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Analysis of variability for qualitative and quantitative traits in *Coleus forskohlii* Briq.

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ABSTRACT

Thirty seven *Coleus forskohlii* genotypes collected from different regions of Tamil Nadu and Karnataka were subjected to diversity analysis based on NBPGR descriptors. Eleven qualitative and fourteen quantitative traits of *C. forskohlii* were evaluated to assess the morphological variations available among the collected genotypes. For qualitative traits, a large number of genotypes out of 37 clustered together at 74 % similarity in four different groups. The dendrogram contract based on fourteen quantitative traits for the same set of genotypes did not reveal a clear pattern in grouping and the genotypes were grouped into ten different clusters. Cluster analysis of various sets of data revealed different groups of genotypes for each of the data set. A poor congruence observed among data sets of qualitative and quantitative traits in the comparison indicated that the morphological traits are not suitable for precise discrimination of closely related genotypes in *C. forskohlii*.

Key words: *Coleus forskohlii*, morphological traits, cluster analysis

INTRODUCTION

Coleus forskohlii Briq is a root medicinal crop recorded in ancient Ayurvedic *Materia Medica* under the Sanskrit name 'Makandi' and 'Mayani" (Shah, 1996). It belongs to the mint family of plants, Lamiaceae. In Ayurveda, the tuberous roots of *Coleus* are used as drug for heart diseases, abdominal colic, respiratory disorder, insomnia and convulsions (Ammon and Muller, 1985). The roots of the plant are a natural source of forskolin, a labdane diterpenoid that increases cellular levels of cyclic Adenosine Mono-Phosphate (cAMP) thereby influencing several aspects of metabolism.The therapeutic properties of forskolin contributed to the emergence of *C. forskohlii* as a taxon of importance in modern medicine. The exclusive presence of forskolin and the current recognition of its status as a unique plant species with high medicinal importance internationally, render a high profile for this particular crop. In this indigenous medicinal plant, knowledge on genetic variability within species will greatly help in direct exploitation of variability as cultivars and indirectly as base materials for various breeding programmes.

MATERIAL AND METHODS

Thirty seven genotypes collected from different regions of Tamil Nadu (17 genotypes) and Karnataka (20 genotypes) were grown in the field in a randomized block design with two replications at the Botanical Garden, Tamil Nadu Agricultural University, Coimbatore. The diversity in terms of morphological variations among the collected genotypes was documented following Singh *et al* (2003). Observations were taken on five randomly selected plants from each genotype for qualitative and quantitative traits.

Qualitative traits that depict an array of characters were converted into binary characters (Sneath and Sokal, 1973) based on the variations present in each trait. The presence or absence of phenotypes was given the score of 1 and 0, receptively. The quantitative data gathered on different traits were standardized to zero mean and a unit variance. Sequential Agglomerative Hierarchical Non-overlapping (SAHN) clustering was performed on squared Euclidean distance matrix and similarity matrix using dice coefficient for quantitative and binary data respectively utilizing the Unweighted Pair Group Method with Arithmetic Averages (UPGMA) method. Analysis of data was done using NTSYSpc version 2.02 (Rohlf, 1994).

RESULTS AND DISCUSSION

Observations for eleven qualitative traits from five randomly selected plants of 37 different *C. forskohlii* genotypes indicated that two traits viz., plant habit and lamina margin did not show any difference between genotypes. The distribution of 37 genotypes based on their phenotype variants for qualitative traits observed is furnished in Table 1. For qualitative traits, a large number of genotypes clustered together at 74% similarity in four different groups (Fig 1). The extent of genetic diversity assessed based on these eleven qualitative traits with the minimum set of NBPGR descriptors of *C. forskohlii* revealed no satisfactory measures of diversity.

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Table 1. Number of phenotype variants observed for various qualitative traits across 37 *Coleus forskohlii* genotypes

Character	Score	Phenotype	No. of genotypes
Plant habit	1	Annual stem with perennial rootstock	37
	2	Biennial	-
	3	Perennial	-
Mode of reproduction	1	Asexual	19
	2	Sexual	18
Plant growth habit	1	Erect	16
	2	Sub - erect	21
Root/tuber branching	1	Profuse	22
	2	Sparse	15
Root/tuber shape	1	Straight	18
	2	Fusiform	19
Stem pubescence	0	Glabrous	2
	3	Sparse	16
	5	Medium	
	7	Dense	19
Lamina margin	1	Crenate	37
Lamina pubescence	3	Sparse	2
	5	Medium	34
	7	Dense	1
Lamina colour	1	Pale green	2
	2	Purple green	-
	3	Dark green	35
Flower colour*	1	Pink-purple	-
	2	Pale-purple	2
	3	Lilac	-
	4	Violet	16
Susceptibility to biotic stress	1	Very low or no visible sign of susceptibility	34
	3	Low	4
	5	Intermediate	-
	7	High	1
	9	Very high	-

*Only flowering genotypes were scored

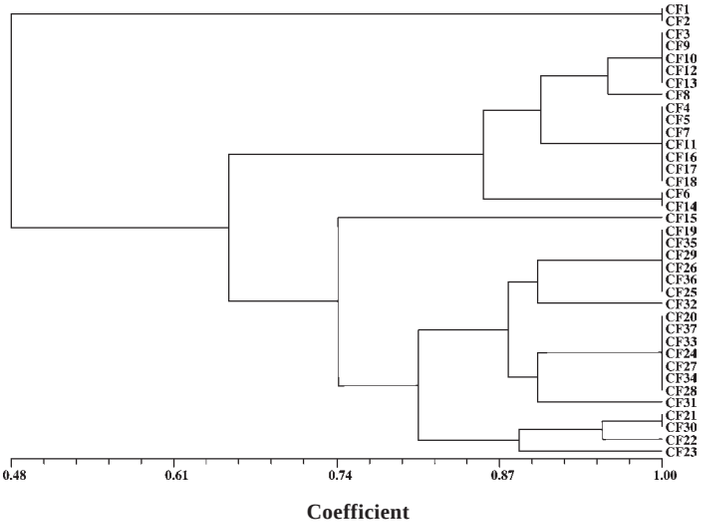

Fig 1. Dendrogram of *Coleus forskohlii* genotypes for qualitative traits using UPGMA based on Dice Coefficient

An additional 14 phenotypic quantitative characters were evaluated to enable diversity comparisons. The percentage of variation for individual traits varied from 4.41 (number of roots/tubers per plant) to 10.37 (root/tuber diameter) (Table 2). In the fourteen traits observed, the root/tuber diameter showed the highest variation ranging from 0.38 cm (CF 3) to 0.90 cm (CF 30). Leaf yield per plant, number of branches per plant and root/tuber length also showed considerable variation. A minimum of 130.41 g and a maximum of 291.20 g leaf yield per plant were observed in CF 8 and CF 14, respectively. The number of branches was maximum in CF 23 (14.97) and minimum in CF 16 (7.62). The root/tuber length was 5.08 cm and 38.27 cm in CF 15 and CF 13, respectively. The dendrogram construction based on fourteen quantitative traits for 37 *C.*

Table 2. Mean, range, coefficient of variation and standard deviation for each of the 14 quantitative traits

Trait	Mean	Range	CV (%)	SD
Number of roots/tubers per plant	25.36	16.12 - 45.77	4.41	1.12
Root/tuber length (cm)	23.60	5.08 - 38.27	7.46	1.76
Root/tuber diameter (cm)	0.63	0.38 - 0.96	10.37	0.07
Number of branches per plant	9.55	7.62 - 14.97	8.57	0.82
Stem diameter	1.53	1.05 - 2.06	7.25	0.11
Number of leaves per plant	172.28	94.00 -368.68	6.26	10.79
Lamina length (cm)	6.06	4.61 - 7.62	7.10	0.43
Lamina width (cm)	3.76	2.43 - 5.12	7.18	0.27
Petiole length (cm)	1.20	0.86 - 1.61	4.17	0.05
Leaf yield per plant (g)	202.21	130.41 -291.20	8.63	17.45
*Days to 50% flowering	84.73	65.00 - 95.00	7.20	8.49
Plant height(cm)	31.07	24.12 - 49.26	5.86	1.82
*Days to fruit maturity	106.25	95 - 115	8.72	9.27
**Forskolin / Coleonol content in roots (%)	1.25	1.14 - 1.40	7.03	0.09

* Only flowering genotypes were scored

** Only non-flowering (tuberous) genotypes were scored

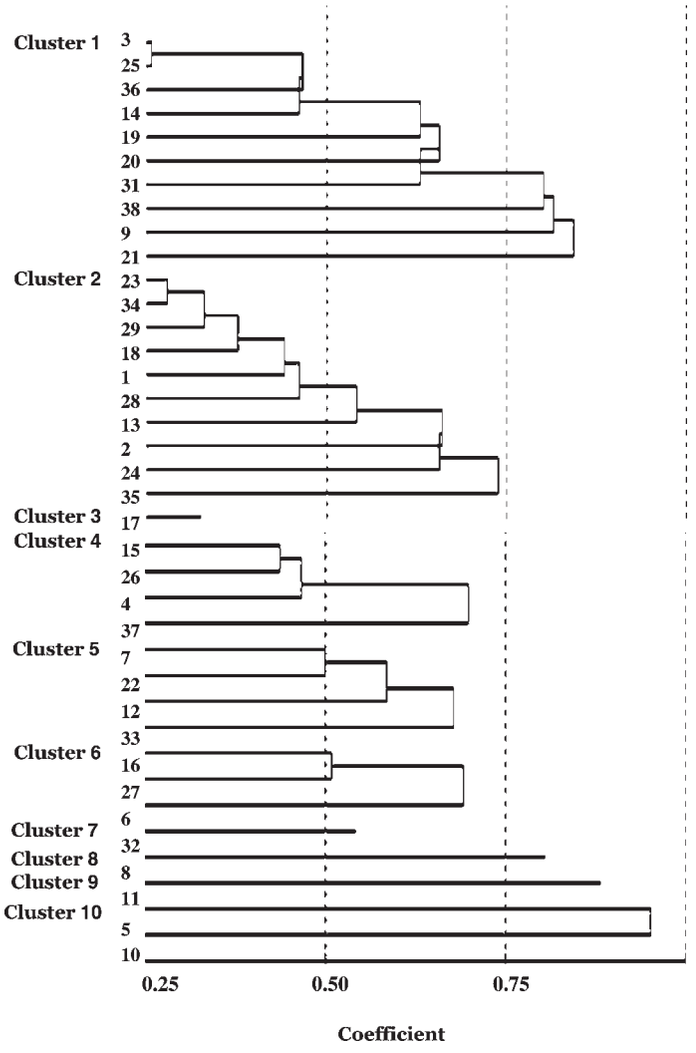

Fig 2. Dendrogram of *Coleus forskohlii* genotypes for quantitative traits using UPGMA based on Squared Euclidean Distance of standardised data Mean

forskohlii genotypes did not reveal a clear pattern in grouping and the genotypes were grouped into ten different clusters (Fig 2).

Morphological description can provide unique identification of genotypes, and are being used as descriptors for initial screening (Troyer, 1986). However they are not reliable us they reflect not only the genetic constitution of the cultivar, but also the interaction of the genotypes with the environment (Patterson and Weatherup, 1984). In the present study, cluster analysis of various sets of data revealed dissimilarity in groups of genotypes for each of the data set. A poor congruence among data sets of qualitative and quantitative traits showed in that the morphological traits alone may not be appropriate to assess the genetic diversity in *C. forskohli* as it is known that multiple genotypes can give phenotypes of similar outward appearance (Ravi, 2000).. In the present study, surveys failed to confirm similar patterns of diversity among combinations of qualitative and quantitative traits. G x E interaction effects were found to cause aberrant means for morphological traits.

Though morphological traits have been used in assessing the genetic diversity of a species, the accuracy of the assessment is questionable. The availability of a limited number of morphological traits, their poor or unknown genetic control, environmental influence on the phenotypic expression, and difficulties in stage-specific identification are major impediments in using these as genetic traits for genetic diversity analysis. Thus morphological traits are inexpensive useful indicators for a preliminary, varietal identification. They can be used as a fast and simple general tool for assessing genetic diversity among phenotypically distinguishable cultivars, although they are inefficient on account of the time and cost involved.

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