

Genetic variability study in biparental derived F_3 families for effective selection in maize

Monisha J.¹ • Talekar S. C.¹ • Kachapur R. M.² • Salakinkop S. R.¹ • Spurthi Nayak²

Abstract The current investigation was carried out to estimate the extent of genetic variability, trait association, direct and indirect effects of yield contributing traits on yield in bi-parental F_3 population of DHKN 509 × CM 111. The experiment was conducted using 287 F_3 progeny families laid out in an un-replicated fashion along with parents and F_1 during *rabi* 2021-22. Nine yield contributing characters were studied; it revealed that there was ample amount of variation among the traits studied. The phenotypic coefficient of variation was higher than genotypic coefficient of variation for all the characters under study. High variability coupled with high heritability and high genetic advance over mean were observed for kernels per row, cob length, pith weight suggesting that these characters can be improved through simple selection. All characters *viz.*, cob length, kernels per row, pith weight, cob girth, 100-grain weight, shelling per cent, pith girth, kernel row number recorded positive and significant relationship with grain yield. Pith weight and shelling per cent recorded highest positive direct effect on grain yield per plant suggesting that selection for these traits results in positive improvement in grain yield during maize improvement programs.

Keywords: Maize • Genetic variability • Correlation • Path analysis

✉ Talekar S. C.: talekarsc@uasd.in

¹All India Coordinated Maize Improvement Project, MARS, Dharwad University of Agricultural Sciences, Dharwad-580005, Karnataka, India

²Department of Biotechnology, University of Agricultural Sciences, Dharwad, Karnataka, India

Introduction

Maize is a major source of calories for humans. As the population expands, the demand for maize-based food, feed, and fuel is increasing. The expanding global population is placing unprecedented pressure on ensuring food security and stabilizing agricultural productivity (Hallauer and Miranda Filho, 1988). In India, maize is the third most important cereal crop after rice and wheat. It is not only important food crop, but also a raw material for many industrial products and basic element for animal feed. Being C_4 and day neutral plant possess high genetic yield potential, but the average productivity of India is 3.38 t/ha, which is still lesser than the global average productivity of 4.76 t/ha (FAOSTAT, 2024). Therefore, India is anticipated to double its maize productivity by 2050 to satisfy future demands (Antony *et al.*, 2023). To meet these challenges, plant breeders have been continuously working to develop high-yielding maize cultivars with better agronomic traits and enhanced stress tolerance (Duvick, 2001).

The basic knowledge on the extent of genetic variability present in the population and relationship between yield and its attributing traits is crucial for any successful plant breeding programmes. The complete view of variability within the population is provided by different genetic parameters like variance, coefficient of variances, heritability and genetic advance (Talekar *et al.*, 2022). The effectiveness of utilizing variability for selection relies on the heritability and genetic advance (GA) of each individual trait (Bilgin *et al.*, 2010). But it is very complex to judge whether observed variability is heritable or not. The genetic parameters such as phenotypic, genotypic and environmental coefficient of variations partition the observed variability into heritable

and non-heritable variation. Heritability coupled with genetic advance estimates indicates the extent of transmissibility of a trait to next generations (Singh *et al.*, 2011)

Yield is a complex quantitative trait and dependent variable, hence knowledge about correlation of yield with other yield contributing traits is essential to improve productivity through indirect selection for significantly correlated traits. However, correlation values alone may not reveal the true association between the two variables since it is occasionally influenced by the third variable (Bello *et al.*, 2010). Thus, path coefficient analysis partitions the correlation coefficients into direct and indirect effects and provides the realistic association between the two traits. Therefore, by considering aforesaid aspects, the present investigation was undertaken to study the genetic variability, correlation and path coefficient studies in F_3 generation of maize.

Materials and methods

Plant materials

The present study was taken up at Main Agricultural Research Station, All India Coordinated Maize Improvement Project, University of Agricultural Sciences, Dharwad, during *rabi* 2021-22. The experimental site is situated in the Northern Transitional Zone of Karnataka (Zone 8) at 15° 26' N latitude and 75° 07' E longitude with an altitude of 678 m above mean sea level with a mean annual rainfall of 740 mm with the medium deep black soil (*Vertic inceptisol*). In this investigation, a bi-parental $F_{2:3}$ population was studied. The experimental material evaluated consisted of 287 $F_{2:3}$ progeny families generated from two parents contrasting for kernel row number, DHKN 509 (20-22 KRN) and CM 111 (12 KRN). The genetic material was evaluated under un-replicated fashion with a spacing of 60×20cm. The recommended dosage of fertilizers (150 N, 65 P_2O_5 , 65 K_2O , and 25 $ZnSO_4$ kg/ha) was applied to raise the healthy crop. The observations were recorded for 287 $F_{2:3}$ progeny families along with five plants each from parents and F_1 for nine characters *viz.* kernel row number, kernels per row, cob length (cm), cob girth (cm), pith girth (cm), pith weight (g), shelling per cent, 100-grain weight and grain yield per plant.

Estimation of variances, heritability and correlation analysis

The variances were calculated using parental, F_1 and F_3 data. Parents and F_1 were evaluated along with the F_3 population to determine the environmental variance using the following formulae suggested by Globerson *et al.* (1987). Phenotypic variance in F_3 population = V_{F_3} , Environmental variance (Error variance) = $(V_{P_{P1}} + V_{P_{P2}} + V_{P_{F1}})/3$ and Genotypic variance = Phenotypic variance - Error variance. Where, $V_{P_{P1}}$ = Phenotypic variance in parent 1; $V_{P_{P2}}$ = Phenotypic variance in parent 2 and $V_{P_{F1}}$ = Phenotypic variance in parent F_1 . Broad sense heritability is estimated as the ratio of genotypic variance to phenotypic variance (Hanson *et al.*, 1956). The data was analysed using the MS-EXCEL to determine genetic variability and 'R' version 4.2.1 software for determining Pearson's correlation and path coefficient analysis between yield and its attributing traits.

Results and discussion

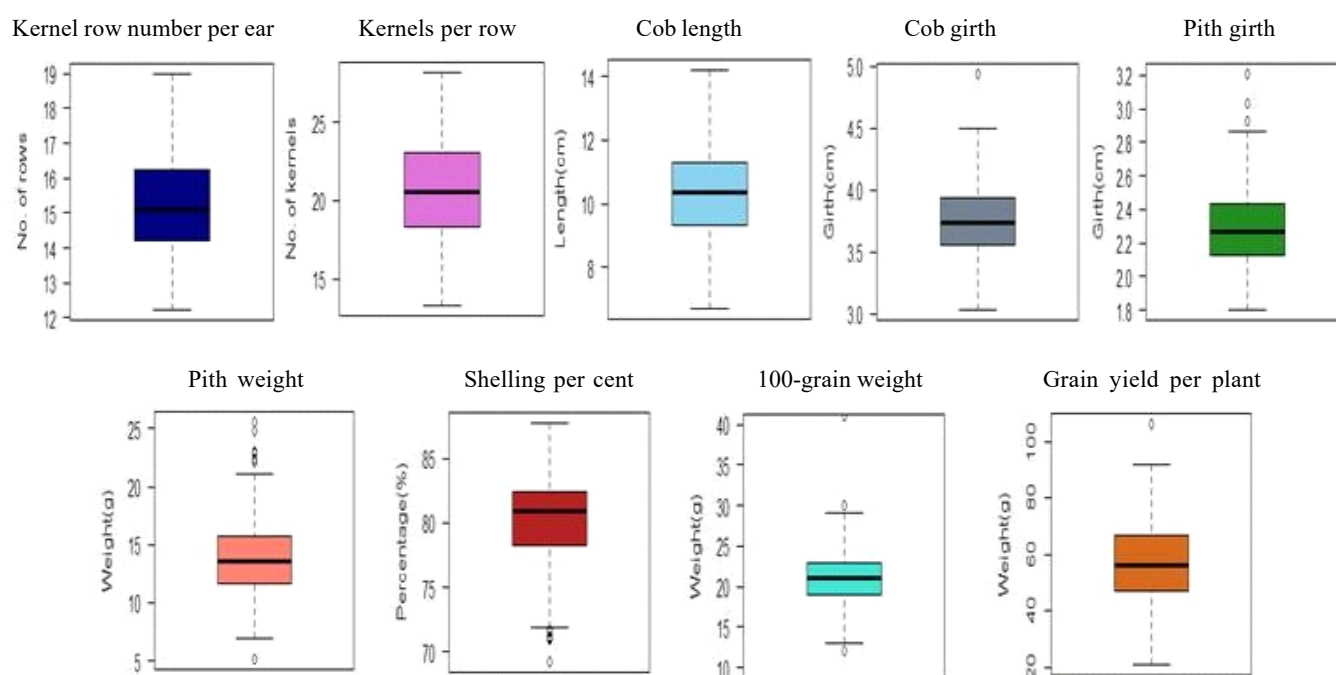
Genetic variability, heritability and genetic advance (per cent of mean)

The F_3 population of the cross DHKN 509 × CM 111 showed wide variation for all the characters studied (Table 1). Among the progeny families, the character kernel row number per ear ranged from 12.22 to 19.00 rows (mean 15.26) ; kernels per row ranged from 13.30 to 28.20 kernels (mean 20.66); cob length ranged from 6.68 to 14.22 cm (mean 10.32); cob girth ranged from 3.03 to 4.94 cm (mean 3.75); pith girth ranged from 1.80 to 3.21 cm (mean 2.29); pith weight ranged from 5.11 to 25.60 g (mean of 13.86); shelling per cent ranged from 69.20 to 87.79% (mean 80.21); 100-grain weight ranged from 12.00 to 41.00 g (mean 21.10); grain yield per plant ranged from 21.00 to 106.40 g (mean 57.08). Thus, the trait grain yield per plant recorded the highest range among all the traits under study indicating greater opportunity for selection (Figure 1). Similar results were recorded by Hosamani *et al.* (2018).

The magnitude of phenotypic coefficient of variation (PCV) was greater than that of genotypic coefficient of variation (GCV) in $F_{2:3}$ population for nine traits studied indicating the effect of environment (Figure 2). Among them, very high estimates of PCV and GCV were observed

Table 1. Estimates of genetic variability parameters for grain yield and its attributing traits in F_3 population of DHKN 509 $\times$ CM 111

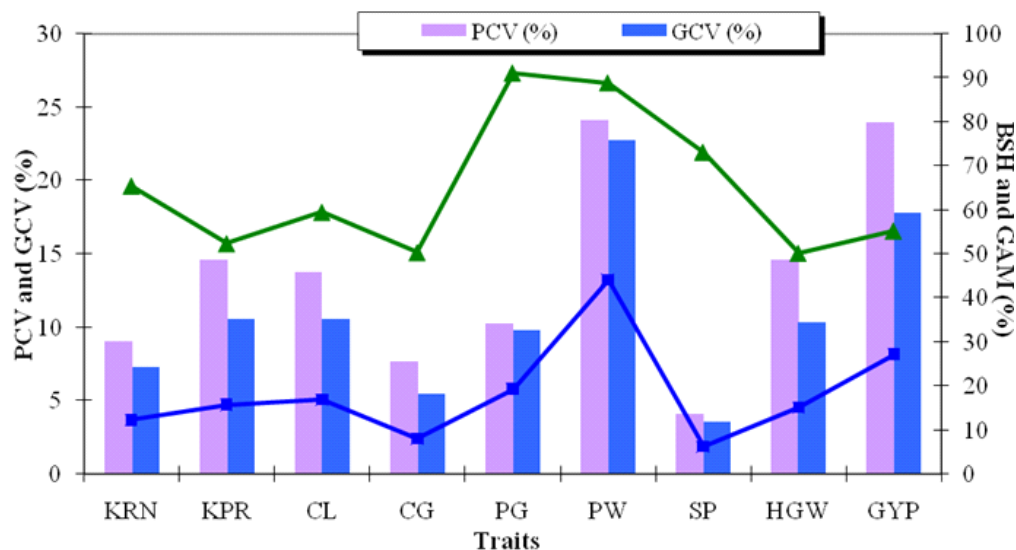
Characters	Mean	Range		PCV (%)	GCV (%)	h^2_{bs} (%)	GAM (%)
		Min	Max				
KRN	15.26	12.22	19.00	9.08	7.34	65.37	12.22
KPR	20.66	13.30	28.20	14.61	10.56	52.27	15.73
CL	10.32	6.68	14.22	13.77	10.61	59.38	16.84
CG	3.75	3.03	4.94	7.70	5.46	50.21	7.97
PG	2.29	1.80	3.21	10.30	9.83	91.05	19.32
PW	13.86	5.11	25.60	24.16	22.76	88.79	44.19
SP	80.21	69.20	87.79	4.14	3.54	73.03	6.24
HGW	21.10	12.00	41.00	14.60	10.33	50.08	15.06
GYP	57.08	21.00	106.40	23.97	17.80	55.14	27.23

**Figure 1.** Box-plots depicting variability in yield and its ancillary traits in $F_{2.3}$ population of DHKN 509 $\times$ CM 111

for pith weight (24.76%, 22.76%) and grain yield per plant (23.97%, 17.80%). Similar results were recorded by Hassan and Hussain (2014) and Reddy *et al.* (2022). Thus, these traits provide a greater chance for effective selection. Moderate values of PCV and GCV were showed by 100-grain weight (14.60%, 10.33%), kernels per row (14.61%, 10.56%), cob length (13.77%, 10.61%) and pith girth (10.30%, 9.83%). Whereas, low PCV and GCV were recorded for kernel row number (9.08%, 7.34%), cob girth (7.70%, 5.46%), and shelling per cent (4.14%, 3.54%). Similar observations of low PCV and GCV were recorded by Bartaula *et al.* (2019), which indicates rigorous selection should be practiced to improve these characters.

High heritability coupled with high to moderate genetic advance was exhibited by pith weight (88.79%, 44.19%), pith girth (91.05%, 19.32%), and kernel row number (65.37%, 12.22%) suggesting that these traits are governed by additive gene action. Similar findings were observed by Khan and Mahmud (2021) and Meena *et al.* (2016) for kernel row number. Moderate heritability with high to moderate genetic advance was recorded for grain yield per plant (55.14%, 27.23%), cob length (59.38%, 16.84%), kernels per row (52.27%, 15.73%) and 100-grain weight (50.08%, 15.06%). Similar results were observed for grain yield per plant by Bhiusal *et al.* (2017). The characters such as shelling per cent (73.03%, 6.24%) and cob girth (50.21% and 7.97%) showed high to

Figure 2. Bar graph depicting phenotypic and genotypic coefficient of variation and line graph showing heritability in broad sense and genetic advance (% of mean) for nine traits



moderate heritability coupled with low genetic advance indicating that the expression for these characters were influenced by non-additive gene action.

Correlation analysis

The correlation study showed all eight characters *viz.*, cob length (0.77), kernels per row (0.76), pith weight (0.65), cob girth (0.61), 100-grain weight (0.43), shelling per cent (0.41), pith girth (0.37) and kernel row number (0.3) were positively and significantly associated with grain yield per plant indicating that individual plant selection can be done and advanced generations for these traits leads to improvement in maize grain yield (Figure 3). Chaurasia *et al.* (2020); Devasree *et al.* (2020); Taiwo *et al.* (2020) and Yahaya *et al.* (2021) also reported the similar findings for relationship of grain yield per plant with other yield-related traits.

Path coefficient analysis

The path coefficient analysis revealed that highest positive direct effect on grain yield per plant is exhibited by pith weight (0.7645), followed by shelling per cent (0.6394), kernels per row (0.1273), kernel row number (0.0610), cob girth (0.0468), 100-grain weight (0.0440), and cob length (0.0429) (Table 2). Highest strong correlation of cob length with grain yield per plant (0.77) may be due to high contribution of kernels per row (0.0942), pith weight (0.4817) and shelling per cent (0.1279) on grain yield through cob length. Moderate association of kernel row number with grain yield per plant may be due to

negative indirect effect of pith girth (-0.0137) and 100-grain weight (-0.0026) on grain yield per plant through kernel row number. These results are parallel with the findings of Reddy *et al.* (2022). Furthermore, the negative direct effect on grain yield per plant was recorded by pith girth (-0.0415) but positive association of pith girth (0.37) with grain yield per plant owed to positive indirect effect of pith weight (0.4740), kernels per row (0.0267), cob girth (0.0262) and kernel row number (0.0201) through pith girth on grain yield per plant.

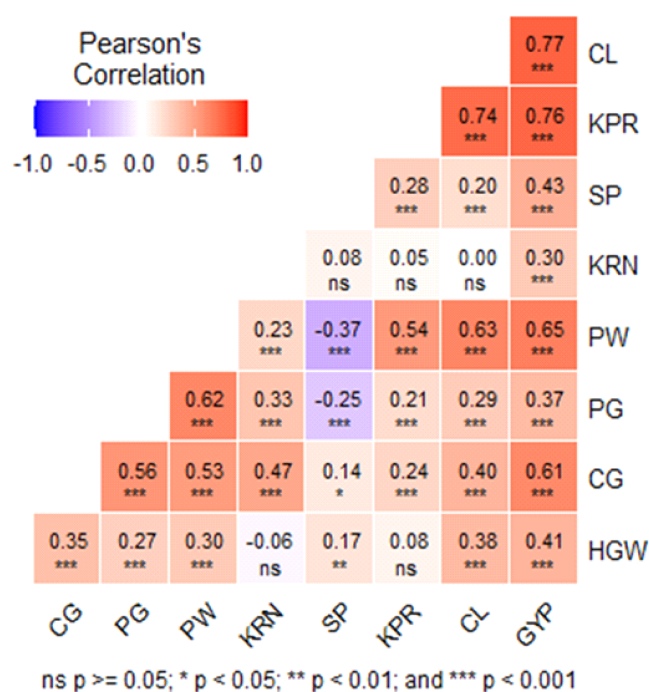


Figure 3. Association between grain yield and its attributing traits
Note: * Significant at 0.05 probability level and ** Significant at 0.01 probability level

Table 2. Direct (diagonal) and indirect effects of eight yield attributing characters on grain yield

Characters	KRN	KPR	CL	CG	PG	PW	SP	HGW	Association with grain yield
KRN	0.0610	0.0064	0.0000	0.0220	-0.0137	0.1758	0.0511	-0.0026	0.30**
KPR	0.0031	0.1273	0.0317	0.0112	-0.0087	0.4128	0.1790	0.0035	0.76**
CL	0.0000	0.0942	0.0429	0.0187	-0.0120	0.4817	0.1279	0.0167	0.77**
CG	0.0287	0.0306	0.0171	0.0468	-0.0233	0.4052	0.0895	0.0154	0.61**
PG	0.0201	0.0267	0.0124	0.0262	-0.0415	0.4740	-0.1598	0.0119	0.37**
PW	0.0140	0.0688	0.0270	0.0248	-0.0258	0.7645	-0.2366	0.0132	0.65**
SP	0.0049	0.0357	0.0086	0.0065	0.0104	-0.2829	0.6394	0.0075	0.43**
HGW	-0.0037	0.0102	0.0163	0.0164	-0.0112	0.2294	0.1087	0.0440	0.41**

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

Residual effect = 0.0488

KRN = Kernel row number per ear; CG = Cob girth (cm); SP = Shelling per cent; KPR = Kernels per row; PG = Pith girth (cm); HGW = 100-grain weight (g); CL = Cob length (cm); PW = Pith weight (g); GYP = Grain yield per plant (g)

Conclusion

The present study showed that there is a wide genetic variability in the F₃ population studied and the characters viz., pith weight, kernels per row, cob length, showed high PCV, GCV, heritability, genetic advance and positive correlation which had direct effect on grain yield per plant and these are the important yield influencing characters in maize. Hence, selection considering these characters could enhance the maize grain yield.

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