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Assessment of genetic variability parameters in sorghum [*Sorghum bicolor* (L.) Moench]

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Abstract

In the present investigation, thirty-eight sorghum genotypes were tested in randomized block design along with three checks viz., CSV-17, CSV-23, CSV-27 with three replications at Instructional Farm, Rajasthan College of Agriculture, MPUAT, Udaipur during *Kharif* 2023-2024 to evaluate for 14 characters. Analysis of variance indicated that mean sum of squares due to genotypes was found significant for all of the characters under study. phenotypic coefficient of variation (PCV) was closer to genotypic coefficient of variation (GCV) for most of the traits indicating little effect of environmental variations on the characters. Traits like dry fodder yield per plant followed by harvest index and plant height displayed high genetic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV), indicating significant genetic variability and potential for improvement through selection. High heritability coupled with high genetic gain was observed for the traits like the plant height, total number of leaves per plant, flag leaf length, dry fodder yield per plant, 100 seed weight, biological yield per plant, harvest index and protein content in grain.

Keywords: Sorghum, genetic variability, heritability and genetic gain

Introduction

Sorghum [*Sorghum bicolor* (L.) Moench] is one of the important crops of semi-arid tropics. In India, sorghum is an essential staple food for the people living in dry regions of the country. Sorghum is commonly known as "Jowar" in India. It is nutritionally superior to other cereals such as rice and wheat having high fiber content, minerals and slow digestibility (Rao *et al.*, 2017) [13]. It has 70% starch, hence a good energy source containing 70% to 80% amylopectin in its starch. It is the source of feed, fodder and bio fuels. It also serves as raw material for the production of starch, fiber, dextrose syrup, alcohol and other products. It is a short-day C4 plant and its easy adaptability to hot and dry agro-ecologies makes it a climate change-compliant crop (Hariprasanna and Patil, 2015) [7]. Sorghum is predominantly a self-pollinated crop but it is considered as an often-cross-pollinated species, with outcrossing up to 6% depending on the genotype and growing conditions. It is cultivated during rainy (*Kharif*) and winter (*Rabi*) season. It is mainly originated from Africa region of Sahara Desert (Legwaila *et al.* 2003) [10].

The prime objective of any plant breeding programme is to increase the yield and improve the quality. A choice of the suitable parents for successful development of superior varieties or hybrids is a major concern to plant breeder. For this purpose, utilization of variability and selection of genotypes is necessary. Genetic variability is the presence of differences in genetic constitution among individuals of plant population. Therefore, genetic variability is essential to study those characters that favor the rise in yield along with resistance to biotic and abiotic factors and adaptability. High degree of genetic variability present in population is important to a plant breeder for starting a judicious breeding programme.

Materials and Methods

The present investigation entitled "Character Association Studies in sorghum [*Sorghum bicolor* (L.) Moench]" was conducted to assess the genetic variability, correlation coefficient and path analysis in sorghum at Instructional Farm Rajasthan College of Agriculture, MPUAT, Udaipur

(Rajasthan). Thirty-eight sorghum genotypes evaluated in randomized block design along with three checks in three replications during kharif 2023. Row to row and plant to plant distance was kept 45 cm. and 15 cm, respectively. All the recommended agronomical practices were adopted to raise the good crop. Five competitive plants from each genotype were selected randomly for recording observations for all the traits under study viz., plant height (cm), number of total leaves per plant, stem girth (cm), panicle length (cm), panicle width (cm), grain yield per plant (g), flag leaf length (cm), 100-seed weight (g), dry fodder yield per plant (g), biological yield per plant (g), harvest index (%), protein content in grain (%), except days to 50 per cent flowering and days to maturity which were recorded on plot basis. The analysis of variance was worked out separately for each character as per the method suggested by Panse and Sukhatme (1985) [12] in order to test the difference among the genotypes. The coefficient of genotypic and phenotypic variation was calculated by using the formula suggested by Burton (1952) [2]. Estimates of heritability (h^2) was calculated as per the formula suggested by Burton and Devane (1953) [1]. Genetic advance and genetic gain were computed as per the

formula described by Johnson *et al.* (1955) [9].

Results and Discussion

Mean sum of squares from analysis of variance for various characters are given in (Table-1) for 14 characters viz., days to 50 per cent flowering, days to maturity per plant, plant height (cm), total number of leaves per plant, stem girth(cm), flag leaf length (cm), panicle length (cm), panicle width (cm), grain yield per plant (g), dry fodder yield per plant (g), 100 seed weight (g), biological yield per plant (g), harvest index (%) and protein content in grain (%), revealed significant mean sum of squares due to genotypes at 1% level of significance for all the characters studied.

The mean, range, phenotypic and genotypic coefficient of variation (%), heritability (%) in broad sense and genetic gain for each trait are presented in Table 2. In this study, the phenotypic coefficient of variation (PCV) was closer to genotypic coefficient of variation (GCV) for most of the traits indicating little effect of environmental variations on the characters. Ghorade *et al.* (2015) [6] also found close GCV and PCV indicating less influence of environment.

Table 1: Mean sum of squares for different characters

Characters	Replication [2]	Genotype [40]	Error [80]
Days to 50 per cent flowering	7.715	85.887**	2.015
Days to maturity per plant	9.764	96.504**	4.848
Plant height (cm)	334.266	4779.868**	92.725
Stem girth (cm)	3.125	1.574**	1.203
Total number of leaves per plant	1.379	15.971**	0.361
Flag leaf length (cm),	5.993	69.053**	0.419
Panicle length (cm),	0.631	14.402**	0.291
Panicle width (cm),	2.885	1.216**	0.184
Grain yield per plant (g)	1.353	116.133**	5.916
Dry fodder yield per plant (g)	1.353	116.133**	5.916
100 seed weight (g)	0.072	0.795**	0.104
Biological yield per plant (g)	5.753	1502.740**	16.048
Harvest index (%)	0.595	165.214**	1.408
Protein content in grain (%)	4.473	4.572**	0.38

** Significant at 1% level of significance

[] degree of freedom

The genotypic coefficient of variation (GCV) reflects the magnitude of genetic variability within each trait, with higher values indicating greater genetic diversity. Notably, traits such as dry fodder yield per plant exhibited substantial GCV (33.99), followed by harvest index (25.25) and plant height (16.25), high lighting significant genetic variability. Conversely, traits like stem girth showed lower GCV (3.44) followed by days to maturity per plant and days to 50% flowering, suggesting less genetic diversity in these characteristics. Almost similar results were obtained by Daniel and Eric (2014) [3] for harvest index, Jain and Patel (2016) [8] for dry fodder yield, Syed *et al.* (2018) [16] for days to maturity per plant and days to 50% flowering, Subramaniam *et al.* (2019) [15] for panicle length, Dhutmal *et al.* (2020) [5] for days to maturity per plant and days to 50% flowering, Deshmukh *et al.* (2021) [4] observed moderate to low values of GCV for plant height, 100 seed weight, panicle length, days to maturity per plant and days to 50% flowering and Santhiya *et al.* (2021) [14] for plant height.

Phenotypic coefficient of variation (PCV) measures the extent of variation in observable traits due to both genetic and environmental factors. Traits like dry fodder yield per plant (34.00), harvest index (25.57), and plant height (16.73)

demonstrated the higher PCV values, indicating considerable phenotypic variability. In contrast, days to maturity per plant (6.33) and days to 50% flowering exhibited lower PCV, suggesting less variation in phenotypic expression among individuals. Almost similar results were obtained by Daniel and Eric (2014) [3] for harvest index, Jain and Patel (2016) [8] for dry fodder yield, Syed *et al.* (2018) [16] for days to maturity per plant and days to 50% flowering, Subramaniam *et al.* (2019) [15] for panicle length, Dhutmal *et al.* (2020) [5] for days to maturity per plant and days to 50% flowering, Deshmukh *et al.* (2021) [4] observed moderate to low values of GCV for plant height, 100 seed weight, panicle length, days to maturity per plant and days to 50% flowering and Santhiya *et al.* (2021) [14] for plant height. High heritability coupled with high genetic gain were recorded for plant height, total number of leaves per plant, flag leaf length, dry fodder yield per plant, 100 seed weight, biological yield per plant, harvest index and protein content in grain. High heritability coupled with high genetic gain was also reported by Subramaniam *et al.* (2019) [15] for panicle length, Mofokeng *et al.* (2019) [11] for plant height, panicle length, 100 seed weight and Santhiya *et al.* (2021) [14] for plant height, 100 seed weight.

Table 2: Estimates of mean, range and variability parameters

Characters	Mean	Range	GCV	PCV	h ²	GG
Days to 50 per cent flowering	61.569	41.33-69.00	8.588	8.892	93.276	17.086
Days to maturity per plant	93.935	81.33-107.00	5.884	6.334	86.306	11.261
Plant height (cm)	243.167	139.07-313.30	16.255	16.73	94.398	32.534
Stem girth (cm)	10.208	9.00-12.41	3.444	11.285	9.313	2.165
Total number of leaves per plant	15.919	10.58-21.88	14.33	14.818	93.516	28.546
Flag leaf length (cm),	37.256	25.94-46.48	12.839	12.956	98.203	26.209
Panicle length (cm),	24.477	20.05-32.00	8.861	9.13	94.178	17.714
Panicle width (cm),	7.275	5.92-9.10	8.06	9.988	65.121	13.399
Grain yield per plant (g)	71.195	52.53-90.13	8.514	9.173	86.131	16.276
Dry fodder yield per plant (g)	112.124	32.07-189.67	33.997	34.001	99.975	70.025
100 seed weight (g)	3.617	1.95-4.74	13.261	15.99	68.784	22.657
Biological yield per plant (g)	191.621	144.67-234.20	11.617	11.804	96.863	23.553
Harvest index (%)	29.264	17.04-46.29	25.251	25.574	97.486	51.358
Protein content in grain (%)	9.75	7.23-12.20	12.125	13.673	78.637	22.15

Broad-sense heritability (h²) estimates the proportion of phenotypic variation attributable to genetic factors alone. Traits such as dry fodder yield per plant (99.97%) showed very high heritability, indicating that nearly all phenotypic variation in these traits is due to genetic differences. In comparison, traits like stem girth had lower heritability (9.31%), suggesting a stronger influence of environmental factors on phenotypic expression. Subramaniam *et al.* (2019) [15] for panicle length, Mofokeng *et al.* (2019) [11] for plant height, panicle length, 100 seed weight and Santhiya *et al.* (2021) [14] for plant height, 100 seed weight gave almost similar findings.

Genetic gain measures the percentage increase in trait values relative to their respective means due to genetic improvement. Traits like dry fodder yield per plant (70.02%) and harvest index (51.35%) showed substantial genetic gain, indicating significant improvements relative to their average values. In contrast, traits like stem girth (2.16%) exhibited lower GA% of means, suggesting more modest improvements relative to their means. Subramaniam *et al.* (2019) [15] for panicle length, Mofokeng *et al.* (2019) [11] for plant height, panicle length, 100 seed weight and Santhiya *et al.* (2021) [14] for plant height, 100 seed weight gave almost similar findings.

Conclusion

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 dry fodder yield per plant followed by harvest index and plant height displayed high genetic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV), indicating significant genetic variability and potential for improvement through selection. All traits examined in the study exhibited high heritability. Maximum heritability was observed for dry fodder yield per plant followed by flag leaf length and harvest index. The study also identified maximum genetic gain for dry fodder yield per plant followed by harvest index and plant height. High heritability coupled with high genetic gain were recorded for plant height, total number of leaves per plant, flag leaf length, dry fodder yield per plant indicating the presence of additive genes. Therefore, these characters can be selected for improvement programmes.

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