



ISSN (E): 2277- 7695

ISSN (P): 2349-8242

NAAS Rating: 5.03

TPI 2018; 7(7): 940-943

© 2018 TPI

www.thepharmajournal.com

Received: 05-05-2018

Accepted: 06-06-2018

## Kumari Shikha

Research Scholar,

Department of Genetics and Plant Breeding, Institute of Agricultural Sciences, Banaras Hindu University, Varanasi, Uttar Pradesh, India

## JP Shahi

Professor, Department of Genetics and Plant Breeding, Institute of Agricultural Sciences, Banaras Hindu University, Varanasi, Uttar Pradesh, India

## Anima Mahato

Department of Genetics and Plant Breeding, Institute of Agricultural Sciences, Banaras Hindu University, Varanasi, Uttar Pradesh, India

## Saurabh Singh

Department of Horticulture, Institute of Agricultural Sciences, Banaras Hindu University, Varanasi, Uttar Pradesh, India

## Correspondence

Kumari Shikha

Research Scholar,

Department of Genetics and Plant Breeding, Institute of Agricultural Sciences, Banaras Hindu University, Varanasi, Uttar Pradesh, India

## Genetic divergence studies in maize hybrids based on morphological traits

Kumari Shikha, JP Shahi, Anima Mahato and Saurabh Singh

### Abstract

The magnitude of genetic variability and divergence was elucidated among 47 hybrids of maize by conducting experimental research in randomized block design. Two composites, Madhuri and Win orange were used as check for comparison. All genotypes were evaluated for 18 agro-morphological traits under open field conditions at Institute of agriculture science, B.H.U, Varanasi. Analysis of variance revealed presence of a wide range of variability between the hybrids for cob yield with husk, cob yield without husk/plot, five cob weight, green fodder weight, number of cobs/plot, TSS%, seedling emergence %, ear height, plant height, kernels/row, ear width, ear length, kernel rows/cob, husk weight and 100 seed weight indicating the scope for selection of suitable hybrid for cultivation. The high heritability with high to moderate estimates of genetic advance were obtained from grain yield, plant height, ear height, number of kernels per row, 100-kernel weight indicating additive gene action for which selection would be effective. Genotypes grouped into eight clusters and maximum intra-cluster distance was shown by cluster VII. The maximum inter-cluster distance was observed between cluster VIII and V. Characters viz., 100 seed weight, TSS%, green fodder weight/plot, number of kernels/ row and husk weight/plot together contributed 80% towards total divergence. These characters should be taken into consideration for further utilization in maize breeding strategies and commercialization of hybrids.

**Keywords:** Characters, heritability, divergence, inter-cluster, intra-cluster and variability

### Introduction

Maize (*Zea mays* L.) belongs to the family graminiae ( $2n=2x=20$ ) and is an important cereal crop having wider adaptability under varied agro-climatic conditions. It is known as queen of cereals due to its high genetic potential. About 9000 years ago maize originated from a single domestication (teosinte) in South Mexico according to Matsuoka *et al* (2002) <sup>[1]</sup>. According to advance estimate it is cultivated in 8.7 m ha (2010-11) mainly during *Kharif* season which covers 80% area.

Maize crop can be grow this crop throughout the year, due to availability of thermos- and photo-insensitive varieties. Usually three crops of maize, viz. *kharif*, *rabi* and spring are grown in India. It requires adequate moisture and warmth from sowing to end of flowering. The optimum temperature for germination is 21° C, while for growth it is 32° C.

Information on genetic diversity (GD) in maize is of fundamental importance as it facilitates plant breeder to know the extent of already existing genetic variability in the material <sup>[2]</sup>. This information also foster classification of germplasm in appropriate heterotic groups for future breeding programs because genetically divergent genotypes are known to have high hybrid vigour and yield <sup>[3]</sup>.

Most of the maize diversity remains un-described, poorly understood and under-utilized largely because of the difficulty of identifying useful hidden genetic variants in the background of low yielding local varieties or lines <sup>[4]</sup>. Thus, identification of existing diversity in maize genotype is crucial for plant breeding programme.

Recently, there is perceptible improvement in maize production in India. However, production and productivity in India is less and ample of scope is prevailing for improvement. 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. Morphological traits are the functional manifestation of underlying genetic constitution of an organism hence they constitute an important set of markers to assess the genetic diversity.

## Materials and methods

The experiment material consisted of 49 maize genotypes (30 sweet corn hybrids, 12 field corn hybrids, five QPMs along with two checks) which were obtained from Department of Genetics and Plant Breeding, Institute of Agricultural Science, Banaras Hindu University, Varanasi. All F<sub>1</sub> hybrids along with two checks were sown in Randomized Block Design with two replications at Agro-farm of B.H.U during Rabi 2015-16. The experimental field length was 27m and width 8m and each plot was 4 meter in length and 0.6 meter in width. A spacing of 60cm between rows and 25 cm between plants were maintained and border of 1.25m width all around the plot. The crop was raised as per the recommended package of practice. Data were recorded on yield and different yield contributing traits viz, seedling emergence%, days to 50% tasseling, days to 50% silking, days to harvesting, plant height (cm), ear height (cm), number of ears per plant, number of kernels per row, ear length (cm), ear width (cm), TSS%, yield with husk per plot (Kg), yield without husk per plot (Kg), 100 seed weight (g), husk weight/plot, green fodder yield/plot (Kg/ha), best five cob weight/plot (Kg).

**Data analysis:** The statistical analysis of data based on the mean value of recorded observations on five random plants, was done for determining the genetic diversity of the hybrid population as well as correlation and regression effects of

various traits on yield. The analysis was carried out by using Indostat software. Recorded data were subjected to Mahalanobis D<sup>2</sup> statistical analysis extended by Rao [5]. Intra-cluster and inter-cluster distance, cluster mean and contribution of each trait to the divergence were estimated as suggested by Singh and Chaudhary [6].

## Result and Discussion

Mean and coefficient of variation of eighteen traits in 49 maize genotypes are presented in Table 1. Analysis of variance revealed significant difference among genotypes for maturity, plant height, ear height, ear length, ear girth, number of kernel rows per ear, number of kernels per ear, 100 seed dry weight, cob yield with husk per plot, cob yield without husk per plot, TSS%, green fodder weight and seedling emergence%. The highest GCV% and PCV% were observed for the husk weight followed by yield without husk weight, five cob weight, yield with husk, number of cobs/plot, Seedling emergence % and ear height. Similar finding reported by Rafiq *et al.* (2010) [7] for grain yield, ear length and ear height; Vashistha *et al.* (2013) [8] for grain yield per plant, ear height and number of grains row per cob. In contrast Kapoor and Batra (2015) [9] reported high estimates of GCV and PCV for plant height, leaf length, stem girth, number of cobs, number of seeds, dry matter yield and green fodder yield.

**Table 1:** Estimation of range, mean, components of variance and genetic advance and genetic parameters for eighteen characters in 48 maize hybrids.

Traits	Mean	V <sub>g</sub>	V <sub>p</sub>	V <sub>E</sub>	GCV%	PCV%	ECV	H <sub>b</sub>	GA as % of mean
Seedling emergence %	71.58	137.7	154.31	16.6	16.39	17.35	5.69	0.89	31.9
Days to 50% tasseling	99.63	12.51	13.42	0.91	3.55	3.67	0.95	0.93	7.05
Days to 50% silking	104.69	8.34	9.25	0.90	2.76	2.90	0.90	0.90	5.40
Days to maturity	149.96	10.88	12	1.11	2.24	2.35	0.71	0.90	4.4
Plant height	145.82	143.52	170.15	26.63	8.21	8.94	3.53	0.84	15.54
Ear height	65.99	74.79	89.32	14.53	13.10	14.32	5.77	0.83	24.70
Yield with husk(Kg)	2.306	0.23	0.32	0.08	20.94	24.62	12.95	0.72	36.68
Yield without husk(Kg)	1.31	0.10	0.12	0.02	24.39	27.48	12.66	0.78	44.59
Husk weight(Kg)	1.037	0.15	0.17	0.02	37.41	39.82	13.67	0.88	72.38
Cobs/plot	13.88	6.14	7.13	0.98	17.85	19.22	7.14	0.86	34.13
Kernel rows/cob	14.07	0.96	1.14	0.17	6.99	7.60	2.98	0.85	13.24
Kernels/row	32.48	8.25	10.07	1.82	8.84	9.77	4.16	0.81	16.48
Ear length	16.98	1.19	1.54	0.34	6.44	7.32	3.46	0.77	11.68
Ear width	3.77	0.06	0.08	0.02	6.62	7.60	3.73	0.75	11.90
5cob weight	0.55	0.018	0.02	0.002	24.54	25.90	8.29	0.89	47.89
TSS%	16.08	9.53	10.63	1.105	19.2	20.28	6.53	0.89	37.44
100 Seed weight	7.91	2.02	2.08	0.05	17.99	18.22	2.88	0.97	36.61
Green fodder weight (Kg)	3.13	0.801	0.86	0.059	28.54	29.58	7.79	0.93	56.71

In contrast, low GCV% and PCV% observed in days to 50% tasseling, days to 50% silking and days to maturity, ear length, ear girth and number of kernel rows per ear and exhibited moderate to high heritability along with low Genetic advance that indicates preponderance of non-additive gene action which provides limited scope for improvement of traits through selection. Similar results were reported by Mahmood *et al.*, 2004 [10], Hemavathy *et al.*, 2008 [11], Jawaharlal *et al.*, 2011 [12] and Vashistha *et al.*, 2013 [7].

The high heritability coupled with high genetic advance noticed for husk weight, green fodder weight, five cob weight, yield without husk, TSS%, yield with husk, 100 seed dry weight, number of cobs/plot, seedling emergence %, ear height traits which indicate the role of additive gene action in controlling the traits, therefore pedigree method of breeding will be employed to improve the traits under investigation.

Days to 50% tasseling, days to 50 per cent silking, days to maturity and number of kernel rows per ear recorded non-significant association.

High to moderate heritability with moderate estimates of genetic advance were observed for grain yield, plant height, ear height, number of kernels per row, 100-kernel weight. High to moderate heritability along with moderate and low estimates of genetic advance were observed for days to 50 per cent tasseling, days to 50 per cent silking, days to maturity. Whereas high to moderate heritability along with low estimates of genetic advance were observed for ear length, ear girth and number of kernel rows per ear were presented in Table 1.

Genetic diversity was assessed by using Mahalanobis's D<sup>2</sup> statistic for eighteen characters. The per cent contribution of each character towards divergence is presented in fig 1. It was

observed that 100 seed dry weight was the single largest contributor (35.63%) towards divergence followed by TSS% (20.58%), green fodder weight (17.86%), kernels/row (4.93%), husk weight (4.34) % etc.

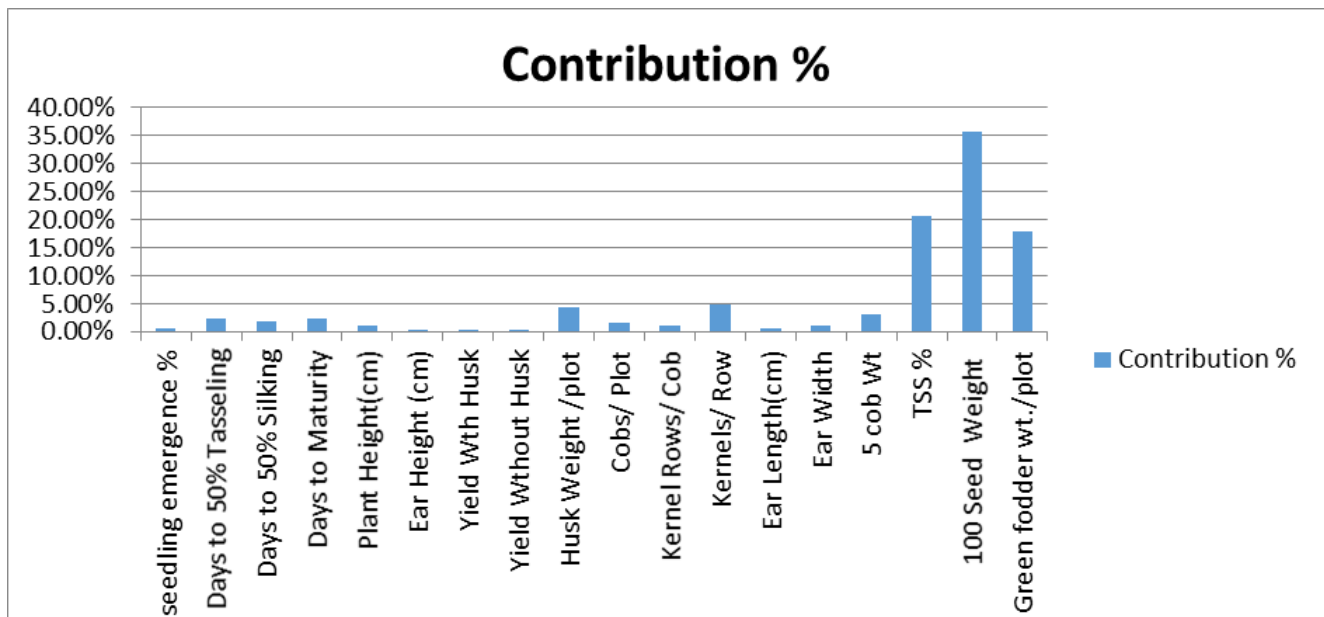


Fig 1: %contribution of each characters towards diversity in forty nine maize hybrids.

Grouping of genotypes into clusters using Ward’s euclidean<sup>2</sup> distance method (Joe H. Ward, 1952) [13] resulted in formation of eight clusters that are presented in Table 2. The average intra and inter-cluster D<sup>2</sup> values for eight clusters in forty nine genotypes of maize are presented in Table 3. The maximum

intra-cluster distance was shown by cluster VII. While, cluster VIII was a solitary cluster. The maximum inter cluster distance was observed between cluster VIII and V (47.71), more heterotic hybrids are likely to be produced by crossing genotypes of these two clusters.

Table 2: The distribution of 49 genotypes of maize into different clusters on the basis of D<sup>2</sup> statistics.

Clusters	Number of genotypes included	Genotypes
I	7	SC Female X DMSC-1, SC female x su2su20202 comp (Red)-BBB-1-BBB 4PI, Su2su20202 comp (y)- BBB-1-BBB 4PI x Win sweet corn, DMSC-8 x DMSC-35, DMSC-8 x DMSC-27, Su2su20202 comp (y)- BBB-1-BBB 4PI x DMSC-2,
II	11	SC Female x DMSC-9, SC Female x DMSC-8, DMSC-8 X Dulce Amanilla (Su Su), DMSC-6 x DMSC-19, Su2su20202 comp (y)- BBB-1-BBB 4PI x DMSC-27, CHECK2- MADHURI, DMSC-8 x DMSC-19, Su2su20202 comp (y)- BBB-1-BBB 4PI x Win sweet corn,
III	8	Su2su20202 comp (Red) BBB-40-BBB x DMSC-9, DMSC-6 X DMSC-9, DMSC-6 X DMSC-8, DMSC-8 x WNCDMRSCY18R716, HUZM-69 x HUZM-246, HUZM-69 x HKI-1025, DMSC-8 X DMSC-9, Su2su20202 comp (Red) BBB-40-BBB x DMSC-8,
IV	9	SC female x su2su20202 comp (Red)-BBB-1-BBB 4PI, (CML421 CML170)-B x HUZM-355, (CML421 CML170)-B x HUZM52-1, Su2su20202 comp (y)- BBB-1-BBB 4PI x WNCDMRSCO8R686(A), HKC-193-1 x 169(469), 466 x 467, HKC-193-1 x 467

Table 3: Average intra (bold) and inter-cluster D<sup>2</sup> and D values for eight clusters in forty nine genotypes of maize

Euclidean <sup>2</sup> : Cluster Distances : Ward								
	1 Cluster	2 Cluster	3 Cluster	4 Cluster	5 Cluster	6 Cluster	7 Cluster	8 Cluster
1 Cluster	161.066 (12.06)	262.157 (16.19)	433.213 (20.81)	427.868 (20.68)	895.001 (29.91)	388.962 (19.72)	434.090 (20.83)	981.401 (31.32)
2 Cluster		199.578 (14.12)	379.852 (19.48)	402.651 (20.06)	1027.841 (32.05)	601.273 (24.52)	737.529 (27.15)	1144.898 (33.83)
3 Cluster			302.815 (17.4)	652.73 (25.54)	797.917 (28.24)	632.463 (25.14)	1012.905 (31.82)	1586.080 (39.82)
4 Cluster				189.611 (13.76)	892.913 (29.87)	521.469 (22.83)	777.502 (27.8)	1281.620 (35.79)
5 Cluster					196.096 (14)	535.536 (23.14)	1268.304 (35.61)	2275.442 (47.71)
6 Cluster						238.452 (15.4)	566.793 (23.8)	1303.304 (36.10)
7 Cluster							392.596 (19.81)	862.272 (29.63)
8 Cluster								0.000

Figures in parenthesis are D values.

The highest mean values for cob yield with husk/plot, five cob weight, ear girth and kernel rows per cob were found in cluster VIII and that of green fodder yield/plot value was in cluster IV. Short duration genotypes, short ear height and high mean ear length accounted for cluster III. Cluster II was the biggest, consisting of eleven genotypes. The inter-cluster distance between cluster V and cluster VIII was maximum, followed by cluster III and cluster VIII. Thereby, inter-crossing between the genotypes clubbed in cluster V and cluster VIII would create a wide spectrum of variability and may produce desirable segregants.

The D<sup>2</sup> study provides useful information that can be used in a breeding program for genetic improvement. On the basis of inter cluster distances, cluster means, per se performance observed in the present study the five hybrids viz, Su2su20202 comp (y)- BBB-1-BBB 4PI x DMSC-8, Su2su20202 comp (y)- BBB-1-BBB 4PI x DMSC-9, Su2su20202 comp (y)- BBB-1-BBB 4PI x DMSC-27, Su2su20202 comp (Red) BBB-40-BBB x DMSC-9, DMSC-8 X DMSC-9 were found to be superior.

### References

1. Matsuoka Y, Vigouroux Y, Goodman MM, Sanchez J, Buckler E, Doebley J. A single domestication for maize shown by multilocus microsatellite genotyping. *Proceedings of the National Academy of Sciences*. 2002; 99(9):6080-6084.
2. Cholastova T, Soldanova M, Pokorny R. Random amplified polymorphic DNA (RAPD) and simple sequence repeat (SSR) marker efficacy for maize hybrid identification. *African Journal of Biotechnology*. 2011; 10(24):4794-4801.
3. Dandolini TS, Scapim CA, Amaral Junior AT, Mangolin CA, Machado MDFPS, Movtt AS *et al*. Genetic divergence in popcorn lines detected by microsatellite markers. *Crop Breeding and Applied Biotechnology*. 2008; 8(4):313-320.
4. Tanksley SD, Mc Couch SR. Seed banks and molecular maps: unlocking genetic potential from the wild. *Science*. 1997; 277(5329):1063-1066.
5. Rao CR. *Advanced statistical methods in biometrical research*. John Wiley and Sons, INC. New York, 1952, 390-395.
6. Singh RK, Chaudhary BD. *Biometrical methods in quantitative genetic*. Biometrical methods in quantitative genetic analysis, 1979.
7. Rafiq CM, Rafique M, Hussain A, Altaf M. Studies on heritability, correlation and path analysis in maize (*Zea mays* L.). *Journal of Agricultural Research*. 2010; 48(1):35-38.
8. Vashistha A, Dixit N, Dipika N, Sharma SK, Marker S. Studies on heritability and genetic advance estimates in Maize genotypes. *Bioscience Discovery*. 2013; 4(2):165-168.
9. Kapoor R, Batra C. Genetic variability and association studies in maize (*Zea mays* L.) for green fodder yield and quality traits. *Electronic Journal of Plant Breeding*. 2015; 6(1):233-240.
10. Mahmood Z, Malik SR, Akhtar R, Rafique T. Heritability and genetic advance estimates from maize genotypes in Shishi Lusht a valley of Krakurm. *International Journal of Agriculture and Biology*. 2004; 6(5):790-791.
11. Hemavathy AT, Balaji K, Ibrahim SM, Anand G, Sankar D. Genetic variability and correlation studies in maize (*Zea mays* L.). *Agricultural Science Digest*. 2008; 28(2):112-114.
12. Jawaharlal J, Reddy GL, Kumar RS. Genetic variability and character association studies in maize. *Agricultural Science Digest*. 2011; 31(3):199-123.
13. Ward Jr JH. Hierarchical grouping to optimize an objective function. *Journal of the American statistical association*. 1963; 58(301):236-244.