



Studies On Genetic Divergence In Maize Genotypes (*Zea mays* L.)

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ABSTRACT

The parental material for the present study comprised of 30 maize inbred lines with 6 checks. The field experiment was laid out in Randomized Block Design with three replications and data were recorded for twelve quantitative characters and nine qualitative characters. The genotypes were grouped under seven clusters in which Cluster I was the largest which accommodated eight genotypes whereas, cluster V had accommodated only one genotype. The highest intra-cluster distance was observed between cluster VI and cluster I and it was zero in cluster V. The highest inter cluster distance was observed between cluster III and V.

Key words: Genetic diversity, D^2 matrix and cluster.

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INTRODUCTION

Maize or corn (*Zea mays* L) is one of the most important cereal crops in the world and a strategic food crop for the majority of the developing countries (**Lopes and Larkins, 1996**). The genus *Zea* is a group of annual and perennial grasses native to Mexico and Central America (**Galinat, 1971**). The genus *Zea* includes the wild taxa, known collectively as teosinte (*Zea* species) and domesticated corn or maize. Globally being one of the most important cereal crops worldwide. Globally the area under maize is 182.0 million ha with production of 987.0 million tonnes and the productivity is 54.23 q/ha. The United States, China, Brazil and Mexico account for 70% of global production. India has 5% of corn acreage and contributes 2% of world production. In India, maize is the third important food crop after rice and wheat. At national level the area under this crop is 9.43 million ha, production 24.26 million tonnes and productivity is 2583 kg/ha. In Jharkhand it is cultivated over 0.2569 million ha production 0.517 million tonnes and productivity 2012 kg/ha.

Assessment on genetic diversity among the genotypes is important for planning an effective hybrid breeding programme as the genetically diverged genotypes are known to produce high heterotic effects. It has become possible to quantify magnitude of genetic diversity among germplasm with the help of advanced biometrical methods such as multivariate analysis (RAO, 1957) based on Mahalanobis (1936) D^2 statistic. A number of maize inbred lines from CIMMYT need assessment of variation among them for evaluation of their potential use in hybrid breeding programme.

MATERIALS AND METHODS

The present investigation was carried out in the experimental area of Department of Plant Breeding & Genetics, Birsa Agricultural University, Ranchi, during Kharif 2015. The parental material for the present study comprised of 30 maize inbred lines with 6 checks. All the 36 maize genotypes were grown in randomized block design (RBD) with three replications during the Kharif 2015. Each entry was sown in 1 row of 4 m in length. The plant to plant spacing within rows was maintained at 20 cm and 70 cm between rows. The data on thirteen quantitative and nine qualitative characters were recorded on five competitive and randomly selected plants in each replication for characters like days to 50% pollen shedding, days to 50% silking, days to maturity, plant height (cm), ear height (cm), cob per plant, cob yield per plant (g), cob length (cm), number of kernel, 100 grain weight (g), harvest index (%), protein content (%) and starch content (%). The mean values were used for statistical analysis. Analysis of variance was based on procedure given by Panse and Sukhatme.

RESULTS AND DISCUSSION

The analysis of variance was carried out with 30 genotypes and 6 checks the analysis of variance revealed highly significant differences among the genotypes for all the yield attributing traits which were presented in Table-1. The D² matrix based on data of quantitative traits for 1296 pair of combinations among 36 maize genotypes have been calculated. It could be observed that the D² values for all the 1296 pair of combinations ranged from 19.29 to 540.42. The highest D² value (540.42) was obtained in combination of genotypes.

The thirty six genotypes including six checks were grouped in seven clusters (Table-2). Out of seven clusters, cluster I was the largest one in size which accommodated eight genotypes followed by cluster IV (seven genotypes and cluster II, III and VII six genotypes respectively). Clusters VI (two genotypes) and V (one genotype). It could be observed that (Table-3) intra and inter cluster distance was maximum differences among the genotypes within the same cluster was registered by cluster VI followed by cluster I, III, II, VII and cluster IV. Clusters V had zero intra cluster distance. The inter cluster distance which measure the diversity between the clusters varied from 100.59 to 432.19. The cluster III and V recorded highest inter cluster distance followed by cluster I and V, cluster V and VII, cluster V and cluster VI, cluster I and cluster VI, cluster III and cluster VI, cluster II and cluster VI, cluster I and cluster VII, cluster VI and cluster VII, cluster IV and cluster V, cluster IV and cluster VI, cluster III and cluster IV, cluster III and cluster VII, cluster I and cluster IV, cluster II and cluster III, cluster I and cluster III, cluster II and cluster VII, cluster II and cluster IV, cluster IV and cluster VII, Whereas, Ganesan *et al.* (2010) studied the genetic diversity among one hundred five adapted maize germplasms and classified into four clusters. Cluster IV consisted of maximum fifty three genotypes followed by cluster II with 32 genotypes. The genotypes accommodated under cluster VI were found early to pollen sheds with their average value of 47.00 with days to silking of 50.50 days and days to maturity with 84.17 days. Average cob yield per plant of genotypes were found in cluster VI with of 125.33 (g) whereas, the genotypes in cluster V having more cob yield per plant followed by cluster IV, cluster I, cluster II, cluster VII and minimum was observed in cluster III (Table-4)

The average length of cob were maximum in cluster V followed by cluster IV, cluster II, cluster I, cluster III, cluster VII and minimum length of cob were observed in cluster VI similar to the result of Marker and Krupakar (2009). The starch content contributed maximum towards divergence followed by cob yield per plant, protein content, 100 grain weight, days to maturity. While the contribution from ear height, kernel per cob, cob length, plant height, days to 50% pollen shedding and harvest index was low in magnitude. Days to 50% silking contributed least to total divergence (Table-5).

Table-1: Analysis of variance (mean sum of square) for twelve yield attributing characters

Sl. No.	Source of variation	d.f	Days to 50% flowering	Days to 50% silking	Days to maturity	Cob yield/plant (g)	Cob length (cm)	Plant height (cm)	Ear height (cm)	Kernel/cob	100 grain weight (g)	Harvest index (%)	Protein content (%)	Starch content (%)
1.	Replication	2	0.36	0.20	1.23	30.19	1.74	24.20	60.57	3.06	0.08	2.99	0.00	0.01
2.	Genotypes	35	8.42**	8.63**	20.21**	6953.72**	3.77*	1216.76**	389.18**	5.92**	31.61**	11.04**	6.13**	26.24**
3.	Error	70	1.04	1.45	1.54	180.70	1.10	125.24	36.35	6.00	1.07	2.68	0.30	0.46
4.	S Em±		0.59	0.69	0.71	7.76	0.60	6.47	3.49	6	0.58	0.94	0.32	0.39
5.	C.D at 5%		6.62	5.78	6.32	102.12	13.12	29.88	38.65	21.77	1.22	8.67	34.14	11.32

*,** significant at 1% and 5%

Table-2: Distribution of genotypes in different clusters based on yield components

Sl. No.	Cluster	No. of genotypes	Name of genotypes
1.	I	8	CML-165, HKI-323B, CML-163-7-2, 2007-1-CML-467, SC FEMALE, Dholi Pop 65-DS-9, CML-468, WNCDMR 19 RYDWS 2025 (A)
2.	II	6	Dholi -M7, Dholi Inbred 2012, HQPM-1, High Oil Population, PFSR-R9-1, HKI-586
3.	III	6	CML-196, JHARGRAMPOP, WNCDMR 08 RYSC 683, Winpop 8-1, WNCDMR 11 R 4602, WNCPOPSELECTION NS
4.	IV	7	HKI-1105, CML-471, 69-828K-CML-115, CML-161, SUWAN, 21-113-CM-411, LM-13
5.	V	1	BIO-9637
6.	VI	2	BVM-2, BM-1
7.	VII	6	CML-150, CML-171, 8-1238-IEC-6189, HKI-193I, Pop-65, 193-I

Table-3: Average Inter and intra- cluster distance based on yield and yield components

Cluster	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI	Cluster VII
Cluster I	80.95	107.03	122.14	144.34	364.99	286.42	210.60
Cluster II		61.40	129.28	100.91	306.04	232.81	105.41
Cluster III			65.90	163.77	432.19	246.21	149.29
Cluster IV				51.22	187.28	175.45	100.59
Cluster V					0.00	309.94	338.09
Cluster VI						127.57	198.11
Cluster VII							54.83

Table-4: Cluster mean of different characters in maize

Clusters	Characters											
	Days to 50% Pollen Shedding	Days to 50% Silking	Days to Maturity	Cob Yield/ Plant (g)	Cob Length (cm)	Plant Height (cm)	Ear Height (cm)	Kernels/ Cob	100 Grain Weight (g)	Harvest Index (%)	Protein Content (%)	Strach Content (%)
Clusters I	52.50	55.83	93.87	116.42	12.43	156.77	71.65	293.16	19.20	35.89	10.22	63.02
Clusters II	52.67	56.22	93.50	98.67	13.33	142.48	64.16	284.71	22.17	35.90	10.64	66.45
Clusters III	53.39	56.89	93.67	79.56	12.27	122.44	57.11	311.46	14.26	35.20	10.63	64.76
Clusters IV	52.00	55.38	93.62	168.29	13.35	161.28	69.64	308.40	20.95	38.14	8.85	67.96
Clusters V	52.33	56.00	91.67	276.67	15.77	166.20	81.67	418.20	26.53	40.33	12.25	69.20
Clusters VI	47.00	50.50	84.17	125.33	11.60	147.80	57.87	317.77	19.23	36.72	10.55	68.80
Clusters VII	52.72	51.17	94.39	91.44	11.77	132.86	57.49	290.97	19.30	35.51	9.26	70.06

Table-5: Contribution of different yield components to total divergence

Characters	Times Ranked first	% Contribution
Days to 50% pollen shedding	1	0.16
Days to 50% silking	0.01	0.00
Days to maturity	34	5.40
Cob yield/plant (g)	139	22.06
Cob length (cm)	3	0.48
Plant height (cm)	3	0.48
Ear height (cm)	19	3.02
Kernels/cob	4	0.63
100 grain weight (g)	89	14.13
Harvest Index (%)	1	0.16
Protein Content (%)	92	14.60
Starch Content (%)	245	38.89

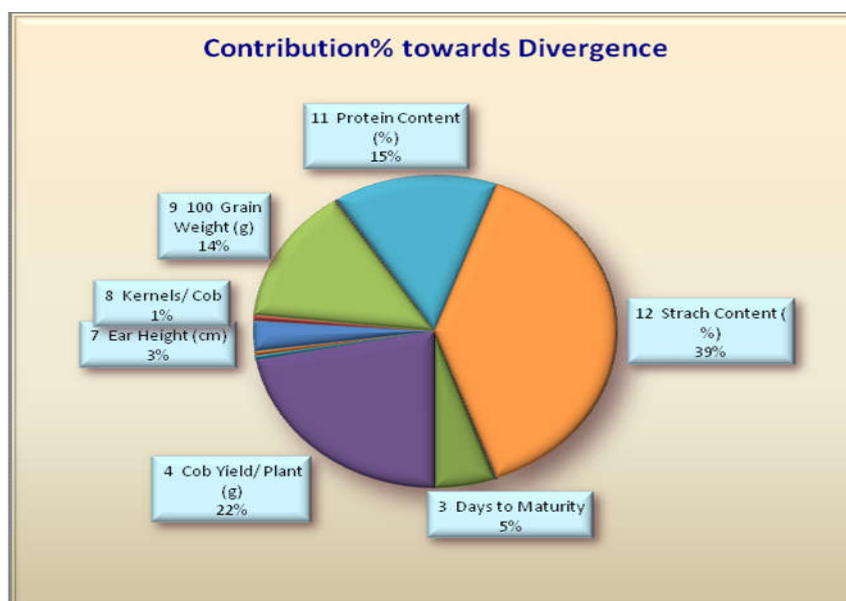


Fig-1: Contribution (%) of different yield components traits

CONCLUSION

The genotypes namely, SC FEMALE (55 days) followed by WNCDMR 08 RYSC 683 (54 days), HQPM -1 (54 days), WNCPOPSELECTION NS (54 days), 193 -I (54 days) and WNCDMR 11 R 4602 (54 days) were found for days to 50% pollen shedding and SC FEMALE (59 days) followed by HQPM -1 (58 days), WNCPOPSELECTION NS (58 days) for days to 50% silking, CML-468, CML-161, HQPM-1, 8-1238-IEC-6189, SUWAN, PFSR-R9-1 and 193-I (95 days) for days to maturity, BIO-9637 (276 g) and 21-113-CM-411 (212 g) for cob yield/plant, HQPM-1 (15.80 cm) and BIO- 9637 (15.77 cm) for cob length, Dholi pop 65-DS-9 (187.23 cm) and HKI-323B for plant height, HKI-323B (87.53 cm) and BIO-9637 (81.67 cm) for ear height, BIO-9637 (418) and BM-1(364) for number of kernel per cob, BIO-9637 (26.53 g) and CML-150 (22.90 g) for 100 grain weight, BIO-9637 (40.33%) and SUWAN (39.09%) for harvest index, WNCDMR08RYSC-683 (13.56%) followed by HQPM-1 (12.25%) and BIO-9637 (12.25%) for protein content and CML-171 (72.98%) and CML-150 (71.20%) for starch content were identified as most diverse genotypes for the trait concerned, based on phenotypic traits and quality components studies considering together which may be used in future breeding programme of maize to get transgressive recombinants in segregating generation and high heterotic F_1 's with respect to maturity and yield as well as improved protein quality.

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