

### Genetic variability studies in sorghum

Sorghum (*Sorghum bicolor* (L.) Moench) is the third most important cereal crop of the country. Genetic improvement for quantitative traits depends upon the nature and amount of variability present in the genetic stock and the extent to which the desirable traits are heritable. Indian sorghum possess wide range of genetic variability. However, the improvement work in land races did not achieve an appreciable increase in their yielding ability. Since green revolution, over decades, hybridization has boosted the yield levels of sorghum, besides improving other characters like resistance to biotic and abiotic stresses that pose a serious problem for its successful cultivation. Assessment of genetic diversity therefore becomes an essential prerequisite for identifying potential parents for hybridization. Diverse parents are expected to yield higher frequency of the heterotic hybrids in addition to generating a broad spectrum of variability in segregating generations.

The experimental material for the present investigation comprised 20 F5 families with 4 checks of *Sorghum bicolor* (L.) Moench. These 24 genotypes were grown at the Experimental Farm, Department of Agricultural Botany, Marathwada Agricultural University, Parbhani during 2006-07 with a spacing 45 cm x 15 cm. The experiment was laid out in randomized block design with three replications. Observations were recorded on five competitive plants in each genotype in each replication for days to 50 per cent flowering, days to maturity, panicle length (cm), panicle width (cm), plant height (cm), number of primary branches per panicle, number of grains per panicle, test weight (g), harvest index and grain yield per panicle (g). The mean values were used for statistical analysis. The data was analyzed statistically for genotype and phenotype coefficients of variation (Burton, 1952), Heritability (Allard, 1960) and genetic advance (Johnson *et al.*, 1955).

The analysis of variance revealed that the significant differences among genotypes for all characters, which indicated presence of variability among the lines being evaluated and ample scope of improvement by selection. The range of variation and the estimate of genetic parameters which include heritability in broad sense, coefficient of variation (GCV and PCV) and genetic advance are presented in table 1. The range was highest for number of grains per panicle (1326.67 - 3625.33) followed by plant height (149.00 - 255.33), grain yield per panicle (20.25 - 89.93), number of primary branches per panicle (40.10 - 83.60), harvest index (14.36 - 55.13), days to maturity (105.00 - 128.00), days to 50 per cent flowering (65.33 - 86.00), test weight (14.80 - 31.30), panicle length (17.30 - 32.47) and panicle width (3.42 - 8.16).

However genotypic and phenotypic variances were exhibited for plant height, number of grains per panicle, grain yield per panicle and number of primary branches per panicle. On the basis of mean, the GCV and PCV observed to be high for harvest index (36.10) followed by grain yield per plant (34.23), panicle width (27.67). The highest value of GCV (35.49) and PCV (36.72) were observed for harvest index. The least values for GCV and PCV were recorded by days to maturity (27.10 and 5.97). High GCV and PCV values for grain yield per panicle was reported by Kumar and Singh (1986). Sharma *et al.* (2006) reported that high GCV and PCV for grain yield per plant and plant height. However, low GCV and PCV for days to 50 per cent flowering was also reported by Mallinath *et al.* (2004).

The effectiveness of selection for any character depends not only on the extent of genetic variability but also in the extent to which it will be transferred from one generation to next. High heritability was observed for grain yield per panicle (95.57) followed by harvest index (93.16), panicle width (92.97)

Table 1. Parameters of genetic variability for yield and yield contributing characters in F5 families of sorghum

Sl. No.	Parameters	Range	Mean	Genotypic variance	Phenotypic variance	GCV (%)	PCV (%)	Heritability (%)	Genetic advance (GA)	Expected genetic advance (EGA) (%)
				( $\delta^2$ g)	( $\delta^2$ p)	(%)	(%)	(%)	(GA)	(EGA) (%)
1	Days to 50 % flowering	65.33 - 86.00	72.15	32.33	36.09	7.56	7.99	89.57	11.09	14.75
2	Days to maturity	105.00 - 128.00	116.03	36.92	47.99	5.23	5.97	76.94	10.99	9.46
3	Panicle length (cm)	17.30 - 32.47	23.96	19.21	21.84	18.29	19.5	87.93	8.46	35.33
4	Panicle width (cm)	3.42 - 8.16	5.81	2.5	2.68	27.17	28.18	92.97	3.14	53.97
5	Plant height (cm)	149.00 - 255.33	211.08	1152.3	1250.9	16.08	16.75	92.12	67.12	31.79
6	Number of primary branches / panicle	40.10 - 83.60	60.38	155.06	166.78	20.62	21.38	92.97	24.74	40.96
7	No. of grain / panicle	1326.67 - 3625.33	2398	422604	457667	27.1	28.21	92.34	1286.8	53.66
8	Test weight (g)	14.80 - 31.30	23.49	13.21	16.35	15.47	17.21	80.79	6.75	28.65
9	Harvest index	14.36 - 55.13	33.6	142.22	152.66	35.49	36.72	93.16	23.72	70.57
10	Grain yield / panicle (g)	20.25 - 89.93	58.03	386.17	404.07	33.86	34.63	95.57	39.57	68.79

number of primary branches per panicle (92.97), plant height (92.12) and number of grains per panicle (92.34). Similar results were obtained by Sharma *et al.* (2006) for number of grains per panicle and plant height. Moderate heritability estimates were obtained for days to 50 per cent flowering (89.57) and panicle length (87.93). Heritability estimates were low for test weight (80.79) and days to maturity (76.94).

High genetic advance was observed for number of grains per panicle (1286.80) and low for panicle width (3.14). High heritability coupled with high genetic advance was observed

for number of grains per panicle, plant height and grain yield per panicle. Whereas, high heritability combined with low genetic advance was recorded by panicle width, panicle length and test weight. Similar results were obtained by Bapat and Shinde (1980) and Tiwari *et al.* (2003). Kishor and Singh (2005) reported high genetic advance for days to 50 per cent flowering. Occurrence of high heritability may be inferred that the genotypic variance for these traits were primary due to additive genetic effect and selection based on phenotypic performance could be worth in achieving desired results.

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