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RESEARCH PAPER

Genetic variability, correlation studies and path analysis in S_2 progenies derived from two diverse populations in maize (*Zea mays* L.)

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Abstract: The present investigation has been undertaken to estimate the genetic variability, correlation coefficient and path analysis among 90 crosses for 13 characters during *rabi* 2017-18 using Augmented design-II. Phenotypic coefficient of variation (PCV)were comparatively higher than that of genotypic coefficient of variation (GCV)and is found in higher magnitude for traits like, grain yield, 100 grain weight, number of kernels per row and cob lengthwhich represents considerable variability and offers scope for genetic improvement through selection. High heritability and high GAM were observed for number of kernels per row and cob length while, high heritability and moderate genetic advance as per cent mean (GAM) estimates were shown by brown husk maturity,100-grain weight. Grain yield was significantly and positively correlated with 100-grain weight of magnitude, cob length, number of kernels per row, number of kernel rows per coband brown husk maturityat genotypic level. Path coefficient analysis at genotypic level depicts characters *viz.*, days to 50 per cent tasseling, brown husk maturity, plant height, cob length, cob girth, shelling percentage and 100-grain weight had positive direct effect on grain yield per hectare indicating that selection for these traits results in more grain yield.

Key words: Genetic advance as per cent mean, Genetic variability, Genotypic coefficient of variation, Heritability, Phenotypic coefficient of variation

Introduction

Maize is the third most important cereal crop after rice and wheat and it has become a staple food in many parts of the world, with total production surpassing that of rice and wheat. Maize is known as queen of cereals because of its high production potential and wider adaptability. Genetic variability among the individuals in population offers effective selection and the magnitude of genetic variability present is of paramount importance for the success of plant breeding program. Heritability alone provides no indication of the amount of genetic improvement that would result from selection of individual genotypes (Rajesh *et al.*, 2013). Hence, knowledge about genetic advance coupled with heritability is most useful.

Grain yield is a complex quantitative trait that depends on a number of factors; hence knowledge of the relationship between grain yield and its contributing components will improve the efficiency of breeding programs through the use of appropriate selection indices (Mohammadi *et al.*, 2003). Therefore, correlation analysis of a particular trait with other trait attributing to yield is of great importance for selecting lines for higher yield while path coefficient analysis helps partitioning the correlation coefficient into its direct and indirect effects.

Material and methods

The breeding materials used for the experimentation are S_2 progenies from two populations namely P-I and P-II. Populations P-I and P-II consisted of 100 and 78 progenies of S_2 generation, respectively. From these two diverse populations 49 (P-I) and 28 (P-II) $S\text{-}_2$ progenies selected for crossing programme based on their *per se* performance on tolerance to charcoal stalk rot. These S_2 progenies derived from populations; P-I (49) and P-II (28) were crossed to two testers *viz.*, CM-501 and Renuka, broad based open pollinated varieties using line x tester design during *kharif* 2017. Totally 154 crosses were attempted but, only 90 crosses were successful. Hence, in *rabi* 2017-18 these 90 crosses (60 crosses from P-I and 30 crosses from P-II) were selected and evaluated against five checks *viz.*, CM-501, Renuka, CP-818, KDMI-16 and GPMH-1101 (Rashmi and Wali, 2020).

A total of 90 successful crosses were evaluated for genetic variability through estimation of genetic parameters like phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability, genetic advance and genetic advance as per cent mean (GAM). This experiment was carried out during *rabi* 2017-18 comprising 95 entries (90 crosses and 5 checks) using Augmented design-II, each entry was raised in two rows with a row length of 3 m with spacing of 60 cm between the rows and 20 cmbetween plants.

The data were collected on 13 quantitative characters *viz.*, days to 50 per cent tasseling,days to 50 per cent silking, brown husk maturity, plant height (cm), ear height (cm), cob length (cm), cob girth (cm), number of kernel rows per cob, number of kernels per row, shelling percentage (%), 100-grain weight (g), grain yield per plot (kg) andgrain yield (q/ha).

Results and discussion

The analysis of variance for augmented design-II was performed for all the 13 characters studied. Significant differences were observed for all the entries and checks indicating the presence of substantial variability among the S_2 progenies (Table 1).

Table 1. Analysis of variance (ANOVA) for augmented design-II

Sources of variation	Block (eliminating check + crosses)	Entries (ignoring blocks)	Checks	Crosses	Checks vs Crosses	Error
Degrees of freedom	9	94	4	89	1	32
Days to 50per cent tasseling	1.38	5.79**	1.77*	5.87**	14.7**	1.27
Days to 50per cent silking	1.08	5.11**	0.80*	4.95*	36.30**	0.76
Brown husk maturity	3.85	37.59*	15.47*	35.08*	349.07**	45.07
Plant height (cm)	1222.42	374.46*	325.95**	248.98**	0.41*	2825.19
Ear height (cm)	320.19	105.24**	53.46*	104.88**	344.53**	109.65
Cob length (cm)	32.47	16.39*	9.81*	16.85*	1.73*	14.55
Cob girth (cm)	1.99	1.36*	1.34*	1.30*	7.04*	1.09
Number of kernel rows per cob	2.55	2.02*	2.31*	2.02*	1.79*	2.36
Number of kernels per row	23.16	18.33*	21.82*	18.21*	14.97*	31.94
Shelling percentage (%)	51.61	21.62*	21.15*	21.23*	58.13*	20.02
100 grain weight (g)	41.00	25.97*	22.64*	26.41*	0.74*	43.25
Grain yield (q/ha)	0.03	0.05*	0.02*	0.05*	0.36*	0.06
Grain yield (q/ha)	59.48	91.84*	35.68*	88.27*	635.10**	107.69

The results of genetic parameters for different characters are presented in Table 2, Fig 1 and Fig 2. Phenotypic coefficient of variation were comparatively higher than that of genotypic coefficient of variation and is found in higher magnitude for traits like, grain yield (27.45 and 22.66 %), 100-grain weight (14.44 and 13.80 %), number of kernels per row (13.60 and 12.83 %) and cob length (12.96 and 12.16 %). Similar results of higher values of PCV and GCV were reported by Rahman *et al*. (2015), Reddy *et al*. (2013) and Srivas and Singh (2010). Lower values of PCV and GCV were noticed for 50 per cent tasseling, 50 per cent silking, brown husk maturity, plant height, number of kernels per cob which are in agreement with the results of Satyanarayana *et al.* (1994) and Murugan *et al.* (2010).

High heritability and high GAM were observed for number of kernels per row (89 % and 24.94) followed by cob length (88 % and 23.53) while, high heritability and moderate GAM estimates were shown by brown husk maturity (89 % and 10.38) followed by 100-grain weight (81% and 27.17) was also reported by Rajesh *et al.* (2013), Vashistha *et al.* (2013) and Kumar *et al.* (2014).

Genotypic correlation for grain yield with other yield components

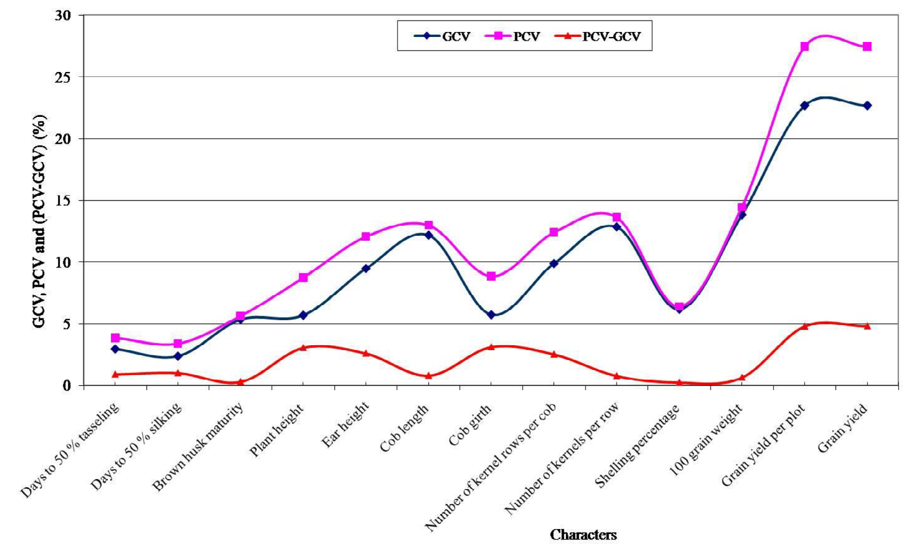

Fig. 1. Contribution of genotypic coefficient of variation, phenotypic coefficient of variation and its difference in crosses derived from S_2 progenies

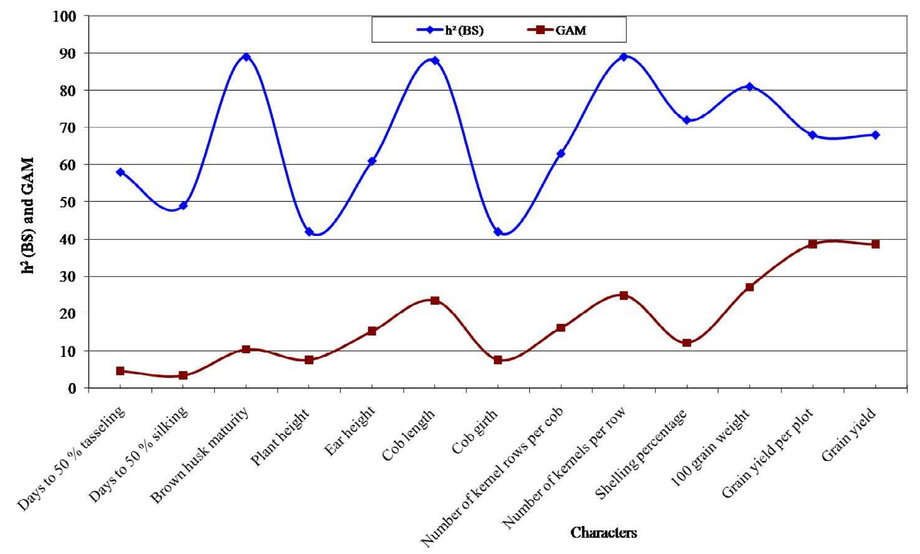

Fig. 2. Contribution of heritability and genetic advance as per cent mean in crosses derived from S_2 progenies

Table 2. Genetic parameters for 13 characters in crosses derived from S_2 progenies

Genetic parameter	Days to 50 per cent tasseling	Days to 50 per cent silking	Brown husk maturity	Plant height (cm)	Ear height (cm)	Cob length (cm)	Cob girth (cm)	Number of kernel rows per cob	Number of kernels per row	Shelling percentage (%)	100 grain weight (g)	Grain yield (q/ha)	Grain yield (q/ha)
Range	67-77.5	69-79	98.5-121	164.5-235	76-127.5	12.48-22.8	3.37-5.29	12-19	24-41.5	69.44-94.24	19.84-36.16	0.44-1.98	18.33-79.17
Mean	70.91	73.26	109.34	196.8	100.23	17.44	4.48	14.41	31.08	84.16	30.16	0.88	36.83
GCV	2.94	2.36	5.32	5.67	9.45	12.16	5.71	9.86	12.83	6.15	13.80	22.66	22.66
PCV	3.84	3.37	5.61	8.72	12.04	12.96	8.82	12.38	13.60	6.38	14.44	27.43	27.45
PCV-GCV	0.9	1.01	0.29	3.05	2.59	0.8	3.11	2.52	0.77	0.23	0.64	4.77	4.79
h^2 (BS)	0.58	0.49	0.89	0.42	0.61	0.88	0.42	0.63	0.89	0.72	0.81	0.68	0.68
Genetic advance	3.29	2.51	11.36	14.96	15.30	4.12	0.34	2.33	7.79	10.26	8.38	0.34	14.13
GAM	4.63	3.42	10.38	7.59	15.28	23.53	7.60	16.17	24.94	12.21	27.17	38.58	38.55

GCV- Genotypic coefficient of variation, PCV- Phenotypic coefficient of variation GAM- Genetic advance as per cent mean,h^2 (BS)-Heritability

Table 3. Genotypic correlation coefficient for grain yield and its components for 12 characters

Sl. No	Characters	Days to 50 per cent tasseling	Days to 50 per cent silking	Brown husk maturity	Plant height (cm)	Ear height (cm)	Cob length (cm)	Cob girth (cm)	Number of kernel rows per cob	Number of kernels per row	Shelling percentage (%)	100 grain weight (g)	Grain yield (q/ha)
1	Days to 50 per cent tasseling	1.00	0.95**	-0.21**	0.11	0.07	0.10	-0.11	-0.30	0.12	0.06	-0.05	-0.04
2	Days to 50 per cent silking		1.00	-0.18*	0.22**	0.06	0.07	-0.13	-0.40**	-0.04	-0.04	-0.06	-0.01
3	Brown husk maturity			1.00	-0.13	0.05	-0.08	0.04	0.03	0.06	-0.06	0.23**	0.26**
4	Plant height (cm)				1.00	0.73**	0.29**	-0.26**	0.01	0.06	-0.21**	-0.04	-0.09
5	Ear height (cm)					1.00	0.43**	-0.11	-0.18*	0.27**	-0.04	0.039	0.14*
6	Cob length (cm)						1.00	0.21**	0.26**	0.75**	-0.19**	0.21**	0.37**
7	Cob girth (cm)							1.00	0.05	0.25**	0.06	0.27**	0.12
8	Number of kernel rows per cob								1.00	0.11	-0.05	0.05	0.26**
9	Number of kernels per row									1.00	-0.03	0.17*	0.29**
10	Shelling percentage (%)										1.00	-0.07	0.12
11	100 grain weight (g)											1.00	0.57**
12	Grain yield (q/ha)												1.00

*-Significant at 5 % level**-Significant at 1 % level

is given in the Table 3. The magnitude of correlation of grain yield was highest with 100-grain weight of magnitude (0.57) followed by cob length (0.37), number of kernels per row (0.29), number of kernel rows per cob (0.26) and brown husk maturity (0.26). A significant and positive correlation of grain yield with ear height, number of kernel per row, number of kernel per row and 100-grain weight was reported by Gazal *et al.* (2018), Jatto *et al.* (2015), Jawaharlal *et al.* (2010), Rafiq *et al.* (2010) and Sadaiah *et al.* (2013) indicating that these are the most important traits to yield. Dagla *et al.* (2015) showed negative correlation of days to 50 per cent tasseling and days to 50 per cent silking with grain yield.

Results from path coefficient analysis at genotypic level (Table 4) depicts characters *viz.*, days to 50 per cent tasseling, brown husk maturity, plant height, cob length, cob girth, shelling percentage and 100-grain weight had positive direct effect on grain yield per hectare indicating that selection for these traits results in more grain yield. While, days to 50 per cent silking, ear height, number of kernel rows per cob and number of kernel per row had negative direct effect on grain yield for genotypic path indicating that selection for these traits results in lesser grain yield. The direct effect on grain yield by plant heightwas reported by Nataraj *et al.* (2014), days to 50 per cent tasseling by Kumar *et al.* (2015), brown husk maturity and 100-grain weight by Gazal *et al.* (2018) and Rafiq *et al.* (2010).

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

Characters	Days to 50 per cent tasseling	Days to 50 per cent silking	Brown husk maturity	Plant height (cm)	Ear height (cm)	Cob length (cm)	Cob girth (cm)	Number of kernel rows per cob	Number of kernels per row	Shelling percentage (%)	100 grain weight (g)	Correlation with grain yield
Days to 50 per cent tasseling	6.85	6.51	-1.49	0.81	0.48	0.74	-0.72	-2.09	0.85	0.44	-0.34	-0.04
Days to 50 per cent silking	-7.22	-7.60	1.41	-1.72	-0.49	-0.57	1.05	3.06	0.34	0.31	0.50	-0.01
Brown husk maturity	-0.23	-0.19	1.06	-0.13	0.06	-0.08	0.05	-0.03	0.07	-0.07	0.25	0.26**
Plant height (cm)	0.22	0.43	-0.25	1.92	1.42	0.57	-0.51	0.01	0.12	-0.41	-0.09	-0.09
Ear height (cm)	-0.15	-0.14	-0.12	-0.16	2.24	-0.97	0.25	0.41	-0.61	0.10	-0.08	0.14*
Cob length (cm)	0.34	0.23	-0.25	0.93	1.36	3.1	0.66	0.84	2.37	-0.61	0.66	0.37**
Cob girth (cm)	-0.01	-0.02	0.01	-0.01	-0.01	0.01	-0.06	0.02	0.01	0.01	0.01	0.12
Number of kernel rows per cob	0.49	0.65	0.05	-0.01	0.29	-0.43	-0.09	-1.62	-0.19	0.08	-0.46	0.26**
Number of kernels per row	-0.34	0.12	-0.18	-0.17	-0.74	-2.05	-0.70	-0.32	2.72	0.08	-0.46	0.29**
Shelling percentage (%)	0.01	-0.01	-0.01	-0.03	0.01	0.03	0.01	-0.01	0.01	0.18	-0.01	0.12
100 grain weight (g)	-0.01	-0.01	0.05	-0.01	0.01	0.04	0.06	0.01	0.04	-0.01	0.23	0.57**

R^2= 0.56, Residual effect = 0.63

Conclusions

The study of genetic variability among S_2 progenies revealed narrow difference between PCV and GCV indicating less influence of environment for all the traits studied. Moderate to high heritability with moderate estimates of GAM were recorded for grain yield per plot, plant height, ear height and 100-grain weight. Significant and positive association of grain yield was shown with ear height, cob length, number of kernel rows per cob, number of kernels per row and 100-grain weight. Further, plant height, cob length, cob girth, shelling percentage and 100-grain weight exhibited positive direct effect on grain yield.

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