

GENETIC VARIABILITY STUDIES IN SELECTED ORCHID GENOTYPES

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Abstract

Orchid genotypes comprising of six genera *i.e.*, Aranda, Aranthera, Kagawara, Mokara, *Renanthera*, and *Vanda* were evaluated using completely randomized design with five replications. The selected materials were evaluated by recording observations on their vegetative and floral characters. Parameters of variability, heritability, and expected genetic advance were calculated. The mean and standard errors were worked out as per standard methods and then coefficients of variation were computed. Genotypic and phenotypic coefficients of variation were high for thickness of leaf, leaf area, and number of aerial roots indicating high variability for these characters and scope for improvement through selection. High heritability (>70%) combined with genetic advance greater than 70 per cent was observed for number of aerial roots, leaf width, leaf thickness, leaf area, number of spikes per shoot, and number of flowers per inflorescence indicating additive gene action for these characters and providing thereby a greater scope for further improvement of these traits in advance generations.

Introduction

ORCHIDS, THE most beautiful flowers in God's creation, occupy top position amongst all the flowering plants valued for cut flower production and cherished as potted plants. They are the most pampered plants and are coveted for their long lasting and bewitchingly beautiful flowers which are the major players in the multibillion dollar floriculture trade in the world (De and Pathak, 2015; Hegde, 2016; Prakash and Pathak, 2019). These orchids are better priced in the international floriculture trade because of their spectacular flowers having numerous colour combinations and patterns (De and Pathak, 2018; Janakiram and Baskaran, 2018; Thomas and Lekha Rani, 2008). Orchids have received very little attention at the hands of geneticists until now and the knowledge about the mode of inheritance of the economic characters in this group of plants is still inadequate. Most of the genetic diversity that exists in orchids today has been the result of exploration, collection, introduction, and conservation (Ramudu and Khasim, 2016). The chances for the selection of better genotypes are greater when the genetic variability is high. The genetic parameters like genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) gives an account of the extent of variability present in a genetic population. The estimates of genetic parameters like heritability and genetic advance help the plant breeder in selecting elite genotypes from heterogeneous populations. It is essential to produce novel and adapted quality hybrids that are acceptable in the national and international markets. There is a wide range of variation for most of the traits studied; these genotypes can be utilised further for the production of novel monopodial orchid hybrids.

Material and Methods

The research programme was undertaken in the Department of Plant Breeding and Genetics, College of Agriculture, Vellayani. The parent materials for investigation were maintained in the green house and observations on vegetative and floral characters were taken. The experiment was laid out in Completely Randomized Design (CRD) with fifteen selected genotypes of orchids belonging to 6 genera, *i.e.*, Aranda, Aranthera, Kagawara, Mokara, *Renanthera*, and *Vanda*. The terminal cuttings of these orchids, with three to five velamen roots, were used as planting material. Epidermis in the roots of the orchids is multiseriate. All the roots have velamen but all roots do not have mycorrhizal pelotons (Kaushik, 1983). These were planted in linear trenches prepared on ground using coconut husk, brick pieces, and wood shavings in the month of December. Nutrients were supplied to the plants following the recommended dose of fertilizer. Important cultural practices were carried out from time to time. The selected materials were evaluated by recording observations on their vegetative and floral characters (both quantitative and qualitative). Parameters of variability, heritability, and expected genetic advance were calculated. The mean and standard errors were worked out as per standard methods and co-efficient of variations were computed.

Results

Genotypic and Phenotypic Coefficients of Variation

The analysis of variance revealed significant differences amongst the 15 orchid genotypes with respect to all the 22 biometric characters studied. The genotypic,

phenotypic, and environmental variances, and coefficients of variation at genotypic and phenotypic levels were studied (Table 1). The phenotypic coefficient of variation was found to be higher than the genotypic coefficient of variation for all the traits studied indicating significant influence of environment in the expression of these characters. The vegetative characters such as thickness of leaf (GCV= 64.442%, PCV= 64.573%), leaf area (GCV= 55.464%, PCV= 55.551%), and number of aerial roots (GCV= 54.4%, PCV= 55.906%) in the descending order exhibited the highest estimates of both

Heritability and Genetic Advance

Heritability per cent was categorized as suggested by Allard (1960) into low (<30%), moderate (30-70%), and high (>70%). Accordingly, all the vegetative characters and floral traits exhibited high heritability. A wide range of genetic advance (at 0.05%) was exhibited by the characters studied. This was the highest for leaf area (36.58) followed by shoot length (21.78), and length of inflorescence (21.19). Genetic advance (% mean) was high (>70%) for six characters considered. It was

Table 1. Components of variance and genetic parameters for different vegetative and morphological characters.

Characters	GCV	PCV	Heritability	Genetic advance
Length of shoot (cm)	17.180	17.351	98.0	35.04
Number of leaves/shoot	19.089	19.995	91.1	37.56
Number of aerial roots	54.400	55.906	94.7	109.03
Length of aerial roots (cm)	27.619	29.729	86.3	52.86
Thickness of shoot (cm)	19.868	20.118	97.5	40.16
Length of internode (cm)	18.998	19.120	98.7	38.82
Leaf length (cm)	32.577	32.721	99.1	66.85
Leaf width (cm)	45.508	45.858	98.5	93.20
Leaf thickness (cm)	64.442	64.573	99.6	133.97
Leaf area (cm ²)	55.464	55.551	99.7	114.09
Days to first flower opening from inflorescence emergence	9.896	10.067	96.6	20.04
Days to last flower opening from first flower opening	24.801	24.902	99.2	50.90
Number of spikes per cane	44.692	47.648	88.0	86.45
Length of inflorescence (cm)	30.884	31.336	97.1	62.71
Length of scape (cm)	33.398	34.808	92.1	66.02
Thickness of inflorescence axis (cm)	17.682	18.097	95.5	35.66
Number of flowers per inflorescence	50.118	52.651	90.6	98.30
Length of internode of inflorescence	28.720	32.070	80.2	53.08
Flower length (cm)	21.982	22.217	97.9	44.87
Flower width (cm)	27.965	28.347	97.3	56.80
Vase life (days)	32.118	33.235	93.4	63.96
Fullness value	23.092	23.271	98.5	47.04

genotypic and phenotypic variances. Amongst the floral traits, number of flowers per inflorescence (GCV= 50.118%, PCV= 52.651%), number of spikes per cane (GCV= 44.692%, PC = 47.648%), and vase life (GCV= 32.118%, PCV= 33.235%) showed the highest genotypic and phenotypic variances in the decreasing order.

exhibited in the range of 30-70 per cent by sixteen characters analyzed. High heritability (>70%) combined with genetic advance greater than 70 per cent was observed for number of aerial roots, leaf width, leaf thickness, leaf area, number of spikes per shoot, and number of flowers per inflorescence indicating additive

gene action for these characters. This suggests that permanent improvement could be attained by practicing selection on the above traits. High heritability (>70%) combined with 30-70 per cent genetic advance was observed for shoot length and thickness, number of leaves per shoot, length of aerial roots, length of internode, leaf length, days to last flower opening from first flower opening, length of inflorescence, length of scape, thickness of inflorescence axis, length of internode of inflorescence, flower length and width, pollen size, vase life, and fullness value. Although days to first flower opening from inflorescence emergence and pollen fertility showed high heritability, their genetic advance was found to be less than 30 per cent. This shows the presence of non-additive gene action.

Discussion

A thorough knowledge of vegetative as well as floral traits is important for understanding the diversity of monopodial orchid genotypes and choosing them as parents for a successful hybridization programme. Leonhardt (1977), while breeding with *Cymbidium* and related genera, made use of fullness value to obtain an estimate of the degree of fullness. Number of flowers per inflorescence is a character of prime importance in orchid breeding, as has been pointed out by Kamemoto (1983) and McConnel and Kamemoto (1983). Length of inflorescence has also been pointed out as a character of prime importance in any orchid breeding programme (McDonald, 1991). Days to first flower opening from inflorescence emergence is primarily decided by the length of inflorescence and its rate of growth (Lekha Rani, 2002). Ninitha Nath (2003) observed that this character was following the same trend as the length of inflorescence in all varieties, while the rate of inflorescence growth did not vary much between varieties. Vegetative growth characters in terms of plant height, number of leaves, and leaf length and width play a key role in ultimately deciding crop yield (Anand *et al.*, 2013). High variability was observed in floral characteristics in the monopodial orchid *Rhynchostylis gigantea* (Anuttato *et al.*, 2017). Heritability determines the degree of resemblance between parents and their offsprings. Heritability estimates along with genetic advance are helpful in predicting the gain under selection than heritability estimates alone (Singh and Chaudhary, 1985). Also while selecting parents for any hybridization programme, the general health and superior vegetative qualities of the plants are of great importance.

Conclusion

It may be concluded from the study that wide range of variability exists amongst the orchid genotypes studied, for most of the biological traits analyzed. Considering

their heritability and genetic advance, the genotypes can be selected and utilized as parents in combination breeding programmes for developing improved cultivars and hybrids.

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