

Original Research Article

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## Genetic Variability, Heritability and Genetic Advance Estimates in Quality Protein Maize (*Zea mays* L.)

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### ABSTRACT

#### Keywords

QPM, Variation,  
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PCV values were slightly higher than GCV values for all the characters under the study. 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. Majority of the characters exhibited higher heritability values in which ear height and ear girth recorded the highest values (99%) followed by days to 50% anthesis (98%), days to 50% silking (97%) and number of kernels per row (97%), ear length (95.1%), grain yield (93.9%), number of kernel rows per ear (92.8%), crude protein (85%), days to maturity (83.7%) and lysine (63%). High heritability indicated that these characters were least effected by the environment and selection is effective for the improvement.

### Introduction

Maize is an important staple food crop next to wheat and rice. It is considered as queen of cereals due to its wider adaptability and production potential. However, the has been experiencing many biotic and abiotic stresses thereby decline in the yield levels and hence availability of variability in the population provides a strong base for selection of elite lines for various purposed and hence determination of genetic variability is the

prime requisite for the purpose. Genetic variability for biometric traits is the key component of breeding programmes for broadening the genetic base of any crop. Genetic diversity constitutes the base material for plant improvement and provides protection against genetic vulnerability to various stresses (Wang and Lu, 2006). The parameters like genotypic and phenotypic coefficients of variation (GCV and PCV) will be useful to understand the extent of variability present in the material. Heritability

and Genetic advance (GA) play a crucial role during the selection process depending upon the extent of variability (Bilgin *et al.*, 2010). Heritability (both in broad & narrow sense) is of interest to plant breeders primarily as a measure of the value of selection for particular trait in various types of progenies and as an index of transmissibility. Heritability in broad sense is defined as a ratio of the total heritable variance (genotypic variance) to total phenotypic variance (Johnson *et al.*, 1955). The necessity for partitioning the phenotypic variability into heritable and non-heritable components was suggested by Panse (1957), because highly heritable characters showed the least influence for environmental fluctuations. The heritability estimate is the important component of predicting genetic advance.

### Materials and Methods

A total of thirty one Quality Protein Maize (QPM) genotypes obtained from Maize Research Centre, Agricultural Research Institute, Rajendranagar, Hyderabad were planted in Randomized Block Design with three replications during *khariif*, 2014 at College Farm, College of Agriculture, Rajendranagar, Hyderabad. The data was collected on characters *viz.*, days to 50 per cent anthesis, days to 50 per cent silking, Anthesis silking interval(ASI),days to maturity, plant height (cm), ear height (cm), ear length (cm), ear girth (cm), number of kernel rows per ear, number of kernels per row, grain yield (g/plant),100 kernel weight (g), shelling percentage, crude protein (%), lysine content (%) and tryptophan content (%). Analysis of variance was computed based on Randomized Block Design for each of the character separately as per standard statistical procedure (Panse and Sukhatme, 1985). The test of significance was carried out by referring to 'F' table values given by Fisher and Yates (1967). For statistical

analysis, windostat version 9.1 software package was used. The model of ANOVA used is presented below.

The analysis of variance for each character was carried out by using the method described by Panse and Sukhatme (1985).

The genotypic and phenotypic variance was calculated as per the formulae given by Burton and Devane (1953).

Genotypic variance ( $\sigma^2g$ )

$$= \frac{(\text{Mean sum of squares due to treatments} - \text{Mean sum of squares due to error})}{\text{Number of replications}}$$

Phenotypic variance ( $\sigma^2p$ ) = ( $\sigma^2g$ ) + ( $\sigma^2e$ )

Where, ( $\sigma^2e$ ) = error variance

### Genotypic and Phenotypic Coefficient of Variation (GCV and PCV)

The genotypic and phenotypic coefficients of variation were calculated according to the formulae given by Falconer (1960).

Genotypic coefficient of variation (GCV)

$$= \frac{\text{Genotypic standard deviation}}{\text{Mean}} \times 100$$

Phenotypic coefficient of variation (PCV)

$$= \frac{\text{Phenotypic standard deviation}}{\text{Mean}} \times 100$$

Categorization of the range of variation was done as proposed by Sivasubramanian and Madhavamenon (1973).

Less than 10 %: Low

10-20 %: Moderate

More than 20 %: High

**Heritability (h<sup>2</sup>)**

Heritability in the broad sense refers to the proportion of genotypic variance to the total observed variance in the total population. Heritability (h<sup>2</sup>) in the broad sense was calculated according to the formula given by Allard (1960).

$$h^2 (bs) = \frac{\sigma^2g}{\sigma^2p}$$

Where,

h<sup>2</sup>(bs) = heritability in broad sense

σ<sup>2</sup>g = genotypic variance

σ<sup>2</sup>p = phenotypic variance (σ<sup>2</sup>g + σ<sup>2</sup>e)

σ<sup>2</sup>e = environmental variance

As suggested by Johnson *et al.*, (1955) (h<sup>2</sup>) estimates were categorized as:

Low : 0-30 %

Medium : 30-60 %

High : above 60 %

**Genetic Advance**

Genetic advance refers to the expected gain or improvement in the next generation by selecting superior individuals under certain amount of selection pressure. From the heritability estimates the genetic advance was estimated by the following formula given by Burton (1952).

$$GA = \sigma p. h^2 (b). K$$

Where,

GA = Expected genetic advance

K = Selection differential, the value of which is 2.06 at 5 % selection intensity

h<sup>2</sup> (b) = Heritability in broad sense

σp = Phenotypic standard deviation

**Genetic advance as per cent of mean (GAM)**

In order to visualize the relative utility of genetic advance among the characters, genetic advance as percent of mean was computed.

Genetic advance as percent of mean

$$= \frac{GA}{\text{Grand mean}} \times 100$$

The range of genetic advance as percent of mean was classified as suggested by Johnson *et al.*, (1955)

Low : Less than 10 %

Moderate : 10-20 %

High : More than 20 %

**Results and Discussion**

The phenotypic and genotypic coefficients of variation did not vary widely in majority of the characters and most of them exhibited low to higher values indicating that sufficient amount of variability was available in the material and selection can be exercised whereas, low values were recorded for days to 50 per cent anthesis, days to 50 per cent silking, shelling percentage and tryptophan content. The PCV estimate for grain yield was maximum (41.45%) followed by 100 kernel weight (23.07%) and number of kernels per row (23.02%). The PCV estimate was the lowest for days to maturity (3.32%). The GCV estimate was maximum for grain yield

(40.16%) followed by number of kernels per row (22.65%) and 100- kernel weight (20.90%). The GCV estimate was the lowest for days to maturity (3.03%). The ECV estimate was maximum for anthesis silking interval (15.12%) followed by number of grain yield per plant (10.26%) and 100-kernel weight (9.75%). The ECV estimate was the lowest for days to 50 per cent anthesis (0.71%).

High PCV and GCV values were recorded for number of kernels per row, 100-kernel weight and grain yield whereas, anthesis silking interval, plant height, ear height, ear length, ear girth, number of kernel rows per ear, crude protein and lysine contents exhibited moderate values while, days to 50 per cent anthesis, days to 50 per cent silking, days to maturity, shelling percentage and tryptophan contents recorded low values (Table 1). It is evident from the table that PCV values were slightly higher than GCV values for all the characters under the study. 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 results are in conformity with the findings of Tengan *et al.*, (2012), Aminu and izge (2012), Elmyhum (2013), Mohan Lal and Dharendra Singh (2014), Ogunniyan and Olakojo (2014), Ulganathan *et al.*, (2015), Jaya Prakash *et al.*, (2017) and Preeti Sharma *et al.*,(2017).

Majority of the characters exhibited higher heritability values in which ear height and ear girth recorded the highest values (99%) followed by days to 50% anthesis (98%), days to 50% silking (97%) and number of kernels per row (97%), ear length (95.1%), grain yield (93.9%), number of kernel rows per ear

(92.8%), crude protein (85%), days to maturity (83.7%) and lysine (63%). High heritability indicated that these characters were least effected by the environment and selection is effective for the improvement whereas, medium heritability values were recorded for anthesis silking interval (43%), shelling percentage (47%) and also for tryptophan (53%). High genetic advance was recorded for plant height (53.81%) and ear height (24.59%); medium value was recorded for grain yield (11.56%) while, low values were recorded for the remaining traits (Table 1 & Figure 1 &2). Genetic advance as per cent mean ranged from 2.49 for shelling percentage to 80.16 for grain yield with medium to higher values for the characters.

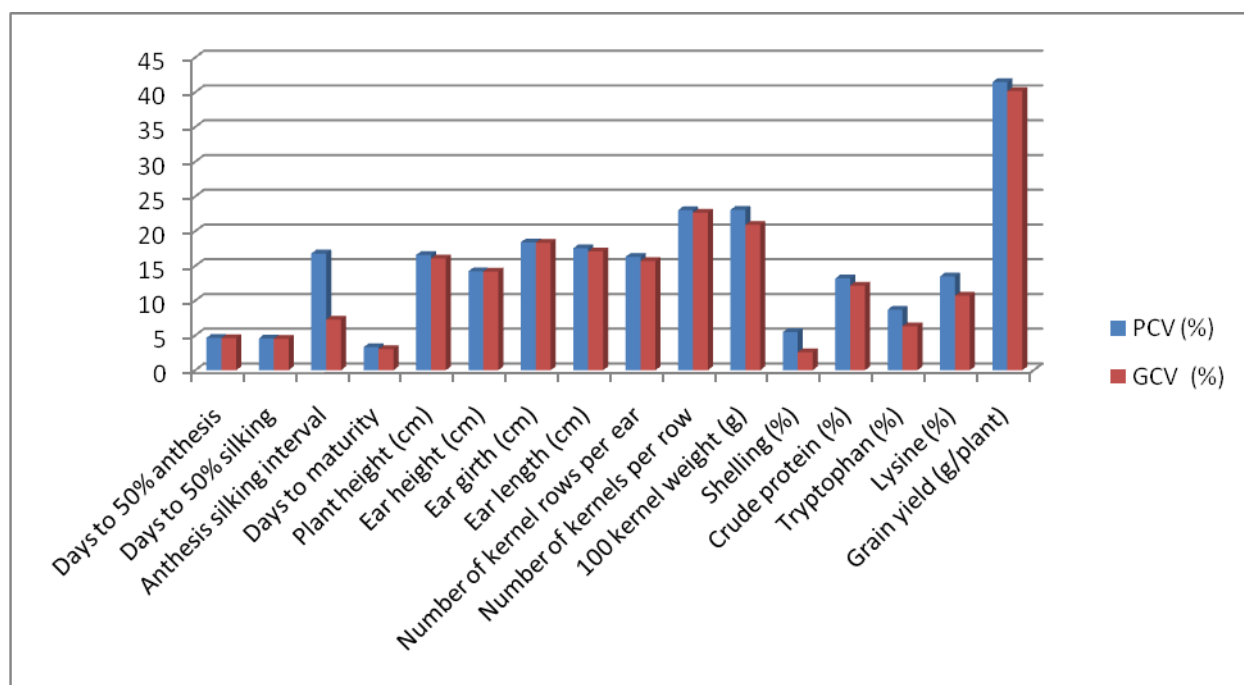
The traits, number of kernels per row, 100-kernel weight and grain yield recorded high heritability coupled with high genetic advance indicating the preponderance of additive gene action where simple selection can be exercised in improvement of these traits whereas, days to 50 per cent anthesis, days to 50 per cent silking, days to maturity and lysine contents recorded high heritability coupled with low genetic advance indicating that these traits were under the control of non additive genes where heterosis breeding is rewarding for improvement of these traits. Medium heritability coupled with low genetic advance was recorded for anthesis silking interval and shelling percentage and tryptophan content revealing the preponderance of non additive genes and hence heterosis breeding is rewarding for the improvement of these traits. The results are in conformity with the findings Tengan *et al.*, (2012), Elmyhum (2013), Mohan Lal and Dharendra Singh (2014), Ogunniyan and Olakojo (2014), Ulganathan *et al.*, (2015) Jaya Prakash *et al.*, (2017) and Preeti Sharma *et al.*, (2017).

**Table.1** Estimation of genetic parameters for sixteen characters in Quality protein maize

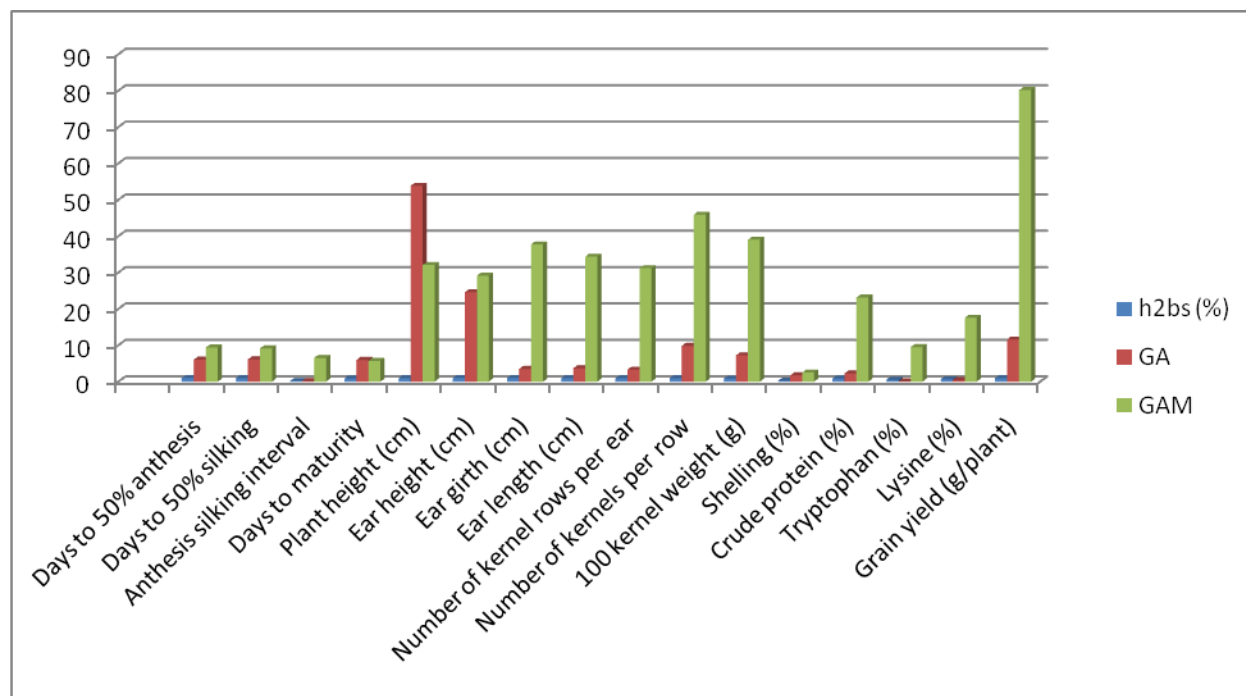
Character	PCV (%)	GCV (%)	ECV (%)	$h^2_{bs}$ (%)	GAM
Days to 50% anthesis	4.66	4.61	0.71	98	9.38
Days to 50% silking	4.57	4.50	0.76	97	9.13
Anthesis silking interval	16.79	7.29	15.12	43	6.52
Days to maturity	3.32	3.03	1.34	84	5.72
Plant height (cm)	16.57	16.06	4.09	94	32.06
Ear height (cm)	14.24	14.19	1.24	99	29.12
Ear girth (cm)	18.40	18.35	1.34	99	37.70
Ear length (cm)	17.54	17.10	3.89	95	34.35
Number of kernel rows per ear	16.32	15.72	4.38	93	31.20
Number of kernels per row	23.02	22.65	4.15	97	45.89
100 kernel weight (g)	23.07	20.90	9.75	82	39.03
Shelling percentage (%)	5.49	2.58	4.85	47	2.49
Crude protein content (%)	13.20	12.18	5.10	85	23.13
Tryptophan content (%)	8.70	6.33	5.96	53	9.49
Lysine content (%)	13.49	10.72	8.20	63	17.54
Grain yield (g/plant)	41.45	40.16	10.26	94	80.16

PCV: Phenotypic coefficient of variation; GCV: Genotypic coefficient of variation  
 ECV: Environmental coefficient of variation;  $h^2_{bs}$ : Broad sense heritability  
 GAM: Genetic advance as per cent mean at 5 % level

**Fig.1** Graphic representations of Phenotypic and Genotypic coefficients of variation for various characters in 31 quality protein maize genotypes



**Fig.2** Graphic representations of heritability and genetic advance for 16 characters in 31 quality protein maize genotypes



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