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RESEARCH ARTICLE

Genetic Divergence Study in Maize (*Zea mays* L.) Inbred Lines under North Western Himalayan Conditions

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Genetic divergence in 50 maize inbreds including five checks was assessed based on some morpho-physiological and yield contributing traits using Mahalanobis D^2 statistics. The experiment was carried out in an augmented block design at Maize Research Station, SKUAST-J, Udhampur, J&K during *Kharif* 2019-20. All the inbreds were grouped into ten clusters based on D^2 analysis. Maximum numbers of genotypes (12) were grouped in cluster III whereas cluster X (1) was the smallest. Maximum inter-cluster distance was observed between cluster VIII and cluster IX indicating presence of maximum diversity among the genotypes falling within these clusters. The genotypes in the cluster VIII showed better performances having high shelling percentage (%), grain yield per plot (g), cob length, kernels per row and 1000 kernel weight (g). It is expected that crossing of inbred lines belonging to high-medium D^2 values may tend to produce high heterosis for yield. Perusal of the data indicated that moisture percentage contributed maximum of 8.90 per cent whereas, days to 50 % silking contributed the lowest of 0.73 per cent to the total genetic divergence.

Key Words: Clusters, Divergence, Inbred, Maize, PCA

Introduction

Maize (*Zea mays* L.) is one of the three most important food crops in the world agricultural economy both as food for human beings and feed for animals. It is grown primarily for grain and secondarily for fodder, raw material for industrial process and diversified products. Maize is a member of Poaceae family (2n=2x=20). Worldwide, approximately 21% of total produced maize is consumed directly as food while the rest part of produce is used in other purposes (Jaiswal *et al.,* 2019). In India, maize is third important cereal crop after rice and wheat. It is cultivated on an area of 9.3 million hectares with a production of 27.2 million metric tonnes and a productivity of 2.92 tonnes per hectare (FAOSTAT, 2018). In Jammu and Kashmir, it is cultivated on an area of 0.29 million hectares with a production and productivity of 5411 thousands quintals and 18.33 quintals per hectare, respectively (Shazia *et al*., 2017). It is mainly concentrated in mid hill zones and rainfed areas of the state. For developing high yielding hybrids in maize, inbred lines need to be evaluated for their diverse gene pool. Precise information about genetic divergence is critical for a productive breeding programme, as genetically diverse parents are known to produce high heterotic effects increasing consequently recovery of yield suitable segregants (Sharma *et al.,* 2020). Information on genetic diversity and relationship among different maize genotypes is very important in hybrid maize breeding programme (Punya *et al.,* 2020*)* Maize shows heterosis in recombinants, particularly when inbreds differing for many genes affecting yield or some other character of importance are used as parents (Udaykumar *et al*., 2013). Several studies on maize have shown that inbred lines from diverse genetic base to be more productive than crosses of inbred lines derived from closely related stocks (Moll *et al*., 1965; Vasal, 1998; Udaykumar *et al*., 2013). It has become possible to quantify magnitude of genetic diversity among germplasm with the help of advanced biometrical methods such as multivariate analysis (Rao, 1952) based on Mahalanobis' (1936) D^2 statistics. Maize inbred lines developed at Maize Research Station, Udhampur and inbred lines received from IIMR, New Delhi as part of coordinated programme needed assessment of diversity

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among them for evaluation of their potential use in hybrid breeding programs. With this view, diversity among 50 maize inbred lines was studied using multivariate approaches of analysis.

Materials and Methods

Fifty inbred lines of maize (*Zea mays* L.) were grown in an Augmented Block Design (ABD) with five blocks including five checks at Maize Research Station, SKUAST-J, Udhampur, J&K during *Kharif* 2019-20. The detail pedigree and source of all fifty maize inbred lines are listed in Table 1. Unit plot size was 3 m x 1.2 m maintaining 60 cm x 20 cm spacing. Intercultural operations were done at appropriate time according to the necessity. Data was recorded on different morpho-physiological and yield contributing traits such as, days to 50% tasseling, days to 50% silking, days to 75% dry husk, plant height (cm), ear height (cm), number of leaves, number of plants per plot, stem girth (cm), number of cobs per plant, shelling percentage (%), moisture percentage (%), grain yield per plot (g), cob length (cm), cob girth (cm), kernel rows per cob, kernels per row and 1000 kernel weight (g). Data was subjected to analysis of Mahalanobis D^2 statistics using windostat 9.1 software. 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).

Results and Discussion

The analysis of variance for significances different genotypes for all the character under study. The highest number of days to 50% flowering was observed in G 29 and G 40 genotypes. The maximum plant height was observed in G 22 and G 40 genotypes. The highest 1000 kernel weight was observed in G 21 and G 45 genotypes. The highest grain yield per plot was observed in G 22 and G 40 genotypes. The variation among the genotypes of 50 inbred lines was studied on a multivariate scale using Mahalanobis, D^2 statistics. Assuming the D^2 values as χ^2, it appears that there were significant variations among all the genotypes. Fifty genotypes were grouped into ten clusters, which are presented in the Table 2. Cluster III was the largest, containing twelve genotypes whereas cluster X was the smallest cluster containing only one genotype. Average intra and inter cluster distance of four clusters are presented in Table 3. The magnitude of intra cluster distances indicated the extent of genetic diversity among genotypes within the same

Table 1. Maize inbred lines studied for morpho-physiological traits

Code	Udhampur code	Inbreds	Source
G1	UDMI 401	CM 153	IIMR
G2	UDMI 402	WN 1069	WNC Hyderabad
G3	UDMI 403	CM 141	IIMR
G4	UDMI 404	CM 212	IIMR
G5	UDMI 405	WN 1207	WNC Hyderabad
G6	UDMI 406	CML 116	CIMMYT
G7	UDMI 407	WN 24249-1	WNC Hyderabad
G8	UDMI 408	WN 689-1	WNC Hyderabad
G9	UDMI 409	CM 140	IIMR
G10	UDMI 410	CML 295	CIMMYT
G11	UDMI 411	WN 1079	CIMMYT
G12	UDMI 412	WN 4615	WNC Hyderabad
G13	UDMI 413	WN 2456	IIMR
G14	UDMI 414	WN 547	CIMMYT
G15	UDMI 415	EV1465	WNC Hyderabad
G16	UDMI 416	WN 2449	IIMR
G17	UDMI 417	WN 2469	IIMR
G18	UDMI 418	PFSR 10109	IIMR
G19	UDMI 419	WN 2436	IIMR
G20	UDMI 420	CML 130	CIMMYT
G21	UDMI 421	CML 31	CIMMYT
G22	UDMI 422	VP14114	CIMMYT
G23	UDMI 423	CM123	IIMR
G24	UDMI 424	VP14109	CIMMYT
G25	UDMI 425	CML 433	CIMMYT
G26	UDMI 426	EV1463	WNC Hyderabad
G27	UDMI 427	WN 4614	WNC Hyderabad
G28	UDMI 428	HKI 323	Karnal
G29	UDMI 429	CML 427	CIMMYT
G30	UDMI 430	WN 52362	IIMR
G31	UDMI 431	CML 300	CIMMYT
G32	UDMI 432	CM 143	IIMR
G33	UDMI 433	WN 52343	CIMMYT
G34	UDMI 434	WN 52218	CIMMYT
G35	UDMI 435	WN 516	IIMR
G36	UDMI 436	WN 52011	MANDYA
G37	UDMI 437	HKI 287	Karnal
G38	UDMI 438	WN 241-1	IIMR
G39	UDMI 439	CM 128	IIMR
G40	UDMI 440	VL144077	CIMMYT
G41	UDMI 441	SNL 142836	CIMMYT
G42	UDMI 442	HKI 139-1	Karnal
G43	UDMI 443	WN 52361	IIMR
G44	UDMI 444	Z490-26	CIMMYT
G45	UDMI 445	WN 52188	CIMMYT
G46	UDMI 446	HKI 1105-2-2	Karnal
G47	UDMI 447	V351	Almora
G48	UDMI 448	CM I52	IIMR
G49	UDMI 449	HKI 536	Karnal
G50	UDMI 450	WN2453-2	IIMR

Table 2. Distribution of 50 genotypes of maize inbreds into ten clusters

Cluster	No. of entries	Name of entries
I	9	G6, G39, G5, G1, G8, G4, G28, G13, G3
II	2	G10, G17
III	12	G7, G42, C47, G15, G9, G48, G24, G26, G35, G41, G25, G50
IV	3	G37, G46, G14
V	6	G34, G36, G38, G31, G44, G2
VI	2	G20, G33
VII	7	G27, G45, G23, G12, G16, G21, G49
VIII	5	G22, G40, G11, G29, G30
IX	3	G32, G43, G19
X	1	G18

cluster. The distance between the clusters were more than the intra clusters distances indicating that diversity in between clusters was more than within clusters. The highest distance was obtained between cluster VIII and cluster IX (10580240.00) indicating the wider genetic divergence between genotypes of these two clusters. Wider diversity shows high heterosis (Singh *et al*., 1980). It was followed by cluster II and cluster IX, cluster V and cluster VIII, cluster IV and cluster IX, and cluster I and cluster VIII. The cluster VIII had the highest distance from the rest indicating that the genotypes in the cluster VIII were distinctly different from others. Low inter cluster distances were observed between cluster I and cluster VI (46018.47) followed by cluster I and cluster V (71727.68) indicating that the genotypes belonging to these clusters were comparatively less diverse. Hence, crossing of genotypes from these clusters may not produce high level of heterotic expression in the F_1's and broad-spectrum of variability in segregating (F_2) populations. The clusters with comparatively less magnitude of divergence showed instability, while widely divergent clusters remained distinct in different environments (Raut *et al*., 1985; Singh *et al*., 1980; Somayajulu *et al*., 1970). Parents for hybridization programmes could be selected on the basis of large inter-cluster distance for isolating useful recombinants in the segregating generations. Increasing parental distance implies a better chance at greater number of constraining alleles at the desired loci, and then to the extent that these loci recombine in the F_2 and F_3 generations, following a cross of distantly related parents, the greater will be the opportunities for successful selection for any character of interest (Ghaderi *et al*., 1984).

Principal Component Analysis (PCA) also helps in assessment of diversity on multivariate scales. The principal components formed were equal to number number of characters. The criteria followed for selecting the principal components to be included in further analysis was based on Eigen values of principal components (Kovacic, 1994). Only 5 principal components were taken having Eigen values greater than one (>1) and they accounted for the 79.99% of total variation. The fact that Eigen values are above unity indicates that the evaluated principal component weight is reliable (Mohammadi and Prassanna, 2003). This clustering pattern confirmed the results obtained by D^2 analysis. For principal component-1, grain yield per plot contributed highest percentage of 36.60. For component-2 highest percentage was contributed by days to 50% tasseling (44.20%), For principal component-3 the highest percentage was contributed by days to 50% silking (29.80%), while as for component-4 and component-5 kernels per row and number of leaves contributed highest with percenatage of 51.10 and 47.90, respectively (Table 4).

Cluster analysis based on PCA scores were compared with the results of the principal component analysis on a visual aid in desecrating clusters in the two dimensional scattered diagram and the genotypes falling in same cluster were present closer to each other in the scattered diagram.

Table 3. Average inter and intra cluster distances in maize inbreds

	1 Cluster	2 Cluster	3 Cluster	4 Cluster	5 Cluster	6 Cluster	7 Cluster	8 Cluster	9 Cluster	10 Cluster
1 Cluster	12532.28	3526052.00	223767.50	2449302.00	71727.68	46018.47	803570.60	5664764.00	778316.50	1680888.00
2 Cluster		296.85	2030856.00	99205.24	4516543.00	2811707.00	1036380.00	287172.10	7578075.00	341690.50
3 Cluster			24011.69	1238961.00	509359.10	76684.87	219682.10	3719944.00	1787615.00	715419.30
4 Cluster				1281.77	3282782.00	1859391.00	506582.30	694161.40	5952360.00	73711.17
5 Cluster					7338.01	204152.80	1295608.00	6897718.00	403977.60	2379302.00
6 Cluster						1013.79	488339.10	4752457.00	1162232.00	1197817.00
7 Cluster							75431.66	2310397.00	3101456.00	208235.20
8 Cluster								106742.80	10580240.00	1201257.00
9 Cluster									18623.37	4711829.00
10 Cluster										0.00

Table 4. Eigen values, proportion of the total variance represented by first five Principal components, cumulative per cent variance and component loading of different characters in maize (*Zea mays* L.)

	PC1	PC2	PC3	PC4	PC5
Eigen Value	2.48	1.82	1.24	1.21	1.04
% variance Expressed	36.18	19.56	9.11	8.71	6.42
Cumulative variance Expressed	36.18	55.74	64.84	73.56	79.99
GYP	0.366	-0.155	0.009	-0.068	-0.020
CL	0.334	-0.133	0.247	0.048	-0.230
CG	0.301	-0.134	0.265	0.115	-0.309
KRPC	0.217	-0.284	0.065	0.066	0.150
1000KW	0.218	-0.047	0.259	-0.519	0.130
KPR	0.173	-0.210	0.012	0.511	-0.309
MP	0.122	0.115	-0.248	-0.213	-0.518
SP	0.070	-0.233	0.295	-0.180	0.388
NCP	0.256	0.067	-0.392	-0.321	-0.044
SG	0.132	0.341	-0.221	0.126	-0.033
NPPP	0.273	0.164	-0.292	-0.197	0.074
NOL	0.147	0.017	-0.325	0.413	0.479
EH	0.350	-0.091	-0.220	0.038	0.099
PH	0.352	-0.142	-0.066	0.070	0.171
DDH	0.184	0.428	0.164	0.018	0.124
DS	0.172	0.432	0.298	0.122	0.0377
DT	0.162	0.442	0.288	0.118	0.037

GYP= grain yield plot-^{1} (g), CL= cob length (cm), CG= cob girth (cm), KRPC= kernels rows cob-^{1}, 1000KW= 1000 kernel weight (g), KPR= kernels row-^{1}, MP= moisture percentage (%), SP= shelling percentage (%), NCP= No. of cobs plant-^{1}, SG= stem girth (cm), NPPP= No. of plants plot-^{1}, NOL= No. of leaves, EH= Ear height (cm), PH= plant height (cm), DDH= days to 75% dry husk, , DS= days to 50% silking, DT= days to 50% tasseling.

Genetically distant parents are usually able to produce higher heterosis (Falconar, 1960; Moll *et al.,* 1962; Mian and Bhal 1989). Endang *et al.,* (1971) 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 variability existed among the studied maize inbreds. The choice of parents for further breeding programme can be made by selecting individuals from the maximum divergent cluster such as cluster VIII and cluster IX and clusters have single or few genotypes II, VI and X in the present study, which would exert high heterosis and wide variability in genetic architecture in subsequent generations. The lines UDMI 433 (G33), UDMI 410 (G10), UDMI 422 (G22), UDMI 440 (G40), UDMI 411 (G11), UDMI 429 (G29), UDMI 430 (G30), UDMI 432 (G32), UDMI 443 (G43) and UDMI 418 (G18) belonging to the distant clusters could be used in hybridization program for obtaining a wide spectrum of variation among the segregants.

Conclusion

Most of the maize inbred lines significantly differed for all the characters under study indicating sufficient amount of variability present in the inbreds. Selection based on characters which are significant positive and direct association with grain yield may increase the grain yield in maize inbreds. High number of clustes and there values for genetic divergence showed presence of significant amount of genetic diversity. The inbred lines showing higher genetic divergence can further be utilised for crossing programme to achieve high yielding hybrids in maize.

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