

Genetic Divergence and Correlations Study in *Chlorophytum borivilianum*

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ABSTRACT. Continuous shrinking of natural resources (forest) led to the cultivation of *Chlorophytum borivilianum*, an ayurvedic crude drug, has necessitated the genetic improvement program of the aforesaid crop. The plant is a member of family liliaceae and naturally occurring populations are open-pollinated, with varying levels of performance. The objective of this study was to assess, characterize, quantify and suitably utilize available genetic variability. Genetic divergence among 31 genotypes was determined using nine characters of *C. borivilianum* of indigenous origin via Mahalanobis D^2 statistic. The genotypes were grouped into eight clusters. Intra-cluster distance was largest for cluster VIII (nine genotypes), followed by cluster I (six genotypes). Inter-cluster D^2 values recorded between cluster II and III and those between cluster III and VI indicated the possibility of raising transgressed hybrids from cross hybridization programs using divergent parents of these four clusters. The clustering pattern

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indicated that geographical diversity was not necessarily related with genetic diversity. Leaf number contributed most toward divergence (15.8%), followed by finger number, length and width (each with at least 13% contribution) and leaf length (12.1%). Correlation analysis for root yield (dependent variable) and the remaining seven plant traits (independent variables) revealed that leaf number, leaf length and finger number, which had contributed highly to divergence, had also significant associations with root yield. The D^2 and correlation results suggested that the variability for the three traits (leaf number, leaf length and finger number) could be reliable selection criterion for root yield in *C. borivilianum*.

KEYWORDS. *Chlorophytum borivilianum*, genetic divergence, correlation, selection parameters, fresh root yield

INTRODUCTION

For a successful genetic improvement program for any crop, conservation of germplasm resources is a basic prerequisite, but to understand the usable variability, grouping or classification of genetic stocks and choice of genetically divergent parents for hybridization is extremely essential. Quantitative classification based on trait measurements offers a quantifiable degree of divergence among genotypes and population. The models of multivariate analysis are Duncan's multiple range test, metroglyph and index score method, D^2 statistic, canonical analysis and factor analysis. Plant breeders have often used D^2 statistic for measuring divergence quantitatively and canonical analysis to determine spatial divergence; both methods have been used to define the relative contribution of different characters to differentiate among genotypes. For determining the divergence among populations in terms of 'generalized group distance,' Prof. PC Mahalanobis (1928, 1936) developed D^2 statistic, which has been successfully used widely in psychometry and anthropometry (Rao 1952). Later on, Chandrashekhariah et al. (1969), Murty and Arunachalam (1966), and Murty et al. (1967) extended it to biology. Nowadays, divergence studies are being made on the basis of molecular markers, which provide precise information about phylogenetic hierarchy or descriptive account of individuals or groups of individuals but lack in quantification of continuous variation, the backbone of practical plant breeding. Mahalanobis's D^2 statistic (Rao 1952) has been widely used in crop plants for rational selection of parents for cross hybridization (Ramanujam et al.

1974; Arunachalam 1981; Gupta et al. 2001; Mononmai et al. 2003; Rabindra Babu et al. 2006). Besides, D^2 – analysis, accompanied by correlation study, could help in formulating selection indexes in crop plants (Singh et al. 1995; Singh et al. 2002). Such a study has not been undertaken in *Chlorophytum borivillianum* (“safed musli”), a plant of immense medicinal importance, especially for its wide uses in Ayurvedic preparations and aphrodisiac formulations. It was, therefore, deemed essential to gather information on important morphometric traits pertaining to genetic divergence among a set of genotypes representing a wide geographical area.

MATERIALS AND METHODS

The experimental material comprised thirty-one genotypes of Safed musli, including one improved population (CIM-OJ) and 30 genotypes from different geographical regions of India. These genotypes were grown in a randomized block design with three replications during Kharif 2006–07 at Research Farm of Central Institute of Medicinal and Aromatic Plants, Lucknow, located at 26.50°N and 80.50° E and 120 m above mean sea levels. Soil of the experimental plot was sandy loam with moderate fertility and pH of 6.5. Each treatment (genotype) was sown in 3-m long rows with a row-to-row spacing of 50 cm and a plant-to-plant spacing of 15 cm on raised beds in the last week of June 2006. The fertilizers like N, P_2O_5 and K_2O were applied (ratio of 60:65:20 kg/h) (Khanuja et al. 2004; Singh et al. 2005). Usually Safed musli does not require any supplement irrigation during June – September, but when rainfed period exceeds 10–12 days, the crop is irrigated. The harvesting of tubers was done in the 1st week of February 2007. Normal cultural practices were followed to raise a good crop of Safed musli (Khanuja et al. 2004; Singh et al. 2005). Five random plants per plot per replication were selected for recording observations on number of leaves per plant, leaf length (cm), leaf width (cm), canopy diameter (cm), length of inflorescence, number of fingers per clump, length of finger (cm), width of finger (cm) and fresh root yield per plant (g). Analysis of variance was carried out and Wilk’s criterion was tested before proceeding to the computation of genetic divergence via Mahalanobis D^2 technique (1928, 1936) using the following equation:

$$D_x^2 = \sum_i^p \sum_j^p (\lambda^{ij}) d_i d_j \text{ or } D^2 = \sum_i^x d_i^2 = \sum_i^x (Y_i^j - Y_i^k)^2 \text{ (j} \neq \text{k)}$$

TABLE 2. Distribution of *Chlorophytum borivilianum* genotypes in different clusters.

Cluster	No. of genotypes	Genotypes
I	6	BLC-1, BLC-2, BLC-6, BLC-11, Jai Samand Centuri-2, Raj-2
II	1	Tapovan-1
III	3	BLC-12, BRFU, Kakroli Rajsamand Navanit Palival
IV	4	BLC-5, BLC-13, Raj Samand-1, Salambhar-1
V	2	BLC-7, Raj-3
VI	3	BLC-9, Jhalod-5, Cv. Sultanpur
VII	3	BLC-10, Salmbhar-3, Cim- OJ
VIII	9	BLC-3, BLC-4, BLC-8, Jai Samand Centuri-1, Salmbhar-2, Jhalod-1, Jhalod-2, Jhalod-3, Jhalod-4

these clusters. The mean performances of each cluster for studied traits are presented in Table 3. The mean of clusters for different characters indicated considerable differences between them for all the characters. Cluster I had the lowest length of inflorescence (18.36) and highest mean (10.67) for number of leaves per plant. Cluster II had lowest mean (29.80) for canopy diameter and highest mean (45.67) for length of inflorescence. Cluster V had highest mean finger width of 0.79, while lowest mean was recorded for number of fingers (6.09) and finger length (5.44). Cluster VI had highest mean for leaf width (2.37) and canopy diameter (69.53). The highest cluster means (11.63, 8.63 and 28.51) for number of fingers per clump, finger length and fresh root yield per plant, respectively were recorded for cluster VIII.

From the perusal of estimates presented in Tables 2 and 3. it is apparent that considerable diversity existed for all characters in various genotypes studied. Clusters V, VI and VIII recorded high mean value for majority of the important traits like number of fingers per clump, length of finger, width of finger, and fresh root yield per plant. The genotypes exhibited random pattern of distribution for various clusters revealing that genetic diversity and geographical diversity were not related. The percent contribution of different characters towards genetic divergence showed that number of leaves had maximum contribution (15.8), followed by number of fingers per clump and finger length and width (each with at least 13% contribution) and leaf length (12.1).

A correlation analysis involving root yield as dependent variable and the rest seven plant traits as the independent variables to know whether the plant traits with high contribution towards divergence had any association with the main economic trait 'root yield'. The results of genotypic and phenotypic correlation coefficients are shown in Table 4. The plant

TABLE 3. Cluster means of eight clusters and contribution of nine characters towards genetic divergence in *Chlorophytum borivilianum*.

Clusters	I	II	III	IV	V	VI	VII	VIII	Number of times ranked first	Percent Contribution towards divergence
No. of leaves per plant	10.67	10.67	6.22	10.00	8.67	10.11	9.11	10.64	3318	15.86
Leaf length (cm)	27.43	32.40	21.24	30.13	30.70	37.44	32.66	32.66	2544	12.16
Leaf width (cm)	1.78	2.33	1.22	2.16	2.00	2.37	1.39	2.07	1926	9.20
Canopy diameter (cm)	54.44	29.80	65.62	51.07	50.00	69.53	63.24	62.94	1250	5.97
Length of inflorescence (cm)	18.36	45.67	26.02	31.16	22.67	39.17	26.82	34.76	1625	7.77
No. of finger/ clump	10.06	11.29	7.96	8.42	6.09	10.32	8.78	11.63	2730	13.05
Finger length (cm)	7.20	8.22	6.43	8.25	5.44	7.48	6.95	8.63	2832	13.53
Finger width (cm)	0.68	0.72	0.53	0.60	0.79	0.66	0.60	0.74	2904	13.88
Fresh root yield per plant (g)	18.96	25.00	10.28	16.48	11.93	24.43	15.26	28.51	1795	8.58

TABLE 4. Estimates of phenotypic (P) and genotypic (G) correlation coefficients among nine characters in *Chlorophytum borivillianum*.

Characters	Leaf length (cm)	Leaf width (cm)	Canopy diameter (cm ²)	Length of inflorescence (cm)	No. of finger/clump	Length of finger (cm)	Width of finger (cm)	Fresh yield per plant (g)
Number of leaves	P 0.322	0.410*	-0.112	0.150	0.319	0.310	0.264	0.508**
	G 0.413*	0.512**	-0.135	0.190	0.541**	0.422*	0.369*	0.646**
Leaf length (cm)	P -	0.515**	0.035	0.439*	0.251	0.199	0.383*	0.358*
	G -	0.578**	0.040	0.454*	0.338	0.264	0.484**	0.397*
Leaf width (cm)	P -	-	-0.150	0.466**	0.246	0.208	0.344	0.390*
	G -	-	-0.161	0.489**	0.373*	0.245	0.419*	0.414*
Canopy diameter (cm)	P -	-	-	0.126	0.046	-0.103	-0.079	0.161
	G -	-	-	0.130	0.074	-0.112	-0.099	0.174
Length of inflorescence (cm)	P -	-	-	-	0.248	0.263	0.181	0.297
	G -	-	-	-	0.345	0.327	0.229	0.314
No. of finger/clump	P -	-	-	-	-	0.421*	0.235	0.528**
	G -	-	-	-	-	0.592**	0.170	0.707**
Finger length (cm)	P -	-	-	-	-	-	-0.016	0.276
	G -	-	-	-	-	-	0.037	0.280
Finger width (cm)	P -	-	-	-	-	-	-	0.291
	G -	-	-	-	-	-	-	0.310

traits, namely leaf number, leaf length and finger number, which had contributed highly towards genetic divergence in evolution, had also significant positive associations with root yield. Taken together, the results of D^2 and correlation study demonstrated that the variability forces (like the variations for leaf number, leaf length and finger number) of genetic divergence act as variability forces for variations in root yield potential in *C. borivilianum*. A great variability in leaf size and fleshy root number was recorded by various workers in their germplasm collection (Jat 1993; Bordia et al. 1995; Jat and Sharma 1996; Kothari and Singh 2001; Geetha and Maiti 2002). Thus, the study raised the possibility that the variability for the three traits (leaf number, length and finger number) could be a reliable selection parameter for the prognosis of higher root yield in this medicinal plant species.

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