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Variability studies on various yield and quality characters in sorghum germplasm accessions

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Abstract
The study was undertaken to evaluate genetic variability, heritability and genetic advance as percent of mean among the 60 sorghum germplasm accessions along with four checks for 14 yield and quality characters. The values of PCV were observed higher than the values of GCV for all the traits, indicating the environmental influence on the expression of these characters. High values of PCV and GCV were noted for plant height, 1000-seed weight, ear head length, harvest index, crude fibre content, total antioxidant activity, dry fodder yield, total phenol content and grain yield per plant, implying high degree of variability in these traits among the genotypes under study. High heritability in addition to high GAM was observed for the traits viz., ear head length, total phenol content, dry fodder yield, days to maturity, plant height, water absorption capacity, protein content, harvest index, grain yield per plant, crude fibre content, days to 50% flowering, total antioxidant activity and 1000-seed weight, suggesting the functioning of additive gene action in the inheritance of these traits. Therefore, simple phenotypic selection is sufficient for improving these traits.

Keywords: PCV, GCV, heritability and genetic advance as percent of mean

Introduction
Sorghum [Sorghum bicolor (L.) Moench] is the 5th most important cereal crop grown in the world with chromosome number, 2n=20 and belongs to the family Poaceae. In India, it occupies 3rd place among the food grains after rice and wheat. It is an important crop of resource for poor, small and marginal farmers in arid and semi-arid regions. It has several economically important uses such as food, feed, fodder, fuel, and fiber (Laavanya et al., 2017) [8]. The basis for genetic advancement in any crop is systematic assessment of genetic variability and diversity available in the germplasm. More chance of heterotic groups is performed if diversity is broad and breeding for biotic and abiotic resistances will be productive (Elangovan and Babu, 2015) [3]. The extent of variability is measured by phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV), which provides the information about relative amount of variation in different characters. Since heritability is also influenced by environment, the information on heritability alone may not help in pin pointing the characters enforcing selection. Nevertheless, the heritability estimates in conjunction with the predicted genetic advance will be more reliable (Johnson et al., 1955) [7].

Materials and Methods
The field experiment was conducted during kharif (rainy season), 2019 at Terraces experimental field, Indian Institute of Millets Research (ICAR-IIMR), Rajendranagar, Hyderabad in augmented block design with 60 sorghum germplasm accessions along with four checks to study the extent of genetic variability, heritability and genetic advance as percent of mean. Each genotype was planted in 4.5m row with 45 x 15cm spacing. The standard agronomic practices were followed throughout the crop growth period. The observations were noted on five randomly selected plants from each entry for the traits, days to 50% flowering, days to maturity, plant height (cm), ear head length (cm), 1000-seed weight (g), dry fodder yield (g), grain yield per plant (g), harvest index (%), total carbohydrate content (g/100g), protein content (g/100g), crude fibre content (g/100g), total phenol content (mg/100g), total antioxidant activity (mg of AAE/100g) and water absorption capacity (ml/100g). Analysis of variance for different characters was done as per standard statistical procedure given by Federer (1956) [4]. The following genetic parameters were estimated.

Phenotypic and genotypic variance
This was estimated according to the method given by Lush (1940) [9].

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$$\text{Genotypic variance } (\sigma^2 g) = \frac{M_t - M_e}{r}$$

$$\text{Phenotypic variance } (\sigma^2 p) = \sigma^2 g + M_e = \frac{M_t - M_e + M_e}{r}$$

The test of significance was carried out using 'F' table value of Fisher and Yates (1963) [5].

Coefficient of Variation
Phenotypic and genotypic coefficients of variation (PCV and GCV) were computed according to the formula given by Burton (1952) [2].

$$\text{GCV} = \frac{\text{Genotypic standard deviation } (\sigma g)}{\text{General mean } (\bar{x})} \times 100$$

$$\text{PCV} = \frac{\text{Phenotypic standard deviation } (\sigma p)}{\text{General mean } (\bar{x})} \times 100$$

The GCV and PCV values were classified as described by Sivasubramanian and Menon (1973) [11].

Classification	GCV/ PCV
Low	Less than 10%
Moderate	10 – 20%
High	More than 20%

Heritability
Heritability in broad sense was computed as the ratio of genetic variance to the total phenotypic variance and narrow sense heritability was the ratio of additive genetic variance to the total phenotypic variance as suggested by Hanson et al. (1956) [6] and expressed as percentage.

$$\text{Heritability } (h^2_{bs}) = \frac{\text{Genotypic variance } (\sigma^2 g)}{\text{Phenotypic variance } (\sigma^2 g)} \times 100$$

Where
h^2_{bs} = Heritability in broad sense
σ^2_g = Genotypic Variance
σ^2_p = Phenotypic Variance

Heritability in broad sense was categorized as per the classification given by Johnson et al. (1955).

Classification	Heritability
Low	0-30%
Moderate	30-60%
High	More than 60%

Genetic advance (GA)
Genetic advance was calculated based on formula given by Johnson et al. (1955) [7].

$$\text{GA} = h^2_{bs} \times \sigma_p \times K$$

Where
h^2_{bs} = Heritability in broad sense
σ_p = Phenotypic standard deviation
K = Standard selection differential which is 2.06 at 5 per cent selection intensity

Genetic advance as per cent of mean (GAM)

$$\text{GAM} = \frac{\text{GA}}{\overline{X}} \times 100$$

Where, GA = Genetic advance

X = Grand mean of the character

The range of genetic advance as per cent of mean was classified as suggested by Johnson et al. (1955) [7].

Classification	GAM
Low	Less than 10%
Moderate	10 – 20%
High	More than 20%

Results and Discussion
The analysis of variance revealed significant differences amid 60 genotypes along with four checks for all the characters under study, intimating the presence of high degree of genetic variability. The details related to analysis of variance for grain yield and quality characters are presented in table 1.
The PCV values were higher than GCV values for all the traits, suggesting the environmental influence on the expression of these traits but the difference between PCV and GCV estimates is very less for all the traits except dry fodder yield, thereby indicating very little environmental influence on the expression of these characters. High PCV and GCV values were observed for plant height, ear head length, 1000-seed weight, dry fodder yield, harvest index, crude fibre content, total phenol content, total antioxidant activity and grain yield per plant thereby denoting the presence of high quantum of variability for these traits. Similar results of high PCV and GCV values for grain yield per plant were reported by Shivaprasad et al. (2019) [10], Swamy et al. (2018) [12] and Badigannavar et al. (2017) [1]. Moderate PCV and GCV values were noticed for days to 50% flowering, days to maturity and protein content which represents moderate variation thereby indicating moderate chance for selection of these traits among the genotypes under study. Similar results of moderate PCV and GCV values for days to 50% flowering were recorded by Badigannavar et al. (2017) [1] and Elangovan and Babu (2015) [3]. Low values of PCV and GCV were noticed for total carbohydrate content and water absorption capacity that represents less quantum of variation for these traits. Similar results of low PCV and GCV values for total carbohydrate content were observed by Usman and Adeyenju (2010) [13]. Estimates of PCV and GCV for 14 characters in 60 sorghum germplasm accessions along with four checks are represented in figure 1.
High heritability together with high GAM was obtained for the traits viz., ear head length, dry fodder yield, protein content, total phenol content, 1000-seed weight, water absorption capacity, harvest index, days to 50% flowering, grain yield per plant, crude fibre content, total antioxidant activity, plant height and days to maturity, indicating the functioning of additive gene action in controlling these traits. Hence, simple phenotypic selection is effective for improving these traits. Similar results of high heritability and high GAM for 1000-seed weight and grain yield per plant were observed by Shivaprasad et al. (2019) [10], Swamy et al. (2018) [12] and Zinzala et al. (2018) [14]. While the trait, total carbohydrate content exhibited high heritability associated with moderate GAM which indicates the presence of both additive and non-

additive gene actions hence further improvement of this trait would be easier through mass selection, progeny selection or any other modified selection procedure aiming to exploit additive gene action rather than simple phenotypic selection. Broad sense heritability and genetic advance as percent of mean for 14 characters in 60 sorghum germplasm accessions along with four checks are represented in figure 2. Estimates of PCV, GCV, heritability and genetic advance as percent of mean for grain yield and quality characters in sorghum [*Sorghum bicolor* (L.) Moench are presented in table 2.

Table 1: Analysis of variance for grain yield and quality characters in sorghum [*Sorghum bicolor* (L.) Moench]

Source of variation	d.f.	Days to 50% flowering	Days to maturity	Plant height (cm)	Ear head length (cm)	1000-seed weight (g)	Dry fodder yield (g)	Grain yield per plant (g)
		Mean sum of squares						
Blocks	5	30.1	17.5	412	3.11	4.8	62	18.4
Entries	63	240.1**	377.8**	3106**	37.64**	54.3**	2552**	203.9**
Checks	3	1335.2**	1940.3**	9375**	85.88**	347.8**	3428*	1947.7**
Genotypes	59	187.8**	304.3**	2779**	35.42**	40.3**	2441**	91.6**
Checks vs Genotypes	1	41.2	27.9	3569**	23.57*	0.1	6496**	1599.8**
Error	15	12.6	16.9	154	2.75	6.8	658	23.8

| Source of variation	d.f.	Harvest index (%)	Total carbohydrate content (g/100g)	Protein content (g/100g)	Crude fibre content (g/100g)	Total phenol content (mg/100g)	Total antioxidant activity (mg of AAE/100g)	Water absorption capacity (ml/100g)
		Mean sum of squares						
Blocks	5	13.7	0.59	0.07	0.0043	0	0	3
Entries	63	123.8**	18.58**	5.39**	0.3293**	3113**	900**	462**
Checks	3	390**	44.7**	27.34**	2.4458**	31721**	8722**	5845**
Genotypes	59	112.4**	12.86**	3.43**	0.2272**	1454**	486**	86**
Checks vs Genotypes	1	0	277.54**	55.22**	0.003	15142**	1859**	6502**
Error	15	13.2	0.62	0.12	0.0043	0	1	2

*Significant at 5% level
** Significant at 1% level

Table 2: Estimates of genetic variability, heritability and genetic advance as percent of mean for grain yield and quality characters in sorghum [*Sorghum bicolor* (L.) Moench

S. No.	Character	Coefficient of variation		Heritability broad sense (%)	Genetic advance as percent of mean
		PCV (%)	GCV (%)		
1	Days to 50% flowering	18.08	17.46	93.28	34.80
2	Days to maturity	15.61	15.17	94.45	30.42
3	Plant height (cm)	22.36	21.73	94.45	43.57
4	Ear head length (cm)	31.07	29.84	92.24	59.12
5	1000-seed weight (g)	27.64	25.21	83.22	47.44
6	Dry fodder yield (g)	42.12	36.00	73.05	63.47
7	Grain yield per plant (g)	35.18	30.27	74.02	53.72
8	Harvest index (%)	50.19	47.15	88.26	91.37
9	Total carbohydrate content (g/100g)	5.43	5.30	95.17	10.67
10	Protein content (g/100g)	17.56	17.25	96.47	34.95
11	Crude fibre content (g/100g)	23.51	23.29	98.13	47.59
12	Total phenol content (mg/100g)	48.98	48.97	99.98	99.02
13	Total antioxidant activity (mg of AAE/100g)	45.17	45.14	99.85	93.05
14	Water absorption capacity (ml/100g)	5.04	4.98	97.72	10.15
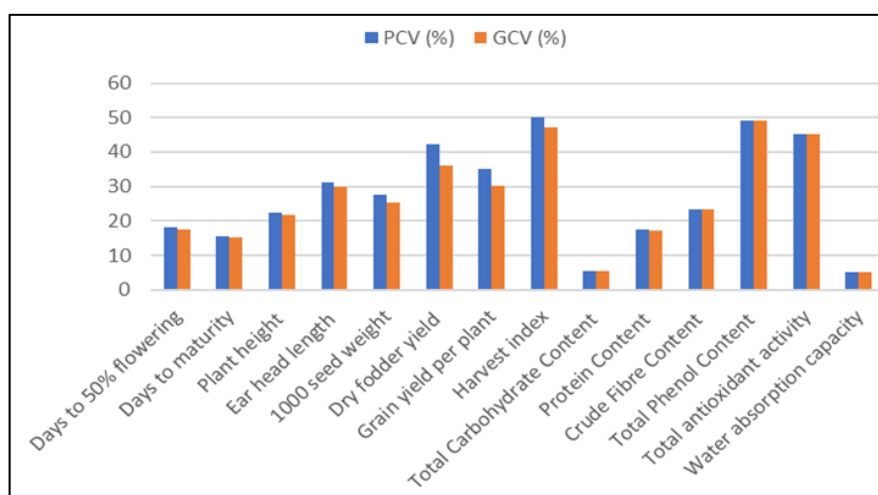
Fig 1: Estimates of PCV and GCV for 14 characters in 60 sorghum germplasm accessions along with four checks
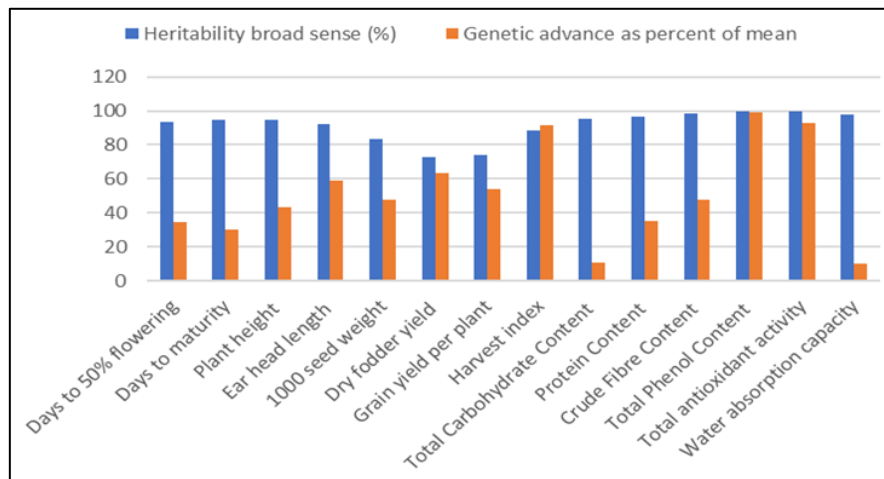
Fig 2: Broad sense heritability and genetic advance as percent mean for 14 characters in 60 sorghum germplasm accessions along four checks

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