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Cluster Analysis and Genetic Diversity of Maize Inbred Lines

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Abstract – **T For the estimation of genetic diversity through cluster analysis forty most promising inbred lines were evaluated for ten different morphological traits. The field experiment was carried out under randomize complete block design (RCBD) in three replications in the field area of maize research station, Ayub Agriculture Research Institute, Faisalabad, Pakistan. According to the statistical analysis of the morphological traits of the inbred lines, wide variability exists for all the characters studied. All the genotypes were grouped into 10 clusters. The parental combinations of the most of developed promising hybrids of the research station exhibited dissimilarity range around 50%. The genotype 24 seems most diverse among all other genotypes with 60 to 80% dissimilarity. The distribution of genotypes in the study indicated that the geographical origin did not have any bearing on clustering pattern.**

Keywords – **Maize Genetic Diversity, Cluster Analysis, AARI.**

I. Introduction

A fundamental step in hybrid development is the development and selection of inbred lines. It is evident from various studies that the hybrids developed from crosses of more diverse and distant parental lines exhibit better heterosis than of related parental material [1]. [2] Reported that the heredity differences of two parental lines are based on expression of heterosis. For hybrid development the selection of genetically distant lines become possible through quantification of hereditary difference using biometrical techniques. Genetic diversity is very helpful in identifying inbred lines appropriate for hybrid development. The genetic diversity between the genotypes is a key to produce high heterotic impacts [3]. The germplasm diversity studies among elite inbred lines are very significant to the crop plant improvement [4]. In corn breeding, depiction of genetic differences in germplasm is of significant importance [5]. Characterization of genetic diversity of maize germplasm is of great importance in hybrid maize breeding [6]. D2 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 [7]. The present investigation was undertaken with a view to estimate the nature and magnitude of genetic diversity in forty maize inbred lines.

II. Materials and Methods

The study was conducted during the year 2016 at the experimental field of the Maize Research Station, Ayub agriculture research institute, Faisalabad, Pakistan. This study was a part of a long-term maize inbred line development program conducted at the research station mentioned above where near-homozygous inbred lines were developed through traditional method self-breeding from different source population (Table. 1). Forty parental lines of most promising maize hybrids were grown in randomize complete block design (RCBD) with three replications during autumn 2016. The seeds of each entry were sown on last week of July 2016 in 5 m long rows with spacing of 0.75 x 0.20 m between rows and hills, respectively. One plant was kept per hill after proper thinning. Recommended doses of fertilizers were applied. The other intercultural operations were done timely and properly to raise the crop uniformly. Ten randomly selected plants were used for recording observations on plant height (PH), ear height (EH), ear length (EL), ear diameter (ED), ears/plant (EPP), number of kernel rows/ear (KRPE), number of grains/row (GPR), number grains/ear (GPE), 1000-kernel weight (g) (TGW) and kernel yield/plant (g) (YPP). Data were subjected to genetic diversity estimation through cluster analysis [9].

III. Results and Discussion

Range, mean, standard error and different yield contributing characters in all these forty maize inbred lines are presented in Table 2. The D2 values ranged from 3.49 to 14.98 and principal component scores also indicated a high degree of genetic diversity among the genotypes. The statistics summary of the morphological traits of the all genotypes, indicated wide variability for all the characters studied and hence ample opportunities exists for genetic improvements of the crop through selection directly from the accessions for development of inbred for future hybrid breeding program. All the genotypes were grouped into 10 clusters. Clusters 1 forming sub cluster a1 and 2, 3, 4 forming sub cluster a2 while 5, 6 and 7 were grouped into sub cluster b1 and 8, 9, 10 into sub cluster b2, the maximum inter cluster difference were observed between sub cluster b1 and A1, especially genotype forming cluster 2 (a1) and genotype forming cluster 7 (b1). The minimum dissimilarity was observed between the genotypes of groups 7 i.e. 6.68 and 9.2 between genotypes 25 and 26. The most possible explanation for the comparatively low genetic distance between the inbred lines was that they were descended from a common ancestor i.e. sister lines. 92.8% dissimilarity is observed between genotypes 24 and 32 while second highest between 24 and 13. Both the combinations have not yet been tried. While most of the existing promising hybrids having dissimilarity range around 50% between their parental combinations. The genotype 24 seems most diverse among all other genotypes having most of the figures from 60 to 80% dissimilarity. The distribution of genotypes in the study indicated that the

geographical origin did not have any bearing on clustering pattern. Clustering pattern of inbred lines under this study revealed that the inbred lines showed considerable genetic diversity among themselves by occupying ten different clusters. Similar, results were reported by [10] and [11] in maize and by [12] in pumpkin. Another study was carried out by [13] 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 [10] and [13].

Table 1. Forty genotypes grouped into ten different clusters along with their origin.

Sr. No	Cluster	No of Genotypes	Name of Genotypes
1	1	3	F-166 (Thailand), F-110 (Local), F-167 (Thailand)
2	2	6	F-132 (Local), F-204 (Mexico), F-208 (Mexico), F-215 (Mexico), F-107 (Nigeria), F-192 (Thailand)
3	3	7	F-155 (Local), F-248 -1 (Local), F-248-2 (Local), F-167 (Thailand), F-271 (Thailand), F-182-1 (Local) , F-182-2 (Local).
4	4	3	F-123 (Mexico), F-249 (Local), F-272 (Thailand)
5	5	3	F-181 (Local), F-196 (USA), F-258 (USA)
6	6	6	F-186 (Thailand), F-187 (Thailand), F-273 (Local), F-210 (Local), F-252 (Local), F-285 (USA)
7	7	2	F-256-1 (Local), F-256-2 (Thailand)
8	8	2	F-297 (USA), F-165 (Thailand)
9	9	5	F-143 (Local), F-279 (USA), F-147 (Local), F-168 (Mexico), F-290 (Local)
10	10	3	F-219 (Local), F-251 (Local), F-260 (Local).

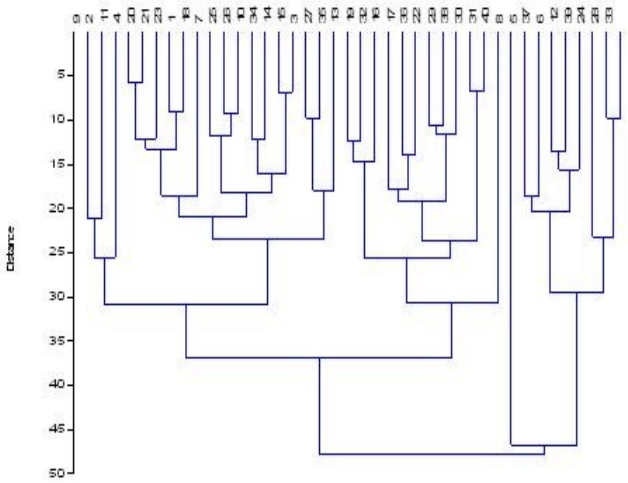

Fig. Cluster analysis of forty inbred lines.

Table 2. Summery statistic of morphological traits.

VARIABLE	MEAN	STDEV	MINI--MUM	MADIAN	MAXI--MUM	RANGE
Days to 5% Tesseling	58.7	3.13	51.0	58.5	64.0	13.0
Days to 50 % Silking	60.4	3.3	52.0	61.0	67.0	15.0
Plant Height (cm)	114.6	19.9	69.0	112.5	150.0	81.0
Ear Height (cm)	44.5	12.4	22.0	45.0	72.0	50.0
Cob L length (cm)	12.5	2.0	7.0	12.8	17.5	10.5
Cob Diameter (cm)	3.9	0.6	2.4	4.0	5.2	2.8
No. of Kernel Rows/ cob	13.2	2.1	8.0	12.0	18.0	10.0
No. of kernel / row	20.35	4.9	10.0	20.0	31.0	21.0
100 Grain Weight (gm)	27.6	4.5	17.0	27.0	37.0	20.0
Total Grain Weight (gm)	56.28	12.8	26.0	57.0	94.0	68.0

REFERENCES

[1] Vasal, S. K. 1998. Hybrid maize technology: Challenges and expanding possibilities for research in the next century. Proc. of 7 th Asian Regional Maize Workshop. Los Banos, Philippines. February 23-27, 58-62, pp

[2] Saxena, V. K., Mathi, N. S., Singh, N. N. and Vasal, S. K. 1998. Heterosis in maize: Grouping and patterns. Proc. of 7th Asian Regional Maize Workshop. Los Banos, Philippines. February 23-27, 124-133, pp.

[3] Mian, M. A. K. and Bahl, P. N. 1989. Genetic divergence and hybrid performance in chickpea. Indian Journal of Genetics, 49: 119-124

[4] Hallauer, A. R., Russell, W. A. and Lamkey, K. R. 1988. Corn Breeding. In: Corn and Corn Improvement, 3rd edn. Agron Monogr 18, ASA-CSSA-SSSA, Madison, Wisconsin, USA. 469-564 pp.

[5] Ahloowalia, B. S. and Dhawan, N. I. 1963. Effect of genetic diversity in combining ability of inbred lines of maize. Indian Journal of Genetics, 23: 158-162.

[6] Xia, X. C., Reif, J. C., Melchinger, A. E., Frisch, M., Hoisington, D. A., Beck, D., Pixley, K. and Warburton, M. L. 2005. Genetic diversity among CIMMYT maize inbred lines investigated with SSR markers. Crop Science, 45; 2573-2582.

[7] Sachan, K. S. and Sharma, J. R. 1971. Multivariate analysis of divergence in tomato. Indian Journal of Genetics, 31: 86- 93.

[8] Anonymous. 2007. Guidelines for the development of crop descriptor lists. Bioversity Tech Bull Series. Bioversity international, Rome, Italy. XII.

[9] Singh R.K. and Chaudhary B.D., 1977, Biometrical Methods in Quantitative Genetic Analysis, Kalyani Publishers, New Delhi, p.266

[10] Singh, P., Sain, D., Dwivedi, V. K., Kumar, Y. and Sangwan, O. 2005. Genetic divergence studies in maize (Zea mays L.). Annals of Agricultural and Biological Research, 10(1): 43-46.

[11] Liu YuAi, Hou Jian Hua, Gao ZhiJun and Zhou Wei 2006. Principal component analysis and cluster analysis of introduced maize varieties. Journal of Maize Science, 14(2): 16-18.

[12] Masud, M. A. T., Chowdhury, M. A., Hossain. M. A. and Hossain, S. M. M. 1995. Multivariate analysis in pumpkin (Cucurbita moschata Duch ex. Poir). Bangladesh Journal of Plant Breeding and Genetics, 8(1&2): 45-50.

[13] Chen FaBo, Yang Ke Cheng, Rong Ting Zhao and Pan Guang Tang 2007. Analysis of genetic diversity of maize hybrids in the regional tests of Sichuan and Southwest China. Acta Agronomica Sinica, 33(6): 991-998.

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