

Genetic analysis of yield and its components traits in diallel cross of maize (*Zea mays* L.) under rainfed condition

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Abstract: Maize is one of the oldest domesticated crops and the world's third most important cereal crop, with a high yield potential. It is currently farmed in most parts of the world, across a wide variety of environmental conditions spanning 50 degrees north and south of the equator. In many regions of the world, it is widely utilized for food, feed, fuel, and fiber. Because of its cross-pollinated nature, maize has a wide range of morphological variability and geographic adaptation. A diallel mating design excluding reciprocals was practised among 8 diverse parents to generate 28 crosses for assessing genetic parameters in maize during *kharif* 2021. Analysis of variance revealed significant variability in the parents for all the characters under study except cob length, cob girth, number of kernel row per cob and 100 grain weight. The ratio of σ^2_{gca} and σ^2_{sca} was found less than unity for most the characters, which revealed prime role of non-additive gene action for expression of the characters under study. Among the traits, grain yield was positively ($P < 0.01$) correlated with plant height, cob length, cob girth, kernel row per cob, hundred grain weight (test weight) and cob weight under rainfed conditions. High

broad-sense heritability was observed for days to tasselling, days to silking, kernel per row, grain yield and, kernel row per cob indicating that additive or genetic factors influenced the expression of these traits and they are less influenced by environmental factors.

Keywords: Maize · Correlation · Heritability · Non-additive · Variance

Introduction

Maize (*Zea mays* L.) is one of the most important strategic and economic crops in the world. It is the third most important food grain in India after wheat and rice. It accounts for around 10 per cent of total food grain production in the country. In India, maize is principally grown in two seasons, rainy (*kharif*) and winter (*rabi*). *Kharif* maize represents around 78-80 per cent of maize area in India, while *rabi* maize correspond to 20-22 per cent maize area. Globally, maize is known as queen of cereals because of its highest genetic yield potential. Maize is the only cereal crop that can be grown in diverse seasons. Being a C4 plant, it is physiologically more efficient and resilient to changing climatic conditions with wider genetic variability and also able to grow successfully throughout the world over a wide range of environmental conditions covering tropical, subtropical and temperate agro-climatic conditions. The method of diallel-crossing is one of the widely used methods of hybridization, because it is possible to determine the performance of the different genotypes in the offspring by calculating general and specific combining ability and their effects. A breeder will be able to determine to what extent the environment impacts yield by determining genotypic and phenotypic variance in yield and its components of diverse

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crop genotypes (Ullah *et al.*, 2012). Heritability assumes that individuals who are closely connected are more likely to resemble one another than those who are distantly related (Falconer and Mackay, 1996). Heritability estimate helps breeders to allocate resources effectively to select desired traits and to achieve maximum genetic gain with little time and resources (Smalley *et al.*, 2004). Characters having a high heritability can be quickly progressed by using simple selection. Grain yield is the polygenic trait that is influenced by a number of morphological and physiological traits. Information on the correlations between traits is crucial in maize breeding to aid the identification of superior genotypes with higher grain yield through indirect selection, of secondary traits. Grain yield can be enhanced by understanding the correlation between yield and its components and influencing the kind of relationship between them (Kalla *et al.*, 2001). Present study was therefore under taken to investigate the trend of the genetic parameters for yield and its attributing traits as well as their correlation under rainfed condition.

Materials and methods

Experimentation

Half diallel crosses were made to generate 28 F_1 crosses during rabi 2020-21. The 28 F_1 crosses and the eight parents were evaluated in a randomized complete-block design (RCBD), with three replications in *kharif* 2021 cropping season at Maize Research Station, Sardarkrushinagar Dantiwada Agricultural University, Bhiloda. Due to limited F_1 seed each entry was grown in 1 row with 4 m in length at one location only. The spacing of 60 cm between the rows and 20 cm between the plants was maintained. All recommended agronomic practices were followed for raising a good maize crop. Twelve phenotypic traits were recorded i.e., days to tasseling, days to silking, anthesis-silking interval, primary ear height (cm), plant height (cm), cob length (cm), cob girth (cm), number of kernel row per cob, number of kernels per row, cob weight per plant (g), grain weight per plant (g) and test weight (g). The mean performance of each parent and hybrids was subjected to statistical analysis.

Statistical analysis

Analysis of variance to test the significance for each character was carried out as per methodology given by

Panase and Sukhatme (1985). The correlation coefficients were calculated to determine the degree of association of characters with yield and also among the yield components themselves. Genotypic correlations were computed by using the formula given by Webber and Moorthy (1952) and Singh and Chaudhary (1985). The significance of 'r' value was tested according to t-test at n-2 degree of freedom. Heritability in broad and narrow sense was estimated depending on the variance of general and specific combining abilities, and on the variance of experimental error according to Singh and Chaudhary (1985). In AGD-R (Analysis of Genetic Designs with R software the proportion of additive and dominance variance components for grain yield and other secondary traits was computed using the Baker's ratio (Baker, 1978), considering that the genetic variance between single-cross progeny is $2\sigma^2A + \sigma^2D$ which is equivalent to addition of the mean squares contribution from the GCA and SCA (Rukundo *et al.*, 2017). The Baker's ratio formula used to generate variance components was: $GCA/SCA = 2\sigma^2 GCA / (2\sigma^2 GCA + \sigma^2 SCA)$.

Results and discussion

The results of analysis of variance (Table 1) revealed that mean square values due to genotypes were found significant for all the characters, indicating the presence of sufficient amount of genetic variability in the material under study. The variance due to parents was found significant for the characters like; days to tasseling, days to silking, anthesis-silking interval, plant height, number of kernels per row and grain weight per plant. The mean square due to hybrids indicated significant difference for all the characters under study except cob girth. Mean sum of squares due to parents vs hybrids showed significant differences for characters under study viz., day to tasseling, days to silking, plant height, cob length, cob girth, number of kernel rows per cob, number of kernels per row, grain yield, 100 grain weight suggesting the existence of differences between parents and hybrids leading to manifestation of heterosis.

The ratio of *gca/ sca* variance for all the characters under study was found less than unity (Table 2) Therefore, prime role of non-additive gene action was observed for inheritance of most the traits. So, exploitation of these traits for improvement of yield through heterosis breeding may be beneficial. Baker's ratio close to zero

Table 2. Estimates of variance, heritability and bakers ratio for different traits

Character	DT	DS	ASI	PEH	PH	CL	CG	KR	KPR	CW	GY	TW
s ² gca	0.08	0.1093	0.0148	9.1544	19	0.2504	0.0191	0.025	1.1093	8.4892	4.7988	-0.0168
s ² sca	1.17	0.9475	0.06	38.165	65.69	1.3129	0.0909	0.3277	5.54	65.63	44.845	1.9641
Ems	0.18	0.27	0.18	42.07	155.56	3.05	0.34	0.37	5.16	67.784	38.489	2.26
s ² gca / s ² sca	0.07	0.1154	0.2463	0.2399	0.2893	0.1907	0.2097	0.0763	0.2002	0.1293	0.107	-0.008
H ² bs	95.68	92.83	59.89	80.11	66.66	64.08	53.25	75.38	81.85	78.52	80.93	71.93
H ² ns	11.51	17.40	19.79	25.97	24.43	17.69	15.76	9.98	23.41	16.14	14.27	-1.25
Bakers ratio	0.12	0.19	0.33	0.32	0.37	0.28	0.30	0.13	0.29	0.21	0.18	-0.02

for flowering traits and kernel yields and its attributing traits implies that SCA estimates were more important. Estimates of Baker's ratio for these traits (grain yields) confirmed the importance of nonadditive gene action. Thus, predicting hybrid performance based on GCA values alone will be ineffective. The predominance of nonadditive gene effects for these traits also suggests that genetic gain could only be achieved through hybridization followed by selection at advanced generations, where the genes are fully fixed and expressed, dominance is dispersed, and undesirable linkage is broken. Estakhr and Heidari (2012) also reported the same results for yield and attributing traits.

For individual traits, the highest heritability (b.s) was observed for DT (95.68%) and the lowest for cob girth (53.25%), (Table 2). High broad-sense heritability observed for DT (95.68%), DS (92.83), KPR (81.85%), GWPP (80.93%) and KRPC (75.38%) indicates that additive or genetic factors influenced the expression of the traits and that the traits were less influenced by environmental factors. Similar results have been reported by Ilyas *et al.* (2019). The high broad-sense heritability estimates mean that the phenotypes were true reflection of the genotypes for the measured traits and that selection based on the phenotypic value could be reliable. On the

contrary, cob girth (53.25%) showed moderately low broad-sense heritability estimates. This indicates that the environment influenced the expression of the traits and that there is little scope for advancement and/or improvement of these traits than the maturity traits.

Information on narrow-sense heritability is of prime importance to the breeder as a measure of efficiency in selection and as an index of transmissibility of favourable additive genes from parents to their offspring's (Falconer *et al.*, 1996). Narrow-sense heritability was moderate for PEH (25.97%), PH (24.43%) followed by KPR (23.41%) and DS (17.40%) suggesting that both additive and non-additive gene effects were primarily responsible for the genetic variation in these traits and improvement of these traits cannot rely upon only through selection. These results are in consonance with findings of Reddy and Jabeen (2016). The variation in the magnitude between broad-sense and narrow-sense heritability of the different traits indicates their levels of environmental influence. The wider difference between the broad- and narrow-sense heritability for all the traits studied suggests a higher environmental influence and therefore leads to difficulty in selection.

The correlation studies were carried out for grain yield per plant and other yield attributing traits (Table 3).

Table 1. Analysis of variance for morphological traits

Source of variation	d.f.	DT	DS	ASI	PEH	PH	CL	CG	KR	KPR	CW	GY	TW
Replications	2	0.108	0.27	0.33	85.20	374.81	6.94	0.823	0.03	10.63	21.41	47.27	0.87
Genotypes (G)	36	3.53*	3.16*	0.41*	185.92*	415.83*	7.65*	0.66*	1.29*	24.70*	273.40*	175.67*	6.821*
Parents (P)	7	3.31*	4.64*	0.66*	201.79*	573.45*	4.14	0.632	0.43	16.02*	185.73*	145.25*	0.94
Hybrids (H)	27	2.05*	1.58*	0.35*	167.78*	318.96*	8.51*	0.515	1.50*	25.19*	226.86*	125.72*	6.77*
Parents vs. Hybrids	1	44.70*	37.46*	0.32	671.06*	2312.76*	13.26*	5.63*	2.60*	91.62*	2229.42*	1717.33*	52.22*
Error	72	0.18	0.27	0.18	42.07	155.56	3.05	0.34	0.48	5.46	187.59	195.38*	3.91

*, ** indicate level of significance at 5% and 1%, respectively.

DT = Days to 50% tasselling, DS = Days to 50% silking, ASI = Anthesis silking interval PEH = Plant ear height PH = Plant height CL = Cob length, CG = Cob girth, KR = No. of row per cobs, KPR = No. of kernels per row NGPR = No. of grains per row, CW = Cob weight, TGW = 1000 grain weight and GY = Grain yield

Table 3. Genotypic correlation coefficient values among all pairs of traits in maize

Character	DT	DS	ASI	PEH	PH	CL	CG	KRPC	KPR	CW	HGW	GY
DT	1											
DS	0.939**	1										
ASI	-0.299 ^{NS}	0.047 ^{NS}	1									
PEH	-0.254 ^{NS}	-0.218 ^{NS}	0.135 ^{NS}	1								
PH	-0.340*	-0.320 ^{NS}	0.101 ^{NS}	0.878**	1							
CL	-0.128 ^{NS}	-0.147 ^{NS}	-0.037 ^{NS}	0.274 ^{NS}	0.386*	1						
CG	-0.331*	-0.362*	-0.044 ^{NS}	0.230 ^{NS}	0.160 ^{NS}	0.392*	1					
KRPC	-0.068 ^{NS}	-0.078 ^{NS}	-0.018 ^{NS}	0.392*	0.292 ^{NS}	0.338*	0.493**	1				
KPR	-0.219 ^{NS}	-0.217 ^{NS}	0.035 ^{NS}	0.298 ^{NS}	0.433**	0.922**	0.332*	0.333*	1			
CW	-0.326 ^{NS}	-0.289 ^{NS}	0.147 ^{NS}	0.296 ^{NS}	0.435**	0.826**	0.400*	0.395*	0.919**	1		
HGW	-0.287 ^{NS}	-0.251 ^{NS}	0.135 ^{NS}	0.328 ^{NS}	0.421*	0.620**	0.434**	0.354*	0.575**	0.639**	1	
GY	-0.335*	-0.297 ^{NS}	0.149 ^{NS}	0.296 ^{NS}	0.427**	0.780**	0.455**	0.420*	0.882**	0.985**	0.630**	1

*, ** indicate level of significance at 5% and 1%, respectively.

Table 4. Weather data year (2021-22)

Standard Week No.	Dates	Maximum Temp. (°C)	Minimum Temp. (°C)	R H (%)	Rain fall (mm)	Days
14	02 April – 08 April	39.5	30.2	92.3	0.0	0
15	09 April – 15 April	42.5	30.5	89.7	0.0	0
16	16 April – 22 April	41.3	29.0	91.3	0.0	0
17	23 April – 29 April	41.5	29.5	91.3	0.0	0
18	30 April – 06 May	43.5	27.5	90.1	0.0	0
19	07 May – 13 May	43.0	28.5	88.6	0.0	0
20	14 May – 20 May	41.7	30.3	91.7	0.0	0
21	21 May – 27 May	43.5	31.5	90.3	0.0	0
22	28 May – 03 June	42.5	31.9	88.2	0.0	0
23	04 June – 10 June	39.6	28.3	83.3	72.2	3
24	11 June – 17 June	38.2	26.6	89.6	0.0	0
25	18 June – 24 June	36.9	27.3	90.0	16.5	1
26	25 June – 01 July	35.1	24.3	90.7	0.0	0
27	02 July – 08 July	37.6	27.2	88.5	0.0	0
28	09 July – 15 July	32.8	27.0	89.0	46.5	4
29	16 July – 22 July	32.3	26.3	90.1	0.0	0
30	23 July – 29 July	30.6	25.7	85.4	44.2	4
31	30 July – 05 August	33.3	26.8	93.5	15.0	4
32	06 August – 12 August	34.3	27.2	87.1	0.0	0
33	13 August – 19 August	34.5	27.1	89.1	3.0	1
34	20 August – 26 August	36.8	25.7	91.4	31.4	2
35	27 August – 02 September	37.4	27.2	88.9	58.8	3
36	03 September – 09 September	36.9	25.3	87.5	24.6	3
37	10 September – 16 September	35.4	24.0	88.7	201.2	6
38	17 September – 23 September	35.5	25.7	89.5	44.6	5
39	24 September – 30 September	34.4	27.1	92.5	48.6	3
40	01 October – 07 October	35.6	24.7	90.7	1.1	1
41	08 October – 14 October	35.8	26.8	90.5	1.0	1
42	15 October – 21 October	36.1	24.5	88.4	0.0	0
43	22 October – 28 October	34.3	22.4	87.3	0.0	0
		37.4	27.2		608.7	41

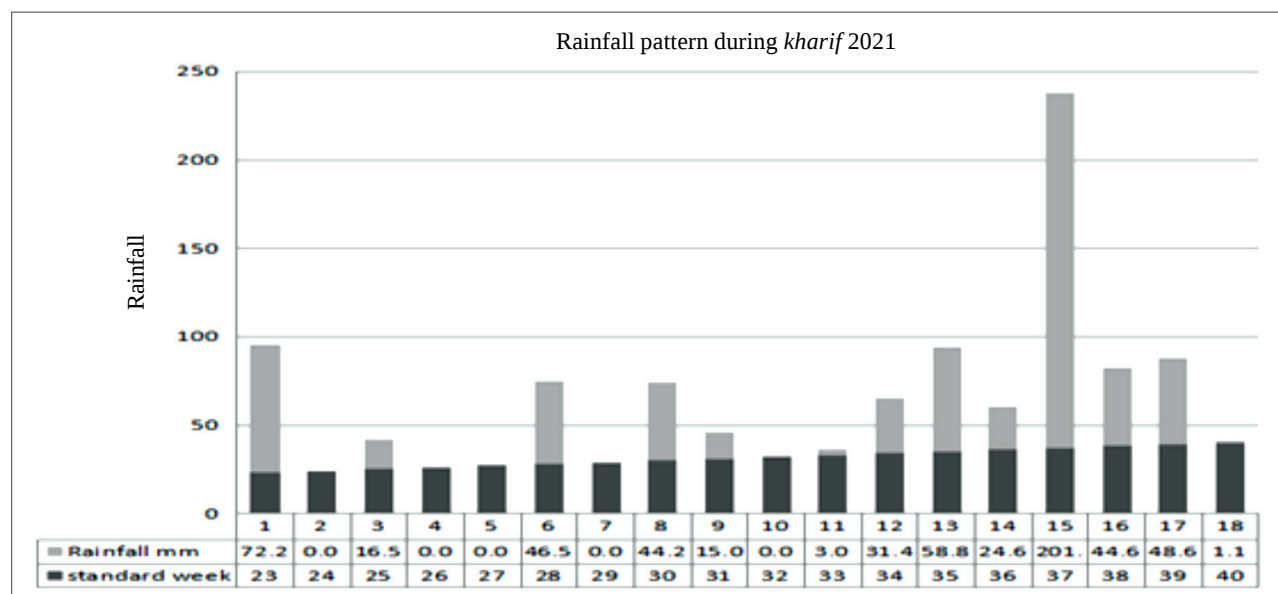


Figure 1. Rainfall pattern during cropping season (*kharif* 2021) at Maize Research Station Bhloda

The association between two variables which can be directly observed is termed as phenotypic correlation, whereas the inherent or heritable association is known as genotypic correlation (Table 4). Among the traits, GY was highly significant and positively correlated with PH ($r = 0.42^{**}$), CL (0.78^{**}), CG (0.45^{**}), KPR (0.88^{**}), HGW (0.98^{**}) and CW ($r = 0.63^{**}$) under rainfed conditions. Days to 50% tasseling showed positive significant association with days to 50% silking (0.93^{**}) and negative significant association with PH (-34^{*}), CG (-0.33^{*}) and GY (-0.33^{*}) (Figure 1). Days to 50% silking also followed the same trend for yield attributing traits and seed yield per plant. This clearly indicates that as the number days taken for tasseling and silking increase, most of the assimilates are diverted towards vegetative growth of the plant as a result of which the ear characters, plant height and ultimately grain yield are reduced significantly. Similar results were also reported by earlier workers viz., Nataraj *et al.* (2014); Talabi *et al.* (2017) and Matongera *et al.* (2023). In the present study, plant height showed positive significant association with cob length, number of kernels per row, cob weight and grain yield. In the present material under study, increased plant height contributed for increase in the length of ear thereby accommodating more kernel rows and more number of kernels per row ultimately resulting in more seed yield per plant. Ear height showed positive significant association with kernel rows. Positive significant association of cob characters with number of kernel rows, number of kernels per row, test weight and grain

yield were observed indicating that increase in length and girth of ears will lead to simultaneous increase in kernel rows as longer and broader kernels can accommodate more number of kernel rows and consequently more number of kernels per row. These are the important yield attributing traits which can be aimed for simultaneous improvement in yield. Similar results were reported by earlier workers viz., Jemal *et al.* (2020) and Shivani and Prasad (2017).

Conclusion

Genotypic correlation coefficients showed that all the traits considered in the study have positive correlation with grain yield except days to 50% tasseling, days to 50% silking, Anthesis silking interval and primary ear height. Plant height, cob length and girth, number of kernels per row, number of kernels row and 100-grain weight showed highly significant and positive correlations with grain yield. Genotypic correlations among traits affecting grain yield explain the true association as they exclude any environmental influences. High broad-sense heritability observed for flowering and yield attributing traits along with grain yield. However, further evaluation of these genotypes at more locations and over years is advisable to confirm the promising results observed in present study. Hence, it can be concluded that cob length, kernel per row, and 100-grain weight were the most effective traits for selection to improve grain yield of the maize genotypes tested in rainfed condition.

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