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# COMPONENTS OF GENETIC VARIATION AND RESPONSE OF SELECTION IN PEARL MILLET (PENNISETUM TYPHOIDES)

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### ABSTRACT

An investigation was conducted in pearl millet composite JOB GT-1 to estimate the components of genetic variance and heritability for yield and related characters using NCD-1. The dominance variation  $(\sigma_D^2)$  was very high for number of ears/plot and ear weight/plot, while the same estimate attained a negative value for plant height and ear length, indicating the preponderance of additive gene action in their inheritance. The heritability in narrow sense was high for ear length. Among the various methods of selection for which theoretical responses were calculated, mass selection appeared suitable for all characters.

Key words: Pearl millet, composite, components of variance, selection response.

Most of the yield improvement in pearl millet in recent years was achieved through the use of hybrids produced by utilizing cytoplasmic genetic male sterility. Encouraged by the presence of adequate additive genetic variance for most characters, population improvement programmes were also started and some of the populations so developed, such as, RHR-1 and RCB-2, have already been released for cultivation in this country [1]. JOB GT-1 is one such composites developed by combining 32 collections of Rajasthan selected for their drought resistance and earliness. To develop superior hybrids, availability of superior inbreds is a prerequisite, and to produce superior inbred lines, the magnitude of additive and dominance variances should be known. The present study is one such effort to estimate the components of genetic variation in pearl millet.

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### MATERIALS AND METHODS

The experimental material consisted of full-sib and half-sib progenies developed according to North Carolina Design I [2] from the composite JOB GT-1. For this, 24 male plants were randomly selected from the population of JOB GT-1 and each male plant was crossed with three randomly selected female plants (different from the selected male plants). The progeny of each female x male plant constituted a full-sib family and the progenies of all the 3 females with a common male plant were designated as one male group. All the 72 full-sib families of the 24 groups were divided into 4 sets of 6 male groups each. The sets were evaluated in RBD with 2 replications. The sets were first randomized in each replication. The males in each set followed by the full-sib families of each male were also randomized afresh in each replication. The progeny of each full- sib family was sown in a plot of 3 x 0.3 m size consisting of two rows of 3.0 m length spaced at 40 cm. The plant-to-plant spacing of 15 cm was adjusted by thinning at 3 to 4 leaf stage. At maturity, the observations on various morphological traits listed in Table 1 were recorded and the data were analysed according to design I of Comstock and Robinson [2] and Robinson et al. [3] using plot means. The estimates of additive  $(\sigma_A^2)$  and  $(\sigma_D^2)$  variances obtained from design I were also used to calculate heritability in narrow sense (h $_{ns}^2$ ) and theoretical responses to different selection schemes according to Pandey [4]. The formulae used for the estimation of responses (R) in various selection schemes are given below:

Mass selection : R = 
$$\frac{i \cdot \sigma_A^2}{\sqrt{\sigma_m^2 + \sigma_f^2 + \sigma_e^2}}$$
 (1)

Full-sib selection : R = 
$$\frac{i \cdot \frac{1}{2} \sigma_A^2}{\sqrt{\sigma_m^2 + \sigma_f^2 + (\sigma_e^2 \setminus r)}}$$
(2)

Half-sib family selection: selection based on half-sib family means and deriving the offspring by inter crosses from a bulked sample of the remnant seed of selected families:

$$R = \frac{i \cdot \frac{1}{4} \cdot \sigma_A^2}{\sqrt{\sigma_m^2 + (\sigma_f^2 \setminus f) + (\sigma_e^2 \setminus rf)}}$$
(3)

where R—response to selection, i—selection intensity (2.06 at 5% intensity,  $\sigma_A^2$  —additive variance,  $\sigma_f^2$  —variance due to females,  $\sigma_m^2$  —variance due to males, r—No. of replications, and f—No. of females in a male.

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### **RESULTS AND DISCUSSION**

The analysis of variance (Table 1) indicated significant differences between males in the sets for all the characters studied. Significant mean squares for females in sets were observed only for plant height, No. of ears, dry fodder weight and ear weight/plot. Similarly, the sum

Source	d.f.	Plant height	Tillers per plot	Ear length	Ears per plot	Dry fodder wt. per plot	Ear wt. per plot
Sets	3	253.0*	5.2	43.6	11.8	10423.0	2578.6
Replications in sets	4	42.2	143.5	6.5	4.6	2935.5	1992.0
Males in sets	20	153.4**	152.3 <sup>*</sup>	33.6**	234.6**	22720.3**	5891.8**
Females in males in sets	48	_ 30.4*	115.1	12.9	184.7 <sup>*</sup>	16749.7**	5736.9 <sup>*</sup>
Error	68	28.9	68.3	8.2	11.5	8115.4	837.3

Table 1. Mean sum of squares for different characters in pearl millet

\*,\*\*Significant at P=0.05 and P=0.01, respectively.

of squares for sets was significant only for plant height. The replications in sets were nonsignificant for all the characters. This indicates that the male groups representing half-sibs and females in males representing full-sibs exhibited significant differences for most of the characters. A perusal of Table 2 shows that plant height and ear length were controlled by additive variance, while the remaining characters exhibited preponderance of dominance. This is also clear from the  $\sigma_A^2 / \sigma_D^2$  ratio which tilted more towards the dominance side. Negative estimates of  $\sigma_D^2$  were observed for plant height and ear length. Theoretically, the variances are never negative. The negative estimates, most probably, resulted from sampling error around mean value zero or very low. The present observations are in agreement with some of the earlier reports [5, 6], while disagree with Sidhu et al. [7], who reported a greater role of additive gene action for most of the traits under study.

The population has shown high variation for ears/plot and ear weight/plant. The variation for other traits was lower. The differences between genotypic (GCV) and phenotypic (PCV) variances are very low for ears/plot and ear weight/plot, indicating that these are least affected by environment. For other traits, the differences are much inflated, indicating a positive role of environment on the expression of genotypes.

The narrow sense heritability  $(h_{ns}^2)$  estimate was highest for ear length. For other characters, the estimates were considerably lower; ear weight and number of ears/plot

Character	$\sigma_A^2$	σ <sub>D</sub> <sup>2</sup>	σ <sub>A</sub> <sup>2</sup> / σ <sub>D</sub> <sup>2</sup>	GCV	PCV	h <sup>2</sup>
Plant height	82.0	- 79.0		1.4	4.6	
No. of tillers/plot	24.8	68.9	0.36	20.5	26.9	15.3
Ear length	13.9	- 4.6	_	14.4	19.8	79.2
No. of ears/plot	33.3	313.1	0.11	47.9	48.7	9.3
Dry fodder wt/plot	3980.4	13288.2	0.30	23.7	28.7	15.7
Ear wt./plot	103.3	9695.9	0.01	40.7	42.4	0.9

Table 2. Estimates of additive  $(\sigma_A^2)$  and dominance  $(\sigma_D^2)$  variances, phenotypic (PCV) and genotypic (GCV)coefficients of variation and narrow sense heritability (h<sup>2</sup>)

When the  $\sigma_D^2$  values were negative, the  $\sigma_A^2 / \sigma_D^2$  and  $h^2$  were not estimated.

exhibited lowest heritability. The results are thus in general agreement with the earlier reports [8, 9].

Genetic advance at 5% selection intensity was negligible for ear weight/plot due to a very high dominance component controlling the inheritance of this character. Low to moderate responses were observed for tillers/plot, ears/plot and dry fodder weight, where as high genetic advance was observed for plant height and ear length (Table 3). Moderate to high genetic advance for tillers per plot, ear length, ears/plot and dry fodder weight has been observed earlier [9–11]. Lal and Singh [10] also reported low response to selection for plant height and ear weight/plot. The results of Table 3 also indicate that high genetic

Character	Genetic	R	Response to selection in	ı
	advance	mass selection	full-sib selection	half-sib selection
Plant height		28.9 (19.6)	14.1 (11.6)	8.4 (6.9)
No. of tillers/plot	4.0 (8.5)	5.2 (10.9)	3.2 (6.8)	2.5 (5.4)
Ear length	6.8 (32.3)	7.6 (36.1)	4.5 (21.5)	3.0 (14.3)
No. of ears/plot	3.6 (9.3)	6.6 (17.1)	3.4 (8.8)	2.7 (7.1)
Dry fodder wt./plot	51.5 (9.3)	10.8 (12.8)	42.4 (7.6)	33.3 (6.0)
Ear weight/plot	2.1 (0.9)	3.7 (1.5)	2.0 (0.8)	1.7 (0.7)

Table 3. Estimates of genetic advance and theoretical response to various selection procedures

Note. Genetic advance was not calculated where h<sup>2</sup> was not estimated. Figures in parentheses are percentages.

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advance was obtained for the characters which had preponderance of  $\sigma_A^2$ , while the opposite was true for the characters having preponderance of  $\sigma_D^2$ .

The estimates of responses in different selection schemes (Table 3) do not lead to any general conclusion. Among the different traits, the ear weight/plot showed minimum response with all the selection schemes while ear length gave maximum response. Among the three different schemes, the responses obtained with mass selection were very high in comparison to the other two schemes. The responses with half-sib selection were the lowest. The above observations are in contrast to Sandhu and Phul [12], who reported higher responses to selection for grain yield in half-sibs. In pearl millet, number of ears and earth length are the major yield components [13], therefore selection based on these characters using mass selection may be used for improving grain yield of pearl millet.

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