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Estimation of genetic variance from full-sib and half-sib families in a maize (*Zea mays* L.) composite

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Abstract

Sixty four randomly selected So plants (used as males) were each mated to four different plants (used as females) to generate 256 full-sib families as per North Carolina Design-1 for the estimation of genetic components of variance and related parameters in a large random mating maize composite Mahidhawal. These 256 full-sib families were evaluated in an incomplete block design with two replications in rainfed farming situations under two different fertility levels. Comparison of the relative magnitude of the additive genetic variance and variance due to dominance deviations revealed that the former was more important for grain yield per plant and its component traits. Variance due to dominance deviations was affected more by the environmental interaction as compared to additive genetic variance. Genes responsible for the expression of majority of the traits showed no dominance to partial dominance, indicating that σ^2_A was the sole contributor to total genetic variability. Heritability (narrow sense) estimates showed that sufficient proportion of additive genetic variance was available for an effective selection procedure to be used.

Key words: Maize composite, additive genetic variance, NC-1 design, heritability (narrow sense)

Introduction

Knowledge on the genetic architecture of populations is necessary to formulate efficient breeding methodology. It is essential to find out the relative magnitude of additive genetic variance and dominance variance with regard to the characters of concern to breeder. Selection within population is advisable if the gene action is mainly additive. On the other hand existence of dominance or epistasis justifies the use of hybrid programme [1]. Mahidhawal is widely cultivated maize composite in the major maize growing belt of the state of Rajasthan, with a average productivity of 35-44 Q/ha. A need was felt to further upgrade the yield level of this composite to make it more suitable for the changing farming situations facing many stresses of both biotic and abiotic nature. Therefore, present investigation was carried out to estimate genetic parameters descriptive of the inheritance of quantitative characters within the open pollinated variety of maize, through analysis of full-sib and half sib families, in order to extract lines and families that may be good parents for conventional and non-conventional hybrids as well as for making synthetics.

Materials and methods

The experimental material consisted of 256 full-sib families developed as per North Carolina Design-1 [2] in maize composite Mahidhawal. 256 full-sib families (64 half-sib families) were developed during rabi 2001-02 at Rajasthan College of Agriculture, Udaipur. To develop full-sib and half-sib families, each 64 randomly chosen male plants were crossed with six random female plants. After harvest out of six female plants, four successfully pollinated female plants that had sufficient seed for field evaluation were retained to constitute a male group (a group of four families involving the same male parent). The sixty-four male groups were assigned to 16 sets with each set comprising four male groups. Each set of four male groups thus have sixteen families (full-sibs) in it. Various male groups were assigned to the sets at random. In each replication sets were randomized and in each set the sixteen full sib families were also randomized.

These 256 full-sib families were evaluated in an incomplete block design (simple lattice design) with two replications in rainfed farming situations of Udaipur under two fertility levels of NPK *viz.*, 120:60:00 kg per hectare (E_1) and 60:60:00 kg per hectare (E_2). Each family was sown in a single row plot of 3 meter length maintaining a crop geometry of 60 × 25 cm. Data on five random competitive plants were recorded for grain yield per plant (g), anthesis-silking interval, ear length

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(cm), ear diameter (cm), kernel rows per ear, 100-grain weight (g), number of cobs per plant, plant height (cm) and ear height (cm) and mean values were used to compute statistical analysis. Combined analysis across environments was followed as per Robinson *et al.* [3]. By using appropriate mean squares obtained from the analysis of variance, estimates of variance components for males (σ^2_M), females within males (σ^2_F) and their interaction with environments (σ^2_{ML} and σ^2_{FL}) were computed. These components were used to estimate additive genetic variance (σ^2_A), variance due to dominance deviation (σ^2_D) and their interactions with environments (σ^2_{AL} and σ^2_{DL}) as per Comstock and Robinson [4].

Results and discussion

Analysis of variance revealed existence of significant genetic variability for all the traits suggesting sufficient variability in population and conforming the heterogeneous nature of composite Mahidhawal (Table 1a and 1b).

The estimates of additive genetic variance (σ^2_A) and variance due to dominance deviation (σ^2_D) from North Carolina Design-1 analysis revealed importance of additive genetic variance in the inheritance of grain yield per plant, 100-grain weight, kernel rows per ear, ear length, ear diameter, number of cobs per plant, plant height, ear height and anthesis silking interval. While, dominance variance was of lower magnitude for these traits (Table 2). These findings are in agreement with earlier reports [5, 6].

Dominance ratio (σ^2_D/σ^2_A) showed that genes responsible for the expression of majority of characters including grain yield per plant showed no dominance to partial dominance (< 0 to < 1) indicating that σ^2_A was major contributor of total genetic variability for most of the traits. Therefore, selection within population is advisable since the gene action is mainly additive. Positive and significant estimates of σ^2_{AL} for all the traits except for anthesis-silking interval, number of cobs per plant and kernel rows per ear suggested major role of additive genetic variance and dominance

Table 1a. Analysis of variance for different characters in population Mahidhawal

S. No.	Source of variation	df	Env.	Grain yield per plant	Anthesis silking interval	Ear length	Ear diameter	Kernel rows per ear	100-grain weight	No. of cobs per plant	Plant height	Ear height
1.	Sets	15	E_1	1693.80**	0.34**	20.21**	17.69**	9.70**	29.11**	0.29**	3336.50**	1638.49**
			E_2	2975.11**	0.46**	22.23**	12.45**	16.03**	23.91**	0.11	1942.11**	921.16**
2.	Replication in sets	16	E_1	9.67	0.16	1.10**	0.73	0.63	3.05	0.16	54.73**	39.63**
			E_2	9.16	0.19	1.40**	1.23**	0.76*	2.75**	0.29**	32.74**	29.04**
3.	Males in sets	48	E_1	1980.33**	0.52**	11.17**	6.31**	12.31**	27.12**	0.78**	1609.85**	895.58**
			E_2	1968.28**	0.65**	5.91**	7.10**	11.59**	21.31**	0.77**	1082.07**	305.14**
4.	Females in sets	192	E_1	720.41**	0.26*	2.87**	1.98**	3.85**	7.06**	0.29**	367.92**	302.82**
			E_2	645.44**	0.15*	1.68**	2.00**	3.68**	6.29**	0.27**	278.11**	132.48**
5.	Error	240	E_1	144.35	0.19	0.34	0.41	0.54	0.28	0.17	28.19	11.81
			E_2	125.09	0.15	0.31	0.28	0.38	0.31	0.12	7.14	4.27

*,** Significant at 1% and 5% level respectively.

Table 1b. Pooled analysis of variance for different characters in population Mahidhawal

S. No.	Source of variation	df	Grain yield per plant	Anthesis silking interval	Ear length	Ear diameter	Kernel rows per ear	100-grain weight	No. of cobs per plant	Plant height	Ear height
1.	Environments	1	33007.50**	0.001	129.71**	109.75**	15.57**	105.76**	2.15**	33653.79**	1692.27**
2.	Sets	15	3841.32**	0.21	40.77**	27.62**	12.22**	51.04**	0.29**	4923.89**	1868.06**
3.	Sets × environments	15	827.59**	0.58**	1.67**	2.52**	13.51**	1.98**	0.11	354.73**	691.60**
4.	Replication in sets in environments	32	9.42	0.17	1.25**	0.98**	0.69*	2.90**	0.22**	43.74**	34.33**
5.	Males in sets	48	3037.16**	0.99**	14.23**	12.06**	12.23**	47.61**	0.60**	2557.10**	932.47**
6.	Females in males in sets	192	328.10**	0.52**	3.11**	1.85**	1.92**	15.67**	0.37**	184.45**	75.05**
7.	Males in sets × environment	48	641.44**	0.45**	2.86**	1.35**	7.67**	0.82**	0.25**	134.81**	268.25**
8.	Females in sets × environments	192	7.75	0.29	0.44**	0.43*	1.62**	0.29	0.22**	61.58**	60.25**
9.	Error	480	134.72	0.17	0.32	0.34	0.46	0.29	0.14	17.67	8.04

*,**Significant at 1% and 5% level respectively.

× environment interaction (σ^2_{DL}) component played very little role in determining the total genetic variability. Further, in main components, additive genetic variance have higher magnitude for most of the traits than its corresponding additive × environment interaction component, indicating that the expression of σ^2_A was more consistent over the environments than that of σ^2_D. Similar results in maize have been reported by Mani and Dubey [7].

Heritability of metric characters is one of the most important properties and in reality in its prediction role for expressing the reliability of phenotypic value and making the effective selection system in separating genotypes [8], Heritability (narrow sense) for different characters in the present study showed that the additive genetic variance appeared to be a relatively high fraction of the total phenotypic variance for grain yield. However, additive genetic variance for characters ear length, ear diameter, kernel rows per ear and 100-grain weight was estimated to 0.5 or more than 0.5 of the total phenotypic variance in both the fertility levels indicating the presence of sufficient proportion of additive genetic variance available in this maize composite for an effective selection programme to be used (Table 2).

Predicted response to selection provides an effective means of comparing various methods of recurrent selection for population improvement in crop plants. In the present study the expected genetic gains were higher from full-sib family selection than from mass selection under both the fertility levels for all the traits studied. For grain yield per plant it was 44.05 percent from full-sib family selection as compared to 25.14 percent from mass selection (pooled basis). Similarly 29.08 and 16.72 percent of expected genetic gain was observed for 100-grain weight and ear diameter through full-sib family selection, which was higher than the expected genetic gain obtained through mass selection for these traits (Table 3). These results clearly suggested continuation of intra population improvement through full-sib family selection. However, for anthesis silking interval higher expected genetic gain was observed in low fertility level (22.66) than high fertility level (16.13), which indicates that selection under low fertility level may also prove usefulness for early maturity. Superiority of full-sib family selection over mass selection in intra population improvement of an open pollinated maize variety have also been reported earlier [9, 10]. Thus, in the present population the synthesis of improved version (through full-sib family selection) would be appropriate to raise the grain yield potential without any appreciable decrease in the nature and magnitude of genetic variability in improved version.

Table 2. Estimates of additive genetic variance to (σ^2_A), dominance variance (σ^2_D), their interaction with environments, dominance ratio and heritability in narrow sense for different characters in population Mahidhawal

S. No.	Genetic component	Env.	Grain yield per plant	Anthesis silking interval	Ear length	Ear diameter	Kernel rows per ear	100-grain weight	No. of cobs per plant	Plant height	Ear height
1.	σ^2_A,	E_1	629.95**	0.12**	4.14**	2.16**	4.23**	10.02**	0.24**	620.96**	296.38**
		E_2	526.42**	0.18*	2.11**	2.55**	3.95**	7.50**	0.23**	401.98**	86.33**
		Pooled	518.84**	0.07	2.17**	2.32**	1.06	7.85**	0.05	574.85*	162.35**
2.	σ^2_D	E_2	522.15**	0.01	0.92	0.98	2.38	3.55	0.001	58.50*	285.63**
		E_2	514.28**	0.01	0.63	0.89	2.66	0.55	0.13	139.95*	170.10**
		Pooled	-	0.15	0.49	-	-	7.53**	0.10	-	-
3.	σ^2_D / σ^2_A, E_1		0.82 0.08	0.22	0.45	0.56	0.35	0.01	0.09	0.96	
		E_2	0.97	0.07	0.30	0.34	0.67	0.07	0.55	0.34	1.97
		Pooled	-	1.93	0.22	-	-	0.95	2.03	-	-
4.	σ^2_{DL}	E_1	-	-	-	-	-	-	-	-	-
		E_1	-	-	-	-	-	-	-	-	-
		Pooled	316.84**	0.07	1.20**	0.46*	0.02	0.26**	0.01	36.61**	103.99**
5.	σ^2_{DL}	E_2	-	-	-	-	-	-	-	-	-
		E_2	-	-	-	-	-	-	-	-	-
		Pooled	-	0.16*	-	-	2.28**	-	0.13	51.20**	0.42
6.	h^2 (ns)	E_1	513.45	54.00	79.04	64.64	61.45	73.11	73.27	89.53	50.41
		E_2	47.71	67.50	73.10	71.16	58.09	61.92	55.55	73.68	33.38
		Pooled	41.81	26.08	59.50	73.40	33.83	49.82	24.90	86.70	82.10

*,** Significant at 1% and 5% level respectively

Table 3. Expected genetic gain (as percent of mean) with different selection schemes at 5 percent selection intensity

S. No.	Selection scheme	Env.	Grain yield per plant	Anthesis silking interval	Ear length	Ear diameter	Kernel rows per ear	100-grain weight	No. of cobs per plant	Plant height	Ear height
1.	Full-sib selection	E_1	37.24	16.13	19.44	13.82	18.64	22.56	41.11	18.90	22.80
		E_2	39.01	22.66	14.00	16.57	19.01	19.18	41.60	15.53	10.95
		Pooled	44.05	7.83	12.47	16.72	7.89	29.08	9.37	22.72	18.99
2.	Mass selection	E_1	24.80	6.83	15.26	9.30	14.39	20.51	18.95	16.13	20.51
		E_2	26.06	10.09	9.80	12.40	14.98	16.96	21.60	14.58	9.92
		Pooled	25.14	3.79	9.16	11.17	14.70	25.20	4.18	19.41	16.28

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