



## Genetic Variability, Heritability and Genetic Advance for Kernel Yield and its Components in Maize (*Zea Mays* L.) Inbreds

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### ABSTRACT

Fifty maize inbred lines were evaluated for genetic potential and variability. Analysis of variance indicated significant differences among 50 genotypes for all the characters studied. The genotypic coefficients of variation for all the characters studied were lesser than the phenotypic coefficients of variation indicating the influence of environment on expression of these traits. High PCV and GCV were recorded for kernel yield per plant and kernels per row while moderate PCV and GCV were recorded for test weight, cob length, plant height and kernel rows per cob indicating that there is considerable amount of variability for majority of the characters studied. The estimates of high heritability coupled with low genetic advance as per cent of mean were recorded by days to 50% tasseling and days to 50% silking indicating the operation of both additive and non-additive gene actions. Days to maturity exhibited moderate heritability and low genetic advance as per cent of mean indicating the predominance of non additive gene action in controlling this trait. While the remaining six traits *viz.*, plant height, cob length, kernal rows per cob, kernels per row, test weight and kernel yield per plant recorded high heritability and high genetic advance as per cent of mean indicating the predominance of additive gene action and hence direct phenotypic selection is useful with respect to these traits.

**Keywords:** *Genitic advance, Genotypic coefficients of variation, Heritability, Phenotypic coefficients of variation.*

Maize (*Zea mays* L.;  $2n=20$ ) is a member of the family Poaceae and is the second most important cereal of the world after wheat. The use of maize varies in different countries and is estimated that approximately 21% of the total grain produced is consumed as food. By origin, maize is native to South America and is a tropical crop but has adapted magnificently to temperate environments with much higher productivity as most of the area is in the warmer parts of temperate regions and in humid-subtropical climate. It is grown from latitude  $58^{\circ}$  N to  $40^{\circ}$  S, from below sea level to higher than 3000 m altitudes and in areas receiving rainfall of 250 mm to 5000 mm per annum.

In India, maize is the third most important food grain after wheat and rice, and maize production accounts for nine per cent of total food grain production. About 28% of maize produced is used for food purpose, about 11% as livestock feed, 48% as poultry feed, 12% in wet milling industry (for starch and oil production) and 1% as seed. In the last one decade, it has registered the highest growth rate among all food grains including wheat and rice because of newly emerging food habits as well as enhanced industrial requirements. In India, maize is cultivated in an area of 9.3 mha with a production and productivity of 21.07 million tonnes and  $2.6 \text{ t ha}^{-1}$ , respectively (Directorate of Economics and Statistics, Department of Agriculture, 2015). While the world average productivity levels are around  $5 \text{ t ha}^{-1}$ . In the present scenario of high demand for maize for different purposes, Indian productivity levels are to be enhanced by breeding high yielding hybrid varieties

which in turn require identification and development of superior inbred lines from the available germplasm.

Choosing an effective breeding method requires a better understanding of the genetic basis of the traits. Genetic improvement depends on the magnitude of genetic variation, heritability and genetic advance of characters of economic importance. Hence knowledge on the variability parameters like GCV, PCV, heritability and genetic advance is of paramount importance in crops like maize to exploit the traits in breeding programmes.

### MATERIAL AND METHODS

The present investigation was carried out during *kharif*, 2014-15 at Agricultural College Farm, Bapatla, Guntur District, Andhra Pradesh, which is located at an altitude of 5.49 m MSL,  $15^{\circ} 54' \text{N}$  latitude and  $80^{\circ} 3' \text{E}$  longitude. The experimental material for the present investigation consisted of fifty genotypes of maize were evaluated in a Randomized Complete Block Design with three replications. Each entry was represented by four rows of 3m length. The spacing of 60 cm between rows and 20 cm within rows was followed. Observations were recorded on ten randomly chosen plants for nine characters *viz.*, plant height, days to 50% flowering, days to maturity, days to 50% tasselling, cob length(cm), test weight(g), kernel rows per cob, kernels per row and kernel yield per plant(g). The mean value of the recorded data was subjected to analysis of variance. The analysis of variance was done as suggested by Panse and Sukhatme (1985). GCV and PCV estimated as per the formula suggested by

Burton (1952). Heritability percentage in broad sense was estimated for various characters as suggested by Hanson *et al.*, (1956). Genetic advance was calculated by the formula given by Johnsen *et al.*, (1955).

## RESULTS AND DISCUSSION

The analysis of variance revealed significant differences among the genotypes for all characters under study, indicating a high degree of variability in the material (Table 1). The estimates of variability, heritability, genetic advance were detailed in the Table 2.

The variation for number of days taken to 50% tasseling ranged from 46 days (BM-256) to 57 days (BM-66-1) with a mean of 51.73 days. The PCV (5.09) and GCV (4.45) estimates were low indicating less variation for days to 50% tasseling among genotypes studied and such estimates of PCV and GCV were earlier reported by Rajitha *et al.* (2015), Maruthi and Rani (2015), Patil *et al.*, (2016) and Begum *et al.*, (2016). High heritability (77.00%) coupled with low genetic advance as per cent of mean (8.03) was noted for this trait which may be due to the predominance of both additive and non-additive gene actions and the desired results may not be obtained by simple selection. These results were in agreement with Begum *et al.*, (2016).

The range of variation for days to 50% silking varied from 49.00 days (BM-256) to 60.67 days (BM-424) with a mean of 55.12 days. The estimates of PCV (5.36) and GCV (4.75) were low indicating less variation among the genotypes studied. Similar results were reported by Patil *et al.*, (2016) and Begum *et al.*, (2016). High heritability (79.00%) coupled with low genetic advance as per cent of mean (8.67) was observed for this trait indicating the operation of both additive and non-additive gene actions and the desired results may not be obtained by simple selection. Similar results were reported by Rajitha *et al.* (2015), Maruthi and Rani (2015) and Begum *et al.* (2016).

The number of days to maturity ranged from 81.67 days (Ra-15-2) to 98.67 days (BM-424) with a mean of 91.13 days. The estimates of PCV (4.39) and GCV (3.09) were low indicating less variation among genotypes studied. Similar results were reported by Patil *et al.* (2016). Moderate heritability (50.00%) coupled with low genetic advance as per cent of mean (4.48) was observed indicating the predominance of non-additive gene action in the inheritance of this trait and the desired results may not be obtained by simple selection. Low genetic advance as per cent of mean was in accordance with the results of Patil *et al.* (2016).

The variation for plant height ranged from 125.23 cm (RNBL-4201) to 216.20 cm (Ra-15-2) with a mean of 172.58 cm. The estimates of PCV (13.31) and GCV (12.22) were moderate. The difference

between PCV and GCV value is less which indicates that there is little role of environmental component in the observed variation. Similar results were reported by Nataraj *et al.*, (2014) and Rajitha *et al.*, (2015). High heritability (84.00%) combined with high genetic advance as per cent of mean (23.12) was observed for this trait indicating the predominance of additive gene action and hence simple selection may be rewarding. These findings are in accordance with that of Reddy *et al.*, (2012) and Reddy *et al.*, (2013).

The range of variation for cob length ranged from 10.60 cm (BM-426) to 19.30 cm (MBSB-3) with a mean of 14.54 cm. The estimates of PCV (13.91) and GCV (13.31) were moderate. The difference between PCV and GCV value is less which indicates that there is little role of environmental component in the observed variation. These results are in agreement with Rajitha *et al.* (2015) and patil *et al.* (2016). High heritability (89.00%) coupled with high genetic advance as per cent of mean (25.54) was observed for this trait revealing the preponderance of additive gene action which may be exploited through simple selection procedures.

The number of kernel rows per cob ranged from 9.60 (BM-426) to 17.70 (MBSB-3) with a mean of 12.83. The estimates of PCV (12.14) and GCV (11.56) were moderate. The difference between PCV and GCV value is less which indicates that there is little role of environmental component in the observed variation. Similar results were reported by Nataraj *et al.*, (2014) and Maruthi and Rani (2015). High heritability (91.00%) and high genetic advance as per cent of mean (22.70) was observed for this trait revealing the preponderance of additive gene action which may be exploited through simple selection procedures.

The number of kernels per row ranged from 11.82 (BM-121) to 36.53 (BM-261) with a mean of 23.44. The estimates of PCV (23.21) and GCV (22.71) were high. The difference between PCV and GCV value is less which indicates that there is little role of environmental component in the observed variation. Similar results were reported by Maruthi and Rani (2015).

High heritability (96.00%) and high genetic advance as per cent of mean (45.76) was observed for this trait revealing the preponderance of additive gene action which may be exploited through simple selection procedures. The above findings are in agreement with the results of Maruthi and Rani (2015) and Patil *et al.* (2016).

The variation for Test weight ranged from 16.73 g (RNBL-4201) to 35.36 g (BM-77) with a mean of 25.57 g. This character possessed moderate PCV (18.67) and GCV (18.59) and there is less difference between them indicating the less influence of

Table 1: Analysis of variance for kernel yield and yield component characters in maize (*Zea mays* L.)

Source of variations	d.f	Days to 50% tasseling	Days to 50% silking	Days to maturity	Plant height (cm)	Cob length (cm)	Kernel rows per cob	Kernels per row	Test weight (g)	Kernel yield per plant (g)
Replications	2	2.68	3.02	0.64	92.81	1.05	0.28	1.47	0.18	31.15
Treatments	49	17.54**	22.43	31.91**	1417.34**	11.38**	6.82**	86.29**	68.02**	2156.33**
Error	98	1.61	1.86	8.08	1.61	0.47	0.22	1.26	0.19	62.98

Table 2: Estimates of variability, heritability and genetic advance as per cent of mean for kernel yield and yield components in maize (*Zea mays* L.)

S. No.	Character	Mean	Range		Coefficient of variation		Heritability (broad sense) (%)	Genetic advance	Genetic advance as per cent of mean
			Minimum	Maximum	PCV (%)	GCV (%)			
1.	Days to 50% tasseling	51.73	46.00	57.00	5.09	4.45	77.00	4.16	8.03
2.	Days to 50% silking	55.12	49.00	60.67	5.36	4.75	79.00	4.78	8.67
3.	Days to maturity	91.13	81.67	98.67	4.39	3.09	50.00	4.09	4.48
4.	Plant height (cm)	172.58	125.23	216.20	13.31	12.22	84.00	39.90	23.12
5.	Cob length (cm)	14.54	10.60	19.30	13.91	13.31	89.00	3.72	25.54
6.	Kernel rows per cob	12.83	9.60	17.70	12.14	11.56	91.00	2.91	22.70
7.	Kernels per row	23.44	11.82	36.53	23.21	22.71	96.00	10.73	45.76
8.	Test weight	25.57	16.73	35.36	18.67	18.59	99.00	9.75	38.14
9.	Kernel yield per plant (g)	70.25	30.42	143.01	39.26	37.60	92.00	52.12	74.18

PCV = Phenotypic coefficient of variation  
 GCV = Genotypic coefficient of variation

environment. These findings were in line with the results of Begum *et al.* (2016) and Patil *et al.* (2016). High heritability (99.00%) coupled with high genetic advance as per cent of mean (38.14) was observed for this trait which revealed the importance of additive gene action. This indicates that this character can be improved through simple selection procedures. These findings were in agreement with the results of Jawaharlal *et al.* (2011), Bharathiveeramani *et al.* (2012), Nataraj *et al.* (2014) Rajitha *et al.* (2015), Begum *et al.* (2016) and Patil *et al.* (2016).

The Kernel yield per plant ranged from 30.42 g (BM-426) to 143.01 g (MBSB-3) with a mean of 70.25 g. The estimates of PCV (39.26) and GCV (37.60) were high indicating more variation among genotypes studied. The magnitude of PCV was higher than GCV revealing the influence of environment in inheritance of this trait. These findings are in conformity with the results of Reddy *et al.* (2012), Nataraj *et al.* (2014) and Rajitha *et al.* (2015). High heritability (92.00%) coupled with high genetic advance as per cent of mean (74.18) indicated the role of additive gene action governing in the inheritance of this character and offers the scope for improvement through simple selection. Similar results were earlier reported by Maruthi and Rani (2015) and Patil *et al.* (2016).

### CONCLUSION

The genotypic coefficients of variation for all the characters studied were lesser than the phenotypic coefficients of variation indicating the influence of environment on expression of these traits. High PCV and GCV were recorded for kernel yield per plant and kernels per row while moderate PCV and GCV were recorded for test weight, cob length, plant height and kernel rows per cob indicating that there is considerable amount of variability for majority of the characters studied.

The estimates of high heritability coupled with low genetic advance as per cent of mean were recorded by days to 50% tasseling and days to 50% silking indicating the operation of both additive and non-additive gene actions. Days to maturity exhibited moderate heritability and low genetic advance as per cent of mean indicating the predominance of non additive gene action in controlling this trait. While the remaining six traits *viz.*, plant height, cob length, kernal rows per cob, kernels per row, test weight and kernel yield per plant recorded high heritability and high genetic advance as per cent of mean indicating the predominance of additive gene action and hence direct phenotypic selection is useful with respect to these traits.

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