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EFFICACY OF SEED SIZE IN DIFFERENTIATING SUBPOPULATIONS IN PEARL MILLET

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ABSTRACT

Twenty six populations of pearl millet, subdivided into large, medium and small seed size groups, revealed that seed size in pearl millet is a major factor in influencing genetic variability of pearl millet populations. The discriminant score of genetic worth of the populations is independent of seed size. Large and small seeded populations had better score than the medium seeded types, which suggests correlated response for important attributes when selection was done for large and small seed size.

Key words: Seed size, subpopulations, discriminant function, genetic worth.

Populations or synthetics of pearl millet (*Pennisetum typhoides* (Burm.) S. & H. are generally uniform for most morphological traits but heterogeneous for seed size. It has been shown that this variability imparts stability to the performance of these populations [1]. Seed size in pearl millet and many other crops has been reported to be an important component affecting early crop establishment, ability to resist drought, yield and yield components [2–4]. The discriminant function analysis is an efficient technique for differentiating between genetically different populations [5]. The objective of this study was to determine whether seed size is a major factor influencing genetic variability of pearl millet populations. These subpopulations have been compared through discriminant function analysis.

MATERIALS AND METHODS

Twenty six populations of pearl millet were divided into three groups based on seed size by the use of standard sieves (15 and 18 mesh per 10 cm^2). The split plot design was used for the analysis. Populations were placed in main plots and seed size was randomly treated as subplot progenies. Grain yield, grain weight, tiller number, and plant height were recorded on ten plants in each "progeny," whereas days to 50% flowering were recorded each individual line. Data were analysed on progeny mean by discriminant function analysis given by Fisher [5].

RESULTS AND DISCUSSION

Pooled analysis of variance over large, medium and small seed size categories for the experimental design (Table 1) revealed highly significant differences among

Table 1. Pooled analysis of variance for plant traits

Source of variation	d.f.	Grain yield	Grain weight	Days to 50% flowering	Tiller number	Plant height
Replications	2	1.5*	0.002	8.9	0.02*	14.1
Populations	25	32.3**	0.110**	57.0**	0.58**	511.6**
Error	50	0.3	0.004	3.8	0.2	27.7
Subpopulations (seed size groups)	2	20.9**	0.510**	257.7**	0.09**	1878.6**
Population × seed size	50	5.6**	0.050**	6.9*	0.05*	118.9*
Error	104	0.3	0.004	2.0	0.02	29.8

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

populations, subpopulations, and populations × seed size interaction for all the traits. This indicated that different seed size populations differ from each other. This was further confirmed by the discriminant function analysis. Thus, selection for seed size is effective or seed size in pearl millet is controlled by a few genes. Index I for each of the pair of seed size groups in large v. medium, medium v. small, and large v. small was constructed in the discriminant function analysis and tested for its significance (Tables 2 and 3). The highly significant differences between

Table 2. Analysis of variance of discriminant function

Source of variation	d.f.	Mean squares		
		large v. medium	medium v. small	large v. small
Between populations	5	2.87**	3.31**	3.57**
Within population	46	0.03	0.04	0.04

Table 3. Discriminant function for comparing seed size groups

Comparison	Discriminant function	F value
Large v. medium	I = 163 TN–2PH–1 DF–22 GY+518 GW	95.7**
Medium v. small	I = 41 TN–1PH–5 DF–2 GY+62 GW	82.7**
Large v. small	I = 19 TN–1PH+10 DF+4 GY–139 GW	89.2**

** Significant at 1% level. TN—tiller number per plant, PH—plant height, DF—days to 50% flowering, GY—grain yield per plant, and GW—grain weight.

populations for all the three pairs of comparison indicate that the seed size can discriminate effectively the genetic worth of subgroups. The uniformly high F values of 95.7, 82.7, and 89.2 over different comparisons (Table 3) indicate that all the comparisons were made with equal precision and different seed size groups have different genetic structure.

Futher, index values on discriminant function were scored for each genotype (Table 4). The discriminant score for all the paired comparisons revealed that genotypes L–72, BCD–5, BCD–17, BCD–21, LC–3, S–530 and K–677 differed over all the paired comparisons, and S–530 exhibited an opposite trend of score in large v. medium seed comparison. Genotypes L–74, L L–75, BCD–3, BCD–8, BCD–16 BCD–18, BCD–21, BCD–26, A 1/3, LC–2, LC–5, LC–6, LC–7 and D–2291 differed over two paired comparisons, and amongst these BCD–8 and BCD–18 showed an opposite trend of score in large v. medium comparison, BCD–18 and BCD–26 in medium v. small. Line BCD–18 also exhibited similar trend in large v. small

Table 4. Score based on discriminant function analysis over different paired comparisons

Genotype	Score in different comparisons					
	large	v. medium	medium	v. small	large	v. small
L-72	506.8	381.4	247.3	266.4	209.6	250.8
L-74	539.4	470.9	241.0	258.1	185.2	251.5
L-75	539.9	454.8	234.4	259.8	200.0	217.9
BCD-3	506.8	420.7	253.0	271.6	219.6	293.7
BCD-5	482.3	302.5	235.6	275.1	228.3	317.9
BCD-8	416.0	493.7	164.5	280.3	241.3	286.8
BCD-12	426.8	371.1	235.7	261.2	237.7	267.5
BCD-16	580.5	472.0	272.6	269.9	205.2	308.6
BCD-17	571.6	416.4	226.9	273.1	220.9	292.9
BCD-18	475.7	576.0	242.4	265.9	273.8	227.5
BCD-19	542.1	496.6	242.7	240.2	198.9	243.5
BCD-21	582.1	481.8	253.4	277.1	227.5	296.4
BCD-26	564.2	470.1	234.9	232.2	196.6	251.5
BCD-31	447.6	453.2	247.5	255.3	206.5	262.1
BCD-34	590.3	543.8	289.8	281.3	202.7	305.3
A 1/3	537.5	495.4	252.8	275.1	181.6	266.5
LC-1	453.9	403.3	243.2	238.0	230.1	278.1
LC-2	549.2	537.5	248.0	272.5	187.6	255.9
LC-3	472.9	381.6	249.8	296.6	241.6	303.2
LC-4	518.0	492.9	233.3	256.8	211.3	180.8
LC-5	597.2	358.2	254.2	301.1	306.2	324.4
LC-6	471.5	303.5	231.2	250.1	229.6	266.3
LC-7	515.9	336.4	271.2	283.3	258.2	435.7
S-530	402.7	518.2	259.1	322.2	293.4	392.0
K-677	475.3	351.5	250.9	282.0	284.9	346.9
D-2291	497.4	417.9	240.5	248.7	195.1	297.6
Mean	508.7	441.7	247.1	268.8	226.4	286.2
Difference of mean	67.0		21.7		59.8	

comparison. This suggests that bold seed may not always have a better genetic value associated with better performance. Line BCD-12, BCD–19, BCD–31, BCD–34 and LC–4 differed in one paired comparison, and BCD-31 among these genotypes showed an opposite trend of score in large v. medium, BCD–19 and BCD–34 in medium v. small, and LC–4 in large v. small comparisons. Only one genotype, LC–1, was similar in all the paired comparisons with opposite trend of score in medium v. small seed comparison.

Thus, almost all the genotypes belonging to different seed size groups differed over populations, except LC-1, which did not differ over populations. Some of the genotypes do not differ for a particular pair(s), indicating the role of genotype in governing such differences. The scores of genotypes did not strictly tally with seed size in medium v. small and large v. small comparisons, indicating that these characters combine better in small seeded categories to give higher genetic worth. Line LC–1, in particular, is composite population synthesized by continuous random mating of plants with high green fodder yield without any selection for seed size and the differences in its seed size may not be large enough to make distinct seed size groups. Thus, in a cross pollinated crop like pearl millet, seed size alone is effective in separating genetically different subpopulations. This may be due to the correlated genetic response for different traits when selection is done for seed size. The separation of subpopulations in a cross-pollinated crop like pearl millet offers an opportunity to exploit intra- and interpopulation heterosis along with a way to have uniformity for agronomic traits.

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