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COMBINING ABILITY OF SOME QUALITY TRAITS IN GRAIN SORGHUM (*SORGHUM BICOLOR* (L.) MOENCH)

A. S. MALLICK,* M. P. GUPTA AND A. K. PANDEY

Department of Plant Breeding & Genetics, C. S. A. University of Agriculture & Technology, Kanpur 208002

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ABSTRACT

A 6×6 diallel analysis of combining ability for 5 quality attributes, e.g. protein, tryptophan, methionine, fat and ash content suggested the importance of both additive and nonadditive gene actions in F_1 and F_2 generations for the control of these traits. The parental performance was a good indication of their gca. The cultivar 5742-1A was a good general combiner for protein, tryptophan and ash content, while CSV 4 and CSV 6 were good general combiners for methionine and fat content.

Key words: Combining ability, quality traits, sorghum.

Considerable amount of variability has been reported for protein as well as essential amino acids such as lysine, methionine, and tryptophan [1–6]. Naik [7], Virupaksha and Sastry [8] and, Wall and Blessin [9] concluded that albumins and globulins are the best proteins in nutritive value. Prolamines are the poorest and glutelins are intermediate. This situation is encouraging, since negative correlation exists between the prolamine and lysine content [10]. Though lysine is the first limiting amino acid in sorghum, there is a good scope to improve the content of other amino acids, such as, methionine and tryptophan in this Crop. The inheritance of lysine is reported to be governed by additive as well as nonadditive gene action [6, 11–13], the inference regarding the gene action for other amino acids, protein, fat and ash content is drawn in this paper.

MATERIALS AND METHODS

The material for the present investigation comprised F_1 and F_2 populations derived from a complete diallel set (excluding reciprocals) of six inbred lines viz., Moti (IS6928), MAUT-1, CSV 4, CSV 6, 5742-1A and IS 165 with diverse genetic background.

A trial consisting of the above mentioned six parents, their 15 F_1 and 15 F_2 was conducted during 1979 rainy season at the university farm. Plants were spaced 50 cm between the rows and 20 cm within the rows, with fertilizer dose of 60:40 NP/ha.

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* Present address: Plant Breeding and Genetics Section, Regional Research Station & Faculty of Agriculture, S.K. University of Agricultural Sciences & Technology, Wadura, Sopore Jammu & Kashmir 193 201.

Recommended agronomic practices were followed for raising the crop. Five randomly selected samples of each of the six parents and 15 F_1 in each replication were analysed for protein (estimated by Kjeldahl method [14]), tryptophan (estimated by the method advocated by Spies and Chamber [15]), methionine (determined by the colorimetric procedure of Horn et al. [16], fat (estimated by the Soxhlet method as described in [14] using petroleum ether B.P. 40-60), and ash content [14] and averaged. In F_2 generation, seeds obtained from 30 plants were mixed and 5 random samples used for biochemical analysis as mentioned above. The combining ability analysis was carried out following Griffing [17].

RESULTS

The mean performance revealed a wide range of variation among parents for all the five traits. Maximum range was observed for protein content (8.6–13.0%). Good amount of variability for protein content in different generations was also reported by Jaya Mohan Rao et al. [18]. Oil content varied from 2.48–4.13%. Highest oil content was recorded in CSV 6. The parent 5742-1A was desirable for protein (12.2%), tryptophan (0.200 g/16 g

Table 1. Superior crosses and their relationship with per se performance and gca effects of the parents in a 6 × 6 diallel cross of sorghum

Character	Generation	Desirable cross	Chemical content		gca effect of parents
			F_1/F_2	best parent	
Protein (%)	F_1	CSV 4 × IS 165*	12.1	12.4	L × H
	F_2	MAUT-1 × 5742-1A	12.1	12.2	H × H
		CSV 4 × IS 165	11.4	12.4	L × H
		5742-1A × IS 165	12.0	12.4	H × H
Tryptophan (g/16 g protein)	F_1	Moti × MAUT-1	0.186	0.189	L × L
		Moti × CSV 6	0.185	0.178	L × L
		Moti × IS 165	0.193	0.199	L × H
		CSV 4 × IS 165*	0.194	0.199	L × H
		5742-1A × CSV 6*	0.190	0.200	H × L
		5742-1A × IS 165	0.200	0.200	H × H
	F_2	CSV 4 × IS 165	0.193	0.198	A × H
		5742-1A × CSV 6	0.189	0.200	H × L
Methionine (g/16 g protein)	F_1	CSV 4 × CSV 6	0.363	0.375	H × H
	F_2	CSV 4 × 5742-1A	0.356	0.363	H × L
		MAUT-1 × CSV 6	0.362	0.375	L × H
Fat (%)	F_1	CSV 4 × CSV 6	3.975	4.126	H × H
	F_2	CSV 4 × CSV 6	4.006	4.126	H × H
Ash (%)	F_1	Moti × IS 165*	1.726	1.794	L × H
		CSV 4 × IS 165	1.698	1.794	L × H
		5742-1A × IS 165	1.702	1.794	H × H
	F_2	MAUT-1 × IS 165	1.704	1.794	H × H
		5742-1A × IS 165	1.693	1.794	H × H

H—high, A—average, and L—low.

* Cross combination common in both F_1 and F_2 generations.

protein) and ash (1.73%) content, and cultivar CSV 4 for methionine (0.362 g/16 g protein) and fat (3.69%) content. The parent IS 165 was also superior for protein (12.4%), tryptophan (0.1999/16 g protein) and ash (1.794%) content. The crosses Moti × CSV 6, Moti × IS 165, MAUT-1×5742-1A, MAUT-I × CSV 6, MAUT-1 × IS 165, CSV 4 × CSV 6, CSV 4 × IS 165, and 5742-1A × IS 165 were desirable combinations in both generations, as they gave high mean performance for one or more characters but in F_1, none of the crosses was significantly superior to the best parent (Table 1). Highly significant differences were observed among parents, F_1, F_2 PVS (F_1+F_2) and F_1 VSF_2 except PVS (F_1+F_2) for protein and F_1 VSF_2 for fat.

COMBINING ABILITY ANALYSIS

The MSS due to gca and sca for all the five characters were highly significant in both generations except sca MSS for protein in F_1 generation and for fat in F_2 generation (Table 2). This means that both additive and nonadditive gene actions were prevalent in the control of these traits. However, the value more than unity for $\hat{\sigma}^2$ gca/$\hat{\sigma}^2$ sca estimates suggested predominant role of additive gene action for protein and fat content in both generations, and for methionine and ash content in F_1 generation. The proportion of $\hat{\sigma}^2$ gca/$\hat{\sigma}^2$sca was less than 1 for tryptophan in both generations and for methionine and ash in F_2 generation only, suggesting nonadditive type of gene action for these traits.

Table 2. ANOVA for combining ability for 5 characters in a 6×6 diallel cross of sorghum (*Sorghum bicolor* (L.) Moench)

Source of variation	Generation	d.f.	Mean squares				
			protein	tryptophan	methionine	fat	ash
gca	F_1	5	4.878**	$15.79 \cdot 10^{-5}$**	$15.74 \cdot 10^{-5}$**	0.966**	0.0323**
	F_2	5	4.648**	$15.79 \cdot 10^{-5}$**	$24.68 \cdot 10^{-5}$**	0.951*	0.0331*
sca	F_1	15	0.156	$4.68 \cdot 10^{-5}$**	$1.73 \cdot 10^{-5}$**	0.040**	0.0010**
	F_2	15	0.334**	$4.90 \cdot 10^{-5}$**	$6.14 \cdot 10^{-5}$**	0.043	0.0086**
Error	F_1	20	0.1326	$0.38 \cdot 10^{-5}$	$0.45 \cdot 10^{-5}$	0.014	0.0004
	F_2	20	0.035	$0.62 \cdot 10^{-5}$	$0.83 \cdot 10^{-5}$	0.023	0.0002
F_1							
$\hat{\sigma}^2$ gca			0.590	$1.38 \cdot 10^{-5}$	$1.75 \cdot 10^{-5}$	0.116	0.0039
$\hat{\sigma}^2$sca			0.030	$4.30 \cdot 10^{-5}$	$1.27 \cdot 10^{-5}$	0.026	0.0006
$\hat{\sigma}^2$ gca/$\hat{\sigma}^2$ sca			19.910	0.321	1.378	4.383	6.0460
$(\hat{\sigma}^2 \text{sca}/\hat{\sigma}^2 \text{gca})^{1/2}$			0.224	1.765	0.852	0.478	0.4067
F_2							
$\hat{\sigma}^2$ gca			0.664	$1.36 \cdot 10^{-5}$	$2.31 \cdot 10^{-5}$	0.113	0.0031
$\hat{\sigma}^2$ sca			0.298	$4.28 \cdot 10^{-5}$	$5.31 \cdot 10^{-5}$	0.020	0.0084
$\hat{\sigma}^2$ gca/$\hat{\sigma}^2$ sca			2.226	0.318	0.435	5.563	0.3650
$(\hat{\sigma}^2 \text{sca}/\hat{\sigma}^2 \text{gca})^{1/2}$			0.670	1.774	1.516	0.424	1.6550

* $p \leq 0.05$, **$p \leq 0.01$.

GCA EFFECTS

The gca effects of the parents 5742-1A and IS 165 for protein, tryptophan and ash content, CSV 4 and CSV 6 for methionine and fat content and MAUT-1 for ash content were positive and significant in both generations (Table 3). MAUT-1 also had significant positive gca effect for protein content in F_2 generation. These parents were, therefore, good general combiners for the respective characters.

SCA EFFECTS

The sca effects of cross CSV 4 × IS 165 were significant for protein and tryptophan content in both generations and for ash content only in F_1 generation. The crosses Moti × IS 165 and 5742-1A × CSV 6 for tryptophan and ash content; Moti × MAUT–1, Moti × CSV 6, and 5742–1A × IS 165 for tryptophan content; and MAUT-I × CSV 6 for ash content and significant positive sca effects in F_1 generation.

Table 3. Estimates of gca effects for 5 characters in a 6×6 diallel cross of sorghum

Parent	Protein		Tryptophan, 10^{-3}		Methionine, 10^{-3}		Fat		Ash	
	F_1	F_2	F_1	F_2	F_1	F_2	F_1	F_2	F_1	F_2
Moti	−0.177	−0.014	−0.68	−0.93	−2.17*	−0.67	0.030	0.014	−0.016*	−0.042**
MAUT-1	0.157	0.258**	−3.90**	−4.63**	−2.90**	−2.41*	−0.107*	−0.118	0.019*	0.024**
5742-1A	0.692**	0.739**	5.54**	4.83**	−4.15**	−4.21**	−0.290**	0.280**	0.049**	0.028**
CSV 4	−0.607**	−0.810**	−0.19	0.79	2.57*	3.82**	0.312**	−0.314**	−0.033**	−0.038**
CSV 6	−1.068**	−1.146**	−5.49**	−5.15**	7.76**	9.14**	0.480**	0.483**	−0.099**	−0.075**
IS 165	1.003**	0.974**	4.71**	5.09**	−1.10	−5.67**	−0.424**	0.412**	0.079**	0.103**
SE $\hat{g}i$	0.115	0.060	0.63	0.80	0.68	0.93	0.038	0.048	0.006	0.004
CD (0.05)	0.178	0.094	0.97	1.25	1.06	1.44	0.058	0.751	0.010	0.006
CD (0.01)	0.462	0.244	2.54	3.24	2.76	3.75	0.152	0.196	0.025	0.016

*p ≤ 0.05, **p ≤ 0.01.

DISCUSSION

The cultivars 5742-1A and IS 165 were the best parents over generations considering the per se performance as well as gca effects for protein, tryptophan and ash content. Similarly cv. CSV 4 and CSV 6 were good general combiners as well as better in per se performance for methionine and fat content. It is evident that, in general, good per se performers were also good general combiners for the respective traits, and, thus, the parents may be selected on the basis of their per se performance, which is a good indicator of their comibining ability for the improvement of the quality traits studied. Since superior alleles are distributed among different parents crosses particularly CSV 4, CSV 6, IS 165 and 5742-1A parents with fixable components of variance, such as, additive variance and additive × additive interaction, are expected to give recombinants with high protein and methionine content in advanced segregating generations. Developing intermating population in sorghum would be easy by incorporating male sterility in these parents.

However, for long time approach in developing intermating population the use of Jensen's [19] method of diallel selective mating as a supplement to conventional breeding systems may also be useful.

Both parents had high gca effects in cross 5742-1A × IS 165, which showed highest tryptophan content (0.200 g/16 g protein). The crosses, Moti × IS 165 for tryptophan, CSV 4 × IS 165 and 5742-1A × IS 165 for ash in F_1 generation involved at least one parent with desirable and high gca effect and the other with poor and low gca effect (Table 1). It means that apparently in these crosses the additive genetic system of good general combiners and epistatic effect of poor combiners acted in a complementary manner to maximise the desirable attributes. Table 1 also shows that the high × high cross 5742-1A × IS 165 for protein and tryptophan content showed only marginal superiority over the best parent. Similarly another high × high cross CSV 4 × CSV 6, though best for methionine and fat content among all the crosses, was not superior than the best parent (CSV 6) involved in it. This shows lack of diversity of alleles among better parents.

The crosses CSV 4 × IS 165 for protein CSV 4 × IS 165 and 5742-1A × CSV 6 for tryptophan, and Moti × IS 165 and MAUT-I × CSV 6 for ash exhibited highly significant positive sca effects in both generations. It indicated the presence of nonadditive type of gene interaction among these crosses.

On the basis of per se performance and sca effects, five crosses were common among nine crosses having desirable effects in F_1 generation. This means that the best cross combination on the basis of high sca effects could not necessarily be the one which would give the highest per se performance while selecting the best crosses. High sca effect itself does not reflect high performance of the hybrids.

The present study reveals substantial amount of additive genetic variance for protein and fat content. While methionine content is governed by both additive and nonadditive genes, tryptophan is controlled by nonadditive genes. Collins and Pickett [20], Nanda and Rao [6], Rana and Murty [21] and, Nayeem and Bapat [22] also reported additive gene action for protein. However, Chinna and Phul [13] reported nonadditive gene action for this trait. Nonadditive gene action for tryptophan was also reported by Nanda and Rao [6] and Chinna and Phul [13]. Therefore, biparental matings or reciprocal recurrent selection programmes which exploit both additive and nonadditive gene action can be utilized for developing better recombinants for these quality traits. The present material has low potential to develop superior quality varieties due to lack of diversity of alleles among parents and failure of high × high crosses to produce significantly superior F_1.

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