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Assessment of genetic diversity based on cluster and principal component analyses for yield and its contributing characters in Mysuru jasmine (Mysore Mallige)

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Abstract
An experiment was carried out to analyze multivariate analysis based on cluster and principal component (PC) for yield and its eighteen contributing traits in 30 Mysore mallige local collections during 2018-19. The cluster analysis categorized all 30 Mysore mallige into 2 major clusters. Extreme genetic divergence was estimated among clusters. Average intra-cluster distance was found maximum (D^2=1254.18) between cluster 1 and cluster 2. The character flower bud weight (53.10%) contributed maximum to the genetic divergence among the genotypes followed by number of petals (18.85%). Highest cluster mean values length of corolla tube, length of the leaf was found in cluster I followed by cluster II. Principal component analysis revealed that first five principal components (PC1, PC2, PC3, PC4 and PC5) accounted for 83.44% of the total variations with the proportionate contribution values of 40.88%, 18.42%, 10.17% and 8.19% respectively. Promising diverse parents identified based on cluster and PC analyses could be selected for future crop improvement.

Keywords: Mysuru jasmine, cluster, dendrogram, principal component, relative contribution

Introduction
Jasmine blossoms have been in use in India for ceremonial purposes since time immemorial. Fragrance has been appreciated by man from beginning of mankind. Jasmine a champion amongst the most significant blossoming plants broadly developed for their attractive fragrant blossoms and concrete extraction. The blooms of jasmine are utilized for making garlands, decorating hair by women, religious and ceremonial functions, for generation of essential oils and perfumery so they are referred as “King of oils” (Bhattacharjee, 1). Mysore mallige is the variety of jasmine grown around Mysuru and Srirangapatna taluk of Mandya district, Southern zone of Karnataka state in India. Owing to the proximity of all these areas to Mysuru city, the erstwhile kingdom of Mysuru, the name Mysore mallige (*Mysuru jasmine*) is prevailing. Mysore mallige flower involves significant position in the commercial floriculture trade in India.

Multivariate analysis of elite germplasm collections is a prerequisite for choosing promising genetically diverse lines for desirable traits (Mladenovic *et al.*, 2). Genetic diversity analysis is well exploited for transferring desirable genes from diverse genetic stock available in the gene pool for broadening the genetic base in crops with narrow genetic base (Haussmann *et al*., 3). Cluster analysis and PC (principal component) analysis are the important genetic diversity measuring tools employed for exhibiting relative genetic differences among the genotype collection of various crop species. However, this crop has got little consideration in the field of genetic improvement. In view of this, the present study was conducted to classify a set of Mysore mallige local collections based on multivariate analysis that may be used for selection of elite genotype.

Material and Methods
The current study was performed to assess multivariate analysis during 2018-19 to evaluate 30 Mysore mallige local collections at College of Horticulture, Mysuru (Karnataka, India)

The experimental field is located at the latitude and longitude of 12°18[11] north and 74.65° 10[11] east respectively at an altitude of 770 meters above mean sea level. The soil type of experimental site was sandy loam. The genotypes under present study were collected from the adjoining districts of old Mysuru region (Table 1). The experiment was conducted in randomized complete block design with two replications to assess the performance of 30 Mysore mallige local collections. The crop was planted in 1.2 m long row, spaced 1.2 m apart. All the recommended agronomic package and practices and protective measures were followed to raise a good crop. Data were recorded for yield and its eighteen contributing traits in Mysore mallige *viz.*, 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), Number of sepal/ calyx teeth, Number of whorls, Number of petals, Petal Length (mm), Petal breadth (mm), Number of stamen, 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 from each local collection was averaged replication wise and mean data was used for statistical analysis. Cluster and PC analysis of 30 Mysore mallige local collections based on yield and its eighteen component traits to assess the magnitude of genetic variation was performed by using statistical software Windostat version 9.3 from Indostat services. Clustering pattern among 30 Mysore mallige local collections exhibiting dendrogram was assessed by using Tocher's method (Table 2, Fig. 1). Average intra- (diagonal) and inter-cluster distance was estimated by using Tocher's method representing Euclidean^2 distances considering yield and its eighteen contributing traits in Mysore mallige local collections (Table 3). Cluster mean value and its deviation from grand mean value for each corresponding contributing traits has been represented in Table 4.

Results and Discussion

The 30 Mysore mallige local collections were categorized into two distinct clusters using Tocher's method (Fig. 1) and their Euclidean^2 distance using D^2 - statistics depicted in Table 3. The Tocher's method of cluster analysis categorized the 30 local collections of Mysore mallige into 2 clusters. 29 genotypes were grouped into Cluster I accounting for 96.66 per cent of the total genotypes. Cluster II had 1 genotype which accounted for 3.33 per cent of the total genotypes. Mysore mallige with 1, 2, 3 and 5 whorls were found in cluster I. whereas, remaining 7 whorls were grouped in cluster II. Present findings in grouping could clearly establish the distinctness of genotypes from morphological traits. Cluster I having 29 genotypes, further clustered in to two sub cluster. First sub cluster was formed at 3.0 euclidean distances for the genotype COHM-UHSB-22. Second sub cluster was formed at 2.0 euclidean distance for the genotype COHM-UHSB-19, COHM-UHSB-17, COHM-UHSB-16, COHM-UHSB-15, COHM-UHSB-18, COHM-UHSB-3, COHM-UHSB-24, COHM-UHSB-20, COHM-UHSB-8, COHM- UHSB-29, COHM-UHSB-21, COHM-UHSB-28, COHM-UHSB-30, COHM-UHSB-14, COHM-UHSB-23, COHM-UHSB-2, COHM-UHSB-13, COHM-UHSB-4, COHM-UHSB-12, COHM-UHSB-26, COHM-UHSB-11, COHM-UHSB-27, COHM-UHSB-1, COHM-UHSB-10, COHM-UHSB-5, COHM-UHSB-7 and COHM-UHSB-6 genotypes. Intra cluster D^2 values ranged from 0.000 to 1254.18. Among the 2 clusters, cluster 1 with twenty nine genotypes showed maximum intra-cluster distance (D^2=1254.18) followed by cluster 2 with one genotypes (COHM-UHSB-25). Similar results were reported by earlier workers, for length of bud and breadth of leaf in Sugarcane (Arrey *et al.*, 4).

In genetic diversity studies using morphological traits, the most important variables describing phenotypic variation are defined by principal component (PC) analysis. Diversity studies using principal component analysis carried out in Mysore mallige prioritize the most essential traits which explain the variability among the studied accessions. Principal component analysis grouped the 19 quantitative traits into 6 components. The first 5 components, with eigen values higher than 1.0, accounted for 83.44 per cent of the total variance in which PC 1 explained 40.88 per cent (Table 5) of the total variation, PC 2 accounted for 18.42 per cent of the total variation, the PC 3 explained 10.17 per cent of the total variation, PC 4 showed 8.19 per cent of the total variation and the PC 5 accounted for 5.78 per cent of the total variation. The PC analysis in this study showed that 83.44% of the total genetic variance encountered among the Mysore mallige local collections was accounted for by the first five principal components considering all the 19 traits studied.

Based on eigen vectors with values greater than or equal to 0.50, traits such as breadth of the bud, petal size were associated with PC 3, length of the bud was major discriminatory characters associated with PC 4 while the PC 5 was dominated by the number of calyx teeth and calyx length. In the present study, it can be deduced that length of the bud, breadth of the bud, number of calyx teeth, calyx teeth, petal size and number of stamen the most important traits which accounted for much of the variability among the Mysore mallige local collections. These findings agree with the results obtained by Sarma, 5 and champa, 6.

The present study found that out of the eighteen yield and its contributing traits, eighteen major traits contributed 100 per cent towards genetic divergence. Out of eighteen major traits, proportionate contribution of flower bud weight (g) and number of petals towards genetic divergence were found 53 and 18 per cent respectively (Table 6).

For future experiment, traits contributing maximum to genetic diversity such as flower bud weight and number of petals should be given top priority as selection parameters and diverse genotypes identified in the present study may be utilized crop improvement.

Table 1: Place of local collections of Mysore mallige

Sl. No.	Place	Germplasm	Genotype code
1	Kadanakuppe, Ramanagara TQ, Ramanagara	*J. sambac*	COHM-UHSB-1
2	Hallikere, Maddur TQ, Mandya	*J. sambac*	COHM-UHSB-2
3	Malavalli, Malavalli TQ, Mandya	*J. sambac*	COHM-UHSB-3
4	Chandagalu, Mandya TQ, Mandya	*J. sambac*	COHM-UHSB-4
5	Nanjangudu, Nanjangudu TQ, Chamarajanagara	*J. sambac*	COHM-UHSB-5
6	Vijayanagara, Mysuru TQ, Mysuru	*J. sambac*	COHM-UHSB-6
7	Bannuru, T-Narasipura TQ, Mysuru	*J. sambac*	COHM-UHSB-7

8	Saraswatipuram, Mysuru TQ, Mysuru	*J. sambac*	COHM-UHSB-8
9	Arasikere, Arasikere TQ, Hassan	*J. sambac*	COHM-UHSB-9
10	T-Bekuppe, Kanakapura TQ, Ramanagara	*J. sambac*	COHM-UHSB-10
11	DMG Halli, Mysuru TQ, Mysuru	*J. sambac*	COHM-UHSB-11
12	Madegowdanadoddi, Channapatna TQ, Ramanagara	*J. sambac*	COHM-UHSB-12
13	Deshahalli, Maddur TQ, Mandya	*J. sambac*	COHM-UHSB-13
14	Yelwala, Mysuru TQ, Mysuru	*J. sambac*	COHM-UHSB-14
15	Chamarajanagara, Chamarajanagara TQ & Dist	*J. sambac*	COHM-UHSB-15
16	Hinkal, Mysuru TQ, Mysuru	*J. sambac*	COHM-UHSB-16
17	Hinkal, Mysuru TQ, Mysuru	*J. sambac*	COHM-UHSB-17
18	Bogadhi, Mysuru TQ, Mysuru	*J. sambac*	COHM-UHSB-18
19	Bogadhi, Mysuru TQ, Mysuru	*J. sambac*	COHM-UHSB-19
20	Maddur, Maddur TQ, Mandya	*J. sambac*	COHM-UHSB-20
21	Bogadhi, Mysuru TQ, Mysuru	*J. sambac*	COHM-UHSB-21
22	Srirangapatna, Srirangapatna TQ, Mandya	*J. sambac*	COHM-UHSB-22
23	Srirampura, K.R.Nagar TQ, Mysuru	*J. sambac*	COHM-UHSB-23
24	Srirangapatna, Srirangapatna TQ, Mandya	*J. sambac*	COHM-UHSB-24
25	Pandavapura, Pandavapura TQ, Mandya	*J. sambac*	COHM-UHSB-25
26	Sugganahalli, Ramanagara TQ, Ramanagara	*J. sambac*	COHM-UHSB-26
27	Pandavapura, Pandavapura TQ, Mandya	*J. sambac*	COHM-UHSB-27
28	Periyapatna, Periyapatna TQ, Mysuru	*J. sambac*	COHM-UHSB-28
29	Veerengere, Mysuru TQ, Mysuru	*J. sambac*	COHM-UHSB-29
30	Veerengere, Mysuru TQ, Mysuru	*J. sambac*	COHM-UHSB-30

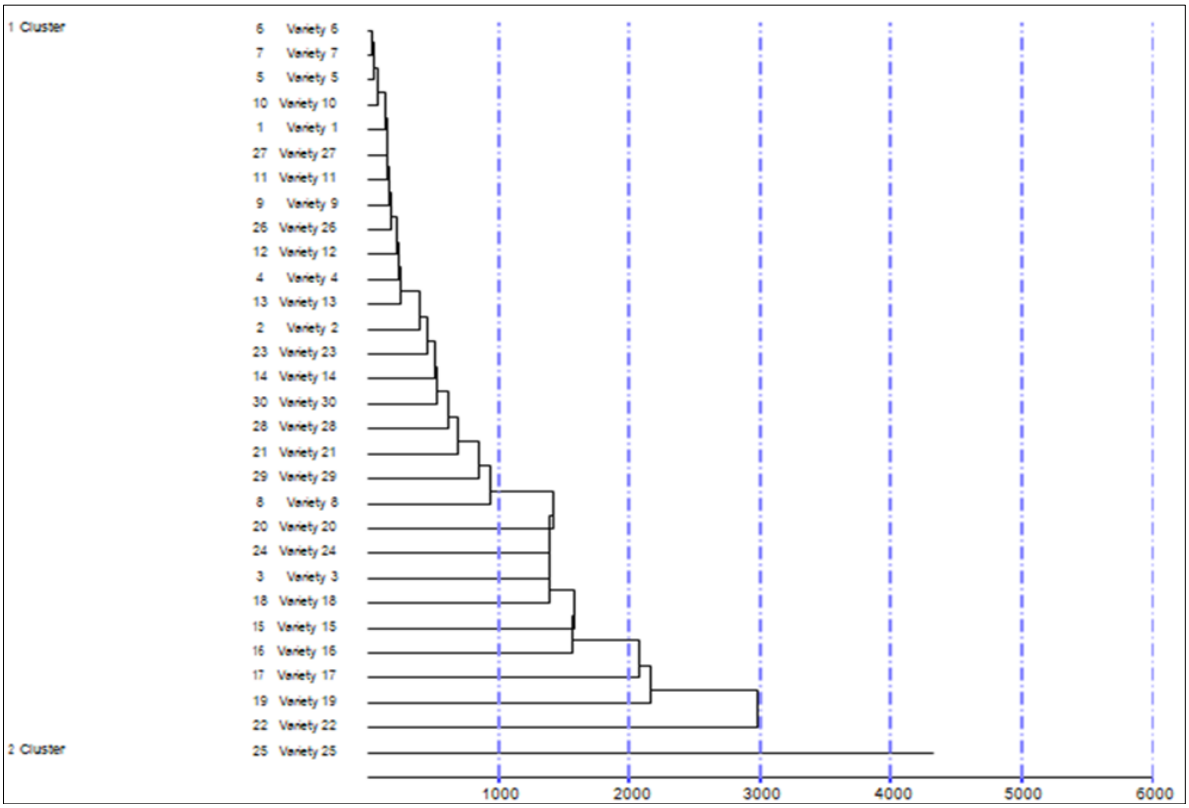

Fig 1: Clustering by Tocher's method showing the relationship and diversity among the 30 local collections of Mysore mallige

Table 2: Clustering pattern of 30 local collections of Mysore mallige based on D^2 values values

Cluster number	Number of genotypes	Genotypes included
I	29	COHM-UHSB-1, COHM-UHSB-2, COHM-UHSB-3, COHM-UHSB-4, COHM-UHSB-5, COHM-UHSB-6, COHM-UHSB- COHM-UHSB-7, COHM-UHSB-8, COHM-UHSB-9, COHM-UHSB-10, COHM-UHSB-11, COHM-UHSB-12, COHM-UHSB-13, COHM-UHSB-14, COHM-UHSB-15, COHM-UHSB-16, COHM-UHSB-17, COHM-UHSB-18, COHM-UHSB-19, COHM-UHSB-20, COHM-UHSB-21, COHM-UHSB-22, COHM-UHSB-23, COHM-UHSB-24, COHM-UHSB-26, COHM-UHSB-27, COHM-UHSB-28, COHM-UHSB-29, COHM-UHSB-30
II	1	COHM-UHSB-25

Table 3: Intra- and inter-cluster D^2 values of 2 clusters for 20 characters formed by 30 local collections of Mysore mallige

	Cluster 1	Cluster 2
Cluster 1	1254.18	12804.66
Cluster 2		0

Table 4: The mean values of 20 characters for 2 clusters formed by 30 local collections in Mysore mallige

Characters	Cluster 1	Cluster 2
Length of the bud (mm)	10.15	8.16
Breadth of the bud (mm)	7.48	9.65
Pedicel length (mm)	10.19	11.48
No. of calyx teeth	7.81	14.50
Calyx length (mm)	7.66	9.89
Length of corolla tube (mm)	12.27	9.11
No. of whorls	1.59	7.00
No. of petals	14.57	50.00
Petal size (mm)	13.36	11.56
Flower diameter (mm)	29.66	35.85
No. of stamen	2.07	3.00
Length of anther (mm)	3.77	3.46
Length of filament (mm)	8.90	5.89
Length of style (mm)	3.64	3.26
Length of stigma (mm)	4.20	5.29
Fragrance	1.30	1.49
Petiole length (mm)	4.07	4.17
Length of leaf (mm)	61.67	50.42
Breadth of leaf (mm)	36.14	30.37
Flower bud weight (g)	0.23	0.83

Table 5: Principal component analysis of quantitative traits in 30 Mysore mallige local collections

Characters	PC 1	PC 2	PC 3	PC 4	PC 5	PC 6
Length of the bud (mm)	0.01	0.20	0.26	0.51	0.44	0.01
Breadth of the bud (mm)	0.11	0.02	0.51	0.36	0.06	-0.10
Pedicel length (mm)	0.03	-0.39	0.00	0.19	0.10	-0.15
No. of calyx teeth	0.25	0.00	-0.02	0.09	-0.50	-0.30
Calyx length (mm)	0.01	-0.11	-0.20	0.44	-0.50	0.42
Length of corolla Tube (mm)	-0.04	0.46	-0.08	-0.12	-0.11	0.03
No. of whorls	0.33	0.01	-0.07	0.03	-0.04	0.01
No. of petals	0.34	-0.01	-0.01	-0.07	0.11	0.04
Petal size (mm)	0.06	0.05	-0.51	0.28	0.24	0.33
Flower diameter (mm)	-0.23	0.29	-0.15	0.28	-0.07	0.04
No. of stamen	0.17	-0.05	-0.35	0.37	0.01	-0.51
Length of anther (mm)	0.14	-0.37	-0.01	-0.09	0.27	0.36
Length of filament (mm)	-0.25	0.28	-0.14	0.02	0.27	-0.19
Length of style (mm)	-0.04	-0.37	-0.32	-0.08	0.21	-0.31
Length of stigma (mm)	0.20	-0.09	0.24	0.08	-0.08	-0.08
Petiole length (mm)	0.27	0.26	-0.19	-0.14	0.09	-0.13
Length of leaf (mm)	0.33	0.12	-0.05	-0.11	0.08	0.09
Breadth of leaf (mm)	0.30	0.24	0.01	-0.09	0.02	0.03
Flower bud weight (g)	0.33	0.11	-0.01	0.04	0.08	-0.04
Eigen Value (Root)	8.18	3.68	2.03	1.64	1.16	0.89
% Var. Exp.	40.88	18.42	10.17	8.19	5.78	4.47
Cum. Var. Exp.	40.88	59.30	69.47	77.66	83.44	87.91

Table 6: Relative per cent contribution of different characters to the total divergence in Mysore Mallige local collections

Sl. No.	Character	Contribution%
1	Length of the bud	2.99%
2	Breadth of the bud	0.23%
3	Pedicel length	1.84%
4	No. of calyx teeth	0.00%
5	Calyx length	0.00%
6	Length of corolla tube	5.75%
7	No. of whorls	0.00%
8	No. of petals	18.85%
9	Petal size	0.69%
10	Flower diameter	0.92%
11	No. of stamen	0.00%
12	Length of anther	1.38%
13	Length of filament	3.45%
14	Length of style	0.23%
15	Length of stigma	4.14%
16	Petiole length	1.84%
17	Length of leaf	2.53%

18	Breadth of leaf	2.07%
19	Flower bud weight	53.10%
	Total	100

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