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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 3 checks genotype 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 twelve quantitative characters revealed significant differences for all the traits under study it 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, test weight had significantly high GCV and PCV 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 having high heritability coupled with a high genetic advance and high genotypic coefficient of variation, 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

Introduction

Sorghum is the fifth most produced cereal crop in the world. It's rich in natural nutrients and easy to add to your diet. It's also widely used as animal feed, and as a natural and cost-effective fuel source. It also referred as poor man's crop, camel crop due to its high tolerance to drought condition and withstand with low soil water condition. 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 genetic improvement of sorghum. This enables simultaneous selection for many traits associated with yield (Mahajan *et al.*, 2011) ^[11]. Sorghum in general possesses a wide range of genetic variability (Sharma *et al.*, 2006) ^[15]. Adequate variability provides options from which selections are made for improvement and possible hybridization. Binodh *et al.* (2008) ^[1] 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 circumvent by the introgression of gene responsible for stay green trait which directly associates with post flowering adaptation (Tuinstra *et al.*, 1997; Kebede *et al.*, 2001) ^[19].

Estimates of heritability with genetic advance are more dependable and important than individual consideration of the parameters (Nwangburuk *et al.*, 2012) ^[13]. The extent of variability is evaluated by GCV and PCV which provides information about relative amount of variation in different traits. According to Tah (2011) ^[18] the extent of variability is measured by GCV and PCV which provide information about relative amount of variation in different traits studied. The present study was aimed to estimate the genetic variations, heritability and expected genetic advance in the selected sorghum varieties.

Materials and Methods

During Kharif 2021-22, twenty six genotypes of sorghum (*Sorghum bicolor* L.) were investigated at College of Agriculture, Latur, under V.N.M.K.V., Parbhani. Each genotype was cultivated in a two row of 45 cm x 15 cm between rows to row and plant to plant by using Randomized Block Design with three replications. To raise a good crop, a recommended package of operations were followed. Five plants were identified and labelled at random from

each row and replication for recording twelve observations, and the mean of the five plants was employed for statistical analysis. The data were recorded for days to 50 per cent 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 (gm), grain yield per plant (gm), fodder yield per plant (gm). 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)^[10]. The genetic advance was calculated in percent as per the formula suggested by Johnson *et al.*, (1995)^[8].

Result and Discussions

The ANOVA for a set of 26 sorghum (*Sorghum bicolor* L.) genotypes for twelve quantitative characters revealed highly significant differences among genotypes for all characters studied. For all twelve characters studied, the mean sum of square 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 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 *viz.* days to 50 per cent 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 (gm) 26.27- 62.53 and fodder yield per plant (gm) 36.92- 157.51.

Genotypic and phenotypic coefficient of variation

High values genotypic variances and phenotypic variance were observed for the characters fodder yield per plant (35.47, 36.45) followed by field grade score (24.15, 25.18), plant height (23.86, 24.68), grain yield per plant (23.85, 27.04), threshed grade score (22.71, 23.45), test weight (20.69, 28.95) denoting the presence high quantum of variability of these character. The characters which have less influence of environment may be improved by simple selection method such as mass selection or by pure line selection. The present findings are in close agreement with those of Jain *et al.* (2014)^[7] and chittuarapur *et al.* (2015).

The moderate genotypic and phenotypic variances were observed for character, number of grains per primary (13.49, 16.20), panicle width (11.55, 18.40), number of primary branches per panicle (10.38, 15.98), and panicle length (14.39) thereby indicating moderate chance for selection these character among the genotype. The similar results were reported by Chavan *et al.* (2010)^[3], Deshmukh *et al.* (2021)^[5].

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 indicates these characters are not suitable for selection. The results are in conformity of Warkad *et al.* (2008)^[20], Godbharle *et al.* (2010)^[6], Syed *et al.* (2018)^[17], and Subramanian *et al.* (2019)^[16].

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

Source of variation	d. f.	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/ panicle	Test weight (gm)	Grain yield/ plant(gm)	Fodder yield/ plant(gm)
		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 per cent level respectively

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

Sr. No.	Characters	Range	General Mean	Geno typic Variance	Pheno typic 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/panicle	34.77-68.47	55.03	32.68	77.36	10.38	15.98	42.24	7.65	13.90
10	Test weight (gm)	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

Heritability and genetic advance

The heritability estimates along with expected genetic advance 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 were 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 *et al.* (2001)^[2], Kalpande *et al.* (2014)^[9], More *et al.* (2019)^[12].

The moderate heritability with moderate genetic advance were observed for the characters panicle length, panicle width and number of primary branches per panicles indicating additive and non-additive gene action which selection was not satisfactory. The similar results were found by Chavan *et al.* (2010)^[3], Deshmukh *et al.* (2021)^[5].

The high heritability with moderate genetic advance were observed for the characters days to 50% flower and days to maturity it indicates non additive gene action. This results are in correspondence with Godbharle *et al.* (2010)^[6], Syed *et al.* (2018)^[17], Subramanian *et al.* (2019)^[16]. The high heritability due to favorable influence of environmental effect rather than genotype and selection of such a traits may not rewarding.

Conclusion

The treatment differences in ANOVA were found statistically significant for all of the characters. The magnitude of genotypic and phenotypic coefficient of variation also indicated the presence of good amount of variability in the experimental materials. In the present study, high estimates of genotypic and phenotypic coefficient of variation were observed for fodder yield per plant followed by field grade score, plant height, grain yield per plant, threshed grade score, test weight. High heritability values in broad sense coupled with high expected genetic advance were associated with the character like characters 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 per cent of mean offers the most effective condition for selection.

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