

GENETIC STUDIES IN RELATION TO POPULATION IMPROVEMENT IN PEARL MILLET

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ABSTRACT

Two hundred reciprocal half sibs (RHS), 200 reciprocal full sibs (RFS) and 200 S_1 families (100 of each kind in each population), derived from two random mating pearl millet populations, PSB-3 and PSB-7, were evaluated at two locations. The S_1 families of both populations generally yielded less than the RHS families for all the characters. The RHS families were poorer than RFS ones. The higher values associated with RHS and RFS progenies indicated the importance of interpopulation heterosis. The variance among S_1 families for different characters invariably exceeded that amongst the RHS families and tended to be higher than that amongst the RFS families. Genetically, more heterogeneous RHS progenies exhibited least interaction with location differences, whereas the other two types had more or less equal sensitivity to variation of locations. Substantial genetic variation was noted among various families for almost all the characters studied, suggesting good scope for intra- and interpopulation improvement.

Key words: Genetic analysis, population improvement, pearl millet.

The population improvement programme has been resorted in recent years to develop genetically broad-based composites and synthetics of pearl millet (*Pennisetum americanum* L. Leeke). The genetic potential of some populations has been found to be quite close to the best available F_1 hybrids and further improvement of such populations is underway [1]. Gill [2] has also emphasised the need for evolution of such populations to minimise the risk due to diseases and unfavourable weather as well as to reduce limitations in seed production. The progress of population improvement depends on appropriate choice of the base material and the recurrent selection method. In making these decisions, the plant breeders are largely guided by the information on the nature and magnitude of genetic variation in populations. Though extensive quantitative genetic information is available about inbred populations but not much work has been done to investigate the genetic structure of interpopulation crosses in pearl millet. This paper describes the means, intra- and interpopulation family variance components and their interactions with locations in the S_1 , reciprocal half sib (RHS) and reciprocal full sib (RFS) families derived from PSB-3 and PSB-7 random mating populations of pearl millet.

MATERIALS AND METHODS

The reference populations were two diverse pearl millet populations, PSB-3 and PSB-7, developed by intermating of 10 inbred lines in a diallel fashion for PSB-3 and by intermating 23 inbred lines in a chain crossing system for PSB-7, i.e., inbred 1 $\times$ inbred 2; inbred 2 $\times$ inbred 3; inbred 3 $\times$ inbred 4, and so on. Both populations were allowed to random mate in isolation for four and two generations, respectively, and were in stable equilibrium [1].

One hundred plants with at least three tillers each of the PSB-3 and PSB-7 populations were randomly selected and used for the synthesis of the experimental materials during 1979 in the following manner.

1. One tiller of each of the 100 plants of PSB-3 was pollinated by bulk pollen from PSB-7 and vice versa to produce total 200 RHS families.
2. The other tiller of each of these 100 plants from PSB-3 was pollinated by a single plant from PSB-7 and vice versa to produce 200 RFS families.
3. The third tiller of each of these 100 plants was self-pollinated to produce 200 S_1 families.

The experimental material consisting of 600 families (100 each of S_1 , RHS and RFS types in both PSB-3 and PSB-7) was evaluated during 1980 at two locations, viz., Ludhiana and Faridkot. A randomized complete block design with two replications as adopted by Eckebil et al. [3] was used to evaluate the material. Each replication was divided into 20 sets to accommodate 30 family progenies and 2 base populations as checks in each set. The 30 families appearing in a set consisted of 5 families taken at random from each of the 6 subpopulations, i.e., three types of families in each of the two base populations. All the 32 entries were randomized in a set, except that the S_1 families were assigned to adjacent rows and separated from RHS and RFS families by a single border row to avoid competition with the S_1 families. Each progeny was grown in a single row plot of 2.5 m length with 60 cm spacing between rows. Ten competitive plants were used for recording data for days to flower (plot basis), plant height (cm), tiller number, ear length (cm), ear girth (cm), ear compactness, seed yield per plant (g), ear weight (g), and ear index (ratio of seed yield per plant to ear weight, %) at both locations. Plot means were subjected to analysis of variance for individual locations as well as over locations for combined analysis. The components of variance for different types of families were estimated by equating observed mean squares to the expected. The standard errors for the estimates of variance components were computed by following Anderson and Bancroft [4].

RESULTS AND DISCUSSION

The character means in RHS, RFS and S_1 families derived from PSB-3 and PSB-7 are presented in Table 1. The S_1 families in both populations generally had lower mean values than RHS and RFS families for all the traits, except days to flower. This low performance of S_1 families over RHS and RFS families was very apparent for seed yield. These differences, however, were only marginal for ear

compactness, ear girth, tiller number and days to flower. The RHS and RFS families also gave quite similar performance. The expression of these characters, therefore, appears to be strongly influenced by nonadditive effects which may have expressed in the interpopulation crosses of PSB-3 and PSB-7.

Table 1. Means for various quantitative characters in reciprocal half-sibs (RHS), reciprocal full-sibs (RFS), and S_1 families derived from two random mating pearl millet populations

Location	Popu- lation	Family type	Days to Flower	Plant height	Tiller num- ber	Ear length	Ear girth	Ear com- pactness	Seed yield/ plant	Ear weight	Ear index
Ludhiana	PSB-7	RHS ₁₂ *	55.2	164.3	2.3	26.7	6.6	5.2	22.9	33.9	69.0
		RFS ₁₂	55.4	165.6	2.8	28.0	7.3	5.6	26.4	36.3	72.8
		S ₁ (7)**	56.5	153.8	1.9	19.1	4.8	4.7	13.8	25.8	53.2
	PSB-3	RHS ₂₁ *	56.0	163.6	2.1	25.2	6.2	4.9	22.3	34.1	65.5
		RFS ₂₁	55.9	164.9	2.6	28.1	6.6	5.0	24.6	34.4	71.6
		S ₁ (3)**	56.1	156.5	1.8	21.8	6.1	4.7	11.2	25.0	44.8
Faridkot	PSB-7	RHS ₁₂	56.0	151.5	1.7	23.6	6.5	5.3	20.5	28.6	71.8
		RFS ₁₂	56.2	151.4	1.5	24.7	6.7	5.3	21.8	29.2	74.6
		S ₁ (7)	56.5	142.5	1.4	17.8	4.9	4.9	12.2	23.5	51.9
	PSB-3	RHS ₂₁	56.5	149.4	1.7	22.9	6.5	5.3	19.7	29.4	67.0
		RFS ₂₁	56.5	150.2	1.7	23.9	6.5	5.3	20.4	31.2	65.5
		S ₁ (3)	56.5	145.0	1.5	20.7	5.1	5.3	10.9	23.8	45.7

*Subscripts 12 and 21 denote population-1 (PSB-3) as male and population-2 (PSB-7) as female; and population-2 (PSB-7) as male and population-1 (PSB-3) as female, respectively.

** (7) and (3) refer to PSB-7 and PSB-3, respectively.

The analysis of variance for the experimental design for inter- and intrapopulation progenies displayed significant mean squares for various characters at Ludhiana and Faridkot, as well as in combined analysis over locations. The estimates of inter- and intrapopulation family variance components and their standard errors obtained from pooled values over locations for each trait are presented in Table 2. The variance among S_1 families was, in general, higher in magnitude than that of RHS and RFS families. This difference was most pronounced for seed yield, tiller number, ear compactness and ear weight. It may be realised that in both the populations, $\sigma_{S_1}^2$ tended to exceed σ_{RHS}^2 and σ_{RFS}^2 tended to exceed σ_{RHS}^2 . This sequence of the magnitude of these variance components directly corresponds to the relative magnitude of additive genetic variance among the three types of families, i.e., 1:0.5:0.25 for S_1 , RHS and RFS, respectively. It is thus apparent that substantial additive genetic differences are available in these populations which can easily be exploited for improving their mean performance.

The estimates of family $\times$ location interaction components of variance are presented in Table 3. The reciprocal half sib families exhibited the least interaction with locations than reciprocal full sibs and S_1 families, as is evident from the lower

Table 2. Estimates of inter- and intrafamily variance components obtained from the combined analysis over locations

Population	Family component	Values for different characters								
		days to flower	plant height	tiller number	ear length	ear girth	ear compactness	seed yield/plant	ear weight	ear index
PSB-7	$\sigma^2_{RHS_{12}}$	0.48 ± 0.23	23.9 ± 11.4	0.04 ± 0.02	1.07 ± 0.38	0.04 ± 0.02	0.10 ± 0.05	8.77 ± 4.04	15.1 ± 7.5	12.6 ± 5.2
	$\sigma^2_{RFS_{12}}$	0.51 ± 0.25	31.7 ± 12.3	0.10 ± 0.03	1.57 ± 0.42	0.17 ± 0.04	0.39 ± 0.11	24.74 ± 8.09	36.1 ± 15.9	28.4 ± 10.9
	$\sigma^2_{S_1(7)}$	0.73 ± 0.27	36.6 ± 17.0	0.13 ± 0.03	1.41 ± 0.37	0.17 ± 0.04	0.49 ± 0.13	28.48 ± 8.82	55.3 ± 15.7	18.7 ± 7.9
PSB-3	$\sigma^2_{RHS_{21}}$	0.56 ± 0.28	29.6 ± 14.0	0.03 ± 0.01	0.88 ± 0.44	0.06 ± 0.02	0.12 ± 0.06	6.86 ± 4.42	17.7 ± 8.7	13.3 ± 6.3
	$\sigma^2_{RFS_{21}}$	0.77 ± 0.34	31.0 ± 13.1	0.08 ± 0.02	1.51 ± 0.43	0.10 ± 0.04	0.39 ± 0.12	25.08 ± 7.60	45.2 ± 18.3	21.8 ± 8.7
	$\sigma^2_{S_1(3)}$	0.85 ± 0.37	39.3 ± 18.8	0.10 ± 0.03	2.00 ± 0.45	0.13 ± 0.04	0.52 ± 0.14	27.53 ± 8.15	63.4 ± 17.3	18.4 ± 8.8

magnitude and mostly nonsignificant values of reciprocal half sib $\times$ locations interaction (σ^2_{RHSL}) variance components. However, in case of ear girth in PSB-7 and ear length in PSB-3, the σ^2_{RHSL} was found to be about more than double the values of σ^2_{SIL} . On the other hand, the variance due to interaction of reciprocal full sibs with locations (σ^2_{RFSL}) was almost equal to σ^2_{SIL} for most of the traits in the two populations. It seemed that both these types of families have reacted more or less equally with location differences. It was also noted that in case of ear weight and ear index in both the populations and days to flower in PSB-7, the σ^2_{RFSL} was higher than σ^2_{SIL} .

Though the breeding behaviour and population structure of pearl millet is similar to maize but the recurrent selection procedures have not been extensively used for the improvement of pearl millet. In order to draw conclusions regarding the choice of breeding material and the breeding system to be used to improve populations, information on the means and magnitude of genetic variation in the populations is essential. The appreciably higher values associated with RFS and RHS families over the S_1 families indicated that interpopulation heterosis would be important in these populations. For efficient interpopulation improvement, the selection of breeding populations should be such that population cross mean(s) are at the highest level possible accompanied by maximum additive genetic variation within each population [1, 5]. This is the key to more effective development of hybrids because the rate of improvement of hybrids will be parallel to the improvement in population cross. The half sib families, which are genetically more heterogeneous than either full sibs or S_1 families, exhibited least interaction with locations for all traits except ear girth in PSB-7 and ear length in PSB-3. Perhaps greater heterogeneity contributes to greater buffering effect or greater stability over a range of environments.

Table 3. Estimates of inter- and intrafamily $\times$ locations interaction variance components with their standard errors for various traits in three types of families from two pearl millet populations

Population	Family $\times$ location component estimates	Days to flower	Plant height	Tiller number	Ear length	Ear girth	Ear compactness	Seed yield/plant	Ear girth	Ear index
PSB-7	$\sigma^2_{RHSL_{12}}$	0.36 ± 0.31	39.0 ± 20.9	0.02 ± 0.02	-0.98 ± 0.48	0.05 ± 0.03	0.12 ± 0.07	13.0* ± 5.6	20.2** ± 10.2	16.7 ± 10.4
	$\sigma^2_{RFSL_{12}}$	0.43 ± 0.33	38.6 ± 24.2	0.03 ± 0.02	0.21 ± 0.32	0.01 ± 0.02	0.26** ± 0.08	30.3** ± 6.8	54.7** ± 17.1	31.9 ± 10.6
	$\sigma^2_{SIL(7)}$	0.41 ± 0.28	41.2* ± 18.9	0.03* ± 0.01	0.35 ± 0.27	0.02 ± 0.02	0.37** ± 0.09	32.6** ± 7.0	52.7** ± 11.5	19.2* ± 8.3
PSB-3	$\sigma^2_{RHSL_{21}}$	0.80 ± 0.42	41.4 ± 25.7	0.01 ± 0.01	1.02 ± 0.68	0.07 ± 0.04	0.13 ± 0.08	10.8 ± 5.9	17.7 ± 11.8	16.9* ± 9.9
	$\sigma^2_{RFSL_{21}}$	0.88* ± 0.36	38.0 ± 24.2	0.02* ± 0.01	0.54 ± 0.34	0.11* ± 0.04	0.37** ± 0.09	26.8** ± 6.0	60.2** ± 18.3	27.7** ± 8.7
	$\sigma^2_{SIL(3)}$	1.01** ± 0.33	45.8** ± 21.2	0.05* ± 0.02	0.58 ± 0.25	0.11* ± 0.03	0.39** ± 0.09	27.3** ± 6.3	58.7** ± 12.1	18.4 ± 10.2

*, **Significant at 5 and 1% probability levels, respectively.

The results are in agreement with those reported in corn [6] and in sorghum [7]. On the other hand, σ^2_{RFSL} was almost equal to σ^2_{SIL} for most of the traits in both the populations, which suggests more or less equal sensitivity of both these types of families to the location differences. Greater homozygosity caused by inbreeding in S_1 may result in greater genotype $\times$ environment interaction. Similarly, narrow genetic base of full sibs compared to half sibs results in greater reaction to environmental variations. Substantial genetic variability was found to occur for almost all the traits under study through enforced mating and selfing in PSB-3 and PSB-7 populations. Results have indicated that reciprocal half sib and full sib selections were equally effective in improving interpopulation cross performance. However, the RFS scheme might prove more rewarding, as in addition to improving the base populations by selection, it is the most effective method to spin off new hybrids from the inbred lines derived from each cycle of selection [8]. Moreover, superior S_1 lines can be intermated to generate improved version of PSB-3 and PSB-7 for effective intrapopulation improvement.

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- Table 3. Estimates of inter- and intrafamily σ^2 for various traits in three types of families from two pearl millet populations errors for various traits in three types of families from two pearl millet populations
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The results are in agreement with those reported in corn [6] and in sorghum [7]. On the other hand, σ^2_{REL} was almost equal to σ^2_{REL} for most of the traits in both the populations, which suggests more or less equal sensitivity of both these types of families to the location differences. Greater homozygosity caused by inbreeding in S_1 may result in greater genotype $\times$ environment interaction. Similarly, narrow genetic base of full sibs compared to half sibs results in greater reaction to environmental variations. Substantial genetic variability was found to occur for almost all the traits under study through enforced mating and selfing in P2B-3 and P2B-7 populations. Results have indicated that reciprocal half sib and full sib selections were equally effective in improving interpopulation cross performance. However, the RFS scheme might prove more rewarding, as in addition to improving the base populations by selection, it is the most effective method to spin off new hybrids from the inbred lines derived from each cycle of selection [8]. Moreover, superior S_1 lines can be intermated to generate improved version of P2B-3 and P2B-7 for effective intrapopulation improvement.

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