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Genetic Diversity in Maize (*Zea mays* L.) Inbred Lines from Kashmir

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ABSTRACT

Genetic diversity in 47 maize inbred lines was assessed based on morphological traits. The Experiment was conducted using RCBD with two replications at Dryland Agriculture Station, Budgam, Jammu & Kashmir in Kharif 2015. D^2 analysis was performed and clustering was done using Tocher's Method. All the inbreds were grouped into 7 clusters. Cluster number IV contained highest number (29) of inbreds and cluster III and VI contained lowest number (2) of inbreds. Cluster II and V, V and VI, VI and VII showed maximum distance between them suggesting higher probability of heterotic hybrids if selection of parents is done from these pairs of groups. Days to tasselling, and days to maturity showed highest contribution to total divergence. This study gave an insight into the variability pattern of the inbred lines which will be helpful in their further utilisation.

Key words: *Maize, inbreds, diversity, D^2, variability*

INTRODUCTION

Maize (*Zea mays* L.) is best known as golden crop because every part of this crop is useful to man, animals and the industries. Maize (*Zea mays* L.) is currently produced on nearly 160 million hectares in 125 developing countries with a production of 850 million tonnes[2]. In Jammu and Kashmir, the crop occupies an area of 0.31 million ha with production of 0.5 million quintals and productivity of 1.64 t/ha[1]. Lower productivity due to locally grown low yielding cultivars is the main limitation of maize production in Kashmir valley. The major objective of most of the maize breeding programmes is to develop better yielding hybrids than the existing cultivars[11], so hybrid breeding remains the choice of the method considering its success over the years. To develop high yielding hybrids in maize, inbred lines need to be evaluated for their genetic diversity which is important for planning an effective hybrid breeding program as genetically diverse parents are known to produce high heterotic effects. Morphological traits are the functional manifestation of underlying genetic constitution of an organism hence they constitute an important set of markers to assess the genetic diversity.

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Several methods have been reported to decipher the pattern and magnitude of variability such as D^2, cluster analysis and principal component analysis. In view of the above status, 47 inbred lines developed at DARS, Budgam were investigated for the extent of variability with respect to their morphological traits.

MATERIAL AND METHODS

Experimental material and location: Forty seven inbred lines of maize (*Zea mays*) at S-9 stage which were developed at DARS were grown in RCBD design with two replications at Dryland Agriculture Station, Budgam, Jammu & Kashmir in *Kharif* 2015. The experimental plot consisted of two rows each of 4 m length maintained with a row to row spacing of 60 cm. Recommended package of practices were followed for raising a good crop. Data were recorded on yield and different yield contributing traits viz, days to tasseling, days to silking, days to maturity, plant height, ear height, ear per plant, kernels per row, hundred grain weight, yield per plot and protein content.

Data analysis: The analysis was carried out by applying standard statistical techniques for analysis of variance to establish significance level among the inbreds for various traits as described by Singh and Choudhary[10] and Steel and Torrie[12]. Data were subjected to principal component and Mahalanobis[6] D^2 statistical analysis extended by Rao[9]. Intra-cluster and inter-cluster distance, cluster mean and contribution of each trait to the divergence were estimated as suggested by Singh and Chaudhary[10]. Windostat 9.1 and SPSS 11 were used for analysis.

RESULTS AND DISCUSSION

Mean and coefficient of variation of eleven (11) traits in 47 maize inbred lines are presented in Table 1. Analysis of variance showed significant differences among the inbreds for all the characters under this investigation indicating considerable variation among studied genotypes. Maximum CV% was found for anthesis-silking interval. Inbred lines viz., IL5, IL9 and IL11 showed longest duration (more than 82 days) to anthesis. Five inbred lines IL7, IL13, IL15, IL26 and IL47 took less than 76 days to tassel showing early flowering behaviour which is of importance in Kashmir scenario. Two inbreds IL7 and IL 47 showed more than 24 kernels per row and these two lines also showed higher 100 gain weight (more than 24gm). Both of these lines were the lines showing highest protein content and highest yield per plot indicating to be useful resources for breeding program. Various genetic parameters, such as GCV (genotypic coefficient of variation), PCV (phenotypic coefficient of variation), h^2_b%, GA (genetic advance) and GA% were estimated for all the characters under study (Table 1). All studied characters showed marked differences between GCV and PCV estimates suggesting that substantial variation for these characters was contributed by environmental components. Higher values of GCV for anthesis-silking interval, grain yield and protein content indicated higher degree of genetic variability in these traits. Similar results have also been observed by Wannows *et al*[13]., and Zaman and Alam[14] in maize inbred lines. Heritability estimates in broad sense were relatively high for all the characters except ASI.

High estimates of h^2_b% along with high GA% for plot yield and protein content suggested that improvement of these characters would be effective through phenotypic selection due to additive gene action. High h^2_b% estimates for plant height, cob height, number of rows/cob and number of kernels/row have been reported in maize by Wannows *et al*[13].

Forty-seven maize inbred lines were grouped into 7 different clusters by using clustering techniques given by Tocher and explained by Rao[9]. Distribution of inbred lines into various clusters is presented in Table 2. The maximum number of inbreds (29) got grouped in cluster IV which was followed by cluster II and VII (4). The cluster III and VI contained two lines and occupied least position.

D^2 analysis carried out involving 47 inbred lines for 11 characters revealed that altogether 7 clusters have been formed (Figure 1). Inter and intra-cluster distance ($D = \sqrt{D^2}$) values were worked out from divergence analysis and are listed in Table 3. From the table, it was revealed that the inter-cluster distances were larger than the intra-cluster distances indicating wide diversity among the inbred lines of different clusters. The maximum intra-cluster distance (D = 54.61) was observed in cluster VII followed by cluster V (D = 50.78) and IV (D = 47.94). The highest inter-cluster distance (D = 3730.93) was observed between clusters V and VI followed by clusters VI and VII (D = 3111.15), suggesting more divergence in genetic makeup of the inbred lines included in these cluster pairs.

The inbred lines 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 and to obtain high heterosis. In this context, inbred lines from cluster V and VI may be selected as parents in hybridization programme for yield improvement in maize inbred lines. The distance between clusters IV and VII was minimum (615.87) followed by the distance between the clusters III and IV (619) indicating that the inbred lines belonging to these clusters were comparatively less diverse. It is expected that the crosses between the lines of clusters V and VI would exhibit high heterosis and also likely to produce new recombinant with desired characters.

The genetic differences between clusters were reflected in their cluster means. Cluster mean values for 11 yield related characters are presented in Table 4. The highest mean values for days to tasseling, silking and ASI were observed in the cluster VII. Plant height, ear height, number of kernels/row, Ear per plant, 100 kernel weight, yield per plot and protein content were found maximum in cluster VI. Required minimum days to tasselling, silking and maturity, were observed in cluster VI indicating the early inbreds in this group. Cluster VII showed minimum plant height indicating that this cluster includes the shorter inbreds. The highest yield was produced by the inbreds of cluster VI followed by cluster II. Considering all the characters it appears that the inbreds in the cluster VI performed better. The inbreds in this cluster had shorter growth duration, highest number of kernels/row, 100 grain weight, grain yield/plant and protein content compared to all other clusters. Similar results have also been reported by Azad *et al*[3]., and Zaman and Alam[14]. Hence, for the improvement of different characters viz. DT, DS, DM, EL and GYP under the present study, inbred lines should be selected from clusters VI, II and I. Contribution of characters towards divergence was obtained from canonical variate analysis (CVA) and is presented in Table 4.

The coefficients pertaining to the different characters in the first two canonical roots are presented in Table 4. The values of vector 1 and vector II revealed that both the vectors had positive values for days to tasseling days to tasseling and days to maturity. These results indicated that these three characters had highest contribution towards divergence among the 11 characters for 47 maize inbred lines. In vector I, other important character responsible for genetic diversity in the major axis of differentiation was number of kernels/row while in vector II (the second axis of differentiation) days to tasseling, days to silking, days to maturity, ear per plant and yield/plant contributed positive impact on divergence. Negative values in both the vectors were for ASI, 100 grain weight, and protein content which indicated that these three characters had lowest contribution to the total divergence. So, the greater divergence in the present materials due to these three characters will offer a good scope for improvement of yield through selection of parents. These results get sufficient validation from the findings of Azad *et al*[3]., and Zaman and Alam[14].

Principal Component Analysis (PCA) also helps in assessment of diversity on multivariate scales. In PCA, the first two components were found to contribute 77.76 %

of the total variation (Table 5). Contribution of different characters as per the PCs is given in Table 5. Graphical display of PCA in biplot indicated the similarity among the traits in their contribution towards total variation (Figure 2). Biplot indicated that the days to silking, days to tasselling, ASI and days to maturity were closely related traits and rest of other traits fell in another group based on the expression of variability (Figure 2).

Table 1: Estimation of mean performance and genetic parameters for grain yields and yield components in maize inbred

Characters	Mean	CV%	F- test	PCV%	GCV%	h2b%	GA	GA (%) of mean
Days to tasseling	78.2575	0.5462	**	3.2002	3.1533	0.971	6.4191	8.2025
Days to silking	81.9383	0.6645	**	3.5163	3.453	0.964	7.3348	8.9516
ASI	3.6809	8.607	**	14.4544	11.6124	0.645	0.9066	24.6291
Plant height (cm)	155.0618	0.1862	**	2.7033	2.6968	0.995	11.0136	7.1027
Ear height	74.5502	0.1841	**	2.7047	2.6984	0.995	5.2986	7.1074
Days to maturity	147.8553	0.3663	**	2.7564	2.7319	0.982	10.5692	7.1483
EPP	1.2298	0	**	6.3248	6.3248	1	0.2053	16.6974
No. of kernels/row	21.849	0.2537	**	5.3961	5.3902	0.998	3.1057	14.2143
100 grain weight	20.6748	0.2287	**	6.0012	5.9968	0.999	3.2708	15.8201
Grain yield/plant (g)	511.0777	0.311	**	15.3201	15.317	1	206.6211	40.4285
Protein content (%)	7.9946	0.5949	**	12.1414	12.1269	0.998	2.5564	31.9764

***, ** Significant at 5% and 1% level of probability, respectively.**

Table 2: Distribution of 47 maize inbred lines in 7 different clusters

Group/Cluster no.	No. of inbred lines	Name of inbred lines present in a cluster
I	3	IL27, IL28, IL6
II	4	IL10, 15, 13, 21
III	2	IL42, 43
IV	29	IL29, 30, 35, 9, 36, 33, 19, 38, 23, 20, 31, 46, 17, 1,
		12, 18, 11, 5, 40, 22, 2, 32, 4, 8, 14, 26, 3, 41, 34
V	3	IL24, 25, 16
VI	2	IL7, 47
VII	4	IL37, 39, 44, 45

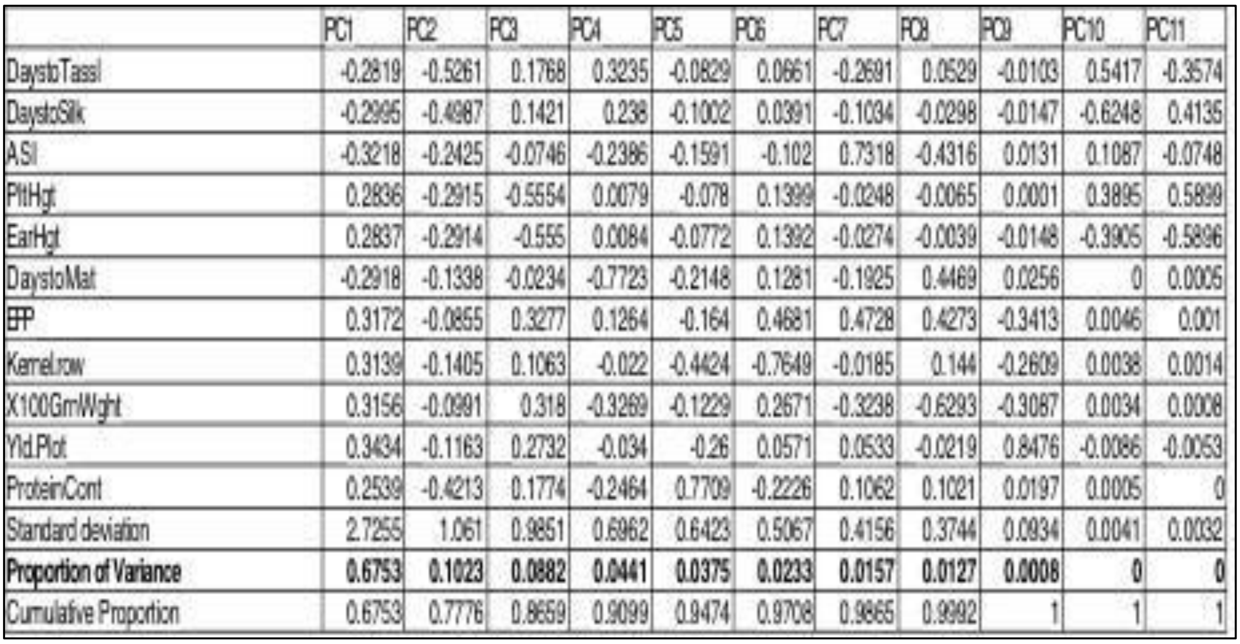
Table 3: Average intra- (bold) and inter-cluster distance (D2) for 25 maize inbred lines obtained on the basis of 11 morphological characters

Clusters	I	II	III	IV	V	VI	VII
I	**6.23**						
II	624.48	**13.18**					
III	625.47	1249.84	**12.71**				
IV	1242.94	1866.77	619	**47.94**			
V	2475.97	3100.01	1850.86	1235.18	**50.78**		
VI	1256.02	631.86	1881.26	2497.95	3730.93	**17.42**	
VII	1856.16	2480.15	1231.32	615.87	622.33	3111.15	**54.61**

Table 4: Cluster means and relative contributions of 11 characters to the total divergence in maize inbreds

Characters	Clusters							Vector 1	Vector 2
	I	II	III	IV	V	VI	VII		
Days to tasseling	75.75	75.56	75.5	79.14	78.5	75	79.25	0.00348	0.09761
Days to silking	78.75	78.56	78.5	82.98	82.5	78	83.38	0.0011	0.01579
ASI	3	3	3	3.84	4	3	4.13	0	0
Plant height (cm)	159.3	159.9	158.78	153.69	155.27	161.34	151.83	-0.00944	-0.37191
Ear height	76.59	76.88	76.37	73.89	74.65	77.57	72.99	-0.00156	-0.05737
Days to maturity	143.1	142.5	144.5	148.78	152.17	142.13	151.25	0.00597	0.07113
EPP	1.3	1.35	1.25	1.2	1.1	1.4	1.15	-0.94766	0.06888
Kennels/row	23.36	23.72	23.11	21.32	21.64	24.12	21.09	0.1194	-0.72172
100 grain weight	22.28	22.63	21.75	20.12	19.8	23.52	20.25	-0.17936	-0.54247
Yield/plant (g)	612.5	656.08	569.53	477.98	435.02	716.24	455.17	-0.24712	0.13782
Protein Content	9.09	9.22	8.98	7.57	7.81	9.81	7.76	-0.0918	-0.06829

Table 5: PCA analysis for morphological traits in maize inbreds



	PC1	PC2	PC3	PC4	PC5	PC6	PC7	PC8	PC9	PC10	PC11
DaystoTassl	-0.2819	-0.5261	0.1768	0.3235	-0.0829	0.0661	-0.2691	0.0529	-0.0103	0.5417	-0.3574
DaystoSilk	-0.2995	-0.4987	0.1421	0.238	-0.1002	0.0391	-0.1034	-0.0298	-0.0147	-0.6248	0.4135
ASI	-0.3218	-0.2425	-0.0746	-0.2386	-0.1591	-0.102	0.7318	-0.4316	0.0131	0.1087	-0.0748
PltHgt	0.2836	-0.2915	-0.5554	0.0079	-0.078	0.1399	-0.0248	-0.0065	0.0001	0.3895	0.5899
EarHgt	0.2837	-0.2914	-0.555	0.0084	-0.0772	0.1392	-0.0274	-0.0039	-0.0148	-0.3905	-0.5896
DaystoMat	-0.2918	-0.1338	-0.0234	-0.7723	-0.2148	0.1281	-0.1925	0.4469	0.0256	0	0.0005
EPP	0.3172	-0.0855	0.3277	0.1264	-0.164	0.4681	0.4728	0.4273	-0.3413	0.0046	0.001
Kernel.row	0.3139	-0.1405	0.1063	-0.022	-0.4424	-0.7649	-0.0185	0.144	-0.2609	0.0038	0.0014
X100GmWght	0.3156	-0.0991	0.318	-0.3269	-0.1229	0.2671	-0.3238	-0.6293	-0.3087	0.0034	0.0008
Yld.Plot	0.3434	-0.1163	0.2732	-0.034	-0.26	0.0571	0.0533	-0.0219	0.8476	-0.0086	-0.0053
ProteinCont	0.2539	-0.4213	0.1774	-0.2464	0.7709	-0.2226	0.1062	0.1021	0.0197	0.0005	0
Standard deviation	2.7255	1.061	0.9851	0.6962	0.6423	0.5067	0.4156	0.3744	0.0934	0.0041	0.0032
Proportion of Variance	**0.6753**	**0.1023**	**0.0882**	**0.0441**	**0.0375**	**0.0233**	**0.0157**	**0.0127**	**0.0008**	**0**	**0**
Cumulative Proportion	0.6753	0.7776	0.8659	0.9099	0.9474	0.9708	0.9865	0.9992	1	1	1

Fig. 1: Distribution of 47 maize inbred lines in 7 different clusters

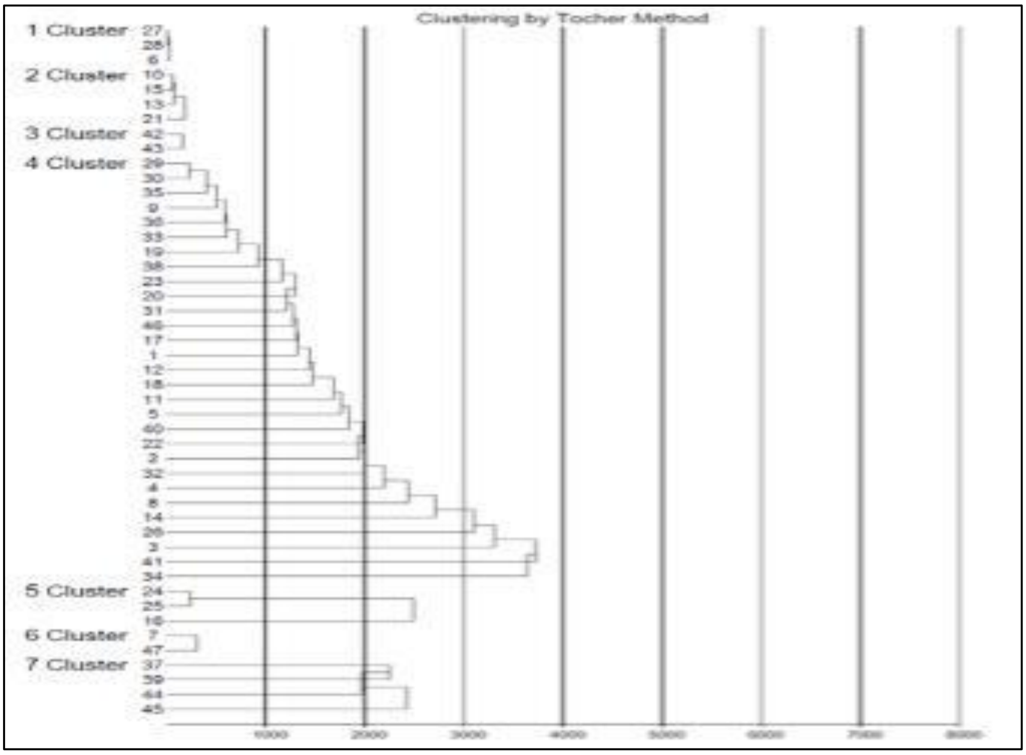
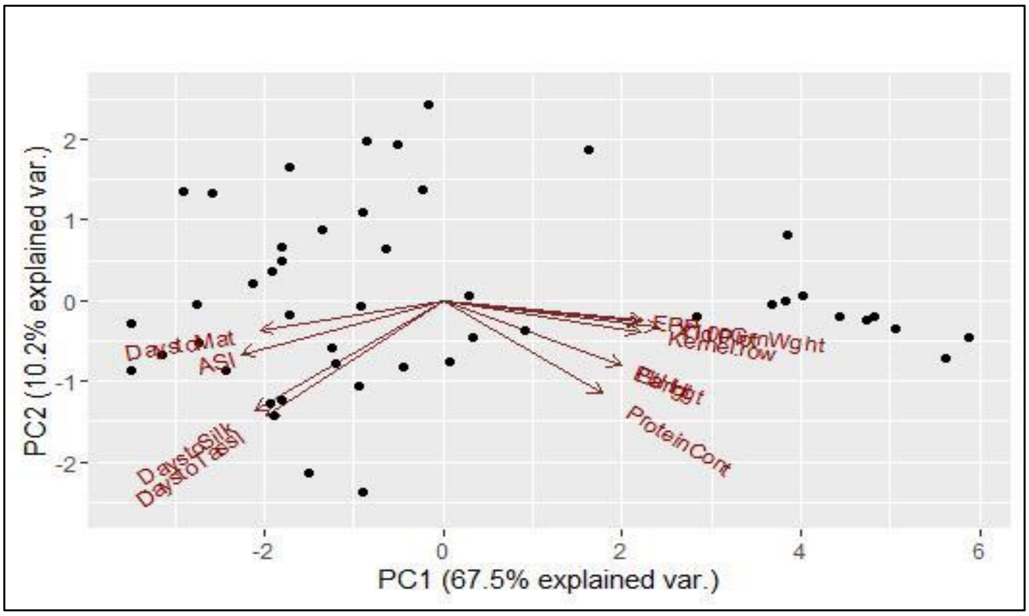


Fig. 2: Biplot of PC1 and PC2



Conclusion

Genetically diverse parents are expected to produce higher heterosis[5,7,8]. Endang *et al*[4]., stated parents from diverse clusters could be selected for crossing which are likely to generate the higher heterosis and good amount of variability for effective selection of various economic traits. Keeping this in view, the findings from the present study indicated that the cluster II and V, V and VI, VI and VII showed higher distance between them. The selection of parents for further breeding programme from these clusters would exert high heterosis in hybrids and wide variability in genetic architecture of subsequent generations. From this study it is evident that the clusters V and VI were highly divergent and the lines belonging to these clusters could be used effectively in hybridization program.

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