

A STUDY OF COMBINING ABILITY FOR GRAIN YIELD AND SMUT SEVERITY IN PEARL MILLET

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ABSTRACT

Combining ability effects were estimated for grain yield and smut severity in a line \times tester crossing programme comprising 70 hybrids produced by crossing 10 lines (5 male sterile and their 5 maintainer lines) with 7 restorers of diverse origin. The material was raised in two environments (dates of sowing) at Hissar. Parents and hybrids differed significantly for gca and sca effects, respectively. 10 A and 10 B among lines and H 833-2 among testers showed consistently high gca effects for grain yield and smut severity. Both additive and nonadditive gene effects seemed to be important in the control of the two characters. No cytoplasmic effect was observed in the development of smut disease. Among hybrids, the best performance was given by cross 10 A \times 77/181-4-4-3-1-5. The results indicated that the performance of hybrids for smut severity can be predicted with greater reliability based on gca alone than for grain yield.

Key words: *Pennisetum typhoides*, pearl millet, combining ability, smut, line \times tester.

Pearl millet [*Pennisetum typhoides* (Burm.) Stapf and Hubb.] is a dual purpose crop and its utility in providing high quality grain both for human and animal consumption will continue to play an important role in the Indian economy. Although there was a significant increase in the productivity and production of pearl millet after the release of hybrid HB 1 in 1965, its yield has remained stagnant during the past decade. Most of the hybrids released so far are susceptible to diseases like downy mildew, smut and ergot. Their effect in terms of losses in quantity of grain is enormous. While downy mildew is of wide spread occurrence, the severity of smut and ergot is often linked with specific geographic areas of cultivation. Haryana state is highly vulnerable to smut and is considered as hot spot of this disease. In India, the disease causes up to 30% reduction in bajra production [1]. Obviously, the evolution of smut resistant male sterile lines, restorer lines, hybrids and varieties is the need of the hour. With the availability of an efficient and reliable screening technique [2] the identification of some of the resistant sources has already been achieved. However, the knowledge about the combining ability of lines, testers and hybrids for smut resistance shall be of immense help in accelerating the pace of breeding programmes. The present investigation has been undertaken to make use of line \times tester analysis for estimating combining ability effects of the parents and hybrids, predictability ratio and identification of desirable genotypes for grain yield and smut resistance in pearl millet.

MATERIALS AND METHODS

The material for the present study consisted of 91 entries, included 5 male

sterile lines (sterile cytoplasm), their 5 maintainer lines (fertile cytoplasm), 7 restorer lines (fertile cytoplasm), selected on the basis of smut severity, their 70 F₁ hybrids, and 4 checks. All these entries were raised in two environments at Hissar: normal sowing (July 5, 1985) and late sowing (July 25, 1985). In both environments, the experimental material was sown in randomized block design with 3 replications.

An aqueous sporidial suspension (~10⁶ sporidia per ml), prepared from smutted pearl millet inflorescences collected in 1984, was used to inject-inoculate at least 10 ear heads of each of the 91 entries at boot stage so that the suspension filled the spaces between the leaf sheath and inflorescence. The boots were bagged immediately after inoculation. High relative humidity was maintained by providing light irrigations at intervals of 7-8 days during the period of inoculation, flowering and grain development. Smut severity (infection index) was estimated on five plants in each plot and in each replication as per cent florets transformed into smut sori 20-25 days after inoculation with the aid of a standard key similar to the one used for estimating ergot severity [3]. Grain yield per plant was recorded on five uninoculated plants. All the ear heads of a plant were hand threshed after sun drying and total grain yield recorded. The line×tester analysis was carried out according to Kempthorne [4]. The general predictability ratio was calculated as suggested by Baker [5].

RESULTS AND DISCUSSION

The mean squares obtained from the line×tester analysis and the values of general predictability ratio for grain yield and smut severity are presented in Table 1.

Table 1. Mean squares obtained from line×tester analysis of variance for grain yield and smut severity in pearl millet grown in two environments

Source	d.f.	Grain yield		Smut severity	
		normal sowing	late sowing	normal sowing	late sowing
Replications	2	14.0	15.3	32.6	263.3
Hybrids	69	139.0**	186.4**	376.6**	638.3**
Lines (sterile and fertile cytoplasm)	9	273.2**	328.3**	690.7**	1092.2**
Sterile cytoplasm	4	219.0**	146.1**	779.8**	1563.9**
Fertile cytoplasm	4	348.5**	592.3**	773.2**	887.9**
Sterile vs fertile cytoplasm	1	188.9**	0.5	4.4	23.0
Testers (fertile cytoplasm)	6	88.7**	27.2**	1069.9**	2286.6**
Lines × testers	54	122.2**	180.5**	247.3**	379.6**
Error	138	5.5	5.8	14.0	17.2
General predictability ratio		0.3	0.2	0.5	0.5

**Significant at 1% level.

This table reveals presence of enough genetic variability among the hybrids. Partitioning of the hybrids indicated that mean squares due to lines, testers and lines \times testers were highly significant for grain yield as well as smut severity, indicating that lines and testers differed for their general combining ability (gca) effects and crosses for their specific combining ability (sca) effects and for both these characters in both environments. However, further partitioning of the item lines revealed that though mean squares due to both sterile (A lines) and fertile (B lines) cytoplasm were highly significant in all four cases, the item sterile vs. fertile cytoplasm was nonsignificant for grain yield under late sowing and for smut severity in both environments. This indicates that cytoplasm (sterile or fertile) had no effect on the development of smut disease, but it may have an effect on grain yield.

The relative importance of gca and sca determining progeny performance should be assessed by estimating general predictability ratio [5]. High values of general predictability ratio for smut severity indicate that performance of hybrids for this character can be predicted with greater reliability based on gca alone than for grain yield.

Table 2 shows that among female lines, 10 A and 10 B emerged to be the best general combiners for the two characters studied. Therefore, these lines are ideal for any breeding programme, particularly when the breeding objective is to obtain high grain yield with substantial degree of resistance against smut disease. Among testers, H 833-2 showed consistently high combining ability effects.

Table 2. Estimates of general combining ability for grain yield and smut severity in pearl millet

Parent	Grain yield/plant		Smut severity	
	normal sowing	late sowing	normal sowing	late sowing
Lines (females)				
111A	-3.24**	-3.92**	-3.38	-0.86
111B	-5.89**	-7.01**	-1.08	5.05**
81A	0.76	0.22	3.19	4.95**
81B	-3.61**	-3.16**	-3.50	-0.58
841A	0.36	0.87	4.62	2.29*
841B	1.54**	3.84**	6.14	2.15*
5141A	4.55**	3.27**	5.14	5.28**
5141B	-1.09*	0.41	5.74	6.85**
10A	3.77**	0.99	-3.95	-15.41**
10B	4.39**	6.22**	-7.95	-9.72**
Testers (males)				
SR/ICMPS-101-1	1.12**	0.74	-1.39*	-2.70**
SR/ICMPS-904-3	2.04**	-0.09	-2.11**	-0.22
SR/ICMPS-1600-3	-0.65	-0.23	-3.14**	-10.11**
77/181-4-4-3-1-5	-2.22**	-0.16	13.08**	14.08**
77/245-7-1-1-5	-2.21**	-1.73**	-0.31	2.61**
H 90/4-5	1.02*	0.14	-1.12	6.41**
H 833-2	0.88	1.34**	-5.02**	10.06**
SE Lines ($g_i - g_j'$)	0.72	0.74	1.16	1.28
SE Tester ($g_j - g_j'$)	0.61	0.62	0.97	1.07

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

The performance of top 20 crosses for these two characters (Table 3) indicated that the number of high×low and low×low combinations was higher than that of high×high combinations. Thus, both additive and nonadditive gene effects were responsible for the control of these characters. However, for grain yield two crosses involved both parents as good general combiners, indicating preponderance of additive gene effects. Chand and Ahmed [6] also reported importance of both additive and nonadditive gene effects in the control of smut severity.

Table 3. The sca performance of 2 top hybrids for grain yield and smut severity in pearl millet

Item	Grain yield	Smut severity
No. of crosses showing significant sca effects	20	20
High × high	2	0
High × low	9	12
Low × low	9	8

Some desirable lines, testers and hybrids identified on the basis of gca and sca effects for smut severity and grain yield are given in Table 4. The hybrids 81

Table 4. Promising lines, tester and hybrids identified on the basis of desirable gca and sca effects for smut resistance and grain yield in pearl millet

Lines		Testers		Hybrids	
normal sowing	late sowing	normal sowing	late sowing	normal sowing	late sowing
10A*	10A	H833-2*	H833-2	L111A×77/245-7-1-1-5	L111B×H90/4-5
10B*	10B	H90/4-5*	H90/4-5	L111A×H833-2	IC181A×SR/ICMPS-101-1
841B	5141B	SR/ICMPS-101-1	SR/ICMPS-1600-4	IC181A×SR/ICMPS-101-1*	IC181A×77/245-7-1-1-5
		SR/ICMPCS-904-3		IC181B×SR/ICMPS-904-3	IC181B×77/×245-7-1-1-5
				IC181B×H90/4-5	841B×H833-2
				841B×77/245-7-1-1-5	841B×77/181-4-4-3-1-5
				5141B×SR/ICMPS-101-1*	514B×SR/ICMPS-101-1
					5141B×SR/ICMPS-904-3
				5141B×SR/ICMPS-904-3*	10A×77/181-4-4-3-1-5
				5141B×H833-2	10B×SR/ICMPS-101-1
				10A×77/181-4-4-3-1-5*	

*Promising in both the environments.

A×SR/ICMPS 101-1, 5141 B×SR/ICMPS 101-1, 5141 B×SR/ICMPS 904-3, and 10 A×77/181-4-4-3-1-5 performed better in both environments. The hybrid 10 A×77/181-4-4-3-1-5 was best among these four combinations. The performance of crosses involving A lines as female parent may be further evaluated in large plot size under environments differing both in time and space. The hybrids confirming superiority over the existing varieties can be recommended for general cultivation. Hybrids involving maintainer lines as female parent may be exploited in population improvement programmes and good inbreds can be derived from the progenies of maintainer combinations.

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