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Research Article

Assessment of genetic diversity of maize (*Zea mays* L.) hybrids under water logging condition

Gayatri Kumawat[1*], Jai Prakash Shahi[2] and Munnesh Kumar[3]

Department of Genetics and Plant Breeding, Institute of Agriculture Science,
Banaras Hindu University, Varanasi-221005, India.
[1] Research Scholar, Department of Plant Breeding and Genetics, Sri Karan Narendra Agriculture University, Jobner, Rajasthan, India
[2] Professor, Department of Genetics and Plant Breeding, Institute of Agriculture Science, Banaras Hindu University, Varanasi, India
[3] Research Scholar, Department of Genetics and Plant Breeding, Institute of Agriculture Science, Banaras Hindu University, Varanasi, India
*E-Mail: kumawatgayatri10@gmail.com

Abstract
The screening of fifty five CIMMYT maize hybrids was carried out to estimate the genetic diversity which was evaluated undermanaged waterlogged or excess soil moisture condition, indicated presence of considerable diversity. The experiment was conducted in an alpha lattice design with two replication and phenotypic data were analyzed using fifteen agro-morphological traits. The fifty five maize single cross hybrids grouped into eight clusters based on Mahalanobis D^2 statistic. Among them cluster I accommodated maximum number of inbred lines (41) followed by cluster V (8). Presence of six solitary clusters indicated larger genetic diversity. The character plant height showed highest contribution towards genetic divergence followed by number of kernel per row, ear height, number of rows per ear, grain weight per plot and 100 seed weight. Based upon the divergence studies suggesting crossing may be made between genotypes of cluster II (P3502) and V (ZH17505, ZH17507, ZH17497, ZH15567, ZH15557, ZH15564, ZH15563 and ZH15562), and the hybrid in these cluster could be used as donor parents for new double cross maize hybrid development for improving yield under water logging condition.

Keywords
Genetic diversity, Mahalanobis D^2 statistic, water logging and clusters.

INTRODUCTION

Maize is known as "Queen of Cereals" because of its highest yield potential and wider adaptability among all cereals. It is the world's most widely cultivated cereal and is the primary staple food in many developing countries (Morris *et al.*, 1999). Karnataka has the highest area 1.2 Mha and production 3.3 M Tonnes whereas Tamil Nadu has the highest productivity 6.5 t/ha. Maize ranks second in yield, third in production and area in India [Economic Survey 2015-16, MoA and FW, GOI].

Among the various abiotic stresses, Excess Soil Moisture (ESM) stress caused by temporary water-logging, due to heavy rains or high ground water table or heavy soil texture is one of the most important constraints for maize production and productivity in Asian regions. So, by exploiting diverse lines in hybridization programme which are water logging resistance/tolerance can reduce this constraints.Precise information on the nature and degree of genetic divergence would help the plant breeder in choosing the perfect parents for different breeding procedures. For developing high yielding double cross hybrids in maize, single cross hybrid lines need to be evaluated for their genetic diversity. Several studies on maize have shown that single crosses from genetically diverse parents tend to be more productive than crosses of single crosses lines from same source (Singh *et al.*, 2015). The manifestation of heterosis in the progeny is usually depends on the genetic divergence of two parents (Saxena *et al.*, 1998). Therefore, characterization of genetic diversity of maize germplasm lines is of great

importance in hybrid maize breeding (Xia *et al.*, 2005). It has become possible to quantify magnitude of genetic diversity among hybrids with the help of advanced biometrical methods such as multivariate analysis (Rao, 1952) based on Mahalanobis (1936) D² statistics. With this view, genetic diversity among 55 newly developed maize hybrids was studied using multivariate approaches of analysis of variation to select out diverse water logging resistance single cross hybrids to develop high yielding double cross hybrid.

MATERIAL AND METHOD
The experiment material comprised of 53 maize single cross hybrids along with two checks (900MG and P3502) which were obtained from CIMMYT (International Maize and Wheat Improvement Center) germplasm under the project: "Climate Resilient Maize for Asia (CRMA)". The experimental hybrids developed initially under optimal, moisture, drought and water logging condition. All maize hybrids along with two checks were sown in alpha lattice design with two replications at the Agriculture Research Farm of Institute of Agriculture Science, Banaras Hindu University during *Kharif* 2017. Each hybrid was planted in two rows of three meters each in length with a spacing of 60x25cm with ten plants per row. The results obtained from the statistical analysis of the data from 55 maize hybrids for 15 characters *viz.*, days to 50% anthesis, days to 50% silking, number of surface roots, number of nodes bearing brace roots, plant height (cm), ear height (cm), ears per plot, plant population, ear length (cm), grain weight per plot, ear diameter (cm), number of kernel rows per ear, number of kernels per row, yield per plant and 100 seed weight.

Water logging /excess moisture stress was managed at approximately 2-3 inch depth for seven days at V_6-V_7 growth stage/ knee height stage of crop growth (35 days after sowing). Proper bunding was done so that water remains within and after seven days, water was drained out (Zaidi *et al.,* 2016). The crop was raised as per the recommended agronomic package of practices. The statistical analysis of data based on the mean value of recorded observations on five random plant basis was done for determining the genetic diversity of the experimental hybrid. The analysis was carried out by using INDOSTAT software.

The data collected on different characters were analyzed using Mahalanobis' D² statistics to determine the genetic divergence among the genotypes (Mahalanobis, 1928). D² value between i^th and j^th genotypes for 'P' characters was calculated as

$$D^2_{ij} = \sum_{t=1}^{p} Y_{it} - Y_{jt_t}$$

Where,

Y_i^t is the uncorrelated mean value of ith genotype for 't'characters

Y_j^t is the uncorrelated mean value of jth genotype for 't' characters

D^2_{ij} is D² between i^th and j^th genotypes.

The D² value obtained for a population pair is taken as a calculated value of ÷² and is tested against the tabulated value of ÷² for P degrees of freedom where P is the number of characters estimated. In the present study P is 15. The grouping of genotypes into different clusters was done using Tocher's method as described by Rao (1952).

RESULT AND DISCUSSION
The percent contribution of individual characters towards genetic divergence by all the fifteen traits is presented in **Table1.** The character plant height showed highest percent contribution (28.48) towards total genetic divergence followed by number of kernels per row (13.67), ear height (8.82), number of kernel rows per ear (7.47), grain weight per plot (7.41), 100 seed weight (6.94), ear length (4.98), days to 50% silking (3.91), ear diameter (3.64),ear per plot (3.1), days to 50% anthesis (2.9), plant population (2.76), yield per plant (2.63),number of surface roots (2.49) and number of nodes bearing brace roots (0.81). These results are in agreement with that of Hoque *et al.* (2017) and Maruthi *et al.* (2015) who also identified above said characters as the principal components contributing maximum to the total variation in maize. These characters should be given importance for selecting diverse parents for water logging resistance breeding programmes in maize (Narayan *et al.*, 2015).

Table 1.Contribution of different characters towards genetic divergence among 55 maize hybrids

Characters	Contribution toward divergence
Number of surface roots	2.49
Number of nodes bearing brace roots	0.81
Days to 50% anthesis	2.90
Days to 50%silking	3.91
Plant height	28.48
Ear height	8.82
Plant population	2.76
Ears per plot	3.10
Grain weight per plot	7.41
Ear length	4.98
Ear diameter	3.64
Number of rows per ear	7.47
Number of kernels per row	13.67
Yield per plant	2.63
100 seed weight	6.94

From the point of selecting the hybrids (parents) for hybridization, which are divergent enough for the character of interest, estimation of the genetic distance is most important. The present estimation of genetic divergence gave clear idea about the diverse nature of the population. Wide range of variation was observed in cluster mean performance for most of the characters studied. All the genotypes were grouped into eight clusters, using the Tocher's method with the criterion that the intra-cluster average D² values should be less than the inter-cluster D² values, indicating the presence of diversity for different traits. The distribution of 55 hybrids into eight clusters is

presented in **Table 2** with the maximum number of 41 hybrids in cluster I. Whereas Cluster V is the second largest with eight hybrids and cluster II (P3502), III (VH11128), IV (ZH17509), VI (ZH17504), VII (ZH17498) and VIII (ZH17494) consists of single hybrid in each. The formation of distinct solitary clusters may be due to the fact that intensive natural and human selection for diverse and adaptable gene complexes otherwise due to geographic barriers preventing gene flow must be responsible for this genetic diversity. The findings were supported by Alam *et al.* (2013) and Mani and Deshpande (2016).

Table 2. The distribution of the 55 maize (*Zea mays* L.) hybrids into different clusters on the basis of D² statistics

Clusters	Number of hybrids included	Genotype
I	41	ZH15546, ZH15547, ZH15548, ZH15549, ZH15550, ZH15551, ZH17495, ZH138260, ZH15553, ZH15554, ZH15555, ZH138267, ZH17229, ZH15558, ZH15559, ZH15560, ZH15561, ZH17499, ZH138269, ZH17501, ZH138294, ZH17230, ZH15565, ZH15566, ZH17502, ZH17503, ZH138303, ZH138305, ZH17506, ZH17508, ZH138312, ZH17231, ZH138278, ZH17232, , ZH15568, ZH15556, ZH17496, ZH17228, ZH17500, ZH17510, 900MG
II	1	P3502
III	1	VH11128
IV	1	ZH17509
V	8	ZH17505, ZH17507, ZH17497, ZH15567, ZH15557, ZH15564, ZH15563, ZH15562
VI	1	ZH17504
VII	1	ZH17498
VIII	1	ZH17494

The average intra and inter cluster D² values estimated as per the procedure was given by Singh and Chaudhary (1977) and were presented in **Table 3** and **fig. 2**. Dendrogram represented the relationship among 55 maize genotypes in eight clusters based on Mahalanobis's D² values are presented in **fig.1**. The intra and inter cluster D² values indicated that inter cluster D² values were higher than intra cluster D² values. The maximum intra cluster

D² value was 266.01 for cluster V followed by 178.75 for cluster I while it was zero for cluster II (P3502), III (VH11128), IV (ZH17509), VI (ZH17504), VII (ZH17498) and VIII (ZH17494). The high intra cluster distance in cluster V indicated the presence of wide genetic diversity among the genotypes *viz.*, ZH17505, ZH17507, ZH17497, ZH15567, ZH15557, ZH15564, ZH15563, ZH15562.

Table 3. Average intra (bold) and inter-cluster D² values for eight clusters in fifty five hybrids of maize (*Zea mays* L.)

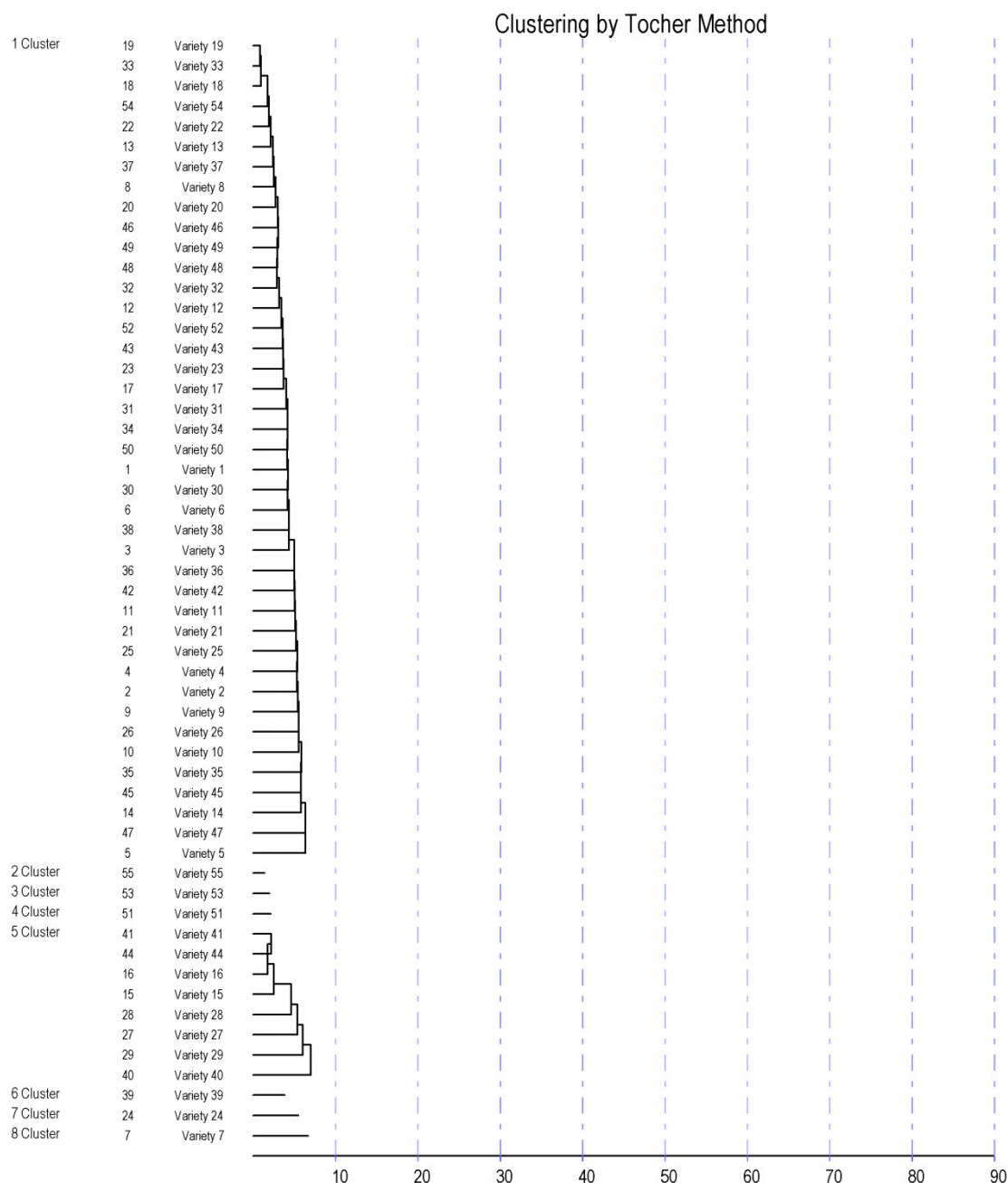|	Cluster1	Cluster2	Cluster3	Cluster4	Cluster5	Cluster6	Cluster7	Cluster8
Cluster1	**178.756**	416.56	341.88	320.76	684.34	541.49	513.92	957.90
Cluster2		**0**	1288.81	35.76	3162.93	1537.42	337.82	2814.30
Cluster3			**0**	484	406.42	570.25	1145.82	736.57
Cluster4				**0**	2209	1182.67	619.01	2566.43
Cluster5					**266.016**	601.72	1765.68	940.64
Cluster6						**0**	658.94	1390.54
Cluster7							**0**	2006.14
Cluster8								**0**

Fig 1.Dendrogram showing relationship among 55 maize (*Zea mays* L.) hybrids in eight clusters based on Mahalanobis's D^2 values.

Maximum inter cluster distance was recorded between the clusters II and V (56.24) followed by cluster II and VIII (53.05) suggesting more variability in genetic makeup of the hybrids included in these clusters. Based on inter cluster D value crosses may be made between genotypes of clusters II (P3502) and cluster V (ZH17505, ZH17507, ZH17497, ZH15567, ZH15557, ZH15564, ZH15563, ZH15562) followed by genotypes of clusters II (P3502)
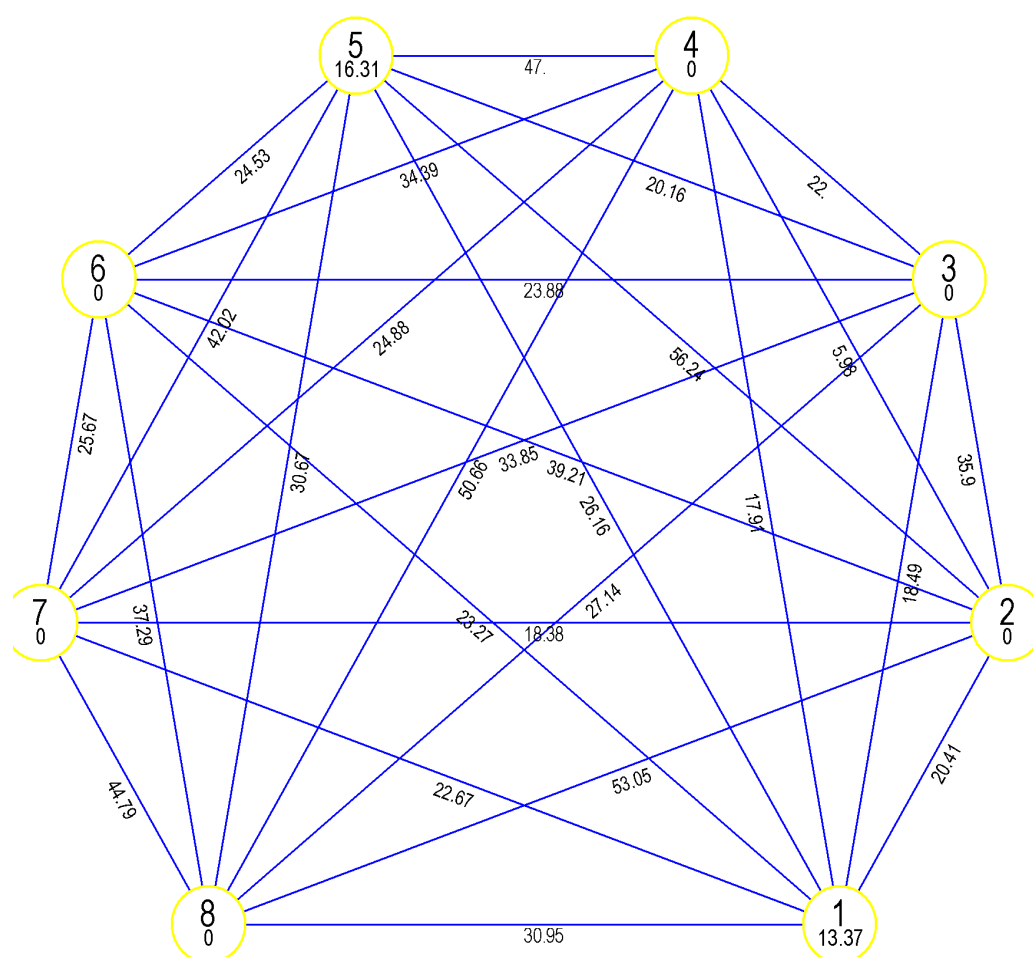
and VIII (ZH17494) to obtain new desirable recombinants in maize. Minimum inter cluster distance was recorded between cluster II and IV (5.98). The genotypes belonging to the clusters separated by high statistical distance could be used in hybridization programme for obtaining a wide spectrum of variation among the segregates. These findings are in conformity with the findings of

Singh *et al.*, (2015) Ganesan *et al.* (2010) and Marker and Krupakar (2009), Williams and Hallauer (2000).

Greater range of mean values among the cluster was recorded for different traits. Analysis of cluster means revealed the relative contribution of different traits to the total divergence by the different clusters. Based on range of means, it is possible to know the characters influencing divergence. It helps to identify clusters having different levels of variability for different characters, based on final ranks it is possible to identify clusters having higher and lesser diversity for more number of characteristics. Utilization of low ranked clusters in breeding programme is expected to yield desirable lines in advanced generation of selection. The mean values of fifteen characters studied in 55 maize genotypes for eight clusters are presented in

Table 5. Cluster II had the highest mean value for days to 50% silking, plant height, ear height. Cluster III had maximum mean value for ear length, number of kernel per row, yield per plant. Cluster IV had the highest mean value for plant population, grain weight per plot. Cluster V had a maximum mean value for days to 50% anthesis. Cluster VIII showed protogyny condition and Cluster I showed less anthesis silking interval which is similarly to Lakshmi (2018). Cluster VI had maximum mean value for number of nodes bearing brace roots and ear per plant. Cluster VII had the highest mean value for ear diameter and number of rows per ear. Cluster VIII had the highest mean value for number of surface roots and seed index. Similar results also reported by Ganesan *et al.* (2010). Therefore, it is suggested that most diverse clusters may be used as parents in hybridization programme to develop high yielding hybrids (Lahane *et al.*, 2016).

Tocher Method

Mahalnobis Euclidean Disatnce (Not to the Scale)

Fig 2. Intra and Inter-cluster distances of 55 maize (*Zea mays* L.) hybrids in eight clusters based on Euclidean D^2 distances

Table 4. The nearest and farthest clusters from each cluster based on D values in maize (*Zea mays* L.) genotype

Cluster No.	Nearest cluster with D values	Farthest cluster with D value
I	IV (17.91)	XIII(30.95)
II	IV (5.98)	V(56.24)
III	I (18.49)	II(35.9)
IV	II (5.98)	VIII(50.66)
V	III(20.16)	II(56.24)
VI	I(23.27)	II(39.21)
VII	II(18.38)	VIII(44.79)
VIII	III(27.14)	II(53.05)

Table 5.Mean values of eight clusters by Tocher's method for 55 genotypes of maize (*Zea mays*L.)

	No. of surface roots	No. of nodes bearing brace roots	Days to 50% anthesis	Days to 50% silking	Plant height (cm)	Ear height (cm)	Plant population	Ears per plot	Grain weight per plot (t/ha)	Ear length (cm)	Ear diameter (cm)	No. of kernel rows per ear	No. of kernels per row	Yield per plant	100 seed weight (gm)
Cluster1	11.44	2.70	61.22	62.40	120.91	54.82	13.77	14.17	1.17	12.48	3.94	13.69	19.70	68.10	25.22
Cluster2	10.50	3.00	60.50	64.00	147.50	77.50	14.00	15.00	1.17	10.10	4.36	14.00	17.50	61.00	26.52
Cluster3	10.00	3.00	59.50	63.00	115.00	45.00	14.00	12.00	1.48	13.52	4.10	11.00	24.90	99.10	28.66
Cluster4	6.50	2.50	59.50	63.00	145.00	70.00	16.50	16.50	1.75	11.75	4.00	13.20	20.50	65.50	27.40
Cluster5	11.06	3.00	61.44	62.94	90.00	32.50	13.06	9.81	0.59	10.89	3.50	11.24	16.21	41.56	23.84
Cluster6	13.00	3.50	57.00	59.50	115.00	52.50	14.00	17.50	1.26	10.98	4.01	10.00	10.70	43.40	24.28
Cluster7	10.50	2.50	60.50	62.50	117.50	60.00	10.00	15.00	1.07	10.91	6.90	14.20	17.10	60.60	25.49
Cluster8	16.00	2.50	60.50	60.00	110.00	40.00	14.00	16.00	1.04	10.44	3.90	14.00	17.60	60.70	48.16

Genetic divergence of hybrids should be assessed in evaluating potential crosses particularly for double cross hybrid. Considering the estimation of genetic diversity the present investigation, crossing among the maize hybrids between cluster II (P3502) and cluster V (ZH17505, ZH17507, ZH17497, ZH15567, ZH15557, ZH15564, ZH15563 and ZH15562) may be recommended which can throw out superior segregants in hybridization. So the genotypes belonging to these clusters can be exploited in future breeding programmes for improving yield under water logging condition.

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