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QUANTITATIVE GENETIC STUDIES IN RELATION TO POPULATION IMPROVEMENT IN PEARL MILLET

P. B. GHORPADE* AND LATHA V. METTA

Department of Agricultural Botany, Punjabrao Krishi Vidyapeeth, Akola 444104

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ABSTRACT

Quantitative genetic studies in WC-C75 population indicated that additive genetic variance was important in the inheritance of all the traits studied. Heritability estimates on progeny mean basis were high for all characters in all families and moderate for grain yield/plant (0.31) in half-sib families. Expected genetic advance for S_1 family selection was high for most traits, particularly for grain yield per plant (25.7%), indicating that S_1 family selection was superior method for population improvement.

Key words: *Pennisetum americanum* (L.), population improvement, genetic advance.

Population improvement has been developed as an important method of breeding cross-pollinated crops. For carrying out an efficient population improvement programme, information about the nature and magnitude of gene effects in the base population, is very important. Therefore, the present study has been undertaken to investigate the genetic nature of grain yield and some agronomic traits in pearl millet and to estimate the genetic advance under three recurrent selection schemes.

MATERIALS AND METHODS

The WC-C75 population was used to develop 100 families each of S_1s, full-sibs and half-sibs. All the three types of families were grown for evaluation in three intermixed 10 x 10 simple lattice design in rainy season during 1986. The plot consisted of single row of 2.1 m with plant-to-plant spacing 15 cm and row-to-row spacing 60 cm. The data were recorded on five competitive plants in each family for plant height, earhead length, earhead diameter and grain yield per plant. The estimates of family components of variances were worked out from the adjusted family mean squares. The estimated genetic components due to variation among family means of S_1, full-sib and half-sibs were used to estimate population genetic variances [1].

*Present address: Department of Agricultural Botany, College of Agriculture, Nagpur 440 010.

RESULTS AND DISCUSSION

The range and mean performance of three types of families (Table 1) revealed that S_1 families displayed wide range for plant height and earhead diameter, whereas full-sib families had wider range for earhead length and grain yield per plant. On the other hand, the half-sib families depicted narrow range for all the characters than full-sib and S_1 families. Higher mean values of half-sib and full-sib families than the S_1 families for all the character indicated the importance of heterosis and inbreeding depression for their attributes. As regards the estimates of genetic variance, additive genetic variance ($\hat{\sigma}^2_A$) was significant for all the characters whereas the dominance components were negative and non-significant. Zaveri [2] also reported importance of additive genetic variation for these characters in PSB-3 and PSB-7 population of pearl millet.

The estimate of $\hat{\sigma}^2_{A*}$ was less than $\hat{\sigma}^2_A$ and also less than unit value of the ratio ($\hat{\sigma}^2_{A*}/\hat{\sigma}^2_A$) for all traits indicate that frequencies of favourable alleles was less than 0.5 and further improvement for grain yield would be expected in subsequent selection cycles. The estimate of heritability, in narrow sense, on progeny mean basis was high for all characters in all families except for grain yield per plant in half-sib families, for which it was moderately high (0.31). High heritability for characters under study were also reported in other pearl millet populations [2–4].

Table 1. Range, mean, genetic variance and heritability in three types of families of pearl millet

	Family type	Range	Mean	$\hat{\sigma}^2_A$	$\hat{\sigma}^2_D$	$\hat{\sigma}^2_{A*}$	$\frac{\hat{\sigma}^2_{A*}}{\hat{\sigma}^2_A}$	h^2
Plant	S_1	116.7-199.1	159.7	231.2 ± 54.4	−112.6 ± 136.7	222.1 ± 51.7	0.96	0.80
height	Full-sib	139.5-203.7	173.3					0.78
(cm)	Half-sib	148.1-198.6	169.4					0.60
Earhead	S_1	18.5-35.9	24.8	8.8 ± 2.0	−3.4 ± 5.6	6.5 ± 1.8	0.74	0.84
length	Full-sib	15.3-33.8	25.7					0.62
(cm)	Half-sib	21.6-31.2	25.6					0.62
Earhead	S_1	4.6-8.9	7.3	0.6 ± 0.1	−0.4 ± 0.3	0.3 ± 0.1	0.51	0.73
diameter	Full-sib	5.8-8.5	7.4					0.96
(cm)	Half-sib	6.1-8.6	7.5					0.61
Grain yield/	S_1	8.9-34.8	19.2	26.7 ± 12.3	−24.3 ± 28.0	14.8 ± 8.0	0.55	0.53
Plant (g)	Half-sib	8.1-34.4	21.4					0.55
	Full-sib	13.2-37.9	22.6					0.31

$\hat{\sigma}^2_{A*}$ — Additive genetic variance in S_1 families. $\hat{\sigma}^2_{A*} = \hat{\sigma}^2_A$ if $P = q = 0.5$.

Table 2. Expected genetic advance per cycle from single trait selection using different intra-population improvement methods

Unit of evaluation and selection	Generation per cycle	Plant height	Earhead length	Earhead diameter	Grain yield per plant
S_1 family	3	23.3	4.13	0.81	4.92
Full-sib family	3	16.7	2.90	0.91	4.77
Half-sib family	3	10.3	2.05	0.51	2.50
Expected genetic advance as percent of the mean					
S_1 family		14.6	16.6	11.1	25.7
		(13.7)	(16.1)	(10.8)	(21.8)
Full-sib family		9.6	11.3	12.4	22.3
		(9.9)	(11.3)	(12.2)	(21.1)
Half-sib family		6.1	8.0	6.8	11.1

Note. Figures in parentheses indicate the expected genetic advance in per cent of mean of the 100 half-sib families.

The expected genetic advance, expressed as per cent of the mean of the highest yielding 100 half-sib families, was high for S_1 family selection for all traits except earhead diameter (Table 2). When 10% of the highest yielding S_1 families were selected, the expected genetic gain in the case of grain yield per plant was 25.7%, followed by full-sib family (22.3%), indicating that S_1 family selection offers greatest promise for population improvement whether calcûlated on cycle basis or on annual basis. With three generations per cycle, full-sib family selection appears to be the second best method. The results are in agreement with earlier studies [2, 5].

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