

ESTIMATION OF GENETIC VARIABILITY, HERITABILITY, AND GENETIC ADVANCE FOR YIELD AND YIELD CONTRIBUTING CHARACTERS IN SORGHUM (*SORGHUM BICOLOR* L.)

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ABSTRACT

The field experiment was conducted at the Experimental Farm of College of Agriculture, Latur, during Kharif – 2021–2022 with 26 genotypes of *Sorghum*, including three checks genotypes as PVK-1009-C, PVK-400-C, and PVK-809-C, with the goal of studying genetic variability, heritability, and genetic advance for yield and yield contributing characters in *Sorghum* (*Sorghum bicolor* L.). An analysis of variance involving 26 *Sorghum* genotypes for 12 quantitative characters revealed significant differences for all the traits under study indicating the presence of wide genetic variability in the experimental materials. Fodder yield per plant field grade score, plant height, grain yield per plant, threshed grade score, and test weight had a significantly high genotypic coefficient of variation (GCV) and phenotypic coefficient of variation magnitudes. The present investigation clarified that plant height, number of grains per primary, field grade score, threshed grade score, grain yield per plant, and fodder yield per plant these character have high heritability coupled with a high genetic advance and high GCV, indicating the role of additive genes in governing the inheritance of these traits, which could be improved through simple selection.

Keywords: Genetic variability, Heritability, Genotypic coefficient of variation, Phenotypic coefficient of variation, Genetic advance, *Sorghum*.

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INTRODUCTION

Sorghum is the fifth most-produced cereal crop in the world. It is rich in natural nutrients and easy to add to your diet. It is also widely used as animal feed and as a natural and cost-effective fuel source. It is also referred to as the poor man's crop, or camel crop due to its high tolerance to drought conditions and withstand low soil water conditions. The amount and types of genetic variability, heritability, and genetic advance in the population, as well as the type of association between yield and yield contributing character, play an important role in the genetic improvement of *Sorghum*. This enables simultaneous selection for many traits associated with yield (Mahajan and Wadikar, 2011). *Sorghum* in general possesses a wide range of genetic variability (Sharma *et al.*, 2006). Adequate variability provides options from which selections are made for improvement and possible hybridization. Binodh *et al.* (2008) reported that information on trait association in crops is essential for effective selection in crop improvement. The post-flowering drought, which significantly lowers the crop's productivity, is the major issue. This problem can be circumvented by the introgression of the gene responsible for the stay-green trait which is directly associated with post-flowering adaptation (Tuinstra *et al.*, 1997; Kebede *et al.*, 2001).

Estimates of heritability with genetic advancement are more dependable and important than individual consideration of the parameters (Nwangburuka and Denton, 2012). The extent of variability is evaluated by the genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) which provides information about the relative amount of variation in different traits. According to Tah and Roychowdhury (2011), the extent of variability is measured by GCV and PCV which provide information about the relative amount of variation in different traits studied. The present study aimed to estimate the genetic variations, heritability, and expected genetic advance in the selected *Sorghum* varieties.

METHODS

During Kharif 2021–2022, 26 genotypes of *Sorghum* (*Sorghum bicolor* L.) were investigated at the College of Agriculture, Latur,

under V.N.M.K.V., Parbhani. Each genotype was cultivated in two rows of 45 cm × 15 cm between row to row and plant to plant using a randomized block design with three replications. To raise a good crop, a recommended package of operations was followed. Five plants were identified and labeled at random from each row and replication for recording 12 observations, and the mean of the five plants was employed for statistical analysis. The data were recorded for days to 50% flowering, plant height (cm), panicle length (cm), panicle width (cm), number of grains per primary branches (no's), field grade score, threshed grade score, days to maturity, number of primary branches per panicle, test weight (g), grain yield per plant (g), and fodder yield per plant (g). Analysis of variance was performed to test the significance of differences between the genotypes for all the characters. The analysis of variance was done as suggested by Panse and Sukhatme (1962). Broad sense heritability was estimated for various characters as per the formulae suggested by Lush (1940). The genetic advance was calculated in percent as per the formula suggested by Johnson *et al.* (1995).

RESULTS AND DISCUSSION

The ANOVA for a set of 26 *Sorghum* (*S. bicolor* L.) genotypes for 12 quantitative characters revealed highly significant differences among genotypes for all characters studied. For all 12 characters studied, the mean sum of squares was non-significant due to replication and all the treatments were significant. The general analysis of variance was carried out for each character to find out the amount of variation for various characters given in (Table 1). Phenotypic variance (V_p) values were more than the genotypic variance (V_g) for all the studied characters. The range for characters, namely days to 50% flowering 67.51–91.93, plant height 103.33–259.33, panicle length 16.50–32.27, panicle length (cm) 16.50–32.27, panicle width (cm) 3.20–7.5, number of grains per primary 21.33–41, field grade score 1.43–4.53, threshed grade score 1.83–4.93, days to maturity 116.67–139.67, number of primary branches per panicle 34.77–68.47, test weight 1.20–4.03, grain yield per plant (g) 26.27–62.53, and fodder yield per plant (g) 36.92–157.51.

Table 1: Analysis of variance for yield and yield contributing characters in Sorghum

Source of variation	d.	Days to 50% flowering	Plant height (cm)	Panicle length (cm)	Panicle width (cm)	No. of grains/ Primary branches	Field grade score	Threshed grade score	Days to maturity	No. of primary branches/ panicles	Test weight (g)	Grain yield/ Plant (g)	Fodder yield/ plant (g)
	f.	1	2	3	4	5	6	7	8	9	10	11	12
Replication	2	6.36	79.26	3.47	0.22	20.80	0.00	0.05	5.69	21.06	0.00	13.57	61.01
Treatment	25	148.93**	583.30**	26.87**	2.10**	67.44**	1.99**	2.15**	137.86**	142.72**	0.80**	244.2**	3733.9**
Error	50	4.36	132.65	9.19	0.713	8.64	0.05	0.04	6.85	44.67	0.19	21.23	67.97

*and **indicates significance at 5 and 1% levels, respectively

Genotypic and PCV

High values of genotypic variances and phenotypic variance were observed for the characters fodder yield per plant (35.47 and 36.45) followed by field grade score (24.15 and 25.18), plant height (23.86 and 24.68), grain yield per plant (23.85 and 27.04), threshed grade score (22.71 and 23.45), test weight (20.69 and 28.95) denoting the presence high quantum of variability of these character. The characters which have less influence on the environment may be improved by simple selection methods such as mass selection or pure line selection. The present findings are in close agreement with those of Jain and Patel (2014) and Chittapur and Biradar (2015).

Moderate genotypic and phenotypic variances were observed for the character, number of grains per primary (13.49 and 16.20), panicle width (11.55 and 18.40), number of primary branches per panicle (10.38 and 15.98), and panicle length (14.39) thereby indicating moderate chance for selection these character among the genotype. Similar results were reported by Chavan *et al.* (2010) and Deshmukh *et al.* (2021).

The low phenotypic variances were observed for character, days to 50% flowering (9.38), days to maturity (5.62), and the low genotypic variance for panicle length (8.99) days to 50% flowering (8.98), days to maturity (5.23). Low GCV and PCV indicate that these characters are not suitable for selection. The results are in conformity with Warkad *et al.* (2008), Godbharle *et al.* (2010), Syed *et al.* (2018), and Subramanian *et al.* (2019).

Heritability and genetic advance

The heritability estimates along with expected genetic advances are more useful in predicting yield under phenotypic selection than heritability estimates alone. The broad sense heritability estimates are always of higher magnitude than narrow sense heritability estimates. Therefore, it should be regarded as crude estimates of gene action, operating for a particular character, and the inference drawn to be viewed accordingly.

In the present investigation, the high broad sense heritability combined with high expected genetic advance was observed for the characters' plant height, number of grains per primary, field grade score, threshed grade score, grain yield per plant, and fodder yield per plant indicating the presence of additive gene action and phenotypic selection effectiveness. These results are in conformity with Chaudhary and Arora (2001), Kalpande *et al.* (2014), and More *et al.* (2019).

Moderate heritability with moderate genetic advance was observed for the characters' panicle length, panicle width, and number of primary branches per panicle indicating additive and non-additive gene action which selection was not satisfactory. Similar results were found by Chavan *et al.* (2010) and Deshmukh *et al.* (2021).

The high heritability with moderate genetic advance was observed for the characters' days to 50% flower and days to maturity indicating non-additive gene action. These results are in correspondence with Godbharle *et al.* (2010), Syed *et al.* (2018), and Subramanian *et al.* (2019). The high heritability due to the favorable influence of environmental effect rather than genotype and selection of such traits may not be rewarding.

CONCLUSION

The treatment differences in ANOVA were found statistically significant for all of the characters. The magnitude of genotypic and PCV also indicated the presence of a good amount of variability in the experimental materials. In the present study, high estimates of genotypic and PCV were observed for fodder yield per plant followed by field grade score, plant height, grain yield per plant, threshed grade score, and test weight. High heritability values in a broad sense coupled

Table 2: Parameters of genetic variability for yield and yield contributing characters in Sorghum

S. No.	Characters	Range	General mean	Genotypic variance	Phenotypic variance	GCV (%)	PCV (%)	h ² (Broad sense)	Genetic advance	Genetic advance (%)
1	Days to 50% flowering	67.51–91.93	77.25	48.16	52.53	8.98	9.38	91.68	13.69	17.72
2	Plant height	103.33–259.33	183.11	19.10	20.42	23.86	24.68	93.50	87.06	47.54
3	Panicle length (cm)	16.50–32.27	26.99	5.85	15.11	8.99	14.39	39.06	3.12	11.58
4	Panicle width (cm)	3.20–7.5	5.8	0.46	1.18	11.55	18.40	39.39	0.88	14.93
5	No. of grains/primary	21.33–41	32.80	19.60	28.25	13.49	16.20	69.38	7.59	23.15
6	Field grade score	1.43–4.53	3.32	0.65	0.70	24.15	25.18	91.96	1.58	47.71
7	Threshed grade score	1.83–4.93	3.69	0.35	0.47	22.71	23.45	93.82	1.67	45.33
8	Days to maturity	116.67–139.67	126.30	43.67	50.52	5.23	5.62	86.43	12.65	10.02
9	No. of primary branches/panicles	34.77–68.47	55.03	32.68	77.36	10.38	15.98	42.24	7.65	13.90
10	Test weight (g)	1.20–4.03	2.17	0.20	0.40	20.69	28.95	51.06	0.66	30.45
11	Grain yield/plant	26.27–62.53	36.14	74.35	95.58	23.85	27.04	77.78	15.66	43.34
12	Fodder yield/plant	36.92–157.51	98.52	5.91	5.99	35.47	36.45	94.73	70.08	71.13

GCV: Genotypic coefficient of variation, PCV: Phenotypic coefficient of variation, h²: Heritability

with high expected genetic advance were associated with the character such as plant height, number of grains per primary, field grade score, threshed grade score, grain yield per plant, and fodder yield per plant. High heritability coupled with a high genetic advance expressed as a percent of the mean offers the most effective condition for selection.

REFERENCES

- Binodh, A. K., Manivannan, N., & Varman, P. V. (2008). Character association and path analysis in sunflower. *Madras Agriculture Journal*, 95(7-12), 425-428.
- Chaudhary, L., & Arora, S. (2001). Genetic variability and character association in Sorghum. *Agricultural Science Digest*, 21(4), 219-222.
- Chavan, U. D., Patil, J. V., & Shinde, M. S. (2010). Nutritional and roti quality of Sorghum genotypes. *Indonesian Journal of Agriculture Science*, 10(2), 80-87.
- Chittapur, R., & Biradar, B. D. (2015). Association studies between quantitative and qualitative traits in Rabi sorghum. *Indian Journal Agriculture Research*, 49(5), 468-471.
- Deshmukh, S. S., Dhutmal, R. R., Kalpande, H. V., & Shinde, A. V. (2021). Studies on genetic variability for yield and yield contributing traits in Colored pericarp Sorghum (*Sorghum bicolor* (L.) Moench). *The Pharma Innovation Journal*, 10, 156-158.
- Godhbarle, A. R., More, A. W., & Ambekar, S. S. (2010). Genetic variability and correlation studies in elite 'B' and 'R' lines in Kharif sorghum. *Electronic Journal of Plant Breeding*, 1(4), 989-993.
- Jain, S. K., & Patel, P. R. (2014). Characters association and path analysis in Sorghum (*Sorghum bicolor* (L.) Moench) F₁S and their parents. *Annals of Plant and Soil Research*, 16(2), 107-110.
- Johnson, H. W., Robinson, H. F., & Comstock, R. E. (1955). Estimates of genetic and environmental variability in soybeans. *Agronomy Journal*, 47, 314-318.
- Kalpande, H. V., Chavan, S. K., More, A. W., Patil, V. S., & Unche, P. B. (2014). Character association, genetic variability and component analysis in sweet Sorghum [*Sorghum bicolor* (L.) Moench]. *Journal of Crop and Weed*, 10(2), 108-110.
- Lush, J. L. (1940). Intra correlation and regression of offspring on dams as a method of estimating heritability of characters. *Record of Proceedings American Society of Animal Production*, 33, 293-301.
- Mahajan, R. C., & Wadikar, P. B. (2011). Genetic divergence analysis in Sorghum [*Sorghum bicolor* (L.) Moench]. *Agricultural Science Digest*, 32(3), 244-246, 2012.
- More, A. W., Dhutmal, R. R., & Karanje M. N. (2019). Variability and correlations studies in F₂ generation of Sorghum (*Sorghum bicolor* (L.) Moench). *Bulletin of Environmental, Pharmacology and Life Sciences*, 8(12), 27-32.
- Nwangburuka, C. C., & Denton, O. A. (2012). Heritability, character association and genetic advance in six agronomic and yield related characters in leaf *Corchorus olitorius*. *International Journal of Agriculture Research*, 7(7), 365-375.
- Panse, V. G., & Sukhatme, P. V. (1985). *Statistical method for agril, workers*. New Delhi, India: ICAR.
- Sharma, H., Jain, D. K., & Sharma, V. (2006). Genetic variability and path coefficient analysis in Sorghum. *Indian Journal of Agricultural Research*, 40(4), 310-312.
- Subramanian, A., Raj, R. N., & Elangovan, M. (2019). Genetic variability and multivariate analysis in Sorghum (*Sorghum bicolor*) under sodic soil conditions. *Electronic Journal of Plant Breeding*, 10(4), 1405-1414.
- Syed, A., More, A., Kalpande, H., & Ambilwade, P. (2018). Variability studies in Sorghum (*Sorghum bicolor* (L.) Moench) Germplasm lines for shoot fly resistance parameters. *An International Quarterly Journal of Life Sciences*, 13, 591-595.
- Tah, J., & Roychowdhury, R. (2011). Genetic variability study for yield and associated quantitative characters in mutant genotypes of *Dianthus caryophyllus* L. *International Journal of Bioscience*, 1(5), pp.38-44.
- Tuinstra, M. R., Grote, E. M., Goldsbrough, P. B., & Ejeta, G. (1997). Genetic analysis of post-flowering drought tolerance and components of grain development in Sorghum *bicolor* (L.) Moench. *Molecular Breeding*, 3, 439-448.
- Warkad, Y. N., Potdukhe, N. R., Deth, A. M., Kahate, P. A., & Kotgire, R. R. (2008). Genetic variability, heritability and genetic advance for quantitative traits in Sorghum germplasm. *Agricultural Science Digest*, 28(3), 165-169.