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Genetic diversity studies in newly developed early maturing yellow inbred lines of maize (*Zea mays* L.)

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Abstract
The present study was conducted to know the genetic diversity among newly developed early maturing yellow inbred lines of maize during Kharif 2017 at Experimental Farm, SAREC, Kangra. In this experiment, forty one inbred lines and two checks were evaluated and observations were recorded for twelve quantitative traits. Analysis of variance revealed significant difference among all inbred lines. Inbred lines were grouped into nine clusters, indicating the presence of genetic diversity. The genotypes were grouped into nine clusters. Cluster III comprised the maximum genotypes (16) which indicated the genetic similarity among them. The highest inter-cluster distance (29.33) was observed between clusters VIII and IV followed by clusters VII and IV (28.01), clusters IV and IV (24.4), clusters IX and IV (23.86), clusters VIII and II (21.66), clusters VII and II (21.48) and clusters IV and III (20.71), suggesting wider diversity between them and the genotypes in these cluster could be used as parents for maize hybrid development. The maximum intra-cluster distance was observed in cluster III (10.26) and the cluster IV was had the least intra cluster distance (6.96). The mean values of cluster II had relatively less days to anthesis and silking, bold grain size, more number of kernels rows/ear and the maximum yielding ability. Cluster IV also showed more kernel weight and reasonable yielding capacity. Plant height and 1000- kernel weight had the greatest contribution to genetic divergence, whereas, other characters like grain yield per plant, ear height, ear length, tassel length, days to silking, days to anthesis, leaf width, number of rows/ear and ear girth contributed very little for divergence.

Keywords: 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 is currently produced on nearly 183 million hectares in 125 developing countries with a production of 1038 million metric tonnes and productivity of 5.66 tonnes/ha. In Himachal Pradesh, the crop occupies an area of 293.6 thousand ha with production of 784.30 thousand tonnes and productivity of 2.67 t/ha (Anonymous, 2018). Lower productivity due to locally grown low yielding cultivars is the main limitation of maize production in State.

The major objective of most of the maize breeding programmes is to develop better yielding hybrids than the existing cultivars, so hybrid breeding remains the choice of the method considering its success over the years (Sreckov *et al.* 2010) [19].

Inbred lines are the prerequisite for hybrid variety development in crop plants. For developing high yielding hybrids in maize, inbred lines need to be developed and evaluated for their diverged gene pool. The genetic diversity between the genotypes is important as the genetically diverged parents are able to produce high heterotic effects (Ghaderi *et al.* 1979) [5]. Several studies on maize have shown that inbred lines from diverse stocks tend to be more productive than crosses of inbred lines from the same variety (Vasal, 1998) [23]. Manifestation of heterosis usually depends on the genetic divergence of the two parental varieties (Saxena *et al.* 1998) [14]. The quantification of genetic diversity through biometrical procedure made it possible to choose genetically diverse parents. Genetic diversity in maize is a valuable natural resource and plays a key role in hybrid breeding program. Knowledge of germplasm diversity and the relationship among elite breeding materials has a significant impact on the improvement of crop plants (Hallauer *et al.* 1988) [6]. In maize, this information is useful in planning crosses for hybrid and line development, in assigning lines to heterotic groups and in plant variety protection. Evaluation of genetic diversity is important to know the source of genes for a particular trait within the available germplasm (Tomooka, 1991) [21]. The importance of genetically diverse genotypes as a source of obtaining transgressive segregants with desirable combinations has been reported by several workers (Peter and Rai, 1978) [11]. Genetic resources are the building blocks and also fundamental not only to a crop improvement program but also for the very survival of the species in time and space

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(Swaminathan, 1983) [20]. Characterization of genetic diversity of maize germplasm is of great importance in hybrid maize breeding (Xia *et al.* 2005) [25]. Several methods have been reported to decipher the pattern and magnitude of variability such as D^2, cluster analysis and principal component analysis. D^2 analysis is a very useful technique in quantifying the degree of divergence between inbred lines or any biological population at genotypic level. It is also helpful in assessment of relative contribution of different components to the total divergence at both intra and inter-cluster level (Sachan and Sharma, 1971) [13]. In view of above importance, 43 newly developed early maturing yellow inbred lines at AICRP on maize at SAREC, Kangra were investigated to study the nature and magnitudes of variability and extent of genetic diversity for yield and yield contributing traits.

Material and Methods

The present investigation was carried out at All India Co-ordinated Maize Improvement Project, Shivalik Agricultural Research and Extension Centre, Kangra during the *Kharif* 2017. The experiment comprised of newly developed 41 lines of tropical origin. These new inbred lines were derived from different source populations by continuous inbreeding. These 41 inbred lines were used along with two testers *viz.*, HKI-1105 and CM-212 to study the genetic diversity. All 43 inbred lines were grown in RBD design with two replications at Experimental Farm, SAREC, Kangra. The experimental unit was two rows for each entry, 2 m row length and 60 cm apart, with intra row distance of 20 cm. Recommended package of practices were followed for raising a good crop. The observations were recorded from five competitive plants in each genotype per replication for 12 quantitative traits *viz.*, days to anthesis, days to silking, anthesis-silking interval, plant height, ear height, ear length, ear girth, number of kernel rows per ear, tassel length, leaf width, 1000-kernel weight and grain yield/ plant. Mahalanobis (1936) [8] D² statistic analysis was used for assessing genetic divergence among 43 maize inbreds and inbreds were grouped into different clusters according to Torcher's method as described by Rao (1952) [12]. Intra-cluster and inter-cluster distance, cluster mean and contribution of each trait to the divergence were estimated as suggested by Singh and Chaudhary (1985) [18].

Results and Discussion

Analysis of variance showed significant differences among the inbreds for all the characters under this investigation indicating considerable variation among studied genotypes (Table1). Coefficient of variation was low for all the traits except anthesis –silking interval and grain yield/ plant. The low CVs is values of traits may be expected because lines have undergone inbreeding depression resulting in the fixation of receive genes and thus increasing homozygousity within the lines. Low coefficients of variation of phenotype and genotype may encourage the use of yield parameters in selection of parents for crosses or lines further improvement. Mean values were used to determine genetic variability, heritability and genetic advance of grain yield and its component traits. Various genetic parameters, such as GCV (genotypic coefficient of variation), PCV (phenotypic coefficient of variation), H^2_b (%) and genetic advance as percent of mean (genetic gain) were estimated for all the characters under study (Table 2). High magnitude of phenotypic and genotypic coefficient of variations as well as high heritability along with high genetic advance as percent of mean (genetic gain) were observed for grain yield/plant,

1000-grain weight, ear length, tassel length, plant and ear heights provides evidence that these parameters were under the control of additive gene effects and effective selection could be possible for the improvement of these characters and might be sources of alleles that can be manipulated with other promising genotypes for higher grain yield in the north-western Himalayas ecology. Reliable selection could be made for these traits on the basis of phenotypic expression. Effective selection for superior inbreds is possible considering grain yield, 1000-kernel weight, ear length, tassel length, plant height and ear heights. High heritability estimates for grain yield/plant, ear height and 1000-kernel weight has been reported in maize by Akbar *et al.* (2006) [1], Wannows *et al.* (2010) [24] and Shazia *et al.* (2017) [15]. Anthesis-silking interval showed marked difference between GCV and PCV estimates suggesting that substantial variation for this trait was contributed by environmental components. Higher values of GCV for anthesis-silking interval and grain yield indicated higher degree of genetic variability in these traits. Similar results have also been observed by Zaman and Alam (2013) [26] and Shazia *et al.* (2017) [15] in maize inbred lines.

Forty-three maize inbred lines were grouped into 9 different clusters by using clustering techniques given by Tocher and explained by Rao (1952) [12]. Distribution of inbred lines into various clusters is presented in Table 3. The maximum number of inbreds (16) got grouped in cluster III which was followed by cluster 1 (14), cluster IV and II (4) and remaining clusters V, VI, VII, VIII and IX were all monogenotypic. The genotypes which are within the clusters by and large exhibit a narrow range of genetic variability. Based on the intra and inter cluster distances using D^2 values (Table 4), the maximum intra cluster distance was recorded within cluster III (10.26), while it was lowest for the genotype of cluster IV (6.96) indicating that the genotypes of these clusters might be differing in their genetic architecture. The highest inter-cluster distance (29.33) was observed between clusters VIII and IV followed by clusters VII and IV (28.01), clusters IV and IV (24.4), clusters IX and IV (23.86), clusters VIII and II (21.66), clusters VII and II (21.48) and clusters IV and III (20.71), suggesting that 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. Hybridization between divergent groups may lead to higher magnitude of heterosis for the characters concerned. Clustering pattern of inbred lines under this study revealed that the inbred lines showed considerable genetic diversity among themselves by occupying nine different clusters. Similar, results were reported by Singh *et al.* (2005) [16] and Liu *et al.* (2006) [7] in maize. Another study was carried out by Chen *et al.* (2007) [3] who reported that 186 maize genotypes could be classified into ten clusters. The crosses involving parents from most divergent clusters are expected to manifest maximum heterosis and generate wide variability in genetic architecture. Intra cluster distance was much lower than the inter cluster one, suggesting, heterogeneous and homogeneous nature between and within groups, respectively. Similar, results have also been reported by Singh *et al.* (2005) [16] and Chen *et al.* (2007) [3]

Mean values of cluster for yield and its different contributing characters were presented in the Table 5. It appeared that the early anthesis and silking genotypes were included in the cluster II (50.88, 54.75)) followed by cluster VII (51, 55). The highest days to anthesis and silking were recorded in cluster

VI (59, 62.5) followed by cluster VIII (56, 60). The dwarf genotypes were included in the cluster VII (137.5) followed by cluster III (138.63) and the tallest genotypes included in the cluster IV (203.88 cm) followed by cluster II (202.63). The highest ear height identified in cluster II (110.38cm) followed by cluster IV (104.13cm). The lowest ear height was included in cluster III (70.47 cm) and the highest in cluster VII (75.00 cm). The bold grain size was found in cluster IV (238.20 g) followed by cluster II (213.90g) and the smallest in cluster VIII (135.5g). The maximum ear length, ear girth and tassel length were observed for cluster IV (13.39, 12.63, 35.63) followed by cluster II (13.00, 11.96, 34.00). The minimum ear length and girth was observed for cluster VII (6.35, 9.35), whereas, minimum tassel length was recorded for cluster VIII (25.00).The more number of kernel rows/ear were observed for cluster VI (13.00) followed by cluster cluster II (12.50) and cluster IV (12.25), whereas, these were lowest in cluster VII (8.00). The maximum leaf width was recorded in cluster VIII (9.30) followed by cluster II (8.34) and cluster IV (8.25), whereas, it was lowest in cluster V (6.10).The highest grain yield/plant was produced by the cluster II (30.35) followed by cluster IX (27.50), and cluster IV (26.19). The lowest yield was recorded in the genotypes of the cluster VIII (12.30) followed by cluster V (16.20). Minmium anthesis –silking interval was recorded in cluster V (2), whereas it was observed maximum in clusters VII, VIII and IX (4.0). However, it is always desirable to look for genotypes having more than one desirable trait and belonging to different clusters. Considering all the characters it appeared that the genotypes in the cluster II had good performance. The genotypes in this cluster had relatively less days to anthesis and silking, bold grain size, more number of kernels rows/ear and the maximum yielding ability. Cluster IV also showed more grain size and reasonable yielding capacity. These findings were in accordance with Singh and Chaudhary (2001) [17], Zaman and Alam (2013) [26] and Mohammad et al. (2017) [9]

While studying contribution of individual characters towards divergence among 13 characters studied (Table 6), plant height (57.92%), and 1000- kernel weight (14.17%) contributed high for divergence, so these characters should be given weightage, for selecting diverse parents for breeding programme. Whereas, other characters like grain yield per plant (7.09%), ear height (5.98%), ear length (4.21%), tassel length (3.99%), days to silking (2.1%), days to anthesis (1.99%), leaf width (1.44%) number of rows/ear (1.00%) and ear girth (0.11%) contributed very little for divergence. More et al. (2006) [10] and Uday Kumar et al. (2013) [22] also reported that plant height and 1000- kernel weights were the major contributors towards divergence.

Table 1: ANOVA for yield and yield related characters

Source of variation	Replications	Treatments	Errors
Degrees of freedom	1	42	1
Grain yield/plant (g)	0.33	76.43**	6.28
1000 -kernel weight (g)	4.92	1236.95**	55.92
Ear length (cm)	1.21	5.30**	1.25
Ear girth (cm)	0.15	2.31**	0.64
Row/Ear	0.74	4.03**	0.93
Tassel length (cm)	0.10	28.85**	4.55
Leaf width (cm)	0.33	1.18**	0.41
Days to anthesis	0.01	14.41**	5.08
Days to silking	0.01	18.75**	7.94
Anthesis to silking interval	0.04	1.91NS	1.54
Plant height (cm)	9.11	1484.76**	22.52
Ear height (cm)	094	438.81**	12.037

** Significant at 5% level of probability

Table 2: Genetic variability parameters for various characters in new inbreds of yellow maize

Characters	Mean+SE	Range	CV%	PCV%	GCV%	Heritibility (broad sense)%	Genetic gain (%)
Grain yield/plant (g)	23.95±1.77	14.65-3260	10.46	25.81	24.72	91.8	48.79
1000-kernel weight (g)	204.36±5.28	135.5-244.2	3.65	12.16	11.89	95.5	23.93
Ear length (cm)	11.72±0.79	6.5-14.8	9.55	13.88	12.14	76.4	21.84
Ear girth (cm)	91.33±0.56	9.23-14.5	7.03	9.49	18.08	72.5	14.18
No. of kernel/rows/ear	11.48±0.68	8-14	8.41	12.36	10.84	76.8	19.57
Tassel length (cm)	31.50±1.50	25.43	6.77	12.05	11.06	84.2	20.92
Leaf width (cm)	8.07±0.45	6.1-9.4	8.02	9.55	7.69	64.7	12.74
Days to anthesis	52.5±1.59	48.5-59	4.28	5.11	4.11	64.7	6.81
Days to silking	56.1±1.99	50.5-62.5	5.02	5.46	4.14	57.7	6.49
Anthesis-silking interval	3.53±0.56	2.0-5.0	35.18	27.67	12.12	19.2	10.95
Plant height (cm)	165.9±3.35	109.5-214.0	2.86	16.42	16.29	70.84	33.18
Ear height (cm)	84.68±2.54	54.5-113.5	4.09	17.49	17.24	97.3	35.04

Table 3: Distribution of 43 inbred lines into different cluster

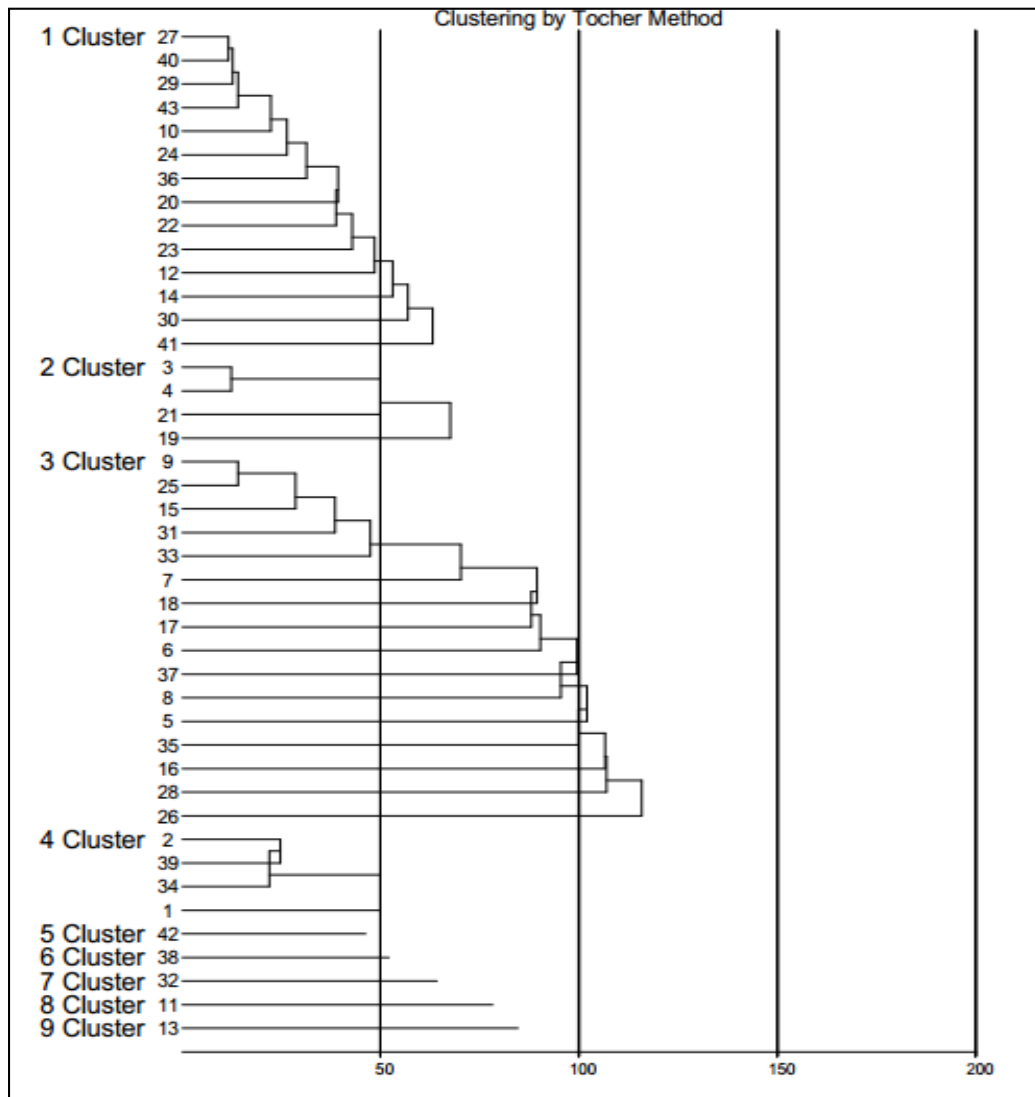| Sr. No.	Cluster	Number of genotypes	Name of genotypes
1.	I	14	$L_{27}, L_{40}, L_{29}, L_{43}, L_{10}, L_{24}, L_{36}, L_{20}, L_{22}, L_{23}, L_{12}, L_{14}, L_{30}, L_{41}$
2.	II	4	L_3, L_4, L_{21}, L_{29}
3.	III	16	$L_9, L_{25}, L_{15}, L_{31}, L_{33}, L_7, L_{18}, L_{17}, L_6, L_{37}, L_8, L_5, L_{35}, L_{16}, L_{28}, L_{26}$
4.	IV	4	L_2, L_{39}, L_{34}, L_1
5.	V	1	L_{42}
6.	VI	1	L_{38}
7.	VII	1	L_{32}
8.	VIII	1	L_{11}
9.	IX	1	L_{13}

Fig 1: Dendrogram showing clustering by Tocher's method

Table 4: Intra (Bold) and inter-cluster distance of 43 inbred lines of maize

Sr. No.	Cluster	I	II	III	IV	V	VI	VII	VII	IX
1.	I	7.02								
2.	II	11.03	8.49							
3.	III	12.40	18.07	10.24						
4.	IV	13.15	13.12	20.71	6.96					
5.	V	14.09	18.31	12.27	24.40	0.00				
6.	VI	10.57	14.19	15.35	18.82	11.90	0.00			
7.	VII	17.43	21.48	13.72	28.01	8.01	15.94	0.00		
8.	VIII	19.12	21.66	17.67	29.33	8.85	14.56	9.06	0.00	
9.	IX	15.68	15.64	19.64	23.86	13.89	9.20	16.34	12.69	0.00

Table 5: Cluster means for 12 different quanititative characters

Sr. No.	Characters	Clusters								
		I	II	III	IV	V	VI	VII	VII	IX
1.	Grain yield/plant (g)	25.19	30.35	22.26	26.19	16.20	21.85	17.85	12.30	27.50
2.	1000 -kernel weight (g)	210.96	213.90	200.96	238.20	163.20	182.9	161.6	135.5	167.3
3.	Ear length (cm)	11.51	13.00	11.77	13.39	10.70	10.00	16.50	11.05	10.90
4.	Ear girth (cm)	11.51	11.96	10.95	12.63	10.65	11.10	9.35	10.80	10.60
5.	Row/Ear	11.79	12.50	11.00	12.25	12.00	13.00	8.00	10.00	11.00
6.	Tassel length (cm)	31.29	34.00	31.16	35.63	27.00	31.00	28.50	25.00	28.00
7.	Leaf width (cm)	7.92	8.34	8.25	7.93	6.10	7.90	7.55	9.30	8.20
8.	Days to anthesis	52.96	50.88	51.94	51.88	56.50	59.00	51.00	56.00	54.50
9.	Days to silking	56.68	54.75	55.25	55.38	58.50	62.50	55.00	60.00	58.50
10.	Anthesis to silking interval	3.71	3.88	3.31	3.50	2.00	3.50	4.00	4.00	4.00
11.	Plant height (cm)	175.36	202.63	138.63	203.88	153.50	184.00	137.50	161.50	198.50
12.	Ear height (cm)	88.11	110.38	70.47	104.13	82.50	85.50	75.00	86.00	93.50

Table 6: Percent contribution of character towards divergence in 43 inbred lines

Sr. No.	Characters	Characters Contribution (%)
1.	Grain yield/plant (g)	7.09
2.	1000- kernel weight (g)	14.17
3.	Ear length (cm)	4.21
4.	Ear girth (cm)	0.11
5.	Kernel rows/ ear	1.00
6.	Tassel length (cm)	3.99
7.	Leaf width (cm)	1.44
8.	Days to anthesis	1.99
9.	Days to silking	2.10
10.	Anthesis-silking interval	0.00
11.	Plant height (cm)	57.92
12.	Ear height (cm)	5.98

Conclusion

The present study was conducted to study the genetic variability and diversity in newly developed early maturing yellow inbreds of maize. High magnitude of phenotypic and genotypic coefficient of variations as well as high heritability along with high genetic advance as percent of mean (genetic gain) were observed for grain yield/plant, 1000-grain weight, ear length, tassel length, plant and ear heights indicated that these traits were under the control of additive gene effects. Genetically diverse parents are expected to produce higher heterosis. Endang *et al.* (1971) [4] stated that the clustering pattern could be utilized in choosing parents for cross combinations which likely to generate the highest possible variability for effective selection of various economic traits. Keeping this in view, the findings from the present study indicated that clusters VIII and IV, VII and IV, IV and IV, IX and IV, VIII and II, VII and II and IV and III showed higher distance between them. Parental material selection from those clusters would provide manifestation of heterosis as well as wide range of variation during hybridization.

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