

Genetic, Heritability and Genetic Advance of Progenies Derived from Hybridization of *Vanda* 'Adrienne' × *Ascocenda* 'Peggy Foo' with *Vanda malinii* × *Vanda denisoniana* Benson & Rchb.f. *in vivo*

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Abstract

Hybridization is the process on interbreeding between individuals of different species or genetically divergent individuals from the same species to produce new progenies with their uniqueness and differences, involving in *Vanda*. Aim of this research was to explore genotypic and phenotypic variability, heritability and genetic advance of progenies derived from hybridization of *Vanda* 'Adrienne' × *Ascocenda* 'Peggy Foo' with *Vanda malinii* × *Vanda denisoniana* Benson & Rchb.f, and to find best characters used for selection. The experiment was conducted at Segunung Experimental Garden of Indonesian Ornamental Crop Research Institute (IOCRI) on altitude of 1100 m above sea level from June 2013 until December 2016. Thirteen genotypes derived from hybridization of *V.* 'Adrienne' × *A.* 'Peggy Foo' with *V. malinii* × *V. denisoniana* of 1A, 2A, 21A, 27A, 50A, 52A, 98A, 101A, 102A, 113A, 116A, 120A, and 120B were used in the study. The experiment was arranged in a Randomized Complete Block Design (RCBD) with three replications. Results of the study indicated that range of genetic variability was varied from 1.2-184.7% with wide genetic variability determined on number of leaves per plant (NLP) up to 26.5% with 184.7% for leaf width (LW) and 24.7% for spike length (SL). Moderate heritability of 25.2% for NLP, 21.0% for LW and 25.2% for SL coupled with high genetic advance percent of mean up to 59.7% for NLP, 939.7% for LW and 33% for SL, reflecting the presence and expression of additive gene action of these traits. The results indicated the importance of these three characters best used as selection criteria for *Vanda* genotypes.

Keywords: genetic gain; selection; *Vanda*; variability; quantitative characters

Introduction

Vanda is tropical orchid consisting of more than 70 species of monopodial epiphytic orchids originated from India, China, The Himalayas, Sri Lanka, Philippines and throughout South East Asia (De *et al.*, 2016), though according to Mabberley (2008) the genus only comprises 45 species. In Indonesia, the orchid is widespread in tropical forests at Java, Bali, Sumatra, Kalimantan, Maluku and Papua (Purwanto and Semiarti, 2009). The *Vanda* is one genus of Orchidaceae family members having monopodial growth habit with stems which vary considerably in size from miniature to several meters in length; leaves from flat to typically broad, ovoid (strap-leaves) and cylindrical (terete); few to many flowers develop on the inflorescences

(Tanee *et al.*, 2012). Many species in the genus are important in hybridization and produce important cut flower commercially (Tanee *et al.*, 2012). The genus is also cross compatible with other genera like *Ascocentrum*, *Aerides*, *Ryncostylis*, *Renanthera* and even *Phalaenopsis* (De *et al.*, 2016). Though new commercials and hybrids on cut flowers of the *Vanda* were successfully developed and grown in Thailand, Singapore, Malaysia and Hawaii, in Indonesia developing the new commercial hybrids for cut flowers are rarely carried out.

Orchids, involving *Vanda*, are highly priced in the international market due to their designed spectacular flowers, brilliant colors, delightful appearance, myriad sizes, shapes, forms, and long-lasting qualities. To improve the orchid genotypes, produce invaluable, commercial and high

economical prices of them, classical approaches via sexual crossing or hybridization are generally applied to produce variation, followed by selecting the variation and stabilizing and multiplying the desired types (Caligari, 2001). The hybridization is one of breeding methods having high significant effect on increasing number of new hybrid varieties, involving in the orchids. Furthermore, the effect is mainly supported by high chances of intergeneric crosses occurred involving two genera (bi-generic), three genera (tri-generic), four genera (tetra-generic), five genera (penta-generic) and six genera (hexa-generic); and now large number of hybrids are registered and listed (De and Bhattacharjee, 2011).

Hybridization of orchids in conjunction to produce new hybrids that transmit desirable characters to them was successfully applied on *Cattleya*, *Cymbidium*, *Dendrobium*, *Odontoglossum*, *Oncidium*, *Paphiopedilum*, *Phalaenopsis*, and *Vanda* (Griesbach, 2002; De and Bhattacharjee, 2011; Teixeira da Silva, 2012; De et al., 2016; Dalstrom and Higgins, 2017; Dehgahi and Joniyas, 2017). For *Vanda*, especially, strap-leaf *Vandas* were first bred with colorful tropical plants to produce hybrids. *Vanda* 'Tatzeri', the hybrid of *Vanda tricolor* and *V. sanderiana*, was registered by the Prague Botanical Gardens in 1919. This cross possesses true hybrid vigor and is an example of the floriferousness that made *Vanda* hybrids desirable (Motes, 1988). From the previous works, significant breeding progresses on *Vanda* were reported and now, new and modern hybrids of *Vanda* such as *Vanda* John DeBiase 'Fuchs' Indigo, *Vandaenopsis* 'Irene Dobkin', *Vanda* Michael's Delight 'Mike' HCC, *Vandachostylis* Charm 'Blue Star' HCC, *Renantanda* How Yin Mun 'Flame Burst' AM, *Mokara* 'Razzmatazz', *Joannara* Scarlet Queen 'Chile Pepper' AM, *Paravanda* Paracentrum Redland Stardust 'Crownfox' HCC, *Vandachostylis* Ladda Gold 'Miramar' HCC, *Vandachostylis* Colmarie 'Sanctuary's Midnight' AM, *Holttumara* Crownfox Speckled Spider 'Crownfox', HCC, etc. were successfully established and registered (American Orchid Society, 2018). These hybrids were derived from bi, tri, tetra, penta and hexa-generic hybrids (Lee et al., 1996; Motes 2000; De and Bhattacharjee, 2011; De et al., 2016; American Orchid Society, 2018).

In the research, unique and interesting progenies derived from tetra-generic hybrids of *V. 'Adrienne' x A. 'Peggy Foo'* with *V. malinii x V. denisoniana* were successfully explored and revealed based on their genetic variability, heritability and genetic advance. Results of the study were evidence that breeding activities of *Vanda* in Indonesia successfully produced new hybrids that can be developed commercially for farmers and growers. New findings in the research were discussed in detail in this paper.

Materials and Methods

Experimental materials and their maintenance

Materials used in the study were thirteen genotypes of *Vanda* derived from hybridization of *V. 'Adrienne' x A. 'Peggy Foo'* (Accession number of IOC01080644) with *V. malinii x V. denisoniana* (Accession number of

IOC01080718). Both were orchid germplasm collections of Indonesian Ornamental Crop Research Institute (IOCRI), Segunung, Pacet, Cianjur, and West Java Indonesia. The thirteen genotypes were 1A, 2A, 21A, 27A, 50A, 52A, 98A, 101A, 102A, 113A, 116A, 120A, and 120B (Fig. 1).

All *Vanda* plants both parental and progenies were maintained optimally under plastic house in hanging pot individually. These plants were watered thrice a week sufficiently and fertilized using combination of Growmore in high nitrogen (32N-10P-10K) and high phosphor and potassium (6N-30P-30K) once a week in 2 g/l dosage each and applied in the morning by spraying their leaves. The plants were also sprayed by a mixture solution of insecticide and fungicide once a week in suggested-dosages. Insecticide used was chlorpirifos 200 g/l; while fungicide was difenokonazole 250 g/l, mancozeb 80% and thiamethoxam 25%.

Treatment and experimental design

In the experiment, thirteen genotypes of 1A, 2A, 21A, 27A, 50A, 52A, 98A, 101A, 102A, 113A, 116A, 120A, and 120B were studied their vegetative and generative characters. The experiment was arranged in a randomized complete block design (RCBD) with three replications. Each treatment was consisted of one plant that was observed its flowers in three flower periods.

Vegetative and generative characters recorded

Variables observed in the study were vegetative and generative characters i.e. plant height (PH, cm), number of leaves per plant (NLP), leaf length (LL, cm), leaf width (LW, cm), spike length (SL, cm), number of flowers per spike, rachis length (RL, cm), flower stalk length (FSL, cm), flower length (FL, cm), flower width (FW, cm). Observation and data collection were carried out when the plants were ± 4 years after acclimatization. The observation was conducted every 4 to 6 months depending on flower immersion period for three years.

Analysis of data

All plants used in this experiment were observed and measured during three times of flowering period. Collected data from each character in the study were subjected to analysis of variance (ANOVA) using Statistical Analysis System (SAS) Release Windows 9.2 (SAS, 2008). If there were significant differences between means, the mean values were further analysed using Tukey test, $p=0.05$ (Mattjik and Sumertajaya, 2006). The statistical data derived from the first analysis was also further analysed using Microsoft Excel to estimate genetic variability, heritability and genetic advance.

Estimation of variance components

Components of variance, σ^2_g =genotypic variance, σ^2_p = phenotypic variance and σ^2_e =error variances were calculated as suggested by Allard (1960):

Environmental variance (σ^2_e) = MSE/r. Where, MSE=error mean square and r=number of replication.

Phenotypic variance (σ^2_p) = MSt/r. Where, σ^2_p =phenotypic variance, MSt = treatment mean square and r=number of replication.



Fig. 1. Male and female parental plants and thirteen progenies derived from hybridization of *V.* 'Adrienne' \times *A.* 'Peggy Foo' with *V. malinii* \times *V. denisoniana* tested in the study A. Female parental plant of *V.* 'Adrienne' \times *A.* 'Peggy Foo', B. Male parental plant of *V. malinii* \times *V. denisoniana*, C. 1A genotype, D. 2A genotype, E. 21A genotype, F. 27A genotype, G. 50A genotype, H. 52A genotype, I. 98A genotype, J. 101A genotype, K. 102A genotype, L. 113A genotype, M. 116A genotype, N. 120A genotype and O. 120B genotype

Genotypic variance (σ_g^2) = (MSt-MSe)/r, where, σ_g^2 =genotypic variance; MSt= treatment mean square; MSE=error mean square and r=number of replication.

Phenotypic coefficient of variation:

$$(PCV) = [(\sigma_p^2)^{1/2} / \bar{X}] \times 100$$

Genotypic coefficient of variation:

$$(GCV) = [(\sigma_g^2)^{1/2} / \bar{X}] \times 100$$

where, σ_p^2 = phenotypic variance, σ_g^2 =genotypic variance and \bar{X} is grand mean of character (Sivasubramanian and Menon, 1973). GCV and PCV values were categorized as low (0-10%), moderate (10-20%) and high (20% and above).

Standard deviation of genotypic and phenotypic variance was determined by equation (Hallauer et al., 2010):

$$\sigma_{\sigma_g^2} = \sqrt{\frac{2}{r^2} \left\{ \frac{MS_E^2}{df_E + 2} + \frac{MS_g^2}{df_g + 2} \right\}} \quad \text{and}$$

$$\sigma_{\sigma_p^2} = \sqrt{\frac{2}{r^2} \left\{ \frac{MS_E^2}{df_E + 2} \right\}}$$

Where, $\sigma_{\sigma_g^2}$ = standard deviation of genotype variance; $\sigma_{\sigma_p^2}$ = standard deviation of phenotype variance; r = number of replication; MS_p = treatment mean square; MSE = error mean square; df_g = degree of freedom of genotype (p-1); df_e = degree of freedom of error p(r-1).

Estimation of heritability in broad sense

Broad sense heritability (H^2_{bs}) of the all traits was calculated according to the formula (Allard, 1960):

$$(H^2_{bs}) = [(\sigma_g^2) / (\sigma_p^2)] \times 100$$

where: h^2_{bs} = heritability in broad sense; σ_g^2 = genotypic variance; σ_p^2 = phenotypic variance. Criteria of heritability was: $H^2_{bs} > 50\%$ = high, $20\% \leq H^2_{bs} \leq 50\%$ = moderate, $H^2_{bs} < 20\%$ = low.

Estimation of genetic advance

Estimation of genetic advance (GA) was calculated using equation as described by Johnson et al. (1955): GA = K (σ_p) h^2 . Where, K = selection differential (k=2, 06 at 5% selection intensity), σ_p = the phenotypic standard deviation of the character and h^2 = broad sense heritability.

The genetic advance as percentage of mean (GAM) was also calculated using formula as described by Johnson et al. (1955):

$$GAM = (GA/x) \times 100\%,$$

where, GAM = genetic advance as percentage of mean; GA = genetic advance; and x = grand mean of a character. Criteria of GAM as follow: 0-10% = low; 10-20% = moderate; > 20% = high (Johnson et al., 1955; Falconer and Mackay, 1996).

Results and Discussion

Vegetative and generative growth performances

In the research, it was successfully revealed that thirteen genotypes studied indicated different growth performances vegetative and generatively. Thirteen genotypes derived from the conventional hybridization of *V. 'Adrienne' x A. 'Peggy Foo'* with *V. malinii x V. denisoniana* indicated variability in all characters observed statistically both $p=0.01$ and $p=0.05$, respectively. Very significant effects on the variability were noted on height of plants, number of leaves per plant, leaf length, leaf width, spike length and flower width; while significant effects were recorded on number of flowers per spike, rachis length, flower stalk length and flower length. Genotype of 102A had bigger flowers with the longest flower stalk length. The genotype had 5.3 cm flower length and 5.7 cm flower diameter (Table 1). The highest plant performances were noted in 98A genotype. The performance had high correlation to number of leaves per plant, leaf length and width, spike length, number flowers per spike and rachis length. The genotype produced 19.7 leaves per plant, 29.3 cm leaf length, 2.72 cm, 10 cm spike length, 6 flowers per spike, 6.3 cm rachis length and 4.7 cm flower stalk length (Table 1). The results strengthened previous studies that the conventional hybridization method stimulated variability in each offspring produced. The variability was presumably affected not only by genetic effect but also by environmental growth condition.

Table 1. Vegetative and generative variables from 13 genotypes derived from conventional hybridization of *V. 'Adrienne' x A. 'Peggy Foo'* with *V. malinii x V. denisoniana*

Genotype	HP (cm)	NLP	LL (cm)	LW (cm)	SL (cm)	NFS	RL (cm)	FSL (cm)	FL (cm)	FW (cm)
1A	12.0	14.0 bcd	25.2 ab	2.4 b	8.2 ab	4.7 ab	4.9 abc	4.9 ab	5.0 ab	5.3 a
2A	7.4 b	11.0 cde	17.6 bc	1.7 b	6.4 bc	2.3 b	1.5 d	4.6 b	4.7 ab	4.9 ab
21A	13.0 ab	14.7 bc	22.0 abc	2.3 b	6.8 abc	2.3 b	2.0 cd	4.9 ab	5.0 ab	5.2 ab
27A	13.0 ab	10.3 de	25.7 ab	1.8 b	5.4 bc	5.0 ab	5.1 abc	4.1 b	4.0 b	4.2 b
50A	9.8 ab	15.3 b	27.5 ab	1.8 b	10.0 a	4.0 ab	5.8 a	6.0 a	4.8 ab	4.7 ab
52A	7.2 b	10.7 cde	18.1 bc	1.9 b	3.8 c	3.0 ab	2.2 bcd	5.0 ab	4.6 ab	5.1 ab
98A	18.0 a	19.7 a	29.3 a	2.7 a	10.0 a	6.0 a	6.3 a	4.7 b	5.1 ab	5.5 a
101A	7.0 b	7.7 e	13.6 c	2.0 b	5.3 bc	3.7 ab	3.5abcd	3.9 b	4.9 ab	4.9 ab
102A	11.0 ab	15.3 b	25.4 ab	2.3 b	7.2 abc	3.3 ab	3.9abcd	6.0 a	5.3 a	5.7 a
113A	9.8 ab	8.7 e	19.8 abc	2.1 b	5.1 bc	2.7 ab	1.8 d	4.6 b	5.0 ab	5.1 ab
116A	6.9 b	8.7 e	23.1 abc	1.9 b	8.4 ab	3.7 ab	3.6abcd	4.6 b	4.7 ab	5.0 ab
120A	9.3 ab	10.7 cde	24.0 abc	2.0 b	6.8 abc	4.7 ab	5.0 abc	4.6 b	5.2 a	5.4 a
120B	7.4 b	10.3 de	21.5 abc	2.0 b	6.9 abc	3.7 ab	3.5abcd	5.1 ab	5.3 a	5.7 a
CV %	13.53	18.40	16.04	10.44	17.28	14.24	16.67	13.81	9.29	7.16

Note : Means followed by the same letter in the same column are not significantly different based on Tukey test, $p=0.05$. HP=height of plant (cm), NLP=number of leaves per plant, LL=leaf length (cm), LW=leaf width (cm), SL=spike length (cm), NFS= number of flowers per spike; RL=rachis length (cm), FSL=flower stalk length (cm), FL=flower length (cm), FW=flower width (cm)

Genetic variability

Based on data analysis, it was clearly revealed that there were several characters with wide variability both phenotypically and genetically. Though wide phenotypic variances were noted on number of leaves per plant (NLP), leaf width (LW), spike length (SL), rachis length (RL), and flower stem length (FSL) with 52.7, 405.0, 49.3, 23.6 and 25.9% respectively; however wide genetic variances were only determined on NLP up to 26.5% GCV with 184.7% for LW and 24.7% for SL (Table 2). Other characters showed narrow to moderate differences. In the study, it was also revealed that wide genetic ranges as recorded at RL and FSL did not always follow wide phenotypic variability. Inversely, the wide genetic variances were always followed by higher phenotypic variability that was noted on NLP, LW and SL.

Heritability and genetic advance

Results of the study indicated that from 10 characters investigated; only NLP, LW and SL had wide genetic variability (Table 2). The characters exhibited moderate in heritability with 25.2, 20.8 and 25.2%, respectively (Table 3), but they induced high genetic advance in percent of mean up to 59.7% for NLP, 939.7% for LW and 33% for SL (Table 3). Though leaf length (LL) and flower width (FW) also had moderate heritability, the character stimulated low genetic advance in percent of mean. These

data indicated that effect of additive gen caused moderate heritability and the high genetic advance in percent of mean leading to the existence of wide genetic variability. Therefore, the NLP, LW and SL characters were the importance characters as selection criteria on breeding program of other Vanda genotypes.

Entirely, from the study, several new findings and evident were successfully revealed under hybridization method, where the results can strengthen all previous results in the similar works. The hybridization, relatively common and easily done, allows combining several genera and generating interspecific, intragenic and intergeneric hybrids (Neto *et al.*, 2011). Each off spring produced from the method is always different from one to another vegetative and generatively in varied ranges. In the study, ten characters observed on thirteen genotypes, wide phenotypic and genotypic variabilities were noted on number of leaves per plant, leaf width, spike length, rachis length and flower stalk length (Table 1). In other studies, Klier *et al.* (1991) reported variation White and Yellow Lady slipper orchids in 23 characters from slipper colour to staminode length and width with high variation on plant height and leaf length. Variation of sixteen characters from plant height to speculum was recorded on a new hybrid of *Ophrys* × *circularium* with high differences in plant height, lip shape and lip length (Pellegrino *et al.*, 2008), variability of 15 characters from plant height to root thickness was reported

Table 2. Genotypic (GCV) and phenotypic (PCV) variabilities and their criteria of 13 genotypes derived from conventional hybridization of *V. Adrienne* × *A. Peggy Foo* with *V. malinii* × *V. denisoniana*

Character	σ^2_g	$\sigma^2_{g_s}$	GCV (%)	GCV criteria	σ^2_p	$\sigma^2_{p_s}$	PCV (%)	PCV criteria
HP (cm)	0.15	0.17	3.8	Narrow	0.84	0.16	9.1	Narrow
NLP	10.28	9.06	26.5	Wide	40.73	9.02	52.7	Wide
LL (cm)	0.07	0.07	1.2	Narrow	0.31	0.07	2.5	Narrow
LW (cm)	14.48	14.45	184.7	Wide	69.59	14.24	405.0	Wide
SL (cm)	3.00	2.65	24.7	Wide	11.90	2.63	49.3	Wide
RL (cm)	0.13	0.15	9.3	Narrow	0.80	0.15	23.6	Wide
NFS	0.01	0.01	2.0	Narrow	0.04	0.01	5.5	Narrow
FSL (cm)	0.24	0.30	9.9	Narrow	1.61	0.29	25.9	Wide
FL (cm)	0.06	0.09	5.1	Narrow	0.52	0.09	14.4	Moderate
FW (cm)	0.14	0.14	7.3	Narrow	0.69	0.14	16.2	Moderate

Note: σ^2_g = genotypic variance, $\sigma^2_{g_s}$ = standard deviation of genotypic variance, GCV = genotypic coefficient variance, σ^2_p = phenotypic variance, $\sigma^2_{p_s}$ = standard deviation of phenotypic variance, PCV = phenotypic coefficient variance. HP=height of plant (cm), NLP=number of leaves per plant, LL=leaf length (cm), LW=leaf width (cm), SL=spike length (cm), NF= number of flower per spike; RL=rachis length (cm), FSL=flower stalk length (cm), FL=flower length (cm), FW=flower width (cm)

Table 3. Heritability estimation value and genetic advance of 13 genotypes derived from conventional hybridization of *V. Adrienne* × *A. Peggy Foo* with *V. Malinii* × *V. denisoniana*

Character	Heritability estimation value			Criteria of H^2_{bs}	GAM (%)	GAM criteria
	σ^2_g	σ^2_p	H^2_{bs} (%)			
HP (cm)	0.15	0.84	17.8	Low	0.73	Low
NLP	10.28	40.73	25.2	Moderate	59.67	high
LL (cm)	0.07	0.31	22.9	Moderate	0.30	Low
LW (cm)	14.48	69.59	20.8	Moderate	939.7	high
SL (cm)	3.00	11.90	25.2	Moderate	33.0	high
RL (cm)	0.13	0.80	15.6	Low	1.16	Low
NFS	0.01	0.04	13.8	Low	0.08	Low
FSL (cm)	0.24	1.61	14.7	Low	5.47	Low
FL (cm)	0.06	0.52	12.6	Low	2.47	Low
FW (cm)	0.14	0.69	20.3	Moderate	5.57	Low

Note: HP=height of plant (cm), NLP=number of leaves per plant, LL=leaf length (cm), LW=leaf width (cm), SL=spike length (cm), NF= number of flower per spike; RL=rachis length (cm), FSL=flower stalk length (cm), FL=flower length (cm), FW=flower width (cm)

on *Dendrobium* with high range measurement values on plant height, spike length, flower durability, and root length (Moniruzzaman *et al.*, 2012), differences of 15 characters from plant length to spike length were noted on fourteen terrestrial orchids and high variation was recorded on leaf length and number of flowers (Erzurumlu *et al.*, 2017), 8 variables from plant to lip performances were determined on Lady's Slipper orchid with high variation on plant height and inflorescence length (Szlachetko *et al.*, 2017). According to Poehlman and Sleper (1995) variability of plant characters was significantly affected by plant genetic and its environmental growth condition. The high variation of plant traits was generally induced by (1) breakdown in reproductive isolation mechanisms, (2) genetic drift (relaxed selection) and (3) natural selection (Ackerman *et al.*, 2011).

Genetic variability is the ability, i.e. capability of a biological system, individual and population that is changing over time. The variability of a trait describes how much that trait tends to vary in response to environmental and genetic influences. In *Cattleya intermedia*, the genetic variability available within this species was high enough to allow genetic progress in flower shape and size characters (Neto *et al.*, 2011). Coefficient variability of 15 characters on *Dendrobium* was varied from 23.74% for plant height, 17.50% for leaf length, 16.95% for leaf breadth, 28% for no of pseudobulb per plant, 27.33% for diameter of pseudobulb, 26.58% for no. of spike/plant, 28.20% for No. of flower per spike, 38.00% for spike length, 35.59% rachis length, 25.00% for flower size, 31.34% for flower durability, 21.58% for pod size, 22.00% for root number, 32.00% for root length, and 15.00% for root thickness (Moniruzzaman *et al.*, 2012); 67.77% for plant height, 64.36% for leaf area, 30.41% for spikes per plant, 24.51% for spike length, 48.86% for flower weight, 40.47% for roots per plant, 37.19% for root length, 25.15% for horizontal spread of flower, 35.90% for vertical spread of flower and 46.30% for flowers per plant on several orchids (Miano *et al.*, 2016). In the study from ten characters observed, wide genetic variability was determined on number of leaves per plant (NLP) up to 26.5% with 184.7% for leaf width (LW) and 24.7% for inflorescence stem length (ISL). The results were lower than other studies reported previously.

In non-orchid plants, 20 characters of *Chrysanthemum* were analyzed and their genetic variability were varied from 11.97 - 90.13% with high value noted on number of suckers per plant (90.13%), flower disc diameter (63.19%) and number of flower per plant (52.27%) (Baskaran *et al.*, 2009); 12 variables of *Polianthes tuberosa* had genetic variability from 1.49 - 24.38% with the highest value noted on number of florets per spike (24.38%) (Ranchana *et al.*, 2013), 14 variables of *Gladiolus* with 8.8 to 70.56% genetic variability with high values recorded on number cormels per plant (70.56%) and weight of cormels per plant (57.11) (Mishra *et al.*, 2014); 28 variables of *Anthurium* with 0.36 - 7.36% genetic variability (Tamuli *et al.*, 2015). In the above studies, wide genetic variability was also noted in 1-3 characters as determined in the study.

Success of genetic advance under selection depends on three factors, i.e. genetic variability, heritability and selection intensity (Allard, 1960). In the study, high genetic

variability recorded on inflorescence stalk length up to 33.0%, 59.7% on number of leaf per plant and 939.7% for leaf width, unfortunately, was not followed by high heritability of them. The characters had moderate heritability of 0.3, 0.2 and 0.3, respectively. The characters can be applied for selection characters for other *Vanda* genotypes. In other orchid studies, fifteen characters of *Dendrobium* dominantly had high genotypic variations that were also followed by high heritability and genetic advance, primarily, on plant height, number of pseudobulb/plant, diameter of pseudobulb, number of spikes/plant, number of flowers/spike, spike length, rachis length, flower size, flower durability, pod size, root number, and root length (Moniruzzaman *et al.*, 2012). In the study, rachis length, durability of flower and number of flowers per spike had contributed maximum direct effects on flower yield and these three characters can be used as selection criteria for other native *Dendrobium* orchids. High genetic variability in plant height (66.7%), leaf area (64.4%), spikes/plant (30.4%), spike length (24.5%), flower weight (48.9%), roots/plant (40.5%), root length (37.2%), horizontal spread of flower (25.2%), vertical spread of flower (35.9%) and flowers/plant (46.3%) was followed by high heritability from 88.1-100% and high genetic advance from 49.3-138.3% (Miano *et al.*, 2016). In the research, ten characters can be applied as selection criteria among orchids.

In *Chrysanthemum*, high genetic variability, heritability and genetic advance were recorded in most of characters, however only number of suckers per plant, flower disc diameter, number of flowers per plant, flower weight, yield per plant and number of ray florets could be exploited for improvement the crop in breeding program (Baskaran *et al.*, 2009). High genetic variability, heritability and genetic advance were clearly observed on number of florets per spike, number of spikes/m², rachis length and yield of florets per plot (2×2 m) (Ranchana *et al.*, 2013). High genotypic coefficient of variance was noted on diameter of neck and vase life, however high heritability in associated with high genetic advance percentage of mean was determined on vase life of flower (Kumar, 2014), high genetic advance in percentage of mean coupled with high heritability on gladiolus was recorded on number of sprouts, number of spikes per plant, length of spike, vase life, weight of corms per plant, weight of cormels per plant, number of corms per plant, number of cormels per plant (Mishra *et al.*, 2014). High genetic variance, heritability coupled with high genetic advance had been exhibited by leaf area, number of suckers, plant height, plant spread, increase in spathe size at third (3rd) day after harvest, water uptake at third (3rd) day after harvest and at senescence, fresh weight of the cut flower at senescence, total chlorophyll and anthocyanin content in spathe and its ratio provide greater scope for further improvement of these traits in advance generations (Tamuli *et al.*, 2015).

Conclusions

Exploring genetic and phenotypic variability on *Vanda* clones derived hybridization of *Vanda* Adrienne x *Ascocenda* Peggy Foo with *Vanda* Malinii x *Vanda* *denisoniana* was carried out to determine the more variable

characters, which might be useful in improving Vanda breeding program. This study has shown that high genotypic, heritability and genetic advance were significantly noted on number of leaves per plant, leaf length and spike length. Therefore, these three characters can be used as selection criteria of the orchid genotypes.

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Conflicts of interest

The authors declare that there are no conflicts of interest related to this article.

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