

Estimation of Genetic Parameters and Association Analysis of Yield and Yield Attributing Traits of sorghum (*Sorghum bicolor* L. moench)

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ABSTRACT: Twenty advance breeding lines of Sorghum were evaluated for their genetic variability with regards to grain yield and yield components. Study of genetic parameters through which heritability of characters and tight association among them can be known and the selection of yield attributes can be easily done for further improvement. Along with variability, heritability and genetic advance as percent mean was also calculated. In addition, association analysis was also taken up for these traits. The results revealed High heritability (>60%) estimates was observed with the characters viz., days to 50% flowering, Plant Height, Panicle length, 100 seed weight indicating the low influence of environment on these characters. Further, high (>20%) estimates of genetic advance as percent mean was observed in Plant height, Panicle length and 100 seed weight. In addition, high heritability coupled with high genetic advance as percent mean was recorded with Plant height, Panicle length and 100 seed weight indicating that these characters are governed by additive gene action and therefore simple selection would be effective for improvement of these characters.

Keywords: Coefficient of variation, Genetic advance as percent mean, Heritability, Sorghum, Variability, Yield.

INTRODUCTION

Sorghum (*Sorghum bicolor* L.) is an important irrigated and rainfed crop and the principal food grain crop next to rice in southern part of Andhra Pradesh cultivated in *kharif maghi* and *rabi* seasons. The area under Sorghum in Andhra Pradesh is 1.55 lakh ha with annual production of 3.89 lakh tonnes yielding about 2510 kg/ha during 2019-20 with major area in Kurnool (55,000 ha), Guntur (40,000 ha) and Ananthapuram (30,000 ha) districts and Scarce Rainfall Zone (Kurnool and Ananthapur districts) alone accounted for 54.8% of total AP state area. Jowar is known for its unique nutritional properties particularly high fibre content, quality protein and mineral composition and contribute significantly to nutritional security.

An attempt was made in the present investigation to study the nature and magnitude of genetic parameters like, coefficient of variation, heritability and genetic advance as percent mean and also to identify promising entries suitable for Andhra Pradesh among the studied genotypes.

MATERIALS AND METHODS

The present investigation was taken up during *rabi* 2017-18 with 20 sorghum advance breeding lines developed at Regional Agricultural Research Station, Nandyal, Andhra Pradesh, India. These genotypes were grown in a randomized block design with three replications with a layout of 6 rows with 6m length by adopting a spacing of 45 cm between rows and 15 cm within the row. All recommended package of practices were adopted to raise a healthy crop. Observations were recorded for different yield components, namely, plant height, panicle length, were recorded for five randomly selected plants for each entry in each replication. However, Initial plant population, Final plant population, Days to 50% flowering, Days to maturity and grain yield were recorded on plot basis. In contrast data on 100 seed weight was obtained from a random grain sample drawn from each plot in each entry and replication. The data obtained was then subjected to standard statistical procedures. The data was analyzed statistically for genotype and phenotype coefficients of variation (Burton, 1952), Heritability (Allard, 1960) and genetic advance (Johnson *et al.*, 1955).

RESULTS AND DISCUSSION

The success of plant breeding programs relies heavily on the presence of genetic variability in plants for a particular character. Estimates of mean sum of squares for replications and genotypes and CV % for the studied genotypes are shown in Table 1. The analysis of variance (ANOVA) revealed highly significant differences among all the 20 sorghum genotypes studied for all the

traits indicating the existence of adequate variation in the experimental material ample scope of improvement by selection. Similar results were observed by Arunkumar *et al.* (2004); Chavan *et al.* (2010); Hamidou *et al.* (2018).

Table 1: Analysis of variance for yield and yield attributes in Sorghum.

Sr. No.	Character	Replication	Treatments	Error	SE m ±	CV (%)
1.	Initial Plant Population	84.11	178.96**	58.88	4.43	6.08
2.	Final Plant Population	181.11	178.96**	58.88	4.43	6.23
3.	Days to 50% flowering	0.51	41.18**	3.60	1.09	2.91
4.	Days to maturity	0.80	44.69**	8.30	1.66	2.80
5.	Plant height (cm)	8.01	4185.36**	107.05	5.97	5.13
6.	Panicle length (cm)	0.97	16.49**	1.34	0.67	5.80
7.	100 seed weight (g)	0.04	1.09**	0.08	0.16	8.14
8.	Grain Yield (kg/ha)	381520.41	1185274.4**	98004.00	180.74	10.35
9.	Fodder Yield (kg/ha)	1092370.71	6147038.71**	236444.55	280.73	7.11

The mean performance of sorghum genotypes for different yield and yield characters are presented in Table 2. The results revealed that the genotypes NJ 2647, NJ 2659, NJ 2657, NJ 2654 and NJ 2651 are high yielders. The higher grain yield of NJ 2647 (4167 kg/ha) recorded in the present study is attributed to its long panicle length (22.3 cm) and high 100 seed weight (4.3g). These varieties are therefore identified as promising varieties for extensive commercial cultivation.

Table 2: Mean performances of sorghum genotypes for yield and yield components.

Sr. No.	Treatment	Initial Plant Population	Final Plant Population	Days to 50 % flowering	Days to maturity	Plant Height (cm)	Panicle length (cm)	100 Seed weight (g)	Grain Yield (kg/ha)	Fodder Yield (kg/ha)
1.	NJ 2647	130.3	127.3	65.7	103.0	119.0	22.3	4.3	4167.0	7315.3
2.	NJ 2659	125.3	122.3	62.7	102.3	230.0	22.8	4.5	4167.0	6883.3
3.	NJ 2657	130.3	127.3	66.7	104.0	202.7	17.5	4.1	3889.0	6883.3
4.	NJ 2654	125.7	122.7	67.7	104.7	171.7	22.5	2.6	3858.0	7037.7
5.	NJ 2651	134.0	131.0	64.7	104.7	176.3	19.9	3.2	3673.3	6389.3
6.	NJ 2660	133.0	130.0	62.0	100.0	222.7	24.2	3.5	3179.3	4938.7
7.	NJ 2664	116.3	113.3	70.7	109.3	267.0	20.2	3.1	3117.7	7716.7
8.	NTJ-2	108.0	105.0	56.3	95.3	205.7	20.5	4.1	3025.0	6019.0
9.	NJ 2653	112.0	109.0	63.3	98.7	176.3	21.6	4.3	2994.0	5093.0
10.	NJ 2652	128.0	125.0	67.7	102.0	181.7	17.3	3.3	2901.3	7099.3
11.	NJ 2655	125.3	122.3	68.7	104.7	244.3	20.5	3.7	2839.7	9414.3
12.	NJ 2668	135.0	132.0	62.7	98.3	239.0	19.6	3.4	2778.0	7840.0
13.	NJ 2665	135.0	132.0	69.0	107.0	235.7	16.5	3.7	2747.3	9105.7
14.	NJ 2662	118.7	115.7	65.7	101.3	169.0	21.4	2.9	2747.0	5556.0
15.	NJ 2667	120.0	117.0	60.3	99.0	220.0	23.1	3.4	2623.7	5401.7
16.	NJ 2656	131.7	128.7	62.0	98.3	189.7	19.6	4.3	2592.7	4568.3
17.	NJ 2661	130.3	127.3	64.7	103.7	208.3	18.3	3.3	2531.0	7932.7
18.	NJ 2663	122.7	119.7	69.3	107.3	135.3	16.4	2.6	2469.3	5185.7
19.	NJ 2658	132.3	129.3	62.0	100.7	236.0	16.7	3.6	2130.0	8951.3
20.	NJ 2666	129.3	126.3	70.0	109.7	197.0	19.3	2.6	2006.3	7346.3
	GMean	126.2	123.2	65.1	102.7	201.4	20.0	3.5	3021.8	6833.9
	Min	108.0	105.0	56.3	95.3	119.0	16.4	2.6	2006.3	4568.3
	Max	135.0	132.0	70.7	109.7	267.0	24.2	4.5	4167.0	9414.3
	S.E.	4.43	4.43	1.10	1.66	5.97	0.67	0.17	180.74	280.74
	C.D.(5%)	12.59	12.59	3.12	4.73	16.98	1.90	0.47	513.78	798.02
	CV(%)	6.08	6.23	2.92	2.81	5.14	5.80	8.15	10.36	7.12

Genotypic and Phenotypic Variation: The range of variation and the estimate of genetic parameters which include heritability in broad sense, coefficient of variation (GCV and PCV) and genetic advance as percent mean are presented in Table 3. A perusal of results revealed that the maximum range was observed for Grain yield per hectare (2006.3 kg– 4167kg) followed by plant height (cm) (119 – 267), fodder yield (kg/ha) (4568.3 – 9414.3). The phenotypic coefficient of variation was higher than genotypic coefficient of variation for all the characters studied showing that all the traits were highly influenced by environment. This result was supported by the scientific writings of Ashok *et al.* (2017); Wadikar *et al.* (2018). High estimates (>20%) of genotypic and phenotypic co-efficient of variation were observed for grain yield (kg/ha) (GCV-22.5) fodder yield (kg/ha)(20.5, 21.7) indicating more variability and scope for selection for the improvement of this character. These results are in line with the results published by Ashok *t al.* (2017) and wadikar *et al.* (2018). Amare *et al.*, (2015); Abraha *et al.*, (2015); Ranjith *et al.*, (2017) also reported similar higher GCV and PCV value for GY and fodder yield of sorghum. The characters plant height, panicle length and 100 seed weight were recorded moderate (10-20%) estimates of genotypic and phenotypic co-efficient of variation. Further, low estimates (<10%) of genotypic and phenotypic co-efficient of variation was observed in initial plant population, final plant population, days to 50% flowering and days to maturity. Similar results were observed by Jain and Patel (2012).

The selection efficiency of any yield component depends on both genetic variability and the extent of heritable nature of that trait from one generation to the next generation. High heritability estimates (>60%) were noticed for days to 50% flowering, plant height, panicle length, 100 seed weight, grain yield and fodder yield. However, moderate estimates (30% -60%) of heritability were recorded for initial plant population, final plant population and days to maturity. The results are in conformity with the results of Chavan *et al.* (2010) and Godbharle *et al.* (2010). The results on genetic advance as percent mean studied for yield and yield characters revealed that high (> 20%) estimates of genetic advance as percent mean for plant height, panicle length, 100 seed weight, grain yield and fodder yield, where as low (<10%) estimates of genetic advance as percent mean recorded for initial plant population, final plant population, days to 50% flowering and days to maturity. Similar findings were reported by Subhashini *et al.* (2020). Further, High heritability coupled with high genetic advance as percent mean was recorded for grain yield/ha (78.7), fodder yield/ha (89.3), 100 seed weight (80.4) and plant height (92.7) revealing that these yield attributing traits are governed by additive gene action and phenotypic selection for these characters will be effective.

Table 3: Estimates of variability and genetic parameters for yield and yield components in sorghum.

Sr. No.	Character	Mean	Range		Coefficient of variation		Heritability in broad sense	Genetic advance as percent of mean
			Min	Max	GCV	PCV		
1.	Initial Plant Population	126.2	108.0	135.0	5.0	7.9	40.5	6.6
2.	Final Plant Population	123.2	105.0	132.0	5.1	8.1	40.5	6.7
3.	Days to 50 % flowering	65.1	56.3	70.7	5.4	6.2	77.7	9.9
4.	Days to maturity	102.7	95.3	109.7	3.4	4.4	59.3	5.4
5.	Plant Height (cm)	201.4	119.0	267.0	18.3	19.0	92.7	36.3
6.	Panicle length (cm)	20.0	16.4	24.2	11.2	12.6	78.9	20.6
7.	100 Seed weight (g)	3.5	2.6	4.5	16.5	18.4	80.4	30.4
8.	Grain Yield (kg/ha)	3021.8	2006.3	4167.0	19.9	22.5	78.7	36.4
9.	Fodder Yield (kg/ha)	6833.9	4568.3	9414.3	20.5	21.7	89.3	40.0

Correlation. Correlation coefficient is a statistical measure, which denotes the degree and magnitude of association between any two casually related variables. This association is due to pleiotropic gene action or linkage or more likely both. However a study on association of yield and yield components is also essential to simultaneously improve the performance of the genotype. Correlation studies provide nature and extent of association between yield and yield contributing characters. The phenotypic and genotypic correlation was presented in Table 4. In general the genotypic correlation was generally of higher magnitude than phenotypic correlation, indicating that inherent association between various characters studied. In the present investigation, grain yield (kg/ha) was positively and significantly correlated with the yield contributing traits namely, initial plant population, final plant population, panicle length and 100 seed weight indicating the increase in these characters will increase the grain yield and prioritizing these characters through selection process. The results are in conformity with the results of Khandelwal *et al.* (2015). In contrast, non significant association of grain yield was observed with days to 50% flowering, days to maturity and plant height. The results obtained are similar to the results obtained by Aml, *et al.* (2012); Godbharle *et al.* (2010).

Table 4: Phenotypic and Genotypic correlation coefficients (rp and rg) of yield and yield attributes in Sorghum.

Sr. No.	Character	r	Days to 50 % flowering	Days to maturity	Plant Height (cm)	Panicle length	100 Seed weight (g)	Grain Yield (kg/ha)	Fodder Yield (kg/ha)
1.	Initial Plant Population	rp	0.1654**	0.2328**	0.0457**	0.1977**	-0.0612	0.0045**	0.2686**
		rg	0.2655**	0.2338**	0.0712**	-0.3732	-0.0891	0.0223**	0.4407
2.	Final Plant Population	rp	0.1654**	0.2328**	0.0457**	-0.1977	-0.0612	0.0045**	0.2686**
		rg	0.2655**	0.2338**	0.0712**	-0.3732	-0.0891	0.0223**	0.4407
3.	Days to 50 % flowering	rp		0.8179	-0.0662	-0.3153	-0.4446	-0.0202	0.3851**
		rg		0.9791	-0.0887	-0.3907	-0.5664	-0.0445	0.4023**
4.	Days to maturity	rp			-0.0007	-0.2259	-0.4339	-0.0521	0.3715**
		rg			0.009	-0.4075	-0.6056	0.0123	0.449
5.	Plant Height (cm)	rp				-0.0277	0.0589**	-0.2013	0.4503
		rg				-0.0387	0.1001**	-0.2454	0.4767
6.	Panicle length (cm)	rp					0.1361**	0.4024**	-0.3774
		rg					0.2117**	0.4798	-0.4216
7.	100 Seed weight (g)	rp						0.3702**	-0.0621
		rg						0.416**	-0.0875
8.	Grain Yield (kg/ha)	rp							-0.0452
		rg							-0.0806

Along with yield association with other characters which determines the performance of the genotypes, inter associations between the yield attributing characters will also be fetching in the selection of those characters for yield improvement. Initial and final plant population was significantly and positively correlated with days to 50% flowering, days to maturity, plant height and panicle length (phenotypically). Plant height and panicle length had positive significant association with 100 seed weight. The significant and positive association of Plant height with 100 seed weight was also reported by Prasad and Sridhar, (2019). Days to 50% flowering, days to maturity and plant height were negatively correlated with grain yield. These results were also reported by Arunkumar *et al.* (2004).

CONCLUSION

The study made in brief can be concluded as selection of yield attributes having high heritability and genetic advance and significant positive association among the yield attributing characters will be more effective for have countability for increasing variability and also can achieve the objective of selection of promising entries for further improvement of breeding programme. Through this selection process the high yielding entries can be further demonstrated on large scale in farmer's fields and thereby can benefit the farming community.

FUTURE SCOPE

Every breeding programme ultimate goal is to broaden the genetic base, variability and heritability among the genetic material used, coming to the present research work an attempt was made to study the genetic advance, heritability, association among the yield and yield attributing characters through which assessment can be done in selection of yield traits for improvement. By selecting the significant positively correlated characters for yield along with high heritability and genetic advance, in near future, considerable yield improvement can be done.

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Conflict of Interest. The authors declare that there is no conflict of interests regarding publication of this article.

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