



## Studies on Genetic Variability for Yield and Quality Traits in Maize (*Zea mays* L.)

Udaya Bhanu Kote, P V Rama Kumar, M Lal Ahamed, Y Ashoka Rani, V Srinivasa Rao and  
D Adilakshmi

Department of Genetic and Plant Breeding, Agricultural College, Bapatla 522101, Andhra Pradesh

### ABSTRACT

An experiment was conducted to study the genetic variability parameters using 45 hybrids, 15 inbred lines, 3 testers and three checks at three locations (Agricultural College Farm, Bapatla, Agricultural Research Station, Madhira and Regional Agricultural Research Station, Anakapalle) and in two seasons (*kharif* and *rabi* 2012-13) for yield and yield attributing traits. High PCV, moderate GCV and high heritability coupled with high genetic advance were observed for the characters *viz.*, ear height, kernels per row and NAR 30-60 DAS. High heritability coupled with high genetic advance were observed for the character yield per plant indicating that additive gene action was prominent and direct selection can be employed for improvement of this character.

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

Maize is the most widely distributed important cereal crop in the world after wheat and rice (Shanthi *et al.* 2011). Superior position of maize is due to very wide utilization. It is an excellent source of carbohydrates, protein and good quality oil. The information of genetic parameters of variability for different characters of economic significance is important for plant breeders before releasing any specific variety or hybrid in any crop. Hence, an attempt is made to study the genetic variability, heritability and genetic advance of various physiological, quality and economic traits in maize to elucidate information on nature and magnitude of genetic variation.

### MATERIAL AND METHODS

Fifteen inbreds and three testers were crossed in line x tester design at Agricultural College Farm, Bapatla during *rabi*, 2011-12. The forty-five crosses along with their parents and three checks (*viz.*, DHM-117, 30V92, 900M Gold) were evaluated in a randomized block design with three replications during *kharif* and *rabi*, 2012-13 at three locations *viz.*, Regional Agricultural Research Station, Anakapalle, Agricultural College Farm, Bapatla and Agricultural Research Station, Madhira representing different agro climatic regions of Andhra Pradesh. Each genotype was planted in three rows of 3 m length with a row to row and plant to plant spacing of 60 and 20 cm respectively.

The data was recorded on eighteen quantitative characters *viz.*, days to 50 % tasseling, days to 50% silking, days to maturity, plant height (cm), ear height (cm), ear length (cm), ear girth (cm), number of kernel rows per cob, number of kernels per row, protein per cent, starch per cent, oil per cent, relative growth rate at 30-60 DAS, relative growth rate at 60-90 DAS, net assimilation rate at 30-60 DAS, net assimilation rate at 60-90 DAS, test weight and seed yield per plant. Data was recorded on ten randomly selected plants in each replication for all the genotypes in all the six environments. Dry weight and leaf area at 30 days, 60 days and 90 days were recorded to derive relative growth rate and net assimilation rate. Two plants per replication were selected and area of total leaves of each plant was taken at 30 days interval from the date of sowing for three times during the crop growth period. The plants which were taken for leaf area were cut up to the base of the stem, oven dried at 80°C for about 72h to attain constant dry weight and thus the dry weight recorded was used for calculation of the physiological growth parameters each time at 30 days interval. Protein percentage, starch percentage and oil percentage were analysed by using NIR analyser. The mean of replications was used for statistical analysis. Genotypic and phenotypic coefficients of variation (Burton and Devane, 1953), heritability and genetic advance as

Table 1. Analysis of variance over environments (pooled) in maize.

Source	d f	Days to 50% tasseling	Days to silking	Days to 50% maturity	Plant height	Ear height	Ear length	Ear girth	No. of kernel rows per cob	No. of kernels/row
Replicates	2.00	1.72	4.78	0.03	Mean squares 99.35	217.46	0.21	0.21	0.19	0.07
Env	5.00	5297.41**	4768.90**	9354.75**	31155.41**	13523.32**	284.73**	153.63**	30.74**	382.67**
Genotypes	65.00	139.03**	130.71**	73.53**	8660.07**	3669.22**	62.58**	21.62**	26.90**	409.23**
Env *	325.00	11.14**	9.95**	17.62**	522.39**	262.43**	5.94**	2.28**	1.39**	18.11**
Error B	790.00	2.05	2.44	2.88	148.83	66.42	1.84	0.67	0.57	6.35
Total	1187.00	34.34	31.60	50.17	847.71	374.31	7.48	2.90	2.36	33.21

  

Source	d f	Protein %	Starch %	Oil %	RGR at 30-60	RGR 60-90	NAR 30-60	NAR 60-90	Test weight	Seed yield/plant
Replicates	2.00	0.08	0.46	0.09	Mean squares 23.12	10.90	0.01	0.01	6.75	206.71
Env	5.00	30.00**	17.92**	71.38**	15256.02**	1044.31**	4.07**	9.34**	87.94**	7521.85**
Genotypes	65.00	3.62**	10.24**	2.14**	748.48**	110.50**	1.06**	0.59**	119.03**	13540.78**
Env *	325.00	1.87**	5.58**	0.64**	196.89**	83.67**	0.24**	0.19**	4.25**	450.89**
Error B	790.00	0.16	0.31	0.10	23.46	10.66	0.02	0.02	1.89	106.35
Total	1187.00	0.94	2.37	0.66	174.81	40.47	0.16	0.14	9.32	967.76

\*\* Significant at 1 % level

\* Significant at 5 % level

Table 2. Estimates of genetic parameters for yield and quality characters over six environments (Pooled).

S. No.	Character	Mean	Range		PCV (%)	GCV (%)	Heritability (broad sense) (%)	Genetic advance as per cent of mean
			Minimum	Maximum				
1.	Days to 50% tasseling	54.87	49.83	61.94	6.36	4.98	61.23	8.03
2.	Days to 50% silking	57.38	52.39	64.17	5.94	4.61	60.30	7.38
3.	Days to maturity	91.17	87.50	95.72	3.62	2.11	33.81	2.52
4.	Plant height (cm)	168.93	112.88	208.22	15.95	12.79	64.31	21.13
5.	Ear height (cm)	80.66	45.46	120.77	22.22	17.40	61.28	28.06
6.	Ear length (cm)	15.90	10.82	18.97	15.85	11.44	52.07	17.00
7.	Ear girth (cm)	13.60	10.23	15.28	11.11	7.84	49.85	11.41
8.	Number of kernel rows per cob	13.88	9.96	16.26	10.84	8.67	64.03	14.29
9.	Number of kernels per row	30.82	18.88	38.63	18.36	15.28	69.31	26.21
10.	Protein %	11.05	9.89	11.80	8.22	3.67	19.93	3.38
11.	Starch %	68.83	66.99	70.56	2.22	0.99	20.00	0.91
12.	Oil %	4.51	3.09	5.13	13.40	7.16	28.58	7.89
13.	RGR at 30-60 DAS( $\text{mg g}^{-1}\text{d}^{-1}$ )	67.97	49.61	79.58	15.56	9.00	33.46	10.73
14.	RGR 60-90 DAS ( $\text{mg g}^{-1}\text{d}^{-1}$ )	21.17	15.31	26.64	28.53	9.85	11.93	7.01
15.	NAR 30-60 DAS( $\text{mg cm}^{-2}\text{d}^{-1}$ )	1.26	0.72	1.71	29.68	18.40	38.46	23.51
16.	NAR 60-90 DAS( $\text{mg cm}^{-2}\text{d}^{-1}$ )	0.87	0.50	1.20	36.17	19.65	29.51	21.99
17.	Test weight (g)	24.86	15.68	29.26	12.11	10.23	71.33	17.80
18.	Seed yield per plant (g)	109.58	50.23	162.99	28.11	24.84	78.08	45.21

PCV = Phenotypic coefficient of variation

per cent of mean (Johnson *et al.*, 1955) were estimated.

Relative growth rate is the rate of increase in the dry weight per unit dry weight already accumulated per unit time and was calculated by using the formula of Blackman (1919).

Net assimilation rate is the rate of dry weight increase per unit leaf area per unit time, which was calculated by the formula as adopted by Gregory (1926).

## RESULTS AND DISCUSSION

In the present investigation, pooled analysis of variance revealed significant differences among the genotypes for all the traits studied at three locations and two seasons indicating the existence of sufficient variation in the material studied (Table-1). The estimates of heritability alongwith expected genetic advance are more useful in predicting the resultant effects on selecting the best individuals. The estimates of genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability ( $h^2$ ) in broad sense and genetic advance as per cent of mean (GAM) were estimated for all the characters and are represented in Table 2.

The overall range of GCV was from 0.99 (starch percentage) to 24.84 (seed yield per plant), while overall range of PCV was from 2.22 (for starch) to 36.17 (net assimilation rate at 60-90 DAS). The highest estimates of GCV and PCV were observed for seed yield per plant (24.84 and 28.11) followed by net assimilation rate at 60-90 DAS, net assimilation rate at 30-60 DAS and ear height where as the characters *viz.*, plant height, ear length, number of kernels per row showed moderate GCV and PCV. However, lower values for GCV and PCV were expressed by the characters *viz.*, days to 50% tasseling, days to 50% silking, days to maturity, protein percent and starch percent.

The heritability estimates ranged from 11.93 (for relative growth rate at 30-60 DAS) to 78.08 (seed yield per plant). The estimates of genetic advance as per cent of mean were found vary from 0.91 (for starch percentage) to 45.21 (seed yield per plant). The heritability and genetic advance were low for the characters *viz.*, protein percentage, starch percentage, oil percentage and relative growth rate at 30-60 DAS. Similar result was earlier

reported by Prakash *et al.* (2006) in maize for these traits. While, days to maturity exhibited moderate heritability and low genetic advance indicating the predominant role of non additive gene action. Improvement of this character is complicated and it might be possible through heterosis breeding. Prakash *et al.* (2006), Singh and Singh (2011), Reddy *et al.* (2012) and Reddy *et al.* (2013) also reported similar results for these traits.

High heritability along with moderate genetic advance as per cent of mean was observed for the characters *viz.*, number of kernel rows per cob and test weight. High heritability coupled with high genetic advance was noticed for seed yield per plant, number of kernels per row, plant height and ear height indicating these traits are controlled by high additive gene effects (Johnson *et al.*, 1955) and thus there is better scope for improvement of these traits through direct selection. Similar results were earlier reported by Choudhary and Chaudhari (2002), Sumathi *et al.* (2005), Singhal *et al.* (2006), Hemavathy *et al.* (2008), Jawaharlal *et al.* (2011), Reddy *et al.* (2012), Bharathiveeramani *et al.* (2012) and Reddy *et al.* (2013).

## LITERATURE CITED

- Burton G W and Devane E W 1953** Estimating heritability in tall fescue (*Festuca arundinaceae*) from replicated clonal material. *Agronomy Journal*, 45: 478-481.
- Bharathiveeramani B, Prakash M and Seetharam A 2012** Variability studies of quantitative characters in maize (*Zea mays* L.). *Electronic Journal of Plant Breeding*, 3 (4): 995-997.
- Blackman V H 1919** Soil plant relationship. 2<sup>nd</sup> edition. *John Wiley and Sons Inc.*, New York Pp. 230-234.
- Choudhary A K and Chaudhari L B 2002** Genetic studies in some crosses of maize (*Zea mays* L.). *Journal of Research, BAU*. 14: 87-90.
- Gregory F G 1926** The effect of climatic conditions on growth of barley. *Annals of Botany*, 40: 1-26.
- Hemavathy A T, Balaji K, Ibrahim S M, Anand G and Sankar D 2008** Genetic variability and correlation studies in maize (*Zea mays* L.). *Agricultural Science Digest*, 28 (2): 112-114.

- Jawaharlal J, Reddy G. L and Kumar R S 2011** Genetic variability and character association studies in maize. *Agricultural Science Digest*, 31 (3): 173-177.
- Johnson H W, Robinson H F and Comstock R E 1955** Estimates of genetic and environmental variability in soybean. *Agronomy Journal*,. 47 (7): 314-318.
- Prakash O, Shanthi P, Satyanarayana E and Saikumar R 2006** Studies on genetic variability exploitation for quality traits and agronomic characters on quality protein maize (QPM) germplasm (*Zea mays* L.). *Annals of Agricultural Research*, 27 (2): 147-153.
- Reddy V R, Rao A S and Sudarshan M R 2012** Heritability and character association among grain yield and its components in maize (*Zea mays* L.). *Journal of Research, ANGRAU*. 40 (2): 45-49.
- Reddy V R, Jabeen F, Sudarshan M R and Rao A S 2013** Studies on genetic variability, heritability, correlation and path analysis in maize (*Zea mays* L.) over locations. *International Journal of Applied Biology and Pharmaceutical Technology*, 4 (1): 195-199.
- Shanthi P, Satyanarayana E, Suresh Babu G and Sai Kumar R 2011** Studies on genetic variability for phonological, yield and quality parameters in quality protein maize (QPM) (*Zea mays* L.). *Crop Research*, 41 (1, 2 & 3): 188-191.
- Singh S B and Singh A K 2011** Heterotic expression and combining ability analysis for yield and yield components over environments in yellow maize (*Zea mays* L.). *Progressive Agriculture*, 11 (2): 409-419.
- Singhal N, Verma S S, Baskheti D C and Kumar A 2006** Heritability, genetic advance, correlation and path-coefficient estimation in high quality protein maize (*Zea mays* L.). *Asian Journal of Biosciences*, 1 (2): 54-56.
- Sumathi P, Nirmalakumari A and Mohanraj K 2005** Genetic variability and traits interrelationship studies in industrially utilized oil rich CYMMIT lines of maize (*Zea mays* L.). *Madras Agricultural Journal*, 92 (10-12): 612 - 617.

(Received on 17.02.2014 and revised on 16.10.2014)