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## Genetic studies on correlation, variability, heritability and genetic advance of grain yield and its components of maize (*Zea mays* L.) single cross hybrids

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### Abstract

In the present investigation sixty-three single cross hybrids were evaluated in 9 x 7 alpha lattice to study the Correlation, genetic variance, heritability and genetic advance among different quantitative traits to determine the efficiency of selection in a breeding programme. Accordingly, the higher phenotypic variance than genotypic variance was recorded for most of the traits. However, the difference between PCV and GCV was very minimal for most of the traits except grain yield indicating selection for grain yield provides less chances as compared to other traits. Plant height, hundred seed weight and cob length recorded high heritability along with high genetic advance indicating positive response upon selection. Correlation study revealed that grain yield was significantly correlated with days to 50 per cent tasseling, days to 50 per cent silking, plant height, ear height, number of kernels per row, cob girth, cob length, and hundred grain weight.

**Keywords:** Maize, heritability, correlation, genetic advance, variability

### 1. Introduction

Maize is an important cereal crop known for its wide adaptability to diverse agro climatic regions and also for high amount of heterosis. High amount of genetic diversity and out crossing nature in the crop provides tremendous scope for genetic improvement for grain yield through application of suitable breeding procedures. As maize is highly cross pollinated crop, hybrid breeding approach is very much lucrative and has witnessed a lot of commercial success in the last two decades globally. However, to develop the inbreds based on the different objectives a suitable selection strategy has to be developed and for this knowledge of genetic correlation among the characters, presence of genetic variability, heritability for the trait of interest among the germplasm lines is desirable in any plant breeding programme. Genetic improvement in traits of economic importance along with maintaining sufficient amount of variability is always the desired objective in maize breeding programmes (Hallauer 1972) [9].

Effective improvement in yield can be brought about through selection for component characters of yield. So, correlation analysis provides the information on nature and magnitude of the association of different components characters with seed yield. Genetic variability is a heritable difference among cultivars and is required in an appreciable level within a population to facilitate and sustain an effective long-term plant breeding programme. Progress from selection has been reported to be directly related to the magnitude of genetic variance in the population (Tabanao and Bernardo, 2005) [22]. Further, the efficiency with which genotypic variability can be exploited by selection depends upon heritability and the Genetic Advance (GA) of individual trait (Bilgin *et al*, 2010) [4].

Knowledge of direction and degree of association between traits is of fundamental importance in making selection during plant breeding programmes. The importance increases, especially if some of the desirable traits present difficulty in assessment/selection or show low heritability such as grain yield. (Cruz *et al*. 2014) [5]. Thus, correlation coefficient helps in understanding the degree and direction of relationship between different traits. Correlation analysis helps in understanding how the improvement of one character will cause simultaneous changes in other characters.

The present study was undertaken to understand the genetic correlation between different quantitative characters for yield and yield contributing traits, variability, heritability and genetic advance among the sixty-three single cross hybrids of maize to decide upon suitable breeding procedure for genetic improvement.

## 2. Material and Method

In the present study sixty-three single cross hybrids were generated by crossing 20 lines and three testers and were evaluated in replicated trial during Kharif 2018. Each hybrid was raised in two rows of 4 meter length with a spacing of 60 cm x 20 cm in 7x9 alpha lattice design following recommended package of practices. Data was recorded on days to 50% tasseling, days to 50% silking which were collected on plot basis, whereas, for yield related traits plant height (cm), ear height (cm), number of kernel rows per cob, number of kernels per row, cob length (cm) and cob girth (cm) data was collected on five randomly chosen competitive plants. Grain yield (GY) was calculated by recording fresh ear weight of the entire plot at the time of harvest and expressed in quintals per hectare (q/ha) at 15% moisture.

### 2.1 Estimation of variance components, Broad sense heritability and Genetic advance

The data was subjected to analysis of variance using INDOSTAT 7.1 software. Correlation, Phenotypic variance, Genotypic variance, Environmental, Phenotypic covariance (PCV) and Genetic covariance (GCV) were calculated according to Singh and Chaudhary (1985). GCV and PCV values were categorized as low when less than 10%, moderate, 10-20% and high, greater than 20% as indicated by Deshmukh *et al.* (1986) [6].

Broad sense heritability was estimated according to the procedure suggested by Singh and Chaudhary (1985):

$$H = \frac{\delta_g^2}{\delta_p^2} \times 100 \quad (1)$$

where,  $\delta_g^2$  is genotypic variance and  $\delta_p^2$  is phenotypic variance. Broad sense heritability percentage was categorized as low when less than 40%, medium, 40 – 59%, moderately high, 60-79% and very high, 80% and above as indicated by Singh (2001) [19].

Genetic advance values were determined by the formula illustrated by Johnson *et al.* (1955) [14]:

$$GA = (K)(\delta A)(H) \quad (2)$$

where, K = 2.063 (selection differential at 5%);  $\delta A$  = phenotypic standard deviation of the mean yield of the hybrids and H = broad sense heritability. Genetic advance was expressed as a percentage of the hybrids mean. This was categorized as high when it is above 20%, moderate, 10-20% and low when it is less than 10%. Genetic advance as percentage of means were obtained using method suggested by Allard (1960) [11].

### 2.2 Genotypic and phenotypic correlation coefficients

Genotypic and phenotypic correlation coefficients were worked out as per the methods suggested by Falconer (1960) [7] to find out the relationship between yield and yield attributing character. The genotypic and phenotypic variance and co-variance components were utilized to calculate

genotypic and phenotypic correlation coefficients by applying the formula.

$$r_{g.1.2} = \frac{COV.g.1.2}{\sqrt{(\sigma^2g_1) \times (\sigma^2g_2)}} \quad (3)$$

$$r_{p.1.2} = \frac{COV.p.1.2}{\sqrt{(\sigma^2p_1) \times (\sigma^2p_2)}} \quad (4)$$

where, Cov.g. 1.2 - Genotypic covariance between two traits (1 and 2), Cov.p. 1.2 - Phenotypic covariance between two traits (1 and 2),  $\sigma^2g_1$  - Genotypic covariance for first trait,  $\sigma^2p_1$  - Phenotypic covariance for first trait.  $\sigma^2g_2$  - Genotypic covariance for second trait and  $\sigma^2p_2$  - Phenotypic covariance for second trait. Referring to correlation table of Fisher and Yates (1963) [8], the significance of correlation coefficient was tested at 5 % and 1 % significance level.

## 3. Results and Discussion

Analysis of variance based on the data recorded for different quantitative traits highlighted the existence of significant difference among the hybrids for the studied traits in the experimental material indicating that the chosen parental lines and hybrids have sufficient genetic variability (Table 1). The block effect was significant for days to 50% tasseling, days to 50% silking, plant height, ear height, number of kernels per row, cob length and grain yield. It indicates scope for selection among the genotypes for further improvement. The mean of the hybrids for grain yield ranged from 25.21 to 75.08 q/ha with an overall mean of 52.30 q/ha. Similarly, the mean number of kernels per row varied from 27.7 to 40.2 kernels with an overall mean of 34.5 kernels/row.

The Phenotypic variance, Genotypic variance, PCV, GCV, Broad sense heritability and Genetic advance is presented in Table 2. The relative magnitudes of the phenotypic as well as genotypic variances between the traits were compared based on the phenotypic and genotypic coefficient of variation. The GCV provides a measure of comparison of variability and give some indication regarding validity of traits for selection. However, it does not provide clean picture of the extent of genetic gain to be expected from selection of phenotypic traits, unless heritable fraction of variation (heritability) is known (Burton, 1952). Low PCV and GCV values were observed for days to 50% tasseling, days to 50% silking, plant height, no. of kernel rows per cob, cob girth and cob length. The results from all the crosses depicted that phenotypic variances ( $\sigma^2p$ ) and phenotypic coefficient of variation (PCV) were higher than genetic variances ( $\sigma^2g$ ) and genotypic coefficient of variation (GCV) for all the characters studied suggesting some environmental influence on the characters, Arunkumar *et al.* (2018) [2] also reported higher PCV than GCV for most of the quantitative traits in their experiment on maize comprising of 422 inbreds. High PCV coupled with moderate GCV was recorded for grain yield. Whereas, moderate PCV was observed for ear height, number of kernels per row and hundred seed weight.

The difference between PCV and GCV was low for traits like days to 50% silking, days to 50% anthesis, plant height, number of kernel rows per ears, number of kernels/row, cob length, cob girth and hundred seed weight. This implies, less environmental influence on these traits, which ensured practically higher chance for selection. While, for ear height and grain yield relatively high difference was observed

between phenotypic and genotypic coefficient of variation and hence these traits provide practically, less chance for selection, due to higher influence of environmental factors. Although GCV is indicative of the presence of high degree of genetic variation, the amount of heritable portion can only be determined with the help of heritability estimates and genetic gain (Rao and Rao, 2015) [17].

High heritability was recorded by plant height, cob length and hundred seed weight indicating lower influence of environment on these traits. Similarly, Sesay *et al.* (2016) [18] reported high heritability for plant height and hundred seed weight. Low heritability was observed for days to 50% tasseling and ear height. Characters days to 50% silking, number of kernel rows per cob, number of kernels per row, cob girth and grain yield showed moderate heritability. High heritability emphasizing that the additive genetic variation was the major component of genetic variation in the inheritance of these traits and the effectiveness of selection in the early segregating generations of the genotypes for improving these traits. Whereas, the traits exhibiting moderate heritability estimates could be improved through heterosis breeding or hybridization (Bello *et al.* 2012) [3]. This implies selection is considerable difficult for such traits due to the masking effect of the environment.

Genetic advance (GA) as a percentage of the mean was higher for traits such as grain yield per hectare (22.46) followed by hundred seed weight (15.62) showing that, these traits are under the control of additive gene action, Low estimates of genetic advances were observed in days to 50 % Tasselling, days to 50% silking and ear height indicating the presence of low genetic variability for these traits which are also reflected by their respective low genotypic and phenotypic variations. This in turn showed the importance of genetic variability for the improvement of the traits through selection

Heritability estimates along with genetic advance is more helpful in predicting the genetic gain under selection than heritability estimates alone. Therefore, high GA was observed only for grain yield whereas, moderate GA was observed for plant height, number of kernel rows per cob, number of kernels per row, cob length and hundred seed weight. Low GA was observed for days to 50% tasseling, days to 50% silking, ear height and cob girth.

High heritability combined with high GA are important indicators of the predominant role of additive gene action in these characters. Predictability of high performance and selection of hybrids based on high heritability and genetic advance would lead to successful maize breeding program. However, none of the traits in the present study could be classified under this group. High heritability estimates coupled with moderate values of GA were recorded for plant

height, hundred seed weight and cob length 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. Moderately high heritability values and low GA values observed, in the present study, for cob girth, number of kernel rows per cob and days to 50 % silking indicating 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. Estimate of GA is more useful as a selection tool when considered jointly with GCV and heritability values (Johnson *et al.* 1955) [14]. Traits such as hundred seed weight and cob length showed moderate GCV, moderately high heritability values and high GA values suggesting that they were principally under genetic control.

Genotypic correlation coefficient is the heritable association between two variables. However phenotypic correlation includes both phenotypic and environmental effect. Hence significant phenotypic correlation without significant genotypic correlation has no value. In the present study the genotypic coefficients were higher than the phenotypic coefficients indicating the effect of environment of these quantitative characters. There was a general agreement in both sign and magnitude between estimates of genotypic and phenotypic correlations. Days to 50 per cent tasseling was significantly correlated with days to 50 per cent silking (0.95), plant height (0.80), ear height (0.77), number of kernels per row (0.33) and grain yield (0.28) at genotypic level. Hundred grain weight has a positive significant association with cob length (0.30, 0.25), cob girth (0.46, 0.53) and grain yield (0.39, 0.52) at phenotypic level and genotypic level respectively. Whereas, at phenotypic level, grain yield had a positive significant correlation with plant height (0.37), ear height (0.37), cob girth (0.28) and hundred grain weight (0.39). At genotypic level grain yield has a positive significant association with days to 50 per cent tasseling (0.28), days to 50 per cent silking (0.34), plant height (0.41), ear height (0.43), number of kernels per row (0.38), cob girth (0.45), cob length (0.28) and hundred grain weight (0.52). Such observations were also made by Mural *et al.* (2012), Jodage *et al.* (2017) [13], Jakhar *et al.* (2017) [12] and Soumya and Kamatar (2017) [21]. Positive behavior of these characters towards grain yield indicated that, these traits can play a crucial role for the development of superior hybrids in maize. Higher genotypic correlations than their corresponding phenotypic correlations showed the higher genetic association among traits with the yield and the lower differences among both GCV and PCV for most of the traits attributed to lower modifying effect of environment on the association of characters (Hossain and Joarder, 2006) [10].

**Table 1:** Analysis of variance, Mean and Range of 63 single cross hybrids for yield and yield related traits.

Source	D.F.	Days to 50% tasselling	Days to 50% Silking	Plant Height (cm)	Ear Height (cm)	No. of kernel rows per cob	No. of Kernels per row	Cob Girth (cm)	Cob Length (cm)	Hundred Seed Weight (g)	Grain yield (q/ha)
Replication	2	4.93	7.31	146.31	28.51	1.96	92.25	0.26	13.1	51.37	103.32
Blocks within Replication	24	22.9*	18.61*	265.08**	291.62**	0.64	12.36*	0.04	1.1*	3.46	198.26**
Hybrids	62	35.74**	40.25**	520.84**	156.68**	3.03**	27.04**	0.18**	4.26**	15.73**	221.14**
Error	100	12.32	10.67	75.23	37.42	0.63	5.71	0.04	0.51	2.53	57.8
Mean		62.79	64.51	183.98	88.88	14.69	34.45	4.49	16.79	25.34	52.30
Range		55 to 70.33	56.67 to 71.33	154.33 to 219.13	70.67 to 108.75	12 to 17.67	27.67 to 40.17	3.45 to 4.98	14.05 to 19.69	18.53 to 31.50	25.21 to 75.08
C.V.		6.04	5.41	5.74	10.45	5.41	7.66	1.98	4.69	6.48	17.59

\* $p < 0.05$ ; \*\* $p < 0.01$ .

**Table 2:** Estimation of phenotypic variance, genotypic variance, Phenotypic covariance (PCV), Genotypic variance (GCV), Broad Sense heritability and Genetic advance as percent of mean for 63 single cross hybrids.

	Days to 50% tasseling	Days to 50% Silking	Plant Height	Ear height	No. of kernel rows per cob	No. of kernels per row	Cob girth	Cob length	Hundred seed weight	Grain yield
Genotypic Variance	9.40	11.30	174.41	47.64	0.91	7.54	0.06	1.45	5.91	71.58
GCV	4.88	5.21	7.17	7.75	6.50	7.95	5.35	7.16	9.56	16.14
Phenotypic variance	23.62	23.43	286.93	133.34	1.56	15.89	0.10	2.27	9.39	156.86
PCV	7.74	7.50	9.20	12.97	8.52	11.54	7.15	8.96	12.05	23.90
Broad Sense Heritability (%)	39.8	48.2	60.8	35.7	58.2	47.5	56	63.9	62.9	45.6
Genetic Advance as percent of Mean	6.35	7.45	11.52	9.55	10.21	11.28	8.24	11.78	15.62	22.46

**Table 3:** Phenotypic correlation coefficient among yield and yield related traits.

Characters	Days to 50 per cent tasseling	Days to 50 per cent silking	Plant height (cm)	Ear height (cm)	Number of kernel rows per cob	Number of kernels per row	Cob girth (cm)	Cob length (cm)	Hundred grain weight (g)	Grain Yield (q/ha)
Days to 50 per cent tasseling	1	0.81**	0.33**	0.22	0.13	0.09	0.08	0.17	-0.10	-0.021
Days to 50 per cent silking		1	0.40**	0.24	0.20	0.22	0.12	0.22	-0.12	0.061
Days to 75 per cent dry husk			0.29*	0.22	0.03	0.03	0.05	0.12	-0.03	0.07
Plant height (cm)			1	0.77**	0.07	0.32*	0.09	0.37**	0.09	0.37**
Ear height (cm)				1	0.06	0.31*	0.09	0.40**	0.10	0.37**
Number of kernel rows per cob					1	0.11	0.25*	0.16	-0.08	0.06
Number of kernels per row						1	0.19	0.54**	0.11	0.22
Cob girth (cm)							1	0.15	0.46**	0.28*
Cob length (cm)								1	0.30*	0.22
Hundred grain weight (g)									1	0.39**
Shelling percentage (%)										0.16
Grain yield (q/ha)										1

\*, \*\* - Significant at 5 % and 1 % level of probability, respectively

**Table 4:** Genotypic correlation coefficient among yield and yield related traits.

Characters	Days to 50 per cent tasseling	Days to 50 per cent silking	Plant height (cm)	Ear height (cm)	Number of kernel rows per cob	Number of kernels per row	Cob girth (cm)	Cob length (cm)	Hundred grain weight (g)	Grain yield (q/ha)
Days to 50 per cent tasseling	1	0.95**	0.80**	0.77**	0.43**	0.33**	0.28*	0.34**	-0.18	0.28*
Days to 50 per cent silking		1	0.80**	0.75**	0.30*	0.52**	0.25*	0.38**	-0.17	0.34**
Days to 75 per cent dry husk			0.39**	0.24	0.09	0.17	0.03	0.20	-0.02	0.14
Plant height (cm)			1	0.84**	0.18	0.48**	0.11	0.49**	0.12	0.41**
Ear height (cm)				1	0.22	0.52**	0.20	0.60**	0.10	0.43**
Number of kernel rows per cob					1	0.24	0.26*	0.30**	-0.20	0.04
Number of kernels per row						1	0.17	0.56**	0.09	0.38**
Cob girth (cm)							1	0.16	0.53**	0.45**
Cob length (cm)								1	0.25*	0.28*
Hundred grain weight (g)									1	0.52**
Shelling percentage (%)										0.14
Grain yield (q/ha)										1

\*, \*\* - Significant at 5 % and 1 % level of probability, respectively

#### 4. Conclusion

Phenotypic variances were higher than genetic variances for all the characters studied. However, the difference between PCV and GCV was low for traits like days to 50% silking, days to 50% anthesis, plant height, number of kernel rows per ears, number of kernels/row, cob length, cob girth and hundred seed weight indicating less environmental influence on these traits and hence, practically higher chance for selection. High heritability was recorded by plant height, cob length and hundred seed weight indicating lower influence of environment on these traits. Genetic advance (GA) as a percentage of the mean was higher for traits such as grain yield per hectare (22.46) followed by hundred seed weight (15.62) showing that, these traits are under the control of additive gene action. High heritability coupled with moderate values of GA were recorded for plant height, hundred seed weight and cob length suggested that the expression of this trait was mostly influenced by additive type of gene action.

#### 5. References

- Allard RW. Principles of Plant Breeding. 1st ed, John Wiley and Sons Inc, New York, 1960.
- Arunkumar B, Gangapp E, Ramesh S, Savithamma DL, Nagaraju N, Lokesh R. Genetic potential, variability, heritability and genetic advance of grain yield and its component traits in maize (*Zea mays* L.) in breds, International Journal of Chemical Studies. 2018; 6(6):2015-2018.
- Bello OB, Ige SA, Azeez MA, Afolabi MS, Abdulmalik SY, Mahamood J. Heritability and Genetic Advance for Grain Yield and its Component Characters in Maize (*Zea mays* L.). International Journal of Plant Research. 2012; 2:138-145.
- Bilgin O, Korkut KZ, Baser I, Dalioglu O, Ozturk I, Kahraman T *et al.* Variation and Heritability for Some Semolina Characteristics and Grain Yield and their Relations in Durum Wheat (*Triticum durum* Desf.).

- World Journal of Agricultural Sciences. 2010; 6:301-308.
5. Cruz CD, Carneiro PCS, Regazzi AJ. Modelos Biométricos Aplicados ao Melhoramento Genético, 3rd ed. UFV, Viçosa, MG, 2014.
  6. Deshmukh SNN, Basu MS, Reddy PS. Genetic Variability, Character Association and Path Coefficients of Quantitative Traits in Virginia Bunch Varieties of Groundnut. Indian Journal of Agricultural Sciences. 1986; 56:816-821.
  7. Falconer DS. Introduction to Quantitative Genetics, Oliver and Boyd, Edinberg and London, 1960, 224-261.
  8. Fisher RA. Yates F. Statistical Tables for Biological, Agricultural and Medical Research, Oliver and Boyd, Edinberg and London, 1963, 63.
  9. Hallauer AR. Third phase in the yield evaluation of synthetic varieties of maize. Crop Science. 1972; 12:16-18.
  10. Hossain MS, Joarder OI. Genetic variability, correlation and path analysis in some quantitative traits in wheat. Bangladesh Journal of Crop Sciences. 2006; 17:1-6.
  11. Ibrahim MM, Hussein RM. Variability, Heritability and Genetic Advance in Some Genotypes of Roselle (*Hibiscus sabdariffa* L.). World Journal of Agricultural Sciences. 2006; 2:340-345.
  12. Jakhar DS, Singh R, Ojha VK, Kumar S. Correlation studies in maize (*Zea mays* L.) for yield and other yield attributing characters. International Journal of Advances in Biological Research. 2017; 7(2):246-248.
  13. Jodage K, Kuchanur PH, Zaidi PH, Patil A, Seetharam K, Vinayan MT, Arunkumar B. Association and path analysis for grain yield and its attributing traits under heat stress condition in tropical maize (*Zea mays* L.). Electronic Journal of Plant Breeding. 2017; 8(1):336-341.
  14. Johnson HW, Robinson HF, Comstock RE. Estimation of Genetic and Environmental Variability in Soybeans. Agronomy Journal. 1955; 47:314-318.
  15. Murtagha S, Ariyo OJ, Kehinde OB. Character Association of Seed Yield and Its Components in Okra (*Abelmoschus esculentus* (L.) Moench). Ogun Journal of Agricultural Sciences. 2004; 3:222-233.
  16. Nwangburuka CC, Denton OA, Kehinde OB, Ojo DK, Popoola AR. Genetic Variability and Heritability in Cultivated Okra (*Abelmoschus esculentus* (L.) Moench). Spanish Journal of Agricultural Research. 2012; 10:123-129.
  17. Rao PJM, Rao VT. Genetic Analysis for Yield and its Components in Pigeon pea (*Cajanus cajan* (L.) Mill Sp). International Journal of Applied Biology and Pharmaceutical Technology. 2015; 6:189-190.
  18. Sesay S, Ojo D, Ariyo OJ, Meseka S. Genetic variability, heritability and genetic advance studies in top-cross and three-way cross maize (*Zea mays* L) hybrids. Maydica, 2016, 61.
  19. Singh BD. Plant Breeding: Principles and Methods. Kalyani Publishers, New Delhi, India, 2001.
  20. Singh RK, Chaudhary BD. Biometrical Methods in Quantitative Genetic Analysis, Kalayani Publishers, New Delhi, India, 1985, 318.
  21. Soumya HH, Kamatar MY. Correlation and path analysis for yield and yield components in single cross maize hybrids (*Zea mays* L.). Journal of Farm Sciences. 2017; 30(2):153-156.
  22. Tabanao DA, Bernardo R. Genetic Variation in Maize Breeding Populations with Different Numbers of Parents. Crop Science. 2005; 45(6):2301-2306.