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A multivariate analysis of morphological variation in the *Hemizygia bracteosa* complex (Lamiaceae, Ocimeae)

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Abstract. The variation and recognition of taxa within the *Hemizygia bracteosa* complex was examined using multivariate techniques. Morphological characters were sampled on 197 herbarium specimens. Phenetically *H. bracteosa* and *H. welwitschii* overlap in many floral characters. However differences in leaf characters and habit maintain their morphological distinctness from each other and they are therefore upheld as species. *Hemizygia ornata*, synonymized under *H. welwitschii* in recent treatments of the genus *Hemizygia*, differentiates from *H. welwitschii* on the basis of differences in leaf and floral characters and its reinstatement at specific level is here proposed. The concept of *H. linearis* is revised on account of the type specimen separating from all other elements of the taxon used in the analyses. The latter form a coherent group with *H. petrensis* and *H. canescens* thus negating any attempt to give any of them specific recognition. It is proposed that they should be synonymized under the earliest name *H. canescens*. The specific boundary of *H. petiolata* is revised but its specific status maintained.

Key words: *Hemizygia bracteosa* complex, phenetics, cluster analysis, discriminant analysis, principal component analysis.

Hemizygia (Benth.) Briq. is placed in the tribe Ocimeae of the Labiatae (Cantino et al. 1992, Paton 1998, Paton et al. 2004). It comprises perennial soft shrubs or annual herbs usually found growing in dry often rocky woodland or grassland. Together with *Syncolostemon*, a closely related genus, they have fused anterior stamens, a putative synapomorphy that sets them apart from other genera in the Ocimeae (Paton 1998, Paton et al. 2004). Initially recognized as a section of *Ocimum* by Bentham (1848), *Hemizygia* was later elevated to generic rank by Briquet (1897). Ashby (1935) recognized 26 species in *Hemizygia* while Codd (1976, 1985) gave an account of 28 species in the genus in southern Africa. Paton (1998) made a new combination *H. comosa* (Wright ex Benth.) A. J. Paton from India, and Paton and Hedge (1999) described a new species *H. madagascariensis* A. J. Paton and Hedge from Madagascar. Another new species, *H. stalmansii* A. J. Paton & K. Balkwill from South Africa was described by Paton and Balkwill (2001). Currently therefore a total of 33 species are recognized in *Hemizygia* including *H. welwitschii* (Rolfe) Ashby (Ashby 1935)

and *H. oritrephes* Wild (Wild 1964). In a phylogenetic study of *Hemizygia* and *Syncolostemon* using molecular and morphological data (Otieno et al., in press), *H. bracteosa*, *H. welwitschii*, *H. linearis*, *H. petrensis*, *H. canescens* and *H. petiolata* form a clade diagnosed by the presence of two lobes and sunken persistent remains of the stamen at the apex of the stylopodium. The present paper focuses on the delimitation of taxa within this group.

All species of *Hemizygia* with the exception of *H. madagascariensis* and *H. comosa* occur in mainland Africa and of these only *H. bracteosa* (Benth.) Briq. and *H. welwitschii* occur beyond the southern African region. The latter two species co-occur in West, East, Central and parts of southern Africa. They also show some overlap in habitat preferences.

Hutchinson and Dalziel (1931) included West African material of *Hemizygia* under the name *Orthosiphon bracteosus* (Benth.) Bak. but Morton (1962, 1963) divided the same material into two species, *H. bracteosa* and *H. welwitschii*, separating them on the basis of differences in leaf and bract shape, pubescence and longevity. This delimitation has led to confusion in the past with several specimens having been misidentified in herbaria. In addition, a preliminary investigation of herbarium material identified some specimens of *H. bracteosa* from Nigeria, Zambia, Mozambique, Malawi and Zimbabwe with rather robust leaf, inflorescence and floral features, which seemed to show affinities with both *H. bracteosa* and *H.* welwitschii, suggesting the possibility of hybridization between the two species. In the southern African region *H. bracteosa* also resembles *H. petrensis* in habit, ecology and distribution and has canescent leaves as in *H. canescens* (Codd 1976, 1985).

Hemizygia ornata S. Moore previously subsumed under *H. welwitschii* (Ashby 1935) was included as a separate species by Otieno et al. (in press) in their phylogenetic study. In that study it emerged in a different clade from that in which *H. welwitschii* was nested. We feel there is need to establish whether this entity is phenetically different from *H. welwitschii* and hence if it warrants being recognized at the specific level as the results of that phylogenetic study seem to suggest. On that basis it has been included in this study. Codd (1976, 1985) in his two accounts of *Hemizygia* in southern Africa noted the close morphological relationships between *H. linearis* (Benth.) Briq., *H. petrensis* (Hiern) Ashby and *H. canescens* (Gürke) Ashby due to their almost identical floral characters and small inconspicuous bracts. In the phylogenetic study of *Hemizygia* and *Syncolostemon* (Otieno et al., in press) the relationships between *H. petrensis*, *H. linearis* and *H. canescens* remained unresolved, with the three emerging as a weakly supported trichotomy. This seems to suggest very close affinities between the three species.

Hemizygia petrensis and *H. linearis* overlap in their geographic distribution in Namibia, Botswana, Zimbabwe, Angola and South Africa. Their distribution also overlaps with that of *H. canescens* in South Africa where the latter is confined. All three species occur more or less in the same kind of habitat and altitudinal ranges. The distinction between *H. petrensis* and *H. canescens* appears to break down in the Waterberg Plateau in Namibia where what seem to be occasional intermediates have been found (Codd 1976). However *H. canescens* is not known to occur in the area and this led Codd (1976) to recommend that further investigations be carried out in that vicinity.

Although Codd (1976, 1985) separated *H. petiolata* from *H. canescens* on account of its more ovate leaves, longer petioles and larger corolla tube, in our preliminary assessments of its morphological variation, we found that sometimes specimens identified as *H. canescens* approached *H. petiolata* and vice versa in leaf shape and pubescence and this presented difficulties in their placement. These difficulties indicate a need for a clarification of the specific boundaries between these two species. In the phylogenetic study of *Hemizygia* and *Syncolostemon* (Otieno et al., in press), *H. petiolata* was very strongly supported as sister to the

H. linearis/*H. canescens* group. The character variation between *H. bracteosa* and *H. welwitschii*; *H. linearis*, *H. petrensis* and *H. canescens* and between *H. petiolata* and *H. canescens* is somewhat intergrading, causing much confusion in their identification in the herbarium and this probably extends to the field as well.

The primary purpose of this study was therefore to use multivariate techniques to analyze the pattern of variation and to determine species' circumscriptions consistent with that pattern. The paper focuses on the following specific taxonomic questions: i) Can *H. bracteosa* be distinguished from *H. welwitschii* and ii) Can *H. welwitschii* be distinguished from what has previously been treated as *H. ornata*? and iii) Are *H. linearis*, *H. petrensis*, *H. canescens* and *H. petiolata* distinct from each other?

Materials and methods

Plant material. This study is based on herbarium material borrowed from K, PRE, NH and NU and collections kept at J. Of the 352 specimens examined, 197 were included in the analysis. Only those with either fully open flowers or fruiting calyces or both and also with mature leaves were included in order to allow standardized measurements to be made. A list of specimens used is available from the corresponding author. Material included was matched to descriptions of *H. welwitschii*, *H. bracteosa*, *H. petrensis*, *H. linearis*, *H. canescens*, *H. petiolata* and what has previously been treated as *H. ornata* (hereafter referred to as "*H. ornata*"). Keys, e.g. in Moore (1911), Hutchinson and Dalziel (1931), Morton (1963), and Codd (1976, 1985) were also consulted. However, because of close morphological similarities between *H. bracteosa* and *H. welwitschii*, *H. linearis*, *H. petrensis* and *H. canescens* and between *H. petiolata* and *H. canescens*, it was still difficult to assign some specimens to some of these taxa. As far as possible herbarium specimens were selected to represent the entire geographical range and to reflect the morphological variability present within each taxon.

Morphological characters. A total of 40 characters were examined on each specimen, comprising 37 quantitative and three qualitative characters (Table 1). The three qualitative characters were scored as binary characters. For each quantitative character, a single measurement was taken from a mature flower and calyx at the base of the inflorescence and the largest leaf at the base of the specimen so as to minimize the confusion that could arise from developmental plasticity if immature samples were measured. Published keys and descriptions of species (e.g. Ashby 1935; Codd 1976, 1985) were consulted to establish characters that had previously been considered to be of taxonomic importance. A number of qualitative characters used by other workers (e.g. flower colour, density of hairs etc) could not be discerned, were too variable or invariant between species, and were therefore omitted from the study. Codd (1976, 1985) used the type of leaf base as a character in his description of the taxa in this complex of species. However in this study we redefined this as the angle at the base of the leaf (Character 6), measured on a scale of 0°–180°. Most characters observed on the herbarium specimens have not been employed in previous studies but were considered to be of potential taxonomic significance and included in the investigation. Data on all characters were entered in a data matrix, which is available from the corresponding author on request. In the matrix all missing data were replaced by an identifying numerical code to ensure that no cells in the matrix were left empty (Rohlf 1998).

Data analyses. Principal Component Analysis (PCA) was carried out to examine the pattern of relationships between OTU's (operational taxonomic units, specimens in this case) as well as among characters employed. This technique projects samples in multivariate space so that maximum variances, which are not correlated, are extracted along different axes. The raw data is thus converted into uncorrelated variables but without any character redundancies (Everrit and Dunn 2001). Several runs of PCA were carried out to i) recognize any distinct groupings of similar OTU's, and ii) separate and re-analyze distinctive groups of OTU's so as to recognize any further patterns of within-group variation. Cluster analysis (CA) based on the UPGMA method and using Average Taxonomic Distance Coefficient as a dissimilarity coefficient was also used as an exploratory method to establish if the data grouped the classes to which the specimens had been assigned. Prior to doing the PCA and CA, the data were standardized to a mean of 0 and a variance of 1 to remove the effects

of characters with large variances. Both the PCA and CA were performed using NTSYS-pc version 2.0 (Rohlf 1998). The groups revealed by PCA and CA were then used as apriori groups for Discriminant Analysis (DA). Discriminant analysis was carried out to extract dominant underlying gradients of variation, also known as canonical variates, among these groups, with the aim of describing maximum differences between them based on a suite of discriminating characteristics (Thorpe 1983, Owen and Chmielewski 1985, McGarigal et al. 2000). Only those characters that contributed most to the variability of the first three axes of the PCA ($r > 0.6$) and that had the least correlation with each other ($r < 0.6$) were used in the DA. To maximize the resolving power of DA, analyses were performed on major clusters revealed by PCA and CA together and then separately. Among the groups produced by CA and DA, patterns or discontinuities in character variation were identified using box-plots. Means and standard deviations were computed for all quantitative characters used and the significance of individual character differences among groups tested using an unpaired T-test. Discriminant and univariate analyses were carried out using the software program STATISTICA (Statsoft, Inc. 2002). A character count procedure (Wilson 1992) was used to establish whether hybrids occur between *H. bracteosa* and *H. welwitschii*. In the procedure individuals are placed in groups representing two putative parental taxa and a putative hybrid taxon (step 1) and then characters that separate the parents are selected (step 2) followed by the tabulation of their values to show whether or not the values for the hybrid are intermediate (step 3). Finally a count is made of the number of characters that are and that are not intermediate (step 4) and judgment made on whether or not the coalescence of intermediate character states is too improbable to represent divergence in the same characters in the same direction.

Results

PCA analyses. The initial PCA carried out using all 40 characters did not produce distinct groupings of the OTU's (data not shown). Characters which were logically interdependent were removed. In addition, Pearson's Correlation Coefficient was used to determine which pairs of characters showed genetic connectedness [i.e. members of the pair showed a high correlation ($r > 0.6$)]. Only one of each pair was retained to ensure that the characters that contributed most to separation along the three axes were not highly correlated hence weighting heavily on the principal components with the possibility of complicating interpretation (McGarigal et al. 2000). Leaf and calyx characters retained in subsequent analyses are shown in Table 1. Of all inflorescence characters, only the character LPTIB (Table 1) was used in the final analysis. Characters that did not load significantly on any component after another run of the PCA and which did not therefore seem important for the study (McGarigal et al. 2000) were also eliminated (see Table 1). A total of 22 characters, including 3 qualitative characters, were then used in all subsequent analyses (Table 1).

In the PCA run using these characters (Fig. 1), the first three principal components (PC) explain 63.1% of the total character variation with 36.0%, 18.9% and 8.1% for the respective axes. In the case of the first PC, eleven characters had loadings with an absolute value greater than 0.6 while in the second, the major variables included LAF, LS, LPCLIP and WMLCLIP (Table 2). The character with the strongest correlation to the third PC was MLWR followed by LALB while three of the highest loadings on PCA correspond to qualitative characters used in the analysis (Table 2). Qualitative characters are thus the most taxonomically useful for partitioning the *H. bracteosa* complex into two assemblages of morphologically coherent taxa.

In this PCA two major groups separated along the first principal axis (Figs. 1A and B). One group comprising OTU's of *H. bracteosa*, *H. welwitschii* and "*H. ornata*" clustered at the positive end of axis 1 while OTU's belonging to *H. petrensis*, *H. linearis*, *H. canescens* and *H. petiolata* occupied the negative end. One specimen (*Drummond 7822*) belonging to *H. linearis* occupied an intermediate position between the two clusters. Within-group structure in the cluster

Table 1. List of qualitative and quantitative characters used in numerical analyses. Quantitative characters used in the final PCA and subsequently in CA and DA are followed by their abbreviations in brackets. Asterisks denote qualitative characters used in all analyses. Their character states are indicated in square brackets. All characters are in mm except character 6 and the three qualitative characters. Characters excluded from PCA, CA and DA due to high correlation are marked with superscript letter [(a)] and those not loading significantly on any component with superscript letter [(b)].

	Character
Leaf	1. Maximum length (ML)
	2. Width at widest point[a]
	3. Width at mid-point[a]
	4. Maximum length/width ratio (MLWR)
	5. Petiole length (LPL)
	6. Lamina angle at leaf base (LALB)
	7. *Sessile glands [absent (0) /present (1)
Inflorescence	8. Length of terminal axis minus stalk[b]
	9. Number of verticils on terminal axis[b]
	10. Distance between last two verticals on terminal axis[b]
	11. Maximum length of terminal inflorescence bract[a]
	12. Maximum width of terminal inflorescence bract[a]
	13. Length/width ratio of terminal inflorescence bract[b]
	14. Length of petiole on terminal inflorescence bract (LPTIB)
Calyx	15. Length of calyx[a]
	16. Circumference of calyx mouth[a]
	17. Circumference of calyx mouth/calyx length ratio[b]
	18. Length of posterior calyx lip[a]
	19. Width of posterior calyx lip (WPCLIP)
	20. Length of longest lobe of posterior calyx lip[a]
	21. Length of shortest lobe of anterior calyx lip (LSLAC)
	22. Difference in length between longest and shortest lobe of anterior calyx lip (DLLSAC)
	23. Maximum width at the base of the lateral lobe of anterior calyx lip (MWLAC)
Corolla	24. Total length of corolla tube[a]
	25. Length of posterior corolla lip (LPCLIP)
	26. Length of median lobe of posterior corolla lip[a]
	27. Width of median lobe of posterior corolla lip (WMLCLIP)
	28. Length of anterior corolla lip[a]
	29. Width of anterior corolla lip at widest point (WACLIP)
	30. Length/width ratio of anterior corolla lip (LWRACLIP)
Androecium	31. Distance from base of corolla to point at which posterior stamens attached (DFBPS)
	32. Length of posterior filament[a]
	33. Length of anterior filament (LAF)
	34. Difference in length between posterior and anterior filaments (DLBPAF)
Gynoecium	35. Length of style (LS)
Nutlet	36. Length of nutlet[b]
	37. Width of nutlet (NW)
	38. Nutlet length/width ratio (NLWR)
	39. * Network of veins on nutlets [absent (0)/present (1)]
	40. * Colour of nutlets [light to dark brown (0)/brownish black to black (1)]

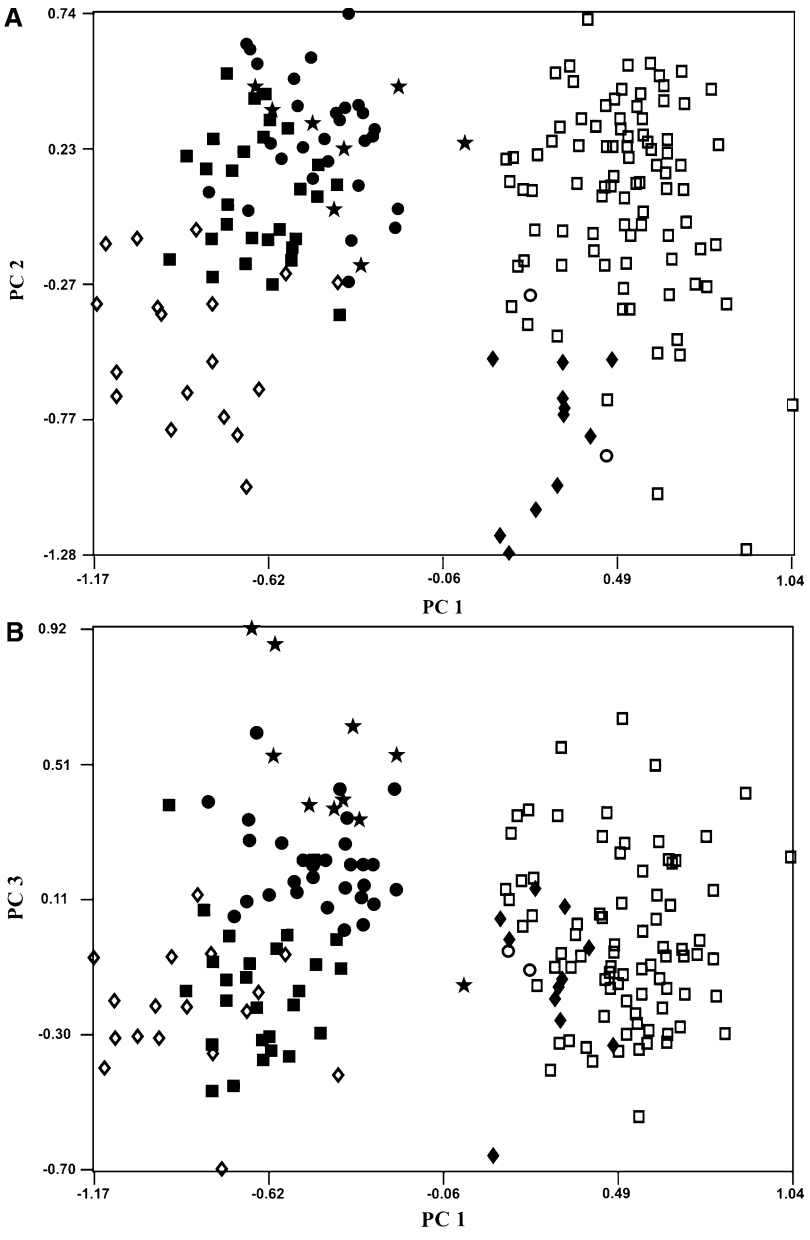


Fig. 1. Scatterplots of the 197 OTU's. **A** OTU's plotted against the first principal component by the second principal component. **B** OTU's plotted against the first principal component by the third pricipal component. □ = *H. bracteosa*, ■ = *H. canescens*, ⋆ = *H. linearis*, ○ = "*H. ornata*", ● = *H. petrensis*, ◇ = *H. petiolata* and ♦ = *H. welwitschii*

comprising *H. bracteosa*, *H. welwitschii* and "*H. ornata*" was not very apparent (Fig. 1A). However, the *H. linearis*-*H. petiolata* cluster appeared to differentiate into two marginally separated subgroups along the second principal axis (Fig. 1A) but with elements of the different taxa mixed in the larger subgroup. In a plot of the first and third principal axes (Fig. 1B) there was separation, along the third axis, of two specimens of *H. linearis* (one of which is the type specimen) and the rest of the *H. linearis*-*H. petiolata* group.

Table 2. Factor loadings on the first three principal components for quantitative and qualitative characters used in the final PCA. Qualitative characters are marked with an asterisk.

Character	PC 1	PC 2	PC 3
1. ML	0.7162	0.0219	0.2574
4. MLWR	0.1923	0.3939	0.7327
5. LPL	−0.6224	−0.4523	−0.3761
6. LALB	−0.3042	−0.4687	−0.6276
7*	0.9292	−0.0778	−0.1268
14. LPTIB	0.7128	−0.4154	0.0326
19. WPCLIP	0.6410	−0.2753	−0.1851
21. LSLAC	0.5936	−0.4203	−0.1147
22. DLLSAC	0.6187	−0.0655	−0.1083
23. MWLAC	0.6064	−0.3696	−0.1700
25. LPCLIP	−0.4332	−0.6868	0.3640
27. WMLCLIP	−0.1717	−0.6092	0.2290
29. WACLIP	0.3084	−0.6358	0.4113
30. LWRACLIP	−0.5599	−0.0112	−0.2538
31. DFBPS	0.4630	−0.5549	0.1133
33. LAF	−0.2798	−0.7938	0.2214
34. DLBPAF	−0.5815	−0.4923	−0.0192
35. LS	−0.2721	−0.7153	0.0968
37. NW	0.8834	−0.1511	−0.0931
38. NLWR	−0.6226	−0.0108	0.0283
39*	0.8449	0.1866	−0.1045
40*	−0.9017	0.1615	0.1752

Cluster analysis. The UPGMA of the OTU's used in the study is shown in Fig. 2. The correlation of the distance and tree matrix was 0.760, indicating a good fit of the phenogram to the distance matrix (e.g. Sneath and Sokal 1973, McGarigal et al. 2000). Cluster analysis revealed the existence of two distinct primary groups (Fig. 2) as in PCA. In addition, a small cluster of two specimens of "*H. ornata*" also emerges as a branch off the two primary groups. Both primary groups show very clear internal structure. The *H. linearis-H. petiolata* cluster is dominated by two sub-clusters, a big one comprising OTU's of *H. linearis*/*H. petrensis*/*H. canescens* (labeled 5) and a slightly smaller one containing elements of *H. petiolata* (labeled 6). There is a third sub-cluster of two specimens of *H. linearis* (labeled 7) which, in the PCA, also separated from the remainder of the *H. linearis-H. petiolata* cluster.

In the bigger sub-cluster (labeled 5) there is further separation of groups, with OTU's belonging to *H. petrensis* and *H. linearis* mixing to form one subgroup and those of *H. canescens* dominating the second one. The third (labeled 9) and fourth (labeled 10) subgroups are considerably smaller. All these subgroups are weakly separated as indicated by the rather short lengths of their subtending branches. The three sub-clusters (labeled 5, 6, 7) are, however, highly dissimilar. Univariate analysis (Table 3) supports their separation on the basis of leaf, floral and nutlet characters.

In the other primary group revealed by CA, comprising specimens of *H. bracteosa* and *H. welwitschii* and one of *H. linearis*, two subclusters can be recognized. The two subclusters appear to be distinct from each other as they separate at quite a high level of dissimilarity. One (labeled 1) comprises exclusively of *H. bracteosa* specimens except for one OTU of *H. linearis* (*Drummond 7822*) which appears misplaced. This specimen had some data missing; its position is probably an

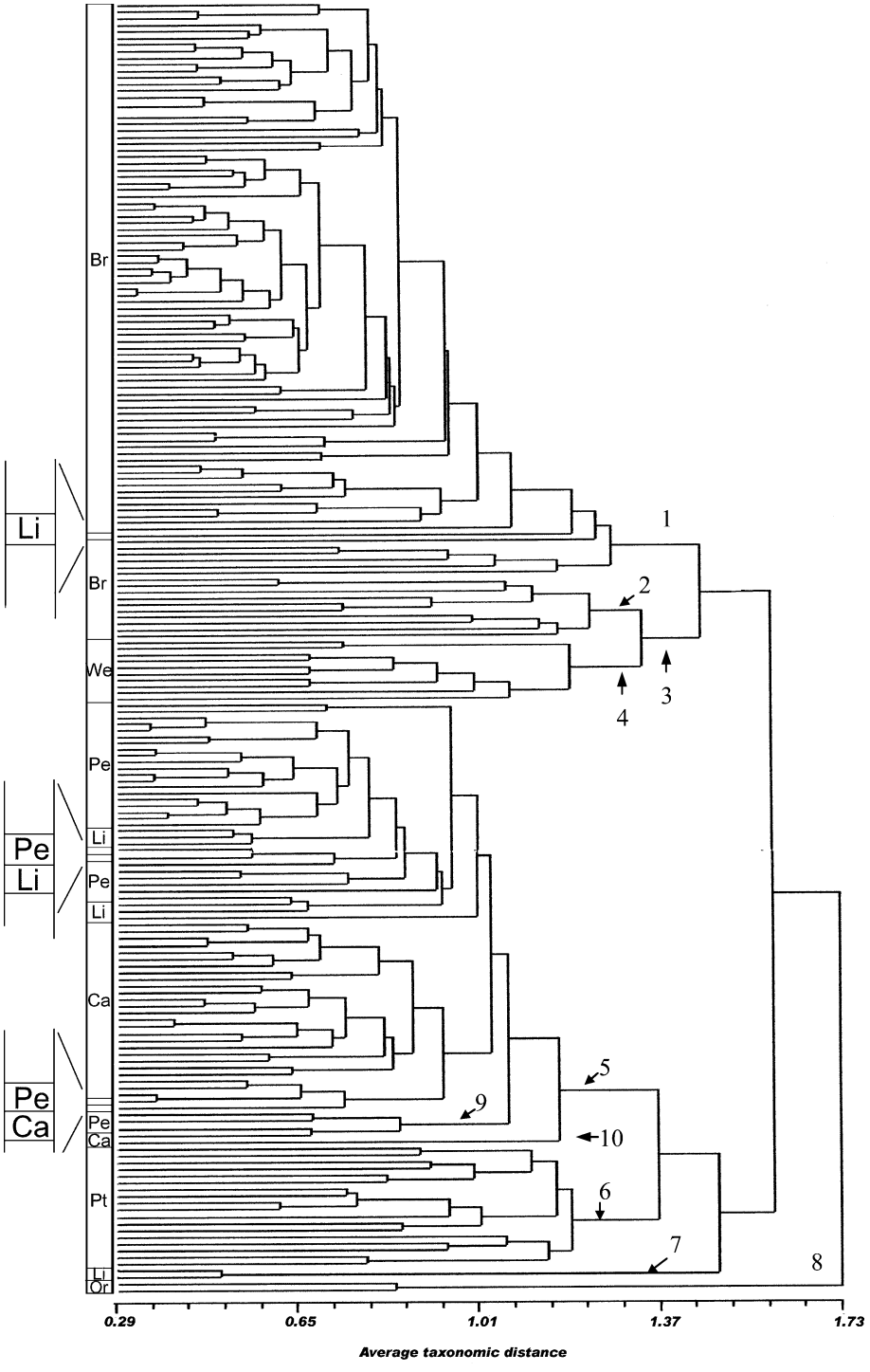


Fig. 2. Cluster analysis (UPGMA) of the *H. bracteosa* complex. OTU's represented by *Br* = *H. bracteosa*, *Ca* = *H. canescens*, *Li* = *H. linearis*, *Or* = "*H. ornata*", *Pe* = *H. petrensis*, *Pt* = *H. petiolata* and *We* = *H. welwitschii*. *1& 2* = subgroups BRAC1 & BRAC2 (= *H. bracteosa*), *3* = BRAC2 & WELW, *4* = subgroup WELW (= *H. welwitschii*), *5* = subgroup PETR (= mixture of *H. canescens*, *H. linearis* s.l. & *H. petrensis*), *6* = subgroup PETI (= *H. petiolata*), *7* = subgroup LINE (= *H. linearis* s.str) and *8* = ORN (= "*H. ornata*")

Table 3. Comparison of quantitative variables used in the final PCA and subsequently in CA and DA for groups in the *H. bracteosa* complex. Sample size (n), mean and standard deviation (SD) are given. Groups denoted by similar symbols (either * or ¤) occur in the same cluster in the PCA, CA and DA performed using all specimens. The results of an unpaired t-test are summarized by the superscripts. Groups from the same cluster having the same letters do not differ significantly for that character ($p < 0.05$). Full description of the variables is given in Table 1. The last two columns of the Table represent the final two steps of the character count procedure for the groups BRAC 1, BRAC 2 and WELW. "BRAC 2 different from" indicates significant differences between BRAC 2 and BRAC 1 or WELW or both or neither based on unpaired t-test comparisons. "BRAC 2 intermediate?" indicates whether or not BRAC 2 was intermediate between BRAC 1 and WELW for that character.

Variable	*BRAC 1		*BRAC 2		*WELW		*ORN	
	n	Mean (SD)	n	Mean (SD)	n	Mean (SD)	n	Mean (SD)
ML	79	77.5 (21.5)	9	96.8 (16.3)	10	48.6 (9.30) [a]	2	43.0 (4.24) [a]
MLWR	78	5.98 (1.84) [a]	9	7.20 (2.88) [a c]	9	2.55 (0.59) [b]	2	2.60 (0.14) [b c]
LPL	87	0.00 (0.00) [a]	9	0.00 (0.00) [a]	7	3.57 (2.35)	1	0.00 – [a]
LALB	76	26.3 (15.9) [a c]	6	23.5 (9.85) [a]	7	57.9 (24.3) [b]	1	58.0 – [b c]
LPTIB	84	1.38 (0.54)	9	3.10 (0.86) [a c]	7	2.28 (0.80) [a b]	1	2.50 – [b c]
WPCLIP	86	4.55 (0.91) [a d]	10	5.06 (1.39) [a b e]	10	5.30 (0.46) [b c]	2	5.00 (0.00) [c d e]
LSLAC	86	2.49 (0.52)	10	2.87 (0.63) [a c]	10	3.41 (0.74) [a b]	2	3.50 (0.70) [b c]
DLLSAC	86	1.78 (0.48) [a b]	10	1.99 (0.53) [a c e]	10	1.68 (0.82) [b c d]	2	1.55 (0.07) [d e]
MWLAC	86	2.53 (0.43) [a d]	10	2.74 (0.58) [a b e]	10	2.90 (0.39) [b c]	2	3.00 (0.70) [c d e]
LPCLIP	85	3.52 (0.65)	10	4.50 (1.02) [a c]	9	5.00 (0.96) [a b]	2	5.05 (0.07) [b c]
WMLCLIP	86	1.25 (0.30)	10	2.19 (1.02) [a b]	9	1.74 (0.29) [a]	2	3.00 (0.00) [b]
WACLIP	72	3.32 (0.76)	6	5.08 (1.28) [a]	5	4.20 (0.83) [a]	0	
LWRACLIP	71	0.98 (0.14) [a b]	5	1.00 (0.20) [a c]	4	1.08 (0.22) [b c]	0	
DFBPS	87	2.88 (0.79) [b]	9	4.27 (0.79) [a]	8	3.56 (0.77) [a]	2	2.00 (0.00) [b]
LAF	85	5.99 (1.74) [b c]	9	9.97 (3.05) [a]	9	11.9 (2.05) [a]	2	6.75 (1.06) [b c]
DLBPAF	85	3.45 (1.26) [c]	9	6.55 (2.16) [a d]	8	4.87 (2.24) [a b]	2	5.25 (3.18) [b c d]
LS	81	12.7 (9.51) [a b e]	9	16.7 (4.85) [a c f]	7	18.1 (3.92) [b c d]	2	12.2 (3.18) [d e f]
NW	85	1.92 (0.16)	10	3.16 (3.32) [a b]	10	2.06 (0.13) [a]	2	2.50 (0.00) [b]
NLWR	85	1.23 (0.19) [a b e]	10	1.25 (0.12) [a c f]	10	1.21 (0.10) [b c d]	2	1.30 (0.14) [d e f]

Variable	*PETR		*PETI		*LINE		BRAC2	*BRAC2
	n	Mean (SD)	n	Mean (SD)	n	Mean (SD)	different from	Intermediate?
ML	65	43.9 (14.5) [b]	18	38.6 (11.8) [b]	2	29.5 (2.12) [b]	both	–
MLWR	64	5.49 (2.51)	18	2.84 (1.03)	2	17.7 (3.18)	WELW	–
LPL	62	2.23 (3.00) [b]	18	8.41 (3.16)	1	0.00 – [b]	WELW	–
LALB	60	29.5 (19.5) [d]	18	65.6 (25.6)	1	5.00 – [d]	WELW	–
LPTIB	54	0.21 (0.22)	18	0.22 (0.57)	0		BRAC 1	–
WPCLIP	66	3.89 (0.73) [f]	18	4.11 (0.68) [f]	1	2.20 –	neither	+
LSLAC	66	1.83 (0.50) [d]	18	1.67 (0.43) [d e]	2	1.10 (0.56) [e]	BRAC 1	+
DLLSAC	66	1.10 (0.39) [f]	18	1.13 (0.48) [f g]	2	0.90 (0.14) [g]		
MWLAC	66	2.12 (0.30) [f]	18	2.06 (0.22) [f]	2	1.50 (0.00)	neither	+
LPCLIP	63	4.22 (0.69) [d]	18	5.32 (0.79) [e]	2	4.95 (0.07) [d e]	BRAC 1	+
WMLCLIP	63	1.44 (0.32) [c]	18	1.69 (0.34) [d]	2	1.40 (0.14) [c d]	BRAC 1	–
WACLIP	55	3.05 (0.74) [b c]	16	3.16 (0.75) [b d]	1	3.50 – [c d]	BRAC 1	–
LWRACLIP	55	1.15 (0.21) [d]	16	1.39 (0.38) [e]	1	0.85 – [d e]		
DFBPS	63	2.16 (0.57) [c]	18	2.5 (0.65) [d]	2	2.00 – [c d]	BRAC 1	–

Table 3. (Continued)

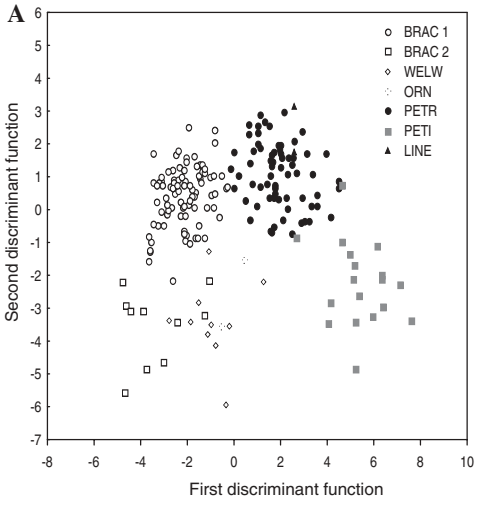
Variable	*PETR		*PETI		*LINE		BRAC2	*BRAC2
	n	Mean (SD)	n	Mean (SD)	n	Mean (SD)	different from	Intermediate?
LAF	62	7.41 (1.24) [d]	17	9.64 (1.32)	2	7.50 (0.70) [d]	BRAC 1	+
DLBPAF	62	5.47 (1.75) [e]	17	9.97 (2.79)	2	5.00 (0.00) [e]	BRAC 1	−
LS	62	12.7 (2.78) [g]	18	18.8 (4.14) [h]	2	12.7 (0.35) [g h]		
NW	64	1.30 (0.23) [c]	17	1.22 (0.25) [c]	2	1.00 (0.00) [c]	BRAC 1	−
NLWR	64	1.54 (0.27) [g]	17	1.49 (0.24) [g]	2	1.50 (0.00) [g]		

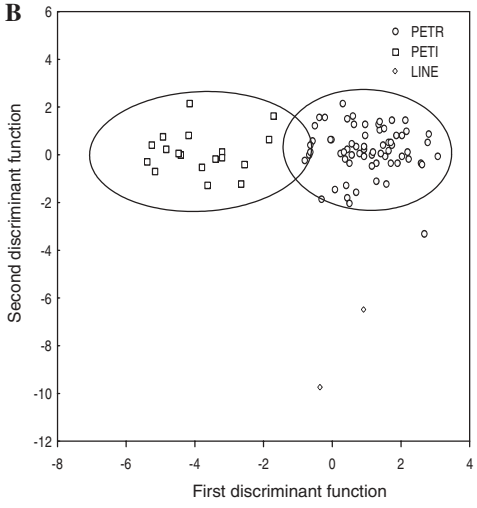
artefact. The other sub-cluster (labeled 3) is made up of an equal number of OTU's belonging to *H. bracteosa* and *H. welwitschii*, which separate into two subgroups (labeled 2 and 4).

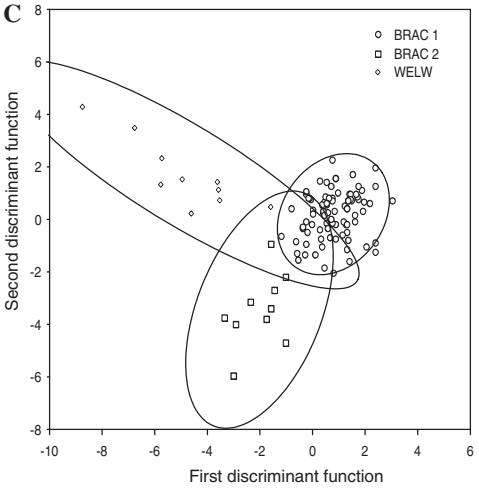
In CA, the two sub-clusters within the *H. linearis-H. petiolata* cluster are distinguished mainly by foliar and floral characters (Table 3) while the two resolved in the *H. bracteosa-H. welwitschii* cluster differentiate significantly on the basis of the sizes of the characters LPTIB and LSLAC (Table 3). The OTU's of *H. bracteosa* and *H. welwitschii*, which separate into two discrete subgroups within the smaller sub-cluster (labeled 3) of the *H. bracteosa-H. welwitschii* cluster, also differ significantly in several leaf and corolla characters (Table 3).

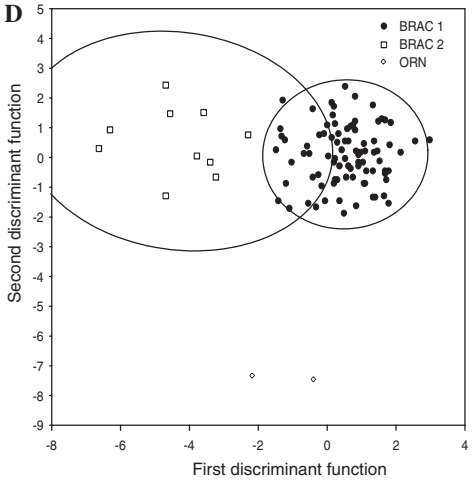
Discriminant analyses. When all specimens were plotted on the first discriminating axis from the DA on the eight main groups discovered by CA (i.e. clusters 1, 2, 3, 4, 5, 6, 7, 8), a configuration more or less similar to that produced by PCA was obtained (Fig. 3A). A phenetic cluster to the left of the plot comprises specimens of *H. bracteosa* (labeled BRAC 1 and BRAC 2), *H. welwitschii* (labeled WELW) and "*H. ornata*" (labeled ORN). It separates along the first axis, with only slight overlap, from the cluster containing specimens of *H. linearis*, *H. petrensis* and *H. canescens* (labeled PETR), *H. petiolata* (labeled PETI) and the two distinctive OTU's of *H. linearis* (labeled LINE). The first two discriminant axes accounted for approximately 80% of the variation, which was largely a function of leaf and floral measurements. The present analysis did not differentiate groups 1, 2, 3, 4, 5, 6, 7 and 8 obtained in CA. In two further DA's run separately for the two major clusters obtained in the original DA (Fig. 3A), subgroup PETI separates from PETR and LINE along axis 1 (Fig. 3B). However there is no sharp morphological distinctness between PETI and PETR as there is a slight overlap of the 95% confidence ellipses around them. Subgroups BRAC 1, BRAC 2 and WELW also show only marginal separation (Fig. 3C). Characters that contribute most to the separation of PETI from PETR and LINE, in order of importance according to the factor structure coefficients, are DLBPAF (−0.441), LPL (−0.424), LS (−0.406), LALB (−0.358) and LPCLIP (−0.319). The separation of subgroup LINE

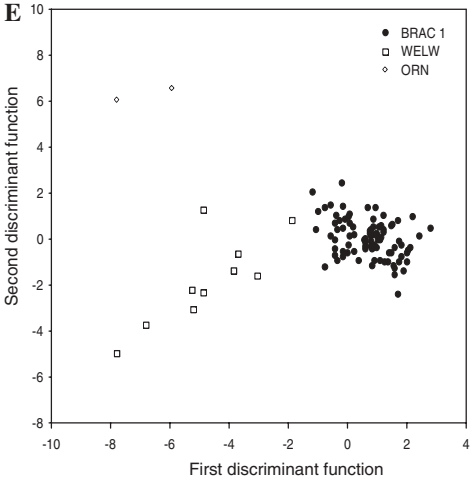
Fig. 3. Discriminant analysis plots. **A** Plot of quantitative data for groups found in the *H. bracteosa* complex after CA. **B** Plot of the first two discriminant functions after DA of individuals in the groups PETR, PETI and LINE with group spread for PETR and PETI shown by 95% confidence ellipses. **C** Plot of the first two discriminant functions after DA of individuals in the groups BRAC 1, BRAC 2 and WELW with 95% confidence ellipses around group spreads shown for all the three groups. **D** Plot of the first two discriminant functions after DA of individuals in the groups BRAC 1, BRAC 2 and ORN with 95% confidence ellipses around group spreads shown for BRAC 1 and BRAC 2. **E** Plot of the first two discriminant functions after DA of individuals in the groups BRAC 1, WELW and ORN


A
BRAC 1
BRAC 2
WELW
ORN
PETR
PETI
LINE
Second discriminant function
First discriminant function


B
PETR
PETI
LINE
Second discriminant function
First discriminant function


C
BRAC 1
BRAC 2
WELW
Second discriminant function
First discriminant function


D
BRAC 1
BRAC 2
ORN
Second discriminant function
First discriminant function


E
BRAC 1
WELW
ORN
Second discriminant function
First discriminant function

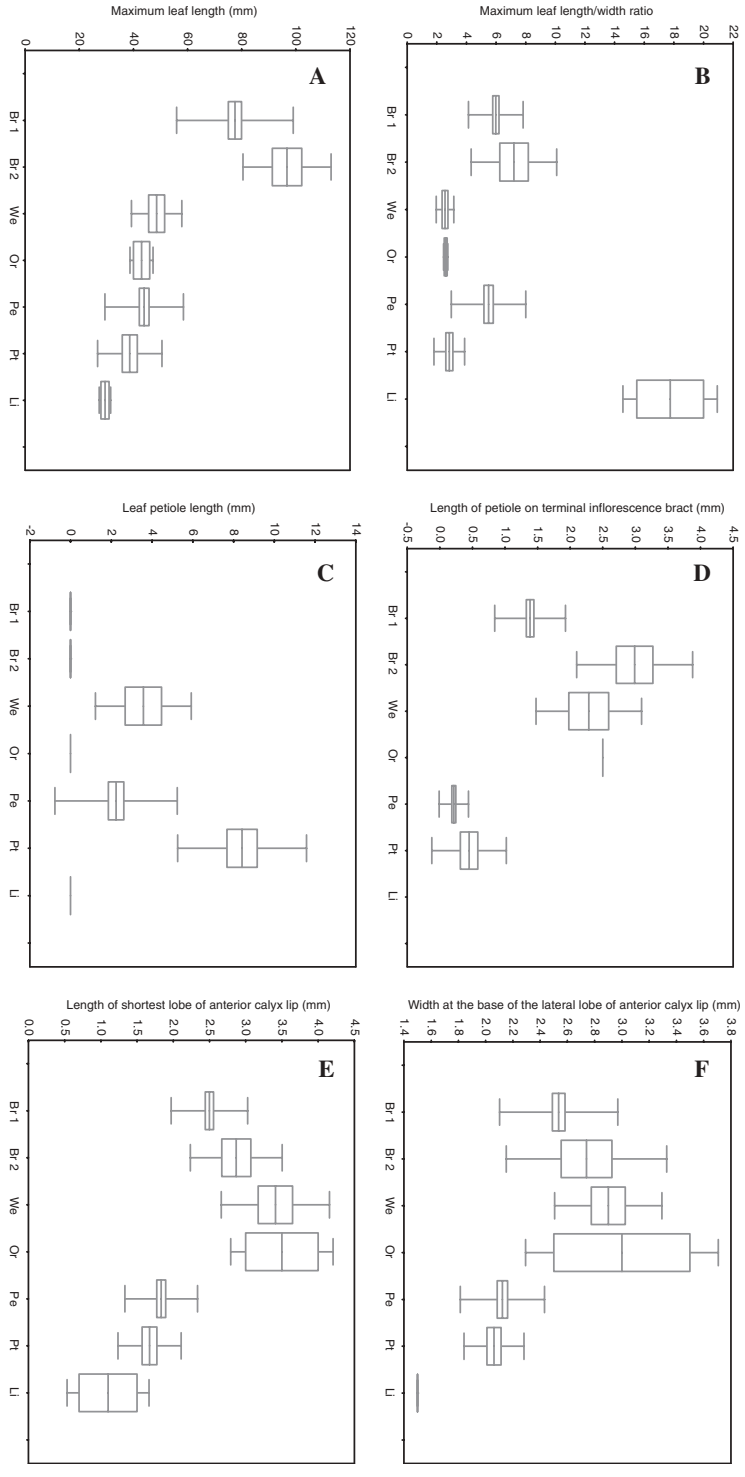


Fig. 4. Boxplots of selected leaf, calyx and floral characters. *Br 1 & Br 2* = *H. bracteosa* (= subgroups BRAC 1 and BRAC 2 respectively in DA), *We* = *H. welwitschii* (= subgroup WELW in DA), *Or* = "*H. ornata*" (= subgroup ORN in DA), *Pe* = *H. linearis* s.l., *H. petrensis* & *H. canescens* (= subgroup PETR in DA), *Pt* = *H. petiolata* (= subgroup PETI in DA), *Li* = *H. linearis* s.str. (= subgroup LINE in DA). Box = standard error, whisker = standard deviation, line in box = mean

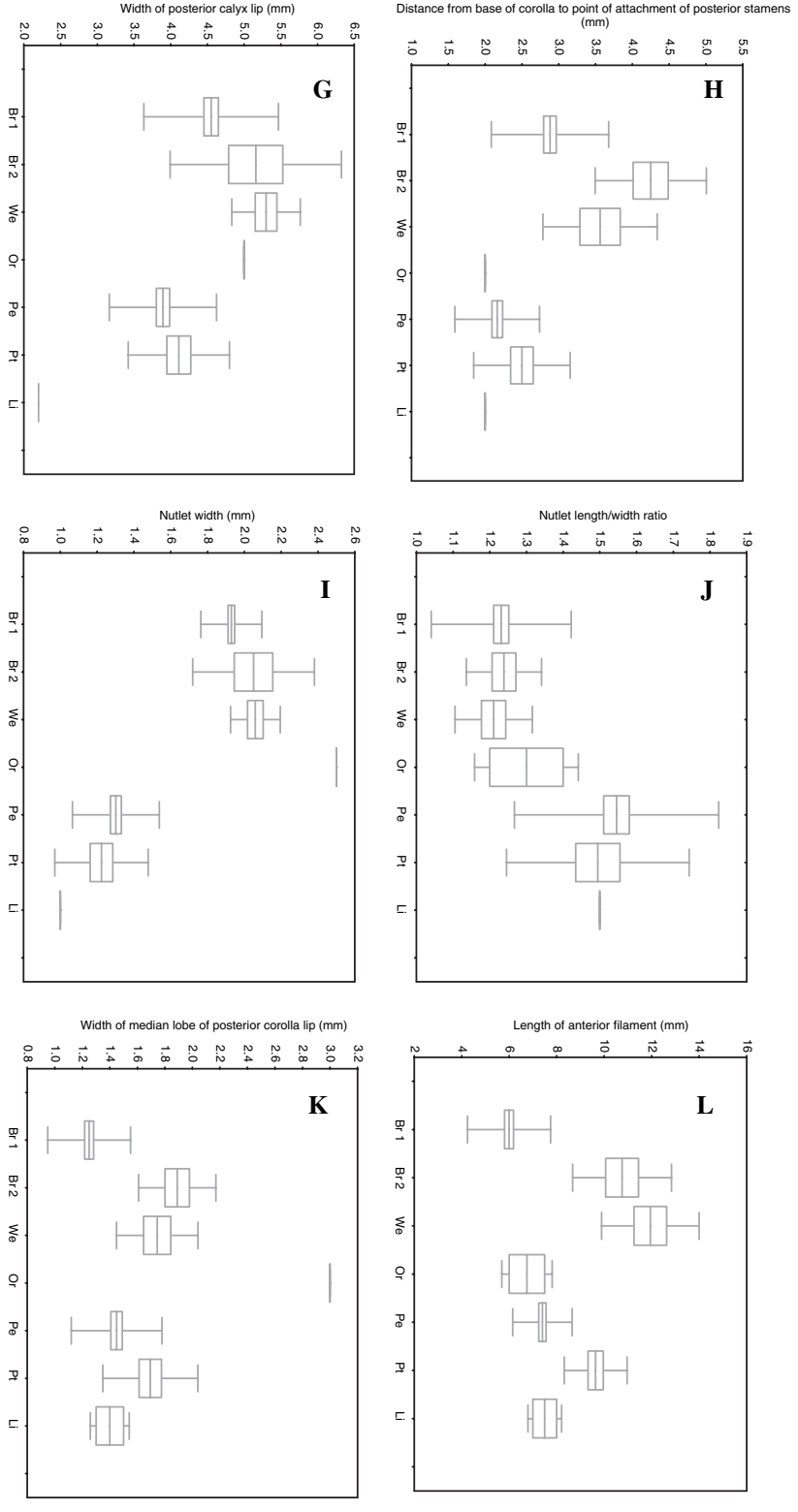


Fig. 4. (Continued)

from PETI and PETR along axis 2 is influenced largely by character MLWR while that of subgroup BRAC 2 partially from BRAC 1 and WELW along axis 2, is influenced by characters LPTIB (−0.463), WMCLIP (−0.391), ML (0.369), LPL (0.353), DLBPAF (−0.353) and MLWR (−0.330). These characters also correlate with axis 1.

The subgroup ORN separates from BRAC 1 and BRAC 2 along axis 2 when the three are analyzed together (Fig. 3D). Characters WMLCLIP (−0.430), MLWR (0.266) and ML (0.266) influence their separation. The subgroups BRAC 1 and BRAC 2 appear to be distinct but the 95% confidence ellipses around them indicate otherwise. Nevertheless characters that contribute most to their partial separation along axis 1, include LPTIB (−0.545), WMLCLIP (0.495) and DLBPAF (−0.419). A DA of the subgroups BRAC 1, WELW and ORN shows a clear discrimination between ORN and the other two along axis 2 (Fig. 3E), largely on the basis of the characters LPL (−0.514), WMLCLIP (0.425), LAF (−0.421) and NW (0.275).

Univariate analyses. Univariate analyses using boxplots (Fig. 4) indicate that the characters LSLAC, WPCLIP, LPTIB, DFBPS, NW and NLWR contribute most to the separation of the two major clusters discovered in all multivariate analyses carried out. The boxplots also indicate that two characters, MLWR and WMLCLIP separate the cluster containing the two distinctive *H. linearis* specimens from all the rest (Fig. 4). Unpaired T-tests done for all characters and different combinations of the subgroups within the two major clusters show significant levels of statistical differences between the subgroups in respect to some of the characters. At the significance level of $p < 0.05$, characters LPTIB, LPCLIP, WMCLIP, WACLIP, DFBPS, LAF, DLBPAF and NW differentiated between subgroups BRAC 1 and BRAC 2 while WELW differed significantly ($p < 0.05$) from BRAC 1 in all the characters studied except characters DLLSAC, LWRACLIP and NW (Table 3). The subgroup WELW differed significantly from both BRAC 2 and ORN in only four of the 19 quantitative characters examined and there were a higher proportion of characters that were significantly different between subgroup ORN and BRAC 1 than between ORN and BRAC 2 (Table 3). In 11 of the 19 characters used, subgroups PETR and PETI were found to be significantly different at $p < 0.05$ (Table 3). A comparison of subgroups PETR and LINE revealed significant differences in only four of the 19 quantitative characters while subgroups PETI and LINE were significantly different in 7 out of the 19 characters used (Table 3).

Character count procedure. Results show that the individuals of subgroup BRAC 2, which we initially thought might be hybrids between subgroups BRAC 1 and WELW, are intermediate between the two in only 5 out of the 15 characters that significantly differentiate between them (Table 3).

Discussion

Morphometric analysis provides a powerful tool for assessing the phenetic relationships among closely related and morphologically similar taxa. In this study, multivariate analyses of morphological characters strongly suggested the existence of two assemblages of species in the *H. bracteosa* complex: one comprising *H. bracteosa*, *H. welwitschii* and "*H. ornata*" and the other *H. linearis*, *H. petrensis*, *H. canescens* and *H. petiolata*. However, "*H. ornata*", is doubtful as a member of the *H. bracteosa*/*H. welwitschii* assemblage as cladistic analysis of sequence and morphological data of *Hemizygia* and *Syncolostemon* (Otieno et al., in press) excludes it from a lineage comprising these two species. In the present study CA also excludes it from the cluster comprising *H. bracteosa* and *H. welwitschii* (Fig. 2). The two species assemblages, excluding "*H. ornata*", resolved at the phenetic level by PCA, CA and DA coincide remarkably well with two monophyletic lineages produced in the phylogenetic analysis (Otieno

et al. in press) by taxa from the two assemblages.

H. bracteosa and *H. welwitschii*. Two of the multivariate techniques applied (CA and DA) were able to discriminate between *H. bracteosa* and *H. welwitschii*. Two components of *H. bracteosa* (BRAC 1 and BRAC 2) were resolved by CA and also by DA, but just marginally. According to CA (Fig. 2) subgroup BRAC 2 appears to be phenetically closer to *H. welwitschii* (subgroup WELW) than to BRAC 1 but not so in DA (Fig. 3C). In PCA the discrimination of the BRAC 2 subgroup is equivocal with a few of its elements mixing with those of *H. welwitschii* or falling in the intervening space between BRAC 1 and *H. welwitschii*. The differences revealed between subgroups BRAC 2 and WELW (Table 3) are consistent with the leaf characters used by Morton (1962, 1963) to differentiate between *H. bracteosa* and *H. welwitschii*. Morton (1963) described *H. bracteosa* as having linear lanceolate leaves that are cuneate at the base and either sessile or shortly petiolate and *H. welwitschii* as having leaves that are ovate to ovate-lanceolate, rounded to cuneate at the base and either sessile or nearly so. In addition to the characters mentioned above, *H. welwitschii* is also significantly different from *H. bracteosa* in calyx and corolla characters (Table 3). The same characters together with one inflorescence character (LPTIB) and an additional corolla character (WACLIP) also differentiate between subgroups BRAC 1 and BRAC 2. In all other characters, except DFBPS, overall size is emphasized, with most characters in BRAC 2 being significantly larger than the ones in subgroup BRAC 1 (see Fig. 4). However, in general facies, habitat and distribution, elements of BRAC 2 fall within the range of BRAC 1.

The extensive overlapping pattern of morphological variation between subgroups WELW and BRAC 2 (Fig. 4) suggests that the two groups form part of a continuum that extends to BRAC 1. According to the character count procedure (Wilson 1992), subgroup BRAC 2 is intermediate between subgroups BRAC 1 and WELW in only five out of the 15 characters separating these two sub-clusters (Table 3). The preponderance of non-intermediate characters seems to suggest a hypothesis of divergence rather than hybridization (Wilson 1992) to account for the partial intermediacy of BRAC 2 between BRAC 1 and WELW. However, given that individuals of BRAC 2 have a wide geographical range (have been collected in Nigeria, Zambia, Mozambique, Malawi and Zimbabwe) and are also not specific to one particular type of habitat (e.g. found in "… dry scrubby roadsides" or "open grassy sites"), their marginal intermediate nature could equally be the result of phenotypic plasticity or hybrids between BRAC 1 and WELW back-crossing with one or both of the putative parents. *Hemizygia bracteosa* is an erect, annual herb (Morton 1962, 1963; Codd 1976, 1985), sometimes woody at the base (Codd 1976, 1985) and often found growing among rocks in watercourses and in open sandy places in relatively dry tropical woodland (Codd 1976, 1985) or in marshy savannah (Morton 1962, 1963). *Hemizygia welwitschii*, on the other hand, is a perennial, bushy, somewhat woody herb of dry stony savannah (Morton 1962, 1963). All the specimens of subgroup BRAC 2 that we examined are robust in stature and this is demonstrated by their always-high measurement values in most characters (Fig. 4). It is therefore not surprising that in CA, they cluster as a group that is phenetically closer to *H. welwitschii* than to the subgroup BRAC 1. However, in facies they are indistinguishable from those of BRAC 1. Clearly, they are not amenable to treatment or recognition as a geographical or ecological race. Since both ordination techniques used in this study also place them in the ordination space between *H. bracteosa* s.str. (BRAC 1) and *H. welwitschii* (WELW) with only a few elements mixing with those of WELW in PCA, it is likely that their clustering with subgroup WELW in CA is an artefact of the analysis. Linkage based CA techniques, like the UPGMA used in this

study, are sometimes known to impose a hierarchical structure even on data that forms a continuum, which can be misleading (Thorpe 1983). The clustering of BRAC 2 individuals with subgroup WELW should therefore not be given too much taxonomic weight.

H. ornata and *H. welwitschii*. In CA (Fig. 2) two specimens of *H. ornata* joined the rest of the clusters produced at a very high level of dissimilarity. When analyzed with sub-clusters BRAC 1 and BRAC 2 or with BRAC 1 and WELW in DA, *H. ornata* was clearly discriminated from the rest (Figs. 3D, 3E). However in PCA, it mixed with specimens of *H. welwitschii* and only separated marginally from *H. welwitschii* when the *H. bracteosa*/*H. welwitschii*/*H. ornata* cluster from the original PCA was analyzed separately from the *H. linearis*/*H. petiolata* cluster (data not shown). In describing the diagnostic features of *H. ornata*, Moore (1911) noted that "among species with large foliaceous bracts, this is known at once by the small ovate leaves". This is confirmed by our data (see Fig. 4B). Cluster analysis and DA in this study show that it is distinct from *H. welwitschii* on account of having sessile leaves, wider median lobes of the posterior corolla lip, broader nutlets, shorter filaments of anterior stamens (Figs. 4C, J, K, L) and styles. Its generally diminutive stature further adds to its distinction from the robust and bushy *H. welwitschii*. This was also noted by Swynnerton who, quoted by Moore (1911), referred to *H. ornata* as "… a low herb with bright pink bracts growing in large clumps amongst short grass …" Good and Taylor (1931) transferred *H. ornata* to *Orthosiphon* as *Orthosiphon ornatus* (S. Moore) R. Good but later, Ashby (1935) included it in the synonymy of *H. welwitschii*. However, the morphometric distinctness of *H. ornata* as demonstrated by CA and DA in this study and its positioning in a clade different from that containing *H. welwitschii* (Otieno et al., in press) suggests that it should probably be treated as a separate species. We therefore here propose its reinstatement at the specific level.

H. petrensis, *H. linearis*, *H. canescens* and *H. petiolata*. Cluster analysis revealed three subgroups (PETR, PETI, LINE) within the *H. linearis*-*H. petiolata* cluster (Fig. 2). Subgroup LINE which was successfully revealed by all analyses (Figs. 1B, 2, 3B), separates from the rest of the sub-clusters on the basis of having filiform leaves, a narrower posterior calyx lip and shorter and narrower lateral lobes of the anterior calyx lip (Figs. 4B, E, F, G). Since in CA it joins with the rest of the sub-clusters in the *H. linearis*-*H. petiolata* cluster at a very high level of dissimilarity (Fig. 2) and it is unequivocally separated from sub-clusters PETI and PETR in ordination space (Fig. 1B) and there is compelling character data offering it morphometric distinctiveness (Figs. 4B, E, F, G), we restrict the use of the name *H. linearis* to this group. Krauss (1996) has however argued that it is unrealistic to use phenetic distinctiveness as the sole criterion for rank recognition since with enough resolution populations and even individuals can be recognized. We, however, regard this argument as moot because so far, there are no universally applied criteria to determine, for example, where or how species boundaries should be located or established. Indeed Verboom and Linder (1998) have noted that with the lack of agreement endemic to the species debate, the definition of species level taxa is left open to the individual taxonomist. We therefore confine our species recognition, in this study, to those groups that are consistently and persistently distinct and distinguishable by ordinary means (Cronquist 1988).

In light of the data presented here, it is evident that all other elements that have previously been included in the concept of *H. linearis* were erroneously classified. *Hemizygia linearis* should therefore be treated in a narrower sense than it has previously e.g. by Ashby (1935) and Codd (1976, 1985). All specimens with features conforming to the type of *H. linearis* s.str., including the type itself, are from Zimbabwe. The species is mostly found growing amongst grass in shallow soil among rocks (Codd 1976, 1985). *Hemizygia canescens*

and *H. petrensis* are more widespread occurring in Zimbabwe, Botswana, Mozambique, Namibia, Swaziland and South Africa and are usually found growing also among rocks in open places, arid moist woodlands and marginal grasslands (Codd 1976, 1985).

Cluster analysis and DA separated subclusters PETI and PETR but in PCA their separation is only marginal (Fig. 1A). Overall, though, the present data indicate a clear divergence between these two sub-clusters. Sub-cluster PETI in both CA and DA is a tight coherent group and corresponds to Ashby (1935) and Codd's (1976, 1985) concept of *H. petiolata*. We therefore maintain it as such. Characters that have been considered diagnostic for *H. petiolata* are its differentiated terminal bracts, the more ovate leaves, longer petioles and longer internodes on the stem (Ashby 1935) and generally larger corolla and strong smell of mint and coconut (Codd 1976, 1985). In addition, we now also include the characters LPTIB, LAF, LS and LALB (Table 1) as defining characteristics for *H. petiolata*. A phylogenetic analysis of combined molecular and morphological data of *Hemizygia* and *Syncolostemon* (Otieno et al., in press) resolved *H. petiolata* as sister to a clade comprising *H. linearis*, *H. petrensis* and *H. canescens*. This result is remarkably consistent with our multivariate analyses, which show the sub-cluster PETI to be close to subgroup PETR (e.g. Figs. 2, 3B).

Hemizygia linearis s.l., *H. petrensis* and *H. canescens* have long been known to form a closely related group of species recognized by the almost identical floral characters and small inconspicuous terminal inflorescence bracts (Codd 1976, 1985). However, they have been distinguished, but with difficulty, on the basis of leaf width and differences in leaf and stem pubescence (Codd 1976, 1985). For example, despite *H. petrensis* and *H. linearis* being different in many morphological aspects, Codd (1976) noted that the stem and leaves of the former occasionally approach the condition of the latter in being sparingly villous. He also mentioned the occurrence of occasional intermediates between *H. canescens* and *H. petrensis* in Namibia (= formerly S. W. Africa), which he considered to fit more in *H. canescens* than in *H. petrensis*. In this study we found the characters Codd used to differentiate between the three taxa to be extremely variable between them, therefore making it difficult to discern any of the species with certainty. Indeed, in all multivariate analyses, specimens of what remains after exclusion of *H. linearis* s.str. from *H. linearis* sensu Codd (1976, 1985) plus OTU's of *H. petrensis* and *H. canescens* were completely interspersed (e.g. Figs. 1, 2).

The continuous pattern of morphological variation between the three taxa [as circumscribed by Codd (1976, 1985)] and their non-separation in ordination space and CA shows that they form a morphological continuum. We consider the lack of morphometric separation between them as strongly favouring their treatment as conspecific and recommend that they should be merged into one taxon and recognized by the earliest epithet *canescens*. It should however be noted that *H. linearis* in our sense is not part of this taxon.

Taxonomic conclusions

These results provide the first comprehensive phenetic analyses of the taxa in the *H. bracteosa* complex. The data presented provide evidence which suggests that *H. bracteosa* could probably be in a state of incipient divergence, though this still requires more thorough verification. The data also show that the specific integrity of *H. bracteosa* and *H. welwitschii* has not been compromised by their apparent morphological continuity in some floral characters. No morphological discontinuities have been established between *H. petrensis*, *H. canescens* and "*H. linearis*" s.l. to warrant their continued recognition as separate taxa. In all morphometric analyses undertaken they mix to form a coherent group. It is therefore recommended here that they should be synonymized under the earliest name, *H. canescens*. The concept of *H. linearis* is revised and the species is here delimited to only include individuals with

filiform leaves, narrow posterior calyx lips and shorter and narrower lateral lobes of the anterior calyx lip. Even though in PCA *H. petiolata* is only marginally separated from the sub-cluster PETR, in CA and DA the two separate unequivocally with clear discontinuities marking the boundary of *H. petiolata*. We therefore maintain *H. petiolata* at the specific status. However, there is no doubt that it is closely allied to elements of sub-cluster PETR. Multivariate techniques in this study and phylogenetic analysis (Otieno et al., in press) suggest that what has previously been treated as *H. ornata* is distinct from *H. welwitschii*. Its recognition and reinstatement at the specific level is proposed. A formal taxonomic treatment of the complex is presented below where name changes of species in the complex are effected following the proposal by Otieno et al. (in press) in their phylogenetic study that, being congeneric, *Hemizygia* and *Syncolostemon* should be merged under the earliest name *Syncolostemon*. This taxonomy will also be followed in the forthcoming treatments of the Lamiaceae in *Flora Zambesiaca* and *Flora of Tropical East Africa*. Hereafter we refer to the complex as the *Syncolostemon bracteosa* complex

Key to taxa of the *Syncolostemon bracteosa* complex

1. Anterior stamens hairy over entire length ……..……..……*S. ornatus*
   Anterior stamens glabrous or sparsely hairy at the base……..2
2. Sessile glands absent on leaves……3
   Sessile glands present on leaves……5
3. Terminal inflorescence bracts inconspicuous although often persisting as a colourful and conspicuous coma; plant with strong smell of mint and coconut;…… ……..…… *S. petiolatus*
   Terminal inflorescence bracts always inconspicuous, never forming a colourful coma; plant without strong smell of mint and coconut……..…….……..…4
4. Leaves filiform, 1.4–3 mm wide, always sessile; lateral lobe of anterior calyx 0.7–1.5 mm wide ……*S. linearis*
   Leaves linear to ovate-lanceolate, 4–25 mm wide, sessile to petiolate; lateral lobe of anterior calyx lip 1–3 mm wide …… ……..…….. *S. canescens*
5. Leaves petiolate, sinus between anterior calyx lobes deeper than between anterior and lateral lobes ……. *S. welwitschii*
   Leaves sessile, sinus between anterior calyx lobes as deep as between anterior and lateral lobes ……. *S. bracteosus*

***S. ornatus* (*S. Moore*) *D.F.Otieno* comb. nov.**

H. ornata S. Moore in J. Linn. Soc., Bot. 40: 172 (1911). Type: Zimbabwe, Mt. Pene (“Singwekive”), 6500–7000 ft, Oct., *Swynnerton* 6078 (holotype, BM; isotype, K not seen).? *Orthosiphon ornatus* (S. Moore) Good in J. Bot. 69: 151 (1931).

***S. petiolatus* (*Ashby*) *D.F.Otieno* comb. nov.**

Hemizygia petiolata Ashby in J. Bot. Lond. 73: 355 (1935); Codd in Bothalia 12: 17 (1976b); Codd in Fl. southern Afr. 30, 4: 207 (1985). Type: Transvaal, Soutspanberg, Tshakoma, *Obermeyer* Sub TRV 31571 (holotype, PRE!).

***S. linearis* (*Benth.*) *D.F.Otieno* comb. nov.**

Orthosiphon linearis Benth. in Hooker’s Icon Pl. t. 1274 (1878). Type: Zimbabwe, Matabeleland, Apr., *Oates* s.n. (holotype, K!). *Hemizygia linearis* (Benth.) Briq. in Bull. Herb. Boiss. sér 2, 3: 997 (1903); Codd in Bothalia 12: 18 (1976b), *pro parte*; Codd in Fl. southern Afr. 30, 4: 208 (1985), *pro parte*.

***S. canescens* (*Gürke*) *D.F.Otieno* comb. nov.**

Orthosiphon canescens Gürke in Bull. Herb. Boiss. sér. 6: 557 (1898). Lectotype: Transvaal, Wonderboompoort, *Rehmann* 4507 (lectotype, K!; isolectotype, Z not seen). *Hemizygia canescens* (Gürke) Ashby in J. Bot. Lond. 73: 354

(1935); Codd in Bothalia 12: 17 (1976b); Codd in Fl. southern Afr. 30, 4: 208 (1985). *O. affinis* N.E.Br., loc. cit. 257 (1910). Type: Transvaal, Woodbush Mts, *Schlechter* 4737 (lectotype, PRE!; isolectype, K!; designated here); near Potgietersrus, *Bolus* 11146 (BOL not seen). *Orthosiphon petrensis* Hiern, Cat. Afr. Pl. Welw. 1: 859 (1900). Type: Angola, *Welwitsch* 5494 (holotype, BM not seen). *H. petrensis* (Hiern) Ashby in J. Bot. Lond. 73: 353 (1935). *H. dinteri* Briq. in Bull. Herb. Boiss. sér. 2, 3: 995 (1903). Type 10 km E of Orumbe, *Dinter* 1320 (holotype, Z not seen). *O. varians* N.E.Br. in Fl. Cap. 5, 1: 256 (1910) Ashby, loc. cit. 357 (1935). Type: Transvaal, Komatipoort, *Schlechter* 11746 (holotype, BOL!) *O. holubii* N.E.Br., loc.cit. 258 (1910). Type: Cape Molopo River, *Holub* s.n. (holotype, K!). *O. engleri* Perkins in Bot. Jahrb. 54: 34 (1917). Type: S.W.A/Namibia, Okahandja, *Engler* 6475 (holotype, B†). *O. mossianus* Good in J. Bot. Lond. 63: 175 (1925). Type: Transvaal, Messina, *Moss & Rogers* 193 (holotype, BM not seen; isotype, PRE!). *H. mossiana* (Good) Ashby. loc.cit. (1935). *H. linearis* (Benth.) Briq. *sensu* Codd in Bothalia 12: 18 (1976b), *pro parte*; *sensu* Codd in Fl. southern Afr. 30, 4: 208 (1985), *pro parte*.

S. bracteosus (Benth.) *D.F.Otieno* comb. nov.

Ocimum bracteosum Benth. Lab. 14 (1832) in Hooker's Icon. Pl. t. 455 (1842); in DC., Prodr. 12: 41 (1848). Type: Senegal, Labsar, in fields, Aug. *Le Prieur & Perrottet* s.n. (holotype, G not seen). *H. bracteosa* (Benth.) Briq. in Ann . Conserv. Jard. Bot. Geneve 2: 248 (1898); Codd in Bothalia 12: 19 (1976b); Codd in Fl. southern Afr. 30, 4: 211 (1985). *Orthosiphon bracteosus* (Benth.) Bak. in F.T.A. 5: 375 (1900); N.E.Br. in Fl. Cap. 5, 1: 248 (1910). *Orthosiphon schinzianus* Briq. in Bot. Jahrb. 19: 173 (1894). Type: S.W.A/Namibia, Amboland, *Schinz* 45 (holotype, Z not seen; isotype, photo of Z specimen in K!). *H. junodii* Briq. in Ann. Conserv. Jard. Bot. Geneve 2: 249 (1898). Lectotype: Mozambique, Delagoa Bay, *Junod* 61 (lectotype, photo of G specimen at K!, designated here). *H. junodii* var. *quintasii* Briq., loc.cit. 249 (1898). Type: Mozambique, Delagoa Bay, *Quintas* s.n. (holotype, photo of G specimen at K!) *H. hoepfneri* Briq. in Bull. Herb. Boiss. sér. 2, 3: 994 (1903). Type: S.W.A/Namibia, Hereroland, *Hopfner* 85 (holotype, photo of Z specimen at K!). *H. serrata* Briq. loc.cit. 996 (1903). Lectotype: S.W.A/Namibia, Amboland, *Wulfhorst* 1 (lectotype, Z!, designated here), *Rautenan* s.n. (isolectotype, Z not seen) *Orthosiphon rhodesianus* S. Moore in J. Bot. Lond. 43: 50 (1905). Type: Zimbabwe, Wankie, *Eyles* 132 (holotype, BM not seen).

S. welwitschii (*Rolfe*) *D.F.Otieno* comb. nov.

H. welwitschii (Rolfe) M.Ashby in J. Bot. Lond. 73: 350 (1935). *Orthosiphon welwitschii* Rolfe in Bolet. Soc. Brot. xi: 88 (1893). Type: Pungo Andongo, woods near Cazella, Oct., *Welwtisch* 5555 (holotype, K!; isotype, BM not seen). *O. adornatus* Briq. in Engl. Bot. Jahrb 19: 176 (1894). Type: Lopollo heights near Ferrao da Sola, in rocky pastures and low thickets, Jan., *Welwitsch* 5519 (holotype, BM not seen; isotype, K!). *O. adornatus* var. *angolensis* Briq. in Engl. Bot. Jahrb 19: 176 (1894). Type as above. *O. adornatus* var. *oblongifolius* Briq. tom. cit. 177. Type: Bas Congo, Lutete, Aug., *Buchner* 570 (holotype, B†) *O. adornatus* var. *chlorococcus* Briq. loc. cit. Type: between Sanza and Malange, Oct., *Pogge* 349 (holotype, B†). *O. adornatus* var. *rotundifolius* Briq. loc. cit. Type: Malange, July-Aug., *Meechow* 166 (holotype, B†). *O. pseudornatus* Good in J. Bot. 69, 151 (1931). Type: Angola, in the bushy thickets behind the Governor's Palace, Malange, Jul., *Gossweiler* 1030 (holotype, BM; isotype, K not seen).

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