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Genetic divergence in maize (*Zea mays* L.) inbred lines

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Abstract
Investigation was carried out to determine the genetic divergence in the 30 maize inbred lines using Mahalanobis D^2 statistic. Analysis of variance revealed highly significant differences among all the inbreds. Inbreds were grouped into seven clusters, indicating the presence of genetic diversity. Cluster IV was the largest having (10) genotypes followed by cluster III having (8) genotypes and cluster I having (6) genotypes. Cluster IV had the highest intra-cluster distance (385.52). The inter-cluster distance was found to be highest between Cluster VI and Cluster VII (4534.03) suggested more variability in genetic makeup of the genotypes included in these clusters and thus inbred lines from cluster VI and VII should be selected as parents in hybridization programme for yield improvement in maize inbred lines. Out of 12 characters studied, plant height and 100 seed weight contributed high for genetic divergence.

Keywords: Genetic divergence, maize inbred lines, Mahalanobis D^2 statistic, intra-cluster distance

Introduction
Maize is one of the three leading global cereals that feeds the world (Shiferaw *et al*., 2011) [11]. Maize is an important cereal crop, which can supply food, feed, fodder, and fuel for domestic use and also raw materials for use in industry. Among food grain crops, globally maize occupies third position in terms of acreage and production. As a versatile crop, it grows successfully throughout the world covering low land, tropical, sub-tropical, and temperate climatic condition (Elias, 1995) [2]. Globally, maize is known as 'Queen of Cereals' because of its highest genetic yield potential among cereals.

Mahalanobis' D^2 statistic of multivariate analysis is recognized as a powerful tool in quantifying the degree of genetic divergence among the inbreds (Hemavathy *et al*., 2008) [5]. D^2 statistics is a powerful tool in quantifying the degree of divergence among biological populations and assessing the relative contribution of different components to the total divergence at intra- and inter- cluster levels. (Murty and Arunachalam, 1966; Panwar, 1970) [8, 9]. Estimation of genetic divergence also allows breeders to eliminate some parents in downsizing the core collections maintained and concentrate their efforts in a smaller number of hybrid combinations (Fuzzato *et al*., 2002) [3]. It also helps to identify the suitable inbreds for hybridization programme on the basis of their clustering pattern. The present investigation was undertaken with a view to estimate the genetic divergence in the 30 maize inbred lines using Mahalanobis D^2 statistic.

Materials and Methods
The present investigation was carried out during *Kharif*, 2018 at Dryland *(*Karewa) Agriculture Research Station (DARS), Budgam, SKUAST-Kashmir using 30 maize inbreds viz., L-1, L-2, L-9, L-18, L-6, L-10, L-8, HKI- 101, CML-129, HKi-1015-W8,CML-470, L-72, CML-488, CML-167,LM-14, DMR-N6,CML-135, CML-415, LM-12, CML-139, CML-425, CML-286, CML-474, V-338, V-5, V-412, V-351, V-405, V-400, V-335. Data was collected on twelve maturity, morphological and yield and traits.and was subjected to analysis of variance. Genetic divergence was computed by multivariate analysis using Mahalanobis D^2 technique and the genotypes were grouped into clusters following Euclidean method as described by Rao (1952) [10].

Results and Discussion
Thirty maize inbreds were evaluated during *Kharif,* 2018 and the data was subjected to

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D^2 analysis. The analysis of variance revealed highly significant differences among the genotypes for all the twelve characters indicating the existence of genetic variability among the experimental material. Based on the performance of the genotypes, thirty inbreds got grouped into 7 clusters (Table-1 and Figure-1) as per the Mahalanobis D^2 analysis employing Tocher's method (Rao, 1952) [10]. Cluster IV was the largest having (10) genotypes indicating genetic similarity among them followed by cluster III having (8) genotypes, cluster I (6) genotypes, cluster II (3) genotypes, cluster V (1) genotype, cluster VI (1) genotype and cluster VII (1) genotype respectively. Clusters V to VII are solitary clusters containing only one genotype indicating the uniqueness of the genotypes included in those clusters when compared to other genotypes included in the study. Genetic diversity is generally associated with geographical diversity, but the former is not necessarily directly related with geographical distribution. The genotypes within the same clusters were originated from different geographical regions of the world, which indicated the geographical distribution and genetic divergence did not follow the same trend which might be due to continuous exchange of genetic material among the countries of the world. Similar conclusions were also drawn by other workers (Singh *et al.*, 1999 and Texeira *et al.*, 2002) [12, 13].
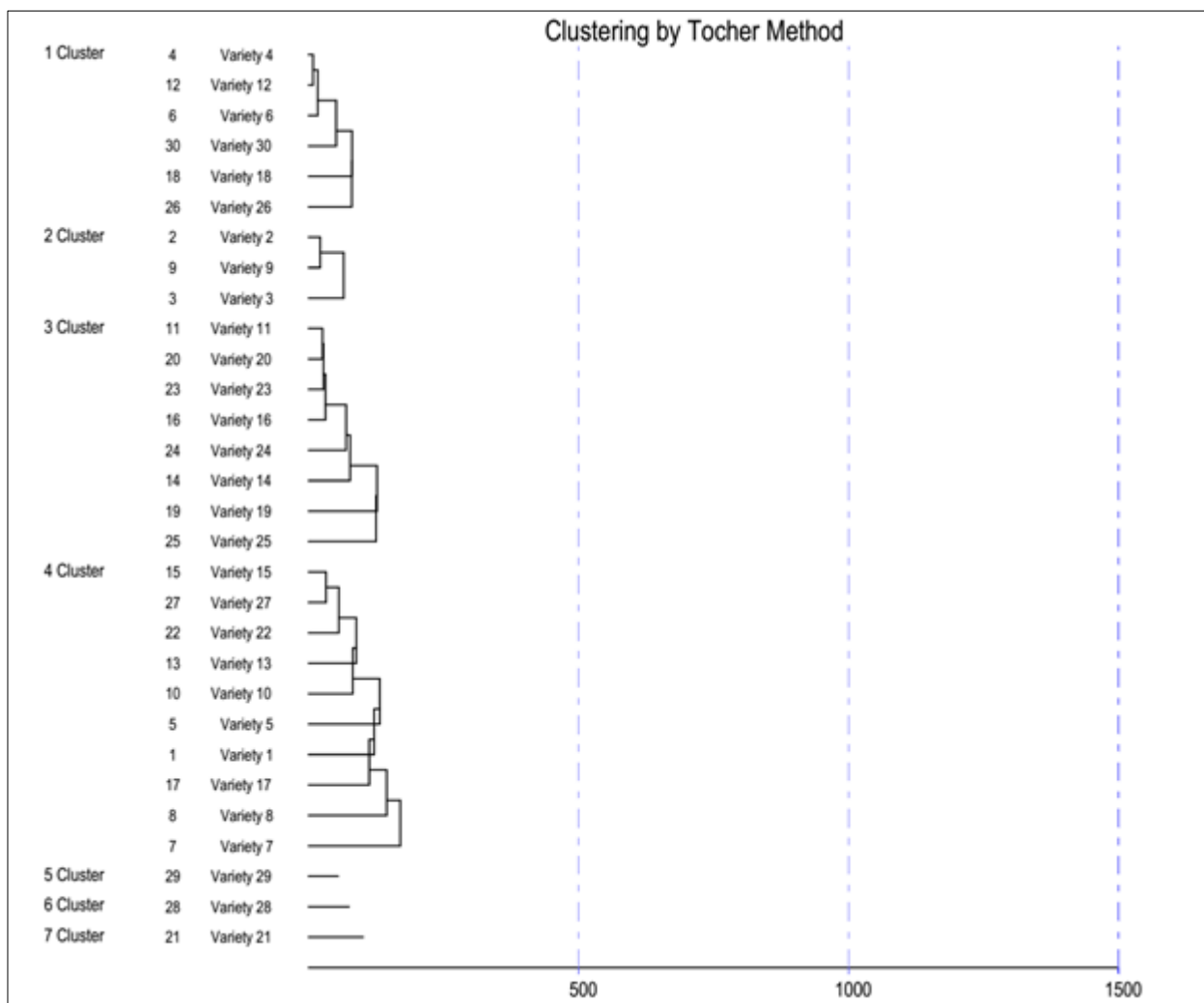

Fig 1: Clustering by tocher method

Table 1: Distribution of different Maize (*Zea mays* L.) inbreds into clusters based on Mahalanobis D^2 statistic

Cluster	Number of genotypes in the cluster	Number of the genotypes
I	6	L-18, L-72, L-10, V-335,CML-415, V-412
II	3	L-2, CML-129, L-9
III	8	CML-470, CML-139, CML-474, DMR-N6, V-338, CML-169, LM-12, V-5
IV	10	LM-14, V-351, CML-286, CML-488, HKI-1015-W8, L-6, L-1, CML-135, HKI-101, L-8
V	1	V-400
VI	1	V-405
VII	1	CML-425

Statistical distance represents the induction of genetic diversity among clusters. The intra-cluster distances and the inter-cluster distances are presented in (Table- 2 and Figure 2)

The intra-cluster distances are lower than the inter-cluster distances. Therefore less diversity was found in the genotypes within cluster. Cluster 4 had the highest intra-cluster D^2

values (385.52), followed by Cluster 3 (278.86), Cluster 1 (203.53) and Cluster 2 (193.11). The inter-cluster distance was found to be highest between Cluster 6 and Cluster 7 (4534.03), followed by Cluster 2 and Cluster 7 (3950.34). Least inter-cluster distance was found between Cluster 1 and Cluster 6 (355.14). Similar results were obtained by (Singh *et al.*, 1999 and Miranda *et al.*, 2003) [12, 7]. The genotypes belonging to the clusters separated by high statistical distance could be used in hybridization programme for obtaining a wide spectrum of variation among the segregates. Selection of parents from the highly divergent clusters is expected to manifest high heterosis in crossing and also wide variability in genetic architecture. Murty and Anand (1966) [5] claimed that there is a positive relationship between the specific combining ability and the degree of genetic diversity.

The cluster mean for twelve characters is presented in Table 3. Greatest range of mean values among the cluster was recorded for different traits. Cluster means revealed that substantial variability existed for all the maturity, morphological and yield traits, confirming their respective

contribution towards divergence. Similar results were obtained by (Gazal *et al.*, 2017; Varaprasad and Shivani, 2017) [4, 15]. Therefore, it is suggested that lines from most diverse clusters may be used as parents in hybridization programme to develop high yielding hybrids or varieties.

Contributions for the characters towards divergence are presented in Table 4. The percent contribution of different characters towards divergence revealed that maximum contribution was by plant height (58.16%), followed by 100 seed weight (30.34%). Higher contribution by traits like plant height and 100 seed weight to total divergence was reported by (Azad *et al.*, 2012). Jagadev and Samal (1991) [1, 6] reported that plant height was higher contributor towards diversity in niger. Thiagarjan *et al.* (1988) [14] observed that plant height as higher contributor towards diversity in cowpea. Based on percent contribution towards genetic divergence, emphasis can be made on selection of those characters with more contribution towards genetic divergence for creating variability in the population.
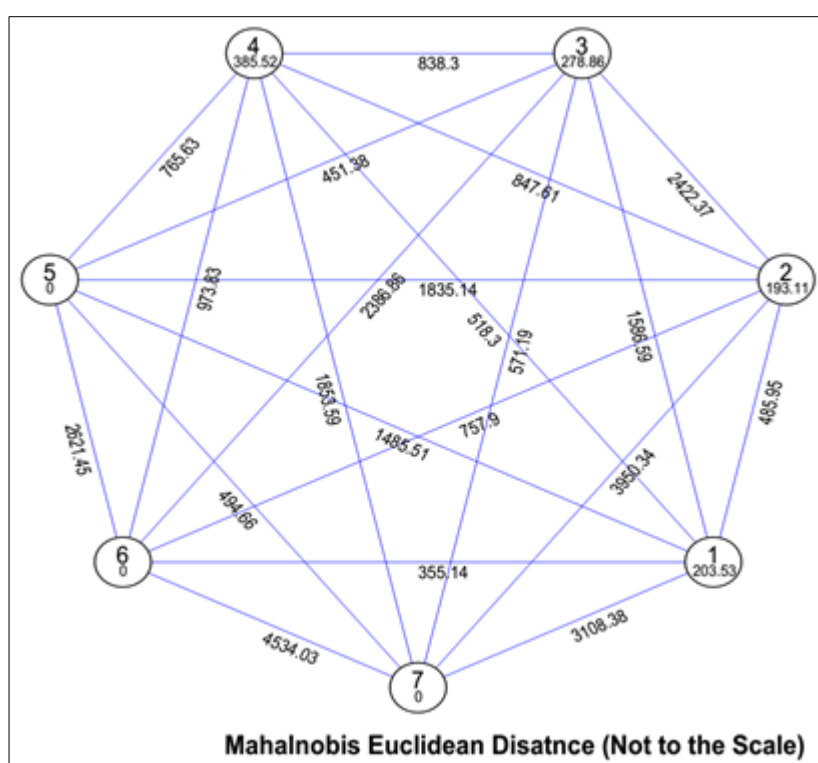

Fig 2: Tochers method

Table 2: Average inter-cluster (above diagonal) and intra-cluster (diagonal) D^2 values among different maize (*Zea mays* L.) inbreds

Cluster	Cluster 1	Cluster 2	Cluster 3	Cluster 4	Cluster 5	Cluster 6	Cluster 7
1	203.53	485.95	1586.59	518.3	1485.51	355.14	3108.38
2		193.11	2422.37	847.61	1835.14	757.9	3950.34
3			278.86	838.3	451.38	2386.86	571.19
4				385.52	765.63	973.83	1853.59
5					0	2621.45	494.66
6						0	4534.03
7							0

Table 3: Cluster means for maturity, morphological and yield traits in different clusters of maize (*Zea mays* L.) inbreds

Clusters	Days to anthesis	Days to silking	Anthesis silking interval	Plant height	Cob height	No. of cobs per plant	Cob diameter	Cob length	No.of kernel rows cob^{-1}	No. of kernels row^{-1}	100 seed weight	Grain yield hac.$^{-1}$
1	71.78	73.89	2.11	126.39	54.82	1.00	2.81	13.92	12.00	17.83	16.97	23.74
2	77.55	79.77	2.22	130.55	53.29	1.00	2.95	13.67	12.00	19.33	15.50	23.82
3	74.75	76.66	1.91	89.06	39.44	1.00	2.59	12.63	10.50	18.79	16.10	20.83

4	76.5	78.83	2.33	110.80	47.34	1.00	2.58	14.10	11.00	18.40	16.31	21.71
5	69.66	70.33	1.34	93.00	37.66	1.00	2.64	13.00	12.00	18.00	14.10	20.13
6	75.33	78.66	3.33	132.66	74.66	1.00	2.95	16.00	10.00	24.00	18.10	27.99
7	70.66	72.00	1.34	73.66	22.66	1.00	2.00	10.00	12.00	16.00	14.70	19.32

Table 4: Percent contribution of individual traits towards total divergence in Maize (*Zea mays* L.) Inbreds

Traits	Number of times ranked Ist	Per cent contribution towards total divergence (%)
Days to tasseling	7	1.61%
Days to silking	-	-
Anthesis silking interal	-	-
Plant height	253	58.16%
cob height	-	-
No. of cobs per plant	4	0.92%
Cob diameter	10	2.30%
Cob length	17	3.91%
No. of kernel rows cob^{-1}	6	1.38%
No. of kernels row^{-1}	-	-
100 seed weight	132	30.34%
Grain yield per ha.	6	1.38%
Total	435	100%

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