

Original Research Article

<https://doi.org/10.20546/ijcmas.2020.905.287>

## Genetic Study of Certain Quantitative Traits in Maize (*Zea mays* L.)

Kanhaiya Lal\*, Sarvendra Kumar, Lokendra Singh, H. C. Singh,  
Mahak Singh and Anurag Kumar

Department of Genetics and Plant Breeding, CS Azad University of  
Agriculture and Technology, Kanpur-208002, India

\*Corresponding author

### ABSTRACT

#### Keywords

Genetic study,  
Maize, Heritability  
in broad sense,  
Genetic advance  
and Quantitative  
traits

#### Article Info

Accepted:  
18 April 2020  
Available Online:  
10 May 2020

Maize (*Zea mays* L.) a member of grass family, poaceae (gramineae) having  $2n = 2x = 20$  chromosomes is one of the most important cereal crops of India. Mexico and Central America are the origin place of this crop. It has more than thirty-two thousand genes in its genome and the size of genome is about 2.3 gigabase. The objective of this study was to evaluate seventy-seven maize genotypes in relation to heritability and genetic advance for fourteen quantitative traits. The estimates of heritability provide information regarding to possibility and extent to which improvement is possible through selection. In this experiment it was found that the mean sum of squares due to genotypes was highly significant for all the characters under study. Indicated that significant amount of variability was available in the genotypes for all the traits. Majority of the traits were found to exhibit moderate to high estimates of genotypic coefficient of variance (GCV) and phenotypic coefficient of variance (PCV), however some traits such as days to 50% tasseling, days to 50% silking, days to 75% dry husk, cob diameter and shelling % had low estimates of GCV and PCV. Highest estimate of GCV was reported for grain yield per plant (35.54) followed by kernels per cob (32.03), cob weight (30.96) while the lowest estimate of GCV was reported for days to 75% dry husk (2.88). High estimates of heritability in broad sense (>61%) were reported for all the fourteen characters under study but among them eight traits such as grain yield per plant (72.7), kernels per cob (65.48), cob weight (63.2), kernels per row (55.25), cobs per plant (29.78), cob length (27.13), 100-kernel weight (26.45) and kernel rows per cob (22.48) had high estimates of genetic advance in percent of mean (>20%). High estimates of heritability coupled with high estimates of genetic advance are the indicative of additive gene effects in the inheritance of above-mentioned traits. Therefore, selection will be rewarding for the improvement of these traits.

### Introduction

Maize (*Zea mays* L.) is one of the most important cereal crops of India. It is a member of grass family, poaceae (gramineae) has  $2n = 2x = 20$  chromosomes. It originated in Mexico and Central America. It possesses over 32,000 genes on ten chromosomes with a genome size of 2.3 gigabase (Hossain *et al.*, 2016). It has assumed greater significance due

to its demand for food, feed and industrial utilization. It is the third most important cereal crop of India after rice and wheat.

In India the annual production of cereals is around 252.02 mt from an area of 124.30 m ha. with productivity level of 2028 kg/ha, Maize contributed around 24.17 mt productions from an area of 9.19 m ha. with productivity level of 2632 kg/ha during 2014-

15 (Agricultural statistics at a glance 2016, DAC&FW). Hybrid cultivars have played a vital role in increasing acreage and productivity of maize but continuous increasing demand of maize required specific attention in maize breeding to develop high yielding maize cultivar suitable for different agroclimatic zones.

However, the breeding objective in maize improvement program is to obtain genetic progress in yield component traits along with maintaining a high amount of variability (Hallauer, 1973).

Welsh, 1981 emphasized the importance of variability and stated that genetic variability is key to any crop improvement programme. Efficiency of selection and genetic improvement of yield and other agronomic traits also depend upon the nature and magnitude of variability and the proportion of total variability which is heritable in nature.

Heritability alone has no reliable for remark of genetic progress from individual genotype selection. Hence knowledge about heritability along with genetic gain is very useful (Johnson *et al.*, 1955). Therefore, the present investigation carried out to evaluate maize genotypes in relation to heritability and genetic advance.

## Materials and Methods

Fifty-four single cross hybrids (obtained through the crossing of 18 lines (females) with 3 testers (males) in line x tester design during *Kharif* 2018) along with their parental lines and 2 check varieties evaluated at Student Instructional Farm, CS Azad University of Agriculture and Technology, Kanpur-208002 (U.P.), India during *Rabi* 2018-19 in Randomized complete block design. Each treatment grown in a single row of 4m length with 60x25cm spacing and

replicated three times. Data on various quantitative traits such as plant height, number of cobs/plant, number of kernel rows/cob, number of kernels/row, cob length (cm), cob diameter (cm), cob weight (g), number of kernels/cob, 100-kernel weight (g), grain yield/plant (g) and shelling percentage (%) were recorded on 5 randomly selected plants per entry per replication while, data on days to 50% tasselling, days to 50% silking, days to 75% dry husk, were recorded on plot basis.

All the recommended cultural practices were followed to raise a good crop. The mean values of recorded data were used for Analysis of variance for Randomized Complete Block Design (Panse and Sukhatme, 1985).

Phenotypic (PCV), genotypic (GCV) and environmental (ECV) coefficients of variation for different characters were estimated by following formulae suggested by Burton and de Vane (1953).

Phenotypic coefficient of variation (PCV)

$$= \frac{\sqrt{\text{Phenotypic variance}}}{\bar{X}} \times 100$$

Genotypic coefficient of variation (GCV)

$$= \frac{\sqrt{\text{Genotypic variance}}}{\bar{X}} \times 100$$

Environmental coefficient of variation (ECV)

$$= \frac{\sqrt{\text{Environmental variance}}}{\bar{X}} \times 100$$

Where,  $\bar{X}$  = Mean of the characters.

As suggested by Sivasubramanian and Menon (1973), GCV and PCV were categorized into Low = Less than 10% Moderate = 10-20% High = More than 20%

Heritability in broad sense ( $h^2b$ ) was calculated as suggested by Hanson, 1963.

$$h^2b (\%) = \frac{\sigma^2g}{\sigma^2p} \times 100$$

Where,

$\sigma^2g$  = genotypic variance

$\sigma^2p$  = phenotypic variance

As suggested by Robinson *et al.*, 1949, heritability in broad sense  $h^2$  (b) estimates were categorized into

Low = 0 – 30 per cent, Moderate = 31- 60 per cent, High = 61 per cent and above

The expected genetic advance (Ga) was estimated using formula suggested by Johnson *et al.*, 1955.

$$Ga = h^2b \times \sigma p \times K$$

Where,

$h^2b$  = Heritability

$\sigma p$  = Phenotypic standard deviation

K = Standardized selection differential (2.06) a constant at 5% selection intensity.

Now Genetic advance as per cent of mean ( $\overline{Ga}$ ) was worked out as:

$$(\overline{Ga}) (\%) = \frac{GA}{\overline{X}} \times 100$$

Where,

Ga = Genetic advance

$\overline{X}$  = Mean of the character

The range of genetic advance as per cent of mean was classified as suggested by Johnson *et al.*, 1955.

Low = Less than 10 per cent, Moderate = 10-20 per cent, High = More than 20 per cent

## Results and Discussion

Efficiency of selection and genetic improvement of yield and other agronomic traits depend upon the nature and magnitude of variability and the proportion of total variability which is heritable in nature. The analysis of variance for different quantitative traits was done and presented in table 1 which revealed that the mean sums of squares due to genotypes were highly significant for all the characters under study.

Indicated that significant amount of variability was available in the genotypes for all the traits. Muhammad *et al.*, 2010, Thakur *et al.*, 2016, Patil *et al.*, 2016, Kumar *et al.*, 2017, Beulah *et al.*, 2018 and Dar *et al.*, 2018 has also reported highly significant variation for all the characters under study. Devkota *et al.*, 2020 has also observed significant variation for grain yield, silking and tasseling, number of kernels per cob and cob length in the genotypes. Adhikari *et al.*, 2018 has reported significant differences among the genotypes for days to tasseling, days to silking, plant height, ear height, ear length, ear diameter and grain yield. Sharma *et al.*, 2018 has also reported significant differences for all growth, yield and yield attributing characters in the genotypes. Considerable genotypic variability among the genotypes for different traits have also observed by Turi *et al.*, 2007.

The estimates of heritability provide information regarding to possibility and extent to which improvement is possible through selection. Heritability alone has no reliable for remark of genetic progress from individual genotype selection. Hence knowledge about heritability along with genetic gain is very useful (Johnson *et al.*, 1955). The estimates of GCV, PCV, heritability and genetic advance presented in table 2.

**Table.1** Analysis of variance for different quantitative traits in maize

Source variation	d.f.	Days to 50% tasseling	Days to 50% silking	Days to 75% dry husk	Plant height (cm)	Number of cobs/plant	Cob length (cm)	Cob diameter (cm)
Replication	2	2.90	2.95	1.60	17.91	0.001	0.33	0.10
Treatment	76	52.68**	52.01**	61.85**	1356.25**	0.090**	15.19**	2.39**
Error	152	18.21	21.67	28.59	73.80	0.002	0.41	0.22

Source variation	d.f.	Cob weight (g)	Number of kernel rows/cob	Number of kernels / row	Number of kernels /cob	100-Kernel weight (g)	Shelling percentage (%)	Grain yield/plant (g)
Replication	2	29.01	0.01	0.07	73.54	0.11	0.25	0.08
Treatment	76	2934.36**	8.13**	125.48**	34164.24**	30.01**	121.02**	2860.67**
Error	152	17.62	0.32	1.10	173.27	0.92	9.40	13.60

\*, \*\* significant at 5% and 1% level, respectively

**Table.2** Estimates of GCV, PCV, heritability and genetic advance for different quantitative traits in maize

Genotypes	Mean	Min	Max	Heritability (%)	Ga	Ga as % mean	GCV (%)	PCV (%)
Days to 50% tasseling	108.28	101.67	117.00	75.21 (H)	7.11	6.56 (L)	3.67 (L)	4.24 (L)
Days to 50% silking	112.34	104.67	120.33	72.87 (H)	6.91	6.15 (L)	3.50 (L)	4.10 (L)
Days to 75% dry husk	144.68	134.67	156.33	64.39 (H)	6.89	4.77 (L)	2.88 (L)	3.59 (L)
Plant height (cm)	207.76	157.66	259.62	85.27 (H)	39.33	18.93 (M)	9.95 (L)	10.78 (M)
Number of cobs/plant	1.14	1.00	1.78	92.96 (H)	0.34	29.78 (H)	14.99 (M)	15.55 (M)
Cob length (cm)	16.18	10.47	21.05	92.27 (H)	4.39	27.13 (H)	13.71 (M)	14.27 (M)
Cob diameter (cm)	11.44	9.55	13.45	76.86 (H)	1.54	13.43 (M)	7.44 (L)	8.49 (L)
Cob weight (g)	100.73	33.65	184.68	98.22 (H)	63.66	63.20 (H)	30.96 (H)	31.24 (H)
No of kernel rows/cob	13.96	10.36	18.64	89.15 (H)	3.14	22.48 (H)	11.56 (M)	12.24 (M)
No of kernels / row	23.70	7.77	39.85	97.43 (H)	13.09	55.25 (H)	27.17 (H)	27.53 (H)
No of kernels /cob	332.35	107.36	609.08	98.49 (H)	217.62	65.48 (H)	32.03 (H)	32.27 (H)
100-Kernel weight (g)	23.19	16.88	30.74	91.37 (H)	6.13	26.45 (H)	13.43 (M)	14.05 (M)
Shelling (%)	75.81	51.78	84.89	79.82 (H)	11.23	14.81 (M)	8.05 (L)	9.01 (L)
Grain yield/plant (g)	86.67	27.70	164.20	98.59 (H)	63.01	72.70 (H)	35.54 (H)	35.80 (H)

Critical analysis of the table showed that four types of GCV and PCV estimates (high GCV and high PCV, moderate GCV and moderate PCV, low GCV and moderate PCV and low GCV and low PCV) could be observed for various traits under study in this investigation. Such type of estimates has also been reported by Beulah *et al.*, 2018, Dar *et al.*, 2018, Thakur *et al.*, 2016 and Sheng, 2017. High estimates of GCV and PCV (>20%) were exhibited by grain yield per plant, kernels per cob, kernels per row and cob weight.

Bisen *et al.*, 2018 has also reported high GCV and PCV for the traits such as grain yield, stover yield, cob weight and cob/plant. Beulah *et al.*, 2018 has reported such estimates for grain yield per plant. Moderate estimates of GCV and PCV were observed for 100-kernel weight, kernel rows per cob, cob length and cobs per plant. Sandeep *et al.*, 2015 has also reported moderate GCV and PCV for cob length, 100-kernel weight and kernels per row. Pandey *et al.*, 2017 has reported such estimates for 100-kernel weight and Thakur *et al.*, 2016 has reported such estimates for cob length. In this way majority of the traits were found to exhibit moderate to high estimates of GCV and PCV, however some traits such as days to 50% tasseling, days to 50% silking, days to 75% dry husk, cob diameter and shelling % had low estimates of GCV and PCV. Similar results have also been reported by Sandeep *et al.*, 2015, Maruthi and Rani (2015), Patil *et al.*, 2016, Pandey *et al.*, 2017 and Adhikari *et al.*, 2018.

High estimates of heritability in broad sense (>61%) were reported for all the fourteen characters under study but among them eight traits such as grain yield per plant (72.7), kernels per cob (65.48), cob weight (63.2), kernels per row (55.25), cobs per plant (29.78), cob length (27.13), 100-kernel weight (26.45) and kernel rows per cob (22.48) had high estimates of genetic advance in percent of mean (>20%). Similar results have also been reported by Maruthi and Rani (2015), Kinfe and Tsehaye (2015) and Thakur *et al.*, 2016. High estimates of heritability coupled with high estimates of

genetic advance are the indicative of additive gene effects in the inheritance of above-mentioned traits. Therefore, selection will be rewarding for the improvement of these traits.

## References

- Adhikari, B.N., Shrestha, J., Dhakal, B., Joshi, B.P. & Bhatta, N.R. (2018). Agronomic performance and genotypic diversity for morphological traits among early maize genotypes. *International Journal of Applied Biology*, 2(2): 33-43.
- Beulah, G., Marker, S. and Rajasekhar, D. (2018). Assessment of quantitative genetic variability and character association in maize (*Zea mays* L.). *Journal of Pharmacognosy and Phytochemistry*, 7(1): 2813-2816.
- Bisen, N., Rahangdale, C.P. and Sahu, R.P. (2018). Genetic Variability and correlation studies of yield and yield component in maize hybrids (*Zea mays* L.) under kymore plateau and satpura hill region of Madhya Pradesh. *International Journal of Agriculture, Environment and Biotechnology*, 11(1): 71-77.
- Burton, G.M. and de Vane, E.H. (1953). Estimating heritability in tall fescue (*Festuca arundinacea*) from replicated clonal material. *Agron. J.*, 45: 471-481.
- Dar, A., Dar, Z.A., Lone, A.A., Kamaluddin, S.P.A., Hussan, S., Dar, M.S. and Alie, W. (2018). Genetic variability studies involving drought tolerance related traits in maize genotypes. *Journal of agriculture and ecology research international*, 14(2): 1-13.
- Devkota, S., Karn, R., Jha, R.K., Marasini, D. and Sah, S.K. (2020). Evaluation of open pollinated and hybrid maize varieties in Dhading district of Nepal. *Journal of Agriculture and Natural Resources*, 3(1): 160-169.
- Hallauer, A.R. Scobs, J.H. (1973). Change in quantitative traits associated with inbreeding in synthetic variety of maize. *Crop Sciences*, 13(3): 327-330.
- Hanson, W.D. (1963). Heritability in: WD Hanson and HF Robinson (Eds.) *Statistical Genetics and Plant Breeding* Publ. 982, Washington,

- DC National Academy of Science, National Research Council, pp 125-139.
- Hossain, F., Muthusamy, V., Bhat, J.S., Jha, S.K., Zunjare, R., Das, A., Konsam, S. and Kumar, R. (2016). Maize. In *Broadening the Genetic Base of Grain Cereals* (eds., Singh, M. and Kumar, S.), Springer Publishers, pp. 67-88.
- Johnson H.W. Robinson H.F. Comstock R.E. (1955) Estimates of genetic and environmental variability in soybean. *Agronomy Journal*, 47: 314-318.
- Kinfe, H. and Tsehaye, Y. (2015). Studies of heritability, genetic parameters, correlation and path coefficient in elite maize hybrids. *Acad. Res. J. Agri. Sci. Res.*, 3(10): 296-303.
- Kumar, R., Dubey, R.B., Ameta, K.D., Kunwar, R., Verma, R. and Bisen, P. (2017). Correlation and path coefficient analysis for yield contributing and quality traits in quality protein Maize (*Zea mays* L.). *Int. J. Curr. Microbiol. App. Sci.*, 6(10): 2139-2146.
- Maruthi, R.T. and Rani, K.J. (2015). Genetic variability, heritability and genetic advance estimates in Maize (*Zea mays* L.) inbred lines. *Journal of Applied and Natural Science*, 7(1): 149-154.
- Muhammad, C.R., Muhammad, R., Hussain, A. and Muhammad, A. (2010). Studies on heritability, correlation and path analysis in Maize (*Zea mays* L.). *J. Agric. Res.*, 48(1): 35-38.
- Pandey, Y., Vyas, R.P., Kumar, J., Singh, L., Singh, H.C., Yadav, P.C. and Vishwanath (2017). Heritability, correlation and path coefficient analysis for determining interrelationships among grain yield and related characters in maize (*Zea mays* L.). *Int. J. Pure App. Biosci.*, 5(2): 595-603.
- Panse, V.G. and Sukhatme, P.V. (1985). *Statistical Methods for Agricultural Workers*. 4<sup>th</sup> Ed. ICAR, New Delhi pp. 361.
- Patil, S.M., Kumar, K., Jakhar, D.S., Rai, A., Borle, U.M. and Singh, P. (2016). Studies on variability, heritability, genetic advance and correlation in maize (*Zea mays* L.). *International Journal of Agriculture, Environment and Biotechnology*, 9(6): 1103-1108.
- Robinson, H.F., Cornstock, R.E. and Harvey, P.H. (1949) Estimates of heritability and degree of dominance in corn. *Agronomy Journal*, 41: 353-359.
- Sandeep, S., Bharathi, M., Reddy, N.V. and Eswari, K.B. (2015). Genetic variability, heritability and genetic advance studies in inbreds of maize (*Zea mays* L.). *Eco. Env. & Cons.*, 21(Suppl.): S445-S449.
- Sharma, B.K., Sharma, S., Kandel, B.P. and Shrestha, J. (2018). Varietal evaluation of promising maize genotypes. *Azarian Journal of Agriculture*, 5(4): 120-124.
- Shengu, M.K. (2017). Genetic Study of Some Maize (*Zea mays* L.) Genotypes in Humid Tropic of Ethiopia. *International Journal of Scientific and Research Publications*, 7(1): 281-287.
- Sivasubramanian, S. and Menon, M. (1973). Heterosis and inbreeding depression in rice. *Madras Agric. J.*, 60: 1139.
- Thakur, S., Sinha, S.K., Mehta, N. and Thakur, D. (2016). Genetic analysis of yield and its components in maize (*Zea mays* L.) inbred lines using line x tester analysis. *International Journal of Agriculture Sciences*, 8(53): 2768-2773.
- Turi, N.A., Shah, S.S., Ali, S., Rahman, H., Ali, T. and Sajjad, M. (2007). Genetic variability for yield parameters in maize (*Zea mays* L.) Genotypes. *Journal of Agricultural and Biological Science*, 2(4-5): 1-3.
- Welsh J. (1981) *Fundamentals of plant breeding and genetics*. Jhon Weliey & Sons, New York.

**How to cite this article:**

Kanhaiya Lal, Sarvendra Kumar, Lokendra Singh, H. C. Singh, Mahak Singh and Anurag Kumar. 2020. Genetic Study of Certain Quantitative Traits in Maize (*Zea mays* L.). *Int.J.Curr.Microbiol.App.Sci*. 9(05): 2508-2513. doi: <https://doi.org/10.20546/ijcmas.2020.905.287>