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# Genetic variability for yield and yield attributing traits in maize (Zea mays. L)

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### Abstract

The present study aims to reveal the existence of genetic variability and importance of some quantitative traits in the 50 maize genotypes. The objectives were to assess the variability, heritability and genetic advance values were computed on 10 characters. Highly significant mean sum of squares due to genotypes and wide range of variability were noticed among the genotypes for all the characters except number of kernels per row. Phenotypic coefficient of variation was higher than the corresponding genotypic coefficient of variation for all the characters studied. High to moderate estimates of PCV and GCV were recorded for grain yield, ear height, ear length, number of kernel row per ear and 100 kernel weight suggesting sufficient variability thus offers scope for genetic improvement through selection. High estimates of heritability were observed for number of kernel rows per ear and days to 50 per cent flowering. High to moderate heritability with moderate estimates of genetic advance recorded for grain yield and ear height, where careful selection may lead towards improvement for these traits. Hence, provides better opportunities for selecting plant material for these traits in maize.

**Keywords:** maize, phenotypic coefficient of variation (PCV), genotypic coefficient of variation (PCV), heritability and genetic advance

## Introduction

Maize (*Zea mays* L.; 2n = 20) is one among the three major cereal crops which contributes to food security after Rice and Wheat. Its importance is uncontestable in the world agricultural economy as food for humans (Morris *et al.*, 1999) <sup>[8]</sup>, feed for animals and as a crop of industrial value (White and Johnson, 2003) <sup>[12]</sup>. It is a miracle C<sub>4</sub> crop and has a very high genetic yield potential. There is no other cereal, which has such an immense genetic potential and thus is rightly called as 'Queen of Cereals'. It is one of the most versatile emerging crops possessing wider adaptability under varied agro-climatic conditions.

Maize is cultivated on an area of 184.2 m ha with a production of about 1021.62 million tonnes of grain and productivity of 5.57 t ha<sup>-1</sup> in world. Among the maize growing countries, USA is the highest producing country (35%) followed by China (22%) (FAOSTAT, 2014) <sup>[6]</sup>. In India maize is produced over an area of 8.69 m. ha and production of 21.80 m. t with an average productivity 2.51 t ha<sup>-1</sup>. Karnataka is the one of most important maize growing states of India with a total area of 1.18 m. ha and production of 3.27 m. t with an average productivity of 2.77 t ha<sup>-1</sup> (Anonymous, 2016) <sup>[2]</sup>. Nutritionally it has highest crude protein of about 9.9 per cent at early and at full bloom stages which decreases to per cent at milking stage and 6 per cent at maturity. It has high nutritive value as it contains 72 per cent starch, 10 per cent protein, 4.80 per cent oil, 9.50 per cent fiber, 3.0 per cent sugar, 1.70 per cent ash, 82 per cent endosperm, 12 per cent embryo, 5 per cent bran testa and 1 per cent tip cap (Ali *et al.* 2014) <sup>[1]</sup>.

The basic information on the existence of genetic variability and diversity in a population and the relationship between different traits is essential for any successful plant breeding programme. Genetic improvement through conventional breeding approaches depends mainly on the availability of diverse germplasm and presence of enormous genetic variability. The characterization and evaluation are the important pre-requisites for effective utilization of germplasm and also to identify sources of useful genes. An insight into the nature and magnitude of genetic variability present in the gene pool is of immense value for starting any systematic breeding programme because the presence of considerable genetic variability in the base material ensures better chances of evolving desirable plant type. Hence, an attempt was made to estimate the extent of variation for yield contributing traits in 50 maize genotypes by studying the genetic parameters like phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability and genetic advance, which may contribute to formulation of suitable selection indices for improvement in this crop. Keeping in this in view, the present investigation was undertaken to assess the genetic variability, heritability and genetic advance for yield and yield attributing traits in maize.

# Materials and Methods

Sixteen best promising inbred lines were selected from two different populations and these selected 16 inbred lines were crossed with three different testers viz., CI-4, KDMI-15, NEI-9202B, using line×tester mating design during kharif 2012 and generated 48 single cross hybrids which were evaluated during rabi/summer 2012-13 along with two commercial checks viz., Bio-9681 and 900M for their performance. These were grown in randomised complete block design with three replications of 4 m length with inter row spacing of 60 cm and intra row spacing of 20 cm at Agriculture College Bheemarayanagudi during rabi/summer 2012-13. The data on Days to 50 % flowering, Days to 50 % silking, Plant height (cm), Ear height (cm,) Ear length (cm), Ear girth (cm), Number of kernel rows per ear, Number of kernels per row, 100 kernel weight (g) and Grain yield kg/ha were recorded and characters were analyzed to estimate genetic variability parameters. Genetic variability was measured and subjected to statistical analysis as suggested by Panse and Sukhatme (1964). Heritability (broad sense), genetic advance (GA) and genetic advance as a percent over mean (GAM) were worked by following the method suggested by Falconer (1981)<sup>[5]</sup>, Robinson et al. (1949).

## **Results and Discussion**

Genetic variability studies provide basic information regarding the genetic properties of the population based on which breeding methods are formulated for further improvement of the crop. These studies are also helpful to know about the nature and extent of variability that can be attributed to different causes, sensitivity of crop to environment, heritability of the character and genetic advance. The analysis of variance showed a wide range of variation and significant differences for all the characters under study, indicating the presence of adequate variability for further improvement. The mean sum of squares due to genotypes showed highly significant differences for all the characters except for number of kernels per row (Table1). This indicates the presence of substantial genetic variability among the genotypes. Similar results were reported by Anshuman et al. (2013)<sup>[3]</sup> for number of cobs per plant. The estimates of mean, range, phenotypic coefficient of variation, genotypic coefficient of variation, heritability, genetic advance and genetic advance as per cent of mean are presented in table 2.

The trait grain yield (4357.75 to 9843.66 kg/ha) revealed highest range followed by plant height (209.66 to 274.00 cm) and ear height (82.66 to 142.00) while, the lowest range was observed in case of ear girth (11.96 to 15.30). Hence, a breeder can concentrate more on these traits which can provide him ample scope for selection. Similar results have been reported by Praveen kumar *et al.* (2014) <sup>[9]</sup>.

In the present investigation, the phenotypic coefficient of variation (PCV) was higher than genotypic coefficient of variation (GCV) for all the characters indicated larger influence of environment for the expression of these characters. The values for PCV ranged from 3.33 to 22.94 per cent. The values for GCV obtained for different characters ranged from 2.57 to 14.64 per cent. The coefficients of

variation at phenotypic and genotypic levels were high for grain yield indicating that this character is more viable in the genotypes. There is a great scope for improvement of this character by direct selection among the genotypes. Similar results were earlier reported by Anshuman *et al.* (2013) <sup>[3]</sup>, Praveen kumar *et al.* (2014) <sup>[9]</sup> and Matin *et al.* (2017) <sup>[7]</sup>. Moderate PCV and GCV were recorded for ear height, ear length, number of kernel rows per ear and 100 kernel weight. These observations are in agreement with the earlier reports of Bikal and Deepika (2015) <sup>[4]</sup>, Sesay (2016) <sup>[11]</sup>. The lowest PCV and GCV were recorded for ear girth. Similar results were reported by Matin *et al.* (2017) <sup>[7]</sup>, Sesay (2016) <sup>[11]</sup> and Praveen kumar *et al.* (2014) <sup>[9]</sup>. Moderate to low variability of these characters indicated the need for improvement of base population.

The considerable differences in heritability values for different characters were observed (Table 2). Estimates of heritability ranged from 9.20 to 69.50 per cent. Number of kernel rows per ear (69.50%) recorded highest heritability followed by days to 50 per cent flowering (60.06%) and moderate heritability for days to 50 per cent silking (41.10%), plant height (35.20%), ear height (48.20%) and grain yield (40.70%). Whereas low estimates of heritability were recorded for ear length (26.50%), ear girth (27.10%), number of kernels per row (9.20%) and 100 kernel weight (15.40%). The estimates of heritability in broad sense computed, which include both additive and non additive effects. Similar results have been reported by Sarma Barua (2017) [10], Matin et al. (2017) <sup>[7]</sup> and Sesay (2016) <sup>[11]</sup>. Heritability which is the heritable portion of phenotypic variance is a good index of transmission of characters from parents to offspring (Falconer, 1960)<sup>[5]</sup>.

Heritability alone provides no indication of the amount of genetic improvement that would result from selection of individual genotypes. Hence, knowledge about genetic advance coupled with heritability is most important selection parameters. Character exhibiting high heritability may not necessarily give high genetic advance. High heritability should be accompanied with high genetic advance to arrive more reliable conclusion. In the present investigation, high to moderate heritability with moderate estimates of genetic advance were observed for grain yield (1352.88) and ear height (13.48).

Expected genetic advance as per cent of mean indicates the mode of gene action in the expression of a trait, which helps in choosing an appropriate breeding method. Moderate heritability along with moderate to low estimates of genetic advance were obtain for days to 50 per cent silking, plant height, ear height and grain yield, which results in intermediate expression for both additive and dominance gene effect. Whereas days to 50 per cent flowering, days to 50 per cent silking, plant height and ear girth exhibited moderate to low heritability along with low GCV and genetic advance indicating limited scope for improvement of these characters through selection. Similar findings were reported by Anshuman *et al.* (2014) for days to 50 per cent flowering, days to 50 per cent silking and ear length in maize.

It is concluded that genetic variability present in the population is mainly used for varietal improvement of future breeding programmes. A high estimate of phenotypic and genotypic coefficient of variation was observed for grain yield. Whereas ear height, ear length, number of kernels rows per ear, number of kernels per row and 100 kernel weight were showed moderate estimates of phenotypic and genotypic coefficient of variation suggesting variability and thus offers scope for genetic improvement through selection. High to moderate heritability with moderate estimates of genetic advance recorded for grain yield and ear height, where careful selection may lead towards improvement for these traits. Hence, improvement of these characters could be effective through single phenotypic selection.

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

Characters	Mean sum of square						
	Replication (Df= 2)	Genotypes (Df= 49)	Error (Df= 98)				
Days to 50 % flowering	1.64	7.94**	1.41				
Days to 50 % silking	6.40	11.01**	3.56				
Plant height (cm)	8693.98**	444.71**	169.05				
Ear height (cm)	2456.23**	362.25**	95.55				
Ear length (cm)	88.02**	7.25**	3.48				
Ear girth (cm)	9.15**	1.44**	0.68				
Number of kernel rows per ear	1.96	5.10**	0.94				
Number of kernels per row	423.75**	28.64	21.93				
100 kernel weight (g)	215.62**	18.10*	11.71				
Grain yield kg/ha	56718.84	4718804.00**	1541531.49				

Table 2: Estimation of genetic parameters for yield and yield components characters in maize

Characters	Range		Maan	PCV	GCV	h <sup>2</sup> bs	GA	CAM
	Min.	Max.	Mean	(%)	(%)	(%)	(%)	GAM
Days to 50 % flowering	55.00	62.33	56.80	3.33	2.57	60.06	2.36	4.16
Days to 50 % silking	55.33	64.66	58.97	4.17	2.67	41.10	2.08	3.53
Plant height (cm)	209.66	274.00	251.04	6.43	3.81	35.20	11.7	4.66
Ear height (cm)	82.66	142.00	111.47	12.18	14.45	48.20	13.48	12.09
Ear length (cm)	13.13	19.86	15.96	13.63	16.01	26.50	1.18	7.44
Ear girth (cm)	11.96	15.30	13.62	7.09	3.69	27.10	0.53	3.95
Number of kernel rows per ear	12.26	18.13	14.73	10.35	13.93	69.50	1.87	12.70
Number of kernels per row	23.30	36.80	29.12	16.80	15.13	9.20	0.93	3.21
100 kernel weight (g)	16.90	30.63	25.34	14.67	15.75	15.40	1.18	4.66
Grain yield kg/ha	4357.75	9843.66	7027.89	22.94	20.64	40.70	1352.88	19.25

**PCV**= Phenotypic coefficient of variation

GCV= Genotypic coefficient of variation

 $\mathbf{h}^2$  bs=Broad sense heritability

**GA** = Genetic advancement at 5 per cent level.

GAM= Genetic advance as per cent of mean at 5 per cent level.

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