

## Estimation of Genetic Variability among Sorghum Genotypes for Different Morphological and Biochemical Traits

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### ABSTRACT

Fifty diverse genotypes of sorghum were evaluated for different metric traits to assess the genetic diversity during *kharif* 2018-19 for yield and its associating traits. Less difference between the estimates of GCV and PCV implying the minimal influence of environmental agencies and importantly, improvement through selection seems feasible. The coefficients of variation (GCV and PCV) for panicle length without peduncle, 100-grain weight, green fodder production, crude protein yield, and other variables were found to be high. Whereas, low genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were recorded for traits, crude protein, height up to flag leaf, plant height, stem diameter, stem diameter and time of panicle emergence. Leaf breadth, panicle length without peduncle, dry matter%, 100-grain weight, green and dry fodder yield, HCN and tannin content, crude protein all had high heritability and genetic advance.

**Keywords** Genetic diversity, Genetic variability parameters, Heritability, Genetic advance, Sorghum.

### INTRODUCTION

Sorghum (*Sorghum bicolor* L.), after wheat, rice, maize, and barley, is the fifth most important cereal crop in the world (Cuevas *et al.* 2014). In contrast to many other cereal grains, sorghum grains are gluten-free and constitute a staple diet in 30 tropical and semi-tropical nations. The crop works well in a wide range of temperatures and may be cultivated in the majority of soil types (Nguyen *et al.* 2013). Moreover, it is a multipurpose crop exploited for its grain, fodder and biofuel potential (Elangovan *et al.* 2014). The worldwide production and area under the sorghum cultivation is 58 million tonnes and 40 Mha, respectively with the largest contribution from the Africa (46.8%). In terms of quantity production the largest producers are USA (9 MT), Nigeria (6 MT), Ethiopia (5 MT) and India (4.7 MT), respectively (Anonymous 2022).

The genetic diversity and the degree to which the targeted traits are heritable have a significant role in the success of a breeding program (Majumder and Shamsuddin 2008). To begin an effective breeding program, genetic variation evaluation that offers data on estimates such as genotypic coefficient of variation, phenotypic coefficient of variation, heritability estimates, and genetic progress is very much required and of the utmost importance (Atta *et al.* 2008). The variability in germplasm is a result of both heritable genetic influences and non-heritable environmental

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impacts (Sami *et al.* 2013). The PCV expresses both the genetic and environmental influences on the trait, whereas the GCV just expresses the heritable component (Bello *et al.* 2007). Breeding program employ heritability as a measure of how well desirable traits are passed on from parents to their offspring. Estimating heritability provides details on the level of genetic influence over the manifestation of a specific trait as well as the reliability of phenotypic prediction of breeding value (Falconer 1981). A trait having high heritability is a good indicator of the revealing the direction in which it can be further improved. However, broad sense heritability might not be accurate in the absence of genetic advance. Therefore, for a more accurate assessment, estimates of broad sense heritability must be combined with estimates of genetic advance (Najeeb *et al.* 2009). Hence, present investigation was undertaken to understand genotypic and phenotypic coefficient of variation, heritability, and genetic advance for green fodder yield and its contributing traits in sorghum.

## MATERIALS AND METHODS

The present study was carried out at the Research Farm Area, Forage Section, Department of Genetics and Plant Breeding, CCS Haryana Agricultural University, Hisar in the year 2018-19 to characterize and to assess genetic diversity for fifteen morpho-biochemical parameters. Hisar has a semi-arid, subtropical climate with hot, dry winds in the summer. The climate in this region is often warm and humid during the monsoon and cold and dry during the winter. The forty nine genotypes were grown in randomized block design, controlling the heterogeneity in one direction, with three replication and each genotype grown as two rows. The plant to plant distance was measured to be 10 cm and row to row distance as 30 cm at the same time keeping the row length at 3 m. The data was recorded on five randomly selected plants in each genotype for 15 morphological and biochemical traits namely; time of panicle emergence (days), height upto flag leaf (cm), total plant height (cm), stem diameter (mm), third leaf length from top (cm), third leaf breadth from top (cm), panicle length without peduncle (cm), dry matter (%), hundred seed weight (g), green fodder yield (q/ha), dry fodder yield (q/ha), HCN content on fresh weight basis ( $\mu\text{g/g}$ ),

protein (%), crude protein yield (q/ha), tannin content on dry weight basis (mg/g). The data were analyzed using R studio software.

## RESULTS AND DISCUSSION

### Analysis of variance

Analysis of variance revealed significant differences among all genotypes for all the studied characters (Table 1), which indicated the existence of substantial genetic variability among the genotypes under study for further selection and improvement. Similar, Sinha and Kumaravadivel (2016), Kisua *et al.* (2015), Kalpande *et al.* (2014) also suggested a large and exploitable variation in different sorghum germplasm, it could be stated that there was ample scope of variation in these traits that could be utilized for improvement through selection for the traits investigated in the present material.

### Mean performance of sorghum genotypes

The performance of the fifty sorghum genotypes was recorded for 15 morpho-biochemical traits (Table 2). For the most of the studied, all genotypes exhibited significant variation. Among grain and fodder yield and its component characters, the mean performance for time of panicle emergence range from lowest 75.3 in genotype IS 285913 to highest 92.7 in genotype IS 651, whereas mean range for height up to flag leaf (cm) range from minimum 145.9 (IS 3947) to maximum 273.4 (IS 2919). Plant height (cm) showed mean range from 170.9 to 293 in genotype IS 285831 and IS 2919, respectively. Likewise stem diameter (mm) mean performance ranged from highest in genotype SOR 5504 (16.4) to lowest in IS 3947 (6.6). Mean values for third leaf length (cm) and third leaf breadth (cm) lies 40 (HC 136) to 75.5 (IS 1328) and 3 (IS 3947) to 8.3 (IS 40927, IS 1004), respectively. Mean values for panicle length without peduncle lies between 4cm to 28cm in genotypes G-800 and GP-311, respectively. Range of mean value for dry matter (%) and 100 seed weight (gm) ranged from lowest to highest 13.5 to 40 and 1.49 to 4.89, respectively. The mean values for economic part i.e. green fodder yield (q/ha) is ranged from maximum 462.8 (GP-236) to minimum 28.3 (GP-297), whereas, for dry fodder

**Table 1.** Analysis of variance of different agro-morphological characters in sorghum.

Source of var	df	TP	HF	PH	SD	TLL	TLB	PL
Replicate	2	7.61	2182.17	2769.96	5.96	2.17	1.75	14.24
Genotypes	48	59.87***	2212.38***	2458.35***	7.86***	92.43***	3.39***	72.17***
Error	96	5	362.91	438.87	1.94	12.16	0.4	2.14

**Table 1.** Continued.

Source of var	df	DM	TW	GFY	DFY	HCN	CP	CPY	Tanin
Replicate	2	476.69	0.02	132127.2	9262.71	795.11	0.04	77.9	0.004
Genotypes	48	315.48***	1.06***	32316.45***	5855.59***	1053.65***	2.10***	54.97***	0.50***
Error	96	20.98	0.01	664.2	78	12.33	0.48	1	0.000

**Table 2.** Mean performance of sorghum genotypes for yield and its component traits.

Genotypes	TP	HF	PH	SD	TLL	TLB	PL	DM	TW	GFY	DFY	HCN	CP	CPY	Tanin
GFS 5	79.30	181.60	202.30	11.30	53.90	6.30	15.90	27.30	2.45	306.10	83.20	26.20	9.38	7.84	0.55
SOR 5504	92.00	186.10	188.10	16.40	64.30	7.40	15.40	32.60	2.86	164.40	51.20	35.80	9.60	4.91	1.34
SOR 668	90.30	219.00	250.20	12.50	65.50	7.70	14.70	30.80	2.48	208.30	64.20	87.40	9.82	6.35	0.89
SOR 6408	84.00	244.60	244.60	16.10	53.20	5.10	12.20	32.70	2.66	167.80	50.00	57.60	8.97	4.51	0.97
IS 585159	87.00	219.40	231.50	14.10	54.90	6.30	12.30	21.80	2.41	75.70	16.30	47.10	8.39	1.37	1.06
IS 585176	83.30	229.00	266.60	12.80	58.40	5.50	23.10	37.70	2.22	287.20	102.70	63.90	10.77	11.07	0.60
IS 585186	82.30	223.20	229.30	12.30	57.30	6.70	6.70	34.70	3.33	194.40	62.80	50.30	9.55	6.04	1.13
SOR 6453	86.70	207.00	233.90	11.80	51.20	6.50	15.50	30.90	2.40	302.80	92.30	25.80	9.26	8.54	1.17
IS 144849	88.30	189.70	219.80	13.30	55.40	6.40	17.90	21.40	3.17	125.60	26.80	71.30	9.63	2.58	1.16
IS 285831	83.00	158.00	170.90	12.60	45.90	5.60	12.80	17.30	2.75	116.20	19.70	60.30	9.99	1.97	0.76
IS 285913	75.30	189.40	221.70	10.60	53.60	5.70	19.40	22.40	2.57	115.60	28.20	88.70	7.89	2.21	0.79
GP-236	75.70	221.40	240.30	12.80	51.30	6.40	16.30	32.80	2.77	462.80	151.60	34.10	9.97	15.10	1.08
GP-237	85.00	181.70	211.50	13.70	52.20	6.00	16.50	40.00	4.89	151.70	55.90	69.60	9.63	5.38	1.80
G-800	76.70	206.30	240.40	12.10	49.50	4.80	16.90	34.10	3.11	265.00	88.70	19.10	10.43	9.26	0.59
IS 3244	83.70	218.40	255.50	11.50	54.30	5.50	20.10	28.10	2.36	334.40	93.60	74.80	9.48	8.85	0.87
IS 3299	83.30	218.90	264.00	12.40	58.60	5.10	23.90	26.60	2.49	342.20	90.10	69.50	10.48	9.40	1.08
SSG 233	88.00	219.20	267.60	11.40	63.30	4.90	25.50	24.10	2.55	180.60	42.80	43.60	8.93	3.79	0.56
SOPPON	84.00	222.90	247.70	12.70	57.90	6.10	15.90	27.30	2.36	336.70	92.20	50.10	8.73	7.97	1.02
GP-297	82.30	166.70	205.50	12.10	61.50	5.70	18.10	31.90	4.56	28.30	9.00	92.40	8.05	0.72	1.63
GP-298	89.30	245.10	280.20	13.40	55.60	5.50	20.70	34.70	2.01	406.70	140.80	54.30	7.53	10.63	1.11
GP-311	79.70	223.70	254.00	13.40	57.30	7.90	17.30	38.20	2.72	298.30	114.50	37.70	8.68	9.91	0.56
PGN 56	84.00	228.70	253.50	13.50	52.10	6.10	14.60	30.00	2.89	303.90	89.30	44.20	9.48	8.50	1.52
SUENT	83.70	224.30	247.30	12.50	53.30	7.00	15.10	27.30	2.49	280.00	75.80	52.50	7.85	5.91	1.75
GP-318	80.00	217.70	246.30	10.00	55.10	5.00	17.10	31.40	2.92	307.80	96.60	72.30	9.70	9.34	1.82
SPV 2191	90.70	223.70	260.20	12.50	57.40	6.70	20.50	29.00	3.10	347.20	100.00	39.70	10.93	11.32	0.75
PGN 66	81.70	232.40	263.10	10.90	51.10	6.80	18.00	34.80	2.52	355.60	123.80	57.10	8.92	11.03	0.60
PGN 9	82.00	166.1	194.90	14.20	57.70	6.60	18.00	39.70	2.77	173.30	65.60	108.50	8.90	5.79	1.40
Dairy green	83.70	179.90	206.50	13.20	62.50	6.50	14.70	34.80	3.05	166.10	58.10	62.00	9.60	5.51	1.69
SOR 5449	85.00	176.20	184.70	15.10	47.90	7.90	10.10	17.50	2.34	62.50	10.90	76.70	9.80	1.07	1.08

Table 2. Continued.

Genotypes	TP	HF	PH	SD	TLL	TLB	PL	DM	TW	GFY	DFY	HCN	CP	CPY	Tanin
SOR 5510	88.30	224.00	238.60	12.60	59.50	7.50	14.40	35.20	2.63	295.00	99.70	86.30	8.07	8.04	1.89
SOR 5578	78.00	215.70	225.90	14.40	56.30	7.90	10.90	27.80	2.86	294.20	82.60	45.80	10.16	8.42	0.87
IS 40398	78.30	210.40	213.50	12.00	50.10	6.50	5.60	26.30	2.36	265.00	70.10	66.20	9.36	6.55	1.68
IS 40717	75.70	235.00	256.00	11.80	56.80	5.80	9.10	23.20	3.12	225.00	52.80	75.00	10.40	5.47	1.06
IS 40921	80.00	235.00	255.40	14.70	62.40	8.30	17.90	35.30	2.61	321.70	239.20	65.70	9.80	23.42	1.62
IS 3947	81.70	145.90	189.10	6.60	55.60	3.00	23.90	22.70	1.49	43.30	9.40	74.80	9.04	0.85	0.92
IS 5127	83.00	212.80	231.60	14.20	57.80	7.50	13.80	32.30	2.39	357.20	114.80	36.70	8.68	9.98	1.89
IS 1328	76.30	216.00	232.00	13.00	75.50	8.00	8.70	28.10	2.07	245.00	165.30	74.60	8.75	14.47	1.24
IS 651	92.70	253.80	265.90	13.80	54.00	7.20	11.80	36.40	1.91	314.40	114.00	50.70	10.94	12.89	1.47
IS 2919	82.30	273.40	293.00	12.20	51.00	6.60	14.50	23.40	2.63	380.00	89.30	66.80	8.97	8.01	1.26
IS 608	87.00	207.40	224.20	13.50	59.70	7.60	13.80	35.90	2.58	271.70	96.20	74.80	10.06	9.67	1.16
IS 1004	83.70	228.80	259.30	15.60	59.60	8.30	16.20	32.90	2.86	331.70	107.20	54.00	9.41	10.08	1.25
HC 171	78.00	248.80	252.10	12.90	59.00	6.70	4.00	27.30	3.29	190.00	50.90	47.00	9.84	5.01	0.32
HC 260	83.70	239.60	265.60	12.30	53.30	5.90	13.50	27.80	4.14	393.30	109.70	57.10	10.20	11.22	1.57
HC136	89.30	253.00	265.00	12.50	40.00	8.10	12.70	13.50	3.06	73.30	9.70	44.10	9.63	0.94	1.33
HC308	78.30	235.30	262.90	13.00	53.10	6.10	17.70	33.30	2.51	376.70	125.30	61.40	10.06	12.62	0.61
HJ 513	84.70	250.70	289.30	14.80	56.90	7.00	23.10	33.80	2.96	256.10	83.60	33.60	8.31	6.95	1.05
HJ 541	78.30	251.10	290.30	14.20	55.10	6.70	28.00	30.80	2.67	203.30	62.60	70.20	7.88	4.93	1.11
S713	88.00	229.90	261.60	13.10	57.10	6.60	16.00	28.70	3.01	328.30	94.30	50.80	8.97	8.46	0.78
SH1591	86.70	224.60	254.40	14.30	51.50	6.20	16.30	29.90	3.42	206.70	62.10	53.50	10.06	6.25	1.50
Mean	83.40	216.60	241.00	12.90	55.80	6.50	15.90	29.70	2.77	249.80	80.30	58.40	9.37	7.57	1.14
MIN	75.30	145.90	170.90	6.60	40.00	3.00	4.00	13.50	1.49	28.30	9.00	19.10	7.53	0.72	0.32
MAX	92.70	273.40	293.00	16.40	75.50	8.30	28.00	40.00	4.89	462.80	239.20	108.50	10.94	23.42	1.89
CV (%)	2.70	8.80	8.70	10.80	6.30	9.80	9.20	14.60	2.97	10.30	11.00	6.00	7.37	13.21	2.89
SEm (±)	1.30	11.00	12.10	0.10	2.00	0.40	0.90	2.60	0.05	14.90	5.10	2.00	0.40	0.58	0.02
CD (5%)	3.60	30.90	34.00	2.30	5.70	1.00	2.40	7.40	0.13	41.80	14.30	5.70	1.12	1.62	0.05

TP: Time of panicle emergence, HF: Height up to flag leaf (cm), PH: Plant height (cm), SD: Stem diameter (mm), TLL: Third leaf length (cm), TLB: Third leaf breadth (cm), PL: Panicle length without peduncle (cm), DM: Dry matter (%), TW: 100 seed weight (g), GFY: Green fodder yield (q/ha), DFY: Dry fodder yield (q/ha), HCN: HCN content ( $\mu\text{g/g}$ ) on fresh weight basis, CP = Crude Protein (%), CPY: Crude protein yield (q/ha), Tanin: Tannin (mg/g) on dry weight basis.

yield (q/ha) it's ranged from 9 (GP-297) to 239.2 (IS 40921). HCN content ( $\mu\text{g/g}$ ) on fresh weight basis varied from 19.1 in genotype G-800 to 108.5 in genotype PGN 9, whereas, tannin (mg/g) on dry weight basis varied from 032 (HC 171) to 1.89 (IS 5127). Mean performance crude protein (%) lies in between 9 (GP-297) to 239.2 (IS 40921) and for crude protein yield (q/ha) ranged from 0720 in genotype GP -297 to 23.42 in genotype IS 40921.

This shows that these characters were respon-

sible for wide variation in grain and fodder yield of various genotypes. These results also indicating that these genotypes are useful as genetic source in forage sorghum improvement program. Furthermore, the genotype namely, IS 49021 might prove very useful in the improvement of forage sorghum aimed for both higher dry fodder yield and crude protein yield simultaneously. Similar results obtained from the study of Kisua *et al.* (2015), Kinfe and Tesfaye (2018), Mengistu *et al.* (2020) which concurred partial results from our study.

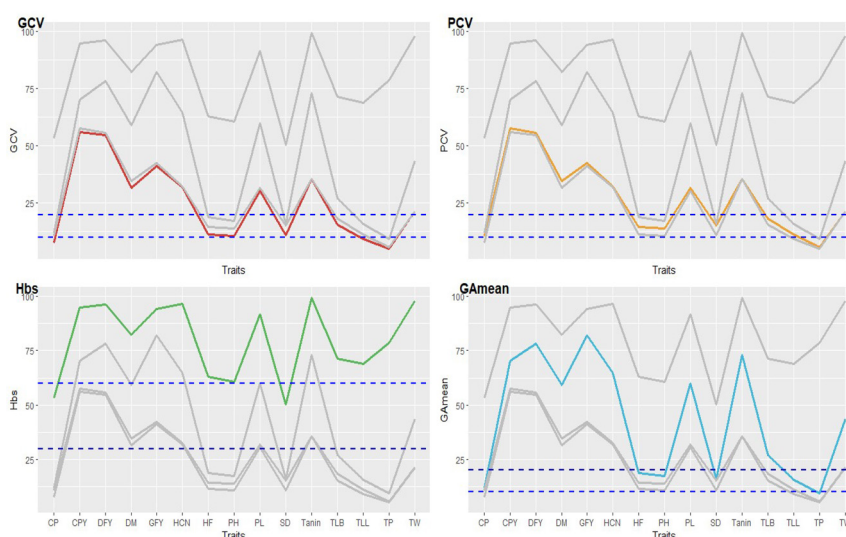
### Phenotypic and genotypic coefficient of variation

Genetic variability parameters i.e genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability (broad sense) and genetic advance as percentage of mean was worked out for all the studied traits (Table 3 and Fig 1). The high estimates of the PCV was observed for the traits viz. crude protein yield (57.5), dry fodder yield (55.7), green fodder yield (42.4) supporting the ANOVA for the presence of considerable genetic variability for the required traits improvement. For the same traits viz. crude protein yield (56.0), dry fodder yield (54.6), green fodder yield (41.1) there is presence of high estimates of GCV. There is less difference between the estimates of GCV and PCV indicating the minimal influence of environmental agencies and importantly, improvement through selection seems feasible. Moderate GCV and PCV Observed for the traits viz., height up to flag leaf (11.47, 14.45, respectively), plant height (10.77, 13.84, respectively), stem diameter (10.87, 15.32, respectively) and third leaf breadth (15.47, 18.30, respectively). Low range of GCV and PCV is recorded for trait time of panicle emergence (5.13, 4.79, respectively). Previously, Kalpande *et al.* (2014) and Mohanraj *et al.* (2011) also reported higher values of PCV value than the corresponding GCV value for all the investigated traits in forage sorghum.

**Table 3.** Genetic variability parameters of the different traits in sorghum genotypes.

Traits	GCV	PCV	h <sup>2</sup> (Broad sense)	GA% mean
TP	5.13	5.79	0.79	9.37
HF	11.47	14.45	0.63	18.74
PH	10.77	13.84	0.61	17.26
SD	10.87	15.32	0.50	15.90
TLL	9.26	11.17	0.69	15.82
TLB	15.47	18.30	0.71	26.94
PL	30.46	31.83	0.92	60.05
DM	31.60	34.81	0.82	59.08
TW	21.35	21.56	0.98	43.56
GFY	41.12	42.40	0.94	82.17
DFY	54.64	55.73	0.96	78.34
HCN	31.91	32.47	0.97	64.60
CP	7.86	10.78	0.53	11.82
CPY	56.00	57.54	0.95	70.29
Tanin	35.59	35.71	0.99	73.09

TP: Time of panicle emergence, HF: Height up to flag leaf (cm), PH: Plant height (cm), SD: Stem diameter (mm), TLL: Third leaf length (cm), TLB: Third leaf breadth (cm), PL: Panicle length without peduncle (cm), DM: Dry matter (%), TW: 100 seed weight (g), GFY: Green fodder yield (q/ha), DFY: Dry fodder yield (q/ha), HCN: HCN content ( $\mu\text{g/g}$ ) on fresh weight basis, CP = Crude protein (%), CPY: Crude protein yield (q/ha), Tanin: Tannin (mg/g) on dry weight basis.



**Fig. 1.** Pictorial representation of genetic variability parameters for different traits in sorghum.

## Heritability and genetic advance

High estimates of broad sense heritability was observed for all the studied viz., tannin content (99.3%), 100-seed weight (98.1%), dry fodder yield (96.1%), green fodder yield (94.1%). except stem diameter (50.4%) and crude protein percentage (53.2%). While high estimates of genetic advance percentage of mean was observed for dry fodder yield, green fodder yield. The traits with high heritability and genetic advance percentage of mean usually corresponds to the additive gene action which make them directly applicable to the selection pressure for their improvement. These results on the parameters of genetic variability are similar with those reported by Kour and Pradhan (2016), Warkad *et al.* (2008) and Jain and Patel (2012).

## CONCLUSION

Genetic improvement and tailoring of high yielding cultivars require knowledge of amount and nature of genetic variability that is present in the primary gene pool. Therefore, we examined genetic variation for 15 quantitative traits of 49 sorghum genotypes in order to have better insight into genetic variability. From study it was clear there is ample amount of variations were present among different genotypes of sorghum for yield and related traits. So, selection among these genotypes for these specified traits will be effective. From results five genotypes GP-236, GP-298, HC 260, IS 2919 and HC 308 were observed superior in term of green fodder yield and its associates. Therefore, to obtain high yielding transgressive segregants, these genotypes should be used in recombinant breeding programs to exploit genetic variability present in sorghum stocks.

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