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

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Authors' contributions

This work was carried out in collaboration among all authors. All authors read and approved the final manuscript.

Original Research Article

ABSTRACT

Aim: The aim of the present research work was to estimate the genetic variability, broad sense heritability and genetic advance for various yield and its contributing characters of 39 maize genotypes.
Methodology: 39 maize genotypes were sown in randomized block design and replicated thrice to evaluate various genetic parameters. The data was recorded on twelve quantitative traits including

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days to fifty percent tasseling, days to fifty percent silking, days to maturity, plant height, ear height, ear length, ear diameter, number of kernel rows/ear, number of kernels/row, 100kernels weight, shelling % and grain yield/plant.

Results: The mean sum of squares due to genotypes for each of the 12 traits under study indicated significant differences in analysis of variance. High to moderate genotypic and phenotypic coefficients of variation as well as genetic advance were observed in the traits yield per plant, plant height, ear height, number of kernels per row, and 100-kernel weight. These findings suggest that the heritability of these traits is most likely the result of additive gene effects and that selection in early generations may be effective for these traits. On the other hand, the remaining characters days to 50% tasseling, days to 50% silking, number of kernel rows per ear, and shelling percentage were recorded with high heritability with low genotypic and phenotypic coefficient of variation and genetic advance suggesting non-additive gene action for control of these traits which provides limited scope for improvement by selection.

Conclusion: Among the characters studied, grain yield, plant height, and ear height had high heritability and high values of genetic advance indicating that these characters were controlled by additive gene action and so phenotypic selection is effective for improvement of these traits.

1. INTRODUCTION

"After rice and wheat, maize (*Zea mays L.*) is the third most produced cereal crop worldwide. It holds a significant place in world agriculture, producing 1215.90 million tones across 206.16 million hectares with a productivity of 5.65 t ha^{-1}. Among the countries that cultivate maize, India ranks fourth in terms of area and seventh in terms of production, with a 9.95 million hectare cultivation area, 33.72 million tones of production and 3.38 tonnes of productivity" [1]. It contributes around 4% of the world's total maize area and 2% of its total production. The area under maize cultivation in Telangana is 0.41 million hectares with 2.22 million tonnes production and 5.40 tonnes per hectare productivity [2]. In India, maize is cultivated in a wider range of climatic situations due to its better adaptability. Maize has many uses as it is used in human food, feed for livestock, built material, fuel and a raw material for the manufacture of various alcoholic and non-alcoholic beverages (Bekric and Radosavljevic, 2008). Maize being a cross pollinated, C4 type plant has high fertilizer responsive resulting in high per day productivity. It offers plant breeders a vast opportunity for the genetic improvement. Effective selection is made possible by presence of genetic variation among population. For the success of plant breeding program depends on the degree of genetic variation present in the population. Assessing the genotypes of maize is necessary in order to take advantage of genetic variations for various economic attributes, which aids in the selection of suitable maize genotypes. The assessment of various genetic parameters will provide the information on nature of gene action in governing the characters and to adopt various breeding strategies to obtain genetic gain [3]. "Genetic parameters like variance, coefficient of variance, heritability, genetic advance are explain the condition of a population with regard to the breeding objective. The estimates of coefficients of variation and variability aid in the selection of superior genotypes and provide information on the genetic variability demonstrated by a variety of quantitative characters. It cannot, however, ascertain the quantum of variation which is heritable. Thus, heritability and coefficient of variation would give a clear picture of the level of gain or progress that may be obtained from selection" [4]. "However, as heritability estimates comprises both additive and non-additive gene effects, it cannot be relied upon alone [5]. When a trait is governed by additive gene action that usually results in higher heritability and genetic advance. On the other hand, a trait is controlled by non-additive gene action, it may resulted in high heritability but low genetic advance" [6]. Thus, a trait with high heritable may not exhibit high genetic advance. When estimating the gain under selection, heritability estimates coupled with genetic advance tend to be more useful than heritability alone. Hence, understanding genetic advance along with heritability is really helpful.

Therefore, this study was undertaken to estimate the genetic parameters *viz.*, genetic variability, heritability and genetic advance for yield and other its contributing characters by evaluating 39 maize genotypes.

2. MATERIALS AND METHODS

2.1 Experimental location

The present experiment was carried out with 39 maize genotypes in randomized block design with three replications during *Kharif* 2019 at Regional Sugarcane and Rice Research Station, Rudrur, Nizamabad. Every entry was planted in two four-meter-long rows, with a 20- centimeter spacing between each plant and a 75-centimeter spacing between each row. Data recorded on five randomly selected plants in each replication for plant height (cm), ear height (cm), ear length (cm), ear diameter (cm), number of kernel rows per ear, number of kernels per row, 100 kernel weight, shelling percentage, and grain yield per plant. Data recorded on plot basis for days to 50% tasseling, days to 50% silking, and days to maturity. Ear diameter without husk was measured in centimeters at the middle of the ear at the time of harvest with vernier calipers.

Data on days to 50%tasseling and silking was calculated based on number of days took from date of sowing to date of 50%plants shedding pollen and plants with silk emergence respectively. Days to maturity recorded as number of days taken from the date of sowing to date of 75 per cent of the cobs turned to brown husk. Plant Height measured in centimeters by measuring the plant stalk from the ground level to the tip of the tassel. Ear Height was expressed in centimeters by measuring the plant stalk from the ground level to the node of the attachment of the upper most ear. Ear length was measured from the base to the tip of the ear in centimeters. Ear diameter without husk was measured in centimeters at the middle of the ear at the time of harvest with vernier calipers. Number of kernel rows per ear was recorded by counting the number of rows per ear at the middle of the ear for five randomly selected ears. The number of kernels per row were counted and recorded in each ear. To measure test weight one hundred kernels were counted and the weight was recorded with the help of electronic top pan balance. The shelling percentage is calculated by using the following formula.

Shelling percentage (%) =

$$\frac{\text{Total grain yield per ear (g)}}{\text{Total weight of the ear}} \times 100$$

Grain yield was recorded in grams per plant after drying and shelling the grains from individual ears. The fertilizers of N, P and K were applied as per the recommended ratio of 120: 80: 60 kg ha-1. The whole dose of P and K and half dose of nitrogen was applied as basal, the other half of the nitrogen dose was given in two equal split doses at knee height and tasseling stages. In order to raise a healthy crop, weeding activities, essential plant protection measures to protect the crop from pests and diseases, and proper irrigation schedules were implemented as per the recommendations.

2.2 Estimation of Variance Components

To determine the genetic variability among the genotypes of maize, variance components were computed. Calculated error ($\sigma 2e$), genotypic ($\sigma 2g$), and phenotypic ($\sigma 2p$) variances from expected mean squares of analysis of variance following the method as per Hallauer and Miranda [7].

Error variance $\sigma^2 e = MSe$

Where MSe= mean square of error

Genotypic variance

$$\sigma^2 g = \left(\frac{MSg - MSe}{r}\right)$$

Where MSg = mean square due to genotype, MSe = mean square due to error and r = number of replications

Phenotypic variance

$$\sigma^2 p = \sigma^2 e + \sigma^2 g$$

Where $\sigma^2 e$ denotes error variance and $\sigma^2 g$ denotes genotypic variance

The Genotypic coefficients of variation and Phenotypic and coefficients of variations were calculated by using the formula as per Singh and Chaudhary [8].

Genotypic coefficient of variation (GCV)

$$GCV = \left(\frac{\sqrt{\sigma^2 g}}{X}\right)100$$

Where $\sigma^2 g$ denotes genotypic variance and xdenotes mean of the trait

Phenotypic coefficient of variation (PCV)

$$PCV = (\frac{\sqrt{\sigma^2 p}}{X})100$$

Where $\sigma^2 p$ denotes phenotype variance and; denotes mean of the trait

The PCV and GCV estimates were classified as low (0-10%), moderate (10-20%), and high (>20%) values as suggested by Sivasubramanian and Menon [9]

2.3 Estimation of Genetic Parameters

Heritability in broad sense was computed by the formula reported by Allard [10]

$$\text{Heritability broad sense (H}^2) = (\frac{\sigma^2 g}{\sigma^2 p})100$$

Where $\sigma^2 g$ denotes genotypic variance and $\sigma^2 p$ denotes phenotypic variance.

The heritability estimates were classified according to Robinson et al. [11] as 0-30% low, 30-60% moderate and >60 high.

Genetic advance (GA) and genetic advance as per cent of the mean (GAM) were computed according to Johnson et al. [12] as follows,

$$GA = k\sigma pH^2$$

Where σp denotes the phenotypic standard deviation of the trait, H^2 denotes broad sense heritability estimate and k is selection differential, where k = 2.063 (at 5 % selection intensity).

To compare the extent of predicted advances of various traits under selection, genetic advance as a percent of the mean (GAM) was computed according to Falconer [13] as follows.

$$GAM = (\frac{GA}{X})100$$

GA = genetic advance; x= mean of the trait

The GAM was categorized as low (0-10%), moderate (10-20%) and high (>20%) according to Johnson et al. [12].

2.4 Data Analysis

The data recorded on each trait were subjected to statistical analysis using statistical software, Windostat Version 9.3.

3. RESULTS AND DISCUSSION

3.1 Analysis of Variance

All the characters under study were shown significant differences among the genotypes as revealed by the analysis of variance, as illustrated in Table 1. Sesay et al. [14], Jio et al. [15] and Rai et al. [16] reported significant differences among the genotypes for most of the yield and other component characters in maize.

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

Source of variation Characters	Replication	Genotype	Error
d.f.	2	38	76
Days to 50% tasseling	1.34	23.04**	0.83
Days to 50% silking	1.13	25.82**	0.86
Days to maturity	3.76	100.56**	3.33
Plant height (cm)	99.33	3825.37**	59.21
Ear height (cm)	77.26	1171.19**	26.08
Ear length (cm)	0.95	18.00**	0.35
Ear diameter (cm)	0.04	0.98**	0.03
Number of kernel rows per ear	0.21	3.43**	0.25
Number of kernels per row	7.78	112.03**	3.04
100-kernel weight (g)	0.32	87.51**	2.04
Shelling percentage	2.57	16.14**	4.58
Grain yield per plant (g)	200.30	7103.01**	107.42

*Significant at 5 percent level; **Significant at 1 percent level*

Table 2. Assessment ofgeneticparameters in maize for various quantitative traits

Characters	$\sigma^2 g$	$\sigma^2 p$	Co-efficientof Variation		h^2(%) (BroadSense)	GA(%)		GAasPercent mean	
			GCV	PCV		GA5%	GA1%	5%	1%
Daysto50%tasseling	7.40	8.23	4.96	5.23	89.9	5.31	6.81	9.69	12.42
Daysto50%silking	8.32	9.18	5.02	5.28	90.6	5.65	7.24	9.85	12.63
Daystomaturity	32.41	35.74	5.93	6.22	90.7	11.16	14.31	11.63	14.90
Plantheight(cm)	1255.38	1314.60	16.13	16.50	95.5	71.32	91.40	32.47	41.61
Earheight(cm)	381.70	407.79	21.43	22.15	93.6	38.93	49.90	42.72	54.75
Earlength(cm)	5.88	6.23	15.18	15.63	94.4	4.85	6.22	30.38	38.94
Eardiameter(cm)	0.31	0.35	13.42	14.09	90.7	1.10	1.42	26.34	33.76
Numberofkernelrows/ear	1.05	1.31	7.34	8.19	80.3	1.89	2.43	13.56	17.38
Numberofkernels/row	36.33	39.37	19.06	19.84	92.3	11.92	15.28	37.72	48.34
100-kernelweight(g)	28.49	30.53	15.87	16.43	93.3	10.62	13.61	31.57	40.46
Shellingpercentage	3.85	8.43	2.39	3.54	45.7	2.73	3.50	3.33	4.27
Grainyieldperplant(g)	2331.86	2439.28	32.47	33.21	95.6	97.26	124.64	65.41	83.82

3.2 Estimation of Genotypic and Phenotypic Variance

Among the characters, highest genetic variability was observed in grain yield per plant (2331.86) followed by the plant height (1255.38), ear height (381.7), number of kernels per row (36.33), days to maturity (32.41) and100-kernel weight (28.49). These characters also recorded high estimates of phenotypic variances; it implies the presence of sufficient inherent genetic variance which enables effective selection. The low genetic variability was observed for ear diameter (0.31), number of kernel rows per ear (1.05) and shelling percentage (3.85). High estimates of genotypic and phenotypic variance was reported earlier by Praveen et al. (2014) and Sesay et al. [14] for plant height, ear height, and100-kernel weight. Mager et al. [17] for plant height, ear height test weight and Oruganti et al. [18] for grain yield and plant height.

3.3 Phenotypic and Genotypic Coefficients of Variation

The estimates of phenotypic (PCV) and genotypic coefficient of variation (GCV) were high for the characters grain yield and ear height. Where as moderate values of PCV and GCV observed for number of kernels per row, plant height, 100-kernel weight, ear length and ear diameter as given in Table 2. Indicating adequate variability present in such traits and provides scope for selection. High estimates of PCV and GCV was also reported for grain yield and ear height by Shrestha et al. [19]. Similarly, Jilo et al. [15], Mager et al. [17], Rai et al. [16], Oruganti et al. [18], Yadav et al. [20] and Thakur et al. [21] were reported for grain yield. The other characters shelling percentage, days to 50%tasseling, days to 50%silking, days to maturity and number of kernel rows per ear were recorded low PCV and GCV. Low genotypic variation in maize genotypes for these traits may be due to the existence of both positive and negative alleles and phenotypic plasticity. These results were also confirmed by results of Jilo et al. [15] and Rai et al. [16] who observed low PCV and GCV for days to 50%tasseling, days to 50 % silking and number of kernel rows per ear. The results of Sravanti et al. [22] and Oruganti et al. [18] also shown low PCV and GCV for days to 50% tasseling, Days to 50% silking and Days to maturity and Thakur et al. [21] for days to maturity, days to 50%

tasseling, days to 50% silking and shelling percentage.

3.4 Estimation of Heritability and Genetic Advance

In this investigation, except shelling percentage almost all the studied characters were recorded high heritability as given in Table 2. Highest heritability was recorded for grain yield (95.6%) followed by plant height (95.5%), ear length (94.4%), ear height (93.6%), 100-kernel weight (93.3%), number of kernels per row (92.6%), ear diameter (90.7%), days to maturity (90.7%), days to 50% silking (90.6%), days to 50% tasseling (89.9%) and number of kernel rows per ear (80.3%). High heritability values, suggests, a large portion of variation present in a trait is genetic, controlled by additive gene effects and less influenced by environment. High heritability values observed also by Jilo et al. [15], Mager et al. [17], Rai et al. [16], Oruganti et al. [18], Yadav et al. [20] and Shrestha et al. [19] for most of these characters. Mager et al. [17] observed high heritability for grain yield and test weight. Shelling percentage (45.7) was shown moderate heritability. It might be due to the environmental impact on the phenotypic nature of trait [23].

"Heritability and genetic advance parameters are two key selection factors. A trait having high heritability may not have high genetic advance. When a character controlled by additive gene effects, it generally resulted with both higher heritability and genetic advance, if a trait controlled by non-additive gene actions, that trait might results in high heritability but low genetic advance" [6]. Hence, to arrive at a more reliable conclusion and to predict gain under selection, heritability along with genetic advance are more helpful. The estimates of genetic advance (GA) was found high for grain yield (97.26%), plant height (71.32%) and ear height (38.93%). shows that additive genes play a major role in expression of these characters, pedigree breeding method may useful for improvement of these characters. High genetic advance for grain yield was also found by Sesay et al. [14], Sravanti et al. [22] and Shrestha et al. [19]. Oruganti et al. [18] observed "high genetic advance for grain yield and plant height. Moderate genetic advance was recorded by number of kernels per row (11.92%), days to maturity (11.16%) and 100-kernel weight (10.62%)". Similarly, Abhishek et al. [24] reported "for number of kernels per row, days to

maturity and 100-kernel weight". Sesay et al. [14], Sravanti et al. [22] and Shrestha et al. [19] found similar results for "100-kernel weight. Low genetic advance was recorded by ear diameter (1.10%), number of kernel rows per ear (1.89%), shelling percentage (2.73%), ear length (4.85%), days to 50% tasseling (5.31%) and days to 50% silking (5.65%)". These findings identical with results found by Muliadi et al. [25]. Low genetic advance was also found by Sesay et al. [14] and Abhishek et al. [24] for days to 50% tasseling and silking, ear length and number of kernel rows/ear. Similarly, by Shrestha et al. [19] "for days to 50% silking and days to 50% anthesis" and Sravanti et al. [19] for "number of kernel rows per ear. Among the traits studied, grain yield, plant height and ear height were recorded high estimates of heritability and genetic advance, indicating that, additive gene action is governing these characters and that phenotypic selection will be effective for these traits". Similar results for grain yield, plant height, ear height was found by Sravanti et al. [19]. Sesay et al. [14] and Shrestha et al. [19] were observed for grain yield. Oruganti et al. [18] for plant height and grain yield per cob. The characters, number of kernels/row, days to maturity and 100-kernel weight recorded high heritability with moderate estimates of genetic advance. High heritability with moderate estimates of genetic advance indicate the existence of intermediate additive and non-additive gene actions and careful selection can lead to improvement of these traits. Shrestha et al. [19] reported high heritability with moderate estimates of GA for thousand kernel weight. Similarly, Sesay et al. [14] observed for ear height and 100-kernel weight. While, high to moderate heritability with moderate estimates of GA reported by Rajesh et al. (2013) reported for "number of kernels/row and 100-kernel weight. Days to 50 % tasseling and silking, ear length, ear girth and number of kernel rows/ear were shown high heritability along with low estimates of genetic advance indicating the influence of non additive gene action on expression of these characters and suggesting hybridization or heterosis breeding for improvement of these characters". Shrestha et al. [19] found "high heritability with low estimates of GA for days to 50% silking and days to 50% anthesis". Low heritability and genetic advance observed for shelling percentage indicating this trait influenced by environment and direct selection may not be effective. Wondimu et al. [26] indicated "management practices rather than selection are needed to

improvement of the performance of such characters. Expected genetic advance as per cent of mean (GAM) determines the nature of gene action involved in expression of a character, which aids in adopting the suitable breeding strategy to improve that trait.In the present investigation, genetic advance as per cent mean (GAM) found high for grain yield (65.41), ear height (42.72), number of kernels per row (37.72), plant height (32.47), 100-kernel weight (31.57), ear length (30.38) and ear diameter (26.34) demonstrating the additive gene action in control of these traits". Similar results of high GAM also observed by Sravanti et al. [22] for "plant height, ear height and grain yield/plant. Jilo et al. [15] for grain yield, 100-kernel weight and ear height". Mager et al. [17] for "grain yield and 1000 grain weight. Rai et al. [16] observed for grain yield and ear height". Oruganti et al. [18] for "plant height, ear length, number of kernels per row, and grain yield per cob" and Thakur et al. [21] for "grain yield, 100 grain wt (g) and number of kernels per row" observed similar results. Moderate genetic advance as per cent mean was exhibited by number of kernel rows per ear (13.56) and days to maturity (11.63). Other researchers Abhishek et al. [24], Oruganti et al. [18] and Thakur et al. [21] were found "moderate GAM for number of kernel rows per ear". Low genetic advance as per cent mean was recorded for shelling percentage (3.33), days to 50% tasseling (9.69) and days to 50% silking (9.85). Similar results of low genetic advance as per cent mean for shelling percentage, days to 50% tasseling and days to 50% silking were reported by Abhishek et al. [24] and Thakur et al. [21]. Rai et al. [16] found "low GAM for days to 50% tasseling and days to 50% silking" and Mager et al. 2021 observed "low GAM for days to 50% anthesis".

High estimates of heritability coupled with low GAM was observed by days to 50 percent tasseling and silking. Similar results of high heritability with low GAM was found by Shrestha et al. [19] and Thakur et al. [21] for days to 50% silking and days to 50% tasseling. High heritability with low GAM suggests the influence of non-additive gene action in control of such traits and poor response to selection. Selection for such characters may not be successful because the high heritability is being shown by the environment rather than genotype [21]. The traits, days to maturity and number of kernel rows per ear exhibited high heritability with moderate GAM. Thakur et al. [21] reported

moderate heritability with moderate GAM for number of kernel rows per ear. Low heritability with low GAM was found for shelling percentage. Tilahun et al. [27] suggested that the improvement of this type of traits need better management methods rather than selection as variation of such characters are effected by environments and governed by non-additive gene action. Thakur et al. [21] reported high heritability with low GAM for shelling percentage**.** In this study, while considering all the genetic parameters, among the characters, plant height, ear height and grain yield were exhibited high heritability along with high estimates of PCV, GCV & GA was [28-31]. It revealed adequate variability present in these traits is genetic, scope for improvement by selection and are under the control of additive gene effects. Similarly, Mager et al. [17], Rai et al. [16] and Oruganti et al. [18] reported for grain yield and Sravanti et al. [22] for ear height. The characters, plant height, ear height, grain yield, ear length, ear diameter, No. of kernels per row and 100-kernel weight were exhibited high heritability along with moderate to high PCV, GCV & GA, demonstrates the heritability is probably the result of additive gene effects and deploying early generation selections may be effective. The remaining characters under study, days to 50 percent tasseling and silking, number of kernel rows per ear and shelling percentage were shown high heritability with low PCV, GCV & GA indicating non-additive gene action. Similar results were reported by Rai et al. [16] for days to 50 percent and silking and number of kernel rows/ear. Sravanti et al. [22] and Oruganti et al. [18] observed for days to 50% tasseling and silking.

4. CONCLUSION

In this investigation, the traits grain yield, plant height and ear height were exhibited high heritability coupled with high estimates of genetic advance suggesting that these traits were governed by additive gene action and hence, amenable for improvement by phenotypic selection. Whereas days to 50 percent tasseling, days to 50%silking, number of kernel rows per ear and shelling percentage recorded high heritability along with low PCV, GCV & GA indicating the presence of non-additive gene action in expression of such traits and limits the scope for selection to enhance the performance of such traits.

COMPETING INTERESTS

Authors have declared that no competing interests exist.

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