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Morphological Variation and Evaluation of Gladiolus (*Gladiolus Hybridus* hort.) Cultivars

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Abstract

An experiment was conducted to evaluate the genetic variability in *Gladiolus* at Horticultural Research Centre (HRC) of Sardar Vallabhbhai Patel University of agriculture and technology, Meerut, during Rabi season of 2014-2015. A total of 53 varieties were evaluated for 27 characters in genetic diversity on the basis of Mahalanobis D^2 results of Cluster and D^2 analysis indicated that the distribution patterns of *Gladiolus* genotypes into 8 clusters. Cluster IV contained maximum number of genotypes (13). The grouping pattern of the genotypes suggested no parallelisms between genetic divergence and geographical distribution of genotypes.

The intra-cluster was maximum in cluster VII (D2=372.852) reveals maximum genetic diversity followed by cluster II (D2=343.392) and cluster V (D2=150.904) and maximum inter-cluster generalized distance (D2=1855.023) was between cluster VII and cluster VIII exhibited maximum divergence followed cluster II and VIII (D2=1568.477). It is suggested that selection of genotypes based upon large cluster distance from all the clusters may lead to favorable broad spectrum genetic variability for corm yield improvement.

The Cluster VII had highest mean values number of corms per plant and genotypes in cluster VIII had highest mean values of weight of corm, weight of corms per plant indicating that by crossing between these clusters may be helpful in genetic improvement of *Gladiolus* germplasm.

Keywords: *Gladiolus*; Cluster and D^2 analysis; Evaluation; Germplasm

Introduction

Gladiolus is one of the most important bulbous ornamentals for cut flower trade in India. It is also ideal both for garden display, floral arrangements for table and interior decoration as well as making high quality bouquet [1]. The main emphasis in *Gladiolus* improvement has been on the development of varieties having attractive color and large number of florets mainly for cut flower, viz long spikes, more number of well-spaced large sized florets and good corm multiplication ability. *Gladiolus* is very rich in varietal wealth and every year there is an addition of new varieties [2]. Multiplication of planting material of *Gladiolus* is most important because the cut flower trade is lagging behind over the recent years, owing to he unavailability of sufficient quality planting material at large scale [3]. Moreover, new varieties also come from other countries, and the performance of these varieties depends upon climatic conditions of the region under which they are grown. As a result, cultivars which perform well in one region may not perform same in other regions of varying climatic conditions [4]. It is also important to study the performance of existing cultivars for their superior desirable characters [5]. Hence, it becomes very much necessary to study the morphological variation and evaluation of genotypes and also to identify the suitable germplasm for further improvement programme in U.P. region.

Studies on genetic diversity for yield traits is important as the individual plant selection is slowly dependent on variability. More the diversity better are chances of improving the economic characters under consideration in the resulting offspring. Crop improvement in *Gladiolus* has so far been achieved by exploiting the available sources of the variability. Naturally the genetic variation or diversity for most of the yield attributes is considerably high in *Gladiolus*. Keeping in view the above facts there is an urgent need to seek improvement in complex quantitative trait such as flower and corm yield of *Gladiolus*. As a result of free exchange of *Gladiolus* germplasm and lot of introgression of characters has taken place in many local *Gladiolus* cultivars resulting in enhancement of variability and new genetic combinations. Mahalanobis D^2 analysis helps in assessing the diversity among the genotypes and to select the divergent parents for future breeding programmes. Currently, such assessment is mainly based on a small number of phenotypic traits. However, environmental conditions may affect their expression and so assessing only morphological traits may not reflect the genetic diversity available.

Material and Methods

The present investigation was carried out with fifty-three varieties of *Gladiolus* obtained from different parts of India and selected on the basis of phenotypic variability in different quantitative and qualitative characters. The experiment was conducted at Horticultural Research centre (HRC) of Sardar Vallabhbhai Patel University of Agriculture and Technology, Meerut, Uttar Pradesh, India during winter season 2014-2015. The collected genotypes of *Gladiolus* were planted in Randomized Block Design with three replications. In each replication corms were sown in a spacing 30 × 20 cm. The corms of different varieties were sown during second fortnight of October, 2014. At the time of final ploughing, well rotten FYM @ 20 tonnes per hectare was incorporated and thoroughly mixed in to field. A dose of NPK @ 180:150:150 kg per hectare was applied in a schedule i.e., full dose of phosphorus, potassium and half dose of nitrogen were given at

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the time of planting of corms and remaining dose of nitrogen were applied in two spilt doses i.e. 30 and 60 days after planting (DAP). After care and plant protection measures had been done during entire period of crop growth. The observations were recorded on the basis of growth, flowering and yield of spikes and its attributing parameters. The concept of Mahalanobis's D^2 statistic is based on the technique of utilising the measurements in respect of aggregate of characters. The D^2 statistic as a measure of genetic divergence was used for the first time in the field of plant breeding by Nair and Mukherjee in the classification of natural and plantation teak.

Result and Discussion

For getting high heterosis or for recovering transgressive segregants, parents chosen for hybridization need to be genetically diverse or distant. The cultivars from widely separated localities with good yield have been usually included in the hybridisation programme, presuming the presence of genetic divergence and maximum likelihood of recovering promising segregants. As per expectations, in practice, this has not yielded very satisfactory and consistent results. Eco-geographical diversity has been regarded as a reasonable index of genetic diversity [6,7].

Mahalanobis D^2 analysis

On the basis of Mahalanobis D^2 values, all the 53 genotypes were grouped under study into 8 clusters. The distribution patterns of *Gladiolus* genotypes into 8 clusters are shown in Figure 1 and Table 1. Cluster IV contained maximum number of genotypes (13). The grouping pattern of the genotypes suggested no parallelisms between genetic divergence and geographical distribution of genotypes. These results are in conformity with the findings of observations have been

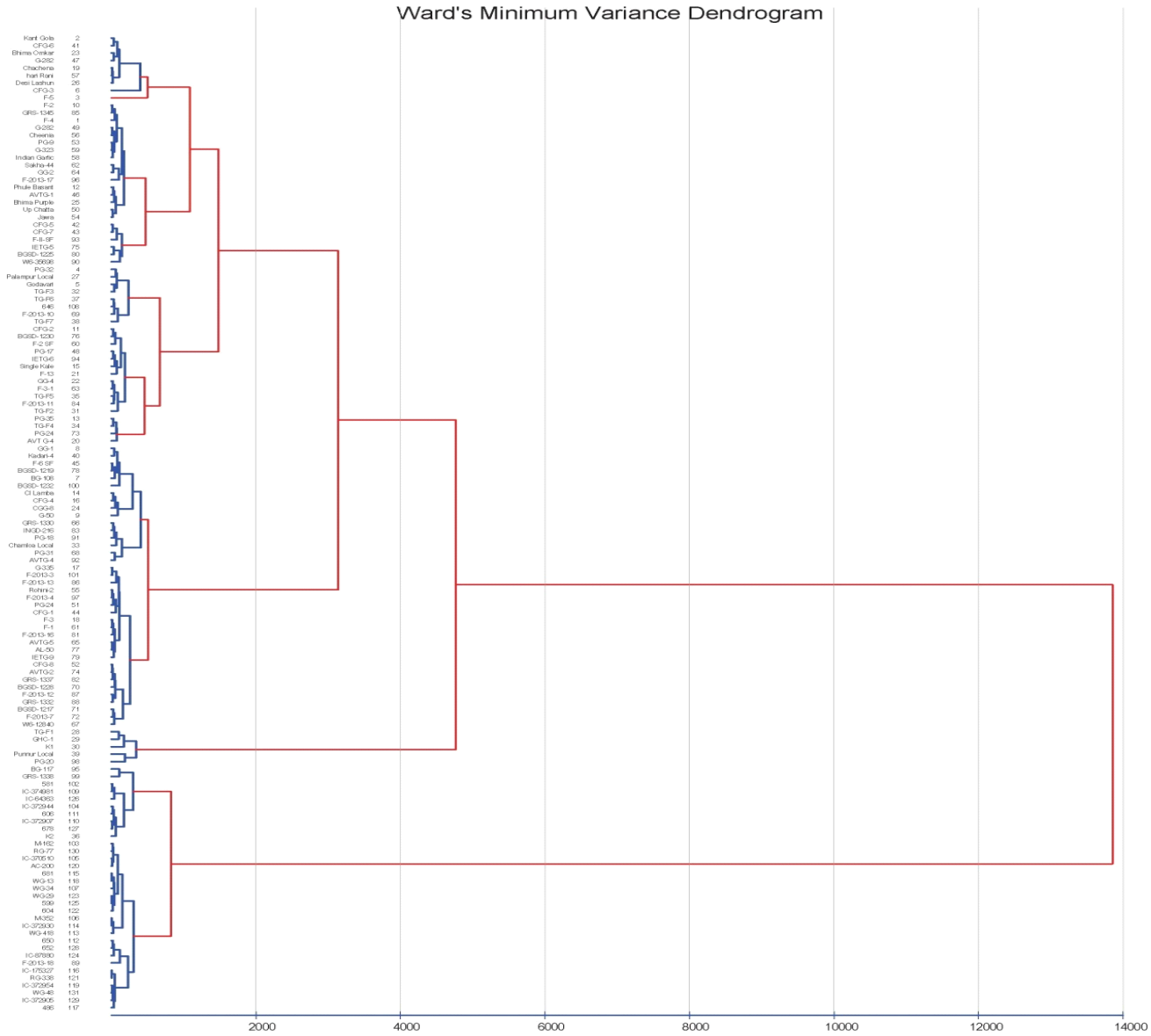

Figure 1: Mahalanobis Euclidean^2 Distance.

observed by Nimbalkar et al. [8]; Pal et al. [9] and Sheikh and Ahmad [10] in *Gladiolus*.

The inter-cluster distance was greater than intra-cluster distance as indicated in Figure 2 and Table 2 revealing considerable amount of genetic diversity among the genotypes studied. The intra-cluster was maximum in cluster VII (D^2 =372.852) reveals maximum genetic diversity followed by cluster II (D^2 = 343.392) and cluster V (D^2 =150.904) and maximum inter-cluster generalized distance (D^2 =1855.023) was between cluster VII and cluster VIII exhibited maximum divergence followed cluster II and VIII (D^2 =1568.477). It is suggested that selection of genotypes based upon large cluster distance from all the clusters may lead to favorable broad spectrum genetic variability for corm yield improvement. Therefore, it is suggested that selection of genotypes based upon large cluster distance from all the clusters may lead to favorable broad spectrum genetic variability for corm yield improvement. Similar findings are reported earlier by of Sheikh and Khanday [11] and Patra and Mohanty [12]. The grouping pattern of the genotypes suggested no parallelisms between genetic divergence and geographical distribution of genotypes.

Cluster Number	No. of genotypes	Genotypes included
1	**10**	Shohangini, Snow Princess, Arka Naveen, Pusa Shuryana, Punjab Glade, Navaleen, Peater Pearl, Pricilla, Victor, Gester Gold
2	**8**	Friendship, Arka Amar, Punjab Pink Elegance, Sagar, Chandni, Arka Baran, Lagent Pink, Tilak
3	**1**	Arka Keshar
4	**13**	Hunting Song, Tiger Flame, White Prospirity, Nova Lux, Pusa Kiran, Darshan, Share Punjab, Flavor Sauvenir, Prince Margaret, Aarti, Mohini, Shobha, Poonam
5	**8**	Inter Pearl, Ocilla, Linoncella, Gold Field, Regency, Sylvia, Punjab Flame, Orange Ginger
6	**1**	Arka Gold
7	**7**	Forta Rosa, Yellow Stone, Sensire White, American Beauty, Prabha, Punjab Down, SVP-1
8	**5**	Arun, Punjab Glance, Pacific, Kum-Kum, Shagun

Table 1: Clustering pattern of 53 genotypes of Gladiolus on the basis of genetic divergence.

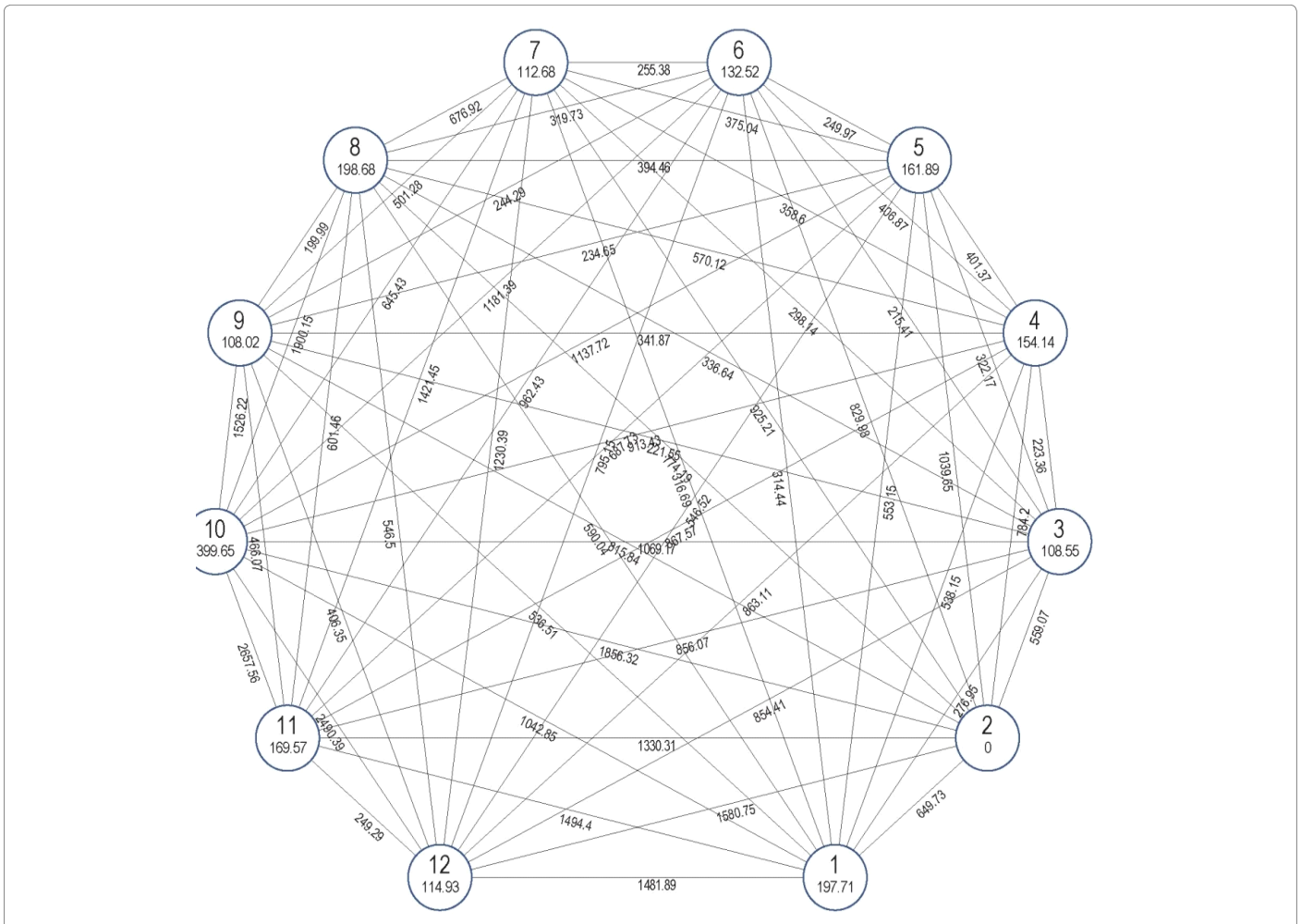

Figure 2: Euclidean^2 Distance.

Cluster No.	1 Cluster	2 Cluster	3 Cluster	4 Cluster	5 Cluster	6 Cluster	7 Cluster	8 Cluster
1 Cluster	**72.833**	245.825	297.203	150.521	117.138	163.716	472.358	1191.271
2 Cluster	-	**343.392**	522.66	319.561	265.618	336.969	582.890	1568.477
3 Cluster	-	-	**0.00**	465.616	448.404	388.297	839.536	964.232
4 Cluster	-	-	-	**125.006**	140.393	186.062	475.774	1013.632
5 Cluster	-	-	-	-	**85.266**	158.752	321.347	1274.666
6 Cluster	-	-	-	-	-	**150.904**	381.330	1115.994
7 Cluster	-	-	-	-		-	**372.852**	1855.023
8 Cluster	-	-	-	-	-	-	-	**0.000**

Values in parenthesis are square root of D^2 value

Table 2: Average of intra and inter cluster distance.

Cluster Number	Characters													
	DTS	PH	NLPP	LLL	WLL	NSPC	VSD	OFFD	NFPS	DF	SPC	DS	LS	LR
1 Cluster	10.679	52.331	6.876	39.084	2.607	2.142	79.126	89.342	13.178	9.239	1.881	0.878	58.484	37.589
2 Cluster	15.457	50.437	7.100	39.497	2.450	2.243	79.583	90.123	13.187	8.603	1.953	0.847	58.690	39.073
3 Cluster	11.377	55.610	7.717	41.370	4.340	1.913	81.870	91.987	15.737	8.517	2.140	0.830	58.870	30.603
4 Cluster	11.143	50.640	6.753	38.807	2.253	2.913	81.380	91.177	11.697	8.443	1.797	0.737	55.280	41.233
5 Cluster	10.160	51.393	7.407	38.787	2.773	3.063	87.763	95.010	13.127	9.537	3.233	1.123	62.420	35.253
6 Cluster	11.723	52.907	6.257	39.450	2.663	2.003	86.770	96.187	14.277	8.617	1.770	0.980	86.137	59.723
7 Cluster	15.457	46.827	7.403	37.200	2.250	2.377	79.580	89.580	14.933	8.103	2.047	0.777	49.210	26.313
8 Cluster	10.520	50.753	7.357	38.967	2.427	1.937	80.463	90.943	21.457	10.987	1.647	0.887	80.283	56.180

Cluster Number	Characters												
	LSD	VLCFRT	FLD	NFOPS	FOP	WU	WC	WCPP	DC	NCPP	CPP	YCPH	YCCPH
1 Cluster	23.175	9.966	5.946	7.999	63.465	45.614	50.821	106.103	6.603	2.079	14.150	127.285	132.373
2 Cluster	21.983	9.453	5.253	8.207	63.630	41.523	30.000	68.820	5.777	2.293	13.470	82.547	87.193
3 Cluster	23.197	11.280	6.760	9.257	60.410	49.570	33.187	62.500	6.880	1.900	14.480	74.950	80.447
4 Cluster	23.063	10.093	6.033	6.757	62.073	43.400	79.970	119.827	7.833	1.513	16.780	143.773	149.380
5 Cluster	31.817	9.907	5.710	8.490	67.167	45.080	48.397	67.420	6.367	1.413	14.267	80.873	86.970
6 Cluster	23.217	10.270	6.213	10.040	73.570	58.110	58.143	98.890	6.807	1.700	14.813	118.650	122.723
7 Cluster	22.503	8.197	4.210	6.957	48.187	28.193	49.697	128.710	6.870	2.583	17.733	154.423	158.797
8 Cluster	22.990	12.093	7.933	15.253	71.503	53.140	112.163	248.697	7.403	2.223	15.333	298.423	301.870

Table 3: Cluster wise mean values of 27 characters in gladiolus.

Cluster mean

Cluster means for 27 characters are present in Table 3. The existence of diversity among the genotypes was also assessed by the considerable amount of variation in cluster means for different characters. The Cluster VII had highest mean values number of corms per plant and genotypes in cluster VIII had highest mean values of weight of corm, weight of corms per plant indicating that by crossing between these clusters may be helpful in genetic improvement of *Gladiolus* germplasm. These results are in conformity with the findings of observations have been observed by Ranchana et al. [13].

D^2 analysis (Rank method)

The percentage contribution of different characters towards genetic divergence is presented in Table 4. Ranking character wise D^2 values and adding the ranks for each character for all the entries identified the variables, which contributed towards the divergence. Characters such as days taken to sprouting contributing maximum (19.01%) towards total divergence and this was followed yield of corms per hectare (15.02%), weight of corm (11.39%) and length of spike (7.69%) these can be used for selecting parents from distinctly placed cluster to obtain higher production. The present findings were accordance with the findings of Desh Raj and Misra [14]; Nayak et al. [15]; Dhillon, [16] and Pal et al. [17].

Conclusion

- The grouping pattern of the genotypes suggested no parallelisms between genetic divergence and geographical distribution of genotypes.
- The selection of genotypes based upon large cluster distance from all the clusters may lead to favorable broad spectrum genetic variability for corm yield improvement.
- On the basis of Mahalanobis D^2 analysis it could be concluded that the *Gladiolus* germplasm at SVPUAT can be used for future breeding programmes.
- Finally, these studies have given important clues in understanding genotypes relationship, which may further assist in developing and planning breeding strategies.

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Source	Times Ranked 1st	Contribution %
1 Days taken to sprouting	262	19.01
2 Plant height (cm)	2	0.15
3 Number of leaves per plant	4	0.29
4 Length of the longest leaf	32	2.32
5 Width of the longest leaf	33	2.39
6 Number of sprouts percorm	10	0.73
7 Days required for visibility of first spike	68	4.93
8 Days required for opening of first flower	0	0.00
9 Number of florets per spike	39	2.83
10 Diameter of flower (cm)	67	4.86
11 Number of spikes per corm	0	0.00
12 Diameter of spike (cm)	56	4.06
13 Length of spike (cm)	106	7.69
14 Length of rachis (cm)	68	4.93
15 Longevity of spike in days	50	3.63
16 Vase life of cut flower at room temperature (days)	4	0.29
17 Floret longevity in days	2	0.15
18 Flowers open per spike	58	4.21
19 Floret Opening (%)	0	0.00
20 Water Uptake (ml)	112	8.13
21 Weight of Corm (gm)	157	11.39
22 Weight of Corms/ Plant (g)	5	0.36
23 Diameter of Corm (cm)	14	1.02
24 Number of corms per plant	14	1.02
25 Number of cormlets per plant	8	0.58
26 Yield of corms per hectare	207	15.02
27 Yield of corm and cormlets per hectare	0	0.00

Table 4: Contribution of various characters towards total genetic divergence.

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