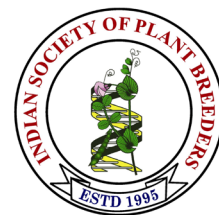


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Research Note

Genetic variability in Mysuru jasmine (*Mysuru mallige*) : A GI crop of Mysuru

S. C. Venkatesha^{1*}, K. N. Rahul², B. Fakrudin², Mukesh L Chavan³,
H. M. Pallavi¹ and Vikram Appanna¹

¹College of Horticulture, Mysuru, University of Horticultural Sciences, Bagalkot

²Department of Genetics and Plant Breeding, College of Horticulture, Bengaluru

³University of Horticultural Sciences, Bagalkot

*E-Mail: venkateshasc@gmail.com

Abstract

At the college of Horticulture, Mysuru, Karnataka, the study was conducted during 2018 *kharif* using RBD with two replications. Quantitative characters namely petiole length, leaf length, leaf breadth, bud length, bud breadth, flower diameter, flower stalks length or pedicel length, calyx length, the number of sepals/ calyx teeth, the number of whorls, the number of petals, petal length, the number of stamens, length of the anther, length of the filament, length of the style, length of the stigma, length of the corolla tube and flower bud weight were recorded. High (>20%) genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) was observed for bud length, bud breadth, the number of whorls, the number of petals, pedicel length, length of corolla tube, length of filament, length of style, length of stigma and flower bud weight. Moderate (10 to 20%) GCV and PCV were observed for petiole length, leaf length, leaf breadth, flower diameter, calyx length, the number of calyx teeth, petal size and the number of stamen and length of the anther. The phenotypic co-efficient of variation was more than the genotypic co-efficient of variation for all characters studied. The higher (>20%) values of genetic advance over mean (GAM) coupled with very high (>80%) estimates of heritability were observed for characters viz., bud length, bud breadth, flower diameter, calyx length, the number of calyx teeth, the number of whorls, the number of petals, petal size, pedicel length, length of the corolla tube, the number of stamens, length of anther, length of the filament, length of the style, length of the stigma and flower bud weight. Moderate heritability (40-60%) with low GAM was observed for petiole length. The variance due to genotypes was highly significant for all the characters except for length of the leaf.

Keywords: Mysuru mallige, genetic advance heritability, PCV, GCV

Mysuru mallige is the variety of jasmine grown around Mysuru and Srirangapatna taluk of Mandya district in the Southern part of Karnataka, India. Owing to the proximity of all these areas to Mysuru city, the erstwhile kingdom of Mysuru, the name Mysuru mallige (Mysuru jasmine) is prevailing. Mysuru mallige not only has unmatched fragrance but also has an inextricable link with the royal city of Mysuru. The unique characteristics vested with the Mysuru mallige are due to the combinations of

inherent genetic constitution of the local variety and the geographical area where it is grown through possible G × E interactions (Anon., 1959). Heritability denotes the proportion of phenotypic variation due to genotypes and thus it helps the breeders to select the elite variety for a character of interest. The genetic advance predicts the amount of gain expected by imposing a particular intensity of selection. However, high heritability alone is not enough to make an efficient selection, unless the

information is accompanied for a substantial amount of genetic advance. The present investigations were, therefore, undertaken to ascertain the magnitude and extent of variability and heritability for yield and yield components of Mysuru mallige.

At the college of Horticulture, Mysuru, Karnataka the study was conducted during 2018 *Kharif*. This study involved 30 Mysuru jasmine local collections, which were collected from Mysuru and its adjoining districts such as Mandya, Chamarajanagara, Hassan, Ramanagar and Bengaluru rural. The experiment was laid out in a randomized block design and replicated twice at a spacing of 1.2 m between rows and 1.2 m between plants. Observations were recorded for petiole length (mm), leaf length (mm), leaf breadth (mm), bud length (mm), bud breadth (mm), flower diameter (mm), flower stalks length or pedicel length (mm), calyx length (mm), the number of sepals/ calyx teeth, the number of whorls, the number of petals, petal length (mm), petal breadth (mm), the number of stamens, length of the anther (mm), length of the filament (mm), length of the style (mm), length of the stigma (mm), length of the corolla tube (mm) and flower bud weight (g).

Data were recorded on two competitive selected plants in each genotype per replications. Variability among the genotypes was studied using Analysis of Variance (ANOVA) as described by Singh and Narayanan (1993). A Genotypic and Phenotypic coefficient of variation (GCV and PCV) was calculated as suggested by Burton (1952). Broad sense heritability was calculated as suggested by Lush (1940), whereas genetic advance was calculated as suggested by Johnson *et al.* (1955). GA and GAM (Johnson *et al.*, 1955) were classified into three groups: low (0-10%), moderate (10.1-20%), and high (>20%). Robinson *et al.* (1949) classified heritability into three categories: low (0-30%), moderate (30.1-60%), and high (>60%).

ANOVA demonstrated significant variation among genotypes (**Table 1**). Petiole length varied from 2.48 to 5.66 mm, leaf length varied from 37.71 to 90.26 mm, leaf breadth varied from 24.75 to 57.95 mm, bud length varied from 7.49 to 15.50 mm, bud breadth varied from 5.18 to 11.61 mm, flower diameter varied from 15.37 to 46.74 mm, calyx length varied from 4.80 to 9.89 mm, the number of sepals varied from 7.0 to 14.5, the number of whorls varied from 1.0 to 7.0, The number of petals ranged from 7.0 to 50.0, the petal size ranged from 7.90 to 18.61mm, the pedicel length ranged from 3.37 to 14.21 mm, the length of the corolla tube ranged from 5.99 to 21.24 mm, the number of stamens ranged from 2.0 to 3.0, the anther length ranged from 1.9 to 5.09 mm, the filament length ranged from 3.90 to 16.53 mm, the style length ranged 1.81 to 7.20 mm, stigma length ranged from 2.82 to 6.84 mm and flower bud weight ranged from 0.06 g to 0.83 g.

The phenotypic coefficient of variation (PCV) was greater

than the genotypic coefficient of variation (GCV) for all of the characters except for the number of whorls and the number of stamens indicating that the environment has an effect on their expression. GCV values ranged between (12.11) and (73.85) for leaf length and the number of whorls. Bud length, bud breadth, the number of petals, pedicel length, length of corolla tube, length of filament, length of style, length of stigma, and the number of whorls had high PCV and GCV values. High PCV and moderate GCV values were observed for petiole length, leaf length, leaf breadth and flower diameter. This indicated that genotypes possessed a high degree of inherent variability for bud length, bud breadth, the number of petals, pedicel length, length of corolla tube, length of filament, length of style, length of stigma, petiole length, leaf length, leaf breadth, the number of whorls and flower diameter, making them ideal for selection. Earlier reports of Ajay *et al.* (2014) in Pigeonpea corroborate the findings of the present study that high PCV and high/moderate GCV indicate the presence of variability among genotypes and offers scope for further selection. Traits namely calyx length, the number of sepal, the number of petiole, the number of stamen, length of anther had moderate PCV and GCV values indicating that limited scope of selection for these traits.

Unless and until the heritability of phenotypic traits is understood, the genotypic coefficient of variation does not provide a precise indication of the level of genetic advantage to be expected (Narasimhulu *et al.*, 2021). **Table 1** contains estimates of heritability in a broad sense for the nineteen traits examined and it ranged from 24.83 percent for leaf length to 100 percent for the number of whorls. Heritability estimates were higher for all the traits except leaf length and leaf breadth.

Heritability estimates along with genetic gain would be more useful than heritability alone in selecting the best individuals (Johnson *et al.*, 1955). Therefore, it is essential to consider the predicted genetic advance along with heritability estimates as a tool in the selection programme for better efficiency. High heritability accompanied with a high genetic advance indicates that most likely the heritability is due to additive gene effects and selection may be effective. High heritability accompanied with a low genetic advance indicates non-additive gene action and selection for such traits may not be rewarding. Low heritability accompanied with a high genetic advance reveals that the character is governed by additive gene effects. Selection may be effective in such cases. Low heritability accompanied with a low genetic advance indicates that the character is highly influenced by environmental effects and selection would be ineffective. High heritability along with high GAM was recorded by all traits except leaf length and leaf breadth. Similar results were observed by Khan and Muthuswamy (1969), Khan *et al.* (1970), Gobade *et al.* (2017), Priyanka *et al.* (2017) and Tuppada *et al.* (2017) in

Table 1. Estimates of mean, heritability and genetic advance for growth parameters in local collections of Mysuru mallige

S. No.	Characters	Mean \pm SEM	Range		GV	PV	GCV (%)	PCV (%)	h ² (%)	GA	GAM (%)
			Minimum	Maximum							
1	Petiole length (mm)	4.07 \pm 0.50	2.48	5.66	0.49	1.00	17.16	24.47	49.16	1.23	30.27
2	Leaf length (mm)	61.29 \pm 9.12	37.71	90.26	55.06	221.74	12.11	24.29	24.83	8.51	13.88
3	Leaf breadth (mm)	35.95 \pm 4.89	24.75	57.95	22.63	70.56	13.23	23.37	32.07	6.38	17.74
4	Bud length (mm)	10.08 \pm 0.35	7.49	15.50	5.30	5.56	22.84	23.39	95.35	6.47	64.22
5	Bud breadth (mm)	7.54 \pm 0.43	5.18	11.61	2.39	2.77	20.49	22.06	86.23	4.04	53.48
6	Flower diameter (mm)	29.86 \pm 1.16	15.37	46.74	35.15	37.88	19.85	20.61	32.07	16.33	54.70
7	Calyx length (mm)	7.73 \pm 0.39	4.80	9.89	1.54	1.84	16.03	17.56	83.27	3.15	40.78
8	Number of sepal/ calyx teeth	8.03 \pm 0.30	7.00	14.50	1.56	1.75	15.55	16.45	89.34	3.35	41.67
9	Number of whorls	1.76 \pm 0.00	1.00	7.00	1.70	1.70	73.85	73.85	100	3.80	215.15
10	Number of petals	15.75 \pm 0.33	7.00	50.00	90.08	90.29	60.26	60.33	99.75	27.60	175.23
11	Petal size (mm)	13.30 \pm 0.50	7.90	18.61	6.07	6.58	18.52	19.28	92.19	6.75	50.77
12	Pedicle length (mm)	10.23 \pm 0.44	3.37	14.21	5.15	5.55	22.18	23.01	92.90	6.26	61.16
13	Length of corolla tube(mm)	12.16 \pm 0.51	5.99	21.24	7.68	8.22	22.79	23.57	93.47	7.68	63.12
14	Number of stamen	2.10 \pm 0.00	2.00	3.00	0.09	0.09	14.53	14.53	100	0.89	42.33
15	Length of anther(mm)	3.75 \pm 0.13	1.90	5.09	0.31	0.35	14.93	15.78	89.52	1.51	40.07
16	Length of filament(mm)	8.80 \pm 0.32	3.90	16.53	4.80	5.01	24.89	25.43	95.82	6.18	70.23
17	Length of style(mm)	3.62 \pm 0.25	1.81	7.20	0.82	0.95	25.02	26.93	86.32	2.37	65.37
18	Length of stigma(mm)	4.23 \pm 0.18	2.83	6.84	1.16	1.23	25.41	26.12	94.61	3.01	71.03
19	Flower bud weight (g)	0.24 \pm 0.01	0.06	0.83	0.03	0.03	67.39	67.87	99.00	0.48	194.28

Holostemma adakodien for yield and yield attributing characters. Leaf length and leaf breadth which recorded moderate heritability and moderate GAM could be exploited through the manifestation of dominance and epistatic components through heterosis in bhendi (Yassin and Anbu, 1997).

Prevalence of a high degree of additive components of genetic variance for characters, bud length, bud breadth, the number of whorls, the number of petals, pedicel length, length of corolla, length of filament, length of style and length of stigma indicated the possibility of achieving a higher degree of genetic improvement for these traits through selection using the existing germplasm stock.

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