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Estimation of genetic parameters for quantitative traits in maize (*Zea mays* L.) Inbred Lines

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Abstract

Thirty maize inbred lines were evaluated during *Kharif*, 2020 at Sri Venkateswara Agricultural College, Tirupati, to determine the nature and magnitude of genetic variability for 16 yield and yield attributes. The analysis of variance revealed significant differences among inbred lines for all the characters under study indicating the presence of considerable amount of genetic variability in the material. High GCV and PCV were recorded for kernel yield plant⁻¹ followed by protein content, specific leaf area, ear length, plant height and number of kernels row⁻¹ indicating the ample amount of variation among the inbred lines and thus, simple selection would be effective for the further improvement of these characters. The traits viz., kernel yield plant⁻¹ followed by protein content, ear length, plant height, tassel length, harvest index, number of kernels row⁻¹ and specific leaf area exhibited high heritability coupled with high genetic advance as per cent of mean indicating the preponderance of additive gene action and selection may be effective for these traits.

Keywords: Genetic variability, heritability, genetic advance, inbred lines and maize

Introduction

Maize (*Zea mays* L.) is the third most important cereal crop after rice and wheat in the present world agriculture scenario contributing maximum (38%) to global food production compared to wheat (30%) and rice (20%). It is known as “Queen of Cereals” due to its several uses and expansive adaptability under diverse agroclimatic conditions. India ranks sixth in maize production with an area of 9.5 million hectares, production of 28.76 million tonnes and productivity of 3008.3 kg ha⁻¹ (FAOSTAT, 2020) [4]. Increasing the maize production and productivity is of paramount importance in order to cater the needs of ever growing population. Efforts have been intensified by the breeders in this direction to develop potential inbred lines for yield and yield attributes which could be utilized in hybridization programme for better exploitation of heterosis.

Understanding various estimates of genetic parameters is important for the better exploitation of heterosis available in the base material for seed yield and yield attributes. Knowledge on genetic variability parameters such as genotypic coefficient of variation, heritability and genetic advance is absolutely necessary for plant breeder to start a judicious breeding programme. Furthermore, heritability measures the relative amount of the heritable portion of variation, while the genetic advance helps to measure the amount of progress that could be expected with selection in a character. High heritable estimates together with high genetic advance are more valid for selection than heritability estimates alone (Johnson *et al.*, 1955) [7]. Estimation of genetic variability along with heritability and genetic advance gives an idea of the possible improvement of the character through selection. Hence, an attempt was made to estimate the genetic variability among 30 inbred lines with the aid of genetic parameters.

Material and Methods

The experimental material consisting 30 maize inbred lines was evaluated in Randomized Block Design (RBD) with three replications during *Kharif*, 2020 at Sri Venkateswara Agricultural College, Tirupati situated in Southern Agro-climatic Zone of Andhra Pradesh (altitude of 182.9 m above mean sea level, 13°N latitude and 79°E longitude). All recommended package of practices were followed to raise the healthy crop. Observations were recorded on randomly tagged five plants for SPAD chlorophyll meter reading, specific leaf area (cm² g⁻¹), plant height (cm), tassel length (cm), ear length (cm), ear girth (cm), number of kernels row⁻¹, number of kernel rows ear⁻¹, 100 kernel weight (g), kernel yield plant⁻¹ (g), harvest index (%) and protein content (%), while days to 50% tasseling, days to 50% silking,

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anthesis-silking interval and days to maturity were recorded on plot basis.

Statistical Analysis

Analysis of variance was worked out by the method suggested by Panse and Sukhatme (1961) ^[10] and the genotypic and phenotypic coefficient of variations were estimated by the method suggested by Burton (1952) ^[3] and heritability (broad sense) as the ratio of genotypic to phenotypic variance. The procedure of Johnson *et al.*, (1955) ^[7] was followed for calculating the expected genetic advance and genetic advance as per cent of mean. The data analysis was carried out with INDOSTAT software.

The GCV and PCV are classified as low (<10%), moderate (10-20%) and high (> 20%) as suggested by Sivasubramanian and Madhavamenon (1973). Heritability was estimated by the formula given by Johnson *et al.* (1955) ^[7] and they classified the heritability as low (below 30%), moderate (30-60%) and high (above 60%). The range of genetic advance as per cent of mean was classified as low (< 10%), moderate (10-20%) and high (> 20%) as suggested by Johnson *et al.* (1955) ^[7].

Results and Discussion

Analysis of variance

The present study was carried out among 30 inbred lines of maize to evaluate genetic parameters for 16 yield and yield attributes. The analysis of variance revealed significant differences among inbred lines for all the characters indicating the presence of considerable amount of genetic variability in the material (Table 1).

Genetic variability studies

Success of any hybrid development program largely depends on the selection of elite parental inbreds. Selection of superior inbreds will be possible only when adequate variability exists in the gene pool. Higher the amount of variation present for character in the breeding material, greater is the scope for its improvement through selection.

The mean performance of inbred lines for 16 characters with their range, genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV) and C.V (%) are presented in Table 2. The phenotypic coefficient of variation was of higher magnitude than genotypic coefficient of variation for all characters indicating the influence of environment on the expression of these characters.

The traits kernel yield plant⁻¹ (GCV: 37.84%; PCV: 38.53%), followed by protein content (GCV: 33.65%; PCV: 34.27%), specific leaf area (GCV: 22.33%; PCV: 25.96%), ear length (GCV: 20.70%; PCV: 21.85%), plant height (GCV: 20.51%; PCV: 22.62%) and number of kernels row⁻¹ (GCV: 20.50%; PCV: 23.20%) showed higher estimates of variability indicating the ample amount of variation among the inbred lines. Therefore, simple selection would be effective for the further improvement of these characters. Similar results were earlier reported by Ghosh *et al.* (2014) ^[5] and Maruti and Jhansi (2015) ^[9] for plant height, Lal *et al.* (2020) ^[8] for kernel yield plant⁻¹, Shazia *et al.* (2017) ^[13] for protein content and Bhadru *et al.* (2020) ^[2] for number of kernels row⁻¹. Moderate estimates of GCV and PCV were observed for harvest index, 100 kernel weight, tassel length, number of kernel rows ear⁻¹ and anthesis-silking interval. High to medium range of coefficient of variation provides great scope for the selection of desirable genotypes.

Heritability in broad sense (h²_b)

The knowledge of heritability enables the plant breeder to decide the course of selection procedure to be followed under a given situation. Broad sense heritability (h²_b) is an estimate of the total contribution of the genetic variance to the total phenotypic variance of trait. It measures the relative amount of heritable portion of total variability and provides information on the extent to which a particular morphogenetic trait can be transmitted to successive generation. Heritability and genetic advance estimates are presented in Table 3.

In the present study, high heritability was recorded for all the traits *viz.*, kernel yield plant⁻¹ (96.45%), protein content (96.41%), ear length (89.74%), days to maturity (84.33%), plant height (82.23%), tassel length (82.07%), days to 50% silking (79.17%), harvest index (79.15%), days to 50% tasseling (78.27%), number of kernels row⁻¹ (78.05%), specific leaf area (73.98%), SPAD chlorophyll meter reading (71.54%), ear girth (67.94%) and number of kernel rows ear⁻¹ (65.78%) except for 100 kernel weight (56.61%) and anthesis-silking interval (39.67%) indicating that these characters were less influenced by environment. Therefore, selection would be effective for improving these traits. These results corroborates the findings of Kharel *et al.* (2017) ^[6] for days to 50% tasseling, days to 50% silking, plant height, SPAD chlorophyll meter reading and number of kernels row⁻¹, Prakash *et al.* (2019) ^[11] for grain yield, tassel length, number of rows cob⁻¹, days to 50% silking, and plant height and Supraja *et al.* (2019) ^[14] for days to anthesis, days to silking, plant height, ear length and number of kernel rows ear⁻¹.

Genetic advance as per cent of mean (GAM)

Genetic advance as per cent of mean (GAM) is a more reliable index for understanding the effectiveness of selection in improving the traits because its estimate is derived by involvement of heritability, phenotypic standard deviation and intensity of selection. Thus, heritability coupled genetic advance as per cent of mean provide clear picture regarding the effectiveness of selection for improving the plant characters (Singh *et al.*, 2018) ^[12].

High genetic advance as per cent of mean was exhibited by kernel yield plant⁻¹ (76.55%), protein content (68.07%), ear length (40.41%), specific leaf area (39.56%), plant height (38.32%) number of kernels row⁻¹ (37.31%), harvest index (28.04%), tassel length (24.13%) and 100 kernel weight (20.47%), while number of kernel rows ear⁻¹ (19.23%), SPAD chlorophyll meter reading (15.04%), anthesis-silking interval (14.72%) and ear girth (14.58%) registered moderate genetic advance as per cent of mean (Table 3).

High heritability coupled with high genetic advance as per cent of mean was observed for kernel yield plant⁻¹ (h²_b = 96.45%, GAM = 76.55%), protein content (h²_b = 96.41%, GAM = 68.07%), ear length (h²_b = 89.74%, GAM = 40.41%), plant height (h²_b = 82.23%, GAM = 38.32%), tassel length (h²_b = 82.07%, GAM = 24.13%), harvest index (h²_b = 79.15%, GAM = 28.04%), number of kernels row⁻¹ (h²_b = 78.05%, GAM = 37.31%) and specific leaf area (h²_b = 73.98%, GAM = 39.56%) indicating the preponderance of additive gene action. Therefore, these characters could be considered as favourable attributes for improvement through selection. These results are in conformation with Bhadru *et al.* (2020) ^[2], Lal *et al.* (2020) ^[8] and Wedwessen and Zeleke (2020) ^[15] for the most of the yield attributing traits.

Days to maturity (h²_b = 84.33%, GAM = 8.97%), days to 50% silking (h²_b = 79.17%, GAM = 8.48%) and days to 50%

tasseling ($h^2_b = 78.27\%$, $GAM = 8.89\%$) exhibited high heritability coupled with low genetic advance as per cent of mean, it indicates non-additive gene action. The high heritability is being exhibited due to favourable influence of environment rather than genotype and selection for such traits

may not be rewarding. Similar results were earlier reported by Ghosh *et al.* (2014) [5] for days to 50% tasseling and days to 50% silking and Maruti and Jhansi (2015) [9] for days to maturity.

Table 1: Analysis of variance for 16 characters in 30 inbred lines of maize

S. No.	Characters	Mean sum of squares		
		Replications (df=2)	Treatments (df=29)	Error (df=58)
1	Days to 50% tasseling	3.03	23.19**	1.96
2	Days to 50% silking	4.87	23.43**	1.88
3	Anthesis-silking interval	0.47	0.66**	0.22
4	Days to maturity	4.23	64.67**	3.77
5	SPAD chlorophyll meter reading (SCMR)	10.81	48.94**	5.73
6	Specific leaf area ($\text{cm}^2 \text{g}^{-1}$)	2288.36	6929.20**	727.29
7	Plant height (cm)	95.69	3639.45**	244.48
8	Tassel length (cm)	1.40	54.98**	3.73
9	Ear length (cm)	0.26	22.55**	0.82
10	Ear girth (cm)	1.07	3.58**	0.48
11	No. of kernels row ⁻¹	14.62	65.53**	5.61
12	No. of kernel rows ear ⁻¹	2.83	6.46**	0.95
13	100 kernel weight (g)	15.79	37.77**	7.68
14	Kernel yield plant ⁻¹ (g)	0.75	1496.17**	18.12
15	Harvest index (%)	18.47	132.93**	10.73
16	Protein content (%)	0.3	9.04**	0.11

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

Table 2: Mean, range, genotypic and phenotypic coefficient of variation for 16 characters in 30 inbred lines of maize

S. No.	Character	Grand Mean + S.E (m)	Range		Variance		Coefficient of Variation		C.V. (%)
			Min.	Max.	Genotypic	Phenotypic	GCV	PCV	
1	Days to 50% tasseling	54.50 ± 0.79	48.00	60.33	4.88	5.51	4.88	5.51	2.57
2	Days to 50% silking	57.89 ± 0.78	51.00	64.33	4.62	5.20	4.62	5.20	2.37
3	Anthesis-silking interval	3.39 ± 0.26	2.33	4.33	11.34	18.01	11.34	18.01	13.99
4	Days to maturity	94.97 ± 1.10	85.33	103.33	4.74	5.16	4.74	5.16	2.04
5	SPAD chlorophyll meter reading	43.95 ± 1.35	35.65	54.20	8.63	10.21	8.63	10.21	5.44
6	Specific leaf area ($\text{cm}^2 \text{g}^{-1}$)	203.59 ± 15.30	118.05	313.43	22.33	25.96	22.33	25.96	13.24
7	Plant height (cm)	163.98 ± 8.87	107.60	246.00	20.51	22.62	20.51	22.62	9.53
8	Tassel length (cm)	31.96 ± 1.09	25.85	41.92	12.93	14.27	12.93	14.27	6.04
9	Ear length (cm)	13.00 ± 0.51	9.33	22.10	20.70	21.85	20.70	21.85	7.01
10	Ear girth (cm)	11.83 ± 0.39	9.83	13.87	8.58	10.42	8.58	10.42	5.90
11	No. of kernels row ⁻¹	21.80 ± 1.34	15.13	34.47	20.50	23.20	20.50	23.20	10.87
12	No. of kernel rows ear ⁻¹	11.77 ± 0.55	9.47	15.73	11.51	14.19	11.51	14.19	8.30
13	100 kernel weight (g)	23.98 ± 1.57	17.70	31.75	13.20	17.55	13.20	17.55	11.56
14	Kernel yield plant ⁻¹ (g)	58.66 ± 2.41	34.15	137.53	37.84	38.53	37.84	38.53	7.25
15	Harvest index (%)	41.71 ± 1.85	30.67	56.00	15.30	17.19	15.30	17.19	7.85
16	Protein content (%)	5.13 ± 0.18	2.76	9.36	33.65	34.27	4.88	5.51	6.99

Table 3: Genetic parameters for 16 characters in 30 inbred lines of maize

S. No.	Character	Heritability in broad sense (h^2_b) (%)	Genetic Advance (GA)	Genetic advance as per cent of mean (%)
1	Days to 50% tasseling	78.27	4.84	8.89
2	Days to 50% silking	79.17	4.91	8.48
3	Anthesis-silking interval	39.67	0.49	14.72
4	Days to maturity	84.33	8.52	8.97
5	SPAD chlorophyll meter reading	71.54	6.61	15.04
6	Specific leaf area ($\text{cm}^2 \text{g}^{-1}$)	73.98	80.55	39.56
7	Plant height (cm)	82.23	62.84	38.32
8	Tassel length (cm)	82.07	7.71	24.13
9	Ear length (cm)	89.74	5.25	40.41
10	Ear girth (cm)	67.94	1.72	14.58
11	No. of kernels row ⁻¹	78.05	8.13	37.31
12	No. of kernel rows ear ⁻¹	65.78	2.26	19.23
13	100 kernel weight (g)	56.61	4.90	20.47
14	Kernel yield plant ⁻¹ (g)	96.45	44.90	76.55
15	Harvest index (%)	79.15	11.69	28.04
16	Protein content (%)	96.41	3.48	68.07

Conclusion

The high estimates of GCV and PCV were observed for kernel yield plant⁻¹ followed by protein content, specific leaf area, ear length, plant height and number of kernels row⁻¹ and therefore, selection would be effective for these traits. Traits viz., kernel yield plant⁻¹, protein content, ear length, plant height, tassel length, harvest index, number of kernels row⁻¹ and specific leaf area showed high heritability coupled with high genetic advance indicating the predominance of additive gene action. Hence, direct selection would be effective for further improvement of these traits.

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