

GENERATION MEAN ANALYSIS OF GRAIN YIELD AND SOME PANICLE CHARACTERS IN TWO EXOTIC x INDIAN RABI SORGHUM CROSSES

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ABSTRACT

Generation mean analysis was carried out in six generations of two crosses involving an exotic (E 36-1), a local (M 35-1), and an improved variety (SPV 86) of rabi sorghum in respect of grain yield and its components. The scaling test and joint scaling tests indicated presence of nonallelic interaction for all the traits in both crosses except for primaries per panicle. Generation mean analysis showed importance of dominance gene effect, followed by additive x additive and dominance x dominance with a small proportion of additive gene effect. Digenic interactions were completely absent for primaries per panicle while a still higher order gene interaction was indicated for panicle width in the cross E 36-1 x M 35-1. Breeding methods which can simultaneously exploit both additive and nonadditive gene effects are suggested.

Key words: Scaling tests, generation means, gene effects, sorghum.

The few varieties/hybrids of sorghum released for general cultivation during rabi in India are susceptible to charcoal rot disease [1]. Since the disease cannot be controlled with the available fungicides, resistance breeding against this disease is the only way to find a possible solution to the problem [2]. For such breeding programme, the genetic architecture of grain yield, its components as well as mechanism of resistance to charcoal rot must be thoroughly understood. The present study is an attempt in this direction.

MATERIALS AND METHODS

An exotic rabi genotype, E 36-1, resistant to charcoal rot was crossed with M 35-1 and SPV 86. The F₁s of both the crosses were backcrossed with their respective parents to get seeds of BC₁ and BC₂ generations and also selfed to obtain F₂ seeds. The experiment with

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eleven entries (3 parent, 2 F₁s, 2F₂s, 2 BC₁s and 2 BC₂s) representing six generations of the two crosses (E 36-1 x M 35-1 and E 36-1 x SPV 86) was laid out in randomized block design with three replications. The parents and F₁s were grown in 3 row-plots, and the backcrosses and F₂ generations were grown in 12- and 30-row plots of 3 m length, respectively. The entries were randomly distributed and the seeds were hand dibbled at 15 cm in rows spaced 45 cm apart. The crop was raised as per the recommended package of practices under rainfed condition. Observations for seven quantitative traits were recorded in ten random plants in the parents and F₁s, 250 plants in each backcross population, and 700 plants in each F₂ populations. Means and variances were computed for each generation irrespective of replications, using the data recorded on individual plants. The data were then subjected to joint scaling test [3] and scaling tests [4] to detect epistasis. The gene effects for each trait were estimated as per [5].

RESULTS AND DISCUSSION

The A, B and C scaling tests as well as joint scaling tests (Table 1) were highly significant in the cross E 36-1 x SPV 86 for all the seven traits studied. This indicated presence of digenic or still higher order epistasis and/or linkage in the inheritance of these traits. Contrary to this, the cross E 36-1 x M 35-1 gave nonsignificant scaling tests and joint scaling test for primaries/panicle, while only C test and joint scaling test were significant at 5% probability level for panicle width. This clearly showed a good fit of the additive dominance model for primaries/panicle and a minor role of gene interaction for panicle width. Digenic or a still higher order interaction was indicated for the remaining five traits since A, B and C tests as well as joint scaling tests were highly significant.

Both additive (\hat{d}) and dominance (\hat{h}) gene effects were significant in respect of all the traits except whorls/panicle in the cross E 36-1 x SPV 86, and in respect of five out of seven traits in E 36-1 x M 35-1 (Table 2). However, the magnitude of dominance (\hat{h}) gene effects was greater than additive (\hat{d}) gene effects, indicating predominant role of dominance gene action in the inheritance of the above traits. Importance of dominance gene action for most of these traits was also reported by several workers [6-8]. On the contrary, predominant role of additive gene effects has been reported in the inheritance of panicle length and panicle width [9, 10]; 1000-grain weight [11, 12]; whorls and primaries/panicle [12, 13] and grain yield/plant [11, 12]. Both additive (\hat{d}) and dominance (\hat{h}) gene effects for 1000-grain weight but only additive (\hat{d}) gene effect for panicle width in the cross E 36-1 x M 35-1 and dominance (\hat{h}) gene effect for whorls/panicle in E 36-1 x SPV 86 were nonsignificant. Similar results have also been reported [8, 14].

Among the epistatic interaction effects, the additive x additive (\hat{i}) gene effect was significant and greater in magnitude for panicle length in both the crosses, for panicle width

Table 1. Scaling tests and joint scaling tests in respect of grain yield and some panicle characters in two intervarietal crosses of sorghum

Cross	Scaling test [2]			Joint scaling test [1] (χ^2 at 3 d.f.)
	A	B	C	
	Panicle length			
E 36-1 x M 35-1	-1.3 ± 0.4**	-1.4 ± 0.4**	-5.0 ± 0.6**	70.4**
E 36-1 x SPV 86	-1.6 ± 0.4**	-2.1 ± 0.4**	-6.7 ± 0.7**	131.1**
	Panicle width			
E 36-1 x M 35-1	-0.6 ± 0.3	-0.3 ± 0.3	-1.3 ± 0.5*	9.6*
E 36-1 x SPV 86	-0.2 ± 0.3	-0.9 ± 0.2**	-2.2 ± 0.4**	40.6**
	Panicle weight			
E 36-1 x M 35-1	-5.6 ± 1.0**	-19.0 ± 0.9**	-59.9 ± 1.5**	2136.9**
E 36-1 x SPV 86	-25.4 ± 1.2**	-28.3 ± 1.3**	-70.2 ± 2.1**	1181.0**
	No. of whorls per panicle			
E 36-1 x M 35-1	-1.0 ± 0.3**	-1.5 ± 0.4**	-0.8 ± 0.6*	61.6**
E 36-1 x SPV 86	-1.7 ± 0.3**	-1.1 ± 0.3**	-1.5 ± 0.5*	19.0**
	No. of primaries per panicle			
E 36-1 x M 35-1	0.7 ± 0.7	-0.9 ± 0.9	-0.8 ± 1.4	4.1
E 36-1 x SPV 86	0.1 ± 0.7	-2.5 ± 0.7	-7.3 ± 1.2**	83.2**
	1000-grain weight			
E 36-1 x M 35-1	1.6 ± 0.5**	1.5 ± 0.5**	0.4 ± 0.7	25.2**
E 36-1 x SPV 86	-0.1 ± 0.5	-3.4 ± 0.5**	-4.9 ± 0.9**	62.9**
	Grain yield per plant			
E 36-1 x M 35-1	-5.8 ± 0.9**	-16.4 ± 0.9**	-64.4 ± 1.3**	1235.3**
E 36-1 x SPV 86	-23.7 ± 1.1**	-26.5 ± 1.1**	-63.5 ± 1.9**	1158.5**

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

and primaries/panicle in E 36-1 x SPV 86, and for panicle weight, whorls/panicle and 1000-grain weight in E 36-1 x M 35-1. Several workers have earlier reported importance of additive x additive interaction effect in the inheritance of panicle length and panicle width [7, 12, 15], panicle weight [12], 1000-grain weight [15, 16], whorls/panicle [9] and primaries/panicle [12]. Additive x dominance effect (\hat{j}) for 1000-grain weight and dominance x dominance (\hat{i}) effect for panicle weight, whorls/panicle and grain yield/plant were significant and higher in magnitude in the cross E 36-1 x SPV 86. The importance of dominance x dominance (\hat{i}) gene effect has been reported for panicle weight [7, 8] and grain yield [6, 7, 9, 13]. All the three epistatic interactions were significant in both crosses

Table 2. Estimates of gene effects for grain yield and some panicle characters in two intervarietal crosses of sorghum

Cross	Gene effects + SE					Epistasis	
	m	(\hat{d})	(\hat{h})	(\hat{i})	(\hat{j})		
Panicle length							
E 36-1 x M 35-1	21.9 ± 0.1**	0.9 ± 0.2**	4.8 ± 0.5**	2.3 ± 0.5**	0.0 ± 0.4	0.4 ± 0.9	—
E 36-1 x SPV 86	22.7 ± 0.1**	0.6 ± 0.2**	7.0 ± 0.5**	3.1 ± 0.5**	0.2 ± 0.2	0.6 ± 0.9	—
Panicle width							
E 36-1 x M 35-1	6.5 ± 0.1**	-0.1 ± 0.1	1.2 ± 0.4**	0.4 ± 0.3	-0.1 ± 0.2	0.5 ± 0.7	—
E 36-1 x SPV 86	6.4 ± 0.1**	0.6 ± 0.1**	2.6 ± 0.3**	1.1 ± 0.3**	0.3 ± 0.1**	0.0 ± 0.6	—
Panicle weight							
E 36-1 x M 35-1	42.5 ± 0.2**	2.2 ± 0.4**	36.2 ± 1.3**	35.4 ± 1.2**	6.7 ± 0.6**	10.9 ± 2.3**	Complementary
E 36-1 x SPV 86	55.1 ± 0.1**	-1.7 ± 0.5**	50.3 ± 1.6**	16.4 ± 1.3**	1.4 ± 0.6**	37.3 ± 2.8**	Complementary
No. of whorls/panicle							
E 36-1 x M 35-1	9.6 ± 0.1**	0.7 ± 0.1**	1.6 ± 0.4**	1.2 ± 0.3**	0.2 ± 0.2	1.7 ± 0.7**	Duplicate
E 36-1 x SPV 86	10.6 ± 0.1**	-0.3 ± 0.1**	0.3 ± 0.4	0.7 ± 0.3**	0.0 ± 0.2	2.9 ± 0.8**	—
No. of primaries/panicle							
E 36-1 x M 35-1	45.6 ± 0.1**	-5.0 ± 0.3**	3.4 ± 1.0**	0.7 ± 0.8	0.8 ± 0.4	-0.5 ± 1.9	—
E 36-1 x SPV 86	46.9 ± 0.2**	-5.0 ± 0.3**	12.6 ± 1.0**	4.9 ± 0.9**	1.3 ± 0.4**	-2.5 ± 1.7	—
1000-grain weight							
E 36-1 x M 35-1	33.3 ± 0.1**	-0.2 ± 0.2	1.2 ± 0.7	2.7 ± 0.6**	0.0 ± 0.3	-5.7 ± 1.2**	—
E 36-1 x SPV 86	31.8 ± 0.1**	2.8 ± 0.2**	3.2 ± 0.7*	1.5 ± 0.6*	1.7 ± 0.3**	2.0 ± 1.2	—
Grain yield/plant							
E 36-1 x M 35-1	31.3 ± 0.2**	3.6 ± 0.4**	40.4 ± 1.2**	42.1 ± 1.1**	5.3 ± 0.5**	-19.9 ± 2.0**	Duplicate
E 36-1 x SPV 86	42.6 ± 0.2**	0.9 ± 0.4**	36.1 ± 1.5**	13.3 ± 1.2**	1.4 ± 0.6**	36.9 ± 2.6**	Complementary

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

for panicle weight and grain yield/plant. On the other hand, none of the gene interaction was significant in respect of panicle width and primaries/panicle in the cross E 36-1 x M 35-1. Since the joint scaling test and C test were significant at 5% probability level in this cross for panicle width, the digenic interaction model may also be insufficient to explain the genetic situation in this cross and a still higher order of epistasis may be involved in the inheritance of this trait. The nonsignificant scaling tests and joint scaling tests for primaries/panicle indicate absence of any nonallelic interaction. Similar results are also

reported for this trait in a single cross of sorghum [13]. Complementary epistasis was operative in respect of panicle weight in both the crosses, while duplicate epistasis was noticed for whorls/panicle and grain yield/plant in the cross E 36-1 x M 35-1, but only complementary epistasis in E 36-1 x SPV 86 for grain yield/plant. In contrast, Kachave and Nandanwankar [14] reported complementary and duplicate epistasis for grain yield per plant in two and four crosses, respectively.

Most of the characters studied in both these crosses are under the control of dominance (\hat{h}) gene effect, followed by either additive x additive (\hat{i}) or dominance x dominance (\hat{j}) interactions with small proportion of additive (\hat{d}) gene effect. However, for 1000-grain weight, dominance x dominance (\hat{j}), followed by additive x additive (\hat{i}) in the cross E 36-1 x M 35-1; and dominance (\hat{h}) followed by additive (\hat{d}) and additive x dominance (\hat{j}) were important in E 36-1 x SVP 86. Since nonadditive gene action is predominant for most of the traits studied, reciprocal recurrent selection or diallel selective mating could simultaneously result in the improvement of these traits.

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