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RESEARCH PAPER

Genetic variability and trait association studies in maize (*Zea mays* L.)

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Abstract: Genetic variability study on 12 quantitative traits in Maize was carried at AICRP on maize, UAS, Dharwad during *Kharif*, 2019. The experiment consisted of 64 single cross maize hybrids obtained by crossing 32 lines with 2 testers in line x tester mating design. These hybrids along with checks were raised in alpha-lattice design in three replications. The phenotypic co-efficient of variation (PCV) was higher than genotypic co-efficient of variation (GCV) for all the traits. Highest PCV was observed for Plant height (20.88 %) and grain yield (24.52 %) and medium for ear height (12.88%), number of kernels per row (12.98 %), cob length (13.58 %) and hundred grain weight (12.42%). High heritability along with high genetic advance was observed for grain yield, 100 grain weight and plant height. The grain yield/ ha had highly significant and positive correlations both at genotypic and phenotypic levels with ear height (r_g=0.66, r_p=0.55), plant height (r_g=0.50,r_p=0.44), cob length (r_g=0.45,r_p=0.34), number of kernels per row(r_g=0.37, r_p=0.28), 100-grain weight (r_g=0.36, r_p=0.31). The highest positive and direct effect was found for days to 50% silking (3.16) followed by ear height (1.10) on grain yield.

Key words: Correlation, Heritability, Maize, Variability

Introduction

Maize (*Zea mays* L.) is the third important cereal crop globally after wheat and rice. Maize being a C_4 plant is physiologically more efficient and has higher grain yield potential and wider adaptation as evident from the wide range of agro climatic zones where it is cultivated. It meets the requirements of food, feed, fodder and fuel and also serves as a source of basic raw material for a number of industrial products *viz.,* protein, starch, oil, food sweeteners and bio-fuel hence it is known as industry oriented crop. Maize has contributed about Rs.308 billion to the Indian economy during the financial year 2018 (www.statista.com). Because of these reasons, the demand for maize is on the increasing trend year after year and the projected demand of maize in India by 2022 is 45 million m.tn (www.ficci.in/2018).To address this growing demand of maize production, the main goal of all maize breeding programes is to develop new inbreds and hybrids that will outperform the existing through exploitation of heterosis for grain yield. However, grain yield is a complex quantitative trait that depends on plant inherent genetic potential complimented with different yield contributing characters and their interaction with environmental conditions. For a systematic improvement of such a complex trait genetic variability is a prerequisite which can be studied through phenotypic and genotypic coefficient of variation. Similalry, correlation analysis of different characters provides useful information to identify desirable traits that may contribute in improvement of grain yield. Path analysis on another hand is an efficient biometrical tool which indicates the direct contribution of characters and its influence through other traits in influencing the yield (Aman, 2021). The present study was aimed at understanding the genetic parameters which determine the relationship between maize yield and its attributing traits.

Material and methods

Thirty-two germplasm lines were crossed with two diverse testers (CM-111 and CM-202) in Line x Tester method during *Rabi*, 2018. The 64 single cross hybrids were evaluated along with checks in a replicated yield trial during *Kharif,* 2019 at AICRP-Maize, MARS, UAS, Dharwad. Each hybrid was raised in two rows of four-meter length with a spacing of 60 × 20 cm in Alpha lattice design with three replications. Recommended cultural practices were adopted to raise a healthy crop.

Observations for the twelve quantitative traits i.e., days to 50 per cent taselling, days to 50 percent silking, days to 75 per cent dry husk, plant height (cm), ear height (cm), cob length (cm), cob girth (cm), number of kernel rows per cob, number of kernels per row, 100-grain weight (g), shelling percentage (%) and grain yield (q/ha) were recorded.

The phenotypic (r_p) and genotypic (r_g) correlation coefficients were calculated by the method suggested by Johnson *et al.* (1955). To establish a cause and effect relationship it is necessary to first partition the genotypic and phenotypic correlation coefficient into direct and indirect effects by path analysis as suggested by Dewey and Lu (1959). The genotypic and phenotypic variances, Heritability in broad sense (H^2_{BS}) and Genetic advance were estimated according to the formula given by Johnson *et al.* (1955). Genotypic and phenotypic co-efficient of variations were estimated according to Burton (1952) and Singh and Choudhury (1985). The analysis was done using Indostat statistical software.

Results and discussion

In the present investigation the analysis of variance for different quantitative traits revealed significant differences among the genotypes for all the yield and yield contributing traits (Table 1) suggesting the presence of genotypic differences among the genotypes under evaluation. Rahman *et al.* (2017) was also of the similar opinion.

Table 1. Analysis of variance for twelve quantitative traits in maize

Source of variation	Replication	Treatments	Blocks within Replication	Error
Degrees of freedom (df)	2	69	27	111
Days to 50 % tasseling	0.871	13.53**	3.54*	0.773
Days to 50 % silking	1.55	8.64**	2.09*	0.73
Days to 75 % dry husk	2.80	20.35**	3.62	1.62
Plant height (cm)	72.19	508.79**	27.43	26.46
Ear height (cm)	30.87	199.71**	10.83	12.77
Cob length (cm)	1.21	9.74**	1.69	1.61
Cob girth (cm)	0.066	0.31**	0.035	0.028
Number of kernel rows per cob	0.005	1.433**	0.412	0.309
Number of kernels per row	3.70	42.09**	11.00	8.67
Shelling percentage (%)	0.066	0.317**	0.035	0.028
100- grain weight (g)	6.04	51.20**	2.53	1.93
Grain yield / ha (q)	25.56	893.04**	17.02	22.35

Genetic variability was measured through phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) and is classified as low if co-efficient of variation is < 10 %, medium (10- 20%) and high (> 20 %) as proposed by Siva Subramanian and Menon (1973). In the present study in general PCV was higher than GCV for most of the quantitative traits (Table 2). However, among them PCV was relatively more higher than GCV for days to 50% silking, number of kernels per row and grain yield indicating that environmental factors were more influential in phenotypic expression of these traits as compared to other traits. Similarly, for number of kernel rows and cob girth PCV and GCV were on par with each other and this low difference between PCV and GCV for these traits indicated that environmental factors had little influence in expression of these traits and these traits were governed by additive gene action (Arati *et al*, 2015) and hence and they could be improved by following different phenotypic selection methods. Ababulgu (2014) and Rahman *et al*., (2017) also reported higher PCV than GCV from their study in maize, suggesting importance of environmental factors. However, PCV was high for Plant height (20.88 %) and grain yield (24.52 %) and medium for ear height (12.88%), number of kernels per row (12.98%), cob length (13.58 %) and hundred grain weight (12.42%).

Heritability of a character is a very important for selections to be effective. The estimated broad sense heritability in the present study ranged from 54.8 % for number of kernel rows per cob to 92.85 % for grain yield. In the present study the heritability estimates for all the characters was either medium or high. Among the yield contributing characters hundred seed weight was highly heritable (89.48 %). Higher heritability suggests the presence of additive gene action and selection for this could be effective in early generations itself.

Heritability estimates along with genetic advance are more helpful in predicting the genetic gain under selection than heritability estimates alone (Johnson *et al*., 1955). Estimated genetic advance was higher for grain yield (33.82) followed by plant height (Table 2). In the present study high GCV, high heritability with high genetic advance was observed for the traits like grain yield, plant height, ear height and 100 grain weight which is desirable and it is amenable for improvement through direct selection. This high genetic advance coupled with high heritability was also reported by Kinfe and Tsehaye (2015) for plant height and grain yield and so also by Bhiusal *et al*., 2017. Similarly, Bekele and Rao (2014) recorded high genetic advance with higher heritability for 100 seed weight which is similar with the present finding. These traits can be improved through simple or progeny selection methods. Moderate heritability coupled with low genetic advance as percent of mean was observed for number of kernel rows, number of kernels per and cob length indicating the presence of non additive gene effects and hence there is a limited scope for selection for improvement in these traits.

Association analyses for various morphophysiological traits were done at both phenotypic and genotypic levels (Table 3). In general, higher genotypic correlation coefficients were observed in the present study than phenotypic correlation indicating that association is reduced at phenotypic level due to significant environmental effects. The grain yield/ ha had highly significant and positive correlations both at genotypic and phenotypic levels with ear height (r_g=0.66, r_p=0.55),plant height (r_g=0.50, r_p=0.44), cob length (r_g=0.45, r_p=0.34), number of kernels per row(r_g=0.37, r_p=0.28) and 100-grain weight (r_g=0.36, r_p=0.31) (Table 3) and hence improvement for these traits will lead to improvement in grain yield indicating that each of two-character pairs could be controlled by closely linked genes, or by genes with pleiotropic effects for these characters. However, number of kernel rows per cob (r_g=0.068, r_p=0.04) had non-significant and positive correlation at both the levels indicating any amount selection for this trait will not bring any improvement in grain yield.

Table 2. Genetic Parameter of different characters of maize

Trait	Days to 50 per cent tasseling	Days to 50 per cent silking	Days to 75 per cent dry husk	Plant height (cm)	Ear height (cm)	Number of kernel rows per cob	Number of kernels per row	Cob girth (cm)	Cob length (cm)	Hundred grain weight (g)	Shelling per cent (%)	Grain yield (q/ha)
GV	4.25	2.64	6.24	160.78	62.31	0.37	11.14	0.094	2.71	16.42	0.10	290.23
PV	5.03	3.37	7.86	187.24	75.08	0.68	19.81	0.122	4.32	18.35	0.12	312.58
Heritability %	84.62	78.32	79.40	85.87	82.99	54.80	56.23	77.05	62.73	89.48	77.48	92.85
PCV (%)	3.67	2.91	2.75	20.88	12.88	0.11	12.98	0.02	13.58	12.42	0.42	24.52
GCV (%)	3.38	1.02	2.55	19.35	11.73	0.08	1.14	0.01	10.10	11.75	0.26	12.28
GA	3.91	2.96	4.59	24.20	14.81	0.93	5.16	0.55	2.69	7.90	0.56	33.82

Table 3. Genotypic and phenotypic correlation coefficient for grain yield and its components in maize

SI. No.	Characters		X1	X2	X3	X4	X5	X6	X7	X8	X9	X10	X11	X12
1	Days to 50 per cent tasseling (X1)	G	1.00	0.99**	0.71**	0.49**	0.54**	0.50**	0.50**	0.29**	0.55**	0.24**	-0.49*	0.14*
		P	1.00	0.94**	0.57**	0.35**	0.42**	0.31**	0.37**	0.21**	0.31**	0.17*	-0.33*	0.13
2	Days to 50 per cent silking (X2)	G		1.00	0.75**	0.52**	0.55**	0.49**	0.49**	0.35**	0.52**	0.21**	-0.42*	0.18*
		P		1.00	0.58**	0.37**	0.40**	0.25**	0.31*	0.20**	0.25**	0.15*	-0.28*	0.14*
3	Plant height (cm) (X3)	G			1.00	0.90**	0.51**	0.52**	0.49**	0.38**	0.47**	0.29**	-0.31*	0.50**
		P			1.00	0.79**	0.40**	0.39**	0.41*	0.26**	0.36**	0.25**	-0.23*	0.44**
4	Ear height (cm) (X4)	G				1.000	0.52**	0.46**	0.48**	0.26**	0.41**	0.40**	-0.29*	0.67**
		P				1.000	0.39**	0.32**	0.36**	0.13	0.26**	0.32**	-0.23*	0.55**
5	Days to 75 per cent dry husk (X5)	G					1.00	0.38**	0.53**	0.18*	0.26**	0.57**	-0.44*	0.32**
		P					1.00	0.28**	0.41**	0.10	0.18**	0.45**	-0.26*	0.26**
6	Cob length (cm) (X6)	G						1.000	0.35**	0.0009	0.79**	0.48**	-0.34*	0.45**
		P						1.000	0.40	0.05	0.79**	0.40**	-0.27*	0.34**
7	Cob girth (cm) (X7)	G							1.00	0.47**	0.19**	0.60**	-0.37*	0.26**
		P							1.00	0.41**	0.28**	0.55**	-0.33*	0.21**
8	Number of kernel rows per cob (X8)	G								1.00	-0.09	-0.06	0.106	0.068
		P								1.00	0.02	-0.047	0.05	0.04
9	Number of kernels per row (X9)	G									1.00	0.13	-0.31*	0.37**
		P									1.00	0.16*	-0.23*	0.28**
10	100-grain weight (g) (X10)	G										1.00	-0.41*	0.36**
		P										1.00	-0.32*	0.31**
11	Shelling percentage (%) (X11)	G											1.00	-0.16
		P											1.00	-0.13
12	Grain yield per hectare (X12)	G												1.00
		P												1.00

Knife and Tsehaye (2015) also observed positive and strong association of grain yield with ear length, ear diameter, plant height and ear height both at phenotypic and genotypic levels. High correlation of grain yield with plant height, ear height, cob length, cob girth, number of kernels per row and100-grain weight was also reported by Dar *et al.* (2015) and Kumar *et al.* (2017).

Most of the character pairs had higher values of genotypic correlations than their corresponding phenotypic correlations. This could be due to masking or modifying effect of the environment. Days to 50 per cent tasseling had highly significant and positive association with all the traits except shelling percentage at both genotypic and phenotypic levels. Plant height exhibited highly significant and positive

Table 4. Direct and indirect effects of different characters on grain yield (Genotypic path)

Characters	X1	X2	X3	X4	X5	X6	X7	X8	X9	X10	X11
X1	-3.29	-3.26	-2.35	-1.63	-1.78	-1.66	-1.67	-0.96	-1.81	-0.79	1.62
X2	3.13	3.16	2.37	1.66	1.73	1.54	1.56	1.12	1.64	0.68	-1.32
X3	-0.55	-0.57	-0.76	-0.69	-0.39	-0.39	-0.38	-0.29	-0.36	-0.22	0.24
X4	0.55	0.58	1.00	1.10	0.57	0.51	0.53	0.29	0.45	0.44	-0.32
X5	-0.08	-0.08	-0.07	-0.07	-0.14	-0.05	-0.07	-0.02	-0.04	-0.08	0.06
X6	0.03	0.03	0.03	0.03	0.02	0.06	0.02	0.00	0.04	0.03	-0.02
X7	0.02	0.02	0.02	0.02	0.02	0.01	0.04	0.02	0.01	0.02	-0.01
X8	-0.01	-0.01	-0.01	0.00	0.00	0.00	-0.01	-0.02	0.00	0.00	0.00
X9	0.19	0.18	0.16	0.14	0.09	0.27	0.07	-0.03	0.35	0.05	-0.11
X10	0.04	0.03	0.04	0.06	0.08	0.07	0.08	-0.01	0.02	0.14	-0.06
X11	0.12	0.10	0.08	0.07	0.11	0.08	0.09	-0.03	0.08	0.10	-0.25
Correlation with grain yield	0.15*	0.18*	0.50**	0.67**	0.32**	0.45**	0.26**	0.07	0.37**	0.36**	-0.17*

R square = 0.626 Residual effect = 0.611

X1 - Days to 50% tasseling
X2 - Days to 50% silking
X5 – Days to 75% dry husk
X3 – Plant height (cm)
X4- Ear height (cm)
X6 – Cob length (cm)
X7 – Cob girth (cm)
X8 – Number of kernel rows per cob
X9 – Number of kernels per row
X10 – 100-grain weight (gm)
X11– Shelling percentage

association with ear height, cob length, cob girth, number of kernel rows per cob, number of kernels per row and 100-grain weight. Cob length had highly significant and positive association with number of kernels per row and 100-grain weight. Cob girth had significant and positive association with number of kernel rows per cob, number of kernels per row and 100-grain weight.

The estimation of correlation coefficients indicates only the nature and extent of association between yield and yield attributes, but does not show the direct and indirect effects of different yield contributing traits on yield. Grain yield is dependent on several characters which are mutually associated these will in turn impair the true association exiting between various component traits and grain yield. The genotypic correlation coefficients calculated for different pairs of characters were subjected to path coefficient analysis for partitioning these values into direct and indirect effects. The highest positive and direct effect was found for days to 50% silking (3.16) followed by ear height (1.10) (Table 4).

Days to 50 per cent tasseling showed highly negative indirect effect for days to 50 per cent silking (-3.26) followed by plant height (-2.35), ear height (-1.63), days to 75 per cent dry husk (-1.78), cob length (-1.66), cob girth(-1.67), number of kernel rows per cob(-0.96),number of kernels per row(-1.81) and 100-grain weight (-0.79). Whereas, it recorded positive indirect effect with shelling percentage (1.62). Similalry, 100-grain weight showed positive indirect effect for all the characters except number of kernel rows per cob (-0.01) and shelling percentage (-0.06). These findings were in agreement with reports of Kanagarasu *et al.* (2013), Kumar *et al*. (2017) and Oyekunle and Badu-Apraku, (2018)

Conclusion

From the present study it was found that PCV was higher than GCV for days to 50% silking, number of kernel rows and grain yield indicating the influence of environmental factors in expression of these traits. Highest broad sense heritability among the yield contributing characters was observed in 100 seed weight (89.48%).Similarly, high heritability with high GCV and high GA was observed in grain yield, plant height and 100 seed weight traits and hence these traits are easily amenable for improvement through direct selection. Among the yield contributing traits grain yield showed significant and positive direct association with cob length, 100 seed weight and number of kernels per row both at genotypic and phenotypic level. Therefore, 100 seed weight, cob length and number of kernels per row are the traits on which the breeders can concentrate leaving out number of kernel rows in pursuit of improving grain yield.

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