ASSESSMENT OF VARIOUS VARIABILITY PARAMETERS AND CORRELATION OF QUANTITATIVE CHARACTERS IN MAIZE (*Zea mays* L.) INBRED LINES

Abstract

The present research problem was carried out to assess the variability parameters, heritability, genetic advance and correlations among various quantitative traits in maize inbred lines. A total of 69 inbred lines were evaluated in alpha lattice design with 2 replications at Winter Nursery Centre, Hyderabad. ANOVA results displays genotypes were significantly different from each other. From the results it was depicted that Phenotypic Coefficient of Variation (PCV) was higher than Genotypic Coefficient of Variation (GCV) indicating the influence of environment. The traits, No. of kernels per row, Cob weight, Grain yield per cob showed high GCV and PCV values likewise Days to 50% tasseling, Days to 50% silking and Days to 75% dry husk showed low GCV and PCV values. Most of the characters showed high heritability and traits such as Plant height, Tassel length, Ear length, No. of kernels per row, Cob weight and Grain yield per cob showed high GAM and its values ranged from 21.5% to 101.30%. So, the traits such as No. of kernels per row, Cob weight and Grain yield per cob can be used for further crop improvement in the breeding programme. Of all the traits under study except, Days to 50% tasseling, Days to 50% silking and Days to 75% dry husk showed positive significant correlation with grain yield per cob indicating selection for the traits will enhance the grain yield whereas the excepted traits showed negative significant association with grain yield per cob indicating selection for these traits is also essential as it reduces duration of crop.

Key words

GCV, PCV, Heritability, Genetic advance, Correlation

1. INTRODUCTION

Maize (*Zea mays* L.) is the 3rd most grown cereal crop after wheat and rice in the world. Millions of people depend on maize as a food source, animal feed, and raw material for industries. Additionally, maize is grown in over 170 countries producing 1147.7 million MT over 193.7 Mha at 5.75 t ha^{-1} productivity (FAOSTAT, 2020). It is reported that by 2050, the demand for maize will double in the developing world at the same time yield is severely limited due to various biotic and abiotic factors (Rosegrant *et al*., 2009). In addition to this climate change forecasts indicates substantial harm to agricultural productivity and the inability of many regions to achieve necessary long-term food security improvements (Cairns *et al*., 2012).

In order to meet the future challenges, plant breeders will need all the genetic diversity that they can get. Landraces and heirloom cultivars, which are still grown by farmers all over the world, have some of this diversity (Dempewolf *et al*., 2014). Crop improvement in a population largely depends on amount of genetic variability present among individuals of population. Variability refers to the presence of difference among the individuals of plant population. Genetic variability is the most important prerequisite for effective improvement through both traditional and modern breeding procedures.

Genetic variability is estimated with the help of certain genetic parameters such as Genotypic Coefficient of Variation (GCV), Phenotypic Coefficient of Variation (PCV) and heritability. Estimates of heritability give accurate information about how faithfully a certain genetic trait will be passed down to next generations. Heritability estimates in combination with genetic advance are often more useful than heritability estimates alone. However, it is not necessary that a character showing high heritability may also exhibit high genetic advance (Johnson *et al*., 1955).

In addition to variability parameters, Correlation study also has the potential to offer reliable and beneficial insights into the nature, extent, and direction of the selection process. (Zeeshan *et al*., 2013). The correlation coefficient helps in ascertaining the extent of the association between two distinct attributes and the degree to which these attributes change together (Bocanski *et al*., 2009; Nagabhushan *et al*., 2011). Grain yield is a complex characteristic that is impacted by various morphological and physiological attributes (Crosbie and Mock. 1981). Enhancing grain yield involves grasping the correlated relationship between yield and its elements, as well as identifying the nature of the connection between them. (Kalla *et al*., 2001). The aim of the present study was to assess the variability and correlation among various quantitative traits in maize inbred lines.

2. MATERIALS AND METHODS

2.1. Location of experiment

The experiment was carried out at Winter Nursey Centre, Rajendranagar, Hyderabad. Winter Nursey Centre, Hyderabad is in Southern Telangana agro climatic zone of Telangana state. Geographically, it lies at 17.19° N latitude, 78.24° E longitude with an altitude of 542.6 meters above Mean Sea Level (MSL). The rainfall of the Research Station ranges from 606 to 853 mm.

2.2. Materials used for the experiment

A total of 69 inbred lines were used. They are grown in alpha lattice design with two replications, each replication consists of seven blocks, and the spacing followed was 60 cm × 20 cm in a row length of 3m in *Rabi*, 2022-23 and standard intercultural practices were followed.

2.3. Collection and analysis of data

Data was recorded on three randomly selected plants for plant height, tassel length, ear length, ear diameter, number of kernel rows per ear, number of kernels per row, cob weight and grain yield per cob in each replication. Flowering and maturity traits *i.e.*, days to 50% tasseling, days to 50% silking, Anthesis Silking Interval (ASI) and days to 75% dry husk were recorded in each replication. The data on all the characters were subjected to standard analysis of variance methods (Patterson and Williams 1976).

The phenotypic and genotypic coefficients of variation (Singh and Chaudhary.

1985), Heritability (broad sense) (Johnson *et al*., 1955), genetic advance (Burton. 1952), and genetic advance as a percentage of the mean (Johnson *et al*., 1955) were all calculated using below formulas.

$$\text{GCV (\%)} = \frac{\sqrt{\delta^2 g}}{\bar{x}} \times 100$$

$$\text{PCV (\%)} = \frac{\sqrt{\delta^2 p}}{\bar{x}} \times 100$$

$$\text{Heritability } (h^2) = \frac{\delta^2 g}{\delta^2 p} \times 100$$

where: δ^2 g = genotypic variance, δ^2 p = phenotypic variance and $\bar{x}$= sample mean.

$$\text{Genetic advance (GA)} = (K)\ (\sqrt{\delta^2}\text{p})\ (h^2)$$

where GA = expected genetic advance, K = selection differential that varies depending up on the selection intensity and stands at 2.056 for selecting 5% of the genotypes, δ^2p = phenotypic variance and h^2 = heritability (in broad sense).

$$\text{Genetic advance as percent of mean (GAM)} = \frac{GA}{\bar{x}} \times 100$$

The Pearson correlation coefficient of growth, yield and its attributing traits was worked out according to the following formulae,

$$r = \frac{\sum_i (x_i - \bar{x})\,(y_i - \bar{y})}{\sqrt{\sum_i (x_i - \bar{x})^2}\,\sqrt{\sum_i (y_i - \bar{y})^2}}$$

where, r= Pearson correlation coefficient x_i = x variable, y_i = y variable

2.4. Statistical analysis

Excel 2010 was used to process the experimental data, while R-studio 3.5.0 was used to analyse it in Alpha lattice design.

3. RESULTS AND DISCUSSION

Investigation at field were carried out to assess the genetic variability and associations among various quantitative characteristics in maize inbred lines. The results were analysed and discussed below, supported by prior research evidence.

3.1. Genetic variability

ANOVA results displays genotypes were significantly different from each other except for Anthesis silking interval which were represented in Table 1.

Genetic variability results were presented in Table 2. Based on the results all the characters under investigation showed lower GCV values compared to PCV values indicating that the characters were influenced by environment. And the results were classified into standard categories into low (0–10%), moderate (10–20%) and high (>20%) as given by Sivasubramanian and Madhavamenon (1973). No. of kernels per row, Cob weight and Grain yield per cob showed high GCV and PCV values (20.68, 25.08; 47.26, 50.30; and 52.12, 55.25 respectively.). Likewise, traits such as Days to 50% tasseling, Days to 50% silking and Days to 75% dry husk showed low GCV and PCV values (6.88, 7.79; 6.28, 7.11; and 2.98, 4.620) and moderate GCV and PCV was shown by Plant height, Tassel length, Ear length and No. of kernel rows per ear. The remaining traits such as Anthesis silking interval had moderate GCV and high PCV (11.49, 42.3) and Ear diameter had low GCV and moderate PCV (9.0, 12.23). The results were in comparable to Kandel *et al*. (2017), Magar *et al.* (2021), Nzuve (2014), Mishra *et al*. 2016, Bharathiveeramani *et al*. (2012) and Hefny *et al*. (2011).

The reliability of a trait for utilization in a breeding initiative is assessed through its coefficient of variation (CV), especially the genetic coefficient of variation (GCV). In breeding programme, a higher proportion of GCV in relation to PCV is favoured. Traits like the number of kernels per row, cob weight, and grain yield per cob exhibited high values for both PCV and GCV.

3.2. Heritability and genetic advance

Form the results it was depicted that heritability of traits can be grouped into low (< 30%), moderate (30%–60%) and (> 60%) high as given by Johnson *et al*. (1955). Most of the characters such as Plant height, Tassel length, Days to 50% tasseling, Days to 50% silking, Ear length, No. of kernels per row, Cob weight and Grain yield per cob showed high heritability ranging from 61%-81%, which were displayed in table- 2, and moderate heritability was shown by Days to 75% dry husk, Ear diameter and No. of kernel rows per cob i.e., 41%, 54% and 46% respectively. Whereas Anthesis silking interval trait showed low heritability i.e., 7%. Likewise, GAM for all the characters under investigation were displayed in table- 2. They were classified into low (less than 10%), moderate (10 –20%), and high (greater than 20%) Johnson *et al*. (1955). Characteristics such as Plant height, Tassel length, Ear length, No. of kernels per row, Cob weight and Grain yield per cob showed high GAM and its values ranged from 21.5% to 101.30% and moderate GAM was shown by Days to 50% tasseling, Days to 50% silking, Ear diameter and No. of kernel rows per ear ranging from 11.42 to 14.77 whereas Anthesis silking interval and Days to 75% dry husk showed low GAM i.e., 6.42 and 3.96 respectively. The above results are on par with Bharathiveeramani *et al*. (2012), Mishra *et al*. (2016), Kharel *et al*. (2017), Jilo *et al*. (2018) and Rai *et al*. (2021).

When a character is governed by additive gene effects, it typically leads to increased heritability and genetic advancement. Conversely, if non-additive gene actions are responsible for controlling a trait, it could lead to high heritability but low genetic advancement. From the present research results Plant height, Tassel length, Ear length, No. of kernel rows per ear, Cob weight, Grain yield per cob showed additive gene action suggesting that selection for these traits increase the grain yield of the crop whereas Traits such as Anthesis silking Interval displayed low estimations of both heritability and genetic advance due to their susceptibility to environmental influence. As their gene action is non-additive in nature selection for this trait is not recommended.

3.3. Phenotypic correlation coefficient

Phenotypic correlation coefficient for all the traits were estimated and displayed in Table 3. Most of the traits such as Plant height (r= 0.54), Tassel length (r= 0.51), Anthesis silking interval (r= 0.481), Ear length (r= 0.848), Ear diameter (r= 0.778), No. of kernel rows per ear (r= 0.635), No. of kernels per row(r= 0.884) and Cob weight(r= 0.99) showed positive significant correlation with Grain yield per cob among them Cob weight exhibited the highest influence on Grain yield per cob followed by No. of kernels per row then Ear length among the attributed traits which indicates selection for these traits will enhance the grain yield, analogous results were obtained by Alvi *et al*. (2003), Bartaula *et al*. (2019), Chinnadurai and Nagarajan (2011), Rajwade *et al.* (2018) and Kharel *et al.* (2017). Whereas Days to 50% tasseling, Days to 50% silking and Days to 75% dry husk showed negative significant correlation with Grain yield per cob which indicates selection for these traits will reduce the duration of crop which is also a major objective of any breeding programme analogous results were reported by Kharel *et al*. (2017), Akshaya *et al*. (2022) and Garko *et al*. (2023).

4. CONCLUSION

All the characters under present investigation exhibited significant variation indicating that there is a presence of genetic variation among maize inbred lines. For all the characters under investigation PCV is greater than GCV, indicating the presence of environmental influence. Traits such as No. of kernels per row, Cob weight and Grain yield per cob exhibited high values for GCV, PCV, Heritability and GAM indicating selection for these traits will enhance the yield of the crop. Most of the traits such as Plant height, Tassel length, Anthesis silking interval, Ear length, Ear diameter, No. of kernel rows per ear, No. of kernels per row and Cob weight exhibited positive significant correlation with grain yield per cob indicating selection for the traits will enhance the grain yield whereas Days to 50% tasseling, Days to 50% silking and Days to 75% dry husk showed negative significant association with grain yield per cob indicating selection for these traits is also essential as it reduces duration of crop.

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Conflict of Interest: None.

REFERENCES:

Akshaya, M., Shantakumar, G., Sridevi, O and Sangamesh, N. 2022. Correlation and path coefficient analysis for determining interrelationships among grain yield and yield related characters in maize hybrids (*Zea mays* L.). *The Pharma Innovation Journal*. 11 (3): 1343-1346.

Alvi, M.B., Rafique, M., Tariq, M.S., Hussain, A., Mahmood, T and Sarwar, M. 2003. Character association and path coefficient analysis of grain yield and yield components maize (*Zea mays* L.). *Pakistan Journal of Biological Sciences*. 6(2):136-138.

Bartaula, S., Panthi, U., Timilsena, K., Acharya, S.S and Shrestha, J. 2019. Variability, heritability and genetic advance of maize (*Zea mays* L.) genotypes. *Research in Agriculture Livestock and Fisheries*. 6 (2): 163-169.

Bharathiveeramani, B., Prakash, M and Seetharam, A. 2012. Variability studies of quantitative characters in Maize (*Zea mays* L.). *Electronic Journal of Plant Breeding.* 3 (4): 995-997.

Bocanski, J., Sreckov, Z and Nastasic, A. 2009. Genetic and phenotypic relationship between grain yield and components of grain yield of maize (*Zea mays* L.). *Genetika-Belgrade*. 41 (2): 145-154.

Burton, G.W. 1952. Quantitative inheritance in grasses. *Proceedings of the 6th International Grassland Congress*, Pennsylvania State College, USA, 23 August 1952. 277-283.

Cairns, J.E., Sonder, K., Zaidi, P.H., Verhulst, N., Mahuku, G., Babu, R., Nair, S.K., Das, B., Govaerts, B., Vinayan, M.T and Rashid, Z. 2012. Maize production in a changing climate: impacts, adaptation, and mitigation strategies. *Advances in agronomy*. 114: 1-58.

Chinnadurai, I.S and Nagarajan, P. 2011. Interrelationship and path coefficient studies for qualitative traits, grain yield and other yield attributes among maize (*Zea mays* L.). *International Journal of Plant Breeding and Genetics*. 5 (2): 1- 4.

Crosbie, T.M and Mock, J.J. 1981. Changes in physiological traits associated with grain yield improvement in three maize breeding programs 1. *Crop Sciences*. 21 (2): 255–259.

Dempewolf, H., Eastwood, R.J., Guarino, L., Khoury, C.K., Muller, J.V and Toll, J. 2014. Adapting agriculture to climate change: a global initiative to collect, conserve, and use crop wild relatives. *Agroecology and Sustainable Food Systems*. 38 (4): 369-377.

FAOSTAT. 2020. [online]Available at: https://www.fao.org/faostat/en/#data/QCL.

Garko, M.S., Dawaki, K.D., Yawale, M.A., Saad, A.M., Daraja, Y.B., Fulani, M.S., Magashi, A.I and Abdussalam, S.S. 2023. Correlation And Path Coefficient Analysis Between Grain Yield and Some Growth And Yield Components Of Maize (*Zea Mays* L.) Genotype As Influenced By Drought And Heat Stress Conditions In Sudan Savannah Of Nigeria. *International Journal of Agriculture and Environmental Research*. 9 (2): 162-169.

Hefny, M. 2011. Genetic parameters and path analysis of yield and its components in corn inbred lines (*Zea mays* L.) at different sowing dates. *Asian Journal of Crop Science*. 3 (3): 106-117.

Jilo, T., Tulu, L., Birhan, T and Beksisa, L. 2018. Genetic variability, heritability and genetic advance of maize (*Zea mays* L.) inbred lines for yield and yield related traits in southwestern Ethiopia. *Journal of plant breeding and crop science*. 10 (10): 281-289.

Johnson, H.W., Robinson, H.F and Comstock, R.E. 1955. Estimates of genetic and environmental variability in soybeans 1. *Agronomy journal*. 47 (7): 314-318.

Kalla, V., Kumar, R and Basandrai, A.K. 2001. Combining ability analysis and gene action estimates of yield and yield contributing characters in maize (*Zea mays* L.). *Crop Research*. 22 (1): 102–106.

Kandel, B.P., Poudel, A., Sharma, S and Subedi, M. 2017. Variability studied in yield attributing traits of early maize genotypes in western hill of Nepal. *Nepalese Journal of Agricultural Sciences*. 15: 13-18.

Kharel, R., Ghimire, S.K., Ojha, B.R and Koirala, K.B. 2017. Estimation of genetic parameters, correlation and path coefficient analysis of different genotypes of maize (*Zea mays* L.). *International Journal of Agriculture Innovations and Research*. 6 (1): 191-195.

Magar, B.T., Acharya, S., Gyawali, B., Timilsena, K., Upadhayaya, J and Shrestha, J. 2021. Genetic variability and trait association in maize (*Zea mays* L.) varieties for growth and yield traits. *Heliyon* 7 (9): 1-8.

Ministry of Agriculture, 2020-2021. Government of India. http:// www.indiaagristat.com.

Mishra, T.K., Pradhan, B and Mishra, D. 2016. Genetic Diversity, Character association and Path-Coefficient study in QPM inbreds. *Electronic Journal of Plant Breeding*. 7 (3): 505-513.

Nagabushan, N.M., Chandrashekhar, H., Shashibhaskar, M.S and Prahalada, G.D. 2011. Genetic variability and correlation studies for yield and related characters in single cross hybrids of maize (*Zea mays* L.). *Current Biotica*. 5 (2): 157-163.

Nzuve, F., Githiri, S., Mukunya, D.M and Gethi, J. 2014. Genetic Variability and Correlation Studies of Grain Yield and Related Agronomic Traits in Maize. *Journal of Agricultural Science*. 6 (9): 166-176.

Patterson, H. D and Williams, E. R. 1976. A new class of resolvable incomplete block designs. *Biometrika*. 63 (1): 83-90.

Rai, R., Khanal, P., Chaudhary, P and Dhital, R. 2021. Genetic variability, heritability and genetic advance for growth, yield and yield related traits in maize genotypes. *Journal of Agriculture and Applied Biology*. 2 (2): 96-104.

Rajwade, J.K., Jagadev, P.N., Lenka, D and Gupta, S. 2018. Correlation and path coefficient studies on elite genotypes of maize inbred lines. *Journal of Pharmacognosy and Phytochemistry*. 7 (2): 2765-2771.

Rosegrant, M.R., Ringler, C., Sulser, T.B., Ewing, M., Palazzo, A., Zhu, T., Nelson, G.C., Koo, J., Robertson, R., Msangi, S and Batka, M. 2009. Agriculture and food security under global change: Prospects for 2025/2050. *International Food Policy Research Institute, Washington, DC*. 1-81.

Sivasubramanian. S and Madhava Menon. P. (1973) Genotypic and phenotypic variability in rice. Madras Agric. J. 60(9 -12):1093 -1096.

Singh, R.K and Chaudhary, B.D. 1977. *Biometrical methods in quantitative genetic analysis.* Kalyani publishers New Delhi.

Zeeshan, M., Ahsan, M., Arshad, W., Ali, S., Hussain, M and Khan, M.I. 2013. Estimate of correlated responses for some polygenic parameters in yellow maize (*Zea mays* L.) hybrids. *International Journal of Advance Research*. 1 (5): 24–29.

Table 1. Analysis of variance for characters in maize

Source of variation	**Degrees of freedom of**	**Mean Sum of squares due to**	**Degrees of freedom of**	**Mean Sum of squares due to**

	Genotypes	**Genotypes**	**Replication**	**Replication**
Plant height	68	685.66**	1	0.50
Tassel length	68	28.54**	1	143.38**
Days to 50% tasseling	68	64.38**	1	78.38**
Days to 50% silking	68	59.58**	1	148.18**
Anthesis silking interval	68	3.35	1	11.02*
Days to 75% dry husk	68	36.67**	1	148.18**
Ear length	68	7.00**	1	0.57
Ear diameter	68	0.29**	1	0.05
No. of kernel rows per ear	68	4.75**	1	0.07
No. of kernels per row	68	49.32**	1	5.68
Cob weight	68	1657.40**	1	78.88
Grain yield per cob	68	1108.37**	1	8.38

*, ** Significant at 5 % and 1 % levels, respectively

Table 2. Estimates of various variability parameters for twelve quantitative traits

Trait	Mean	δ^2g	δ^2p	GCV (%)	PCV (%)	Hbs (%)	GA	GAM

Plant height	113.51	317.74	367.91	15.70	16.89	86	34.12	30.06
Tassel length	24.64	11.28	17.25	13.63	16.85	65	5.59	22.70
Days to 50% tasseling	77.14	28.21	36.16	6.88	7.79	78	9.66	12.52
Days to 50% silkling	81.31	26.09	33.48	6.28	7.11	77	9.28	11.42
ASI	4.16	0.22	3.11	11.49	42.3	7	0.26	6.42
DT75DH	110.13	10.77	25.89	2.98	4.620	41	4.36	3.96
Ear length	12.32	2.67	4.32	13.27	16.87	61	2.64	21.50
Ear diameter	3.51	0.10	0.18	9.00	12.23	54	0.47	13.64
NKRPE	11.77	1.51	3.23	10.46	15.26	46	1.73	14.77
NKPR	21.59	19.95	29.36	20.68	25.08	67	7.58	35.12
Cob weight	58.97	777.16	880.23	47.26	50.30	88	53.96	91.49
Grain yield per cob	43.82	521.93	586.43	52.12	55.25	89	44.39	101.30

Where, δ^2 g= genotypic variance, δ^2 p= phenotypic variance, GCV= Genotypic Coefficient of Variation, PCV= Phenotypic Coefficient of Variation, Hbs= Heritability broad sense, GA= Genetic Advance, GAM= Genetic Advance as percent of Mean, ASI= Anthesis Silking Interval, DT75DH= Days to 75% Dry Husk, NKRPE= No. of Kernel Rows per Ear, NKPR= No. of Kernels per Row.

Table 3. Pearson's correlation coefficient for twelve quantitative traits of maize inbred lines

Trait	**PH**	**TL**	**DFT**	**DFS**	**ASI**	**DT75DH**	**EL**	**ED**	**NKRPE**	**NKPR**	**CW**	**GYPC**
PH	1											
TL	0.692**	1										
DFT	-0.177	-0.074	1									
DFS	-0.182	-0.108	0.996**	1								
ASI	0.019	-0.331**	-0.462**	-0.387**	1							
DT75DH	-0.236	-0.209	1.018**	0.998**	-0.654**	1						
EL	0.549**	0.522**	-0.197	-0.164	0.440**	-0.267*	1					
ED	0.378**	0.358**	-0.49**	-0.45**	0.635**	-0.513**	0.622**	1				
NKRPE	0.169	0.291*	-0.575**	-0.537 **	0.644**	-0.696**	0.356**	0.889**	1			
NKPR	0.415**	0.429**	-0.282*	-0.227	0.701**	-0.379**	0.763**	0.805**	0.596**	1		
CW	0.536**	0.527**	-0.359 **	-0.327 **	0.497**	-0.486**	0.861**	0.785**	0.649**	0.882**	1	
GYPC	0.54 **	0.515**	-0.383**	-0.354 **	0.481**	-0.498**	0.848**	0.778**	0.635**	0.884**	0.999**	1

Where, PH= Plant height, TL= Tassel Length, DFT= Days to 50% Tasseling, DFS= Days to 50% Silking, EL= Ear Length, ED= Ear Diameter, NKRPE= Number of Kernel Rows per Ear, NKPR= Number of Kernels per Row, CW= Cob Weight, GYPC= Grain Yield per Cob.

*, ** Significant at 5 % and 1 % levels, respectively