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RESEARCH PAPER

Estimation of genetic variability, correlation and path coefficient analysis in early segregating generation of maize (*Zea mays* L.)

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Abstract: The present investigation was carried out to assess the extent of genetic variability, character association, direct and indirect effects of yield attributes on yield in bi-parental F_2 population of DHKN 509 × CM 111. The experiment was conducted using 421 F_2 progeny plants laid out in an un-replicated trial along with parents and F_1 during *Rabi* 2020-21. The observations were recorded for ten traits in all the F_2 plants and ten plants each from parents and F_1. It was revealed that there was significant variation among the traits studied. The extent of phenotypic coefficient of variation was higher than genotypic coefficient of variation for all the traits studied. High variability coupled with high heritability and high genetic advance over mean were observed for number of kernels per row, pith weight and grain yield per plant suggesting that these traits are controlled by additive gene action and less influenced by environment and can be improved through simple selection. The traits *viz.*, cob girth, number of kernels per row, pith weight and shelling per cent recorded positive and significant association with grain yield. Pith weight and shelling per cent exhibited highest direct positive effect on grain yield per plant. Hence, it would be rewarding to lay emphasis on these traits while formulating crop improvement programs.

Key words: Correlation, Genetic variability, Maize, Path analysis

Introduction

Maize (*Zea mays* L.) is the only cereal crop cultivated in varied seasons and ecosystems. It is a popular grain serves as a staple food crop for human consumption in many tropical and sub-tropical countries, and as a raw material for industrial products like ethanol, starch, corn syrup and so on. It is mostly used as feed to poultry and livestock (60%) in India. The rising population, commercialization and industrialization put a lot of pressure to enhance grain yields per capita. Hence, researchers are focusing on improving the grain yield in maize. The extent of genetic variability in any germplasm or gene pool is the major determinant in any crop improvement program for selecting superior genotypes. Selection is effective only when there is an enormous amount of variability among the individuals of the population. Phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) provides the extent of variability in the population. Heritability gives the extent of trait transmission to the next generation. Selection is effective if the traits show high heritability and high genetic advance (Johnson *et al*., 1955). Heritability and genetic advance give the type of gene action involved in governing the trait and suggests practicing appropriate breeding program.

Maize grain yield is a complicated trait that is genetically controlled by a large number of genes with moderate genetic effects, and is further complicated by substantial interactions between genotype and the environment. The correlation coefficient and path coefficients of various traits are a valuable criterion for identifying desirable traits that help to improve the grain yield variable (Wright, 1921). Through the use of proper selection indices, a thorough understanding of the interaction between grain yield and its contributing components can greatly increase the effectiveness of a breeding program. Hence, the present study was focused to assess the variability for ten characters; correlation among the characters and direct and indirect effects of the characters on the grain yield in F_2 population of maize.

Material and methods

The experimental material consisted of 421 F_2 progeny plants of cross combination DHKN 509 × CM 111, and their parents, and F_1. The present investigation was taken up at Agricultural Research Station, Mugad, during *Rabi* 2020-21. The site of experiment is situated in the Northern transitional tract of Karnataka at $15^0.15'$ N latitude and $74^0.40'$ E longitude at an altitude of 697m above mean sea level. The site receives mean annual rainfall of 1017.0 mm with the soil type being lateritic. The genetic material was evaluated under un-replicated fashion with a spacing of 60×20cm. Parents and F_1 were evaluated along with the F_2 population to calculate the environmental variance using the following formulae (Globerson *et al.,* 1987).

Environmental variance (Error variance) = $(V_{pP1} + V_{pP2} + V_{pF1})/3$

Genotypic variance of F_2 population = Phenotypic variance of F_2 population - Error variance, where V_{pP1}= Phenotypic variance in parent 1; V_{pP2}=Phenotypic variance in parent 2 and V_{pF1} = Phenotypic variance in parent F_1.

The recommended fertilizer dose of 150:65:65 NPK kg per hectare was applied to raise the healthy crop. The observations were recorded for 421 F_2 progeny plants along with ten plants each from parents and F_1 for ten characters *viz*. days to tasseling, days to silking, anthesis-silking interval, plant height (cm), ear height (cm), cob girth (cm), number of kernels per row, pith weight (g), shelling per cent and grain yield per plant (g). The data was analyzed using the MS-EXCEL for estimating genetic variability and R studio software for correlation and path coefficient analysis.

Results and discussion

Estimates of genetic variability parameters for grain yield and yield attributes

The F_2 population of the cross DHKN 509 × CM 111, exhibited wide variation for all the traits studied (Table 1; Fig. 1). Days to tasseling ranged from 62 to 82 days with a mean of 70 days; days to silking ranged from 65 to 84 days with a mean of 72 days; anthesis-silking interval ranged from -2 to +6 days with a mean of 2 days; plant height ranged from 95 to 228 cm (mean 177.06 cm), ear height ranged from 16.0 to 185 cm with a mean 107.79 cm; cob girth ranged from 2.40 to 5.20 (mean 4.09 cm), number of kernels per ear ranged from 9 to 35 with a mean of 20.22; pith weight ranged from 4.0 to 37.80 g (mean 16.18 g), shelling per cent ranged from 65.0 to 91.61 (mean 78.46) and the grain yield per plant ranged from 21 to 136 g with a mean of 60.92 g.

Genetic variability studies showed that phenotypic coefficient of variation was higher than the genotypic coefficient of variation for all the traits studied (Table 1), which indicated the effect of environment on expression of those traits.PCV and GCV estimates were high for anthesis-silking interval (85.93 % and 82.96 %) followed by grain yield per plant (36.45 % and 33.66 %), pith weight (34.76 % and 32.58 %) and number of kernels per row (24.27 % and 21.75 %) indicating a greater scope for selection to improve these traits. These results are in accordance with Chandana (2018). Whereas, moderate PCV and GCV was recorded for ear height (19.29 % and 18.54 %) followed by plant height (13.93 % and 13.49 %) and cob girth (12.05 % and 11.56 %). Furthermore, low PCV and GCV was observed for shelling per cent (6.80 % and 6.63 %) followed by days to silking (5.04 % and 4.88 %) and days to tasseling (4.11 % and 4.00 %). Similar results of low PCV and GCV for days to tasseling and days to silking were observed by Tasfaye *et al.*(2021).

Table 1. Estimates of genetic variability parameters for grain yield and nine yield attributes in F_2 population of DHKN 509 × CM 111

	MEAN	RANGE		PCV(%)	GCV(%)	Heritability in broad-sense	GAM(%)
		MIN	MAX				
Days to tasseling	70.00	62.00	82.00	4.11	4.00	94.51	8.00
Days to silking	72.00	65.00	84.00	5.04	4.88	93.80	9.73
Anthesis-silking interval	2.15	-2.00	6.00	85.93	82.96	93.20	84.99
Plant height	177.06	95.00	228.00	13.93	13.49	93.74	26.90
Ear height	107.79	16.00	185.00	19.29	18.54	92.35	36.70
Cob girth	4.09	2.40	5.20	12.05	11.56	92.06	22.85
No. of kernels per row	20.22	9.00	35.00	24.27	21.74	80.23	40.10
Pith weight	16.18	4.00	37.80	34.76	32.58	87.86	62.92
Shelling per cent	78.46	65.00	91.61	6.80	6.63	94.79	13.29
Grain yield per plant	60.92	21.00	136.00	36.45	33.66	85.27	64.03

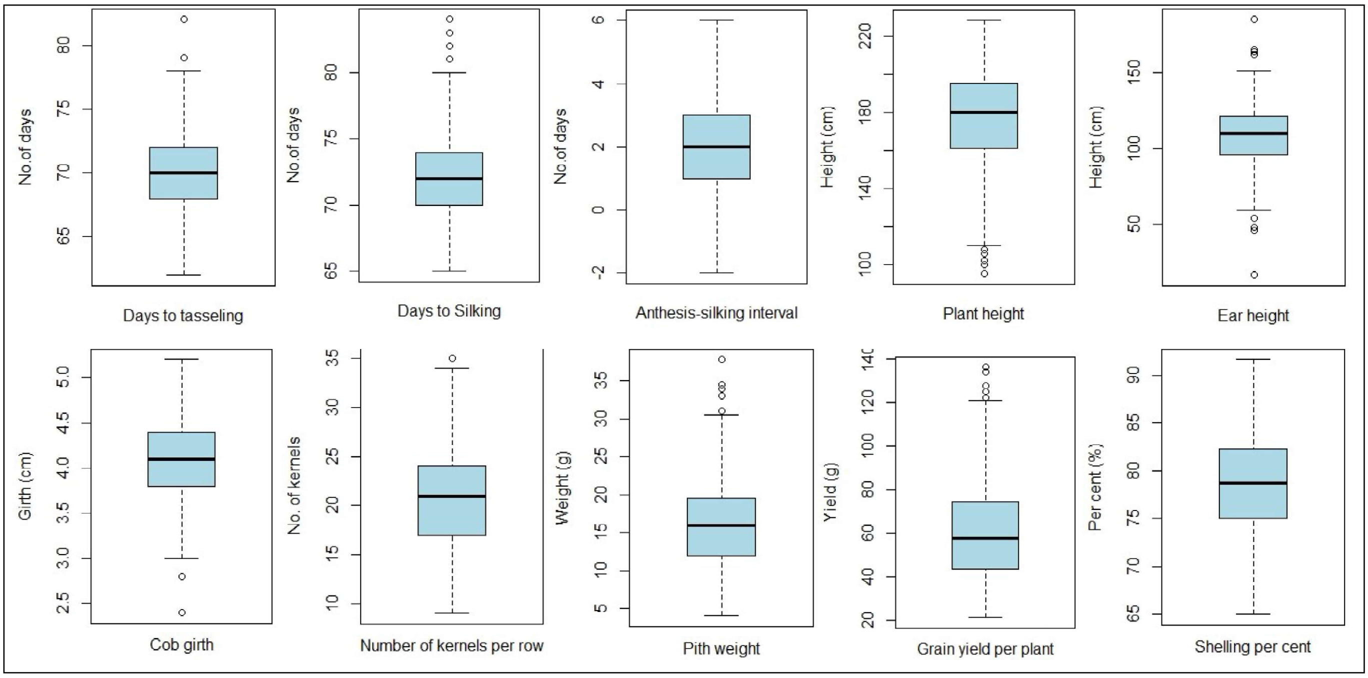

Fig. 1. Box plots showing variability in yield and its attributes in F_2 population of DHKN 509 × CM 111

Heritability in broad sense was high for shelling per cent (94.79 %), days to tasseling (94.51 %),days to silking (93.80 %), plant height (93.74 %), anthesis-silking interval (93.20 %), ear height (92.35 %) and cob girth (92.06 %) where in the heritability was over 90 per cent. The results were in accordance with Pandey *et al.* (2017). Genetic advance as per cent of mean (GAM) was high for anthesis-silking interval (84.99 %) followed by grain yield per plant (64.03 %), pith weight (62.92 %), number of kernels per row (40.10 %), ear height (36.70 %), plant height (26.90 %) and cob girth (22.85 %) suggesting that these traits are controlled by additive gene action and hence selection can be practiced. Chandana (2018) reported similar results for all these traits. Moderate GAM was recorded for shelling per cent (13.29 %) which was in accordance with Pandey *et al.* (2017) and Chandana_(2018). However, low GAM was observed for days to silking (9.73 %) and days to tasseling (8.0 %). These findings were in parallel with the results of Neelima *et al.* (2020) and Tasfaye *et al.* (2021).

Association among grain yield and its component traits in F_2 population of DHKN 509 × CM 111

High heritability coupled with high genetic advance as per cent of mean was observed for anthesis-silking interval followed by pith weight, ear height, number of kernels per row, plant height and cob girth suggesting that for these traits are under the control of additive gene action, selection could be effective for desired genetic improvement. This was in accordance with Reddy *et al.* (2012) and Nataraj *et al.* (2014). The character association studies exhibited that grain yield per plant recorded highly significant and positive association with cob girth (0.70) followed by number of kernels per row (0.66), pith weight (0.60), shelling per cent (0.45) and plant height (0.15) suggesting that selection for these traits could bring yield improvement in maize (Table 2). Such kind of association was reported by Chaurasia *et al.* (2020) and Yahaya *et al.* (2021). Ear height exhibited no significant association with grain yield per plant. The characters *viz.,*days to tasseling (-0.23), days to silking (-0.29) and anthesis to silking interval (-0.22) showed negative and significant association with grain yield per plant suggesting that these traits can be used for identifying early maturing genotypes. These results were in accordance with the studies of Pandey *et al.* (2017) and Chaurasia *et al.* (2020).

Path coefficient analysis of different characters on grain yield per plant in F_2 population of DHKN 509 × CM 111

The path coefficient analysis (Table 3) revealed that highest positive direct effect on grain yield per plant was exhibited by days to silking (0.8758) followed by pith weight (0.8233), shelling per cent (0.7464), number of kernels per row (0.0703), plant height (0.0483) and cob girth (0.0412). Although the direct effects of cob girth and number of kernels per row are relatively lower, these traits have indirectly contributed largely through pith weight and shelling per cent which led to realize higher

Table 2. Association among grain yield and its component traits in F_2 population of DHKN 509 × CM 111

	DTT	DTS	ASI	PH	EH	CG	NKR	PW	SP	GYP
DTT	1.00	0.86**	0.14**	-0.13**	0.01	-0.25**	-0.18**	-0.33**	0.12*	-0.23**
DTS		1.00	0.62**	-0.18**	-0.05	-0.33**	-0.20**	-0.38**	0.10*	-0.29**
ASI			1.00	-0.15**	-0.11*	-0.26**	-0.11*	-0.24**	0.02	-0.22**
PH				1.00	0.78**	0.24**	0.06	0.18**	-0.02	0.15**
EH					1.00	0.08	0.01	0.03	0.01	0.01
CG						1.00	0.40**	0.54**	0.23**	0.70**
NKR							1.00	0.39**	0.33**	0.66**
PW								1.00	-0.39**	0.60**
SP									1.00	0.45**
GYP										1.00

Note: * Significant at 0.05 probability level and ** Significant at 0.01 probability level.

Table 3. Path coefficient analysis of nine characters on grain yield per plant in F_2 population of DHKN 509 × CM 111

	DTT	DTS	ASI	PH	EH	CG	NKR	PW	SP	Phenotypic correlation with grain yield
DTT	-0.7065	0.7532	-0.0648	-0.0063	-0.0006	-0.0103	-0.0127	-0.2717	0.0896	-0.23**
DTS	-0.6076	0.8758	-0.2869	-0.0087	0.0032	-0.0136	-0.0141	-0.3128	0.0746	-0.29**
ASI	-0.0989	0.5430	-0.4627	-0.0073	0.0070	-0.0107	-0.0077	-0.1976	0.0149	-0.22**
PH	0.0918	-0.1577	0.0694	0.0483	-0.0493	0.0099	0.0042	0.1482	-0.0149	0.15**
EH	-0.0071	-0.0438	0.0509	0.0377	-0.0632	0.0033	0.0001	0.0247	0.0075	0.01
CG	0.1766	-0.2890	0.1203	0.0116	-0.0051	0.0412	0.0281	0.4446	0.1717	0.70**
NKR	0.1272	-0.1752	0.0509	0.0029	0.0001	0.0165	0.0703	0.3211	0.2463	0.66**
PW	0.2331	-0.3328	0.1111	0.0087	-0.0019	0.0222	0.0274	0.8233	-0.2911	0.60**
SP	-0.0848	0.0876	-0.0093	-0.0010	-0.0006	0.0095	0.0232	-0.3211	0.7464	0.45**

Note: *Significant at 0.05 probability level and ** Significant at 0.01 probability level.

Residual effect =0.077982

DTT = Days to tasseling
DTS = Days to silking
ASI = Anthesis-silking interval
PH = Plant height
EH = Ear height
CG = Cob girth
NKR = No. of kernels per row
PW = Pith weight
SP = Shelling percent
GYP = Grain yield per plant

association of these two characters with grain yield. Hence, it would be rewarding to lay emphasis on these traits while developing selection strategies in maize. Similarly, days to silking exhibited negative association (-0.29) with grain yield, it recorded positive direct effect which is due to the negative indirect effects of the other traits. Furthermore, highest negative direct effect was observed for days to tasseling (-0.7065) followed by anthesis-silking interval (-0.4627) and ear height (-0.0632).These findings were in parallel with the experiments of Kumar *et al.* (2017) and Hosamani *et al*. (2018).

Conclusion

From the present study, it was concluded that there was an ample amount of genetic variability in the F_2 population studied and the traits *viz.,* cob girth, number of kernels per row, pith weight and shelling per cent, showed high heritability, genetic advance, positive association which had direct effect on grain yield per plant and these are the important yield influencing traits in maize. Hence, selection considering these traits could enhance the grain yield in maize.

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