



International Journal of Research in Agronomy

E-ISSN: 2618-0618

P-ISSN: 2618-060X

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www.agronomyjournals.com

2024; SP-7(7): 360-362

Received: 13-05-2024

Accepted: 18-06-2024

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Genetic variability in sorghum [*Sorghum bicolor* (L.) Moench]

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DOI: <https://doi.org/10.33545/2618060X.2024.v7.i7Se.1053>

Abstract

Genetic variability among 60 genotypes with three checks of Sorghum was estimated in augmented design by Federer's (1956) standard statistical methodology during *kharif*, 2023 at the Instructional Farm, Rajasthan College of Agriculture, Maharana Pratap University of Agriculture and Technology, Udaipur for fourteen characters. The analysis of variance revealed highly significant mean sum of squares attributed to genotypes for all traits, indicating substantial variability observed in each trait. The traits like biological yield per plant and harvest index exhibited high GCV values and the highest PCV was recorded for grain yield per plant followed by biological yield per plant, harvest index and dry fodder yield per plant. The magnitude of heritability was high for all the traits, with number of leaves per plant exhibiting the highest heritability and days to maturity was lowest, indicating a strong genetic component for these traits. The genetic gain was highest for harvest index, biological yield per plant, protein content, dry fodder yield, number of leaves per plant, flag leaf length, grain yield, panicle width, 100-seeds weight, panicle length, stem girth, days to 50 percent flowering, plant height and days to maturity had a moderate genetic gain, suggesting a lesser scope for improvement through selection.

Keywords: Analysis of variance, genetic variability, genotypic coefficient of variation, phenotypic coefficient of variation, heritability, genetic gain

Introduction

Sorghum (*Sorghum bicolor* [L.] Moench) is the fifth most important millet crop grown in nearly 100 countries in the world (Hariprasanna and Patil, 2015) [7]. Sorghum is nutritionally good and comparable with other cereals and so it is indicated as "nutritious grain" (Aruna *et al.* 2020) [2]. Nutritionally, sorghum contains an average of 70-75 percent carbohydrates, 11-12 percent protein, 1.8 percent fat, 1.6 percent fiber, 1.9 percent minerals and 1.40-2.80 percent amino acids. For 500 million people living in the semi-arid tropics in more than 30 countries, sorghum is a source of food, feed and fodder, and is also used as fencing, building material or broom (Dogget, 1988) [5]. India being its secondary center of origin it is rich in diversity of sorghum (Vavilov, 1951) [17]. In India, sorghum is cultivated in 3.81 million hectares with production of 4.23 million metric tonnes and productivity of 1110 kg per hectare (Agricultural statistics at a glance 2022-23). In Rajasthan, sorghum is cultivated in 5.6 lakh hectares with the production of 5.4 lakh tonnes and productivity of 964.28 kg per hectare (Agricultural statistics at a glance 2022-23). The crop is highly popular amongst farmers because of its greater adaptability to wide range of environmental fluctuation and utilization in numerous forms like green fodder, stover, silage and hay to suit the diverse needs of farming systems, besides its grain. It is rich in antioxidants and flavonoids which play a major role in the field of medicine. Similarly, on the economic basis, when antioxidants are present in more concentration, they have a direct impact on the yield (Hithamani *et al.* 2014) [8]. The knowledge of genetic parameters like genetic-advance and heritability among characters under selection is useful for the development of efficient breeding strategies and for the prediction of genetic progress in breeding programme (Akatwijuka *et al.* 2016) [1]. Therefore, the present study was carried out to estimate genetic variability present in a collection of 60 genotypes with 3 checks of Sorghum.

Materials and Methods

The present investigation entitled “Character Association and Diversity Analysis in Sorghum [*Sorghum bicolor* (L.) Moench]” was laid out in Augmented design in four blocks during *Kharif*, 2023 at the Instructional Farm, Rajasthan College of Agriculture, Maharana Pratap University of Agriculture and Technology, Udaipur. Single row per genotype were sown with inter and intra row spacing of 45 x 15 cm and 3 m row length. The quantitative character analysis was carried out in compliance with Federer's (1956) [6] standard statistical methodology for augmented design. GCV and PCV were calculated using the formula suggested by Burton (1952) [3]. Heritability was computed using the formula stated by Burton and De vane (1953) [4] and genetic gain was computed as per the formula of Johnson *et al.* (1955) [9].

Traits observed: Observations were made for all the characters *viz.*, plant height, total number of leaves per plant, stem girth, flag leaf length, panicle length, panicle width, grain yield per plant, dry fodder yield per plant, 100 seeds weight, biological yield per plant, harvest index, protein content on five randomly selected plants for each treatment except days to 50 percent flowering and days to maturity which were recorded on a plot-by-plot basis. For determining the protein content, the nitrogen content of the grains was measured using the standard Micro Kjeldahl method. The nitrogen content was then converted to crude protein percentage by multiplying it with a factor of 6.25 and average protein percentage was calculated. Finally, statistical analysis was performed using the mean data of all the measured traits.

Table 1: Analysis of variance for different characters in Sorghum genotypes.

SN	Character	Block	Treatment	Check	Germplasm	C v/s G	Error
		[3]	[62]	[2]	[59]	[1]	[6]
1	Days to 50 Percent flowering	4.31	28.09*	132.33**	25.22*	205.51**	4.56
2	Days to maturity	9.89	70.05*	333.25**	61.49*	552.54**	14.47
3	Plant height (cm)	94	212.08*	1004.44**	178.58*	1340.04**	37.45
4	Number of leaves per plant	0.01	3.00**	0.03*	1.76**	102.32**	0.01
5	Stem girth (cm)	0.01	0.02*	0.10*	0.02*	0.12**	0.01
6	Flag leaf length (cm)	11.85**	32.98**	0.37	16.06**	1081.46**	0.07
7	Panicle length (cm)	1.61	4.34*	2.96	5.76*	7.82*	1.08
8	Panicle width (cm)	1.23**	1.19**	0.04	0.76**	33.61**	0.08
9	Grain yield per plant (gm)	99.70*	71.20*	277.36**	108.59**	566.51**	10.26
10	100 seed weight (gm)	0.18*	0.05*	0.24**	0.07**	0.02	0.01
11	Biological yield per plant (gm)	6302.53**	9311.47**	4416.75**	9600.56**	22341.38**	311.86
12	Harvest index (%)	18.11*	70.84**	0.55	73.82**	0.77	2.66
13	Dry fodder yield per plant (gm)	3327.55**	776.28**	2211.50**	1249.19**	6563.84**	105.77
14	Protein content (%)	0.93	3.17**	0.42	3.39**	11.17**	0.38

** Significant at 1 percent and 5 percent level

Table 2: Mean, range, variability, heritability (broad sense), genetic advance and genetic gain of Sorghum genotypes for grain yield and its contributing attributes.

Character	Mean	Range		GCV (%)	PCV (%)	h ² bs (%)	GA (%)	GG (%)
		Mini.	Maxi.					
Days to 50 percent flowering	61.4	51.25	77.75	7.4	8.17	81.94	8.49	13.83
Days to maturity	103.58	87.25	122.5	6.62	4.66	76.46	12.37	11.94
Plant height (cm)	167.75	140.67	212.52	7.08	16.86	79.03	21.79	12.99
Number of leaves per plant	10.77	7.64	13.36	12.31	12.32	99.73	2.73	25.35
Stem girth (cm)	1.67	1.36	2.13	7.54	18.75	80.9	0.23	14
Flag leaf length (cm)	37.31	26.67	46	10.72	15.39	99.56	8.23	22.06
Panicle length (cm)	28.13	23.42	37.08	7.7	8.54	81.28	4.03	14.31
Panicle width (cm)	7.45	5.6	9.65	11.05	10.11	89.68	1.61	21.58
Grain yield per plant (gm)	89.93	74.32	113.76	11.03	27.46	90.55	19.47	21.65
100-seeds weight (gm)	2.47	2.04	3.14	10.12	16.07	89.17	0.49	19.71
Biological yield per plant (gm)	353.27	166.92	552.58	27.28	27.63	96.75	195.57	55.36
Harvest index (%)	27.42	10.81	53.94	30.76	25.58	96.39	17.09	62.3
Dry fodder yield per plant (gm)	255.93	207.9	338.33	13.21	36.38	91.53	66.74	26.08
Protein content (%)	9.54	6.4	13.35	18.2	19.3	88.91	3.38	35.4

Results and Discussion

Genotypes exhibited wide range of variation for different characters, *viz.*, days to 50 percent flowering (51.75-77.75 days), days to maturity (87.25-122.5 days), plant height (140.67-212.52 cm), total number of leaves per plant (7.64-13.36), stem girth (1.36-2.13 cm), flag leaf length (26.67-46 cm), panicle length (23.42-37.08 cm), panicle width (5.6-9.65 cm), 100-seeds weight (2.04-3.14 gm), biological yield per plant per plant (166.92-552.58 gm), harvest index (10.81-53.94%), dry fodder yield per plant (207.9-338.33 gm), protein content (6.4-13.35%) and grain yield per plant (74.32-113.76 gm).

The extent of GCV ranged from 7.08 percent for plant height to 30.76 percent for harvest index. Harvest index (30.76%) and biological yield per plant (27.28%) showed high estimates of GCV (>20%). GCV estimates were moderate (10-20%) for traits such as protein content (18.20%), dry fodder yield per plant (13.21%), number of leaves per plant (12.31%), 100-seeds weight (10.12%), panicle width (11.05%), grain yield per plant (11.03%) and flag leaf length (10.72%). On the other hand, panicle length (7.70%), stem girth (7.54%), days to 50 percent flowering (7.40%), plant height (7.08%) and days to maturity (6.62%) exhibited a low GCV. The extent of PCV varied from

4.66 percent for days to maturity to 36.38 percent for dry fodder yield per plant. Dry fodder yield per plant (36.38%), biological yield per plant (27.63%), grain yield per plant (27.46%) and harvest index (25.58%) displayed high PCV estimates (>20%), while protein content (19.30%), stem girth (18.75%), plant height (16.86%), 100-seeds weight (16.07%), flag leaf length (15.39%), number of leaves per plant (12.32%), panicle width (10.11%) exhibited moderate estimates of PCV, while panicle length (8.54%), days to 50 percent flowering (8.17%) and days to maturity (4.66%) showed a low PCV.

The high magnitude of heritability (>60%) were noticed in all the characters viz., number of leaves per plant (99.73%), flag leaf length (99.56%), biological yield per plant (96.75%), harvest index (96.39%), dry fodder yield per plant (91.53%), grain yield per plant (90.55%), panicle width (89.68%), 100-seeds weight (89.17%), protein content (88.91%), days to 50 percent flowering (81.94%), panicle length (81.28%), stem girth (80.90%), days to maturity (76.46%) and plant height (79.03%). The genetic advance was found high (>20%) in the characters like biological yield per plant (195.57%), dry fodder yield per plant (66.74%) and plant height (21.79%), while grain yield per plant (19.47%), harvest index (17.09%) and days to maturity (12.37%) exhibited moderate (10-20%) genetic advance. However, lower genetic advance (<10%) was observed for days to 50 percent flowering (8.49%), flag leaf length (8.23%), panicle length (4.03%), protein content (3.38%), number of leaves per plant (2.73%), panicle width (1.61%), 100-seeds weight (0.49%) and stem girth (0.23%).

The harvest index (62.30%) exhibited the highest genetic gain followed by biological yield per plant (55.36%), protein content (35.40%), dry fodder yield (26.08%), number of leaves per plant (25.35%), flag leaf length (22.06%), grain yield per plant (21.65%) and panicle width (21.58%). However, the genetic gain for 100-seeds weight (19.71%), panicle length (14.31%), stem girth (14.00%), days to 50 percent flowering (13.83%), plant height (12.99%) and days to maturity (11.95%) was moderate.

These results are in accordance with the results of Kalpande *et al.* (2014)^[10], Khandelwal *et al.* (2015)^[11], Senbetay *et al.* (2020)^[16], Nirosh *et al.* (2021)^[14], Navya *et al.* (2021)^[13] and Rathod *et al.* (2022)^[15].

Conclusions

The study revealed significant genetic variability for all the studied traits, as indicated by highly significant mean sum of squares attributed to genotypes. There was substantial variation among genotypes for all the characters. Traits like Harvest index and biological yield per plant displayed high genetic coefficient of variation (GCV). Dry fodder yield per plant, biological yield per plant, grain yield per plant and harvest index displayed high phenotypic coefficient of variation (PCV), indicating significant genetic diversity and potential for improvement through selection. All traits examined in the study exhibited high heritability. Traits like plant height, biological yield per plant and dry fodder yield per plant displayed both high heritability and high genetic advance, indicating that these traits are primarily governed by genetic factors and can be efficiently passed on to offspring through breeding. The study also identified the highest genetic gain in the harvest index, followed by the biological yield per plant, protein content, dry fodder yield, number of leaves per plant, flag leaf length, grain yield per plant and panicle width. The research highlights the significant genetic diversity and heritability of the studied traits, providing valuable insights for targeted breeding programs

aimed at improving key characters, ultimately enhancing crop productivity and performance.

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