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Genetic variability, heritability and genetic advance estimates in maize (*Zea mays* L.) inbred lines

R. T. Maruthi [1*] and K. Jhansi Rani [2]

[1]Crop Improvement Division, Central Research Institute for Jute & Allied Fibres, Barrackpore, Kolkata- 700 120 (West Bengal), INDIA
[2]Department of Seed Science and Technology, ANGRAU, Rajendranagar, Hyderabad- 500 030 (Andhra Pradesh), INDIA
[*]Corresponding author. E-mail: maru7806@gmail.com

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Abstract: Forty three genotypes of maize were evaluated for eleven traits at the College Farm, College of Agriculture, Rajendranagar, Hyderabad to study the genetic divergence and various genetic parameters. There was a significant ($P<0.01$) difference between genotypes for all the characters, which revealed wide range of variability and high heritability for all the characters. The genetic advance as percent of mean was high for grain yield per plant (73.19%), ear height (51.05%), number of kernels per row (44.40%), plant height (43.46%), 100 grain weight (42.88%), ear length (30.79%), number of kernel rows per ear (25.23%), and ear girth (22.37%) indicating additive gene action for these traits. D^2 analysis partitioned the forty three genotypes in to six clusters. The maximum inter cluster distance (39.38) was observed between cluster I and cluster V. Grain yield per plant (38.43%), plant height (14.29%), 100 grain weight (12.85%) and number of kernels per row (12.07%) contributed greatly towards diversity.

Keywords: Cluster analysis, Genetic advance, Heritability, Maize

INTRODUCTION

In India, the production of maize over the years has increased linearly and major breakthrough was experienced at the dawn of 21st century, associated with the development and release of more number of hybrids during this period. Recent emphasis on development of high yielding hybrids in preference to a continued dependence on composites has yielded rich dividends. This emphasis is likely to ensure still higher growth rates in productivity of this versatile crop in the years to come. There is still a considerable scope to improve productivity and adaptability by breeding heterotic hybrids (Grzesiak, 2001).

Achievements in hybrid development should be adequately backed up by germplasm enhancement, synthesizing of gene pools and heterotic populations representing variability for diverse requirement (Reif *et al*., 2005). The knowledge of nature and magnitude of genotypic and phenotypic variability present in the crop species plays a vital role in formulating a successful breeding programme to evolve superior cultivars (Abdurakhmonov and Abdukarimov, 2008). Progress in any breeding programme depends upon the magnitude of useful variability present in the population and the extent to which the desirable characters are heritable. Thus, the study and utilization of existing variability becomes highly essential. Keeping the foregoing points in view, the present investigation was undertaken with a view (a) to estimate genetic variance, heritability and genetic advance (b) to investigate the nature and magnitude of genetic diversity in 43 maize genotypes.

MATERIALS AND METHODS

The experimental material used in the study comprised of forty stabilized inbred lines and three hybrid checks and were obtained from Maize Research Centre, Acharya N. G. Ranga Agricultural University (ANGRAU), Hyderabad (Table 1). The seeds were sown in a randomized complete block design (RCBD) with three replications at the College Farm, College of Agriculture, Rajendranagar. Each entry in each replication consisted of two rows of fifteen plants. Spacing between rows and between plants was 60 cm and 15 cm, respectively. The crop was raised as per the recommended package of practices to obtain proper plant stand in the experiment. The pre and post-harvest observations like days to 50% tasseling, days to 50% silking, days to maturity, plant height (cm), ear height (cm), ear length (cm), ear girth (cm), no. of kernel rows per ear, no. of kernels per row, 100 grain weight (g), grain yield/plant (g) were recorded on five plants selected at random from each genotype in each replication.

Standard statistical procedure was used for analysis of variance, and for genotypic and phenotypic coefficient of variation (Burton and Devane, 1953), heritability (Hanson *et al*., 1956) and genetic advance. Multivariate analysis was done as per Mahalanobis's D^2 statistics

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and the genotypes were grouped into different clusters following Tochers's method (Rao, 1952).

RESULTS AND DISCUSSION

Analysis of variance revealed highly significant (P<0.01) differences among the genotypes for all the characters indicating presence of sufficient amount of variability in all the characters studied (Table 2). The phenotypic coefficient of variability (PCV) and genotypic coefficient of variability (GCV) were highest for plant height, ear height, number of kernels per row and 100 grain weight suggesting that these characters are under the influence of genetic control (Table 3). Likewise Kumar *et al*., (2014) and Nzuve *et al*., (2014) also reported highest GCV and PCV for plant height, ear height, 100-grain weight and number of kernels per row. Hence, these characters can be relied upon and simple selection can be practiced for further improvement. Days to 50 per cent tasseling recorded low GCV indicating the predominance of non-additive gene action. Similarly, while studying variability for protein content and grain yield in maize genotypes Krishnam Raju, (2001) also found predominance of non-additive gene action for days to 50 per cent tasseling.

Heritability estimates revealed the heritable portion of variability present in different characters (Table 3). The knowledge of heritability enables the plant breeder to decide the course of selection procedure to be followed under a given situation (Li and Yang, 1985). However heritability values coupled with genetic advance would be more reliable and useful in formulating selection procedure. In the present study, heritability estimates were high for all the characters studied. This suggested the greater effectiveness of selection and improvement to be expected for these characters in future breeding programme as the genetic variance is mostly due to the additive gene action. Similarly, high heritability estimates for plant height, number of kernels per row and 100 grain weight were reported by Choudhary and Chaudary, (2002) and for grain yield per plant by Zahid -Mahmood *et al.,* (2004) and Sofi and Rather, (2007).

Genetic advance as per cent of mean was also high for grain yield per plant, ear height, plant height, number of kernels per row, number of kernel rows per ear, ear length, ear girth and 100 grain weight (Table 3). Similarly Bekele and Rao, (2014) also reported high genetic advance for plant height, number of kernel rows per ear, 100 grain weight, ear height, grain yield per plot. The high heritability coupled with high genetic advance noticed for these traits indicate the role of additive gene action in controlling the traits, hence pedigree method of breeding will be a rewarding one to improve the traits under investigation. Other traits like days to 50 per cent tasseling, days to 50 per cent silking and days to maturity recorded high heritability with low genetic advance as per cent of mean, indicating that the characters were influenced by the environment and were not stable.

Forty three inbred lines of maize were grouped into 6 clusters (Table 4). The magnitude of D values (Table

Table 1. List of forty three maize genotypes.

S. N.	Genotypes	Source	S. N.	Genotypes	Source
1.	CM 104	A.Theo-21	23	3001	MMH – 9807
2.	CM 105	Peru-330	24	3002	Suwan – 1 (ps)
3.	CM 114	Eto 25A	25	3003	Suwan – 1(ws)
4.	CM 115	Eto 182	26	3004	Suwan – 3
5.	CM 118	PTR (Petro)	27	3005	NC – 300
6.	CM 119	R 109	28	3008	Nech – 02
7.	CM 120	C 103	29	3009	SRRL – 65
8.	CM 121	Adec-C	30	3010	Tolumen
9.	CM 130	CM-111	31	3012	Nizambad local
10.	CM 131	X-131	32	3014	Across
11.	CM 132	B-57	33	3016	BML 15
12.	CM 133	A 670	34	3017	CML 226
13.	CM 149	(X2Y pool-inbred x Suwan-inbred)	35	3022	CM 213
14.	CM 201	G 715	36	3023	Pro 322
15.	CM 202	C 121	37	3025	LM 6
16.	CM 206	SS-III	38	3026	BML 13
17.	CM 208	C 121E	39	3030	BH (JK2293 x LM5) derived inbred
18.	CM 209	RN-6	40	3035	Danphong
19.	CM 210	SS-III		**Checks**	
20.	CM 211	C 121E	41	BH-40625	BML 6 x BML 7
21.	BML-6	SRRL 65	42	BH-1576	BML 6 x BML 15
22.	BML-7	X_2Y Pool x CML 226	43	BH-2187	CM 148 x CM 149

Table 2. Analysis of variance for eleven characters in maize.

Sources of Variation	df	Days to 50% tas-seling	Days to 50%silking	Days to maturity	Plant height (cm)	Ear height (cm)	Ear length (cm)	Ear girth (cm)	No of kernel rows/ ear	No of kernels per row	100 grain weight (g)	Grain yield/ plant (g)
Replications	2	1.98	12.84	12.79	13.37	23.87	0.54	0.01	0.03	2.8	2.58	35.44
Genotypes	42	53.82**	48.64**	49.32**	1764.10**	593.42**	13.79**	7.43**	10.18**	98.80**	102.11**	2906.01**
Error	84	2.21	2.92	2.74	6.06	10.43	0.34	0.34	0.41	2.83	1.26	90.82
SEm ±		0.86	0.99	0.96	1.44	1.87	0.34	0.34	0.37	0.97	0.65	5.5
CV (%)		1.9	2.16	1.51	2.19	5.9	4.24	4.38	4.63	6.69	4.1	11.58
CD (5%)		2.42	2.78	2.69	4.05	5.26	0.94	0.94	1.05	2.74	1.82	15.5

* and ** significant at P = 0.05 and P = 0.01 level of significance, respectively.

Table 3. Estimation of variability, heritability and genetic advance as per cent of mean for eleven characters in forty three genotypes of maize.

S.N.	Characters	Mean ± Sem	Range		PCV (%)	GCV (%)	h^2_{bs} (%)	GA as per cent of mean
			Minimum	Maximum				
1	Days to 50 percent tasseling	78.00±0.86	71.00	86.00	5.32	5.65	88.63	10.31
2	Days to 50 percent silking	79.00±0.99	72.00	87.00	4.92	5.37	83.90	9.29
3	Days to maturity	109.00±0.96	102.00	118.00	3.60	3.91	84.98	6.84
4	Plant height (cm)	113.81±1.44	78.00	177.67	21.21	21.31	98.98	43.46
5	Ear height (cm)	54.74±1.87	27.67	88.33	25.48	26.21	94.56	51.05
6	Ear length (cm)	13.67±0.34	08.53	19.27	15.49	16.06	93.05	30.79
7	Ear girth (cm)	13.25±0.34	10.47	16.47	11.61	12.40	87.55	22.37
8	Number of kernel rows per ear	14.00±0.37	10.00	18.00	13.00	13.80	88.76	25.23
9	Number of kernels per row	25.00±0.97	14.00	40.00	22.49	23.46	91.87	44.40
10	100 grain weight (g)	27.35±0.65	15.67	35.00	21.00	21.59	96.40	42.88
11	Grain yield per plant (g)	82.33±5.50	31.67	176.67	37.21	38.97	91.18	73.19

Table 4. Grouping of forty three maize genotypes based on D^2 analysis.

Cluster	*No. of genotypes*	Genotypes
I	18	CM 104, CM 105, CM 114, CM 115, CM 118, CM 119, CM 120, CM 121, CM 130, CM 131, CM 132, CM 133, CM 149, CM 201, CM 202, CM 206,3001 and 3010.
II	7	CM 208, CM 208, CM 210, CM 211, BML-6, 3003 and 3030.
III	3	BML-7, 3008 and 3035.
IV	12	3002, 3004, 3005, 3009, 3012, 3014, 3016, 3017, 3022, 3023, 3025 and 3026.
V	2	BH-40625 and BH-1576.
VI	1	BH-2187.

Table 5. Average intra (bold) and inter-cluster $D^2$and D values for six clusters in forty three genotypes of maize.

Cluster	I	II	III	IV	V	VI
I	246.95 (15.72)	294.66 (17.17)	570.39 (23.89)	340.81 (18.46)	1550.70 (39.38)	480.84 (21.93)
II		306.70 (17.51)	398.97 (19.98)	295.49 (17.19)	1203.68 (34.70)	431.09 (20.76)
III			135.82 (11.66)	313.77 (17.71)	453.76 (21.30)	319.68 (17.88)
IV				291.67 (17.08)	1048.89 (32.39)	426.18 (20.65)
V					95.00 (9.75)	953.03 (31.87)
VI						0.00 (0.00)

Figures in parenthesis are D values

5) suggested that there was considerable amount of diversity in the experimental material used in investigation. The genotypes exhibited random pattern of distribution into various clusters showing that genetic diversity and geographical diversity are not related. This suggests that forces other than geographic origin such as genetic drift, natural and artificial selection, exchange of genetic material might have played an important role in the diversity of genotypes. Similar conclusions were also drawn by Teixeira *et al.*, (2002) while estimating diversity from the maize genotypes of north eastern region of Brazil.

Statistical distance represents the induction of genetic diversity among clusters. The inter cluster distance was minimum between cluster I and II indicating close relationship and similarity for most of the characters of the genotypes (Table 6). The maximum inter cluster distance was observed between clusters I and V indicating wider genetic diversity among genotypes in these groups. Selection of parents from these diverse clusters for hybridization programme would help in achieving novel recombinants. Similar results were obtained by Azad *et al.,* (2012) while studying genetic diversity in maize, thirty inbreds were grouped into six distinct clusters. Highest inter-cluster distance was observed between cluster I and cluster IV and the lowest between the cluster II and III. Cluster V displayed least intra cluster distance denoting the similarity of genotypes (Table 5). While maximum intra cluster distance was recorded in cluster II and this might be due to limited gene exchange or selection practices among the genotypes for diverse characters.

Emphasis should be laid on characters contributing maximum D^2values for choosing the cluster for the purpose of further selection and choice of parents for hybridization. Highest contribution towards divergence in this regard was put forth by grain yield per plant followed by plant height, number of kernels per row and 100 grain weight (Table7). Similarly higher contribution by traits like plant height, number of kernels per row, 1000 grain weight and grain yield per plant to the total divergence was reported by Azad *et al.,* (2012). The above results imply that in order to select genetically diverse genotypes for hybridization, the material should be screened for the important traits like grain yield per plant, plant height, number of kernels per row and 100 grain weight.

Conclusion

Genetic diversity was studied to find out the more diverse inbred lines in maize which might be used in

Table 6. The nearest and farthest clusters from each cluster based on D^2 values in maize genotypes.

Cluster	*Nearest cluster with D values*	Farthest cluster with D^2 value
I	II (17.17)	V (39.38)
II	I (17.17)	V (34.7)
III	IV (17.71)	I (23.89)
IV	II (17.19)	V (32.39)
V	III (21.30)	I (39.38)
VI	III (17.88)	V (31.87)

Table 7. Per cent contribution of characters towards diversity in maize genotypes.

S. N.	Character	Times ranked 1st	Per cent contribution
1.	Days to 50 percent tasseling	0.33	0.33
2.	Days to 50 percent silking	0	0
3.	Days to maturity	0	0
4.	Plant height (cm)	129	14.29
5.	Ear height (cm)	81	8.97
6.	Ear length (cm)	41	4.54
7.	Ear girth (cm)	27	2.99
8.	Number of kernel rows per ear	50	5.54
9.	Number of kernels per row	109	12.07
10.	100 grain weight (g)	116	12.85
11.	Grain yield per plant (g)	347	38.43
	Total	903	100

hybridization programme. There was significant difference between genotypes for all the characters studied. The genetic advance as percent of mean was high for majority of yield contributing traits indicating predominance of additive gene action and selection will be effective for the improvement of these traits. D^2 analysis partitioned the forty three genotypes in to six clusters. The maximum inter cluster distance was observed between cluster I and cluster V. The crosses involving parents/inbred lines from most divergent clusters are expected to manifest maximum heterosis and generate wide variability in genetic architecture.

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