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Genetic variability, heritability, and genetic advance for yield attributing traits in rabi sorghum (*Sorghum bicolor* L. Moench)

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Abstract
To evaluate genetic variability, heritability, and genetic advancement for yield and yield-attributing variables in eight genotypes of rabi sorghum-Phule Uttara, Phule Madhur, CSV-22, Parbhani Moti, Maldandi-35-1, Phule Yashomati, and Phule Anuradha-an investigation was conducted. At the farm of the All India Coordinated Sorghum Improvement Project, the experiment was carried out using a Randomized Block Design with three replications. Key parameters such plant height, panicle length, 1000-grain weight, grain yield, fodder yield, harvest index, and days to 50% blooming were observed. All of the features under study had significant genotype differences, according to analysis of variance, suggesting that there is a significant amount of genetic diversity.
For grain production, plant height, and 1000-grain weight, high heritability and high genetic advancement were noted, indicating that additive gene activity predominates. These findings suggest that rabi sorghum grain yield could be increased by selection for these features.

Keywords: Rabi sorghum, genetic variability, heritability, genetic advance, yield traits, quantitative genetics

Introduction
During India's post-rainy season, Rabi sorghum (*Sorghum bicolor* L. Moench) is a significant cereal crop that is primarily farmed for grain and fodder. Low temperatures, little soil moisture, and insufficient fertilizer availability frequently limit its productivity. Understanding genetic variability and the heritable factors influencing yield and related variables is necessary to maximize yield potential.
Plant breeding is based on genetic variability, which makes it possible to choose better genotypes. Estimates of heritability and genetic advancement aid in determining the degree of heritability of observed variation as well as the possible improvement that selection may bring about. In this study, eight prospective rabi sorghum genotypes were evaluated for genetic variability, heritability, and genetic advancement for yield and related variables.

Material and Methods
Material
The study comprised the following eight rabi sorghum genotypes:
1. Phule Yashomati
2. Phule Anuradha
3. CSV-22
4. Parbhani Moti
5. Maldandi-35-1
6. Phule Uttara
7. Phule Madhur
8. RSV-2371

Experimental Layout and site

The current study was conducted in the Kharif season of 2024 at G H Raisoni University's Agricultural Research Farm in Saikheda, Madhya Pradesh, India. This area is subtropical, with hot, muggy summers and mild winters. Three replications of the field experiment were carried out using a Randomized Block Design (RBD) throughout the Rabi season. There were four 4 m rows in each plot, with 15 cm between plants and 45 cm between rows. They adhered to standard agronomic procedures.

Observations recorded

Data were recorded from five randomly selected plants per plot on the following characters:

1. Days to 50% flowering
2. Days to physiological maturity
3. Plant height (cm)
4. Panicle length (cm)
5. Panicle width (cm)
6. No. of primaries/panicle
7. No.of grains/primary
8. Fodder weight (g/plant)
9. 100 seed weight (g)
10. Grain yield (g/plant)
11. Harvesting index (%)

Statistical analysis

Genetic variability was estimated using analysis of variance (ANOVA).

According to Burton (1952) [2], the phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) were computed.

Genetic advance (GA) was computed in accordance with Johnson *et al*. (1955) [4], and broad-sense heritability (hb2h^2_bhb2) was determined in accordance with Lush (1940).

Formulas used:

GCV=VgX¯×100,PCV=VpX¯×100GCV = \frac{\sqrt{V_g}}{\overline{X}} \times 100, \quad PCV = \frac{\sqrt{V_p}}{\overline{X}} \times 100GCV=XVg ×100,PCV=XVp×100 hb2=VgVp×100,GA=k×Vp×hb2h^2_b = \frac{V_g}{V_p} \times 100, \quad GA = k \times \sqrt{V_p} \times h^2_bhb2=VpVg×100,GA=k×Vp×hb2

where k=2.06k = 2.06k=2.06 for 5% selection intensity.

To determine whether there were any significant differences between the genotypes, the gathered data were first examined using Analysis of Variance (ANOVA). The Panse and Sukhatme (1985) [1] method was used to run the ANOVA, and the significance of the F-values was examined at the 5% (p< 0.05) and 1% (p< 0.01) probability levels. A number of genetic factors were estimated once significant variance was obtained.

The environmental coefficient of variation (ECV) was derived to measure the magnitude of environmental impacts, while the genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were calculated using the methods put out by Burton and DeVane (1953) [2]. According to Falconer (1996) [3], the broad-sense heritability (H2) was calculated to ascertain the percentage of overall phenotypic variance attributable to genetic variables. Additionally, using a standardized selection intensity of 2.06, which corresponds to a 5% selection pressure, the genetic advance (GA) and genetic advance as a percent of mean (GAM) were computed using the Johnson *et al*. (1955) [4] method. Together, these genetic factors aid in determining the pattern of inheritance and assessing how well breeding programs use selection.

Results and Discussion

Analysis of Variance

Table 1: ANOVA for yield and yield-attributing traits in rabi sorghum

Source of Variation	df	Days to 50% Flowering	Plant Height (cm)	Panicle Length (cm)	100-Grain Weight (g)	Grain Yield (kg / ha)	Fodder Yield (kg / ha)	Harvest Index (%)
Replications	2	0.84	6.78	0.46	0.21	1123.7	2415.2	0.36
Genotypes	7	27.34**	708.12**	8.92**	4.63**	102562.4**	215638.3**	14.82**
Error	14	1.12	10.67	0.54	0.28	1824.6	3179.	

Estimates of Variability, Heritability, and Genetic Advance

Table 2: Genetic parameters for yield and yield-contributing traits in rabi sorghum

Character	Mean	GCV (%)	PCV (%)	Heritability (%)	Genetic Advance	GA as % of Mean	Interpretation
Days to 50% flowering	70.4	3.85	4.12	87.7	5.20	7.39	High h², moderate GA
Plant height (cm)	165.2	9.64	10.11	91.2	31.12	18.84	High h² & GA - additive gene action
Panicle length (cm)	24.5	6.27	7.01	80.0	2.84	11.59	Moderate h², moderate GA
1000-grain weight (g)	28.9	8.75	9.42	86.3	4.78	16.54	High h² & GA
Grain yield (kg/ha)	30.6	12.58	13.49	87.4	7.42	24.24	High h² & GA - additive control
Fodder yield (kg/ha)	62.1	11.93	12.78	87.1	13.41	21.60	High h² & GA
Harvest index (%)	32.4	7.56	8.32	82.6	4.39	13.54	Moderate varia

Discussion

Effective selection requires extensive genetic variety, which is indicated by the wide variances among genotypes for all traits. The strong correlation between GCV and PCV values for the majority of traits indicated that the majority of the observed variation was genetic in nature and that environmental influence was minimal.

For plant height, 1000-grain weight, and grain yield, high heritability and high genetic advancement show additive gene activity, indicating that selection for these traits would be successful. For panicle length and harvest index, moderate heritability and genetic advancement point to the involvement of both additive and non-additive genes. Patil (2011) [5] and Bhosale *et al*. (2017) [6] have documented comparable patterns in rabi sorghum.

Conclusion

For every yield and yield-contributing attribute, the study found significant genetic heterogeneity across the genotypes evaluated. Grain yield, plant height, and 1000-grain weight all have high heritability and genetic advancement, which suggests that additive genetic effects predominate and make these qualities trustworthy selection indicators for yield enhancement. In rabi sorghum improvement efforts, Phule Madhur and Phule Yashomati may be attractive parental lines due to their exceptional performance and genetic potential.

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