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Research Article

Determination of genetic diversity in indigenous cultivars of onion (*Allium cepa L.*) by multivariate analysis under mid hill zone of North-Western Himalayas, India

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Abstract

The present investigation was carried out at the Experimental Farm of the Department of Vegetable Science and Floriculture, CSK HPKV Palampur to assess the genetic divergence in indigenous cultivars of onion. Fifty eight genotypes were evaluated in Randomized Block Design with three replications during *rabi* 2016-17. Data were recorded on 11 yield and yield related traits. The multivariate analysis revealed considerable genetic diversity in the 58 genotypes. Genotypes were arranged into eight clusters with maximum genotypes in cluster II. Marketable yield contributed maximum towards total genetic divergence followed by equatorial diameter and polar diameter. Eleven genotypes namely, ON14-27, ON15-16, ON16-35, ON16-17, ON16-25, ON16-24, ON16-11, ON16-22, ON14-23, ON15-42, ON15-33 along with the standard check Palam Lohit could offer promise for their direct use as varieties and as potential parents in future breeding programmes to isolate transgressive segregants.

Keywords

Genetic divergence, genotypes, marketable yield, onion, transgressive segregants

Introduction

Onion (*Allium cepa* L.) (2n = 16) is the most important bulb crop and an indispensable item in every kitchen as vegetable and condiment used to flavour many of the food stuffs. Therefore, onion is popularly referred as “Queen of Kitchen” belonging to the family Alliaceae and genus *Allium* which is one of the largest genera of monocots encompassing over 900 species (Fritsch and Abbasi, 2013). The genus *Allium* was earlier included in the family Liliaceae due to its superior ovary. It was later shifted to Amaryllidaceae as flowers are borne in a bracted umbel on top of a scape (scapose umbellate). The cultivated onion is most frequently a biennial, but is usually treated as an annual and harvested in its first growing season. It is a native of Central Asia (Vavilov, 1951), but a rich diversity also exists in Greece, North–West India, Pakistan, Turkey and Russia. Today onions are cultivated and used around the world. The whole plant is edible and is used as food in one form or other.

A genetic diverse origin plays an important role in varietal improvement programme of a particular crop for economic characters. Determination of genetic diversity of any given crop species is a suitable precursor for improvement of the crop because it generates baseline data to guide selection of parental lines and design of a breeding scheme (Maesen, 1990). Amongst various tools to assess genetic diversity, D^2 statistic is a powerful tool for estimating genetic diversity among different genotypes and to identify the parents for hybridization to obtain desirable recombinants. The assessment of genetic divergence helps in short listing the number of breeding lines from the large germplasm and the progenies derived from diverse parents are expected to show a broad spectrum of genetic variability and provide better scope to isolate superior recombinants. Keeping this in view, the present investigation was carried out to assess the degree of divergence in 58 cultivars of indigenous onion.

Material and Methods

The experimental material for present study comprised of 58 indigenous cultivars of onion. These 58 genotypes were evaluated at the Experimental Farm of the Department of Vegetable Science and Floriculture, CSK HPKV, Palampur during *rabi* 2016-17 in Randomized Complete Block Design with three replications. The standard cultural practices were followed to raise the crop. The seeds of these genotypes were procured from Directorate of Onion and Garlic Research, Pune, Indian Agricultural Research Institute, New Delhi, Indian Institute of Horticultural Research, Bengaluru, and CSK HPKV, Palampur, India. The nursery beds were prepared 1 m wide and 3 m long and elevated up to 15 cm from ground levels for sowing the seeds. The seeds were sown on 15th of October. The seeds were treated with Bavistin (3g /kg of seed) and were sown on the nursery beds in rows 5 cm apart. After 30 DAS, the seedlings were applied 5% of urea @ 10 days interval for proper growth of the seedlings. The nursery beds were also sprayed with DM-45 @ 2.5% at 10-15 days interval. Eight week old healthy seedlings were transplanted on 15th of December, 2016. Seedling were uprooted from the nursery bed and transplanted in the plots at a spacing of 15 cm (row to row) and 10 cm (plant to plant). Transplanting was done in the afternoon or evening hours immediately followed by sprinkler irrigation for proper establishment of the seedlings. A week after transplanting, gap filling was done.

The observations were recorded on randomly selected 10 plants of each genotype over the replications for 11 traits, viz., plant height (cm), number of leaves/plant, neck thickness (cm), bulb maturity (days), polar diameter (cm), equatorial diameter (cm), shape index (cm), average bulb weight (g), total bulb yield (kg/ plot), biological yield (kg/ plot) and marketable yield (kg/ plot). Wilk’s criterion was used to test the significance of difference in mean values for all the 11 characters. The data were subjected to multivariate analysis utilizing Mahalanobis D^2 statistic as suggested by Mahalanobis (1936) and Rao (1952) using statistical software WINDOSTAT 8.0 developed by Indostat Services. Genotypes were grouped into various clusters following Tocher’s method as suggested by Rao (1952).

Results and Discussion

In the present investigation, with non-hierarchical Euclidean cluster analysis, fifty eight genotypes of onion were grouped into eight clusters, where in four clusters were monogenotypic (solitary) and four were polygenotypic based on genetic divergence (Table 1 and Fig 1). Different clustering patterns in onion were also reported by earlier workers *viz.,* Sharma *et al.,* (2015), Akter *et al.,* (2015) and Ghodke *et al.,* (2018) in their respective studies. The cluster II was the largest consisting of twenty genotypes namely, ON16-15, ON14-17, ON16-05, ON15-48, Patna Red, ON16-39, ON16-32, ON15-20, Palam White, Pusa Red, Pusa Madhvi, ON16-52, ON14-29, ON14-27, Pusa Riddhi, ON16-54, ON16-27, ON16-13, ON15-16 and ON16-35 which constituted for 34.00 per cent of the total population. Different genetic material was also arranged into different clusters by Sharma *et al.,* (2015), Akter *et al.,* (2015) and Ghodke *et al.,* (2018) in their respective studies. Clusters I contained sixteen genotypes *viz.,* ON16-29, ON15-11, ON15-01, ON16-30, ON15-18, ON14-11, ON16-18, ON14-15, Arka Bheem, ON14-04, ON14-09, ON14-25, ON15-06, ON16-37, ON15-13 and ON16-41, Cluster IV had nine genotypes *viz.,* ON15-27, ON14-06, Arka Niketan, ON15-23, ON15-37, ON15-45, ON14-01, Arka Kalyan and Arka Bindu and, Cluster V also constituted nine genotypes *viz.,* ON16-17, ON16-25, ON16-57, Palam Lohit, ON16-24, ON16-11, ON16-48, ON16-20 and ON15-39. While cluster III, VI, VII and VIII were monogenotypic clusters containing one genotype each *viz.,* ON16-22, ON14-23, ON15-42 and ON15-33 respectively, suggesting diverse origin of these genotypes. Monogenotypic clusters were also observed by Ningadalli (2006) and Dhotre *et al.,* (2010). They further suggested that such genotypes were more divergent from others.

The intra-cluster distance varied from 7.926 (2.185) in cluster I to 28.058 (5.297) in cluster V, while for remaining monogenotypic clusters, the intra-cluster distance was zero (Table 2 and Figure 2). Maximum intra-cluster variation among genotypes was also reported by Sharma *et al.,* (2015), Akter *et al.,* (2015) and Ghodke *et al.,* (2018) in their respective genetic materials and locations of studies. Since the intra-cluster distance was low, the chances of developing good segregants by hybridization among parents within cluster would be low. Therefore, it is logical to attempt crosses between genotypes falling in different clusters based on inter-cluster distance.

The inter-cluster distance ranged 12.655 (3.557) between Cluster I and III to 121.635 (11.029) between Cluster VI and VIII (Table 2 and Figure 2). The highest inter-cluster level genetic divergence was recorded between clusters VI and VIII followed by VI and VII, IV and VIII, II and VIII, and III and VI. The inter-cluster proximity was the minimum between clusters I and III followed by III and IV and III and VII. This clearly indicates that the genotypes included in the clusters with high inter-cluster distance showed sufficient genetic diversity and selection of parents from these diverse clusters would be useful in hybridization programme for improving yield and other desirable horticultural traits. The crosses involving the diverse genotypes would be expected to manifest maximum heterosis and are more likely to evolve desirable recombinants in segregating generations. Based on inter-cluster distance, the earlier workers have also suggested selection of parents from diverse clusters for utilization in hybridization programme to obtain desirable transgressive segregants. Different clustering patterns in onion were also reported by earlier workers namely Singh *et al.*, (2013), Sharma *et al.*, (2015), Akter *et al.*, (2015) and Ghodke *et al.*, (2018).

The composition of cluster means for different characters showed considerable differences among the clusters for each character (Table 3). Cluster V was observed to be important with desirable cluster means for the most valuable traits *viz.*, polar diameter, equatorial diameter, total bulb yield and marketable yield. On the same line, Cluster VI showed maximum cluster means for plant height, number of leaves/plant, shape index, average bulb weight and biological weight. Cluster IV showed minimum cluster means for neck thickness. Cluster VIII had minimum cluster mean for plant height and bulb maturity. Hence, different clusters of genotypes on the basis of means revealed divergence for different characters and can be utilized as indicators for selecting diverse parents for specific trait in hybridization programmes. It is worthy to note that in calculating cluster mean, the superiority of a particular genotype with respect to a given character could get diluted by other genotypes that are grouped in the same cluster but are inferior or intermediate for the character in question (Million, 2012). Hence, apart from selecting genotypes from the clusters which have higher inter-cluster distance for hybridization, one can also think of selecting parents based on the extent of divergence with respect to a character of interest (Nigussie and Becker, 2002; Gemechu *et al.,* 2005; Fikreselassie *et al.,* 2012).

The contribution of individual characters to divergence has been worked out in terms of number of times it appeared first (Table 4). Marketable yield contributed maximum towards total genetic divergence followed by equatorial diameter and polar diameter. Therefore, it could also be used as parameters based on specific trait(s) in selecting genetically diverse parents for hybridization to create variability in the population. The contribution of equatorial diameter and polar diameter towards total genetic divergence was also reported by Singh *et al.*, (2013), Arya *et al.,* (2017) and Ghodke *et al.*, (2018).

Selection of genotypes as superior and diverse parents for hybridization programme should be based on diverse clusters. Accordingly, best performing genotypes *viz.,* ON14-27, ON 15-16 and ON16-35 from cluster II whereas, ON16-11, ON16-17, ON16-24, ON16-25, and Palam Lohit from cluster V along with genotypes grouped in monogenotypic clusters namely, ON16-22, ON14-23, ON15-42 and ON15-33 from cluster III, VI, VII and VIII respectively offer promise for their direct use as varieties and as potential parents in future breeding programmes to isolate transgressive segregants.

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Table 1. Cluster composition in onion following multivariate analysis

Cluster number	No. of genotypes	Genotype (s)
I	16	ON16-29, ON15-11, ON15-01,ON16-30, ON15-18, ON14-11, ON16-18, ON14-15, Arka Bheem, ON14-04, ON14-09, ON14-25, ON15-06, ON16-37, ON15-13, ON16-41
II	20	ON16-15, ON14-17, ON16-05, ON15-48, Patna Red, ON16-39, ON16-32, ON15-20, Palam White, Pusa Red, Pusa Madhvi, ON16-52, ON14-29, ON14-27, Pusa Riddhi, ON16-54, ON16-27, ON16-13, ON15-16, ON16-35
III	1	ON16-22
IV	9	ON15-27, ON14-06, Arka Niketan, ON15-23, ON15-37, ON15-45, ON14-01, Arka Kalyan, Arka Bindu
V	9	ON16-17, ON16-25, ON16-57, Palam Lohit, ON16-24,ON16-11, ON16-48, ON16-20, ON15-39
VI	1	ON14-23
VII	1	ON15-42
VIII	1	ON15-33

Table 2. Average intra and inter-cluster distances in 8 clusters of onion genotypes

Clusters	I	II	III	IV	V	VI	VII	VIII
I	7.926	33.126	12.655	28.418	33.648	78.312	30.487	74.921
	(2.185)	(5.756)	(3.557)	(5.331)	(5.801)	(8.849)	(5.522)	(8.656)
II		13.632	43.284	41.006	42.435	34.384	66.892	108.695
		(3.692)	(6.579)	(6.404)	(6.514)	(5.864)	(8.179)	(10.426)
III			0.000	15.894	56.720	101.495	26.244	79.230
			(0.000)	(3.987)	(7.531)	(10.074)	(5.123)	(8.901)
IV				14.713	77.333	98.510	50.263	118.446
				(3.836)	(8.794)	(9.925)	(7.090)	(10.883)
V					28.058	54.929	61.120	73.737
					(5.297)	(7.411)	(7.818)	(8.587)
VI						0.000	119.409	121.635
						(0.000)	(10.927)	(11.029)
VII							0.000	33.711
							(0.000)	(5.806)
VIII								0.000
								(0.000)

Values in bold figures are intra-cluster distances; Values in parenthesis are $\sqrt{D^2} = D$ value

Table 3. Cluster means for different characters in onion

Clusters Traits	I	II	III	IV	V	VI	VII	VIII	Mean	Max.	Min.
Plant height (cm)	45.29	43.91	51.94	45.24	46.95	57.10	43.99	41.90	47.04	57.10	41.90
Number of leaves/plant	9.47	8.96	8.44	8.45	8.05	11.42	9.55	8.35	9.09	11.42	8.05
Neck thickness (cm)	0.81	0.70	0.69	0.62	0.79	0.99	0.63	0.72	0.74	0.99	0.62
Bulb maturity (days)	161.67	160.37	160.79	160.19	159.40	176.78	159.48	158.09	162.09	176.78	158.09
Polar diameter (cm)	5.21	5.45	6.51	4.43	6.93	6.49	4.65	5.35	5.63	6.93	4.43
Equatorial diameter (cm)	5.68	5.85	6.69	4.39	6.99	6.06	4.68	5.89	5.78	6.99	4.39
Shape index (cm)	0.92	0.93	0.98	1.01	1.00	1.07	1.00	0.91	0.98	1.07	0.91
Average bulb weight (g)	47.34	50.20	64.32	40.43	67.40	67.81	41.17	50.90	53.70	67.81	40.43
Total bulb yield (kg/ plot)	9.47	10.03	12.86	8.02	13.43	13.00	8.20	10.17	10.65	13.43	8.02
Biological yield (kg/plot)	0.74	0.71	0.71	0.68	0.65	0.78	0.72	0.69	0.71	0.78	0.65
Marketable yield (kg/plot)	6.91	8.69	11.16	6.56	13.43	13.00	8.20	10.17	9.77	13.43	6.56

Max-Maximum; Min-Minimum

Table 4. Contribution of various traits towards genetic divergence in onion

Characters	Contribution (%)	Times ranked Ist
Plant height (cm)	1.21	20.00
Number of leaves/plant	1.03	17.00
Neck thickness (cm)	2.54	42.00
Bulb maturity (days)	0.48	8.00
Polar diameter (cm)	16.09	266.00
Equatorial diameter (cm)	22.63	374.00
Shape index (cm)	0.42	7.00
Average bulb weight (g)	0.54	9.00
Total bulb yield (kg/ plot)	3.93	65.00
Biological yield (kg/ plot)	2.00	33.00
Marketable yield (kg/ plot)	49.12	812.00

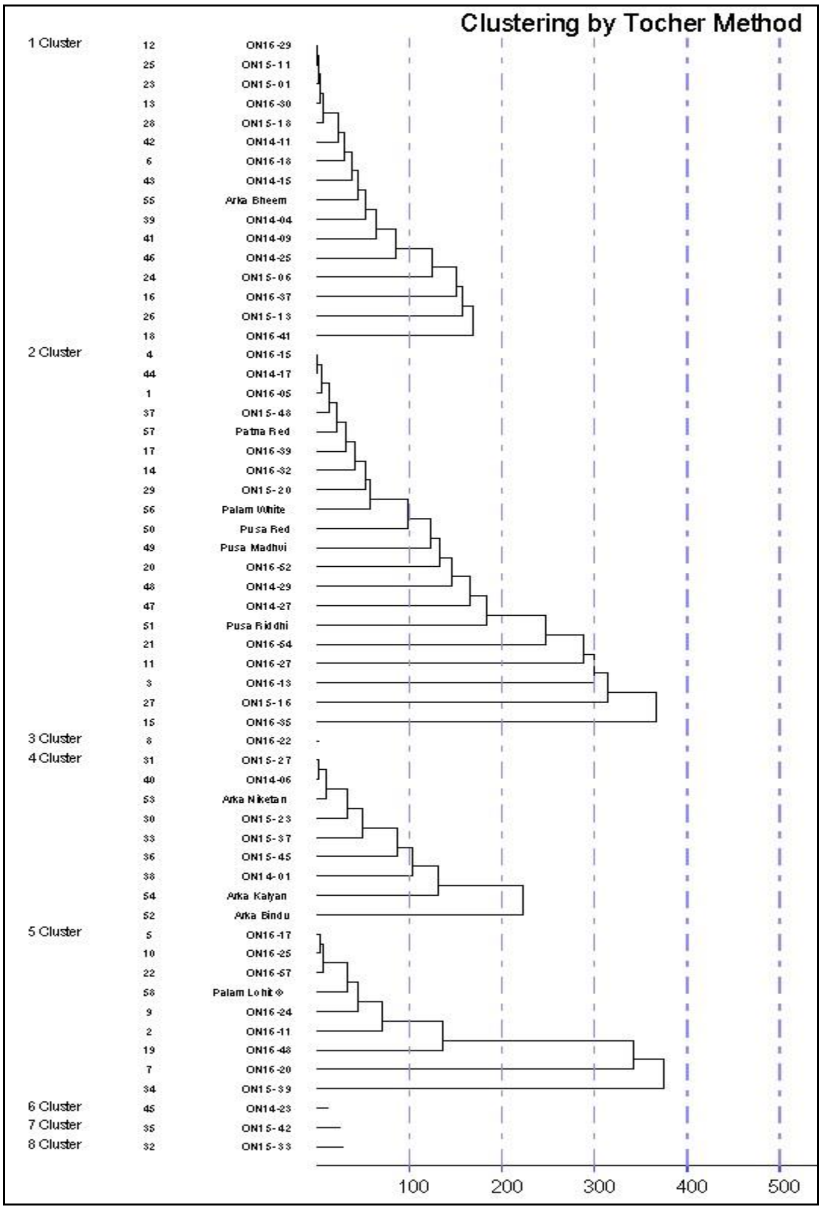


Fig. 1. Dendrogram showing grouping of fifty eight onion genotypes based on D^2 statistics using Tocher's method

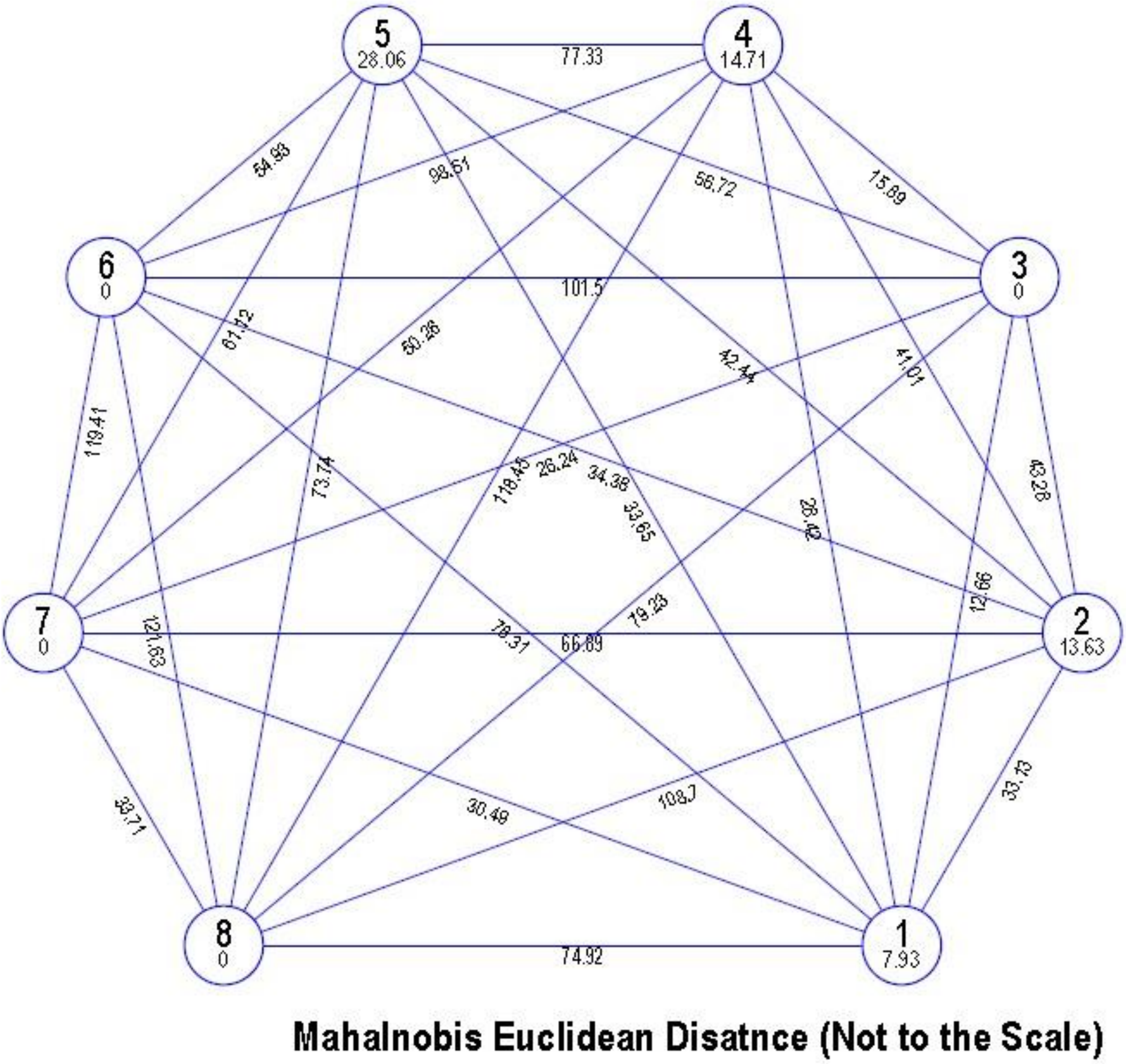
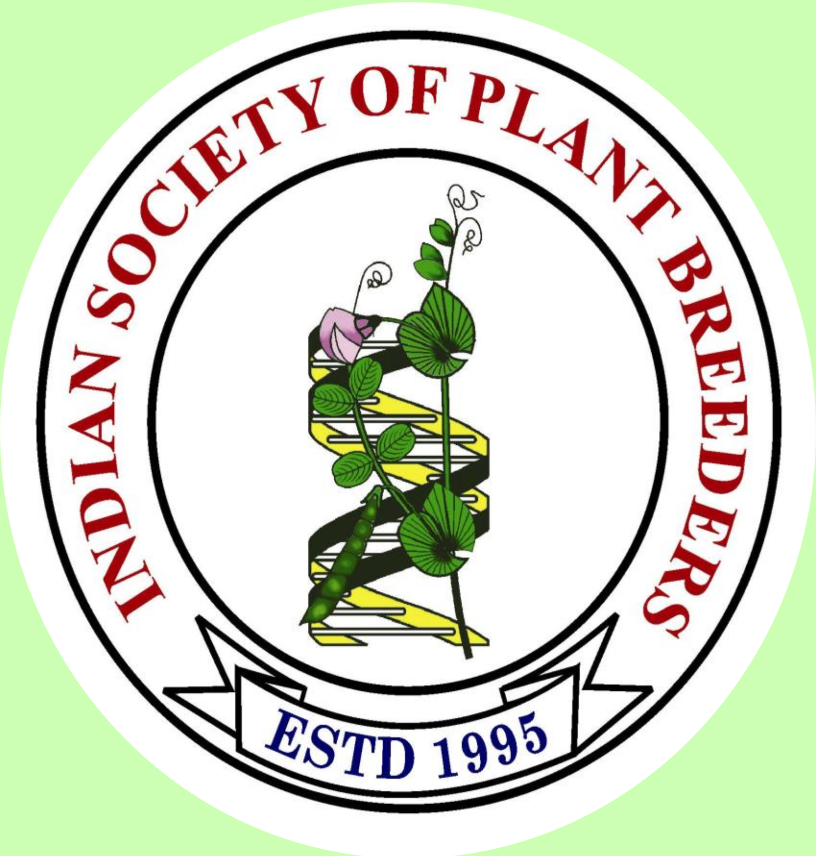


Fig. 2. Intra and Inter-cluster distances using Mahalanobis Euclidean Distance



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