

RESEARCH ARTICLE :

Heritability, variability and genetic advance for grain yield and its component characters in maize (*Zea mays* L.)

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SUMMARY : Knowledge of the magnitude of genetic variability, heritability and genetic gains in selection of desirable characters could assist the plant breeder in ascertaining criteria to be used for the breeding programmes. Eighteen (15 lines and 3 testers) open pollinated maize genotypes were evaluated at Agricultural Research Station, Madhira, Prof. Jayashanker Agricultural University of Telangana during 2015 and 2016 cropping seasons to estimate genetic variability, heritability and genetic advance of grain yield and its component characters. The effect of genotype and genotype by year interaction were significant for ear height and seed yield, while the effect of year was highly significant ($P < 0.01$) for all the characters. Low to moderate genotypic and phenotypic co-efficients of variation were observed for all the characters except for ear height and seed yield which recorded high variation both at phenotypic and genotypic levels indicating profound influence of environment in the expression of these traits. High heritability estimates were recorded by all the characters whereas high heritability along with high genetic advance was recorded for plant height, ear height and seed yield per plant which provides evidence that these parameters were under the control of additive gene effects and effective selection could be possible for improvement for these characters. Moderately high values for genetic advance as percentage of mean was recorded for plant height, ear height, ear length, number of kernels per row, test weight and seed yield per plant indicating responsiveness of selection for bringing improvement in these characters for ultimate yield improvement in maize genotypes under study.

KEY WORDS :

Heritability,
Variability, Maize

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BACKGROUND AND OBJECTIVES

Maize (*Zea mays* L.) belong to family Poaceace and is primarily a cross pollinated species, a feature that has contributed to its broad morphological variability and geographical adaptability. Morphologically

corn exhibits a greater diversity of phenotypes than perhaps any other grain crop and is extensively grown in temperate, subtropical and tropical regions of the world. Maize is rich in starch, proteins, oil and sucrose, due to which it has assumed significant industrial

importance. Maize and its main by-products starch, syrup, glucose, gluten and oil are used in diversified industries like alcohol production, textile, paper, pharmaceuticals, cosmetic industry, edible oil industry, poultry feed and many chemical industries.

Maize offers tremendous scope for the plant breeders for genetic improvement. Genetic variability among individuals in population offers effective selection. The magnitude of genetic variability present in population is of paramount importance for the success of any plant breeding program. 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 useful.

Among the various traits, grain yield in maize is the most important and complex quantitative traits controlled by numerous genes. Yield being a complex trait, is considerably influenced by different contributing yield components like ear height, plant height and test weight. Improvements in yield can be achieved by selection for grain yield, plant height and ear height. The additive genetic variance component is the most important component of genetic variability for all traits. The main objective of the present investigation was to estimate of genetic variance, heritability and genetic advance for some morphological and yield traits of fifteen maize genotypes and their utilization for future maize breeding programs.

RESOURCES AND METHODS

The study of genetic potential and genetic variability of various parameters in maize was conducted at Agricultural Research Station, Madhira during *Kharif* 2015. Eighteen maize genotypes *viz.*, 15 lines and 3 testers possessing a wide genetic background were obtained from Maize Research Station, Rajendranagar. The genotypes were evaluated in Randomized Block Design with three replications. Each plot consisted of four rows of five-meter length with row spacing and plant spacing of 75 and 25 cm, respectively. A basal fertilizer dose of 120 kg N and 50 kg P₂O₅ was applied in the form of DAP and urea. A full dose of P₂O₅ and half of N was applied at the time of sowing. The remaining half of the N was given when the plants reached knee-height. Thinning was carried out when plants were 10-15 cm tall. Standard cultural practices were adopted from sowing till harvest to raise a healthy crop.

Data collection and statistical analysis :

Data were recorded on days to 50% tasselling, days to 50% silking, days to maturity, plant height (cm), ear height (cm), ear length (cm), ear girth (cm), number of kernel rows, number of kernel per row, test weight (gm), seed yield per plant. All the data were subjected to statistical analysis to test the differences among maize genotypes for various traits. The mean data were subjected to statistical analysis for estimating genetic parameters, phenotypic and genotypic co-efficient using formula suggested by Burton and Devane (1953), heritability according to Falconer (1989) and genetic advance over mean was predicted by formula given by Johnson *et al.* (1955).

OBSERVATIONS AND ANALYSIS

The analysis of variance revealed highly significant variation among the genotypes for yield and yield related characters indicating existence of sufficient variability for the characters studied and considerable scope for improvement. The estimates of GCV, PCV, heritability (broad sense), genetic advance and genetic advance as per cent of mean for all the characters studied are given in Table 1. Moderate values for genotypic and phenotypic co-efficients of variation were recorded for plant height, ear length, kernels per row and test weight whereas moderately high values were observed for ear height and seed yield per plant indicating moderate to high amount of variability for these traits. These results are in agreement with the earlier findings of Nigussie and Saleh (2007), Kashiani, *et al.* (2008) and Reddy, *et al.* (2012).

Low estimates of genotypic and phenotypic co-efficients of variation were observed for days to 50% tasselling, days to 50% silking, days to maturity, ear girth and number of kernel rows for the genotypes under study. These results are in agreement with the earlier findings of Sumathi, *et al.* (2005), Akbar *et al.* (2008), Najeeb, *et al.* (2009) and Kashiani, *et al.* (2010). This indicated the narrow genetic base and hence, variability has to be generated in these characters either through introduction or hybridizing divergent genotypes to recover transgressive segregants or by mutation breeding.

Co-efficient of variation indicates only the extent of variability present in germplasm for different characters, but for the prediction of response to selection, heritability estimates are useful. Very high (>80%) broad sense heritability was observed for days to 50% tasselling, days

Table 1: Variability, heritability and genetic advance values for yield and yield components in eighteen maize genotypes

Character	Days to 50% tasselling	Days to 50% silking	Days to maturity	Plant height (cm)	Ear height (cm)	Ear length (cm)	Ear girth (cm)	Number of kernel rows	Number of kernels per row	Test weight (g)	Seed yield per plant (g)
GCV	5.086	4.89	2.377	15.791	20.614	15.313	8.893	9.124	15.269	11.2	23.74
PCV	5.688	5.407	3.1	18.054	23.258	18.188	10.413	10.58	16.888	12.162	25.506
h ² (broad sense)	0.8	0.818	0.588	0.765	0.786	0.709	0.729	0.744	0.818	0.848	0.866
Genetic advance (5%)	5.187	5.275	3.413	45.651	27.811	4.105	2.2	2.32	8.909	5.383	48.145
Genetic advance (1%)	6.647	6.76	4.374	58.504	35.641	5.261	2.819	2.974	11.418	6.898	61.701
Genetic advance as % of mean (5%)	9.368	9.109	3.753	28.453	37.636	26.558	15.646	16.208	28.441	21.248	45.52
Genetic advance as % of mean (1%)	12.006	11.673	4.81	36.464	48.233	34.036	20.052	20.772	36.448	27.23	58.336

to 50% silking, number of kernels per row, test weight and seed yield per plant whereas moderately high heritability estimates were observed for plant height, ear height, ear length, ear girth and number of kernel rows. Similar results were obtained by Nigussie and Saleh (2007), Kashiani, *et al.* (2008), Najeeb, *et al.* (2009) and Ali, *et al.* (2010).

Considering heritability in broad sense along with genetic advance may reveal the prevalence of specific components (additive or non additive) of genetic variance and thus, helps in judging the effectiveness of selection for the trait more accurately. The high estimates of heritability coupled with high values of genetic advance over mean were observed for seed yield per plant, number of kernels per row, test weight, days to 50% tasselling and days to 50% silking indicating additive gene action and effectiveness of selection for the improvement of these traits. Higher degree of genetic improvement for these can be achieved through selection using the existing germplasm stock in this study. Similar results were recorded by earlier workers viz., Sumathi, *et al.* (2005), Akbar *et al.* (2006), Kashiani, *et al.* (2008) and Kashiani, *et al.* (2010). Moderate heritability estimates with high genetic advance as per cent of mean was recorded for plant height, ear height, ear length, ear girth and number of kernel rows. This indicated the importance of additive gene effects for these traits and there can be better response to selection. Moderate to low heritability with moderate to low values for genetic advance as per cent of mean were recorded by days to maturity. These

findings elucidate prevalence of higher influence of environment on these traits and hence, selection would be ineffective. Similar findings were also obtained by Akbar, *et al.* (2008), Kashiani, *et al.* (2008), Ali, *et al.* (2010) and Reddy, *et al.* (2012).

Conclusions :

This study revealed that information about the extent of variation, estimates of heritability and expected genetic advance in respect of maize grain yield and yield contributing characters constitutes the basic requirement for a crop improvement programme. Broad sense heritability is useful for measuring the relative importance of additive portion of genetic variance that can be transmitted to the offspring. The preponderance of additive gene effects controlling a trait usually resulted to both high heritability and genetic advance, while those governed by non-additive gene actions could give high heritability with low genetic advance. However, in the present research, expected genetic advance values were based on broad sense heritability, which integrates additive portion of the total phenotypic variance. Effective selection for superior genotypes is possible considering seed yield per plant, test weight and number of kernels per row and could be used as target traits to improve maize grain yield.

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