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Genetic Divergence Studies for Morphological Traits in Sorghum [*Sorghum bicolor* (L.) Moench] over the Environments

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Authors' contributions

This work was carried out in collaboration between authors VK and AK. Author VK designed the study, performed the statistical analysis, planned and conducted the experiment and wrote the first draft of the manuscript. Authors AK and MD managed the analyses of the study. Author MD also managed the literature searches. All authors read and approved the final manuscript.

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ABSTRACT

Genetic diversity is an essential prerequisite for improving the genetic makeup of any crop. Inclusion of genetically diverse parents in hybridization programme helps in isolation of superior recombinants. So, an experiment was conducted to investigate the genetic diversity among 150 genotypes of sorghum [*Sorghum bicolor* (L.) Moench] Rajasthan during *Kharif* - 2013, 2014 and 2015 in a Randomized Block Design (RBD) with three replications. Present study reveals that the clustering pattern based on D^2 statistics grouped 150 genotypes into 6 clusters, out of which cluster 1 shows the highest intra cluster value (142.62) followed by cluster 2 (119.47). While maximum inter cluster distance (*i.e.*652.68) was observed between cluster 5 and cluster 6, indicating there is presence of wide range of genetic diversity among the sorghum genotypes. Such genotypes with wide genetic diversity based on their mean values can either be utilized for breeding programmes for genetic improvement in sorghum or directly adopted as a variety.

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1. INTRODUCTION

Sorghum crop [*Sorghum bicolor* (L.) Moench) is genetically suited to hot and dry agro-ecologies with frequent drought, where it is difficult to grow other crops [1]. Sorghum is preferred over maize in *kharif* season because of its high tolerance to various stresses and its superiority to pearlmillet in having lower oxalate and fiber content. Sorghum stover is valued over all other sources of fodder (paddy straw, pearlmillet straw and wheat straw). Thus sorghum is also used as fodder to the domestic animals for its better performance. At present the country faces a net deficit of 61.1% green fodder, 21.9% dry crop residues and 64% feeds. In last 15 years, area under grain sorghum is decreasing in favour of other crops. However, it still occupies first position (2.6 million ha) among the forage crops and in addition supply significantly large quantity of stover from grain crop for live stock. It is therefore of paramount importance that technological developments are extended to increase the productivity and sustainability of sorghum production.

Landraces or farmer varieties constitute the basic material for developing any variety or hybrid. An autochthonous landrace is a variety with a high capacity to tolerate biotic and abiotic stress, resulting in high yield stability and an intermediate yield level under a low input agricultural system. Fodder yield is a complex trait which depends upon many independent contributing traits. Knowledge of the magnitude and type of association between fodder yield and its components themselves greatly help in evaluating the contribution of different characters towards fodder yield. Quantitative trait like fodder yield is highly influenced by the fluctuations in environment. Hence, selection of plants based directly on fodder yield would not be very reliable. Breeders are sometimes concerned with the selection of superior genotypes which is dependent on the phenotype expression. Often selection based on phenotypic performance does not lead to expected genetic advance mainly due to presence of genotype x environment interactions as well as due to undesirable association between the component characters at genetic level. Thus, knowledge of correlation between complex traits and genetic variability will be helpful in designing an efficient selection criterion for isolating ideal plant types. As information on the nature and degree of genetic divergence would help the plant breeder in choosing the right type of parents for breeding programme, more emphasis should be given on the study of genetic diversity among genotypes of sorghum with respect to yield related growth characters.

So, present investigation was under taken according to its precision and versatility with an objective to study of genetic diversity in 150 popular genotypes of sorghum using morphological traits, keeping in the view that it will provide systematic approach and basic information on which the success of further breeding programme.

2. MATERIALS AND METHODS

One hundred fifty sorghum accessions collected from Directorate of sorghum, Hyderabad, Sorghum Research Station, Dessa, SDAU, and NAU, Surat, Gujarat, Rajasthan College of Agriculture, Udaipur and farmer field of Rajasthan were used for present study. These accessions were evaluated under rainfed condition at ICAR-CAZRI, Regional Research Station, Pali, Marwar (25°46′N, 73°50′E; 225 masl) Rajasthan during *Kharif*-2013, 2014 and 2015 in a Randomized Block Design (RBD) with three replications. The experimental soil was fine sandy clay loam in texture, mixed hyper thermic belonging to the family Lithic calciorthids having shallow depth of 25-45 cm and underlying dense layer of murrum (highly calcareous weathered granite fragments coated with lime) up to 10-15 m depth. The soil of the experimental farm was moderately saline with pH 8.2 and contains low organic carbon 0.37%. Nutrient profile of soil contains 215 kg ha^{-1} available N, 11.3 kg ha^{-1}Olesn’s extractable P and 225 kg ha^{-1} available K at the time of sowing. The experiment unit was a single row plot of 3.5 m long, spaced 0.5 m apart. The standard agronomic practices were followed throughout the period of crop growth. The observations were based on the five randomly selected plants from each genotype and replication for different agro-morphological traits *i.e.* plant height, number of leaves, leaf area, peduncle length, peduncle width, fodder weight/ plant, dry weight/ plant, 1000 seed weight and grain yield/plant. The observation for days to 50% flowering and days to maturity was recorded on the plot basis.Analysis of variance for the individual character and analysis of co-variance for character pairs were carried out as described by Cochran and Cox [2]. Wilk criteria was used to test the significance of pooled differences [3]. Genetic divergence was estimated by Mahalanobis's [4] D^2 statistics method andgenotypes were clustered into different groups on the basis of minimum generalised distance using Tocher's method as described by Rao [5]. The data were analyzed statistically using the software WINDOSTAT, developed by INDOSTAT services Ltd. [6] Hyderabad, India.

3. RESULTS AND DISCUSSION

The analysis of variances for genetic divergence showed highly significant differences among the genotypes for all the eleven growth characters studied, indicating appreciable amount of variability among the genotypes (Table 1).

The clustering based on D^2 statistics grouped genotypes into six clusters, indicating the presence of wide range of genetic diversity among the genotypes under investigation (Table 2).The maximum numbers of genotypes were grouped into cluster1 followed by cluster 2 each comprising of 132 and 14 genotypes respectively. While remaining clusters were solitary. Similar results were observed by Sarwate [7], Barhate [8], Shridher et al. [9], Patankar et al. [10], Ganesamurthy [11], Damor et al., [12], Ahalawat et al. [13] and Karadi et al. [14] who has reported 14, 13, 23, 10 and 14 clusters respectively.

The intra and inter cluster D^2 values among 150 genotypes (Table 3) revealed that cluster 1 shows the highest intra cluster value (142.62) followed by cluster 2 (119.47). Selection among these clusters based on higher mean values of a concerned character related to grain yield could be useful for improvement in sorghum through inter varietal hybridization programme. Similar results have been reported in the past by other workers, Kadam et al. [15], Ganesamurthy, [11], Ahalawat et al. [13], More et al. [16] and Karadi et al. [14]. While null intra cluster distances were recorded by the clusters 3, 4, 5 and 6 having single genotype. Similar results have been reported earlier by other workers, Shridher et al. [9], Patankar et al. [10], Ganesamurthy, [11], Ahalawat et al. [13], Karadi et al. [14]. Maximum inter cluster distance (*i.e.*652.68) was observed between cluster 5 and cluster 6, indicating that genotypes belonging to these groups were genetically most divergent. Simultaneously, cluster 5 recorded higher values of inter cluster distances with cluster 3 (572.3), cluster 2 (522.96) and cluster 1 (389.28). Similar higher value of inter cluster were recorded between cluster 2 and 4 (573.33) which indicates that genotypes included in these clusters also possess considerable genetic diversity among themselves. Such genetically diverse sorghum genotypes can be effectively utilized as parents in hybridization programme. This type of hybridization would be useful for obtaining highest number of valuable segregates along with maximized vigour. Similar instances for intra and inter cluster distances were recorded by Kadam et al. [15], Shridher et al. [9], Patankar et al. [10], Ganesamurthy [11], Shinde et al., [17], Damor et al., [11], Ahalawat et al. [13] and More et al. [16]. The cluster mean values estimated over genotypes for eleven growth characters in sorghum (Table 4). Minimum cluster mean values for days to fifty per cent flowering and days to maturity was recorded in cluster 4 followed by cluster 6. These clusters were also showed maximum mean value for penducle length and penducle width. It reveals that genotypes included in these clusters are useful in inducing earliness in sorghum varieties [15], Patankar et al., [10], Ahalawat et al. [13], More et al. [16] and Karadi et al. [11]. Maximum plant height and number of leaves were observed in genotypes of cluster 2 followed by cluster 5, 1 and 3. Highest mean values for grain yield/plant were recorded in genotypes of cluster 3 followed by genotypes of cluster 1 and 5. These clusters were also having highest mean values for leaf area, fodder weight/ plant, dry weight/ plant and 1000 seed weight. As characters such as number of leaves, penducle length, penducle width, leaf area, dry weight per plant, fodder yield per plant, 1000 seed weight and grain yield per plant has been proved to be major contributors to its economic superiority Bala et al. [18], Almodares et al. [19] and More et al. [16].

The character contribution of various clusters towards the genetic diversity by Tochers clustering method indicated that peduncle length (35.45%) followed by days to 50% flowering (34.11%) were the major contributors towards total divergence (Table 5).

Genetic diversity instigated in present study among these characters can be a base for genetic improvement in sorghum. Such more diverse genotypes in accordance with their mean values on any cluster as per desire can be used in hybridization programme for sorghum improvement. While, the cluster contributing maximum to the divergence were given greater

Table 1. ANOVA for grain yield and its components

Source of variations	df	Days to 50% flowering	Days to maturity	Plant height	Number of leaves	Leaf area	Peduncle length	Peduncle width	Fodder wt. / plant	Dry wt / plant	1000SW	Grain yield/plant
Replications	2	0.535	4.682*	1043.798**	6.683**	1011.666*	5.716**	2.136**	1082.635**	94.413*	4.339	98.19**
Genotypes	149	191.196**	131.706**	3265.658**	6.189**	14672.171**	101.749**	10.540**	7420.630**	938.719**	16.110**	130.56**
Error	298	0.927	1.064	78.978	0.348	294.808	0.582	0.253	107.516	28.798	1.823	5.585
General Mean		68.237	101.931	239.476	11.047	363.955	17.598	6.105	159.025	56.029	22.024	12.928
CD (5%)		1.547	1.658	14.279	0.948	27.589	1.225	0.809	16.661	8.623	2.17	3.797
CD (1%)		2.038	2.184	18.811	1.249	36.343	1.614	1.065	21.948	11.359	2.858	5.002

Table 2. Distribution of one hundred fifty genotypes of sorghum in to different clusters

Clusters	No. of genotypes	Genotypes
Cluster 1	132	CSV-15, EB-12, EJ-38, IS-6910, EJ-34, EJ-28, E-4, ES-7, EB-18, IS-19231, EB-11, EJ-42, IS-14008, EB-22, EB-6, E-14, IS-6953, ES-10, IS-13996, E-76, E-47, ES-5, E-68, EJ-71, E-102, IS-22518, IS-19065, IS-20582, IS-15664, SMU-1, IS-15448, IS-11497, EG-6, IS-12326, EJ-75, IS-13974, E-70, E-112, CSV-17, E-71, IS-23599, IS-41397, Pr. C-1080, SPV-1822, SU-45 (RC-2), SU-52 (RC-1), GPU-1, GPU-2, GPU-3, GPU-4, GPU-5, GPU-6, GPU-7, GPU-9, GPU-10, GPU-13, GPU-14, GPU-17, SMU-4, E-4, E-5, E-7, E-14, EJ-17, EJ-18, EJ-19, EJ-30, EJ-42, EJ-54, EJ-55, EJ-57, EJ-59, EJ-67, EJ-68, EJ-71, EJ-72, Raj-3, Raj-5, Raj-6, Raj-7, Raj-8, Raj-9, Raj-12, Raj-13, Raj-14, Raj-15, Raj-16, Raj-18, Raj-19, Raj-20, Raj-24, Raj-30, Raj-32, EG-48, E-169, EG-40, ERS-13, E-171, E-173, EG-1, E-210, Gundari, EJ-42, E-168, E-145, EG-55, ERN-8, ERN-4, EJN-33, EJ-77, E-178, Malwan, FM-303, FM-645, SL-44, PSC-1, Rampur Local, GJ-37, GJ-40, GJ-35, GJ-38, GJ-39, GPP-4, GPP-6, GPP-7, GPP-8, GPP-10, GPP-15, GPP-17, GPP-18, GPP-19 and GPP-22
Cluster 2	14	E-152, FM-205, FM-331, EB-1, E-205, E-177, ERN-7, KatarKhatu, Raj-21, EJN-32, EJN-26, MP-Chari, FM-94 and CO-FS-29
Cluster 3	1	GPU-8
Cluster 4	1	E-13
Cluster 5	1	CSV-22
Cluster 6	1	GPP-21

Table 3. Average Intra (diagonal) and Inter-cluster distance (D) value for eleven growth characters in sorghum

	Cluster 1	Cluster 2	Cluster 3	Cluster 4	Cluster 5	Cluster 6
Cluster 1	142.62	272.56	221.11	283.39	383.86	389.28
Cluster 2		119.47	282.01	573.33	555.26	522.96
Cluster 3			0	334.64	173.3	572.3
Cluster 4				0	273.65	238.77
Cluster 5					0	652.68
Cluster 6						0

Table 4. Cluster means for eleven growth characters in sorghum (Tocher method)

Cluster	Days to 50% flowering	Days to maturity	Plant height	Number of leaves	Leaf area	Peduncle length	Peduncle width	Fodder wt. / plant	Dry wt / plant	000SW	Grain yield/plant
Cluster 1	66.89	100.71	238.42	10.85	362.51	17.24	5.93	158.62	55.69	22.5	13.53
Cluster 2	82.38	113.74	257.16	13.16	377.61	18.96	6.83	128.44	48.88	18.02	4.4
Cluster 3	72.67	108	220.53	10.5	538.53	19.3	4.9	306.37	114	28.37	22.8
Cluster 4	52.33	97.33	190.87	8.93	268.43	27.23	8.3	260.53	82.83	16.5	5.63
Cluster 5	70	100.33	249.5	10.97	388.17	21.2	6.17	407.73	119.7	24.73	13.3
Cluster 6	58.33	98	189.53	9.77	259.77	30.47	18.2	142.57	52.8	12.03	4.33

Table 5. % contribution of different characters towards diversity

S.N.	Chatacters	Contribution %
1	Days to 50% flowering	34.11
2	Days to maturity	5.79
3	Plant height	3.1
4	Number of leaves	0.12
5	Leaf area	4.92
6	Peduncle length	35.45
7	Peduncle width	2.29
8	Fodder wt. / plant	8.24
9	Dry wt / plant	3.81
10	1000SW	0.97
11	Grain yield/plant	1.21

emphasis for deciding the type of cluster for the purpose of further selection and the choice of parents for hybridization.

4. CONCLUSION

Based on above discussion, genetic improvement in sorghum for various morphological characters. Highest mean values for grain yield/plant were recorded in genotypes of cluster 3 (GPU-8) followed by genotypes of cluster 1 and 5. These clusters were also having highest mean values for leaf area, fodder weight/ plant, dry weight/ plant and 1000 seed weight. The highest intra cluster value (142.62) followed by cluster 2 (119.47). Maximum inter cluster distance (*i.e.* 652.68) was observed between cluster 5 and cluster 6, indicating that genotypes belonging to these groups were genetically most divergent. Therefore, genotypes from these two clusters were recommended for use in hybridization programme for further improvement.

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COMPETING INTERESTS

Authors have declared that no competing interests exist.

REFERENCES

1. Jain SK, Elangovan M, Patel NV. Correlation and path coefficient analysis for agronomical traits in forage sorghum [*Sorghum bicolor* (L.) Moench]. Indian J. Plant Genet. Resour. 2010;23(1):15-18.
2. Cochran WG, Cox GM. Experimental designs. J. Willey and Sons N.Y. London. 1957;62-90:403-412.
3. Wilk SS. Certain generalization in the analysis of variance. Biometrics. 1932;24: 471-494.
4. Mahalanobis PC. On the generalized distance in statistics. Proc. Nat. Inst. Sci. India. 1936;2:49-55.
5. Rao CR. Advanced statistical methods in biometric research. J. Wiley and Sons., New York; 1952.
6. Indostat Services. Windostat. Hyderabad: Indostat Services; 2004.
7. Sarwate CD. Genetic analysis of yield and yield contributing characters in sorghum. Part II. The Study of Genetic Divergence in Sorghum. Thesis abst. MPKV, Rahuri India; 1985.
8. Barhate KK. Genetic divergence, combining ability and stability studies in sorghum. Ph. D thesis MPKV, Rahuri, India; 1996.
9. Shridher K, Gangaiah B, Ramesh CR. Genetic diversity studies in forage sorghum, Sorghum Research Report. 2003;44:3-6.
10. Patankar AB, Sonone AH, Patil JV, Sarode ND. Genetic divergence in Sweet Sorghum. J. of Maharashtra Agric. Univ. 2005;30(2):175-177.
11. Ganesamurthy D, Punitha K, Elangovan M. Genetic diversity among the land races of sorghum collected in Tamil Nadu. Electronic J. Plant Breeding. 2010;1(6): 1375-1379.
12. Damor HI, Parmar HP, Parmar DJ. D2 analysis in forage sorghum [*Sorghum bicolor* (L.) Moench]. Int. J. of Chemi. Studi. 2017;5(4):337-341.

13. Ahalawat NK, Arya VK, Kumar P, Singh SK. Genetic divergence in forage sorghum (*Sorghum bicolor* L. Moench). J. Appl. Nat. Sci. 2018;10(1):439-444.
14. Karadi A, Kajjidoni ST. Genetic variability and diversity for productivity traits and grain quality including nutritional quality traits in selected mini core and promising released varieties of sorghum. J. Pharmacog. Phytoche. 2019;8(4):2091-2097.
15. Kadam DE, Patil FB, Bhor TJ, Harer PN. Diversity studies in sweet sorghum. J. Maharashtra Agric. Uni. 2001;26(2):140-143.
16. More AW, Kalpande HV, Dhutmal RR. Genetic Divergence Studies in Sorghum (*Sorghum bicolor* L.) Land Races for Yield and Yield Parameters. Int. J. Curr. Microbiol. App. Sci. 2018;6: 393-399.
17. Shinde D, Chavan S, Jadhav BD. Study of genetic divergence in sweet sorghum [*Sorghum bicolor* (L.) Moench]. The Bioscan. 2013;8(1):135-138.
18. Bala RS, Biswas PK, Ratnawati CV. Advances in value addition of kharif sorghum. Crop Improv. 1996;23: 31-36.
19. Almodares A, Taheri R, Adeli S. Stalk yield and carbohydrate composition of sweet sorghum [*Sorghum bicolor* (L.) Moench] cultivars and lines at different growth stages. J. Malesian Appl. Biol. 2008;37:31-36.

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