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Studies on genetic variability, heritability and genetic advance in maize (*Zea mays* L.) populations for yield and its contributing traits

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Abstract

Availability of appropriate germplasm is a key to any crop improvement programme. The knowledge and understanding of genetic variation present within the populations are useful for the efficient use of genetic resources in breeding programme. Hence, the present investigation was carried out to assess the genetic variability, heritability and genetic advance in twenty- six maize lines for agro morphological characters. The analysis of variance revealed the presence of significant variation among maize populations under study and the variability studies indicate the estimates of phenotypic coefficient of variation were slightly higher than its genotypic coefficient of variation for all the traits indicating there is less influence of environment. Among all the characters under study, yield exhibited highest phenotypic coefficient of variation (58.20) and genotypic coefficient of variation (57.89) whereas lowest PCV (5.97) and GCV (5.52) were recorded for days to 50% silking. High heritability with high genetic advance as percent of mean were recorded for plant height, ear height, cob length & girth, no. of kernel rows, no. of kernels per row, 100 - seed weight and yield which indicated the preponderance of additive gene action in controlling these traits. Emphasis should be given on these characters, while selection is made to improve yield potential.

Keywords: Maize, variability, heritability, genetic advance, yield

Introduction

Maize (*Zea mays* L.) is one of the most important cereal crops & occupies a prominent position in global agriculture after wheat and rice. Yield augmentation is major breeding objective in maize crop breeding programme and knowledge on the nature and amount of the genetic variation governing the inheritance of quantitative traits like yield and its component traits is important for effective genetic improvement. Based on the diversity of material with in the crop species, genetic improvement can be achieved. The variability provides options from which selections are made for improvement and possible hybridization.

The knowledge and understanding on the genetic variability parameters such as PCV, GCV, heritability and genetic advance for different characters of economic importance is a main pre-requisite for any plant breeder to work with crop breeding programmes.

The progress of a breeding programme is conditioned by the magnitude and the nature of the genotypic and non-genotypic variation in the various characters of study. Since, most of the economic characters are complex in inheritance and are greatly influenced by various environmental conditions, it is very difficult to judge whether observed variability is heritable or not-heritable.

Again, the heritable portion of the total variation might not always due to additive gene action. It is also essential to find out the relative magnitude of additive & non-additive genetic variances with regard to the characters of concern. Therefore, heritability should be combined with information on genetic advance. Heritability estimates along with genetic advance are normally more helpful in predicting the gain under selection than heritability estimates alone.

Keeping in view the importance of these aspects, the present investigation was undertaken to study the genetic variability, heritability and genetic advance among the populations of maize.

Materials and Methods

In the present investigation, twenty six maize entries (Supplied from MRC, Rajendranagar) were evaluated in randomized block design with two replications at Agricultural Research Station, Tarnala during *Kharif*, 2020. Each entry was raised in four rows of four meters length with a spacing of 60 cm x 20 cm between the rows and plants respectively.

The data was recorded on five randomly selected plants for plant height (cm), ear height (cm), cob length (cm), cob girth (cm), no. of kernel rows, no. of kernels per row, shelling % and grain yield (kg/ha), whereas for days to 50% tasselling and days to 50% silking was recorded on plot basis. 100 - grain weight was recorded per replication in each genotype. The data collected on all the characters were subjected to standard methods of analysis of variance (Panse and Sukhatme, 1985) [8]. Phenotypic and genotypic coefficient of variation was calculated as per Falconer, 1981 [4]. Heritability (Broad sense) according to Johnson *et al.*, 1955 [5], genetic advance (Burton, 1952) [3] and genetic advance as percent of mean (Johnson *et al.*, 1955) [5].

Results and Discussion

Analysis of Variance

The analysis of variance revealed the presence of considerable genetic variability among the experimental material under study as there is existence of significant difference among the material for all the traits as represented in Table 1. The mean values, genotypic and phenotypic coefficient of variation, heritability and genetic advance as percent of mean (Table 2) of 26 maize entries were calculated for yield and its contributing traits.

Phenotypic and genotypic coefficient of variation

For all the characters under study, phenotypic coefficient of variation values were higher than the corresponding genotypic coefficient of variation values and difference between them was narrow. Therefore response to direct selection may be effective for improving these traits (Sravanti *et al.* 2017) [12] as these characters were less influenced by the environment.

The characters studied in the present investigation was exhibited low (<10%), moderate (10-20%) and high (>20%) phenotypic and genotypic coefficients of variation and represented in graphical form in Fig. 1.

High phenotypic and genotypic coefficients of variation were observed for yield character (58.20/57.89), 100 kernel weight (29.24/25.45), kernels/row (32.65/31.88) and cob length (22.02/21.83). These results are in conformity with the findings of Archana *et al.* (2022) [11] for yield and kernels/row, while Sathish *et al.* (2022) [11] for 100 - kernel weight and length of the cob. For the parameters like plant height and ear height, GCV was less than its corresponding estimates of PCV which indicated significant role of environment in the expression of trait.

The estimates of phenotypic and genotypic coefficients of variation were moderate for cob girth (15.03/14.79) and no. of kernel rows (14.05/12.93). These findings are in accordance with those of Sathish *et al.* (2022) [11]. Whereas, phenotypic and genotypic coefficients of variation were observed as low for days to 50% tasselling (6.49/6.00), days to 50% silking (5.97/5.52) and shelling % (7.58/5.29). Similar results were reported by Kumar *et al.* (2014) [6].

Heritability

All the characters under investigation except shelling % recorded high estimates of heritability in broad sense ranging from 68.4% (Ear height) to 98.9% (yield). High heritability estimates indicate the selection for these characters will be effective being less influenced by environmental effects. Similar results were reported by Dawaki *et al.* (2023) [14] for days to 50% tasselling and silking. However, moderate value of heritability in broad sense was reported for shelling % (48.7). This might be due to the environmental impact on the phenotypic nature of trait. These results are in conformity with the findings of Begum *et al.* (2016) [2] and Kumar *et al.* (2024) [7].

Genetic advance

Genetic advance as percent of mean is classified as low (<10%), moderate (10-20%) and high (>20%). Among the traits under study, plant height (33.75%), ear height (33.32%), cob length (44.59%), cob girth (30.01%), no. of kernel rows (24.51%), no. of kernels/row (64.11) and 100 - seed weight (45.62%) expressed high genetic advance as percent of mean, which showed the presence of the additive gene action. Similar results were reported by Reddy *et al.* (2024) for the characters like yield, ear height and no. of kernels/row. Remaining two traits days to 50% tasselling (11.42%) and 50% silking (10.52%) recorded moderate estimates of genetic advance as percent of mean, which showed non-additive gene action these results are in conformity with the findings of Rasheed *et al.* (2023) [9]. However shelling % (7.60%) exhibited low estimates of genetic advance as percent of mean.

Among all the characters under study, days to 50% tasselling and silking expressed high heritability coupled with moderate genetic advance as percent of mean, which suggested that, the expression of this trait was mostly influenced by additive gene of action. Hence, response to selection is would be effective in improving the seed yield. Plant height, ear height, cob length, cob girth, no. of kernel rows, no. of kernels/row, 100 seed weight and yield had high heritability coupled with high genetic advance as percent of mean, which indicates preponderance of additive gene action in controlling the traits. Hence direct selection of such characters would be effective in improving the yield. However, shelling % expressed moderate heritability coupled with low genetic advance as percent of mean.

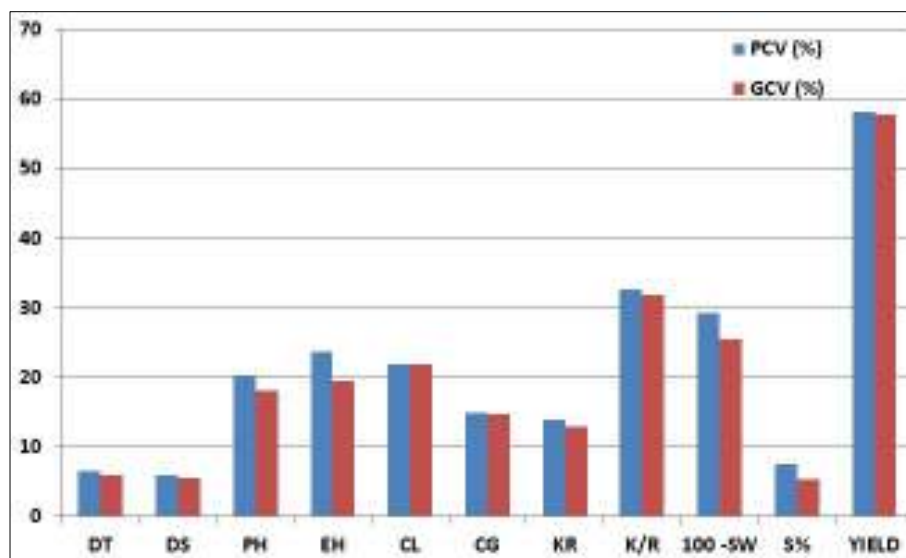


Fig 1: Graphical representation of phenotypic and genotypic coefficients of variation for various characters in maize population

DT- Days to 50% tasselling; DS - Days to 50% silking; PH - Plant Height; EH- Ear height; CL- Cob length (cm); CG - Cob girth (cm); KR- No. of kernel rows; K/R- No. of

kernels/row; 100 - SW - 100 seed weight(g); S %- Shelling %; Yield - Yield (kg/ha)

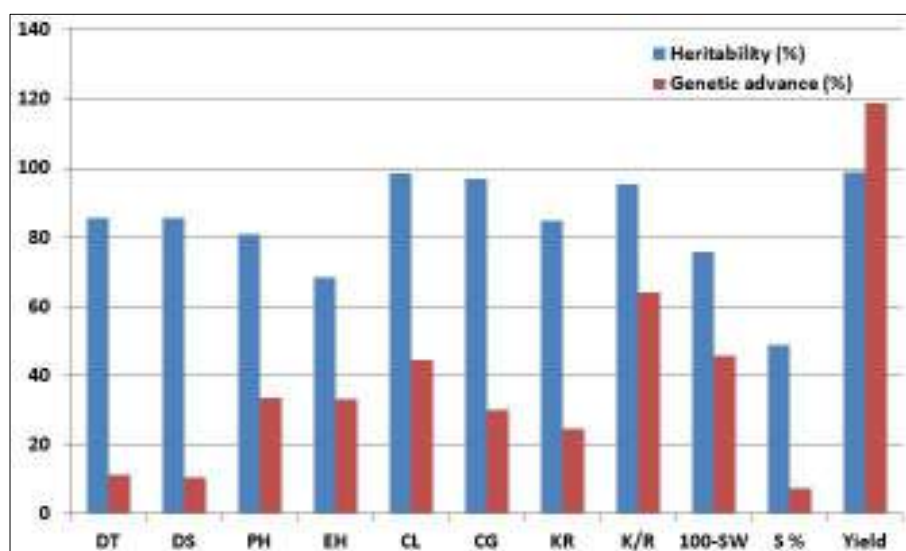


Fig 2: Graphical representation of heritability in broad sense and genetic advance as a percent of mean (5%) for various characters in maize population

DT- Days to 50% tasselling; DS - Days to 50% silking; PH - Plant Height; EH- Ear height; CL- Cob length (cm); CG - Cob girth (cm); KR- No. of kernel rows; K/R- No. of

kernels/row; 100 - SW - 100 seed weight(g); S %- Shelling %; Yield - Yield (kg/ha)

Table 1: Analysis of variance for quantitative traits of maize

S. No.	Traits	Mean sum of squares		
		Replication (d. f. = 1)	Genotypes (d. f. = 25)	Error (d. f. = 25)
1	Days to 50% tasselling	0.308	29.231**	2.308
2	Days to 50% silking	0.308	26.588**	2.068
3	Plant height (cm)	256.543	1197.896**	126.484
4	Ear height (cm)	44.308	276.260**	51.876
5	Cob length (cm)	0.314	19.067**	0.163
6	Cob girth (cm)	0.111	6.252**	0.097
7	Kernel rows (no.)	0.278	4.877**	0.404
8	Kernels/row (no.)	13.100	135.357**	3.253
9	100 seed weight (g)	8.643	104.110**	14.373
10	Shelling (%)	127.136	53.512**	18.463
11	Yield (kg/ha)	1199268.500	29885900.00**	25107039.600

* Significant at 5% level ** Significant at 1% level

Table 2: Estimation of genetic parameters for yield and its contributing characters of maize

S. No.	Traits	Mean	PCV (%)	GCV (%)	Heritability in broad sense (h^2) (%)	GA (5%)	GA as percent of mean (5%)
1	Days to 50% tasselling	61.15	6.49	6.00	85.4	6.98	11.42
2	Days to 50% silking	63.42	5.97	5.52	85.6	6.67	10.52
3	Plant height (cm)	127.07	20.25	18.22	80.9	42.89	33.75
4	Ear height (cm)	54.15	23.66	19.56	68.4	18.04	33.32
5	Cob length (cm)	14.08	22.02	21.83	98.3	6.28	44.59
6	Cob girth (cm)	11.85	15.03	14.79	96.9	3.56	30.01
7	Kernel rows (no.)	11.56	14.05	12.93	84.7	2.84	24.51
8	Kernels/row (no.)	25.50	32.65	31.88	95.3	16.34	64.11
9	100 seed weight (g)	26.32	29.24	25.45	75.7	12.01	45.62
10	Shelling (%)	79.18	7.58	5.29	48.7	6.02	7.60
11	Yield (kg/ha)	5432.14	58.20	57.89	98.9	6443.40	118.62

PCV- Phenotypic Coefficient of Variation; GCV - Genotypic Coefficient of Variation; GA- Genetic Advance

Conclusions

A perusal of genetic parameters *viz.*, phenotypic and genotypic coefficients of variation revealed less influence of environment on the characters under study. Therefore, response to direct selection may be effective in improving these traits. The traits having high heritability coupled with high genetic advance as percent of mean for plant height, ear height, cob length, cob girth, no. of kernel rows, no. of kernels/row, 100 seed weight and yield, indicates preponderance of additive gene action in controlling the traits. Hence direct selection of such characters would be effective in improving the yield.

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