

Estimates of Heritability for Some Quantitative Characters in Maize

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ABSTRACT

Seventy-four S_1 families obtained from maize population C-17 were grown in a triplicated randomized complete block design (RCBD) to estimate significance of differences among S_1 families for number of days taken to tasseling, number of days taken to silking, number of ears per plant, 100-grain weight and grain yield per plant. Highly significant differences were observed among S_1 families for all the traits except for number of ears per plant where it was non-significant. Genotypic variances were greater than the environmental variances for all the traits except for number of ears per plant. Heritability estimates were moderate to high for all the plant traits except for number of ears per plant where they were low in magnitude.

Key Words: Maize; S_1 families; Heritability; Quantitative characters

INTRODUCTION

Grain yield in maize is a complex phenomenon, which results from the interaction of a number of factors, which are highly influenced by the environmental variation. It can not be improved directly by phenotypic selection of desirable plants, especially, when dealing with heterozygous crop like maize (Grafius, 1960). To overcome this problem, yield is partitioned into its contributing components and to study the heritability of the components among various lines/varieties of maize. S_1 family selection in maize is considered as an efficient method of population improvement but has not been extensively exploited compared to other methods. S_1 family selection is used to improve the performance of inbred lines, hybrids, synthetics and that of populations with broad genetic base.

Nelson (1979) reported that genetic improvements in gain of 3-4% per cycle in maize can be expected from S_1 and S_2 progeny selection. Kevern (1981) evaluated 98 S_1 lines from different maize populations to investigate the changes in means and genotypic variances after eight cycles of selection. Decrease in genotypic variability was found in grain yield and number of days to anthesis. Mulamba *et al.* (1983) reported estimates of genetic variability among S_1 progenies for grain yield which showed a decrease in genetic variance for the S_1 and half-sib derived maize population for most traits and no change for the mass selected maize population. Getchman and Hallauer (1991) studied genetic variation among and within S_1 progenies of maize and concluded that on an average, 70.7% greater genetic gains would be realized with among S_1 progeny selection vs. within S_1 progeny selection. Burgess and West (1993) evaluated the responses to S_1 selection and test cross selection for grain yield in maize and concluded that the response to S_1 selection was 44 % yield increase after four cycles, and test cross selection resulted in a 21 % yield gain

in random-mated populations. The present study was, therefore, initiated to evaluate the performance of 74 S_1 families from one maize population for some quantitative characters.

MATERIALS AND METHODS

The studies were conducted in the experimental area of the Department of Plant Breeding and Genetics, University of Agriculture, Faisalabad during the year 1998-1999. The research material was sown during July, 1998. Maize population C-17 was used as source material. Seventy-four S_1 families developed from the population were assigned to two blocks, each block containing 37 families in a triplicate randomized complete block design (RCBD). The experimental unit consisted of single row plot of 4.50 m length with plant to plant and row to row distances of 30 and 75 cm, respectively. The data were recorded for number of days taken to tasseling, number of days taken to silking, number of ears per plant, 100-grain weight and grain yield per plant. The data were subjected to analysis of variance following Steel and Torrie (1980). Phenotypic, genotypic and environmental variances were computed from the respective mean squares. Broad-sense heritability for each trait was calculated as the ratio of the genotypic variance to phenotypic variance.

RESULTS AND DISCUSSION

Analysis of variance for number of days taken to tasseling showed highly significant differences among S_1 families (Table I). The genotypic variance was greater than the environmental variance (Table II). Genotypic coefficient of variation (1.27%) was less than the phenotypic coefficient of variation (1.45%). Broad-sense heritability was high (0.759) indicating sufficient genetic variability in

Table I. Mean square values and their significance from analysis of variance for number of days taken to tasseling, number of days taken to silking, number of ears per plant, 100-grain weight and grain yield per plant

Source of variation	df	Number of days taken to tasseling	Number of days taken to silking	Number of ears per plant	100-grain weight	Grain yield per plant
Blocks	1	2.180	10.378**	0.001**	13.626*	1.013
Rep/Blocks	4	1.293	0.428	0.0003	11.234**	764.184**
S ₁ Families/Blocks	72	2.453**	2.779**	0.00001	7.767**	190.700**
Error	144	0.589	0.622	0.0001	2.030	75.726

* = Significant; ** = Highly Significant

Table II. Estimates of phenotypic variance, genotypic variance, environmental variance, heritability (BS), genotypic coefficient of variation and phenotypic coefficient of variation for number of days taken to tasseling, number of days taken to silking, number of ears per plant, 100-grain weight and grain yield per plant

Characters	Phenotypic variance	Genotypic variance	Environmental variance	Heritability (BS)	Genotypic coefficient of variation (%)	Phenotypic coefficient of variation (%)
Number of days taken to tasseling	0.818	0.621	0.196	0.759	1.27	1.45
Number of days taken to silking	0.926	0.718	0.207	0.776	1.18	1.34
Number of ears per plant	0.000063	0.000004	0.000058	0.077	0.22	0.79
100-grain weight	2.589	1.912	0.676	0.738	7.17	8.35
Grain yield per plant	63.567	38.324	25.242	0.602	4.91	6.33

total phenotypic variation suggesting the possibility of selection for this trait.

Analysis of variance for number of days taken to silking revealed highly significant differences among S₁ families (Table I). The genotypic variance was smaller than the phenotypic variance and both these variances were greater than the environmental variance (Table II). Genotypic coefficient of variation (1.18%) was smaller than the phenotypic coefficient of variation (1.34%). The estimate of broad-sense heritability was high (0.776) indicating the presence of considerable amount of genetic variation in total phenotypic variation. The results are in accord with El-Nagouli *et al.* (1983) and Pal *et al.* (1986) who also reported high broad-sense heritability for number of days to 50% silking.

Number of ears per plant showed non-significant differences among S₁ families of maize (Table I). Genotypic variance was smaller than the environmental variance as well as from the phenotypic variance. Genotypic coefficient of variation was low (0.22%) than the phenotypic coefficient of variation (0.79%). Broad-sense heritability was very low (0.077) in magnitude indicating that selection for this trait will not be effective.

Analysis of variance for 100-grain weight (Table I) showed highly significant differences among the S₁ families. Genotypic variance was greater than the environmental variance (Table II). Genotypic coefficient of variation was smaller (7.17%) than the phenotypic coefficient of variation (8.35%). The estimate of broad-sense heritability (0.738) was considerably high.

Analysis of variance for grain yield per plant (Table II) revealed highly significant differences among the S₁

families. Genotypic variance was greater than the environmental variance (Table II). Genotypic coefficient of variation (4.91%) was smaller than the phenotypic coefficient of variation (6.33%). The estimate of broad-sense heritability (0.602) was moderately high.

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