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Mohammedi Begum
Vasantrao Naik Marathwada
Krishi Vidyapeeth, Parbhani,
Maharashtra, India

More AW
Vasantrao Naik Marathwada
Krishi Vidyapeeth, Parbhani,
Maharashtra, India

Kalpande HV
Vasantrao Naik Marathwada
Krishi Vidyapeeth, Parbhani,
Maharashtra, India

Tirkar AN
Vasantrao Naik Marathwada
Krishi Vidyapeeth, Parbhani,
Maharashtra, India

Kute KG
Vasantrao Naik Marathwada
Krishi Vidyapeeth, Parbhani,
Maharashtra, India

Ritu Rani
Vasantrao Naik Marathwada
Krishi Vidyapeeth, Parbhani,
Maharashtra, India

Kadam KV
Vasantrao Naik Marathwada
Krishi Vidyapeeth, Parbhani,
Maharashtra, India

Yogesh S Borde
Vasantrao Naik Marathwada
Krishi Vidyapeeth, Parbhani,
Maharashtra, India

Lagad SL
Vasantrao Naik Marathwada
Krishi Vidyapeeth, Parbhani,
Maharashtra, India

Corresponding Author:
Mohammedi Begum
Vasantrao Naik Marathwada
Krishi Vidyapeeth, Parbhani,
Maharashtra, India

A study on the genetic variability and heritability for grain yield and its parameters in brown midrib sorghum [*Sorghum bicolor* (L.) Moench]

Mohammedi Begum, More AW, Kalpande HV, Tirkar AN, Kute KG, Ritu Rani, Kadam KV, Yogesh S Borde and Lagad SL

Abstract
The present experiment was carried out with 28 diverse genotypes of brown midrib sorghum including three checks (Parbhani Moti, CSV-22R and CSV 23 BMR) in Randomized Block Design with two replications during *rabi*, 2023. Observations were recorded for 12 characters. High estimates of genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV) was observed for traits *viz.* plant height (cm), grain yield per plant, while moderate GCV and PCV was observed for number of primaries / panicle, number of leaves, panicle length, panicle width, leaf area, stem girth, leaf: stem ratio, 100-seed weight, fodder yield per plant and low genotypic and phenotypic coefficient of variation was observed for days to 50% flowering. High heritability coupled with high expected genetic advance were exhibited for the traits *viz.* plant height, panicle length, number of leaves, leaf: stem ratio, fodder yield per plant, 100-seed weight, grain yield per plant.

Keywords: Genetic advance, Co-efficient of variation, genetic variability, brown midrib sorghum, heritability

Introduction
In terms of production and utilisation, sorghum is the fifth most significant cereal crop, following rice, wheat, maize, and barley across the globe. It is known as Jola (Karnataka), Jowar (Hindi), Jonna (Andhra Pradesh) and Cholam (Tamil Nadu) in the Indian subcontinent. It is highly suited to a wide range of agro-ecologies subjected to abiotic stress problems such as drought, aluminium toxicity, low fertility, and salinity (Santosh and PK Pandey, 2020) [18]. It has an array of uses, including forage sorghum, grain sorghum, and sweet sorghum, which provide food, fodder, feed, fuel, and fibre.

Sorghum is an excellent option for te semi-arid areas and arid areas of the globe due to its terminal drought tolerance, yield stability, and adaptability across a broad variety of climates.

It is the most efficient C4 plant in terms of photosynthetic efficiency, with a very high biomass production potential. Because of its terminal drought tolerance, yield stability, and adaptability across a broad variety of temperatures, sorghum is an excellent choice for arid and semi-arid areas across the globe. In terms of efficiency of photosynthetic activity and biomass production potential, it is the most efficient C4 plant. *Sorghum bicolor* (2n=2x=20) is a member of the Poaceae family, Panicoidae subfamily, Andropogonae tribe, Sorghastrae subtribe, and Sorghum genus. The five basic sorghum races are Bicolor, Guinea, Kafir, Durra, and Caudata (Harlan and Dewet, 1972) [7].

Brown midrib is a phenotype linked with low lignin concentration. This lowered lignin concentration is critical because it improves the digestibility and palatability of the fodder and provides nutritional advantages to the animals which consume it. The mutations characterizing brown midrib in maize have been found and in sorghum it is chemically produced (Porter *et al.*, 1978) [17]. When compared to their normal (white midrib) counterparts, brown midrib mutants generate less lignin and have a chemically changed lignin content (Cherney *et al.*, 1986) [5]. It is a well-known fact that crop improvement is dependent on the degree of variability in the desired character of the base material.

Genetic variability for agronomic characteristics is an important aspect of breeding programmes for gene pool development, and precise estimates of heritability are required to establish an effective breeding programme.

Yield component breeding would be most efficient if the components involved are highly heritable, genetically independent, or strongly associated with grain yield. However, determining whether observed variability is substantially heritable or not is quite challenging. Furthermore, understanding heritability is critical for selection-based improvement since it reveals the amount to which a feature is transmissible to future generations.

Materials and Methods
Experimental Materials
The experimental material for present research work included 25 brown midrib sorghum genotypes (13 BMR sorghum genotypes derived from cross PVR 906 X N 952, 4 Parbhani Moti BMR mutants and 8 different BMR sources *viz* BMR 1, BMR2, BMR 6 and BMR 12) and 3 checks Parbhani Moti, CSV 22R and CSV BMR 43. These genotypes were grown at the Sorghum Research station, VNMKV Parbhani during *rabi* 2023 with 45 cm x 15 cm spacing. The experiment was set up in a randomised block design that included two replications. The crop was raised using all of the prescribed cultural and plant protection practises. Five competitive plants from each genotype were used to record the Observations in each replication for twelve grain yield and its component traits: days to 50% flowering, plant height (cm), number of primaries/ panicle, number of leaves, panicle length (cm),

panicle width (cm), leaf area (cm^2), stem girth (cm), leaf: stem ratio, 100-seed weight (g), fodder yield per plant (g), grain yield per plant (g). The mean value of the collected data was provided to analysis of variance (ANOVA) utilising Panse and Sukhatme (1985) [16] statistical analysis techniques. The phenotypic and genotypic variations were also determined according to Burton's (1952) [3] approach. Heritability (h2) in the broad sense for all characters was calculated using Allard's (1960) [1] method. Johnson *et al*. (1955) [12] algorithm was used to calculate genetic gain for each character.

Results and Discussion
The occurrence of genetic diversity in plants for a certain attribute is critical to the success of plant breeding programmes. Table 1 displays estimates of the mean sum of squares for replications and genotypes, as well as CV% for the genotypes tested. The above analysis revealed that the differences between the treatments respective of all the characters studied were found to be significant at 1% and 5% level of significance, indicating the presence of a sufficient amount of variability for these characters and there is a plenty of scope for improvement via selection. In general, estimates of phenotypic coefficient of variation (PCV) were partly greater than the corresponding genotypic coefficient of variation (GCV), therefore indicating that the expression of the characters is relatively less influenced by environment.

Table 1: Mean, range and character wise promising genotypes for the grain yield and it's component traits.

SL. No.	Characters	Treatment (27 d.f)	Mean	Range	Promising Genotypes
1	Days to 50% flowering	20.382**	79	72-85	PBMR 6, PBMR 3, PBMR 4 and Bmr-14-04-07
2	Plant height (cm)	2754.824**	202.40	88-242.7	CSV 22 R, PBMR 1, CSV 43 BMR, PBMR 11 and PBMR 9
3	No. of primaries/ panicle	75.560**	54	39.25-63.10	PBMR 15 and CSV-22R (63), PBMR 5 (61)
4	Number of leaves	2.964**	10	8.202-11.90	PBMR 7, PBMR 14, PBMR 4, PBMR 8 and CSV-22R, PBMR 1 and PBMR 5
5	Panicle length (cm)	16.894**	19.04	13.702-26.4	CSV 43 BMR and CSV 22R
6	Panicle width (cm)	0.3857**	5.46	4.592-6.29	PBMR 5 and CSV 43 BMR
7	Leaf area (cm^2)	6086.311**	486.79	376.41-568.24	PBMR 5, PBMR 7 and PBMR 12
8	Stem girth (cm)	0.417**	5.03	4.25-5.893	PBMR 15 and PBMR 14
9	Leaf: Stem ratio	0.001**	0.22	0.16-0.257	PBMR 2, PBMR 7 and BMR 14-50-20
10	100-seed weight (g)	0.569**	3.71	2.98-5.08	Parbhani Moti, PBMR 11 and PBMR 12
11	Fodder yield per plant (g)	170.893**	109.57	78.95-144.9	PBMR 14, CSV 22R and PBMR 1
12	Grain yield per plant (g)	683.164**	36.19	21.30-63.60	CSV 22 R, Parbhani Moti and BMR 14-50-20

**Significance at 1% level and *Significance at 5% level.

Mean performance
The Genotypes CSV 22 R (63.6 g) followed by Parbhani Moti (54.1 g), BMR 14-50-20 (44 g) exhibited the highest grain yield per plant. Twelve brown midrib genotypes were found to be significantly higher in performance over the check CSV43 BMR (29.3 g)

GCV and PCV
The coefficient of variation (CV) revealed significant genetic variation in various morphological traits (Table 2). The measure of coefficient of variation is an important tool in the comparison of variation in a set of data with multiple units. Furthermore, a high CV indicates dispersion in the variable. The above analysis revealed that the differences between the treatments respective of all the characters studied were found to be significant at 1% and 5% level of significance, indicating the presence of sufficient amount of variability for these characters.

In the present study, high estimates of genotypic and phenotypic coefficient of variation were observed for the

characters *viz*. plant height (cm), grain yield per plant (g). High genetic variability was reported by Jain *et al*. (2009) [11], Santosh and Pandey (2020) [18] for plant height and for grain yield by Arunkumar (2013) [2]. While moderate GCV and PCV was observed for number of primaries / panicle, number of leaves, panicle length, panicle width, leaf area, stem girth, leaf: stem ratio, 100-seed weight, fodder yield per plant and low GCV and PCV was observed for days to 50% flowering. El- Sagheer *et al*. (2020) [9] and Malik *et al*. (2015) [14] also reported the moderate GCV and PCV for the trait 100 seed weight. Kumar *et al*. (2011) [13] and Malik *et al*. (2015) [14] found the similar results for the trait stem girth and for the trait leaf area, Santosh *et al*. (2020) [18], Malik *et al*. (2015) [14] and Kumar *et al*. (2011) [13] recorded moderate GCV and PCV. More *et al*. (2019) [15] also observed moderate GCV for panicle width and low GCV and PCV for days to 50% flowering. Whereas for panicle length similar results were obtained by Dhutmal *et al*. (2020) [8], El - Sagheer *et al*. (2020) [9].

The PCV was higher than the GCV for all the traits, although

the magnitude of the difference was small for all of them. The small variations between PCV and GCV revealed that they were more resistant to environmental changes, implying that they had a better opportunity of improving these characteristics through selection based on phenotypic performance.
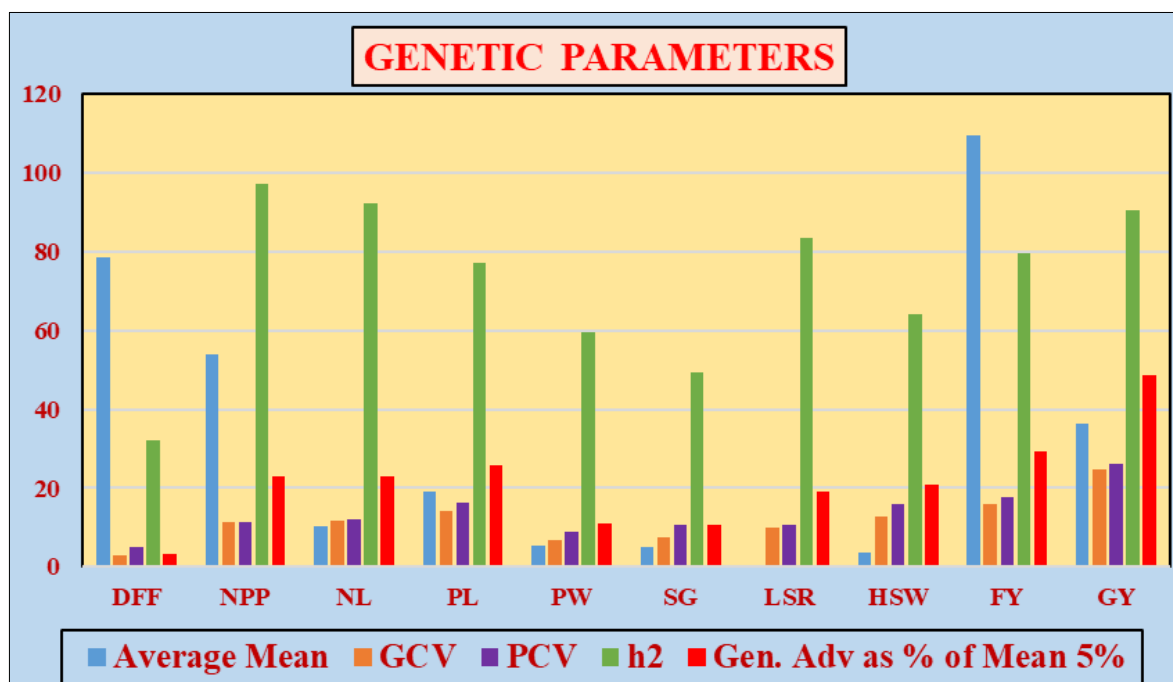

Fig 1: The Genetic parameters for grain yield and contributing traits

Heritability and genetic advance

The high degree of heritability estimates indicated that the traits were under genotypic control, and selection might be relatively simple, with improvement practicable through selective breeding for these traits (Table 2). The estimates of heritability ranged from 98.67% for plant height to 32.20% for days to 50% flowering. The trait plant height has highest heritability (98.67%), followed by number of primaries per panicle (97.17%), number of leaves (92.36%), grain yield per plant (90.37%) and Leaf: Stem ratio (83.33%).

The amount of genetic advance predicted from selection may be calculated by measuring heritability and the coefficient of variability, making it certain that there is ample scope for improvement through selection. The highest GAM was 48.72% for Grain yield per plant (g) followed by plant height (cm) 37.39%, fodder yield per plant (g) 29.22%, panicle length (cm) 25.78%, number of primaries / panicle 22.88%, number of leaves 22.85%, 100-seed weight (g) 20.95%.

The estimates of heritability combined with expected genetic advance are more useful than heritability estimates alone for estimating yield under phenotypic selection. High heritability coupled with high expected genetic advance suggests that the additive gene action predominates, and selection may be successful in such cases. High heritability along with high expected genetic advance were exhibited for the characters *viz.* plant height, number of leaves, panicle length, leaf: stem ratio, 100-seed weight, fodder yield per plant, grain yield per plant (Fig. 1)

Buttar *et al.* (2008) [4], Santosh and Pandey (2020) [18], Gebregergs and Mekbib (2020) [10], Dev *et al.* (2019) [6], Sen *et al.* (2019) [19] observed high heritability combined with high expected genetic advance, whereas similar results for number of leaves were observed by Santosh and Pandey (2020) [18]. Dev *et al.* (2019) [6], Sen *et al.* (2019) [19] for fodder yield per plant and Gebregergs and Mekbib (2020) [10], Jain *et al.* (2009) [11], Malik *et al.* (2015) [14] for grain yield per plant got similar results.

Table 2: Genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), Heritability and Genetic advance for grain yield and its component traits.

	Days to 50% flowering	Plant height (cm)	Number of primaries / panicle	Number of leaves	Panicle length (cm)	Panicle width (cm)	Leaf area (cm²)	Stem girth (cm)	Leaf: Stem ratio	100-seed weight (g)	Fodder yield per plant (g)	Grain yield per plant (g)
Mean	78.69	202.40	53.89	10.33	19.04	19.04	486.79	5.03	0.22	3.71	109.57	36.19
Range	73 to 85	88 to 242.7	39.25 to 63.10	8.2 to 11.9	13.64 to 26.40	4.59 to 6.29 cm	568.24 to 376.41	4.258 to 5.89	0.16 to 0.25	2.98 to 5.08	78.95 to 145.05	21.30 to 63.60
GCV	2.79	18.27	11.27	11.54	14.24	6.93	9.53	7.37	10.10	12.70	15.88	24.88
PCV	4.92	18.39	11.43	12.01	16.20	9.00	12.88	10.49	10.68	15.86	17.79	26.17
h²	32.20	98.67	97.14	92.36	77.23	59.42	54.75	49.36	83.33	64.11	79.72	90.37
Genetic Advancement 5%	2.57	75.68	12.33	2.36	4.911	0.60	70.72	0.53	0.04	0.77	32.01	17.63
Gen. Adv as % of Mean 5%	3.26	37.39	22.88	22.85	25.78	11.02	14.52	10.66	18.97	20.95	29.22	48.72

Conclusion

The present study revealed the considerable amount of difference among the genotypes as revealed by analysis of variance, which validated further on the basis of genetic and statistical analysis of data. The characters plant height, panicle length, leaf: stem ratio, number of leaves, 100-seed weight, fodder yield per plant, grain yield per plant had high heritability combined with high expected genetic advance. Further selection of these characters will improve the breeding efficiency of genotypes. The range of heritability, GCV, PCV and genetic advance as percent of mean was observed from low to high in different yield contributing traits. The traits which has desired value of variability parameters and mean performance can be utilized in crop improvement programme. This study indicated that there was significant genetic variability among the brown midrib sorghum genotypes studied. Thus, there is an opportunity of direct selection of genotypes for different yield contributing traits which would be helpful for enhancing the food security and breeding potential of crops.

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