

Original Research Article

<https://doi.org/10.20546/ijcmas.2017.610.263>

Evaluation of Maize Genotypes (*Zea mays* L.) for Variability, Heritability and Genetic Advance

K. Sravanti^{1*}, I. Swarnalatha Devi², M.R. Sudarshan² and K. Supriya²

¹Department of Genetics and Plant Breeding, College of Agriculture, Rajendranagar-500030, Hyderabad, Telangana, India

²PJTSAU, Rajendranagar, Hyderabad-500030, Telangana, India

*Corresponding author

ABSTRACT

Keywords

Genetic advance, Genotypic coefficient of variation, Heritability and phenotypic coefficient of variation.

Article Info

Accepted:
21 September 2017
Available Online:
10 October 2017

The present investigation was carried out to assess the variability, heritability and genetic advance in forty two maize genotypes for twelve yield and its contributing traits. The analysis of variance revealed the presence of significant variability among the maize genotypes under study. Among all the characters under study, ear eight exhibited highest PCV (27.52) and GCV (26.42), whereas lowest PCV (3.45) and GCV (3.07) were recorded for days to maturity. Ear height and grain yield/plant expressed high heritability coupled with high genetic advance, which indicated the preponderance of additive gene action in controlling the traits. Hence direct selection of such characters would be effective in improving the yield. Emphasis should be given on these characters, while selection to improve yield potential of crop.

Introduction

Maize (*Zea mays* L.) is one of the important cereal crops and occupies a prominent position in global agriculture after wheat and rice. Maize has diversified uses as food and industrial raw materials. Maize acreage and production have an increasing tendency with the introduction of hybrids due to its high yield potential. It possesses one of the most well studied genetic systems among cereals which have motivated a rich history of research into the genetics of various traits in maize. It offers tremendous scope for the plant breeders for genetic improvement. The success of plant breeding depends on the

extent of genetic variability present in a crop. Knowledge on the nature and magnitude of genetic variation governing the inheritance of quantitative characters like yield and its components is essential for genetic improvement. A critical analysis of genetic variability present in the germplasm of a crop and its estimation is a pre-requisite for initiating any crop improvement programme as well as adopting appropriate selection techniques.

Partitioning of observed variability into heritable and non-heritable components is

very much essential to get a true indication of the genetic coefficient of variability as a useful measure of the magnitude of genetic variance present in the population. It is very difficult to judge whether observed variability is heritable or not. Heritability indicates the extent of transmissibility of a character into future generations. Moreover, knowledge of heritability is also essential for selection of component traits for yield improvement.

Again the heritable portion of the total variation might not be always due to additive gene action. Thus estimates of heritability alone will not give a clear indication of the associating genetic progress that would result from selecting the best plants. It is also essential to find out the relative magnitude of additive and non-additive genetic variances with regard to the characters of concern. Therefore it should be combined with information on genetic advance. Thus a character possessing high heritability along with high genetic advance will be valuable in the selection programme. Keeping in view the importance of aforesaid aspects, the present investigation was undertaken to study the genetic variability, heritability and genetic advance among the maize genotypes for yield and yield contributing traits.

Materials and Methods

In the present investigation 42 maize genotypes were evaluated in randomized block design with three replications at Seed Research and Technology Centre, Rajendranagar, Hyderabad during *Kharif*, 2013. Each entry was raised in four rows of four meters length with a spacing of 75 cm between rows and 20 cm between plants. The recommended package of practices was followed to raise a good crop. Observations were recorded on five randomly tagged plants for plant height, ear height, ear length, ear girth, number of kernel rows per ear, number

of kernels per row, 100-kernel weight and grain yield per plant. Whereas, observations for the characters namely days to 50 per cent tasseling, days to 50 per cent silking, days to maturity, grain yield per plot were recorded on plot basis. The data collected on all the characters were subjected to standard methods of analysis of variance (Panse and Sukhatme, 1985). Phenotypic and genotypic coefficient of variation was calculated as suggested by Falconer (1981). Heritability (broad sense) (Johnson *et al.*, 1955), genetic advance (Burton, 1952) and genetic advance as a percent of mean (Johnson *et al.*, 1955) were also estimated.

Results and Discussion

Genetic variability

The analysis of variance revealed the existence of significant differences among the genotypes for all the traits (Table 1), indicating the presence of considerable genetic variability among the experimental material under study. Thus there is ample scope for improvement of different quantitative and qualitative traits through selection. The mean values, genotypic and phenotypic coefficient of variation, heritability, genetic advance and genetic advance as per cent of mean (Table 2) for two genotypes were calculated for yield and its contributing traits.

For all the characters under study, phenotypic coefficient of variation values are slightly higher than the genotypic coefficient of variation values indicating that the characters were less influenced by the environment. Therefore, response to direct selection may be effective in improving these traits.

The characters studied in the present investigation exhibited low (less than 10 %), moderate (10-20 %) and high (more than 20

%) phenotypic and genotypic coefficients of variation. The estimates of phenotypic (27.52) and genotypic (26.42) coefficients of variation were found to be high for ear height. Similar results were obtained by Akbar *et al.*, (2008) and Reddy *et al.*, (2013). Plant height (17.35/16.61), ear length (13.77/11.04) and grain yield/plant (13.22/11.77) had moderate phenotypic and genotypic coefficients variations. These results were in confirmity with the findings of Choudhary and Choudhary, 2002 and Singh *et al.*, (2003) for plant height and ear length, respectively.

Phenotypic and genotypic coefficients of variation were low for days to 50% tasseling (7.05/6.68), days to 50 % silking (6.90/6.53) and days to maturity (3.45/3.07). These results were in accordance with the findings of Kumar *et al.*, (2014). While five traits namely ear girth (11.43/8.82), No. of kernel rows/ ear (10.40/5.48), No. of kernels/ row

(13.12/6.92), 100-kernel weight (15.22/9.82) and Grain yield / plot (13.92/9.53) expressed moderate PCV values coupled with low GCV values indicating high influence of environment on these characters.

Heritability and genetic advance

Seven characters under investigation *viz.*, days to 50 % tasseling (89.7 %), days to 50 % silking (89.5 %), days to maturity (79.0 %), ear height (91.6 %), ear length (92.1 %), ear girth (64.2 %) and grain yield/plant (79.3 %) expressed high estimates of heritability in broad sense. High heritability for these characters indicates the scope of genetic improvement of these characters through selection, which revealed that these characters are less influenced by environment and there could be greater correspondence between phenotypic and breeding values. Similar results were reported by Rajesh *et al.*, (2013).

Table.1 Analysis of variance for randomized block design for yield and yield component characters in maize

Source of variation Characters	Replication	Genotypes	Error
d.f.	2	41	82
Days to 50% Tasseling	0.413	56.118**	2.071
Days to 50% Silking	0.222	61.495**	2.304
Days to maturity	2.294	37.478**	3.050
Plant height(cm)	209.188	2369.623**	70.170
Ear height (cm)	21.882	821.508**	22.761
Ear length (cm)	5.167	12.148**	1.903
Ear girth (cm)	3.424	6.639**	1.224
No. of kernel rows/ear	0.503	3.923**	1.822
No. of kernels/row	24.965	28.460**	13.207
100 kernel weight (g)	24.053	40.688**	12.950
Grain yield/plant (g)	2.603	1024.524**	82.008
Grain yield/plot (kg)	0.103	1.216**	0.333

* Significant at 5 per cent level; ** Significant at 1 per cent level

Table.2 Estimation of variability, heritability and genetic advance for yield and yield component characters in Maize genotypes

S.No.	Character	Mean	Phenotypic Variance	Genotypic Variance	PCV (%)	GCV (%)	h ² (%)	GA	GA as % of Mean
1.	Days to 50% tasseling	63.50	20.08	18.01	7.05	6.68	89.7	8.28	13.03
2.	Days to 50% silking	67.94	22.03	19.73	6.90	6.53	89.5	8.65	12.74
3.	Days to maturity	110.27	14.52	11.47	3.45	3.07	79.0	6.20	5.62
4.	Plant height (cm)	166.62	836.65	766.48	17.35	16.61	91.6	54.58	32.76
5.	Ear height (cm)	61.75	289.01	266.24	27.52	26.42	92.1	32.26	52.24
6.	Ear length (cm)	16.73	5.31	3.41	13.77	11.04	64.2	3.05	18.22
7.	Ear girth (cm)	15.21	3.02	1.80	11.43	8.82	59.6	2.13	14.03
8.	No. of kernel rows/ear	15.25	2.52	0.70	10.40	5.48	27.8	0.90	5.95
9.	No. of kernels/row	32.58	18.29	5.08	13.12	6.92	27.8	2.44	7.51
10.	100 kernel weight (g)	30.94	22.19	9.24	15.22	9.82	41.7	4.04	13.06
11.	Grain yield/plant (g)	150.47	396.18	314.17	13.22	11.77	79.3	32.51	21.60
12.	Grain yield per plot	5.68	0.62	0.29	13.92	9.53	46.9	76.5	13.45

Min-Minimum; Max-Maximum; PCV-Phenotypic Coefficient of variation; GCV-Genotypic coefficient of variation; h²-Heritability in broad sense; GA-Genetic Advance

Ear girth (59.6 %), 100-kernel weight (41.7 %) and grain yield/plot (46.9 %) had moderate heritability, whereas no. of kernel rows /ear (27.8 %) and no. of kernels/row (27.8 %) recorded low heritability.

Genetic advance as a per cent of mean is classified as low (less than 10 %), moderate (10-20 %) and high (more than 20 %). Among the characters under study, days to maturity (5.62 %), No. of kernel rows/ear (5.95 %), no. of kernels/row (7.51 %) exhibited low genetic advance as a per cent of mean. These results were in trends with the findings of Kumar *et al.*, (2014) and Nayak *et al.*, (2014) for days to maturity, Alake *et al.*, (2008) and Hepziba *et al.*, (2013) for no. of kernels rows/ear and no. of kernels/row. Days to 50 % tasseling (13.03 %), days to 50 % silking (12.74 %) ear length (18.22 %), ear girth (14.03 %), 100 kernel weight (13.06 %) and grain yield/plot (13.45 %) had moderate genetic advance as a per cent of mean. Remaining three traits namely plant height (32.76 %), ear height (52.24 %) and grain yield/plant (21.60 %) exhibited high estimates of genetic advance as a per cent of mean. Reddy *et al.*, (2013) and Kumar *et al.*, (2014) reported similar results for plant height and ear height.

Among all the characters studied, days to maturity exhibited high heritability coupled with low genetic advance as a per cent of mean. High heritability coupled with low genetic advance as a per cent of mean indicates that the expression of the trait is under the control of non-additive type of gene action, and its response to selection would be poor. In such case hybridization programme is rewarded.

Days to 50 % tasseling, days to 50 % silking and ear length expressed high heritability coupled with moderate genetic advance as a per cent of mean. High heritability coupled with moderate genetic advance as per cent of mean, suggested that the expression of this

trait was mostly influenced by additive type of gene action. Hence its response to selection would be effective in improving the seed yield.

Plant height, ear height and grain yield/plant expressed high heritability coupled with high genetic advance, which indicated the preponderance of additive gene action in controlling the traits. Hence direct selection of such characters would be effective in improving the yield. These results were in accordance with the findings of Rajesh *et al.*, (2013). Moderate heritability coupled with moderate genetic advance values were reported for ear girth, 100-kernel weight and grain yield/plot, while no. of kernel rows/ ear and no. of kernels/row exhibited low heritability coupled with low genetic advance.

A perusal of genetic parameters *viz.*, phenotypic and genotypic coefficients of variation revealed less influence of environment on the characters under study. Therefore, response to direct selection may be effective in improving these traits.

Plant height, ear height and grain yield/plant expressed high heritability coupled with high genetic advance, which indicated the preponderance of additive gene action in controlling the traits. Hence direct selection of such characters would be effective in improving the yield. Days to 50 % tasseling, days to 50 % silking and ear length expressed high heritability coupled with moderate genetic advance as a per cent of mean, suggesting that the expression of this traits was mostly influenced by additive type of gene action. Hence its response to selection would be effective in improving the seed yield. While days to maturity exhibited high heritability coupled with low genetic advance as a per cent of mean, indicates that the expression of the trait is under the control of non-additive type of gene action and its response to selection would be poor.

References

- Akbar, M., Shakoor, S., Hussain, A., and Sarwar, M. 2008. Evaluation of maize 3-way crosses through genetic variability, broad sense heritability, character association and path analysis. *Journal of Agricultural Research*. 46 (1): 39-45.
- Alake, C.O., Ojo, D.K., Oduwaye, O.A., and Adekoya, M.A. 2008. Genetic variability and correlation studies in yield and yield related characters of tropical maize (*Zea mays* L.) *Agricultural & Environment*. 8 (1/2): 14-27.
- Burton, G.W., 1952. Quantitative inheritance in grasses. *Proceedings of 6th International Grassland Congress*. 1: 277-283.
- Choudhary, A.K., and Chaudhary, L.B. 2002. Genetic studies in some crosses of maize (*Zea mays* L.). *Journal of Research Birsa Agricultural University*.5 (1/2): 10-16.
- Falconer, D.S., 1981. *Introduction to Quantitative Genetics*. Oliver and Boyd, London. 340.
- Hepziba, S.J., Geetha, K., and Ibrahim, S.M. 2013. Evaluation of genetic diversity, variability, character association and path analysis in diverse inbreds of maize (*Zea mays* L.). *Electronic Journal of Plant Breeding*. 4 (1): 1067-1072.
- Johnson, H.W., Robinson, H.F., and Comstock, R.E. 1955. Estimates of genetic and environmental variability in soybean. *Agronomy Journal*. 47: 314-318.
- Kumar, G.P., Reddy, V.N., Kumar, S.S., and Rao, P.V. 2014. Genetic variability, heritability and genetic advance studies in newly developed maize genotypes (*Zea mays* L.) *International Journal of Pure and Applied Biosciences*. 2 (1): 272-275.
- Nayak, V.H., Singh, R., and Potla, K.R. 2013. Genetic variability analysis of yield and yield related traits in inbred lines of maize (*Zea mays* L.). *Environment and Ecology*. 31 (4): 1669-1671.
- Panse, V.G., and Sukhatme, P.V. 1985. *Statistical Methods for Agricultural Workers*. ICAR, New Delhi. 235 – 246.
- Rajesh, V., Kumar, S.S., Reddy, V.N., and Shankar A.S. 2013. Studies on genetic variability, heritability and genetic advance estimates in newly developed maize genotypes (*Zea mays* L.). *International Journal of Applied Biology and Pharmaceutical Technology*. 4 (4): 242-245.
- Reddy, V.R., Jabeen, F., Sudarshan, M.R., and Rao, A.S. 2013. Studies on genetic variability, heritability, correlation and path analysis in maize (*Zea mays* L.) over location. *International Journal of Applied Biology and Pharmaceutical Technology*. 4 (1): 195-199.
- Singh, P., Das. S., Kumar, Y and Dutt, Y., and Sangwan, O. 2003. Variability studies for grain yield and its component traits in maize (*Zea mays* L.). *Annals of Agri Bio Research*. 8: 2-31.

How to cite this article:

Sravanti, K., I. Swarnalatha Devi, M.R. Sudarshan and Supriya, K. 2017. Evaluation of Maize Genotypes (*Zea mays* L.) for Variability, Heritability and Genetic Advance. *Int.J.Curr.Microbiol.App.Sci*. 6(10): 2227-2232. doi: <https://doi.org/10.20546/ijcmas.2017.610.263>