Indian J. Genet., **61**(2): 111-114 (2001)

Estimation of genetic variances in a maize composite

Gul Zaffar, G. H. Zargar and Wani A. Shafiq

Division of Plant Breeding and Genetics, Sher-e-Kashmir University of Agricultural Sciences & Technology,
Shalimar Campus, Srinagar 191 121 (J&K)

(Received: June 2000; Revised: November, 2000; Accepted: February 2001)

Abstract

Sixty four randomly selected S_0 plants (used as males) were each mated to four different plants (used as females) to generate 256 full sib families as per NC Design-I and simultaneously selfed to produce 64 S_1 families for the estimation of genetic components of variance and related parameters. Both full-sib and S_1 families were evaluated in incomplete block design and randomized block design, respectively in two random environments. Observations were recorded on grain yield per plant, test weight, kernel rows per ear, kernels per row, ear length, ear diameter, plant height, ear height and days to silk.

Comparison of the relative magnitude of the additive genetic variance and variance due to dominance deviation revealed that the former was more important for all the traits studied both under NC-Design-I and the one factor design (S_1 families) except for kernels per row and ear length in in (NC-Design-I) and days to silk (in both the designs).

Variance due to dominance deviations was affected more by the environmental interaction as compared to additive genetic variance. Estimates of heritability estimates (narrow sense) for grain yield per plant were high in the S_1 (73.0%) than Design-I. Expected genetic gain in the reconstituted population introgressed from the elite families would be more in S_1 (29.77%) than full sib (7.77%) families.

Key Words : Maize composite, genetic variances, G x E interaction, heritability, expected genetic gain

Introduction

Estimates of additive and dominance genetic variances help to choose the most effective breeding procedure for a crop specie. Selection within populations would be advisable only if the gene action is mainly additive, on the other hand, existence of dominance or epistasis justifies the use of hybrid programme.

The one and two factor designs have been more frequently used than other designs to generate information on genetic components of variation. Estimation of the dominance components of variation in N. C. Design-I is not independent and more often than not is biased [1, 2]. Comparison of the estimates of components of genetic variation from N.C. Design-I and S_1 line analysis provides a measure for a more realistic approach to be adopted in the maize improvement programme.

The present investigation was carried out to estimate genetic architecture of a random mating maize composite C_8 through analysis of full sib and S_1 families.

Materials and methods

Full-sib and S_1 families were developed from a large random mated and nearly linkage equilibrium population of composite C_8 one hundred plants (S_0) were selected at random (used as male parents) and each crossed to four different plants (seed parents) to produce half-sib and full-sib families as per the procedure suggested by Robinson *et al.* [3]. The male parents were simultaneously selfed to produce S_1 families. After harvest, female ears with adequate seeds in each of the half-sib group were identified and such 64 male groups representing 256 full-sib families and 64 S_1 families were finally selected. The full sib and S_1 families were both evaluated at two random locations during 1997. The 64 male groups (half-sibs) were assigned at random to 16 sets, each set containing four half-sib groups or 16 full-sib families and were evaluated in incomplete block design with 2 replications. Progenies within a set and sets within a replication were randomly assigned to reduce random residual variation. The S_1 families were planted in a randomized complete block design with 2 replications. Each plot in both the experimental designs consisted of one row of 5m length spaced 75 cm apart. Two seeds at each hill were planted along the row spaced 20cm apart and later thinned to single plant/hill to maintain 66,000 plants ha^{-1} approximately. Border rows were planted all along the replications to avoid border row effect. Data on grain yield $plant^{-1}$, test weight, kernel rows per ear, kernels per row, ear length, ear diameter, plant height, ear height and days to silk were recorded and the mean values (median values for days taken to silk) were used to compute the analysis of variance.

Table 1a. Analysis of variance of Design-1 progenies for various characters pooled over environments

Source of variance	d.f	Mean Square								
		Grain yield Plant“	Test weight	Kernel row ear^{-1}	Kernels row^{-1}	Kernels row^{-1}	Ear length	Ear diameter	Plant height	Ear height
Environments	1	85764.0**	109.13**	66.07**	2527.69**	808.38**	1.36**	552473.9**	494789.1**	3536.3**
Sets	15	7647.1**	67.92**	6.50**	128.33**	23.80**	2.17**	3383.0**	1860.5**	150.4**
Environments × sets	15	1702.2**	10.46**	0.90**	33.29*	13.66**	0.63**	1210.5**	550.3**	25.2**
Replication in sets In environments	32	20.2	0.79	0.07	0.53	0.27	0.04	22.0	2.8	3.4
Males in sets	48	1686.2**	33.14**	3.31**	37.24**	6.57**	0.84**	148.1**	979.1**	32.4**
Females in males in sets	192	705.3**	15.87**	1.48**	15.21**	3.56**	0.31**	419.4**	275.7**	14.4**
Males in sets × Environments	48	783.1**	10.76*	0.98	13.88**	2.97*	0.26**	460.3**	394.8**	12.6**
Females in males in sets × environments	192	402.4**	8.94**	0.75**	6.44	2.15**	0.19**	191.1**	118.6**	6.8**
Pooled error	480	73.8	2.24	0.37	1.96	0.17	0.15	22.3	9.3	3.8

*, **Significant at 5 and 1 per cent respectively

Table 1b. Analysis of variance of S_1 progenies for various characters

Source of variance	d.f	Mean square								
		Grain yield Plant^{-1}	test weight	Kernel row ear^{-1}	Kernels row^{-1}	Ear length	Ear diameter	Plant height	Ear height	Days to silk
Environments	1	49625.9**	640.40**	17.79**	616.59**	153.60**	10.66	68072.72**	19776.46**	1008.06**
Replications/Environment	2	0.7	0.02	0.01	0.08	0.02	0.02	3.71	0.05	0.50
Lines	63	207324**	46.98**	3.03**	42.95**	8.38**	0.54**	765.71**	765.71**	15.89**
Lines × environments	63	399.4**	11.12**	1.11**	6.63**	1.41**	0.19**	278.01**	278.01**	9.23*
Pooled error	126	42.6	1.48	0.32	2.29	0.29	0.09	13.73	13.73	3.36

*, **Significant at 5 and 1 per cent respectively

Combined analysis across environments was followed as suggested by Hallauer and Miranda [1]. Estimates of variance components for males, females within males and their interaction with environments and those of S_1 lines (lines, lines × environments) were computed using the VARCOMP procedure (method = REML) of the SAS Programme [2]. These components were used to estimate additive genetic variance (σ^2_A), variance due to dominance deviations (σ^2_D) and their interaction with environments (σ^2_{AL}, σ^2_{DL}) as per Hallauer and Miranda [1].

The genotypic variance (σ^2_g) is the total of additive genetic variance and variance due to dominance deviations among full-sib families and is equal to (assuming no epistasis).

$$\sigma^2_g = \sigma^2_A + \sigma^2_D ; \qquad \sigma^2_{gl} = \sigma^2_{AL} + \sigma^2_{DL}$$

Inbred lines (S_1), Pooled analysis over locations

The data recorded on different characters in S_1 families were analyzed as per the procedure proposed by Hallauer and Miranda [1]

Results and discussion

Analysis of variance (Table-1a, b) revealed existence of significant genetic variability for all the traits in the base population confirming its heterogenous nature.

Estimates of genetic variance (σ^2_g) genetic × environment variance (σ^2_{gl}) and heritability (h^2) from Design-I and S_1 line design (Table-2) revealed that, in general, the total genetic variance (σ^2_g) estimated from S_1 lines was higher in magnitude than that from Design-I analysis except in case of kernels row per ear, ear diameter, plant and ear height and days to silk. The variance arising from genotype × environments interaction (σ^2_{gl}) was higher in the Design-I (full sib families) than S_1 families except for kernel rows per ear, ear height and days to silk. S_1 families are expected to be more influenced by genotype × environments interaction as increase in the homozygosity through inbreeding generally leads to less buffering capacity to environmental fluctuations and results in greater interaction with environment (however, this contention was not evident in the present study). Similar results have been reported earlier [4]. Narrow genetic base of full-sibs compared to half-sibs families results in greater reaction to environmental variation [6]. Estimates of heritability (h^2) from S_1 lines were higher in magnitude than those from Design-I families for all the characters except ear height and days to silk. The estimate from S_1 lines was highest for grain yield plant^{-1} (73.0%) whereas, it was 30.0% for Design-I.

The estimates of additive genetic variance (σ^2_A) and variance due to dominance deviations (σ^2_D) from Design-I analysis revealed equal importance of both the components in the inheritance of grain yield plant^{-1}. Whereas, in S_1 family analysis, additive genetic variance was nearly ten times more than corresponding variance due to dominance deviation (Table 3). Additive genetic variance also played a greater role in the expression of test weight, kernel rows ear^{-1}, ear diameter, plant height and ear height in Design-I families, while variance due to dominance deviations was of higher magnitude for kernels row^{-1}, ear length and days to silk. In S_1 family analysis predominant role of additive genetic variance (σ^2_A) for all the traits except days to silk was observed.

Table 2. Estimates of total genetic variance (σ^2_g), genotypic × environments (σ^2_{gl}) and heritability in narrow sense (h^2) from N.C-Design I (D-I) and S_1 progenies

Characters		σ^2_g	σ^2_{gl}	σ^2_{gl}/σ^2_g	σ^2_e	h^2
Grain yield plant^{-1}	D-I	302.92**	657.16**	2.16	73.81	30.0
	S_1	418.43**	178.44**	0.42	42.61	73.0
Test weight	D-1	6.92**	13.36**	1.93	2.24	29.0
Kernel rows Ear^{-1}	D-1	0.73*	0.46*	0.63	0.37	39.0
	S_1	0.48**	0.39**	0.81	0.22	52.0
Kernels row^{-1}	D-1	8.76**	8.96**	1.02	1.96	32.0
	S_1	9.08**	2.17**	0.23	2.29	72.0
Ear length	D-1	1.40*	3.16**	2.25	0.57	27.0
	S_1	1.74**	0.55**	0.31	0.31	72.0
Ear diameter	D-1	0.12*	–0.01	NE	0.15	47.0
	S_1	0.08**	0.05*	0.62	0.09	61.0
Plant height	D-1	228.28**	337.64**	1.48	22.32	46.0
	S_1	121.92**	132.14*	1.08	13.73	59.0
Ear height	D-1	157.16**	218.54**	1.39	9.34	37.0
	S_1	38.55**	86.90**	2.25	4.65	31.0
Days to silk	D-1	7.59*	5.98*	0.78	3.83	30.0
	S_1	1.66*	2.93**	1.76	3.36	13.0

Interaction of components of genetic variance with the environments revealed that both the components of variance [additive (σ^2_A) and dominance (σ^2_D)] were significantly interacting with the environments. However, the magnitude of σ^2_{DL} was more than σ^2_{AL} in Design-I families (1.05 times for days to silk to 14.18 times for test weight) indicating that the expression of σ^2_A was more consistent over the locations than that of σ^2_D.

The reduction in the mean performance of most of the traits in S_1 generation (Table 4) revealed that significant level of heterozygosity existed at many loci for these traits which has maintained the population at a higher fitness and performance. Ear height showed maximum inbreeding depression (31.84%) followed by plant height (26.16%) and grain yield plant^{-1} (14.76%). Inbreeding depression of 46.54 per cent for grain yield plant^{-1}, 13.52 per cent for plant height and –4.19 per cent for days to silk in S_1 generations has also been reported [7]. The magnitude of inbreeding depression observed within a maize population for a trait is a function of the number of segregating loci, the level of directional dominance and the allelic frequency, with inbreeding depression being maximum at an allelic frequency of 0.5 [1,7].

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 gains were higher from S_1 family selection than from full-sib family selection for most of the traits except ear height and days to silk. For grain yield it was maximum from S_1 family selection (29.67%) as compared to full-sib family selection in Design-I families (7.37%).

The results clearly indicated that S_1 selection was expected to give higher response than through full sib family selection for all traits studied, and in the present case corresponded the theoretical expected gains which

Table 3. Estimated genetic variance for various characters studied in C_8 random mating maize population in NC Design-I and S_1 progenies

Characters	NC Design-I					S_1 lines		
	σ_A^2	σ_D^2	σ_{AL}^2	σ_{DL}^2	σ_D^2/σ_A^2	σ_A^2	σ_D^2	σ^2/σ_A^2
Grain yield $plant^{-1}$	150.04	152.88	190.32^{*}	466.84^{**}	1.01	380.21	38.22	0.10
Test weight	3.84^{*}	3.08	0.88	12.48^{**}	0.80	8.19	0.77	0.09
Kernel rows ear	0.40^{*}	0.33	0.04	0.42^{*}	0.83	0.39	0.08	0.20
Kernels row^{-1}	3.64^{*}	5.12^{*}	3.72^{*}	5.24^{**}	1.40	7.80	1.28	0.16
Ear length	0.54	0.86	0.40	2.76^{**}	1.59	1.52	0.21	0.13
Ear diameter	0.11^{*}	0.01	0.03	0.04	0.11	0.08	0.001	0.01
Plant height	198.12^{*}	30.16	134.56^{*}	203.08	0.15	114.38	7.54	0.06
Ear height	106.76^{*}	50.40	138.12^{*}	80.42^{*}	0.47	25.95	12.60	0.48
Days to silk	3.03^{*}	4.56^{*}	2.92^{*}	3.06	1.50	0.52	1.14	2.19

Table 4. Expected genetic gains (per cent mean) through full sib family (Design-I) selection and S_1 line selection, and inbreeding depression in S_1 progenies compared to mean performance of parental population

	N.C-Design-I		S_1 Lines		
Characters	Mean	ECG (per cent of mean)	Mean	ECG (per cent of mean)	Inbreeding depression (%)
Grain yield $plant^{-1}$	136.00	7.37	115.92	29.67	14.76
Test weight (g)	36.16	4.83	33.01	13.92	8.71
Kernels rows per ear	12.51	4.97	12.33	7.49	1.43
Kernels per row	29.87	5.52	28.22	17.37	5.52
Ear length	15.30	3.75	14.40	15.03	5.88
Ear diameter (cm^2)	7.45	NE	7.01	6.83	5.90
Plant height (cm)	220.64	7.07	162.91	10.45	26.16
Ear height (cm)	118.61	8.72	80.84	7.25	31.84
Days to silk	90.71	1.76	89.82	0.61	0.98

predict that S_1 selection is more effective than full-sib family selection on a per cycle basis [8]. Efficiency of S_1 selection over full-sib family selection in the intra-population improvement of the open pollinated maize varieties have been reported [6, 8, 9].

Thus, in the present population the synthesis of improved version (through S_1 family selection) would be appropriate to raise the grain yield potential without any appreciable decrease in the nature and magnitude of genetic variability in the improved version.

References

1. **Benson D. L. and Hallaver A. R.** 1994. Inbreeding depression rates in maize population before and after recurrent selection. Journal of Heredity, **85**: 122-128.
2. **Livini C., Pirovano L., Brandolini A., Lorenzoni C. and Motto M.** 1993. Evaluation of three cycles of recurrent selection for yield in an opaque-2 variety of maize. Maydica, **37**: 89-93.
3. **Robinson H. F., Comstock R. E. and Harvery P. H.** 1949. Estimates of heritability and the degree of dominance in Corn. Agronomy Jour., **41**: 353-359.
4. SAS Institute Inc. 1989. SAS/STAT user's guide. Version 6, 4th ed., vols. 1 and 2. SAS Institute Inc., Cary, NC.
5. **Pal S. S.** 1980. Genetic analysis and selection advance for yield and quality in an opaque-2 population of maize (*Zea mays* L.) Unpubl. Ph.D Dissertation, Punjab Agri. University Ludhiana.
6. **Garay E, Igortua E. and Alvarez A.** 1996. Responses to S1 selection in flint and dent synthetic maize populations. Crop. Sci., **36**: 1129-1134.
7. **Empig L. T., Gardner C. O. and Compton W. A.** 1972. Theoretical gains for different population improvement procedures. University of Nebraska Agri. Expt Station. Miscellaneous Publication 26 (Revised).
7. **Joshi D. P.** 1980. Components of genetic variability and advance through selection in an early maturing open-pollinated variety of maize (*Zea mays* L.) Unpubl. Ph.D. Dissertation, Punjab Agri. University, Ludhiana.
8. **Crow J. F. and Kimura I.** 1970. An introduction to population genetic theory. Minneopolis. Burgess Publishing Co.
9. **J. Jan.orn, Gardner and Ross W. M.** 1976. Quantitative genetic studies of the NP3GR random mating grain sorghum population. Crop Sci., **16**: 489-496.
10. **Lamkey K. R. and Smith O. S.** 1987. Performance and inbreeding depression of population representing seven ears of maize breeding. Crop Sci., **27**: 695-699.