# ASSESSMENT OF GENETIC DIVERSITY AMONG ORCHIDS

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### Abstract

Twenty five orchids were explored for genotypic and phenotypic variations and placed in five groups on the basis of similarity in phenotypic characters. Non-hierarchical clustering of these orchids of five main groups were placed according to their morphological traits. Group I had maximum plant height (158.87 cm), leaf area (160.42 cm<sup>2</sup>), flower weight (9.31 g) and roots/plant (57.84). While number of spikes per plant (2.57), spike length (3.43 cm), root length (9.67 cm), horizontal spread of flower (12.47) and number of flowers/plant (20.53) were attempted by orchids of group V. However, the orchids of group III exhibited maximum vertical flower size (46.03 cm). Clustering pattern revealed that geographical diversity was not associated with genetic diversity i.e., orchids collected from same location were grouped into different clusters or groups. Group II had the maximum intra-group distance (16.158) than other groups. The minimum intra-group distance was observed in the Group III (5.56). The inter-group (D<sup>2</sup>) values varied from 3.579 to 18.724 indicating wide diversity among orchids. The maximum inter-group distance was observed between groups IV and I; minimum in between the groups IV and II. Considering cluster mean values the orchids of groups III and IV could be selected for yield and flower contributing characters.

# Introduction

Orchidaceous is most numerous and the second largest group of flowering plants in the plant kingdom. There are about 788 genera and 25,000 to 30,000 known species of orchids around the world (Mabberley 1997). Orchids attracting botanists, naturalists, and ecologists since the time immemorial due to their incredible range of diversity in shape, size, and colour of flowers. This highly advanced family of monocots is comprised mostly of herbaceous plants characterized by distinct floral morphology, pollination mechanism and minute seeds (Pridgeon et al. 1999). In 2011, imports of orchids for bouquets and ornamental purposes have increased 13.06 per cent, from US\$ 944,370 in 2010 to US\$ 1.07 million imports of orchid plants, including roots, cuttings and slips were also expanded by 18.46 per cent in 2011 to US\$ 1.32 million from US\$ 1.12 million recorded in 2010. The worldwide suppliers in 2011 were the Netherlands (87.2 per cent), Taiwan (7.97 per cent), China (3.00 per cent), Thailand (1.23 per cent) and the United States (0.60 per cent), (SAGARPA 2012). Among many reasons, the lack of high yielding is one of the reasons for less export of this flower. In crop improvement program, genetic diversity has been considered as an important factor for obtaining varieties with important desirable characters like disease resistant, earliness or quality of a particular character (Chowdhury 1975). The present study was undertaken with the objective to estimate genetic variation, its components especially heritability, GCV (%), PCV (%), GA and GA (%) for selection the best characters for future breeding program in orchids. Using the morphological characters, genetic diversity among the collected orchids were carried out through univariate and multivariate analyses techniques. Genetic parameters such as genotypic coefficient of variation, phenotypic coefficient of variation, heritability in broad sense, genetic advance were calculated. For multivariate analyses, non-hierarchical clustering and intra

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and inter cluster distance were done. Moniruzzaman et al. (2012) observed that out of 15 quantitative characters studied in orchids, spike length, rachis length, plant height, floret number and flower durability exhibited high heritability. The characters exhibiting high hb<sup>2</sup> with high genetic advance were spike length (94.00 and 98.29%), rachis length (95.34 and 93.85%) and flower durability (94.00 and 89.00%). The characters exhibited high  $H^2$  along with low genetic advance in orchid were plant height (87.00 and 40.99%) and pod size (74.00 and 48.51%). High broad sense heritability with high genetic advance was observed in spike length (94.00 and 98.29%), rachis length (95.34 and 93.85%), flower durability (94.00 and 89.00%) and floret number (70.50 and 65.47%) indicating additive gene action, suggested the possibility of improvement of these traits through selection. Hybridization and geographic distribution can be involved in the differentiation of the species and lineages in this complex (Fabio and Barros 2009). According to Roychowdhury and Tah (2011), genetic improvement of any crop largely depends on the magnitude of several genetic parameters like analysis of variance of each mean value, phenotypic and genotypic variance, phenotypic and genotypic coefficient of variation (PCV and GCV), broad sense heritability ( $H^2$ ) and genetic advance (GA) on which the breeding methods are formulated for its further improvement.

#### Materials and Methods

Available 25 orchids of 8 years old were collected from different places of Bangladesh including commercial orchid farm (Dipta Orchids, District Mymensingh) and BAU campus located 60 km away from Dipta orchid farm. The genotypic, phenotypic coefficient of variation and genetic advance (GCV, PCV and GA) were computed on morphological data for the 10 most important quantitative characters according to the method advocated by Singh and Chaudhary (1985). Broad-sense heritability ( $H^2$ ) was calculated as the ratio of the genotypic variance to the phenotypic variance using the formula according to Allard (1960). Cluster analysis as performed by  $D^2$  analysis (Rao 1952), which divides the orchids based on the data set into more or less homogenous groups.  $D^2$  is the sum of squares of differences between any two populations for each of the uncorrelated variables (obtained by transforming correlated variables through pivotal condensation method). Clustering was done using non-hierarchical and hierarchical classification (Rao 1952). The procedure for calculating inter-group distance between groups II and I, between groups III and I; between IV and I and so on were taken one by one and their distances from other groups were calculated through multivariate analysis in Gen-Stat 5.3 version.

### **Results and Discussion**

Significant results were observed among 25 orchids for the ten morphological characters indicating the prevalence of genetic variability. The mean is given in Table 1. The variation in shape and color of the orchids studied is presented in Fig. 1. Coefficient of phenotypic and genotypic variations, heritability estimates and expected genetic advance in per cent of mean are given in Table 1. A wide range of variation was observed for the ten characters. The phenotypic variation was higher than genotypic variation in all the characters indicating environmental influence. Average mean values for ten characters showed wide variations for the orchids (Table 1). Mean values were highest for plant height (67.96 cm) and leaf area (62.43 cm<sup>2</sup>). While, lowest mean values were observed for flower weight (2.43 g).

Heritability estimates indicated significant variations among characters of horizontal and vertical spread of flower (100%, respectively) and flower weight (99.29%) than remaining characters. However it was moderate for spikes per plant (88.09). The maximum genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) values were recorded for plant height (67.77 and 68.42%, respectively) followed by leaf area (64.36 and 65.61%,

respectively), than number of flowers per plant (47.59%). Similarly genetic advance (GA) and genetic advance (GA%) in per cent value were maximum for plant height (93.98 and 138.28%, respectively) followed by leaf area (81.17 and 130.01%, respectively). Very little variations were observed between GCV and PCV values for all the characters. Maximum genetic diversity was observed for all the characters under GA and GA% (Table 1).

 Table 1. Mean, heritability, genotypic and phenotypic coefficients of variation, genetic advance and genetic advance in per cent of mean for ten characters among orchids.

Characters	Mean	$H^{2}(\%)$	GCV (%)	PCV (%)	GA	GA (%)
Plant height (cm)	67.96	98.13	67.77	68.42	93.98	138.28
Leaf area (cm <sup>2</sup> )	62.43	96.21	64.36	65.61	81.17	130.01
Spikes/plant	2.00	88.09	30.41	32.40	1.16	58.00
Spike length (cm)	41.34	95.43	24.51	25.09	20.38	49.29
Flower weight (g)	2.43	99.29	48.86	49.03	2.43	100.00
Roots/plant	6.90	96.05	40.47	41.29	5.61	81.30
Root length (cm)	40.09	95.76	37.19	38.01	30.04	74.93
Horizontal spread of flower (cm)	7.01	100.00	25.15	25.15	3.62	51.64
Vertical spread of flower (cm)	6.94	100.00	35.90	35.90	5.12	73.77
Flowers/plant	16.59	94.64	46.30	47.59	15.38	92.70

 $H^2$  = Heritability in broad sense (%), GCV = Genotypic coefficients of variation, PCV = Phenotypic coefficients of variation, GA = Genetic advance, GA% = Genetic advance in per cent of mean.

Results on non -hierarchical clustering of 25 orchid germplasms formed five main groups or classes (Table 2) where orchids were placed according to their morphological traits resemblance. On the basis of similarity in morphological characteristics Mokara Orange, Mokara Yellow Annie, Mokara Robin Red were placed in group I with maximum mean value for plant height (158.87 cm), leaf area (160.42 cm<sup>2</sup>), flower weight (9.31 g) and number of aerial roots/plant (57.84). Group II had Dendrobium Earsakul, Dendrobium Miss Singapore, Dendrobium Kultana Blue, Dendrobium Violate White, Dendrobium Sacula Pink, Dendrobium Sonia, Dendrobium Qasim Gold all these orchids had zero aerial roots (Table 2).

According to their mean value for characters group I and group II had Mokara Aranda Blue, Dendrobium White 5N, Mokara Carol Pink, Mokara Nora Blue, Mokara Dieheard Red, Dendrobium Chaingama pink, Ascosands, Mokara Chalk Guar Pink, Mokara Jitti, group IV placed Dendrobium Satu Pink, Dendrobium Red Bull, Ascocentrum, Vanda, Oncidium with maximum value for vertical spread of flower (46.03 cm) and group V had only Cattleya with maximum values for spikes per plant (2.57), spike length 93.43 cm), root length (9.67 cm), horizontal spread of flower (12.47 cm) and number of flowers per plant (20.53).

The intra-group distance was highest in the group II (116.159) followed by the group IV (9.476) (Table 3). The minimum intra-group distance was observed in the Group 3 (5.560) which included nine orchids. Inter-group (D<sup>2</sup>) values varied from 3.579 to 18.724 indicating wide diversity among orchids. Inter-group distance was the highest between group IV and I (18.724) followed by the distance between group II × I (16.159). The orchids grouped in group IV × I showed maximum inter-group distance are expected to show wide diversity in genetic make-up. The lowest inter-group distance observed in group IV × II suggests that orchids of this group had closeness among themselves (Table 4). Results showed that phenotypic coefficients of variation

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Mokara Orange



Mokara Yellow Annie



Mokara Robin Red



Mokara Aranda Blue



Dendrobium White 5N



Dendrobium Earsakul



Dendrobium Miss Singapore



Mokara Carol Pink



Dendrobium Kultana Blue



Dendrobium Satu Pink



Dendrobium Violate White



Dendrobium Red Bull

(Fig. 1 contd.)



Dendrobium Chaingama Pink



Dendrobium Sacula Pink



Dendrobium Sonia



Ascocentrum garayi (E.)



Cattleya percivaliana (R.)



Vanda coerulea (G.)



Oncidium crista (R.)



Ascosanda sp

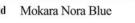


Mokara Chalk Guar Pink



Mokara Jitti





Mokra Dieheard Red

Fig. 1. Orchid flowers with variation in colors.

were slightly higher than the genotypic coefficients of variation for all the traits studied. This indicated the presence of environmental influence to some degree in the phenotypic expression of the characters. Sultana (2003) observed similar findings. Similarly Faroque (2003) and Roychowdhury et al. (2011) found environmental influence on genetic variability for these traits

in orchids. High to medium broad sense heritability estimates observed for horizontal and vertical spread of flower, flower weight, plant height, leaf area, roots per plant, root length, flowers per plant and spike length. It suggests high component of heritable portion of variation, it

Characters	Groups					
	Ι	II	III	IV	V	
Plant height (cm)	158.87	49.21	86.26	19.42	4.49	
Leaf area (cm <sup>2</sup> )	160.42	49.45	52.99	34.04	86.32	
Spikes/ plant	1.86	1.95	2.02	2.01	2.57	
Spike length (cm)	3.08	2.14	2.60	1.93	3.43	
Flower weight (g)	9.31	0.00	6.18	0.95	1.33	
Roots/plant	57.84	0.00	33.48	4.52	23.73	
Root length (cm)	7.12	6.64	7.67	5.76	9.67	
Horizontal spread of flower (cm)	7.29	5.94	7.63	5.79	12.47	
Vertical spread of flower (cm)	38.42	42.87	38.07	46.03	45.33	
Flowers/plant	17.18	15.52	13.96	21.69	20.53	

Group I - Mokara Orange, Mokara Yellow Annie, Mokara Robin Red; Group II - Dendrobium Earsakul , Dendrobium Miss Singapore, Dendrobium Kultana Blue, Dendrobium Violate White, Dendrobium Sacula Pink, Dendrobium Sonia, Dendrobium Qasim Gold; Group III - Mokara Aranda Blue, Dendrobium White 5N, Mokara Carol Pink, Mokara Nora Blue, Mokara Dieheard Red, Dendrobium Chaingama Pink, Ascosands, Mokara Chalk Guar Pink, Mokara Jitti; Group IV - Dendrobium Satu Pink, Dendrobium Red Bull, Ascocentrum, Vanda, Oncidium; Group V - Cattleya.

Groups	1	2	3	4	5
1	0.000				
2	16.159	0.000			
3	13.997	5.560	0.000		
4	18.724	3.579	7.194	0.000	
5	16.061	9.814	11.267	9.476	0.000

Table 3. Intra and inter-group distances  $(D^2)$ .

is the portion which is exploited by breeders (Moniruzzaman *et al.* 2012). Different geographical conditions might have possessed a slight difference because of variations in environmental influenced characters like, leaf length, plant height and spike length. Therefore, diversity of morphological-based markers for genetic diversity of varieties and interaction of environment are expected to be quite high as reported by Trapnell *et al.* (2004), Pellegrino *et al.* (2005) and Jacquemyn *et al.* (2007). Non-hierarchical clustering and Intra and inter-group distance analysis avoided possible distortions produced by a specific method (Everitt 1978), relationship of these methods is very clear from the results, which maximized the variance between characters by choosing axes that were linear combinations of biological variables. Therefore, the results concluded that these characters are contributing traits and selection based on these traits would be most effective for plant breeders in developing new orchid varieties.

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