



E-ISSN: 2278-4136
P-ISSN: 2349-8234
www.phytojournal.com
JPP 2020; 9(6): 816-819
Received: 05-08-2020
Accepted: 15-09-2020

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Genetic analysis for grain yield and its component traits in maize (*Zea mays* L.) in bred lines

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Abstract

An investigation was carried out to assess the genetic potentiality present among 422 maize inbred lines. Analysis of variance revealed, mean sum of squares for different sources of variation differed significantly for all traits indicating the existence of ample variability among the inbreds. Characters, fodder yield /plant at harvest (6145.00; 4279.36), grain yield / plant (2542.08; 1378.94) and number of leaves (1088.99; 1088.32) recorded higher values of phenotypic and genotypic variance, respectively, indicating the presence of sufficient inherent genetic variability for these characters. GCV was less than its corresponding estimates of PCV for all traits indicated the role of environment in the expression of these traits. Characters, anthesis silking interval (82.41; 65.58), number of leaves (236.66; 236.60), number of cobs / plant (36.01; 23.07), grain yield / plant (47.45; 34.95) and fodder yield / plant at harvest (40.90; 34.13) recorded highest estimates of PCV and GCV, respectively. Wide difference between PCV and GCV estimates were observed for all the traits. Higher estimates of heritability in broad sense were reported for anthesis (0.87), silking (0.89), cob length (0.79), cob girth (0.87), test weight (0.71), fodder yield / plant at harvest (0.70), anthesis silking interval (0.63), number of leaves (1.00), and number of kernel rows (0.63). Highest value of genetic advance as *per cent* of mean was recorded for number of leaves (487.22) followed by anthesis silking interval (107.51). High heritability coupled with low genetic advance was reported for silking, anthesis, anthesis silking interval, cob length, cob girth, number of kernel rows and test weight indicating the role of non additive gene action. High heritability coupled with high genetic advance was reported for number of leaves, plant height and fodder yield / plant at harvest indicating the role of additive gene action.

Keywords: Genetic, grain, component, maize, *Zea mays* L.

Introduction

Maize is one of the most important cereal crops in the world. Maize is known as “queen of cereals” due to its highest potential of per day carbohydrate production, genetic yield and productivity among the cereals. It serves as a source of basic raw material for a number of industries *viz.*, starch, protein, oil, alcoholic beverages, food, sweeteners, cosmetics and bio-fuels (Khan and Dubey, 2015) [10]. Globally, maize is cultivated on nearly 183.24 m ha with 1036.07 m. tonnes of production and 5.65 tonnes of productivity. In India, maize is grown both in *kharif* and *rabi* seasons with a share of 85 per cent and 15 per cent, respectively (Anon, 2017) [1] in an area of 9.22 m. hectare with the productivity of 3.12 tonnes ha⁻¹ (USDA, 2018). However, in India, maize production and productivity is still remains far below the world averages. Lower production and productivity of maize are attributed to limited availability and use of high yielding, disease and insect resistant varieties, moisture stress, high incidence of pests and diseases, use of traditional and lack of knowledge on improved cultural practices, poor soil fertility and changing rainfall patterns, etc. Genetic improvement of maize provides an option to address some of these constraints through exploitation of the genetic variability present in maize germplasm.

Information on the nature and magnitude of variability and heritability in a population is one of the prerequisites for successful breeding program in selecting genotypes with desirable characters (Dudly and Moll, 1969) [5]. Genetic improvement in traits of economic importance along with maintaining sufficient amount of variability is always the desired objective in maize breeding programs. Grain yield in maize is a complex quantitative trait that depends on a number of factors. It's highly influenced by environmental conditions; has complex mode of inheritance and low heritability. Because of this, during selection for grain yield, attention is given first to determine mean values, components of variance and the heritability of yield related traits in order to establish the best selection criteria (Falconer and Mackay, 1996) [6]. In order to improve the genetic diversity of local germplasm, it is important to know the extent of already existing genetic variations in the material.

The productivity and quality of maize are assured through initially evaluating, identifying and properly selecting of promising parental lines from available maize inbred lines. With this premise, the present investigation on was undertaken to analyze the variance, genetic variability, heritability and genetic gain among 422 inbreds of maize.

Materials and Methods

The study was undertaken in summer, 2012 at K-block, Department of Genetics and Plant Breeding, UAS, GKVK, Bengaluru. Geographically, the study location is situated at 13° 05' N latitude and 77° 34' E longitude and at an altitude of 924 meters above mean sea level. The average annual rainfall is about 915 mm. The experimental material consisted of 422 inbred/breeding lines collected from AICRP on Maize, ZARS, VC Farm, Mandya, AICRP on Maize, ARS, Arabhavi, College of Agriculture, Bheemaranagudi and CYMMIT, c/o. ICRISAT Campus, Hyderabad and three checks viz., MAI 105, NAI 137 and SKV 50.

The inbred/breeding lines were evaluated in augmented block design (Federrer, 1956) [7]. The design consisted of 15 blocks containing 32 genotypes in each with 29 test inbred / breeding lines and three check entries. In each block the checks were allotted randomly. Each inbred line was sown in a single row of 3 m length with row to row and plant to plant spacing of

0.60 m and 0.30 m, respectively. All the recommended packages of practices were followed to raise a healthy crop. Data on the 12 quantitative traits was collected from five randomly selected competitive plants on various yield and yield contributing traits. The statistical analysis was carried out using WINDOSTAT software developed by Indostat services, Hyderabad installed at Department of Genetics and Plant Breeding, UAS, GKVK, Bengaluru.

Results

Analysis of variance

The Analysis of variance (Table 1) revealed, mean sum of squares for different sources of variation differed significantly for all traits studied. Mean sum of squares for blocks (ignoring treatments) (un adj), entries (ignoring blocks) and varieties was significant for all the traits. Treatments (eliminating blocks) and checks + var. vs. var. differed significantly for all the traits except cobs / plant. Mean sum of squares for checks was significant for all the traits except plant height, cobs / plant and test weight. Effect of block (eliminating check + var.) were non-significant for all the traits except number of leaves and plant height. Checks vs. varieties effect was significant for all the traits except plant height, cob length and kernel rows.

Table 1: Analysis of variance for grain yield and its component traits in maize inbreds

Character Source of variation	df	Anthesis (Days)	Silking (Days)	Anthesis silking interval (Days)	Number of Leaves	Plant height (cms)	Cobs/Plant	Cob length (cms)	Cob girth (cms)	Kernel rows	Kernels / row	Grain yield / plant (gram)	Test weight (gram)	Shellin g%	Fodder yield /plant (gram) at harvest
Blocks (ignoring Treatments) (un adj)	14	80.61**	75.44*	5.70**	1081.04**	6062.70**	1.24**	36.97**	10.86**	9.49**	219.23**	11788.23**	81.93**	94.98**	43412.42**
Treatments (eliminating Blocks)	424	24.68**	28.80*	2.4**	1125.60**	720.09*	0.22	8.31**	2.79**	3.79**	52.92**	2295.22*	23.07**	64.52**	5307.47**
Checks	2	120.75*	125.61**	6.21**	13.39**	74.94	0.29	32.91**	55.66**	162.31**	861.53**	8464.29*	5.76	442.18*	42071.67**
Checks + Var. Vs. Var.	422	24.23**	28.34*	2.38**	1130.88**	723.15*	0.22	8.2**	2.54**	3.04**	49.09**	2265.98*	23.16**	62.73**	5133.23**
Block (eliminating Check + Var.)	14	1.24	3.15	0.91	1.90**	459.00*	0.09	1.27	0.17	0.90	18.83	186.76	10.41	21.34	1488.50
Entries (ignoring Blocks)	24	27.30**	31.18*	2.56**	1161.24**	905.13*	0.26*	9.5**	3.14**	4.07**	59.54*	2678.29*	25.44**	66.95**	6691.75**
Varieties	421	26.86**	30.57**	2.49**	1169.12**	911.22*	0.25*	9.40**	2.87**	3.32**	55.58**	2643.62*	25.28**	64.92**	6460.10**
Checks Vs. Varieties	1	26.67**	100.90**	25.49**	136.87*	3.31	2.0**	3.22	13.65**	2.81	124.86*	5703.54*	128.59**	172.16*	33453.46**
Error	28	3.37	3.08	0.87	0.67	195.66	0.15	1.88	0.33	1.17	22.95	1163.13	6.92	27.57	1865.63

df- Degrees of freedom * Significant at P=0.05 ** Significant at P=0.01

Estimation genetic variability, heritability and genetic advance

Fodder yield /plant at harvest (6145.00; 4279.36) followed by grain yield / plant (2542.08; 1378.94) and number of leaves (1088.99; 1088.32) recorded higher values of phenotypic and genotypic variance, respectively. PCV and GCV estimates were classified as low (0-10%), moderate (10.1-20%) and high (> 20%) (Sivasubramanian and Mahadevmenon, 1973) [18]. In the present investigation silking (8.45; 7.98), anthesis (8.17; 7.60) and shelling % (9.70; 7.44) recorded lower estimates of PCV and GCV, respectively. Moderate estimates were recorded for plant height (16.92; 14.88), cob length (17.35; 15.40), cob girth (11.93; 11.16), kernel rows (12.70; 10.10) and test weight (14.89; 17.65). The characters, anthesis silking interval (82.41; 65.58), number of leaves (236.66;

236.60), cobs / plant (36.01; 23.07), grain yield / plant (47.45; 34.95) and fodder yield /plant at harvest (40.90; 34.13) recorded highest estimates of PCV and GCV, respectively. However, kernels / row recorded high PCV (24.26) but moderate GCV (18.31) values. Difference between PCV and GCV were highest for anthesis silking interval (16.83) followed by cobs / plant (12.94) and grain yield / plant (12.5). Heritability in broad sense was classified as suggested by Robinson *et al.* (1949) [15], the traits viz., cobs / plant (0.40), kernels / row (0.57), grain yield / plant (0.54) and shelling % (0.56) recorded moderate values of heritability. Higher estimates of heritability in broad sense were reported for anthesis (0.87), silking (0.89), number of leaves (1.0), cob length (0.79), cob girth (0.87), test weight (0.71), fodder yield /plant at harvest (0.70), anthesis silking interval (0.63) and

kernel rows (0.63). However, none of the characters studied recorded lower estimates of heritability in broad sense.

The genetic advance as per cent of mean was categorized as suggested by Johnson *et al.* (1955) [8]. Anthesis (14.58), silking (15.54), kernel rows (16.54) and shelling % (11.45) recorded moderate values of genetic advance as per cent of mean. Highest value of genetic advance as per cent of mean was recorded for number of leaves (487.22) followed by anthesis silking interval (107.51). However, none of the character recorded lower estimates of genetic advance as per cent of mean.

Discussion

Analysis of variance (ANOVA) helps in detecting the genetic variability among the inbreds or breeding lines. It is evident from the analysis of variance that means sum of squares for varieties differed significantly for all the characters indicating the existence of ample variability among the inbreds for traits of economic importance. Earlier workers such as Saleem *et al.* (2011) [16], Kashiani *et al.* (2014) [9], Praveen Kumar *et al.* (2014) [13] and Mushtaq *et al.* (2016) [12] have reported similar results in maize.

Presence of genetic variability in the breeding materials is essential for a successful plant breeding programme. Genetic variability, heritability and genetic advance, estimates of means, range, genotypic and phenotypic variances and their coefficients of variation, heritability in broad sense and genetic advance as percentage of means among 422 maize inbreds / breeding lines are presented in Table 2. Higher estimates of genotypic and phenotypic variability values recorded for fodder yield / plant at harvest, grain yield / plant, number of leaves and plant height indicated the presence of sufficient inherent genetic variability for these characters, over which selection can be more effective. Similarly, Rather *et al.*, (2003) [14] reported high estimates of genotypic and phenotypic variability for grain yield per plant and Anshuman vashistha *et al.*, (2013) [3] for grain yield per plant and plant height in maize.

The genotypic coefficient of variation (GCV) was less than its corresponding estimates of phenotypic coefficient of variation (PCV) for all traits which indicated significant role of environment in the expression of these traits. Relatively higher estimates of GCV for grain and fodder yield per plant, number of leaves and anthesis silking interval suggested that the selection can be effective for these traits. In the present study, lower PCV and GCV were recorded for anthesis, silking and shelling %. Previously, Sesay *et al.*, (2016) [17] reported low PCV and GCV for anthesis and silking. Moderate estimates of PCV and GCV were estimated for test weight, cob length, cob girth, kernel rows, kernels / row and plant height. Whereas, higher estimates were observed for fodder yield / plant at harvest, number of leaves, cobs / plant, kernels / row, grain yield / plant and anthesis silking interval. Earlier, Sravanti *et al.*, (2017) [19] reported moderate phenotypic and genotypic coefficients variations for plant height and ear length in their study.

Wide difference between PCV and GCV estimates were observed for all the traits revealing greater role of environment interaction with the genetic factors in the expression of the traits, whereas, anthesis (0.57), silking (0.47) and number of leaves (0.06) exhibited lower differences indicating more influence of genetic factors in determining variability. Similarly, Mruthunjaya and Vishwe Gowda (2015) [11] and Sravanti *et al.*, (2017) [19] reported

lower differences between PCV and GCV for silking, while wide difference for grain yield / plant, kernels / row, kernel rows, plant height, cob length, shelling %, test weight and cob girth. The estimates of genotypic coefficient of variation (GCV) reflect the total amount of genotypic variability which is transmitted from parents to the progeny is reflected by heritability. In the present investigation the heritability estimates were found to be high for fodder yield / plant at harvest, test weight, kernel rows, cob girth, cob length, plant height, number of leaves, silking and anthesis and moderate for shelling %, grain yield / plant and kernels / row. Whereas, low estimates of heritability was recorded for cobs / plant (40%). High value of heritability in broad sense indicates that the character is least influenced by environmental effects. Similarly, Anshuman vashistha *et al.*, (2013) [3] reported high heritability estimates for test weight, plant height, silking and anthesis and moderate heritability estimates were reported for kernels / row by Sravanti *et al.*, (2017) [19].

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 most useful. Character exhibiting high heritability may not necessarily give high genetic advance. Johanson *et al.*, (1955) showed high heritability should be accompanied by high genetic advance to arrive at more reliable conclusion. In the present investigation high heritability estimates were recorded for fodder yield / plant at harvest, cob length, cob girth, kernel rows, test weight, anthesis, silking, anthesis silking interval, number of leaves and plant height, indicated that these characters are less influenced by environment whereas, moderate heritability was exhibited by shelling %, grain yield / plant, kernel / row and cobs / plant and none of the characters reported low heritability. The lower heritability indicated low genetic potential and high effects of environment in determining these traits. Earlier, Praveen Kumar *et al.*, (2014) [13] reported high heritability for plant height, cob girth, kernel rows, anthesis and silking and Sravanti *et al.*, (2017) [19] also reported high heritability for silking, anthesis, grain yield per plant and ear girth. Characters *viz.*, number of leaves, plant height, grain yield / plant, fodder yield / plant at harvest exhibited high genetic advance. Whereas, silking, anthesis silking interval, shelling %, cobs / plant, cob length, cob girth, kernel rows, kernels / row, test weight and anthesis recorded low genetic advance. Medium heritability coupled with low genetic advance was exhibited by kernels / row and cobs / plant. High heritability coupled with low genetic advance was reported for silking, anthesis, anthesis silking interval, cob length, cob girth, kernel rows and test weight which is an indication of involvement of non-additive gene action in controlling these characters. Previously, Begum *et al.*, (2016) [4] reported high heritability and low genetic advance for anthesis, silking and ear girth. In the present investigation medium heritability coupled with high genetic advance was reported for grain yield / plant. High heritability coupled with high genetic advance was reported for number of leaves, plant height and fodder yield / plant at harvest, which indicated that these characters are governed by additive gene action and phenotypic selection for these traits is effective. Earlier, Praveen Kumar *et al.*, (2014) [13] reported high heritability and high genetic advance for plant height and Sesay *et al.*, (2016) [17], reported low genetic advance for silking, anthesis, cob girth and high genetic advance for grain yield / plant.

Table 2: Estimates of parameters and descriptive statistics specifying variability for grain yield and its component traits in maize inbreds

Characters	Range		Mean	Std. Error	Std. Dev	Variance		Coefficient of variance		h ² (heritability (Broad sense))	Genetic Advancement	Gen. Adv. as % of Mean
	Min	Max				Phenotypic	Genotypic	Phenotypic	Genotypic			
Anthesis (Days)	51.9	83.25	61.57	0.25	5.22	25.25	21.88	8.17	7.60	0.87	8.97	14.58
Silking (Days)	52.9	84.75	63.54	0.27	5.61	28.68	25.60	8.45	7.98	0.89	9.84	15.54
Anthesis silking interval (Days)	-3.25	11.83	1.95	0.08	1.65	2.37	1.50	82.41	65.58	0.63	2.01	107.51
Number of leaves	6.3	17	13.77	1.66	34.14	1088.99	1088.32	236.66	236.60	1.00	67.93	487.22
Plant height (cms)	70.00	291.67	173.50	1.61	33.12	862.14	666.47	16.92	14.88	0.77	46.75	26.94
Cobs / plant	1.00	2.00	1.36	0.02	0.53	0.25	0.10	36.01	23.07	0.40	0.42	30.38
Cob length (cms)	9.33	27.17	17.15	0.15	3.21	8.88	7.00	17.35	15.40	0.79	4.83	28.18
Cob girth (cms)	8.33	17.67	13.81	0.08	1.71	2.69	2.35	11.93	11.16	0.87	2.96	21.51
Kernel rows	8.67	20.00	14.00	0.09	1.85	3.17	2.00	12.70	10.10	0.63	2.32	16.54
Kernels / row	8.67	46.33	29.93	0.4	8.07	53.33	30.39	24.26	18.31	0.57	8.57	28.47
Grain yield /plant (gram)	14.00	242.00	105.12	2.51	51.77	2542.08	1378.94	47.45	34.95	0.54	56.34	53.02
Test weight (gram)	14.00	42.00	27.97	0.27	5.51	24.02	17.10	17.65	14.89	0.71	7.18	25.88
Shelling %	41.67	95.56	79.21	0.4	8.72	62.35	34.78	9.70	7.44	0.56	9.07	11.45
Fodder yield /plant (gram) at Harvest	50.00	550.00	188.92	4.21	86.94	6145.00	4279.36	40.90	34.13	0.70	112.45	58.67

Genetic advancement and genetic advance as % of mean at 5% level

Conclusion

Presence of genetic variation in the base genetic material is the key for success of any breeding program. The greater the genetic variability, the higher would be the heritability and hence the better the chances of success to be achieved through selection. There was considerable variability present in the genetic materials studied. As such these results will be useful for choosing inbred / breeding lines to be used in developing new improved maize populations or hybrids. In the light of results obtained in present study, it can be suggested that traits such as cob length, cob girth, kernel rows, test weight, anthesis, silking, anthesis silking interval, test weight and number of leaves should be used as target traits to improve maize grain yield.

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