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Genetic Variability, Heritability and Genetic Advance for Grain Yield and its Components in Maize (*Zea mays* L.)

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ABSTRACT

An investigation was carried out to assess the variability, heritability and genetic advance for nine characters viz., days to 50% tasseling, days to 50% silking, days to maturity, plant height, cob length, kernel rows per cob, 100-seed weight, protein content and grain yield per plant in 24 genotypes (fifteen hybrids, their eight parents along with a check). The results revealed that high PCV and GCV were observed for the character grain yield per plant. High heritability accompanied with high genetic advance had shown by the characters viz., 100-seed weight, grain yield per plant, cob length and plant height indicating the preponderance of additive gene action which may be exploited through breeding methods involving simple selection like mass selection, ear-to-row method, etc. are to be followed to improve these traits.

Key words : Genetic advance, Heritability, Maize, Variability.

The success of any breeding programme depends upon the quantum of genetic variability present in the population. Wider range of genetic variability helps in selecting desired genotypes. In addition to the genetic variability, knowledge on heritability and genetic advance helps the breeder to employ the suitable breeding strategy. Therefore, it is necessary to have knowledge of genetic variability, heritability and genetic advance present in the available genetic material.

MATERIAL AND METHODS

The fifteen hybrids (obtained by crossing five lines with three testers), their eight parents along with a check, DHM-117 were evaluated during *kharif,* 2012 at Agricultural College Farm, Bapatla in a Randomized Block Design with three replications. Observations were recorded on ten randomly chosen plants for nine quantitative characters viz., days to 50% tasseling, days to 50% silking, days to maturity, plant height, cob length, kernel rows per cob, 100-seed weight, protein content and grain yield per plant. The seeds were directly sown by dibbling. Each genotype was represented by five rows of 3m length. The plot size was 9 sq.m. The spacing of 60 cm between rows and 25 cm between the plants was followed. A basal dose of 50 kg N/ha, 50 kg P_2O_5/ha and 40 kg K_2O/ha was applied at the time of sowing. All recommended cultural practices were carried out during crop growth period. The data were subjected to statistical analysis and genetic parameters such as Phenotypic coefficient of variation (PCV) and Genotypic coefficient of variation (GCV) as per Burton (1952), heritability in broad sense and expected genetic advance as percent of mean were worked out as per Johnson *et al.* (1955) and Hanson (1963).

RESULTS AND DISCUSSION

The analysis of variance revealed significant differences among all the 24 genotypes for all the characters studied, indicating a high degree of variability in the material (Table 1). In the present study, the variation among genotypes was estimated as coefficient of variation (Table 2). The phenotypic coefficient of variance (PCV) was slightly higher in magnitude than genotypic coefficient of variance (GCV) for all the characters studied indicating the influence of environment on expression of these traits. Highest PCV and GCV (32.32 and 29.32) was exhibited by grain yield per plant, whereas lowest PCV and GCV (4.74 and 2.54) was recorded by days to maturity. These results were in accordance with the findings of Reddy *et al.* (2012) and Reddy *et al.* (2013).

Table 1. Analysis of variance for 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	Cob length	Kernel rows per cob	100-seed weight	Protein content	Grain yield per plant
Replications	2	0.931	0.375	1.347	10.040	3.934	0.732	0.599	0.167	152.771
Entries	23	12.722**	16.674**	26.896*	2204.450**	13.537**	2.972**	31.378**	1.362**	2577.008**
Error	46	1.423	2.636	12.217	312.672	1.446	0.530	0.733	0.120	172.492

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

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

S. No.	Character	Mean	Range		Coefficient of variation		Heritability (broad sense)	Genetic advance as per cent of mean
			Minimum	Maximum	PCV (%)	GCV (%)		
1.	Days to 50% tasseling	47.97	45.00	54.00	4.75	4.05	72.57	7.10
2.	Days to 50% silking	51.42	48.33	60.00	5.26	4.21	63.97	6.93
3.	Days to maturity	87.19	83.00	96.00	4.74	2.54	28.60	2.79
4.	Plant height (cm)	169.22	124.80	211.27	18.15	14.84	66.85	24.99
5.	Cob length (cm)	15.37	11.97	18.95	15.22	13.06	73.60	23.08
6.	Kernel rows per cob	14.28	12.32	15.77	8.12	6.32	60.58	10.13
7.	100-seed weight (g)	21.91	16.33	26.20	15.10	14.58	93.30	29.02
8.	Protein content (%)	8.02	7.25	9.18	9.10	8.02	77.56	14.55
9.	Grain yield per plant (g)	96.55	52.79	130.03	32.32	29.32	82.29	54.79

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

Moderate PCV and GCV was recorded for plant height, cob length and 100-seed weight. While protein content, kernel rows per cob, days to 50% silking, days to 50% tasseling and days to maturity exhibited low PCV and GCV.

Heritability estimates were high for days to 50% tasseling, days to 50% silking, plant height, cob length, kernel rows per cob, 100-seed weight, protein content and grain yield per plant. Low heritability was recorded for days to maturity. Similar results were obtained by Reddy *et al.* (2012) for all characters except protein content and Shanthi *et al.* (2011) for protein content. The maximum value for heritability was recorded by number of 100-seed weight (93.30%) and minimum was recorded by days to maturity (28.60%).

Heritability estimates along with genetic advance are more helpful in predicting the gain under selection than heritability estimates alone. The estimates of heritability and genetic advance as per cent of mean were high for 100-seed weight, grain yield per plant, cob length and plant height indicating that these characters were less influenced by environment and governed by additive gene action which may be exploited through breeding methods involving simple selection like mass selection, ear-to-row method, etc. These findings were in agreement with Bharathiveeramani *et al.* (2012) and Reddy *et al.* (2012).

High heritability coupled with moderate genetic advance as per cent of mean was observed for kernel rows per cob and protein content.

Whereas days to 50% tasseling and days to 50% silking expressed high heritability accompanied with low genetic advance indicating the role of both additive and non-additive gene actions in the inheritance of these traits and can be improved either by population improvement methods or even heterosis breeding methods like production of hybrids and synthetics. While low heritability coupled with low genetic advance as per cent of mean was observed for days to maturity indicating the role of non-additive gene action and can be improved by population improvement methods involving selection, intermating among selected ones and reselection may help to improve these traits besides exploiting the methods of heterosis breeding.

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