAAACAGTTGTGTGTCAGGGGGCGGATATTGGTCTCCCATGCCTTTGGTGTGGTTGGCCTAAATCAGAGTCCCCTYGGTGGACGCACGGCTAGTGG
 heterochaetaRM1348 TAC-CCTTCCTGTTGGGAAACAGTTGTGTGTCAGGGGGCGGATATTGGTCTCCCATGCCTTTGGTGTGGTTGGCCTAAATCAGAGTCCCCTYGGTGGACGCACGGCTAGTGG
 heterochaetaRM1255 AAC-CCTTCCTGTTGGGAAACAGTTGTGTGTCAGGGGGCGGATATTGGTCTCCCATGCCTTTGGTGTGGTTGGCCTAAATCAGAGTCCCCTYGGTGGACGCACGGCTAGTGG
 tenuifoliaM7219_10 AACTCCTCCCTGTTGGGAAACAGTTGTGTGTCAGGGGGCGGATATTGGTCTCCCATGCCTTTGGTGTGGTTGGCCTAAATCAGAGTCCCCTYGGTGGACGCACGGCTAGTGG
 tenuifoliaRM1352 AACTCCTCCCTGTTGGGAAACAGTTGTGTGTCAGGGGGCGGATATTGGTCTCCCATGCCTTTGGTGTGGTTGGCCTAAATCAGAGTCCCCTYGGTGGACGCACGGCTAGTGG
 ciliarisSR705 AACTCCTCCCTTTTGGGAAACAGTTGTGTGTCAGGGGGCGGATATTGGTCTCCCATGCCTTTGGTGTGGTTGGCCTAAATCAGAGTCCCCTYGGTGGACGCACGGCTAGTGG
 jurineifolia_scabCAM1953 AACTCCTCCCTGTTGGGAAACAGTTGTGTGTCAGGGGGCGGATATTGGTCTCCCATGCCTTTGGTGTGGTTGGCCTAAATCAGAGTCCCCTYGGTGGACGCACGGCTAGTGG
 rigens_unifl_Boknes1 AACTCCTCCCTGTTGGGAAACAGTTGTGTGTCAGGGGGCGGATATTGGTCTCCCATGCCTTTGGTGTGGTTGGCCTAAATCAGAGTCCCCTYGGTGGACGCACGGCTAGTGG
 linearis_linear_Boknes2 AACTCCTCCCTGTTGGGAAACAGTTGTGTGTCAGGGGGCGGATATTGGTCTCCCATGCCTTTGGTGTGGTTGGCCTAAATCAGAGTCCCCTYGGTGGACGCACGGCTAGTGG
 linearis_ovalM041001_2g AACTCCTCCCTRTTGGGAAACAGTTGTGTGTCAGGGGGCGGATATTGGTCTCCCATGCCTTTGGTGTGGTTGGCCTAAATCAGAGTCCCCTYGGTGGACGCACGGCTAGTGG
 rigens_leuco_M070704_1 AACTCCTCCCTGTTGGGAAACAGTTGTGTGTCAGGGGGCGGATATTGGTCTCCCATGCCTTTGGTGTGGTTGGCCTAAATCAGAGTCCCCTYGGTGGACGCACGGCTAGTGG
 krebsiana_krebM071001_1g AACTCCTCCCTATTGGGAAACAGTTGTGTGTCAGGGGGCGGATATTGGTCTCCCATGCCTTTGGTGTGGTTGGCCTAAATCAGAGTCCCCTYGGTGGACGCACGGCTAGTGG
 krebsiana_krebM071001_3g1 AACTCCTCCCTGTTGGGAAACAGTTGTGTGTCAGGGGGCGGATATTGGTCTCCCATGCCTTTGGTGTGGTTGGCCTAAATCAGAGTCCCCTYGGTGGACGCACGGCTAGTGG
 krebsiana_arctM071001_3pg AACTCCTCCCTGTTGGGAAACAGTTGTGTGTCAGGGGGCGGATATTGGTCTCCCATGCCTTTGGTGTGGTTGGCCTAAATCAGAGTCCCCTYGGTGGACGCACGGCTAGTGG
 rigidaM100903_4 AACTCCTCCCTGTTGGGAAACAGTTGTGTGTCAGGGGGCGGATATTGGTCTCCCATGCCTTTGGTGTGGTTGGCCTAAATCAGAGTCCCCTYGGTGGACGCACGGCTAGTGG
 rigidaM100904_4 AACTCCTCCCTGTTGGGAAACAGTTGTGTGTCAGGGGGCGGATATTGGTCTCCCATGCCTTTGGTGTGGTTGGCCTAAATCAGAGTCCCCTYGGTGGACGCACGGCTAGTGG
 rigidM110805_10 AACTCCTCCCTGTTGGGAAACAGTTGTGTGTCAGGGGGCGGATATTGGTCTCCCATGCCTTTGGTGTGGTTGGCCTAAATCAGAGTCCCCTYGGTGGACGCACGGCTAGTGG
 rigidaM120805_80 AACTCCTCCCTGTTGGGAAACAGTTGTGTGTCAGGGGGCGGATATTGGTCTCCCATGCCTTTGGTGTGGTTGGCCTAAATCAGAGTCCCCTYGGTGGACGCACGGCTAGTGG
 leiopodaM160704_5 AACTCCTCCCTGTTGGGAAACAGTTGTGTGTCAGGGGGCGGATATTGGTCTCCCATGCCTTTGGTGTGGTTGGCCTAAATCAGAGTCCCCTYGGTGGACGCACGGCTAGTGG
 pectinataM180904_5 AACTCCTCCCTGTTGGGAAACAGTTGTGTGTCAGGGGGCGGATATTGGTCTCCCATGCCTTTGGTGTGGTTGGCCTAAATCAGAGTCCCCTYGGTGGACGCACGGCTAGTGG
 krebsiana_krebM210902_1 AACTCCTCCCTRTTGGGAAACAGTTGTGTGTCAGGGGGCGGATATTGGTCTCCCATGCCTTTGGTGTGGTTGGCCTAAATCAGAGTCCCCTYGGTGGACGCACGGCTAGTGG
 krebsiana_krebM230803_8 AACTCCTCCCTGTTGGGAAACAGTTGTGTGTCAGGGGGCGGATATTGGTCTCCCATGCCTTTGGTGTGGTTGGCCTAAATCAGAGTCCCCTYGGTGGACGCACGGCTAGTGG
 serrM230901_7g AACTCCTCCCTGTTGGGAAACAGTTGTGTGTCAGGGGGCGGATATTGGTCTCCCATGCCTTTGGTGTGGTTGGCCTAAATCAGAGTCCCCTYGGTGGACGCACGGCTAGTGG
 leiopodaM250901_34 AACTCCTCCCTGTTGGGAAACAGTTGTGTGTCAGGGGGCGGATATTGGTCTCCCATGCCTTTGGTGTGGTTGGCCTAAATCAGAGTCCCCTYGGTGGACGCACGGCTAGTGG
 pectinataM250901_37 AACTCCTCCCTGTTGGGAAACAGTTGTGTGTCAGGGGGCGGATATTGGTCTCCCATGCCTTTGGTGTGGTTGGCCTAAATCAGAGTCCCCTYGGTGGACGCACGGCTAGTGG
 pectM260901_2g AACTCCTCCCTGTTGGGAAACAGTTGTGTGTCAGGGGGCGGATATTGGTCTCCCATGCCTTTGGTGTGGTTGGCCTAAATCAGAGTCCCCTYGGTGGACGCACGGCTAGTGG
 maritimaM260901 AACTCCTCCCTGTTGGGAAACAGTTGTGTGTCAGGGGGCGGATATTGGTCTCCCATGCCTTTGGTGTGGTTGGCCTAAATCAGAGTCCCCTYGGTGGACGCACGGCTAGTGG
 krebsiana_krebM261001_2 AACTCCTCCCTGTTGGGAAACAGTTGTGTGTCAGGGGGCGGATATTGGTCTCCCATGCCTTTGGTGTGGTTGGCCTAAATCAGAGTCCCCTYGGTGGACGCACGGCTAGTGG
 maritimaM270901_5g AACTCCTCCCTGTTGGGAAACAGTTGTGTGTCAGGGGGCGGATATTGGTCTCCCATGCCTTTGGTGTGGTTGGCCTAAATCAGAGTCCCCTYGGTGGACGCACGGCTAGTGG
 rigens_rigensM7293 AACTCCTCCCTGTTGGGAAACAGTTGTGTGTCAGGGGGCGGATATTGGTCTCCCATGCCTTTGGTGTGGTTGGCCTAAATCAGAGTCCCCTYGGTGGACGCACGGCTAGTGG
 rigens_rigensM7298_2 AACTCCTCCCTGTTGGGAAACAGTTGTGTGTCAGGGGGCGGATATTGGTCTCCCATGCCTTTGGTGTGGTTGGCCTAAATCAGAGTCCCCTYGGTGGACGCACGGCTAGTGG
 rigens_rigensM7527_2 AACTCCTCCCTGTTGGGAAACAGTTGTGTGTCAGGGGGCGGATATTGGTCTCCCATGCCTTTGGTGTGGTTGGCCTAAATCAGAGTCCCCTYGGTGGACGCACGGCTAGTGG
 leiopodaM200901_22g AACTCCTCCCTGTTGGGAAACAGTTGTGTGTCAGGGGGCGGATATTGGTCTCCCATGCCTTTGGTGTGGTTGGCCTAAATCAGAGTCCCCTYGGTGGACGCACGGCTAGTGG
 spnov_M7237_4 AACTCCTCCCTGTTGGGAAACAGTTGTGTGTCAGGGGGCGGATATTGGTCTCCCATGCCTTTGGTGTGGTTGGCCTAAATCAGAGTCCCCTYGGTGGACGCACGGCTAGTGG
 serrataHerm_NB AACTCCTCCCTGTTGGGAAACAGTTGTGTGTCAGGGGGCGGATATTGGTCTCCCATGCCTTTGGTGTGGTTGGCCTAAATCAGAGTCCCCTYGGTGGACGCACGGCTAGTGG
 krebsiana_krebNB1465 AACTCCTCCCTGTTGGGAAACAGTTGTGTGTCAGGGGGCGGATATTGGTCTCCCATGCCTTTGGTGTGGTTGGCCTAAATCAGAGTCCCCTYGGTGGACGCACGGCTAGTGG
 linearis_linearRM1013 AACTCCTCCCTGTTGGGAAACAGTTGTGTGTCAGGGGGCGGATATTGGTCTCCCATGCCTTTGGTGTGGTTGGCCTAAATCAGAGTCCCCTYGGTGGACGCACGGCTAGTGG
 rigens_leucoRM1021 AACTCCTCCCTGTTGGGAAACAGTTGTGTGTCAGGGGGCGGATATTGGTCTCCCATGCCTTTGGTGTGGTTGGCCTAAATCAGAGTCCCCTYGGTGGACGCACGGCTAGTGG

Appendix 6: Additional nrDNA sequence data for Chapter 4

rigens_leucoRM919	GCGGGACTACCCGCTGAGGGTAGCATTCTCTTCGACGCAACCCGCCACGCATGGACTAGCCAACACGCGACGAG-TG-ATCGTTTTAGAGAAGCGAGAACGCTAATCAA
krebsiana_krebrM929	GCGGGACTACCCGCTGAGGGTAGCATTCTCTTCGACGCAACCCGCCACGCATGGACTAGCCAACACGCGACGAG-TG-ATCGTTTTAGAGAAGCGAGAACGCTAAACAA
krebsiana_krebrM949	GCGGGACTACCCGCTGAGGGTAGCATTCTCTTCGACGCAACCCGCCACGCATGGACTAGCCAACACGCGACGAG-TG-ATCGTTTTAGAGAAGCGAGAACGCTAAACAA
krebsiana_krebrM950	GCGGGACTACCCGCTGAGGGTAGCATTCTCTTCGACGCAACCCGCCACGCATGGACTAGCCAACACGCGACGAG-TG-ATCGTTTTAGAGAAGCGAGAACGCTAAACAA
linearis_linearRM951	GCGGGACTACCCGCTGAGGGTAGCATTCTCTTCGACGCAACCCGCCACGCATGGACTAGCCAACACGCGACGAG-TG-ATCGTTTTAGAGAAGCGAGAACGCTAAACAA
krebsiana_krebrM960	GCGGG?????????????GGTAGCATTCTCTTCGACGCAACCCGCCACGCATGGACTAGCCAACACGCGACGAG-TG-ATCGTTTTAGAGAAGCGAGAACGCTAAACAA
krebsiana_krebrM962	GCGGGACTACCCGCTGAGGGTAGCATTCTCTTCGACGCAACCCGCCACGCATGGACTAGCCAACACGCGACGAG-TG-ATCGTTTTAGATAAGCGAGAACGCTAAACAA
krebsianaRM966	GCGGGACTACCCGCTGAGGGTAGCATTCTCTTCGACGCAACCCGCCACGCATGGACTAGCCAACACGCGACGAG-TG-ATCGTTTTAGAGAAGCGAGAACGCTAAACAA
krebsiana_krebrM968	GCGGGACTACCCGCTGAGGGTAGCATTCTCTTCGACGCAACCCGCCACGCATGGACTAGCCAACACGCGACGAG-TG-ATCGTTTTAGAGAAGCGAGAACGCTAAACAA
krebsiana_krebrM992	GCGGGACTACCCGCTGAGGGTAGCATTCTCTTCGACGCAACCCGCCACGCATGGACTAGCCAACACGCGACGAG-TG-ATCGTTTTAGAGAAGCGAGAACGCTAAACAA
krebsiana_RM996	GCGGGACTACCCGCTGAGGGTAGCATTCTCTTCGACGCAACCCGCCACGCATGGACTAGCCAACACGCGACGAG-TG-ATCGTTTTAGAGAAGCGAGAACGCTAAACAA
krebsiana_krebrM1403	GCGGGACTACCCGCTGAGGGTAGCATTCTCTTCGACGCAACCCATCAGCATGGACTAGCCAACACGCGACGAG-TG-ATCGTTTTAGAGAAGCGAGAACGCTAAACAA
linearis_linearRM1406_1	GCGGGACTACCCGCTGAG?????????????????????????????????????CATGGACTAGCCAACACGCGACGAG-TG-ATCGTTTTAGAGAAGCGAGAACGCTAAACAA
linearis_linearRM1406_2	GCGGGACTACCCGCTGAGGGTAGCATTCTCTTCGACGCAACCCCTCAGCATGGACTAGCCAACACGCGACGAG-TG-ATCGTTTTAGAGAAGCGAGAACGCTAAACAA
leipodaRM1466	GCGGGACTACCCGCTGAGGGTAGCATTCTCTTCGACGCAACCCGCCACGCATGGACTAGCCAACACGCGACGAG-TG-ATCGTTTTAGAGAAGCGAGAACGCTAAACAA
serrataHerm_RM	GCGGGACTACCCGCTGAGGGTAGCATTCTCTTCGACGCAACCCGCCACGCATGGACTAGCCAACACGCGACGAG-TG-ATCGTTTTAGAGAAGCGAGAACGCTAAACAA
krebsiana_RVC162	GCGGGACTACCCGCTGAG?TAGCATTCTCTTCGACGCAACCCGCCACGCATGGACTAGCCAACACGC-ACGAG-TG-ATCGTTTTAGAGAAGCGAGAACGCTAAACAA
krebsiana_krebrSH110	GCGGGACTACCCGCTGAGGGTAGCATTCTCTTCGACGCAACCCGCCACGCATGGACTAGCCAACACGCGACGAG-TG-ATCGTTTTAGAGAAGCGAGAACGCTAAACAA
krebsiana_krebrSH111_1	GCGGGACTACCCGCTGAGGGTAGCATTCTCTTCGACGCAACCCGCCAC-CATGGACTAGCCAACACGCGACGAG-TG-ATCGTTTTAGAGAAGCGAGAACGCTAAACAA
krebsiana_krebrSH111_2	GCGGGACTACCCGCTGAGGGTAGCATTCTCTTCGACGCAACCCGCCACGCATGGACTAGCCAACACGCGACGAG-TGGATCGTTTTAGAGAAGCGAGAACGCTAAACAA
krebsiana_krebrSH112	GCGGGACTACCCGCTGAGGGTAGCATTCTCTTCGACGCAACCCGCCACGCATGGACTAGCCAACACGCGACGAG-TG-ATCGTTTTAGAGAAGCGAGAACGCTAAACAA
krebsianaSH115	GCGGGACTACCCGCTGAGGGTAGCATTCTCTTCGACGCAACCCGCCACGCATGGACTAGCCAACACGCGACGAG-TG-ATCGTTTTAGAGAAGCGAGAACGCTAAACAA
linearis_linearSH116	GCGGGACTACCCGCTGAGGGTAGCATTCTCTTCGACGCAACCCGCCACGCATGGACTAGCCAACACGCGACGAG-TG-ATCGTTTTAGAGAAGCGAGAACGCTAAACAA
linearis_linearSH117	GCGGGACTACCCGCTGAGGGTAGCATTCTCTTCGACGCAACCCGCCACGCATGGACTAGCCAACACGCGACGAG-TG-ATCGTTTTAGAGAAGCGAGAACGCTAAACAA
krebsianaSH118	GCGGGACTACCCGCTGAGGGTAGCATTCTCTTCGACGCAACCCGCCACGCATGGACTAGCCAACACGCGACGAG-TG-ATCGTTTTAGAGAAGCGAGAACGCTAAACAA
linearis_linearSH131	GCGGGACTACCCGCTGAGGGTAGCATTCTCTTCGACGCAACCCGCCACGCATGGACTAGCCAACACGCGACGAG-TG-ATCGTTTTAGAGAAGCGAGAACGCTAAACAA
linearis_linearSH132	GCGGGACTACCCGCTGAGGGTAGCATTCTCTTCGACGCAACCCGCCACGCATGGACTAGCCAACACGCGACGAG-TG-ATCGTTTTAGAGAAGCGAGAACGCTAAACAA
krebsianaSH133	GCGGGACTACCCGCTGAGGGTAGCATTCTCTTCGACGCAACCCGCCACGCATGGACTAGCCAACACGCGACGAG-TG-ATCGTTTTAGAGAAGCGAGAACGCTAAACAA
krebsianaSH135	GCGGGACTACCCGCTGAGGGTAGCATTCTCTTCGACGCAACCCGCCACGCATGGACTAGCCAACACGCGACGAG-TG-ATCGTTTTAGAGAAGCGAGAACGCTAAACAA
krebsianaSR480	GCGGGACTACCCGCTGAGGGTAGCATTCTCTTCGACGCAACCCGCCACGCATGGACTAGCCAACACGCGACGAG-TG-ATCGTTTTAGAGAAGCGAGAACGCTAAACAA
krebsianaSR520	GCGGGACTACCCGCTGAGGGTAGCATTCTCTTCGACGCAACCCGCCACGCATGGACTAGCCAACACGCGACGAG-TG-ATCGTTTTAGAGAAGCGAGAACGCTAAACAA
linearis_linearSR523	GCGGGACTACCCGCTGAGGGTAGCATTCTCTTCGACGCAACCCGCCACGCATGGACTAGCCAACACGCGACGAG-TG-ATCGTTTTAGAGAAGCGAGAACGCTAAACAA
krebsianaSR564	GCGGGACTACCCGCTGAGGGTAGCATTCTCTTCGACGCAACCCGCCACGCATGGACTAGCCAACACGCGACGAG-TG-ATCGTTTTAGAGAAGCGAGAACGCTAAAAA
linearis_linearSR571	GCGGGACTACCCGCTGAG?GTAGCATTCTCTTCGACGCGACCCGCCACGCATGGACTAGCCAACACGCGACGAG-TG-ATCGTTTTAGAGAAGCGAGAACGCTAAACAA
rigens_rigSR574	GCGGGACTACCCGCTGAGGGTAGCATTCTCTTCGACGCAACCCGCCACGCATGGACTAGCCAACACGCGACGAG-TG-ATCGTTTTAGAGAAGCGAGAACGCTAAACAA
rigens_rigSR575	GCGGGACTACCCGCTGAGGGTAGCATTCTCTTCGACGCAACCCGCCACGCATGGACTAGCCAACACGCGACGAG-TG-ATCGTTTTAGAGAAGCGAGAACGCTAAACAA
rigensSR581	GCGGGACTACCCGCTGAGGGTAGCATTCTCTTCGACGCAACCCGCCACGCATGGACTAGCCAACACGCGACGAG-TG-ATCGTTTTAGAGAAGCGAGAACGCTAATCAA
rigens_uniflSR625	GCGGGACTACCC?????????????????????????????????????CCGCCACGCATGGACTAGCCAACACGCGACGAG-TG-ATCGTTTTAGAGAAGCGAGAACGCTAATCAA
krebsiana_krebrSVHF1	GCGGGACTACCCGCTGAGGGTAGCATTCTCTTCGACGCAACCCGCCACGCATGGACTAGCCAACACGCGACGAG-TG-ATCGTTTTAGAGAAGCGAGAACGCTAAACAA
krebsiana_arctSV_HF2	GCGGGACTACCCGCTGAGGGTAGCATTCTCTTCGACGCAACCCGCCACGCATGGACTAGCCAACACGCGACGAG-TG-ATCGTTTTAGAGAAGCGAGAACGCTAAACAA

[780	790	800	810	820	830	840	850	860	870	880]
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lichtensteiniRM1323	GGACATAAAAAGATCATCTAAGACCCCATGCCACATCAGGTTCCGTATCCAAGACACCAAGCGAAACTCAACAAGCCACATCGACGAA-G--TGTTTTACAACGACAAAA
lichtesteiniM050906_2	GGACATAAAAAGATCATCTAAGACCCCATGCCACATCAGGTTTCYGTATCCAAGACACCAAGCGAAACTCAACAAGCCACATCGACGAA-G--TGTTTTACAACGACAAAA
heterochaetaM160901_5g	GGACATAAAAAGATCATCTAAGACCCCATGCCACATCAGGTTCCGTATCCAAGACACCAAGCGAAACTCAGCAAGCCACATCAACGAA-G--TGTTTTACAACGACAAGA
heterochaetaRM1348	GGACATAAAAAGATCATCTAAGACCCCATGCCACATCAGGTTCCGTATCCAAGACACCAAGCGAAACTCAGCAAGCCACATCAACGAA-G--TGTTTTACAACGACAAGA
heterochaetaRM1255	GGACATAAAAAGATCATCTAAGACCCCATGCCACATCAGGTTCCGTATCCAAGACACCAAGCGAAACTAAGCAAGCCACATCAACGAA-G--TGTTTTACAATGACAAGA
tenuifoliaM7219_10	GGACATAAAAAGATCATTTAAGACCCCATGCCACATCAGGTTCCATATCCAAGACACCAAGCGAAACTCAGCAAGCCACATTCGCCGAA-G--TGTTTTACAACGACAAGA
tenuifoliaRM1352	GGACATAAAAAGATCATTTAAGACCCCATGCCACATCAGGTTCCATATCCAAGACACCAAGCGAAACTCAGCAAGCCACATTCGCCGAA-G--TGTTTTACAACGACAAGA
ciliarisSR705	GGACATAAAAAGATCATTTAAGACCCCATGCCACATCAGGTTCCGTATCCAAGACACCAAGCGAAACTTAGCAAGCCACATCGTCGAA-G--TGTTTTACAACGACAAGA

Appendix 6: Additional nrDNA sequence data for Chapter 4

jurineifolia_scabCAM1953 GGCATAAAAAGGATCATGTTAAGACCCCTATGCCACATCAGGTTCCGATATCCAAGACACCAAGCGAAACTCAGCAAGCCATATCGTCGTA-G--TGTTTACAACAACAAGA
 rigens_unifl_Boknes1 GGACATAAAAAGATCATTTAAGACCC-ATGCCACATTAGGTTCCATATCCAAGACACCAAGCGAAACTCAGCAAGCCACATCGCCGAT-G--TGTACACAACGACAAGA
 linearis_linear_Boknes2 GGACATAAAAAGATCATTTAAGACCC-ATGCCACATTAGGTTCCATATCCAAGACACCAAGCGAAACTCAGCAAGCCACATCGCCGAT-G--TGTACACAACGACAAGA
 linearis_ovalM041001_2g GGACATAAAAAGATCATTTAAGACCC-ATGCCACATTAGGTTCCATATCCAAGACACCAAGCGAAACTCAGCAAGCCACATCGCCGAT-G--TGTACACAACGACAAGA
 rigens_leuco_M070704_1 GGACATAAAAAGATCATTTAAGACCC-ATGCCACATTAGGTTCCATATCCAAGACACCAAGCGAAACTCAGCAAGCCACATCGCCGAT-G--TGTACACAACGACAAGA
 krebsiana_krebM071001_1g GGACATAAAAAGATCATTTAAGACCC-ATGCCACATTAGGTTCCATATCCAAGACACCAAGCGAAACTCAGCAAGCCACATCGCCGAT-G--TGTACACAACGACAAGA
 krebsiana_krebM071001_3g1 GGACATAAAAAGATCATTTAAGACCC-ATGCCACATTAGGTTCCATATCCAAGACACCAAGCGAAACTCAGCAAGCCACATCGCCGAT-G--TGTACACAACGACAAGA
 krebsiana_arctM071001_3pg GGACATAAAAAGATCATTTAAGACCC-ATGCCACATTAGGTTCCATATCCAAGACACCAAGCGAAACTCAGCAAGCCACATCGCCGAT-G--TGTACACAACGACAAGA
 rigidaM100903_4 GGACATAAAAAGATCATTTAAGACCC-ATGCCACATTAGGTTCCATATCCAAGACACCAAGCGAAACTCAGCAAGCCACATCGCCGAT-G--TGTACACAACGACAAGA
 rigidaM100904_4 GGACATAAAAAGATCATTTAAGACCC-ATGCCACATTAGGTTCCATATCCAAGACACCAAGCGAAACTCAGCAAGCCACATCGCCGAT-G--TGTACACAACGACAAGA
 rigidM110805_10 GGACATAAAAAGATCATTTAAGACCC-ATGCCACATTAGGTTCCATATCCAAGACACCAAGCGAAACTCAGCAAGCCACATCGCCGAT-G--TGTACACAACGACAAGA
 rigidaM120805_80 GGACATAAAAAGATCATTTAAGACCC-ATGCCACATTAGGTTCCATATCCAAGACACCAAGCGAAACTCAGCAAGCCACATCGCCGAT-G--TGTACACAACGACAAGA
 leiopodaM160704_5 GGACATAAAAAGATCATTTAAGACCC-ATGCCACATTAGGTTCCATATCCAAGRCACCAAGCGAAACTCAGCAAGCCACATCGCCGAT-G--TGTACACAACGACAAGA
 pectinataM180904_5 GGACATAAAAAGATCATTTAAGACCC-ATGCCACATTAGGTTCCATATCCAAGACACCAAGCGAAACTCAGCAAGCCACATCGCCGAT-G--TGTACACAACGAAAAGA
 krebsiana_krebM210902_1 GGACATAAAAAGATCATTTAAGACCC-ATGCCACATTAGGTTCCATATCCAAGACACCAAGCGAAACTCAGCAAGCCACATCGCCGAT-G--TGTACACAACGACAAGA
 krebsiana_krebM230803_8 GGACATAAAAAGATCATTTAAGACCC-ATGCCACATTAGGTTCCATATCCAAGACACCAAGCGAAACTCAGCAAGCCACATCGCCGAT-G--TGTACACAACGACAAGA
 serrM230901_7g GGACATAAAGATGATCGTTTACCACCC-ATGACAACATTAGGT-CCATATCCAAGAACCAAGCGAAACTCAGCAAGCCACATCGCCGAT-G--TGTACACAACGACAAGA
 leiopodaM250901_34 GGACATAAAAAGATCATTTAAGACCC-ATGCCACATTAGGTTCCATATCCAAGACACCAAGCGAAACTCAGCAAGCCACATCGCCGAT-G--TGTACACAACGACAAGA
 pectinataM250901_37 GGACATAAAAAGATCATTTAAGACCC-ATGCCACATTAGGTTCCATATCCAAGACACCAAGCGAAACTCAGCAAGCCACATCGCCGAT-G--TGTACACAACGACAAGA
 pectM260901_2g GGACATAAAAAGATCATTTAAGACCC-ATGCCACATTAGGTTCCATATCCAAGACACCAAGCGAAACTCAGCAAGCCACATCGCCGAT-G--TGTACACAACGACAAGA
 maritimaM260901 GGACATAAAAAGATCATTTAAGACCC-ATGCCACATTAGGTTCCATATCCAAGACACCAAGCGAAACTCAGCAAGCCACATCGCCGAT-G--TGTACACAACGACAAGA
 krebsiana_krebM261001_2 GGACATAAAAAGATCATTTAAGACCC-ATGCCACATTAGGTTCCATATCCAAGACACCAAGCGAAACTCAGCAAGCCACATCGCCGAT-G--TGTACACAACGACAAGA
 maritimaM270901_5g GGACATAAAAAGATCATTTAAGACCC-ATGCCACATTAGGTTCCATATCCAAGACACCAAGCGAAACTCAGCAAGCCACATCGCCGAT-G--TGTACACAACGACAAGA
 rigens_rigensM7293 GGACATAAAAAGATCATTTAAGACCC-ATGCCACATTAGGTTCCATATCCAAGACACCAAGCGAAACTCAGCAAGCCACATCGCCGAT-G--TGTACACAACGACAAGA
 rigens_rigensM7298_2 GGACATAAAAAGATCATTTAAGACCC-ATGCCACATTAGGTTCCATATCCAAGACACCAAGCGAAACTCAGCAAGCCACATCGCCGAT-G--TGTACACAACGACAAGA
 rigens_rigensM7527_2 GGACATAAAAAGATCATTTAAGACCC-ATGCCACATTAGGTTCCATATCCAAGACACCAAGCGAAACTCAGCAAGCCACATCGCCGAT-G--TGTACACAACGACAAGA
 leiopodaM200901_22g GGACATAAAAAGATCATTTAAGACCC-ATGCCACATTAGGTTCCATATCCAAGACACCAAGCGAAACTCAGCAAGCCACATCGCCGAT-G--TGTACACAACGACAAGA
 spnov_M7237_4 GGACATAAAAAGATCATTTAAGACCC-ATGCCACATTAGGTTCCATATCCAAGACACCAAGCGAAACTCAGCAAGCCACATCGCCGAT-G--TGTACACAACGACAAGA
 serrataHerm_NB GGACATAAAAAGATCATTTAAGACCC-ATGCCACATTAGGTTCCATATCCAAGACACCAAGCGAAACTCAGCAAGCCACATCGCCGAT-G--TGTACACAACGACAAGA
 krebsiana_krebNB1465 GGACATAAAAAGATCATTTAAGACCC-ATGCCACATTAGGTTCCATATCCAAGACACCAAGCGAAACTCAGCAAGCCACATCGCCGAT-G--TGTACACAACGACAAGA
 linearis_linearRM1013 GGACATAAAAAGATCATTTAAGACCC-ATGCCACATTAGGTTCCATATCCAAGACACCAAGCGAAACTCAGCAAGCCACATCGCCGAT-G--TGTACACAACGACAAGA
 rigens_leucoRM1021 GGACATAAAAAGATCATTTAAGACCC-ATGCCACATTAGGTTCCATATCCAAGACACCAAGCGAAACTCAGCAAGCCACATCGCCGAT-G--TGTACACAACGACAAGA
 pectinataRM1044_1 GGACATAAAAAGATCATTTAAGACCC-ATGCCACATTAGGTTCCATATCCAAGACACCAAGCGAAACTCAGCAAGCCACATCGCCGAT-G--TGTACACAACGACAAGA
 hybrRM1061 GGACATAAAAAGATCATTTAAGACCC-ATGCCACATTAGGTTCCATATCCAAGACACCAAGCGAAACTCAGCAAGCCACATCRCCGAT-G--TGTACACAACGACAAGA
 leiopodaRM1063 GGACATAAAAAGATCATTTAAGACCC-ATGCCACATTAGGTTCCATATCCAAGACACCAAGCGAAACTCAGCAAGCCACATCGCCGAT-G--TGTACACAACGACAAGA
 rigidaRM1082 GGACATAAAAAGATCATTTAAGACCC-ATGCCACATTAGGTTCCATATCCAAGACACCAAGCGAAACTCAGCAAGCCACATCGCCGAT-G--TGTACACAACGACAAGA
 linearis_linearRM1090 GGACATAAAAAGATCATTTAAGACCC-ATGCCACATTAGGTTCCATATCCAAGACACCAAGCGAAACTCAGCAAGCCACATCGCCGAT-G--TGTACACAACGACAAGA
 linearis_linearRM1092 GGACATAAAAAGATCATTTAAGACCC-TTGCCACATTAGGTTCCATATCCAAGACACCAAGCGAAACTCAGCAAGCCACATCGCCGAT-G--TGTACACAACGACAAGA
 linearis_linearRM1094 GGACATAAAAAGATCATTTAAGACCC-ATGCCACATTAGGTTCCATATCCAAGACACCAAGCGAAACTCAGCAAGCCACATCGCCGAT-G--TGTACACAACGACAAGA
 linearis_linearRM1103 GGACATAAAAAGATCATTTAAGACCC-ATGCCACATTAGGTTCCATATCCAAGACACCAAGCGAAACTCAGCAAGCCACATCGCCGAT-G--TGTACACAACGACAAGA
 krebsiana_serrRM1137 GGACATAAAAAGATCATTTAAGACCC-ATGCCACATTAGGTTCCATATCCAAGACACCAAGCGAAACTCAGCAAGCCACATCGCCGAT-G--TGTACACAACGACAAGA
 linearis_linearRM1182 GGACATAAAAAGATCATTTAAGACCC-ATGCCACATTAGGTTCCATATCCAAGACACCAAGCGAAACTCAGCAAGCCACATCGCCGAT-G--TGTACACAACGACAAGA
 rigidaRM1210 GGACATAAAAAGATCATTTAAGACCC-ATGCCACATTAGGTTCCATATCCAAGACACCAAGCGAAACTCAGCAAGCCACATCGCCGAT-G--TGTACACAACGACAAGA
 serrataRM1216 GGACATAAAAAGATCATTTAAGACCC-ATGCCACATTAGGTTCCATATCCAAGACACCAAGCGAAACTCAGCAAGCCACATCGCCGAT-G--TGTACACAACGACAAGA
 serrataRM1241 GGACATAAAAAGATCATTTAAGACCC-ATGCCACATTAGGTTCCATATCCAAGACACCAAGCGAAACTCAGCAAGCCACATCGCCGAT-G--TGTACACAACGACAAGA
 serrataRM1245 GGACATAAAAAGATCATTTAAGACCC-ATGCCACATTAGGTTCCATATCCAAGACACCAAGCGAAACTCAGCAAGCCACATCGCCGAT-G--TGTACACAACGACAAGA
 rigidaRM1254 GGACATAAAAAGATCATTTAAGACCC-ATGCCACATTAGGTTCCATATCCAAGACACCAAGCGAAACTCAGCAAGCCACATCGCCGAT-G--TGTACACAACGACAAGA
 serrataRM1260 GGACATAAAAAGATCATTTAAGACCC-ATGCCACATTAGGTTCCATATCCAAGACACCAAGCGAAACTCAGCAAGCCACATCGCCGAT-G--TGTACACAACGACAAGA
 rigidaRM1270 GGACATAAAAAGATCATTTAAGACCC-ATGCCACATTAGGTTCCATATCCAAGACACCAAGCGAAACTCAGCAAGCCACATCGCCGAT-G--TGTACACAACGACAAGA
 serrataRM1280 GGACATAAAAAGATCATTTAAGACCC-ATGCCACATTAGGTTCCATATCCAAGACACCAAGCGAAACTCAGCAAGCCACATCGCCGAT-G--TGTACACAACGACAAGA
 leiopodaRM1291 GGACATAAAAAGATCATTTAAGACCC-ATGCCACATTAGGTTCCATATCCAAGACACCAAGCGAAACTCAGCAAGCCACATCGCCGAT-G--TGTACACAACGACAAGA

Appendix 6: Additional nrDNA sequence data for Chapter 4

krebsianaSH118 GGACATAAAAAGATCATTTAAGACCC-ATGCCACATTAGGTTCCATATCCAAGACACCAAGCGAAACTCAGCAAGCCACATCGCCGAT-G--TGTACACAACGACAAGA
linearis_linearSH131 GGACATAAAAAGATCATTTAAGACCC-ATGCCACATTAGGTTCCATATCCAAGACACCAAGCGAAACTCAGCAAGCCACATCGCCGAT-G--TGTACACAACGACAAGA
linearis_linearSH132 GGACATAAAAAGATCATTTAAGACCC-ATGCCACATTAGGTTCCATATCCAAGACACCAAGCGAAACTCAGCAAGCCACATCGCCGAT-G--TGTACACAACGACAAGA
krebsianaSH133 GGACATAAAAAGATCATTTAAGACCC-ATGCCACAWTAGGTTCCATATCCAAGACAACAAGCGAAACTCAGCAAGCCACATCGCCGAT-G--TGTACACAACGACAAGA
krebsianaSH135 GGACATAAAAAGATCATTTAAGACCC-ATGCCACATTAGGTTCCATATCCAAGACACCAAGCGAAACTCAGCAAGCCACATCGCCGAT-G--TGTACACAACGACAAGA
krebsianaSR480 GGACATAAAAAGATCATTTAAGACCC-ATGCCACATTAGGTTCCATATCCAAGACACCAAGCGAAACTCAGCAAGCCACATCGCCGAT-G--TGTACACAACGACAAGA
krebsianaSR520 GGACATAAAAAGATCATTTAAGACCC-ATGCCACATTAGGTTCCATATCCAAGACACCAAGCGAAACTCAGCAAGCCACATCGCCGAT-G--TGTACACAACGACAAGA
linearis_linearSR523 GGACATAAAAAGATCATTTAAGACCC-ATGCCACATTAGGTTCCATATCCAAGACACCAAGCGAAACTCAGCAAGCCACATCGCCGAT-G--TGTACACAACGACAAGA
krebsianaSR564 GGACATAAAAAGATCATTTAAGACCC-ATGCCACATTAGGTTCCATATCCAAGACACCAAGCGAAACTCAGCAAGCCACATCGCCGAT-G--TGTACACAACGACAAGA
linearis_linearSR571 GGACATAAAAAGATCATTTAAGACCC-ATGCCACATTAGGTTCCATATCCAAGACACCAAGCGAAACTCAGCAAGCCACATCGCCGAT-G--TGTACACAACGACAAGA
rigens_rigSR574 GGACATAAAAAGATCATTTAAGACCC-ATGCCACATTAGGTTCCATATCCAAGACACCAAGCGAAACTCAGCAAGCCACATCGCCGAT-G--TGTACACAACGACAAGA
rigens_rigSR575 GGACATAAAAAGATCATTTAAGACCC-ATGCCACATTAGGTTCCATATCCAAGACACCAAGCGAAACTCAGCAAGCCACATCGCCGAT-G--TGTACACAACGACAAGA
rigensSR581 GGACATAAAAAGATCATTTAAGACCC-ATGCCACATTAGGTTCCATATCCAAGACACCAAGCGAAACTCAGCAAGCCACATCGCCGAT-G--TGTACACAACGACAAGA
rigens_uniflSR625 GGACATAAAAAGATCATTTAAGACCC-ATGCCACATTAGGTTCCATATCCAAGACACCAAGCGAAACTCAGCAAGCCACATCGCCGAT-G--TGTACACAACGACAAGA
krebsiana_krebSVHF1 GGACATAAAAAGATCATTTAAGACCC-ATGCCACATTAGGTTCCATATCCAAGACACCAAGCGAAACTCAGCAAGCCACATCGCCGAT-G--TGTACACAACGACAAGA
krebsiana_arctSV_HF2 GGACATAAAAAGATCATTTAAGACCC-ATGCCACATTAGGTTCCATATCCAAGACACCAAGCGAAACTCAGCAAGCCACATCGCCGAT-G--TGTACACAACGACAAGA

[890 900 910 920 930 940 950 960 970 980 990]

lichtensteiniRM1323 TGGCTTACAGAGACCACCTTACTGGTCCGTCATGCACCACAAGTGCATGCGTGACGGAAACAGATTCAATCGGTCCATACAATGCCCTTTGATTAGGTACGCAACACAGGA
lichtesteiiniM050906_2 TGGCTTACAGAGACCACCTTACTGGTCCGTCATGCACCACAAGTGCATGCGTGACGGAAACAGATTCAATCGGTCCATACAATGCCCTTTGATTAGGTACGCAACACAGGA
heterochaetaM160901_5g TGGCTTACAGAGACCACCTTACTGGTCCGTCATGCACCAC-AGTGCATGCGTGACAAAAACAGATTCAATCGGTCCATACAATGCCCTTTGATTAGGTACGCAACACAGGA
heterochaetaRM1348 TGGCTTACAGAGACCACCTTACTGGTCCGTCATGCACCAC-AGTGCATGCGTGACAAAAACAGATTCAATCGGTCCATACAATGCCCTTTGATTAGGTACGCAACACAGGA
heterochaetaRM1255 TGGCTTACAAAGACCACCTTACTGGTCCGTCATGCACCACAAGTGCATGCGTGACGGAAACAGATTCAATCGGTCCATACAATGCCCTTTGATTAGGTACGCAACACAGGA
tenuifoliaM7219_10 TGGATTACGGAGACCACCTTACTGGTCCGTCATGCACCACAAGTGCATGCGTGACGGAAACAGATTCAATCGGTCCATACAATGCCCTTTGATTAGGTACGCAACACAGGA
tenuifoliaRM1352 TGGATTACGGAGACCACCTTACTGGTCCGTCATGCACCACAAGTGCATGCGTGACGGAAACAGATTCAATCGGTCCATACAATGCCCTTTGATTAGGTACGCAACACAGGA
ciliarisSR705 CGGATTACAGAGAATGCTTACTGGTCCGTCATGCACCACATGTCGATGCGTGACGGAAACAGATTCAATCGGTCCATACAATGCCCTTTGATTAGGTACGCAACACAGGA
jurineifolia_scabCAM1953 TGGATTACAGAGACCACCTTACTGGTCCGTCATGCACCACAAGTGCATGCGTGACGGAAACAGATTCAATCGGTCCATACAATGCCCTTTGATTAGGTACGCAACACAGGA
rigens_unifl_Boknes1 TGGATTACTAAGACCACCTTACCGGTCCATCATGCACCACCTTGTGCGATGCGTGACGGATACATATTCATTTCGGTCCATACAATGCCCTTTGATTAGGTACGCAACACAGTA
linearis_linear_Boknes2 TGGATTACTAAGACCACCTTACCGGTCCATCATGCACCACCTTGTGCGATGCGTGACGGATACATATTCATTTCGGTCCATACAATGCCCTTTGATTAGGTACGCAACACAGTA
linearis_ovalM041001_2g TGGATTACTAAGACCACCTTACCGGTCCATCATGCACCACCTTGTGCGATGCGTGACGGATACATATTCATTTCGGTCCATACAATGCCCTTTGATTAGGTACGCAACACAGTA
rigens_leuco_M070704_1 TGGATTACTAAGACCACCTTACCGGTCCATCATGCACCACCTTGTGCGATGCGTGACGGATACATATTCATTTCGGTCCATACAATGCCCTTTGATTAGGTACGCAACACAGTA
krebsiana_krebM071001_1g TGGATTACTAAGACCACCTTACCGGTCCATCATGCACCACCTTGTGCGATGCGTGACGGATACATATTCATTTCGGTCCATACAATGCCCTTTGATTAGGTACGCAACACAGTA
krebsiana_krebM071001_3g1 TGGATTACTAAGACCACCTTACCGGTCCATCATGCACCACCTTGTGCGATGCGTGACGGATACATATTCATTTCGGTCCATACAATGCCCTTTGATTAGGTACGCAACACAGTA
krebsiana_arctM071001_3pg TGGATTACTAAGACCACCTTACCGGTCCATCATGCACCACCTTGTGCGATGCGTGACGGATACATATTCATTTCGGTCCATACAATGCCCTTTGATTAGGTACGCAACACAGTA
rigidaM100903_4 TGGATTACTAAGAACACCTTACCGGTCCATCATGCACCACCTTGTGCGATGCGTGACTGATACATATTCATTTCGGTCCATACAATGCCCTTTGATTAGGTACGCAACACAGTA
rigidaM100904_4 TGGATTACTAAGAACACCTTACCGGTCCATCATGCACCACCTTGTGCGATGCGTGACTGATACATATTCATTTCGGTCCATACAATGCCCTTTGATTAGGTACGCAACACAGTA
rigidM110805_10 TGGATTACTGAGACCACCTTACCGGTCCATCATGCACCACCTTGTGCGATGCGTGACGGATACATATTCATTTCGGTCCATACAATGCCCTTTGATTAGGTACGCAACACAGTA
rigidaM120805_80 TGGATTACTGAGACCACCTTACCGGTCCATCATGCACCACCTTGTGCGATGCGTGACGGATACATATTCATTTCGGTCCATACAATGCCCTTTGATTAGGTACGCAACACAGTA
leiopodaM160704_5 TGGATTACTGAGACCACCTTACCGGTCCATCATGCAGCACATGTCGATGCGTGACGGAAACATATTCATTTCGGTCCATACAATGCCCTTTGATTAGGTACGCAACACAGCA
pectinataM180904_5 TGGATTACTGAGACCACCTTACCGGTCCATCATGCACCACCTTGTGCGATGCGTGACGGATACATATTCATTTCGGTCCATACAATGCCCTTTGATTAGGTACGCAACACAGTA
krebsiana_krebM210902_1 TGGATTACTAAGACCACCTTACCGGTCCATCATGCACCACCTTGTGCGATGCGTGACGGATACATATTCATTTCGGTCCATACAATGCCCTTTGATTAGGTACGCAACACAGTA
krebsiana_krebM230803_8 TGGATTACTAAGACCACCTTACCGGTCCATCATGCACCACCTTGTGCGATGCGTGACGGATACATATTCATTTCGGTCCATACAATGCCCTTTGATTAGGTACGCAACACAGTA
serrM230901_7g TGGATTACTGAGACCACCTTACCGGTCCATCATGCACCACCTTGTGCGATGCGTGACGGATACATATTCATTTCGGTCCATACAATGCCCTTTGATTAGGTACGCAACACAGTA
leiopodaM250901_34 TGGATTACTGAGACCACCTTACCGGTCCATCATGCACCACCTTGTGCGATGCGTGACGGATACATATTCATTTCGGTCCATACAATGCCCTTTGATTAGGTACGCAACACAGTA
pectinataM250901_37 TGGATTACTRAGACCACCTTACCGGTCCATCATGCACCACCTTGTGCGATGCGTGACGGATACATATTCATTTCGGTCCATACAATGCCCTTTGATTAGGTACGCAACACAGTA
pectM260901_2g TGGATTACTGAGACCACCTTACCGGTCCATCATGCACCACCTTGTGCGATGCGTGACGGATACATATTCATTTCGGTCCATACAATGCCCTTTGATTAGGTACGCAACACAGTA
maritimaM260901 TGGATTACTGAGACCACCTTACCGGTCCATCATGCACCACCTTGTGCGATGCGTGACGGATACATATTCATTTCGGTCCATACAATGCCCTTTGATTAGGTACGCAACACAGTA
krebsiana_krebM261001_2 TGGATTACTAAGACCACCTTACCGGTCCATCATGCACCACCTTGTGCGATGCGTGACGGATACATATTCATTTCGGTCCATACAATGCCCTTTGATTAGGTACGCAACACAGTA
maritimaM270901_5g TGGATTACTAAGACCACCTTACCGGTCCATCATGCACCACCTTGTGCGATGCGTGACGGATACATATTCATTTCGGTCCATACAATGCCCTTTGATTAGGTACGCAACACAGTA
rigens_rigensM7293 TGGATTACTAAGACCACCTTACCGGTCCATCATGCACCACCTTGTGCGATGCGTGACGGATACATATTCATTTCGGTCCATACAATGCCCTTTGATTAGGTACGCAACACAGTA

Appendix 6: Additional nrDNA sequence data for Chapter 4

krebsiana_arctRM903	TGGATTACTAAGAACACTTACCGGTCCATCATGCACCACCTTGTGCGATGCATGACGGATACATATTCATTCCGGTCCATACAATGCCCTTCGATTAGGTACGCAACACAGTA
krebaRM904	TGGATTACTAAGAACACTTACCGGTCCATCATGCACCACCTTGTGCGATGCATGACGGATACATATTCATTCCGGTCCATACAATGCCCTTCGATTAGGTACGCAACACAGTA
krebsiana_krebrM906	TGGATTACTAAGAACACTTACCGGTCCATCATGCACCACCTTGTGCGATGCATGACGGATACATATTCATTCCGGTCCATACAATGCCCTTCGATTAGGTACGCAACACAGTA
rigens_leucoRM919	TGGATTACTAAGACCACCTTACCGGTCCATCATGCACCACCTTGTGCGATGCATGACGGATACATATTCATTCCGGTCCATACAATGCCCTTCGATTAGGTACGCAACACAGTA
krebsiana_krebrM929	TGGATTACTAAGACCACCTTACCGGTCCATCATGCACCACCTTGTGCGATGCATGACGGATACATATTCATTCCGGTCCATACAATGCCCTTCGATTAGGTACGCAACACAGTA
krebsiana_krebrM949	TGGATTACTAAGAACACTTACCGGTCCATCATGCACCACCTTGTGCGATGCATGACGGATACATATTCATTCCGGTCCATACAATGCCCTTCGATTAGGTACGCAACACAGTA
krebsiana_krebrM950	TGGATTACTAAGAACACTTACCGGTCCATCATGCACCACCTTGTGCGATGCATGACGGATACATATTCATTCCGGTCCATACAATGCCCTTCGATTAGGTACGCAACACAGTA
linearis_linearRM951	TGGATTACTAAGACCACCTTACCGGTCCATCATGCACCACCTTGTGCGATGCATGACGGATACATATTCATTCCGGTCCATACAATGCCCTTCGATTAGGTACGCAACACAGTA
krebsiana_krebrM960	TGGATTACTAAGACCACCTTACCGGTCCATCATGCACCACCTTGTGCGATGCATGACGGATACATATTCATTCCGGTCCATACAATGCCCTTCGATTAGGTACGCAACACAGTA
krebsiana_krebrM962	TGGATTACTAAGACCACCTTACCGGTCCATCATGCACCACCTTGTGCGATGCATGACGGATACATATTCATTCCGGTCCATACAATGCCCTTCGATTAGGTACGCAACACAGTA
krebsianaRM966	TGGATTACTAAGACCACCTTACCGGTCCATCATGCACCACCTTGTGCGATGCATGACGGATACATATTCATTCCGGTCCATACAATGCCCTTCGATTAGGTACGCAACACAGTA
krebsiana_krebrM968	TGGATTACTAAGACCACCTTACCGGTCCATCATGCACCACCTTGTGCGATGCATGACGGATACATATTCATTCCGGTCCATACAATGCCCTTCGATTAGGTACGCAACACAGTA
krebsiana_krebrM992	TGGATTACTAAGACCACCTTACCGGTCCATCATGCACCACCTTGTGCGATGCATGACGGATACATATTCATTCCGGTCCATACAATGCCCTTCGATTAGGTACGCAACACAGTA
krebsiana_RM996	TGGATTACTAAGACCACCTTACCGGTCCATCATGCACCACCTTGTGCGATGCATGACGGATACATATTCATTCCGGTCCATACAATGCCCTTCGATTAGGTACGCAACACAGTA
krebsiana_krebrM1403	TGGATTACTAAGAACACTTACCGGTCCATCATGCACCACCTTGTGCGATGCATGACGGATACATATTCATTCCGGTCCATACAATGCCCTTCGATTAGGTACGCAACACAGTA
linearis_linearRM1406_1	TGGATTACTAAGACCACCTTACCGGTCCATCATGCACCACCTTGTGCGATGCATGACGGATACATATTCATTCCGGTCCATACAATGCCCTTCGATTAGGTACGCAACACAGTA
linearis_linearRM1406_2	TGGATTACTAAGACCACCTTACCGGTCCATCATGCACCACCTTGTGCGATGCATGACGGATACATATTCATTCCGGTCCATACAATGCCCTTCGATTAGGTACGCAACACAGTA
leiopodaRM1466	TGGATTACTGAGACCACCTTACCGGTCCATCATGCAGCACATGTGCGATGCATGACGAAACATATTCATTCCGGTCCATACAATGCCCTTCGATTAGGTACGCAACACAGTA
serrataHerm_RM	TGGATTACTAAGACCACCTTACCGGTCCATCATGCACCACCTTGTGCGATGCATGACGGATACATATTCATTCCGGTCCATACAATGCCCTTCGATTAGGTACGCAACACAGTA
krebsiana_RVC162	TGGATTACTAAGAASCACTTACCGGTCCATCATGCACCACCTTGTGCGATGCATGACGGATACATATTCATTCCGGTCCATACAATGCCCTTCGATTAGGTACGCAACACAGTA
krebsiana_krebrSH110	TGGATTACTAAGAACACTTACCGGTCCATCATGCACCACCTTGTGCGATGCATGACGGATACATATTCATTCCGGTCCATACAATGCCCTTCGATTAGGTACGCAACACAGTA
krebsiana_krebrSH111_1	TGGATTACTAAGAACACTTACCGGTCCATCATGCACCACCTTGTGCGATGCATGACGGATACATATTCATTCCGGTCCATACAATGCCCTTCGATTAGGTACGCAACACAGTA
krebsiana_krebrSH111_2	TGGATTACTAAGAACACTTACCGGTCCATCATGCACCACCTTGTGCGATGCATGACGGATACATATTCATTCCGGTCCATACAATGCCCTTCGATTAGGTACGCAACACAGTA
krebsiana_krebrSH112	TGGATTACTAAGAACACTTACCGGTCCATCATGCACCACCTTGTGCGATGCATGACGGATACATATTCATTCCGGTCCATACAATGCCCTTCGATTAGGTACGCAACACAGTA
krebsianaSH115	TGGATTACTAAGAACACTTACCGGTCCATCATGCACCACCTTGTGCGATGCATGACGGATACATATTCATTCCGGTCCATACAATGCCCTTCGATTAGGTACGCAACACAGTA
linearis_linearSH116	TGGATTACTAAGAACACTTACCGGTCCATCATGCACCACCTTGTGCGATGCATGACGGATACATATTCATTCCGGTCCATACAATGCCCTTCGATTAGGTACGCAACACAGTA
linearis_linearSH117	TGGATTACTAAGACCACCTTACCGGTCCATCATGCACCACCTTGTGCGATGCATGACGGATACATATTCATTCCGGTCCATACAATGCCCTTCGATTAGGTACGCAACACAGTA
krebsianaSH118	TGGATTACTAAGACCACCTTACCGGTCCATCATGCACCACCTTGTGCGATGCATGACGGATACATATTCATTCCGGTCCATACAATGCCCTTCGATTAGGTACGCAACACAGTA
linearis_linearSH131	TGGATTACTAAGACCACCTTACCGGKCCATCATGCACCACCTTGTGCGATGCATGACGGATACATATTCATTCCGGTCCATACAATGCCCTTCGATTAGGTACGCAACACAGTA
linearis_linearSH132	TGGATTACTAAGACCACCTTACCGGKCCATCATGCACCACCTTGTGCGATGCATGACGGATACATATTCATTCCGGTCCATACAATGCCCTTCGATTAGGTACGCAACACAGTA
krebsianaSH133	TGGATTACTAAGAACACTTACCGGTCCATCATGCACCACCTTGTGCGATGCATGACGGATACATATTCATTCCGGTCCATACAATGCCCTTCGATTAGGTACGCAACACAGTA
krebsianaSH135	TGGATTACTAAGACCACCTTACCGGTCCATCATGCACCACCTTGTGCGATGCATGACGGATACATATTCATTCCGGTCCATACAATGCCCTTCGATTAGGTACGCAACACAGTA
krebsianaSR480	TGGATTACTAAGAACACTTACCGGTCCATCATGCACCACCTTGTGCGATGCATGACGGATACATATTCATTCCGGTCCATACAATGCCCTTCGATTAGGTACGCAACACAGTA
krebsianaSR520	TGGATTACTAAGACCACCTTACSGGTCCATCATGCACCACCTTGTGCGATGCATGACGGATACATATTCATTCCGGTCCATACAATGCCCTTCGATTAGGTACGCAACACAGTA
linearis_linearSR523	TGGATTACTAAGACCACCTTACCGGTCCATCATGCACCACCTTGTGCGATGCATGACGGATACATATTCATTCCGGTCCATACAATGCCCTTCGATTAGGTACGCAACACAGTA
krebsianaSR564	TGGATTACTAAGACCACCTTACCGGTCCATCATGCACCACCTTGTGCGATGCATGACGGATACATATTCATTCCGGTCCATACAATGCCCTTCGATTAGGTACGCAACACAGTA
linearis_linearSR571	TGGATTACTAAGACCACCTTACCGGTCCATCATGCACCACCTTGTGCGATGCATGACGGATACATATTCATTCCGGTCCATACAATGCCCTTCGATTAGGTACGCAACACAGTA
rigens_rigSR574	TGGATTACTAAGACCACCTTACCGGTCCATCATGCACCACCTTGTGCGATGCATGACGGATACATATTCATTCCGGTCCATACAATGCCCTTCGATTAGGTACGCAACACAGTA
rigens_rigSR575	TGGATTACTAAGAACACTTACCGGTCCATCATGCACCACCTTGTGCGATGCATGACGGATACATATTCATTCCGGTCCATACAATGCCCTTCGATTAGGTACGCAACACAGTA
rigensSR581	TGGATTACTAAGACCACCTTACCGGTCCATCATGCACCACCTTGTGCGATGCATGACGGATACATATTCATTCCGGTCCATACAATGCCCTTCGATTAGGTACGCAACACAGTA
rigens_uniflSR625	TGGATTACTAAGACCACCTTACCGGTCCATCATGCACCACCTTGTGCGATGCATGACGGATACATATTCATTCCGGTCCATACAATGCCCTTCGATTAGGTACGCAACACAGTA
krebsiana_krebrSVHF1	TGGATTACTAAGACCACCTTACCGGTCCATCATGCACCACCTTGTGCGATGCATGACGGATACATATTCATTCCGGTCCATACAATGCCCTTCGATTAGGTACGCAACACAGTA
krebsiana_arctSV_HF2	TGGATTACTAAGAMCACTTACCGGTCCATCATGCACCACCTTGTGCGATGCATGACGGATACATATTCATTCCGGTCCATACAATGCCCTTCGATTAGGTACGCAACACAGTA
[1000 1010 1020 1030 1040 1050 1060 1070 1080 1090 1100]
lichtensteiniRM1323	AACCCACAATACGAGCAAGTCTACAACAAGCCTTGCTACGTAATGAAGAGGTAAGCACGCATGGAAGTTGCTTCGCTAGAAGACATCCAACCACCCGTAACAAACCAA
lichtesteiniM050906_2	AACCCACAATACGAGCAAGTCTACAACAAGCCTTGCTACGTAATGAAGAGGTAAGCACGCATGGAAGTTGCTTCGCTAGAAGACATCCAACCACCCGTAACAAACCAA
heterochaetaM160901_5g	AACCCACAAAACGAGCAAGTCTACAACAAGCCTTGCTACGTAATGAAGAGGTAAGCACGCATGGAAGTTGCTTCGCTAGAAGACATCCAACCACCCGTAACAAACCAA
heterochaetaRM1348	AACCCACAAAACGAGCAAGTCTACAACAAGCCTTGCTACGTAATGAAGAGGTAAGCACGCATGGAAGTTGCTTCGCTAGAAGACATCCAACCACCCGTAACAAACCAA
heterochaetaRM1255	AACCCACAATACGAGCAAGTCTACAACAAGCCTTGCTACGTAATGAAGAGGTAAGCACGCATGGAAGTTGCTTCGCTAGAAGACATCCAACCACCCGTAACAAACCAA

Appendix 6: Additional nrDNA sequence data for Chapter 4

tenuifoliaM7219_10	ACAAGGCAACCTTCATCG-----
tenuifoliaRM1352	AACCCACAATACGAGCAAGTCTATAACAAGCCTTGCTACGTAATGAAGAGGTAAGCAGCGCATGGAAGTTGCTTCGCAAGAAGACATCCAACCACCCGTAACAAACCAA
ciliarisSR705	AACCCACAATATAGCAAGTCTAAAACAAGACTTGCTACGTAATGAAGAGGTAAGCAGCGCATGGAAGTTGCTTCGCTAGAAGACATCCAACCACCCGTAACAAACCAA
jurineifolia_scabCAM1953	AACCCACAATACGAGCAAGTCTAAAACAAGCCTTGCTACGTAATGAAGAGGTAAGCAGCGCATGGAAGTTGCTTCGCTAGAAGACATCCAACCACCCGTAACAAACCAA
rigens_unifl_Boknes1	AACCCACAATACGAGCAACACTAAATTAAGCCTTGCTACGTAATGAAGAGGTAAGCAGCGCATGGAAGTTGCTTCGCTAGAAGACATCCAACCACCCGTAACAAACCAA
linearis_linear_Boknes2	AACCCACAATACGAGCAACACTAAATTAAGCCTTGCTACGTAATGAAGAGGTAAGCAGCGCATGGAAGTTGCTTCGCTAGAAGACATCCAACCACCCGTAACAAACCAA
linearis_ovalM041001_2g	AACCCACAATACGAGCAACACTAAATTAAGCCTTGCTACGTAATGAAGAGGTAAGCAGCGCATGGAAGTTGCTTCGCTAGAAGACATCCAACCACCCGTAACAAACCAA
rigens_leuco_M070704_1	AACCCACAATACGAGCAACACTAAATTAAGCCTTGCTACGTAATGAAGAGGTAAGCAGCGCATGGAAGTTGCTTCGCTAGAAGACATCCAACCACCCGTAACAAACCAA
krebsiana_krebM071001_1g	AACCCACAATACGAGCAACACTAAATTAAGCCTTGCTACGTAATGAAGAGGTAAGCAGCGCATGGAAGTTGCTTCGCTAGAAGACATCCAACCACCCGTAACAAACCAA
krebsiana_krebM071001_3g1	AACCCACAATACGAGCAACACTAAATTAAGCCTTGCTACGTAATGAAGAGGTAAGCAGCGCATGGAAGTTGCTTCGCTAGAAGACATCCAACCACCCGTAACAAACCAA
krebsiana_arctM071001_3pg	AACCCACAATACGAGCAACACTAAATTAAGCCTTGCTACGTAATGAAGAGGTAAGCAGCGCATGGAAGTTGCTTCGCTAGAAGACATCCAACCACCCGTAACAAACCAA
rigidaM100903_4	AACCCACAATACGAGCAACACTAAATTAAGCCTTGCTACGTAATGAAGAGGTAAGCAGCGCATGGAAGTTGCTTCGCTAGAAGACATCCAACCACCCGTAACAAACCAA
rigidaM100904_4	AACCCACAATACGAGCAACACTAAATTAAGCCTTGCTACGTAATGAAGAGGTAAGCAGCGCATGGAAGTTGCTTCGCTAGAAGACATCCAACCACCCGTAACAAACCAA
rigidM110805_10	AACCCACAATACGAGCAACACTAAATTAAGCCTTGCTACGTAATGAAGAGGTAAGCAGCGCATGGAAGTTGCTTCGCTAGAAGACATCCAACCACCCGTAACAAACCAA
rigidaM120805_80	AACCCACAATACGAGCAACACTAAATTAAGCCTTGCTACGTAATGAAGAGGTAAGCAGCGCATGGAAGTTGCTTCGCTAGAAGACATCCAACCACCCGTAACAAACCAA
leiopodaM160704_5	AACCCGCAATACGAGCAACACTAAATTAAGCCTTGCTACGTAATGAAGAGGTAAGCAGCGCATGGAAGTTGCTTCGCTAGAAGACATCCAACCACCCGTAACAAACCAA
pectinataM180904_5	AACCCATAATACGAGCAACACTAAATTAAGCCTTGCTACGTAATGAAGAGGTAAGCAGCGCATGGAAGTTGCTTCGCTAGAAGACATCCAACCACCCGTAACAAACCAA
krebsiana_krebM210902_1	AACCCACAATACGAGCAACACTAAATTAAGCCTTGCTACGTAATGAAGAGGTAAGCAGCGCATGGAAGTTGCTTCGCTAGAAGACATCCAACCACCCGTAACAAACCAA
krebsiana_krebM230803_8	AACCCACAATACGAGCAACACTAAATTAAGCCTTGCTACGTAATGAAGAGGTAAGCAGCGCATGGAAGTTGCTTCGCTAGAAGACATCCAACCACCCGTAACAAACCAA
serrM230901_7g	AACCCACAATACGAGCAACACTAAATTAAGCCTTGCTACGTAATGAAGAGGTAAGCAGCGCATGGAAGTTGCTTCGCTAGAAGACATCCAACCACCCGTAACAAACCAA
leiopodaM250901_34	AACCCACAATACGAGCAAGACTGAATTAAGCCTTGCTACGTAATGAAGAGGTAAGCAGCGCATGGAAGTTGCTTCGCTAGAAGACATCCAACCACCCGTAACAAACCAA
pectinataM250901_37	AACCCACAATACGAGCAACACTAAATTAAGCCTTGCTACGTAATGAAGAGGTAAGCAGCGCATGGAAGTTGCTTCGCTAGAAGACATCCAACCACCCGTAACAAACCAA
pectM260901_2g	AACCCACAATACGAGCAACACTAAATTAAGCCTTGCTACGTAATGAAGAGGTAAGCAGCGCATGGAAGTTGCTTCGCTAGAAGACATCCAACCACCCGTAACAAACCAA
maritimaM260901	AACCCACAATACGAGCAACACTAAATTAAGCCTTGCTACGTAATGAAGAGGTAAGCAGCGCATGGAAGTTGCTTCGCTAGAAGACATCCAACCACCCGTAACAAACCAA
krebsiana_krebM261001_2	AACCCACAATACGAGCAACACTAAATTAAGCCTTGCTACGTAATGAAGAGGTAAGCAGCGCATGGAAGTTGCTTCGCTAGAAGACATCCAACCACCCGTAACAAACCAA
maritimaM270901_5g	AACCCACAATACGAGCAACACTAAATTAAGCCTTGCTACGTAATGAAGAGGTAAGCAGCGCATGGAAGTTGCTTCGCTAGAAGACATCCAACCACCCGTAACAAACCAA
rigens_rigensM7293	AACCCACAATACGAGCAACACTAAATTAAGCCTTGCTACGTAATGAAGAGGTAAGCAGCGCATGGAAGTTGCTTCGCTAGAAGACATCCAACCACCCGTAACAAACCAA
rigens_rigensM7298_2	AACCCACAATACGAGCAACACTAAATTAAGCCTTGCTACGTAATGAAGAGGTAAGCAGCGCATGGAAGTTGCTTCGCTAGAAGACATCCAACCACCCGTAACAAACCAA
rigens_rigensM7527_2	AACCCACAATACGAGCAACACTAAATTAAGCCTTGCTACGTAATGAAGAGGTAAGCAGCGCATGGAAGTTGCTTCGCTAGAAGACATCCAACCACCCGTAACAAACCAA
leiopodaM200901_22g	AACCCGCAATACGAGCAACACTAAATTAAGCCTTGCTACGTAATGAAGAGGTAAGCAGCGCATGGAAGTTGCTTCGCTAGAAGACATCCAACCACCCGTAACAAACCAA
spnov_M7237_4	AACCCACAATACGAGCAACACTAAATTAAGCCTTGCTACGTAATGAAGAGGTAAGCAGCGCATGGAAGTTGCTTCGCTAGAAGACATCCAACCACCCGTAACAAACCAA
serrataHerm_NB	AACCCACAATACGAGCAACACTAAATTAAGCCTTGCTACGTAATGAAGAGGTAAGCAGCGCATGGAAGTTGCTTCGCTAGAAGACATCCAACCACCCGTAACAAACCAA
krebsiana_krebNB1465	AACCCACAATACGAGCAACACTAAATTAAGCCTTGCTACGTAATGAAGAGGTAAGCAGCGCATGGAAGTTGCTTCGCTAGAAGACATCCAACCACCCGTAACAAACCAA
linearis_linearRM1013	AACCCACAATACGAGCAACACTAAATTAAGCCTTGCTACGTAATGAAGAGGTAAGCAGCGCATGGAAGTTGCTTCGCTAGAAGACATCCAACCACCCGTAACAAACCAA
rigens_leucoRM1021	AACCCACAATACGAGCAACACTAAATTAAGCCTTGCTACGTAATGAAGAGGTAAGCAGCGCATGGAAGTTGCTTCGCTAGAAGACATCCAACCACCCGTAACAAACCAA
pectinataRM1044_1	AACCCACAATACGAGCAACACTAAATTAAGCCTTGCTACGTAATGAAGAGGTAAGCAGCGCATGGAAGTTGCTTCGCTAGAAGACATCCAACCACCCGTAACAAACCAA
hybrRM1061	AACCCRCAATACGAGCAACACTAAATTAAGCCTTGCTACGTAATGAAGAGGTAAGCAGCGCATGGAAGTTGCTTCGCTAGAAGACATCCAACCACCCGTAACAAACCAA
leiopodaRM1063	AACCCACAATACGAGCAACACTAAATTAAGCCTTGCTACGTAATGAAGAGGTAAGCAGCGCATGGAAGTTGCTTCGCTAGAAGACATCCAACCACCCGTAACAAACCAA
rigidaRM1082	AACCCACAATACGAGCAACACTAAATTAAGCCTTGCTACGTAATGAAGAGGTAAGCAGCGCATGGAAGTTGCTTCGCTAGAAGACATCCAACCACCCGTAACAAACCAA
linearis_linearRM1090	AACCCACAATACGAGCAACACTAAATTAAGCCTTGCTACGTAATGAAGAGGTAAGCAGCGCATGGAAGTTGCTTCGCTAGAAGACATCCAACCACCCGTAACAAACCAA
linearis_linearRM1092	AACCCACAATACGAGCAACACTAAATTAAGCCTTGCTACGTAATGAAGAGGTAAGCAGCGCATGGAAGTTGCTTCGCTAGAAGACATCCAACCACCCGTAACAAACCAA
linearis_linearRM1094	AACCCACAATACGAGCAACACTAAATTAAGCCTTGCTACGTAATGAAGAGGTAAGCAGCGCATGGAAGTTGCTTCGCTAGAAGACATCCAACCACCCGTAACAAACCAA
linearis_linearRM1103	AACCCACAATACGAGCAACACTAAATTAAGCCTTGCTACGTAATGAAGAGGTAAGCAGCGCATGGAAGTTGCTTCGCTAGAAGACATCCAACCACCCGTAACAAACCAA
krebsiana_serrRM1137	AACCCACAATACGAGCAACACTAAATTAAGCCTTGCTACGTAATGAAGAGGTAAGCAGCGCATGGAAGTTGCTTCGCTAGAAGACATCCAACCACCCGTAACAAACCAA
linearis_linearRM1182	AACCCACAATACGAGCAACACTAAATTAAGCCTTGCTACGTAATGAAGAGGTAAGCAGCGCATGGAAGTTGCTTCGCTAGAAGACATCCAACCACCCGTAACAAACCAA
rigidaRM1210	AACCCACAATACGAGCAACACTAAATTAAGCCTTGCTACGTAATGAAGAGGTAAGCAGCGCATGGAAGTTGCTTCGCTAGAAGACATCCAACCACCCGTAACAAACCAA
serrataRM1216	AACCCACAATACGAGCAACACTAAATTAAGCCTTGCTACGTAATGAAGAGGTAAGCAGCGCATGGAAGTTGCTTCGCTAGAAGACATCCAACCACCCGTAACAAACCAA
serrataRM1241	AACCCACAATACTAGCAAGACTGAATTAAGCCTTGCTACGTAATGAAGAGGTAAGCAGCGCATGGAAGTTGCTTCGCTAGAAGACATCCAACCACCCGTAACAAACCAA
serrataRM1245	AACCCACAATACGAGCAACACTAAATTAAGCCTTGCTACGTAATGAAGAGGTAAGCAGCGCATGGAAGTTGCTTCGCTAGAAGACATCCAACCACCCGTAACAAACCAA
rigidaRM1254	AACCCACAATACGAGCAACACTAAATTAAGCCTTGCTACGTAATGAAGAGGTAAGCAGCGCATGGAAGTTGCTTCGCTAGAAGACATCCAACCACCCGTAACAAACCAA
serrataRM1260	AACCCACAATACGAGCAACACTAAATTAAGCCTTGCTACGTAATGAAGAGGTAAGCAGCGCATGGAAGTTGCTTCGCTAGAAGACATCCAACCACCCGTAACAAACCAA

Appendix 6: Additional nrDNA sequence data for Chapter 4

krebsianaSH115 AACCACAATACGAGCAACACTAAATTAAGCCTTGCTACGTAATGAAGAGGTAAGCACGCATGGAAGTTGCTTCGCTAGAAGACATCCAACCACCCGTAACAAACCAA
 linearis_linearSH116 AACCACAATACGAGCAACACTAAATTAAGCCTTGCTACGTAATGAAGAGGTAAGCACGCATGGAAGTTGCTTCGCTAGAAGACATCCAACCACCCGTAACAAACCAA
 linearis_linearSH117 AACCACAATACGAGCAACACTAAATTAAGCCTTGCTACGTAATGAAGAGGTAAGCACGCATGGAAGTTGCTTCGCTAGAAGACATCCAACCACCCGTAACAAACCAA
 krebsianaSH118 AACCACAATACGAGCAACACTAAATTAAGCCTTGCTACGTAATGAAGAGGTAAGCACGCATGGAAGTTGCTTCGCTAGAAGACATCCAACCACCCGTAACAAACCAA
 linearis_linearSH131 AACCACAATACGAGCAACACTAAATTAAGCCTTGCTACGTAATGAAGAGGTAAGCACGCATGGAAGTTGCTTCGCTAGAAGACATCCAACCACCCGTAACAAACCAA
 linearis_linearSH132 AACCACAATACGAGCAACACTAAATTAAGCCTTGCTACGTAATGAAGAGGTAAGCACGCATGGAAGTTGCTTCGCTAGAAGACATCCAACCACCCGTAACAAACCAA
 krebsianaSH133 AACCACAATACGAGCAACACTAAATTAAGCCTTGCTACGTAATGAAGAGGTAAGCACGCATGGAAGTTGCTTCGCTAGAAGACATCCAACCACCCGTAACAAACCAA
 krebsianaSH135 AACCACAATACGAGCAACACTAAATTAAGCCTTGCTACGTAATGAAGAGGTAAGCACGCATGGAAGTTGCTTCGCTAGAAGACATCCAACCACCCGTAACAAACCAA
 krebsianaSR480 AACCACAATACGAGCAACACTAAATTAAGCCTTGCTACGTAATGAAGAGGTAAGCACGCATGGAAGTTGCTTCGCTAGAAGACATCCAACCACCCGTAACAAACCAA
 krebsianaSR520 AACCACAATACGAGCAACACTAAATTAAGCCTTGCTACGTAATGAAGAGGTAAGCACGCATGGAAGTTGCTTCGCTAGAAGACATCCAACCACCCGTAACAAACCAA
 linearis_linearSR523 AACCACAATACGAGCAACACTAAATTAAGCCTTGCTACGTAATGAAGAGGTAAGCACGCATGGAAGTTGCTTCGCTAGAAGACATCCAACCACCCGTAACAAACCAA
 krebsianaSR564 AACCACAATACGAGCAACACTAAATTAAGCCTTGCTACGTAATGAAGAGGTAAGCACGCATGGAAGTTGCTTCGCTAGAAGACATCCAACCACCCGTAACAAACCAA
 linearis_linearSR571 AACCACAATACGAGCAACACTAAATTAAGCCTTGCTACGTAATGAAGAGGTAAGCACGCATGGAAGTTGCTTCGCTAGAAGACATCCAACCACCCGTAACAAACCAA
 rigens_rigSR574 AACCACAATACGAGCAACACTAAATTAAGCCTTGCTACGTAATGAAGAGGTAAGCACGCATGGAAGTTGCTTCGCTAGAAGACATCCAACCACCCGTAACAAACCAA
 rigens_rigSR575 AACCACAATACGAGCAACACTAAATTAAGCCTTGCTACGTAATGAAGAGGTAAGCACGCATGGAAGTTGCTTCGCTAGAAGACATCCAACCACCCGTAACAAACCAA
 rigensSR581 AACCACAATACGAGCAACACTAAATTAAGCCTTGCTACGTAATGAAGAGGTAAGCACGCATGGAAGTTGCTTCGCTAGAAGACATCCAACCACCCGTAACAAACCAA
 rigens_uniflSR625 AACCACAATACGAGCAACACTAAATTAAGCCTTGCTACGTAATGAAGAGGTAAGCACGCATGGAAGTTGCTTCGCTAGAAGACATCCAACCACCCGTAACAAACCAA
 krebsiana_krebSVHF1 AACCACAATACGAGCAACACTAAATTAAGCCTTGCTACGTAATGAAGAGGTAAGCACGCATGGAAGTTGCTTCGCTAGAAGACATCCAACCACCCGTAACAAACCAA
 krebsiana_arctSV_HF2 AACCACAATACGAGCAACACTAAATTAAGCCTTGCTACGTAATGAAGAGGTAAGCACGCATGGAAGTTGCTTCGCTAGAAGACATCCAACCACCCGTAACAAACCAA

[1110 1120 1130 1140 1150 1160 1170 1180 1190 1200 1210]

lichtensteiniRM1323 CACCACCTCATGCACCTTTACGGTAAACATTTCCCGAAACCACCCGACTAGTAGCCACCCACTTAACACAAA--TGCAAGCAAGCAACCAAAAGCCAAAGCAATCCCAAAA
 lichtesteiniM050906_2 CACCACCTCATGCACCTTTACGGTAAACATTTCCCGAAACCACCCGACTAGTAGCCACCCACTTAACACAAA--TGCAAGCAAGCAACCAAAAGCCAAAGCAATCCCAAAA
 heterochaetaM160901_5g CACCACCTCATGCACCTTTACGGTAAACATTTCCCGAAACCACCCGACTAGTAGCCACCCACTTAGCACAGA--TGCAAGCAAGCAACCAAAAGCCAAAGCAATCCCAAAA
 heterochaetaRM1348 CACCACCTCATGCACCTTTACGGTAAACATTTCCCGAAACCACCCGACTAGTAGCCACCCACTTAGCACAAA--TGCAAGCAAGCAACCAAAAGCCAAAGCAATCCCAAAA
 heterochaetaRM1255 CACCACCTCATGCACCTTTACGGTAAACATTTCCCGAAACCACCCGACTAGTAGCCACCCACTTAGCACAAA--TGCAAGCAAGCAACCAAAAGCCAAAGCAATCCCAAAA
 tenuifoliaM7219_10 -----
 tenuifoliaRM1352 CACCACCTCATGCACCTTTACGGTAAACATTTCCCGAAACCACCCGACTAGTAGCCACCCACATAGCACAAA--TGCAAGCAAGCAACCAAAAGCCAGAGCAATCCCAAAA
 ciliarisSR705 CACCACCTCATGCACCTTTACGGTAAACATTTCCCGAAACCACCCAACACTAGTAGCCACCCACATAGCACAAA--GGCAAGCAAGCAACCAAAAGCCAAAGCAATCCCAAAA
 jurineifolia_scabCAM1953 CACCACCTCATGCACCTTTACGGTAAACATTTCCCGAAACCACCCGACTAGTAGCCACCCACATAGCACAAA--TGCAAGCAAGCAACCAAAAGCCAAAGCAATCCCAAAA
 rigens_unifl_Boknes1 CACCACCTCATGCACCTTTACGGTAAACATTTCCCGAAACCACCCGACTAGTAGCCACCCACATAGCACAAA--TGCAAGCAAGCAACCAAAAGCCAAAGCAATCCCAAAA
 linearis_linear_Boknes2 CACCACCTCATGCACCTTTACGGTAAACATTTCCCGAAACCACCCGACTAGTAGCCACCCACATAGCACAAA--TGCAAGCAAGCAACCAAAAGCCAAAGCAATCCCAAAA
 linearis_ovalM041001_2g CACCACCTCATGCACCTTTACGGTAAACATTTCCCGAAACCACCCGACTAGTAGCCACCCACATAGCACAAA--TGCAAGCAAGCAACCAAAAGCCAAAGCAATCCCAAAA
 rigens_leuco_M070704_1 CACCACCTCATGCACCTTTACGGTAAACATTTCCCGAAACCACCCGACTAGTAGCCACCCACATAGCACAAA--TGCAAGCAAGCAACCAAAAGCCAAAGCAATCCCAAAA
 krebsiana_krebM071001_1g CACCACCTCATGCACCTTTACGGTAAACATTTCCCGAAACCACCCGACTAGTAGCCACCCACATAGCACAAA--TGCAAGCAAGCAAGCAACCAAAAGCCAAAGCAATCCCAAAA
 krebsiana_krebM071001_3gl CACCACCTCATGCACCTTTACGGTAAACATTTCCCGAAACCACCCGACTAGTAGCCACCCACATAGCACAAA--TGCAAGCAAGCAACCAAAAGCCAAAGCAATCCCAAAA
 krebsiana_arctM071001_3pg CACCACCTCATGCACCTTTACGGTAAACATTTCCCGAAACCACCCGACTAGTAGCCACCCACATAGCACAAA--TGCAAGCAAGCAACCAAAAGCCAAAGCAATCCCAAAA
 rigidaM100903_4 CACCACCTCATGCACCTTTACGGTAAACATTTCCCGAAACCACCCGACTAGTAGCCACCCACATAGCACAAA--TGCAAGCAAGCAACCAAAAGCCAAAGCAATCCCAAAA
 rigidaM100904_4 CACCACCTCATGCACCTTTACGGTAAACATTTCCCGAAACCACCCGACTAGTAGCCACCCACATAGCACAAA--TGCAAGCAAGCAACCAAAAGCCAAAGCAATCCCAAAA
 rigidM110805_10 CACCACCTCATGCACCTTTACGGTAAACATTTCCCGAAACCACCCGACTAGTAGCCACCCACATAGCACAAA--TGCAAGCAAGCAACCAAAAGCCAAAGCAATCCCAAAA
 rigidaM120805_80 CACCACCTCATGCACCTTTACGGTAAACATTTCCCGAAACCACCCGACTAGTAGCCACCCACATAGCACAAA--TGCAAGCAAGCAACCAAAAGCCAAAGCAATCCCAAAA
 leiopodaM160704_5 CACCACCTCATGCACCTTTACGGTAAACATTTCCCGAAACCACCCGACTAGTAGCCACCCACATAGCACAAA--TGCAAGCAAGCAACCAAAAGCCAAAGCAATCCCAAAA
 pectinataM180904_5 CACCACCTCATGCACCTTTACGGTAAACATTTCCCGAAaCCACCCGACTAGTAGCCACCCACATAGCACAAA--TGCAAGCAAGCAACCAAAAGC????????????
 krebsiana_krebM210902_1 CACCACCTCATGCACCTTTACGGTAAACATTTCCCGAAACCACCCGACTAGTAGCCACCCACATAGCACAAA--TGCAAGCAAGCAACCAAAAGCCAAAGCAATCCCAAAA
 krebsiana_krebM230803_8 CACCACCTCATGCACCTTTACGGTAAACATTTCCCGAAACCACCCGACTAGTAGCCACCCACATAGCACAAA--TGCAAGCAAGCAACCAAAAGCCAAAGCAATCCCAAAA
 serrM230901_7g CACCACCTCATGCACCTTTACGGTAAACATTTCCCGAAACCACCCGACTAGTAGCCACCCACATAGCACAAA--TGCAAGCAAGCAACCAAAAGCCAAAGCAATCCCAAAA
 leiopodaM250901_34 CACCACCTCATGCACCTTTACGGTAAACATTTCCCGAAACCACCCGACTAGTAGCCACCCACATAGCACAAA--TGCAAGCAAGCAACCAAAAGCCAAAGCAATCCCAAAA
 pectinataM250901_37 CACCACCTCATGCACCTTTACGGTAAACATTTCCCGAAACCACCCGACTAGTAGCCACCCACATAGCACAAA--TGCAAGCAAGCAACCAAAAGCCAAAGCAATCCCAAAA
 pectM260901_2g CACCACCTCATGCACCTTTACGGTAAACATTTCCCGAAACCACCCGACTAGTAGCCACCCGCATAGCACAAA--TGCAAGCAAGCAACCAAAAGCCAAAGCAATCCCAAAA

Appendix 6: Additional nrDNA sequence data for Chapter 4

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linearis_linearRM884      CACCACTCATGCACCTTTACGGTAAACATTTTCCGAAACCACCCGACTAGTAGCCACCCACATAGCACAAA--TGCAAGCAAGCAACCAAAGCCAAAGCAATCCCAAAA
linearis_linearRM885      CACCACTCATGCACCTTTACGGTAAACATTTTCCGAAACCACCCGACTAGTAGCCACCCACATAGCACAAA--TGCAAGCAAGCAACCAAAGCCAAAGCAATCCCAAAA
krebianaRM888            CACCACTCATGCACCTTTACGGTAAACATTTTCCGAAACCACCCGACTAGTAGCCACCCACATAGCACAAA--TGCAAGCAAGCAACCAAAGCCAAAGCAATCCCAAAA
rigidaRM900_1           CACCACTCATGCACCTTTACGGTAAACATTTTCCGAAACCACCCGACTAGTAGCCACCCACATAGCACAAA--TGCAAGCAAGCAACCAAAGCCAAAGCAATCCCAAAA
krebiana_arctRM903      CACCACTCATGCACCTTTACGGTAAACATTTTCCGAAACCACCCGACTAGTAGCCACCCACATAGCACAAA--TGCAAGCAAGCAACCAAAGCCAAAGCAATCCCAAAA
krebarm904              CACCACTCATGCACCTTTACGGTAAACATTTTCCGAAACCACCCGACTAGTAGCCACCCACATAGCACAAA--TGCAAGCAAGCAACCAAAGCCAAAGCAATCCCAAAA
krebiana_krebRM906      CACCACTCATGCACCTTTACGGTAAACATTTTCCGAAACCACCCGACTAGTAGCCACCCACATAGCACAAA--TGCAAGCAAGCAACCAAAGCCAAAGCAATCCCAAAA
rigens_leucoRM919       CACCACTCATGCACCTTTACGGTAAACATTTTCCGAAACCACCCGACTAGTAGCCACCCACATAGCACAAA--TGCAAGCAAGCAACCAAAGCCAAAGCAATCCCAAAA
krebiana_krebRM929      CACCACTCATGCACCTTTACGGTAAACATTTTCCGAAACCACCCGACTAGTAGCCACCCACATAGCACAAA--TGCAAGCAAGCAACCAAAGCCAAAGCAATCCCAAAA
krebiana_krebRM949      CACCACTCATGCACCTTTACGGTAAACATTTTCCGAAACCACCCGACTAGTAGCCACCCACATAGCACAAA--TGCAAGCAAGCAACCAAAGCCAAAGCAATCCCAAAA
krebiana_krebRM950      CACCACTCATGCACCTTTACGGTAAACATTTTCCGAAACCACCCGACTAGTAGCCACCCACATAGCACAAA--TGCAAGCAAGCAACCAAAGCCAAAGCAATCCCAAAA
linearis_linearRM951     CACCACTCATGCACCTTTACGGTAAACATTTTCCGAAACCACCCGACTAGTAGCCACCCACATAGCACAAA--TGCAAGCAAGCAACCAAAGCCAAAGCAATCCCAAAA
krebiana_krebRM960      CACCACTCATGCACCTTTACGGTAAACATTTTCCGAAACCACCCGACTAGTAGCCACCCACATAGCACAAA--TGCAAGCAAGCAACCAAAGCCAAAGCAATCCCAAAA
krebiana_krebRM962      -----
krebianaRM966           CACCACTCATGCACCTTTACGGTAAACATTTTCCGAAACCACCCGACTAGTAGCCACCCACATAGCACAAA--TGCAAGCAAGCAACCAAAGCCAAAGCAATCCCAAAA
krebiana_krebRM968      CACCACTCATGCACCTTTACGGTAAACATTTTCCGAAACCACCCGACTAGTAGCCACCCACATAGCACAAA--TGCAAGCAAGCAACCAAAGCCAAAGCAATCCCAAAA
krebiana_krebRM992      CACCACTCATGCACCTTTACGGTAAACATTTTCCGAAACCACCCGACTAGTAGCCACCCACATAGCACAAA--TGCAAGCAAGCAACCAAAGCCAAAGCAATCCCAAAA
krebiana_RM996          CACCACTCATGCACCTTTACGGTAAACATTTTCCGAAACCACCCGACTAGTAGCCACCCACATAGCACAAA--TGCAAGCAAGCAACCAAAGCCAAAGCAATCCCAAAA
krebiana_krebRM1403     CACCACTCATGCACCTTTACGGTAAACATTTTCCGAAACCACCCGACTAGTAGCCACCCACATAGCACAAA--TGCAAGCAAGCAACCAAAGCCAAAGCAATCCCAAAA
linearis_linearRM1406_1  CACCACTCATGCACCTTTACGGTAAACATTTTCCGAAACCACCCGACTAGTAGCCACCCACATAGCACAAA--TGCAAGCAAGCAACCAAAGCCAAAGCAATCCCAAAA
linearis_linearRM1406_2  CACCACTCATGCACCTTTACGGTAAACATTTTCCGAAACCACCCGACTAGTAGCCACCCACATAGCACAAA--TGCAAGCAAGCAACCAAAGCCAAAGCAATCCCAAAA
leopodaRM1466          CACCACTCATGCACCTTTACGGTAAACATTTTCCGAAACCACCCGACTAGTAGCCACCCACATAGCACAAA--TGCAAGCAAGCAACCAAAGCCAAAGCAATCCCAAAA
serrataHerm_RM         CACCACTCATGCACCTTTACGGTAAACATTTTCCGAAACCACCCGACTAGTAGCCACCCACATAGCACAAA--TGCAAGCAAGCAACCAAAGCCAAAGCAATCCCAAAA
krebiana_RVC162        CACCACTCATGCACCTTTACGGTAAACATTTTCCGAAACCACCCGACTAGTAGCCACCCACATAGCACAAA--TGCAAGCAAGCAACCAAAGCCAAAGCAATCCCAAAA
krebiana_krebSH110      CACCACTCATGCACCTTTACGGTAAACATTTTCCGAAACCACCCGACTAGTAGCCACCCACATAGCACAAA--TGCAAGCAAGCAACCAAAGCCAAAGCAATCCCAAAA
krebiana_krebSH111_1    CACCACTCATGCACCTTTACGGTAAACATTTTCCGAAACCACCCGACTAGTAGCCACCCACATAGCACAAA--TGCAAGCAAGCAACCAAAGCCAAAGCAATCCCAAAA
krebiana_krebSH111_2    CACCACTCATGCRCCTTTACGGTAAACATTTTCCGAAACCACCCGACTAGTAGCCACCCACATAGCACAAA--TGCAAGCAAGCAACCAAAGCCAAAGCAATCCCAAAA
krebiana_krebSH112     CACCACTCATGCACCTTTACGGTAAACATTTTCCGAAACCACCCGACTAGTAGCCACCCACATAGCACAAA--TGCAAGCAAGCAACCAAAGCCAAAGCAATCCCAAAA
krebianaSH115          CACCACTCATGCACCTTTACGGTAAACATTTTCCGAAACCACCCGACTAGTAGCCACCCACATAGCACAAA--TGCAAGCAAGCAACCAAAGCCAAAGCAATCCCAAAA
linearis_linearSH116    CACCACTCATGCACCTTTACGGTAAACATTTTCCGAAACCACCCGACTAGTAGCCACCCACATAGCACAAA--TGCAAGCAAGCAACCAAAGCCAAAGCAATCCCAAAA
linearis_linearSH117    CACCACTCATGCACCTTTACGGTAAACATTTTCCGAAACCACCCGACTAGTAGCCACCCACATAGCACAAA--TGCAAGCAAGCAACCAAAGCCAAAGCAATCCCAAAA
krebianaSH118          CACCACTCATGCACCTTTACGGTAAACATTTTCCGAAACCACCCGACTAGTAGCCACCCACATAGCACAAA--TGCAAGCAAGCAACCAAAGCCAAAGCAATCCCAAAA
linearis_linearSH131    CACCACTCATGCACCTTTACGGTAAACATTTTCCGAAACCACCCGACTAGTAGCCACCCACATAGCACAAA--TGCAAGCAAGCAACCAAAGCCAAAGCAATCCCAAAA
linearis_linearSH132    CACCACTCATGCACCTTTACGGTAAACATTTTCCGAAACCACCCGACTAGTAGCCACCCACATAGCACAAA--TGCAAGCAAGCAACCAAAGCCAAAGCAATCCCAAAA
krebianaSH133          CACCACTCATGCACCTTTACGGTAAACATTTTCCGAAACCACCCGACTAGTAGCCACCCACATAGCACAAA--TGCAAGCAAGCAACCAAAGCCAAAGCAATCCCAAAA
krebianaSH135          CACCACTCATGCACCTTTACGGTAAACATTTTCCGAAACCACCCGACTAGTAGCCACCCACATAGCACAAA--TGCAAGCAAGCAACCAAAGCCAAAGCAATCCCAAAA
krebianaSR480          CACCACTCATGCACCTTTACGGTAAACATTTTCCGAAACCACCCGACTAGTAGCCACCCACATAGCACAAA--TGCAAGCAAGCAACCAAAGCCAAAGCAATCCCAAAA
krebianaSR520          CACCACTCATGCACCTTTACGGTAAACATTTTCCGAAACCACCCGACTAGTAGCCACCCACATAGCACAAA--TGCAAGCAAGCAACCAAAGCCAAAGCAATCCCAAAA
linearis_linearSR523    CACCACTCATGCACCTTTACGGTAAACATTTTCCGAAACCACCCGACTAGTAGCCACCCACATAGCACAAA--TGCAAGCAAGCAACCAAAGCCAAAGCAATCCCAAAA
krebianaSR564          CACCACTCATGCACCTTTACGGTAAACATTTTCCGAAACCACCCGACTAGTAGCCACCCACATAGCACAAA--TGCAAGCAAGCAACCAAAGCCAAAGCAATCCCAAAA
linearis_linearSR571    CACCACTCATGCACCTTTACGGTAAACATTTTCCGAAACCACCCGACTAGTAGCCACCCACATAGCACAAA--TGCAAGCAAGCAACCAAAGCCAAAGCAATCCCAAAA
rigens_rigSR574        CACCACTCATGCACCTTTACGGTAAACATTTTCCGAAACCACCCGACTAGTAGCCACCCACATAGCACAAA--TGCAAGCAAGCAACCAAAGCCAAAGCTATCCCAAAA
rigens_rigSR575        CACCACTCATGCACCTTTACGGTAAACATTTTCCGAAACCACCCGACTAGTAGCCACCCACATAGCACAAA--TGCAAGCAAGCAACCAAAGCCAAAGCTATCCCAAAA
rigensSR581            CACCACTCATGCACCTTTACGGTAAACATTTTCCGAAACCACCCGACTAGTAGCCACCCACATAGCAAAA--TGCAAGCAAGCAACCAAAGCCAAAGCAATCCCAAAA
rigens_uniflSR625      CACCACTCATGCACCTTTACGGTAAACATTTTCCGAAACCACCCGACTAGTAGCCACCCACATAGCACAAA--TGCAAGCAAGCAACCAAAGCCAAAGCAATCCCAAAA
krebiana_krebSVHF1     CACCACTCATGCACCTTTACGGTAAACATTTTCCGAAACCACCCGACTAGTAGCCACCCACATAGCACAAA--TGCAAGCAAGCAACCAAAGCCAAAGCAATCCCAAAA
krebiana_arctSV_HF2    CACCACTCATGCACCTTTACGGTAAACATTTTCCGAAACCACCCGACTAGTAGCCACCCACATAGCACAAA--TGCAAGCAAGCAACCAAAGCCAAAGCAATCCCAAAA

[                               1220           1230           1240           1250           1260           1270           1280           1290           1300           1310           1320]

lichtensteiniiRM1323     ATGAACCGAACGATGCGAGAAACAATAAAGCTACGAAACCGACACGATGCGCCTCATCAAACGCTCGCTTCATGMTTTTCT-A-CACACAACGCATCGCAAGACTAGGCT

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Appendix 6: Additional nrDNA sequence data for Chapter 4

lichtesteiniiM050906_2 ATGAACCGAACGATGCGAGAAAACAATAAAGCTACGAAACCGACACGATCGCCTCATCAAACCGCTCGCTTCATGCTTTTCT-A-CACACAACGCATCGCAAGACT--AGG
heterochaetaM160901_5g ATGCACCGAACGACGCGAGAAAACAATTAAGCTACGAAACCGACACGATCGCCTCATCAAACCGCTCGCTTCATGATTTTCT-A-CACACAACGCATCGCTAGACTAGGCT
heterochaetaRM1348 ATGCACCGAACGACGCGAGAAAACAATTAAGCTACGAAACCGACACGATCGCCTCATCAAACCGCTCGCTTCATGATTTTCT-A-CACACAACGCATCGCTAGACTGGGCT
heterochaetaRM1255 ATGCACCGAACGATGCGAGAAAACAATAAAGCTACGAAACCAACAGATCGCCTCATCAAACCGCTCGCTTCATGATTTTCT-A-GACACAATGCATCGCCAGACTGGGCT
tenuifoliaM7219_10 -----CCAACCCGCCTCATCAAACCGCTCGCTTCATCGTTTTC-A-CACACAACGCATCGCAAGCCA-GGCT
tenuifoliaRM1352 ATGCACCGAACGATGCGAGAAAACAATTAAGCTACGAAACCGACACGATCGCCTCATCAAACCGCTCGCTTCATGTTTTC-A-CACACAACGCATCACAAGCCA-GGCT
ciliarisSR705 ATGCACCGAACGATGCGAGAAAACAATAAAGCTACGAAACCGACATGATCGCCTCATCAAACCGCTCGCTTCACGATTTTCTTA-GACACCACGCATCGCTAGCCG-GGCT
jurineifolia_scabCAM1953 ATGCACCGAACGATGCGAGAAAACAATAAAGCTACGAAACCAACATGATCGCCTCATTAACCGCTCGCTTCATGATTTTCT-A-CGCACAACGATCGCTAGCCG-GGCT
rigens_unifl_Boknes1 ATGTACCGAACGATGCGAGAAAACAGTAAAGCTACGAAACCAACAGGATCGCCTCATCAAACCGCTCGCTTCATTATTTCCA-A-CACACAACGCATCGCTAGCAA-GGCT
linearis_linear_Boknes2 ATGTACCGAACGATGCGAGAAAACAGTAAAGCTACGAAACCAACAGGATCGCCTCATCAAACCGCTCGCTTCATTATTTCCA-A-CACACAACGCATCGCTAGCAA-GGCT
linearis_ovaM041001_2g ATGTACCGAACGATGCGAGAAAACAGTAAAGCTACGAAACCAACAGGATCGCCTCATCAAACCGCTCGCTTCATTATTTCCA-A-CACACAACGCATCGCTAGCAA-GGCT
rigens_leuco_M070704_1 ATGTACCGAACGATGCGAGAAAACAGTAAAGCTACGAAACCAACAGGATCGCCTCATCAAACCGCTCGCTTCATTATTTCCA-A-CACACAACGCATCGCTAGCAA-GGCT
krebsiana_krebM071001_1g ATGTACCGAACGATGCGAGAAAACAGTAAAGCTACGAAACCAACAGGATCGCCTCATCAAACCGCTCGCTTCATGATTTCCG-A-CACACAACGCATCGCTAGCAA-GGCT
krebsiana_krebM071001_3g1 ATGTACCGAACGATGCGAGAAAACAATAAAGCTACGAAACCAACAGGATCGCCTCATCAAACCGCTCGCTTCATTATTTCCA-A-CACACAACGCATCGCTAGCAA-GGCT
krebsiana_arctM071001_3pg ATGTACCGAACGATGCGAGAAAACAATAAAGCTACGAAACCAACAGGATCGCCTCATCAAACCGCTCGCTTCATTATTTCCA-A-CACACAACGCATCGCTAGCAA-GGCT
rigidaM100903_4 ATGTACCGAACGATGCGAGAAAACAGTAAAGCTACGAAACCAACAGGATCGCCTCATCAAACCGCTCGCTTCATTATTTCCA-A-CACACAACGCATCGCTAGCAA-GACT
rigidaM100904_4 ATGTACCGAACGATGCGAGAAAACAGTAAAGCTACGAAACCAACAGGATCGCCTCATCAAACCGCTCGCTTCATTATTTCCA-A-CGCACAACGCATCGCTAGCAA-GGCT
rigidM110805_10 ATGCACCGAACGATGCGAGAAAACAGAAAAGCTACGAAACCAACAGGATCGCCTCATCAAACCGCTCGCTTCATTATTTCCA-A-GACACAACGCATCGCTAGCAA-GGCT
rigidaM120805_80 ATGCACCGAACGATGCGAGAAAACAGAAAAGCTACGAAACCAACAGGATCGCCTCATCAAACCGCTCGCTTCATTATTTCCA-A-GACACAACGCATCGCTAGCAA-GGCT
leiopodaM160704_5 ATGCACCGAACGATGCGAGAAAACAGTAAAGCTACGAAACCAACAGGATCGCCTCATCAAACCGCTCGCTTCATTATTTCCA-A-CACACAACGCATCGCTAGCCG-GGCT
pectinataM180904_5 ???
krebsiana_krebM210902_1 ATGTACCGAACGATGCGAGAAAACAGTAAAGCTACGAAACCAACAGGATCGCCTCATCAAACCGCTCGCTTCATTATTTCCA-A-CACACAACGCATCGCTAGCAA-GGCT
krebsiana_krebM230803_8 ATGTACCGAACGATGCGAGAAAACATTAAGCTACGAAACCAACAGGATCGCCTCATCAAACCGCTCGCTTCATTATTTCCA-A-GACACAACGCATCGCTAGCAA-GGCT
serrM230901_7g ATGTACCGAACGATGCGAGAAAACAGTAAAGCTACGAAACCAACAGGATCGCCTCATCAAACCGCTCGCTTCATTATTTCCA-A-CACACAACGCATCGCTAGCAA-GGCT
leiopodaM250901_34 ATGTACCGAACGATGCGAGAAAACAGTAAAGCTACGAAACCAACAGGATCGCCTCATCAAACCGCTCGCTTCATTATTTCCA-A-CACACAACGCATCGCTAGCAA-GGCT
pectinataM250901_37 ATGTACCGAACGATGCGAGAAAACAGTAAAGCTACGAAACCAACAGGATCGCCTCATCAAACCGCTCGCTTCATTATTTCCA-A-CACACAACGCATCGCTAGCAA-GGCT
pectM260901_2g ATGTACCGAACGATGCGAGAAAACAGTAAAGCTACGAAACCAACAGGATCGCCTCATCAAACCGCTCGCTTCATTATTTCCA-A-CACACAACGCATCGCTAGCAA-GGCT
maritimaM260901 ATGCACCGAACGATGCGAGAAAACAGTAAAGCTACGAAACCAACAGGATCGCCTCATCAAACCGCTCGCTTCATTATTTCCA-A-CACACAACGCATCGCTAGCAA-GGCT
krebsiana_krebM261001_2 ATGTACCGAACGATGCGAGAAAACAGTAAAGCTACGAAACCAACAGGATCGCCTCATCAAACCGCTCGCTTCATTATTTCCA-A-CACACAACGCATCGCTAGCAA-GGCT
maritimaM270901_5g ATGTACCGAACGATGCGAGAAAACAGTAAAGCTACGAAACCAACAGGATCGCCTCATCAAACCGCTCGCTTCATTATTTCCA-A-CACACAACGCATCGCTAGCAA-GGCT
rigens_rigensM7293 ATGTACCGAACGATGCGAGAAAACAGTAAAGCTACGAAACCAACAGGATCGCCTCATCAAACCGCTCGCTTCATTATTTCCA-A-CACACAACGCATCGCTAGCAA-GGCT
rigens_rigensM7298_2 ATGTACCGAACGATGCGAGAAAACAGTAAAGCTACGAAACCAACAGGATCGCCTCATCAAACCGCTCGCTTCATTATTTCCA-A-CACACAACGCATCGCTAGCAA-GGCT
rigens_rigensM7527_2 ATGTACCGAACGATGCGAGAAAACAGTAAAGCTACGAAACCAACAGGATCGCCTCATCAAACCGCTCGCTTCATTATTTCCA-A-CACACAACGCATCGCTAGCAA-GGCT
leiopodaM200901_22g ATGCACCGAACGATGCGAGAAAACAGTAAAGCTACGAAACCAACAGGATCGCCTCATCAAACCGCTCGCTTCATTATTTCCA-A-CACACAACGCATCGCTAGC??????
spnov_M7237_4 ATGTACCGAACGATGCGAGAAAACAGTAAAGCTACGAAACCAACAGGATCGCCTCATCAAACCGCTCGCTTCATTATTTCCA-A-CACACAACGCATCGCTAGCAA-GGCT
serrataHerm_NB ATGTACCGAACGATGCGAGAAAACAGTAAAGCTACGAAACCAACAGGATCGCCTCATCAAACCGCTCGCTTCATTATTTCCA-A-CACACAACGCATCGCTAGCAA-GGCT
krebsiana_krebNB1465 ATGTACCGAACGATGCGAGAAAACAGTAAAGCTACGAAACCAACAGGATCGCCTCATCAAACCGCTCGCTTCATTATTTCCA-A-CACACAACGCATCGCTAGCAA-GGCT
linearis_linearRM1013 ATGTACCGAACGATGCGAGAAAACAGTAAAGCTACGAAACCAACAGGATCGCCTCATCAAACCGCTCGCTTCATTATTTCCA-A-CACACAACGCATCGCTAGCAA-GGCT
rigens_leucoRM1021 ATGTACCGAACGATGCGAGAAAACAGTAAAGCTACGAAACCAACAGGATCGCCTCATCAAACCGCTCGCTTCATTATTTCCA-A-CACACAACGCATCGCTAGCAA-GGCT
pectinataRM1044_1 ATGCACCGAACGATGCGAGAAAACAGTAAAGCTACGAAACCAACAGGATCGCCTCATCAAACCGCTCGCTTCATTATTTCCA-A-CACACAACGCATCGCTAGCAA-GGCT
hybrRM1061 ATGYACCGAACGATGCGAGAAAACAGTAAAGCTACGAAACCAACAGGATCGCCTCATCAAACCGCTCGCTTCATTATTTCCA-A-CACAC????????????????????
leiopodaRM1063 ATGTACCGAACGATGCGAGAAAACAGTAAAGCTACGAAACCAACAGGATCGCCTCATCAAACCGCTCGCTTCATTATTTCCA-A-CACACAACGCATCGCTAGCAA-GGCT
rigidaRM1082 ATGCACCGAACGATGCGAGAAAACAGTAAAGCTACGAAACCAACAGGATCGCCTCATCAAACCGCTCGCTTCATTATTTCCA-A-CACACAACGCATCGCTAGCAA-GGCT
linearis_linearRM1090 ATGTACCGAACGATGCGAGAAAACAGTAAAGCTACGAAACCAACAGGATCGCCTCATCAAACCGCTCGCTTCATTATTTCCA-A-CACACAACGCATCGGTTTCAA-GGCT
linearis_linearRM1092 ATGTACCGAACGATGCGAGAAAACAGTAAAGCTACGAAACCAACAGGATCGCCTCATCAAACCGCTCGCTTCATTATTTCCA-A-CACACAACGCATCGCTAGCAA-GGCT
linearis_linearRM1094 ATGTACCGAACGATGCGAGAAAACAGTAAAGCTACGAAACCAACAGGATCGCCTCATCAAACCGCTCGCTTCATTATTTCCA-A-CACACAACGCATCGCTAGCAA-GGCT
linearis_linearRM1103 ATGTACCGAACGATGCGAGAAAACAGTAAAGCTACGAAACCAACAGGATCGCCTCATCAAACCGCTCGCTTCATTATTTCCA-A-CACACAACGCATCGCTAGCAA-GGCT
krebsiana_serrRM1137 ATGTACCGAACGATGCGAGAAAACAGTAAAGCTACGAAACCAACAGGATCGCCTCATCAAACCGCTCGCTTCATTATTTCCA-A-CACACAACGCATCGCTAGCAA-GGCT
linearis_linearRM1182 ATGTACCGAACGATGCGAGAAAACAGTAAAGCTACGAAACCAACAGGATCGCCTCATCAAACCGCTCGCTTCATTATTTCCA-A-CGCACAACGCATCGCTAGCAA-GGCT
rigidaRM1210 ATGCACCGAACGATGCGAGAAAACAGTAAAGCTACGAAACCAACAGGATCGCCTCATCAAACCGCTCGCTTCATTATTTCCA-A-GACACAACGCATCGCTAGCAA-GGCT
serrataRM1216 ATGCACCGAACGATGCGAGAAAACAGTAAAGCTACGAAACCAACAGGATCGCCTCATCAAACCGCTCGCTTCATTATTTCCA-A-SACACAACGCATCGCTAGCAA-GGCT

Appendix 6: Additional nrDNA sequence data for Chapter 4

krebsiana_krebSH110 ATGTACCGAACGATGCGAGAAACAGTAAAGCTACGAAACCAACACGATCGCCTCATACAAACGCTCGCTTCATTATTTCCA-A-CGCACAACGCATCGCTAGCAA?????
krebsiana_krebSH111_1 ATGTACCGAACGATGCGAGAAACAGTAAAGCTACGAAACCAACACGATCGCCTCATACAAACGCTCGCTTCATTATTTCCA-A-CGCACAACGCATCGCTAGCAA-GGCT
krebsiana_krebSH111_2 ATGTACCGAACGATGCGAGAAACAGTAAAGCTACGAAACCAACACGATCGCCTCATACAAACGCTCGCTTCATTATTTCCA-A-CGCACAACGCATCGCTAGCAA-GGCT
krebsiana_krebSH112 ATGTACCGAACGATGCGAGAAACAGTAAAGCTACGAAACCAACACGATCGCCTCATACAAACGCTCGCTTCATTATTTCCA-A-CACACAACGCATCGCTAGCAA-GGCT
krebsianaSH115 ATGTACCGAACGATGCGAGAAACAGTAAAGCTACGAAACCAACACGATCGCCTCATACAAACGCTCGCTTCATTATTTCCA-A-CGCACAAGCGCATCCTAGCAA-GGCT
linearis_linearSH116 ATGTACCGAACGATGCGAGAAACAGTAAAGCTACGAAACCAACACGATCGCCTCATACAAACGCTCGCTTCATTATTTCCA-A-CRCACAACGCATCGCTAGCAA-GGCT
linearis_linearSH117 ATGTACCGAACGATGCGAGAAACAGTAAAGCTACGAAACCAACACGATCGCCTCATACAAACGCTCGCTTCATTATTTCCA-A-CACACAACGCATCGCTAGCAA-GGCT
krebsianaSH118 ATGTACCGAACGATGCGAGAAACAGTAAAGCTACGAAACCAACACGATCGCCTCATACAAACGCTCGCTTCATTATTTCCA-A-CACACAACGCATCGCTAGCAA-GGCT
linearis_linearSH131 ATGTACCGAACGATGCGAGAAACAGTAAAGCTACGAAACCAACACGATCGCCTCATACAAACGCTCGCTTCATTATTTCCA-A-CACACAACGCATCGCTAGCAA-GGCT
linearis_linearSH132 ATGTACCGAACGATGCGAGAAACAGTAAAGCTACGAAACCAACACGATCGCCTCATACAAACGCTCGCTTCATTATTTCCA-A-CACACAACGCATCGCTAGCAA-GGCT
krebsianaSH133 ATGTACCGAACGATGCGAGAAACAGTAAAGCTACGAAACCAACACGATCGCCTCATACAAACGCTCGCTTCATTATTTCCA-A-CGCACAACGCATCGCTAGCAA-GGCT
krebsianaSH135 ATGTACCGAACGATGCGAGAAACAGTAAAGCTACGAAACCAACAGATCGCCTCATACAAACGCTCGCTTCATTATTTCCA-A-CACACAACGCATCGCTAGCAA-GGCT
krebsianaSR480 ATGTACCGAACGATGCGAGAAACAGTAAAGCTACGAAACCAACACGATCGCCTCATACAAACGCTCGCTTCATTATTTCCA-A-CGCACAACGCATCGCTAGCAA-GGCT
krebsianaSR520 ATGTACCGAACGATGCGAGAAACAGTAAAGCTACGAAACCAACAGGATCGCCTCATACAAACGCTCGCTTCATTATTTCCA-A-CACACAACGCATCGCTAGCAA-GGCT
linearis_linearSR523 ATGTACCGAACGATGCGAGAAACAGTAAAGCTACGAAACCAACAGGATCGCCTCATACAAACGCTCGCTTCATTATTTCCA-A-CACACAACGCATCGCTAGCAA-GGCT
krebsianaSR564 ATGTACCGAACGATGCGAGAAACAGTAAAGCTACGAAACCAACAGGATCGCCTCATACAAACGCTCGCTTCATTATTTCCA-A-CACACAACGCATCGCTAGCAA-GGCT
linearis_linearSR571 ATGTACCGAACGATGCGAGAAACAGTAAAGCTACGAAACCAACACGATCGCCTCATACAAACGCTCGCTTCATTATTTCCA-A-CACACAACGCATCGCTAGCAA-GGCT
rigens_rigSR574 ATGTACCGAACGATGCGAGAAACAGTAAAGCTACGAAACCAACACGATCGCCTCATACAAACGCTCGCTTCATTATTTCCA-A-CACACAACGCATCGCTAGCAA-GGCT
rigens_rigSR575 ATGTACCGAACGATGCGAGAAACAGTAAAGCTACGAAACCAACACGATCGCCTCATACAAACGCTCGCTTCATTATTTCCA-A-CACACAACGCATCGCTAGCAA-GGCT
rigensSR581 ATGTACCGAACGATGCGAGAAACAGTAAAGCTACGAAACCAACAGGATCGCCTCATACAAACGCTCGCTTCATTATTTCCA-A-CACACAACGCATCGCTAGCAA-GGCT
rigens_uniflSR625 ATGTACCGAACGATGCGAGAAACAGTAAAGCTACGAAACCAACAGGATCGCCTCATACAAACGCTCGCTTCATTATTTCCA-A-CACACAACGCATCGCTAGCAA-GGCT
krebsiana_krebSVHF1 ATGTACCGAACGATGCGAGAAACAGTAAAGCTACGAAACCAACACGATCGCCTCATACAAACGCTCGCTTCATTATTTCCA-A-CACACAACGCATCGCTAGCAA-GGCT
krebsiana_arctSV_HF2 ATGTACCGAACGATGCGAGAAACAGTAAAGCTACGAAACCAACACGATCGCCTCATACAAACGCTCGCTTCATTATTTCCA-A-CACACAACGCATCGCTAGCAA-GGCT

[1330 1340 1350 1360 1370 1380 1390 1400 1410 1420 1430]

lichtensteiniIRM1323 --TGCGAACACGTCATGCATCGAAAAGTAATCA--GCTTGCCATCCTCCATGGTGTGCGAAGCGACAACACCACATCATCG????????????????????
lichtesteiniM050906_2 CTTGCGAACACGTCATGCATCGAAAAGTAATCA--GCTTGCCATCCTCCATGGTGTGCGAAGCGACAACACCACATCATCGGT---AAACCGTAACTACGTGCGCTT
heterochaetaM160901_5g --TGCAAACA-CGTCATGCATCGAAAACAAATCA--GCTTGCCACCCCTCCATGGTGTGCGAAGCGACAACACCACATCATTTGGC---ACACCGTAACTACGTGCGCTT
heterochaetaRM1348 --TGCAAACA-CGTCATGCATCGAAAACAAATCA--GCTTGCCACCCCTCCATGGTGTGCGAAGCGACAACACCACAT????????????????????
heterochaetaRM1255 --TGCAAACA-CGTCATRCATCGAAAACAAATCA--GCTTGCCACCCCTCAATGGTGTGCGAAGCGACAACACCACATCATTTG????????????????
tenuifoliaM7219_10 TGTGCCAACACGTCATGCATCGAAAACAAATCA--GCTTGCCACCCCTCCATGGTGTGCGAAGCGACAACACCACATCATCGGGTACGCACCGTTCACTACGTCGCTT
tenuifoliaRM1352 TGTGCCAACACGTCATGCATCGAAAACAAATCA--GCTTGCCACCCCTCCATGGTGTGCGAAGCGACAT????????????????????
ciliarisSR705 TGTGCCAACACGTCATGCTTCGAAAACAAATCA--GCTTGCCACCCCTCCATGGTGTGCGAAGCGACACCACCAGATCCTCGGGTACGCACCGTTCACTACGTGCGCTT
jurineifolia_scabCAM1953 AGTGCCAACA-CGTCATGCGTCGAAAACAAATCA--GCTTGCCACCCCTCAATGG????????????????????
rigens_unifl_Boknes1 AGTGCCAACA-CGTCGCTGCTTTGAAAACAAATCA--GCTTGCCATCCTCACTGATGTTGCGAAGCGACAACACCAGATCAT????????????????
linearis_linear_Boknes2 AGTGCCAACA-CGTCGCTGCTTTGAAAACAAATCA--GCTTGCCATCCTCACTGATGTTGCGAAGCGACAACACCAGATCATCG---TCACCGTTCCTACTACGTGCGCTT
linearis_ovalM041001_2g AGTGCCAACA-CGTCGCTGCTTTGAAAACAAATCA--GCTTGCCATCCTCACTGATGTTGCGAAGCGACAACACCAGATCATCG---TCACCGTTCCTACTACGTGCGCTT
rigens_leuco_M070704_1 AGTGCCAACA-CGTCGCTGCTTTGAAAACAAATCA--GCTTGCCATCCTCACTGATGTTGCGAAGCGACAACACCAGATCATCG---TCACCGTTCCTACTACGTGCGCTT
krebsiana_krebM071001_1g AGTGCCAACA-CGTCGCTGCTTTGAAAACAAATCA--GCTTG????????????????????
krebsiana_krebM071001_3g1 AGTGCCAACA-CGTCGCTGCTTTGAAAACAAATCA--GCTTGCCATCCTCACTGATGTTGCGAAGCGACAACACCAGATCATCG---TCACCGTTCCTACTACGTGCGCTT
krebsiana_arctM071001_3pg AGTGCCAACA-CGTCGCTGCTTTGAAAACAAATCA--GCTTGCCATCCTCACTGATGTTGCGAAGCGACAACACCAGATCATCG---TCACCGTTCCTACTACGTGCGCTT
rigidaM100903_4 AGTGCCAACA-CGTCGCTGCTTTGAAAACAAATCA--GCTTGCCATCCTCACTGATGTTGCGAAGCGACAACACCAGATCATCG---TCACCGTTCCTACTACGTGCGCTT
rigidaM100904_4 AGTGCCAACA-CGTCGCTGCTTTGAAAACAAATCA--GCTTGCCATCCTCACTGATGTTGCGAAGCGACAACACCAGATCATCG---TCACCGTTCCTACTACGTGCGCTT
rigidM110805_10 AGTGCCAACA-CGTCGCTGCTTTGAAAACAAATCA--GCTTGCCATCCTCACTGATGTTGCGAAGCGACAACACCAGATCATCG---TCACCGTTCCTACTACGTGCGCTT
rigidaM120805_80 AGTGCCAACA-CGTCGCTGCTTTGAAAACAAATCA--GCTTGCCATCCTCACTGATGTTGCGAAGCGACAACACCAGATCATCG---TCACCGTTCCTACTACGTGCGCTT
leopodaM160704_5 AGTGCCAACA-CGTCGCTG????????????????????
pectinataM180904_5 ???
krebsiana_krebM210902_1 AGTGCCAACA-CGTCGCTGCTTTGAAAACAAATCA--GCTTGCCATCCTCACTGATGTTGCGAAGCGACAACACCAGATCATCG---TCACCGTTCCTACTACGTGCGCTT
krebsiana_krebM230803_8 AGTGCCAACA-CGTCGCTGCTTTGAAAACAAATCA--GCTTGCCACCCCTCACTGATGTTGCGAAGCGACAACACCAGATCATCG---TCACCGTTCCTACTACGTGCGCTT
serrM230901_7g AGTGCCAACA-CGTCGCTGCTTTGAAAACAAATCA--GCTTGCCATCCTCACTGATGTTGCGAAGCGACAACACCAGATCATCG---ACACCGTTCCTACTACGTGCGCTT

Appendix 6: Additional nrDNA sequence data for Chapter 4

leiopodaM250901_34 AGTGCCAACA-CGTCGTGGTTTAAAAACAAATCA--GCTTGCCATCCTCACTGATGTTGCGAAGCGACAACACCAGATCATCGG----TCACCGTTCACTACGTGCGC???

pectinataM250901_37 AGTGCCAACA-CGTCGTGGTTTAAAAACAAATCA--GCTTGCCATCCTCACTGATGTTGCGAAGCGACAACACCAGATCATCGG----TCACCGTTCACTACGTGCGCCTT

pectM260901_2g AGTGCCAACA-CGTCGTGGTTTAAAAACAAATCA--GCTTGCCATCCTCACTAATGTTGCGAAGCGACAACACCAGATCATCGG----TCACCGTTCACTACGTGCGCCTT

maritimaM260901 AGTGCCAACA-CGTCGTGCTTTGAAAAACAAATCA--GCTTGCCATCCTCACTGATGTTGCGAAGCGACAACACCAGATCA????????????????????????????

krebsiana_krebM261001_2 AGTGCCAACA-CGTCGTGGTTTAAAAACAAATCA--GCTTGCCATCCTCACTGATGTTGCGAAGCGACAACACCAGATCATCGG----TCACCGTTCACTACGTGCGCCTT

maritimaM270901_5g AGTGCCAACA-CGTCGTGGTTTAAAAACAAATCA--GCTTGCCATCCTCACTGATGTTGCGAAGCGACAACACCAGATCATCGG----TCACCGTTCACTACGTGCGCCTT

rigens_rigensM7293 AGTGCCAACA-CGTCGTGCTTTGAAAAACAAATCA--GCTTGCCATCCTCACTGATGTTGCGAAGCGACAACACCAGATCATCGG----TCACCGTTCACTACGTGCGCCTT

rigens_rigensM7298_2 AGTGCCAACA-CGTCGTGCTTTGAAAAACAAATCA--GCTTGCCATCCTCACTGATGTTGCGAAGCGACAACACCAGATCATCGG----TCACCGTTCACTACGTGCGCCTT

rigens_rigensM7527_2 AGTGCCAACA-CGTCGTGGTTTAAAAACAAATCA--GCTTGCCATCCTCACTGATGTTGCGAAGCGACAACACCAGATCATCGG----TCACCGTTCACTACGTGCGCCTT

leiopodaM200901_22g ???

spnov_M7237_4 AGTGCCAACA-CGTCGTGGTTTAAAAACAAATCA--GCTTGCCATC??

serrataHerm_NB AGTGCCAACA-CGTCGTGGTTTAAAAACAAATCA--GCTTGCCATCCTCACTGATGTTGCGAAGCGACAACACCAGATCATCGG----TCACCGTTCACTACGTGCGCCTT

krebsiana_krebNB1465 AGTGCCAACA-CGTCGTGGTTTAAAAACAAATCA--GCTTGCCATCCTCACTGATGTTGCGAAGCGACAACACCAGATCATCGG----TCACCGTTCACTACGTGCGCCTT

linearis_linearRM1013 AGTGCCAACAGCGTCGTGGTTTAAAAACAAATCA--GCTTGCCATCCTC??

rigens_leucoRM1021 AGTGCCAACA-CGTCGTGGTTTAAAAACAAATCA--GCTTGCCATCCTCACTGATGTTGCGAAGCGACAACACCAGATCA????????????????????????????

pectinataRM1044_1 AGTGCCAACA-CGTCGTGCTT??

hybrRM1061 ???

leiopodaRM1063 AGTGCCAACA-CGTCGTGGTTTAAAAACAAATCA--GCTTGCCATCCTCACTGATGTTGCGAAGC??

rigidaRM1082 AGTGCCAACA-CGTCGTGCTTTGAAAAACAAATCA--GCTTGCCATCCTCACTGATGTTGCGAAGCGACAACACCAGATCATCGG----TCACCGTTCACTACGTGCGCCTT

linearis_linearRM1090 AGTGCCAACA-CGTCGTGGTTTAAAAACAAATCA??

linearis_linearRM1092 AGTGCCAACA-CGTCGTGGTTTAAAAAC??

linearis_linearRM1094 AGTGCCAACA-CGTCGTGCTTTGAAAAACAAATCA--GCTTGCCATCCTCACTGATGTTGCGAAGCGACAACACCAGATCATCGG----TCACCGTTCACTACGTGCGC???

linearis_linearRM1103 AGTGCCAACA-CGTCGTGGTTTAAAAACAAATCA--GCTTGCCATCCTCACTGATGTTGCGAAGCGACAACACCAGATCATCGG----TCACCGTTCACTACGTGCGCCTT

krebsiana_serrRM1137 AGTGCCAACA-CGTCATGGTTTAAAAACAAATCA--GCTTGCCATCCTCACTGATGTTGCGAAGCGACAACACCAGATCATCGG----TCACCGTTCACTACGTGCGCCTT

linearis_linearRM1182 AGTGCCAACA-CGTCGTGG??

rigidaRM1210 AGTGCCAACA-CGTCGTGCTTTGAAAAACAAATCA--GCTTGCCATCCTCACTGATGTTGCGAAGCGACAACACCAGATCATCGG----TCACCGTTCACTACGTG????

serrataRM1216 AGTGCCAACA-CGTCGTGCTTTGAAAAACAAATCA--GCTTGCCATCCTCACTGATGTTGCGAAGCGACAACACCAGATCATCGG----TCACCGTTCACTACGTGCGCCTT

serrataRM1241 AGTGCCAACA-CGTCGTGGTTTAAAAACAAATCA--GCTTGCCATCCTCACTGATGTTGCGAAGCGACAACACCAGATCATCGG----TCACCGTTCACTACGTGCGCCTT

serrataRM1245 AGTGCCAACA-CGTCGTGGTTTAAAAACAAATCT--GCTTGCCATCCTCACTGATGTTGCGAAGCGACAACACCAGATCATCGG----TCACCGTTCACTACGTGCGCCTT

rigidaRM1254 AGTGCCAACA-CGTCGTGGTTTAAAAACAAATCA--GCTTGCCATCCTCACTGATGTTGCGAAGCGACAACACCAGATCATCG????????????????????

serrataRM1260 AGTGCCAACA-CGTCGTGGTTTAAAAACAAATCA--GCTTGCCATCCTCACTGATGTTGCGAAGCGACAACACCAGATCATCGG----TCACCGTTCACTACGTGCGCCTT

rigidaRM1270 AGTGCCAACA-CGTCGTGGTTTAAAAACAAATCA--GCTTGCCATCCTCACTGATGTTGCGAAGCGACAACACCAGATCATCGG----TCACCGTTCACTACGTGCGCCTT

serrataRM1280 AGTGCCAACA-CGTCGTGGTTTAAAAACAAATCA--GCTTGCCATCCTCACTGATGTTGCGAAGCGACAACACCAGATCATCGG----TCACCGTTCACTACGTGCGCCTT

leiopodaRM1291 AGTGCCAACA-CGTCGTGCTTTGAAAAACAAATCA--GCTTGCCATCCTCACTGATGTTGCGAAGCGACAACACCAGATCATCGG----ACACCGTTCACTACGTGCGCCTT

leioRM1320 ???

pectinataRM1390 AGTGCCAACA-CGTCGTGGTTTAAAAACAAATCA--GCTTGCCATCCTCACTGATGTTGCGAAGCGACAACACCAGATCATCGG----TCACCGTTCACTACGTGCGCCTT

krebsiana_krebRM713 AGTGCCAACA-CGTCGTGGTTTAAAAACAAATCA--GCTTGCCATCCTCACTGATGTTGCGAAGCGACAACACCAGATCATCGG----TCACCGTTCACTACGTGCGCCTT

krebsiana_arctrM770_2 AGTGCCAACA-CGTCGTGGTTTAAAAACAAATCA--GCTTGCCATCCTCACTGATGTTGCGAAGCGACAACACCAGATCATCGG----TCACCGTTCACTACGTGCGCCT?

rigens_rigensRM772_1 AGTGCCAACA-CGTCGTGCTTTGAAAAACAAATCA--GCTTGCCATCCTCACTGATGTTGCGAAGCGACAACACCAGATCATCGG----TCACCGTTCACTACGTGCGCCTT

linearis_linearRM780 AGTGCCAACA-CGTCGTGGTTTAAAAACAAATCA--GCTTGCCATCCTCACTGATGTTGCGAAGCGACAACACCAGATCATCGG----TCACCGTTCACTACGTGCGCCTT

rigens_uniflRM782_1 AGTGCCAACA-CGTCGTGCTTTGAAAAACAAATCA--GCTTGCCATCCTCACTGATGTTGCGAAGCGACAACACCAGATCATCGG----TCACCGTTCACTACGTGCGCCTT

rigens_uniflRM783 ???

rigens_uniflRM785 AGTGCCAACA-CGTCGTGGTTTAAAAACAAATCA--GCTTGCCATCCTCACTGATGTTGCGAAGCGACAACACCAGATCATCGG----TCACCGTTCACTACGTGCGCCTT

linearis_linearRM787 AGTGCCAACA-CGTCGTGGTTTAAAAACAAATCA--GCTTGCCATCCTCACTGATGTTGCGAAGCGACAACACCAGATCATCGG----TCACCGTTCACTACGTGCGCCTT

linearis_linearRM789 AGTGCCAACA-CGTCGTGCTT??

linearis_linearRM794 AGTGCCAACA-CGTCGTGGTTTAAAAACAAATCA--GCTTGCCATCCTCACTGATGTTGCGAAGCGACAACACCAGATCATCGG----TCACCGTTCACTACGTGCGCCTT

linearis_linearRM804 AGTGCCAACA-CGTCGTG??

serrataRM812 AGTGCCAACA-CGTCGTGGTTTAAAAACAAATCA--GCTTGCCATCCTCACTGATGTTGCGAAGCGACAACACCAGATCATCAG----TCACCGTTCACTACGTGCGCCTT

rigidaRM813 AGTGCCAACA-CGTCGTGGTTTAAAAACAAATCA--GCTTGCCATCCTCACTGATGTTGCGAAGCGACAACACCAGATCATC????????????????

serrataRM821 AGTGCCAACA-CGTCGTGCTTTGAAAAACAAATCA--GCTTGCCATCCTCACTGATGTTGCGAAGCGACAACACCAGATCATCGG----TCACCGTTCACTACGTGCGCCT?

krebsiana_arctrM831_1 AGTGCCAACA-CGTCGTGGTTTAAAAACAAATCA--GCTTGCCATCCTCACTGATGTTGCGAAGCGACAACACCAGATCATCGG----TCACCGTTCACTACGTGCGCCTT

