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STABILITY FOR QUALITY IN SORGHUM

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ABSTRACT

Stability for protein, lysine, tryptophan and total sugar content was examined in 40 diverse genotypes of sorghum [*Sorghum bicolor* (L.) Moench] in six environments. Both linear and non-linear components of genotype × environment interaction were significant for protein while non-linear components were significant for others. In general, hybrids were more stable than varieties and advanced breeding lines. Varieties CSH 9, D 71196, CSH 5 and SPV 225 were stable for most characters and hence can be used in breeding for nutritionally superior cultivars.

Key words: *Sorghum bicolor*, stability, protein, lysine, tryptophan, sugar content.

Sorghum is an important source of protein in semiarid tropics. Breeding effort for improving nutritional quality is inadequate and hence screening of diverse genotypes across environments would be useful for such programmes. The present study is such an attempt to evaluate stability of genotypes for quality characters.

MATERIALS AND METHODS

Forty genotypes of sorghum, including 4 commercial varieties, 33 advanced breeding lines, and 3 hybrids were grown in randomized block design with two replications for two years at Ludhiana and Faridkot. At Ludhiana, it was grown under two environments, irrigated and limited moisture (only one irrigation 15 days after sowing) conditions, and at Faridkot under irrigation only. There were thus six environments; Ludhiana, irrigated (1982); Ludhiana, irrigated. (1983); Faridkot (1982); Faridkot (1983); Ludhiana, limited moisture (1982), and Ludhiana, limited moisture (1983). Single-row plots of 4 m length were used with the spacing of 45 cm between rows and 15 cm between plants.

Grains from five randomly selected plants were used to estimate nitrogen content by the method of McKenzie and Wallace [1] and the value was multiplied by 6.25 to obtain protein content. Lysine was determined by dye binding method of Udy [2] (expressed as percentage of protein), tryptophan by that of Opienska-Blauth and Charenzinski [3] as modified by Dalbi and Tsai [4] (expressed as percentage of protein) and, total sugars as per Yemm and Willies [5]. The concentration of total sugars (mg/g dry weight) were calculated from a standard curve (expressed in %). Stability analysis was done by the method of Eberhart and Russell [6].

RESULTS AND DISCUSSION

The differences among genotypes and genotype × environment interaction were significant for all the characters (Table 1) (see also [7]). Significant environment (linear) M.S. showed that the environments tested were different. Significant genotype

Table 1. Stability analysis of variance for some quality characters

Source	d.f.	Protein	Lysine	Tryptophan	Total sugar
Genotypes	39	17.2*	0.03*	0.08*	0.10*
Environments	5	12.8	0.03	0.06	0.36
Genotype × environment	195	1.7*	0.004*	0.01*	0.02*
Env. + (var. × env.)	200	2.0	0.01	0.01	0.03
Environment (linear)	1	63.9*	0.16*	0.30*	1.80*
Genotype × environment (linear)	39	3.4*	0.01	0.01	0.01
Pooled deviations	160	1.3*	0.004*	0.01*	0.02*
Pooled error	234	0.116	0.001	0.001	0.004

*Significant at 1% level.

× environment (linear) and pooled deviation M.S. for protein indicated that they were important for this character. The significance of linear component further indicated possibilities of prediction across environments when its value is known in one of them. Only nonlinear component of genotype × environment interaction was significant for lysine, tryptophan and total sugar content. Hence only the deviation from regression (S^2) was considered in interpreting the stability for these characters [8, 9]. In general, the hybrids under test were more stable than the varieties and advanced breeding lines. This may be attributed to the higher buffering capacity of heterozygotes. For example, hybrids CSH 9 and D 71196 were stable for all the characters though their mean performance was low for some of them (Table 2).

Table 2. Performance of selected genotypes which were stable for 2 or more characters

Variety/hybrid	Protein (%)			Lysine (% of protein)		Tryptophan (% of protein)		Total sugar	
	mean	b_i	S^2_{di}	mean	S^2_{di}	mean	S^2_{di}	mean	S^2_{di}
D 71196	11.3	0.83	0.277	1.7	0.001	0.7	0.0008	1.4	−0.001
CSH 9	8.0	0.72	0.218	1.9	0.003	0.7	0.0002	1.6	0.001
CSH 5	8.6	0.57	0.192	1.8	0.001	0.8	0.0015*	1.7	0.002
SPV 225	7.6	1.03	−0.094	2.0	0.005*	0.9	0.0007	1.5	0.000
SPV 104	10.9	1.25	0.229	1.7	0.002	0.8	0.006*	1.8	0.028*
SPV 101	8.5	0.72	0.587*	2.0	0.003	0.9	0.002*	1.6	0.008
SPV 270	7.9	0.89	0.039	2.0	0.007*	0.8	0.0003	1.6	0.026*
SE	0.5	0.90		0.04		0.03		0.04	

*Significant at 1% level.

CSH 5 was stable for protein, lysine and sugar and SPV 225 for protein, tryptophan and sugar content. Many genotypes showed stability for only one character (Table 2). These desirable genotypes can be used in breeding for nutritionally superior cultivars with stable performance.

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