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Research Article

Genetic divergence study for duration and biomass traits in sorghum [*Sorghum bicolor* (L.) Moench]

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Abstract
Germplasm can be exploited efficiently by determining its genetic diversity and identifying desirable parents for crop improvement programs. In this study, 200 diverse sets of sorghum accessions were evaluated during *rabi,* 2019 with an aim of assessing genetic diversity for fodder component traits using D^2 statistics. Fresh biomass contributed the highest (47.4%) towards divergence followed by days to flowering (35.9%) and plant height (16.7%). All the 200 genotypes were grouped into 6 clusters with Cluster I having the maximum number of genotypes (108) followed by cluster IV (47), VI (39) and clusters II, III, V having the least genotype number (2). Cluster I had the highest (10.61) intra cluster distance while cluster II had the least (0.41) intra cluster distance. Inter cluster distance between I and IV was observed the highest (10.43) while the least was observed between III and V. Genotypes from Cluster II and IV were observed to be the best suited for fodder improvement programs.

Key words
Sorghum, D^2 statistics, genetic diversity, clusters, fodder

INTRODUCTION

Sorghum (*Sorghum bicolor* (L.) Moench) is the fifth most important cereal crop worldwide after rice, wheat, maize and barley in terms of area and production (FAOSTAT, 2018). Globally sorghum is cultivated in about 105 countries with an area of 42.14 m.ha and production of around 54.34 m.t (Rakshit *et al.,* 2014). Africa contributes to half of the global sorghum production (50.2%) followed by the Americas (32.4%) and Asia (13.4%) (FAOSTAT, 2018). It is rich in carbohydrates, protein, vitamins and minerals and serves as a main source of energy in Africa and South Asia (Duodu *et al.,* 2003). It also serves as an important source of fodder and biofuel (Doggett, 1988). Sorghum fodder is considered a demand in developed countries (FAOSTAT, 2018) as 97 per cent of total sorghum use is mainly confined to livestock feed. Sorghum fodder is preferred more than other forage crops due to its drought tolerance, quick growth, high dry matter content, high yield and wider availability. Some fodder sorghum can produce stalks by regenerating after cutting, yielding higher biomass than other forage crops.

In addition to fodder purpose, the stalks from sorghum are used as an alternative for the production of syrups, jaggery, citric acids and modified starch (Reddy *et al.,* 2005). Due to these multipurpose uses from fodder sorghum, several crop improvement programs were made to maximize biomass production as sorghum is still considered a choice of crop for the marginal environment (Patel *et al.,* 2020). One of the best crop improvement program involves screening the diversity residing in a natural population for identifying the superior genotypes withstanding diverse conditions which can meet up with human needs. So the present study has attempted to understand the divergence for fodder component traits including plant height, days to flowering and fresh biomass in a population of 200 genotypes using Mahalanobis's D^2 statistics (Mahalanobis, 1936).

MATERIALS AND METHODS

A diverse collection of 200 sorghum accessions were assembled (**Table 1**) and raised during *rabi* 2019

at Agricultural Research Station (ARS), Kovilpatti, TNAU (Latitude 9.17′N, Longitude 77.88′E). Complete Randomized Block Design (CRBD) was followed for assessing genetic diversity in three fodder related traits *viz*. days to flowering, plant height (cm) and fresh biomass (g) with three replications. Accessions were raised in 2 m rows with spacing of 45 x 10 cm and were maintained with the standard cultivation practices. The fodder traits were observed for five randomly selected plants from the replicates of each accession.

Genetic diversity in the collection was assessed by determining Mahalanobis (1936) D^2 statistics. Clustering of genotypes was performed by Tocher's method (Rao, 1952) using GENRES statistical package (GENRES, 1994).

Table 1. List of accessions taken for the study

S. No.	NBPGR Accession	Experimental ID
1	IS 6997	TNAU_Sor1
2	IS 7022	TNAU_Sor2
3	IS 7129	TNAU_Sor3
4	IS 7175	TNAU_Sor4
5	IS 7204	TNAU_Sor5
6	IS 7333	TNAU_Sor6
7	IS 7358	TNAU_Sor7
8	IS 7405	TNAU_Sor8
9	IS 7459	TNAU_Sor9
10	IS 7649	TNAU_Sor10
11	IS 7686	TNAU_Sor11
12	IS 7737	TNAU_Sor12
13	IS 7748	TNAU_Sor13
14	IS 7752	TNAU_Sor14
15	IS 7777	TNAU_Sor15
16	IS 7794	TNAU_Sor16
17	IS 7877	TNAU_Sor17
18	IS 7887	TNAU_Sor18
19	IS 7935	TNAU_Sor19
20	IS 7991	TNAU_Sor20
21	IS 8028	TNAU_Sor21
22	IS 8113	TNAU_Sor22
23	IS 8569	TNAU_Sor23
24	IS 8609	TNAU_Sor24
25	IS 8613	TNAU_Sor25
26	IS 8616	TNAU_Sor26
27	IS 8621	TNAU_Sor27
28	IS 8622	TNAU_Sor28
29	IS 8688	TNAU_Sor29
30	IS 8714	TNAU_Sor30
31	IS 8717	TNAU_Sor31
32	IS 8723	TNAU_Sor32
33	IS 8724	TNAU_Sor33
34	IS 8725	TNAU_Sor34
35	IS 8794	TNAU_Sor35
36	IS 8826	TNAU_Sor36
37	IS 8853	TNAU_Sor37
38	IS 8900	TNAU_Sor38
39	IS 8942	TNAU_Sor39
40	IS 8946	TNAU_Sor40
41	IS 8962	TNAU_Sor41
42	IS 8968	TNAU_Sor42
43	IS 9094	TNAU_Sor43
44	IS 9108	TNAU_Sor44
45	IS 9151	TNAU_Sor45
46	IS 9185	TNAU_Sor46
47	IS 9200	TNAU_Sor47
48	IS 9203	TNAU_Sor48
49	IS 9262	TNAU_Sor49
50	IS 9295	TNAU_Sor50
51	IS 9325	TNAU_Sor51
52	IS 9348	TNAU_Sor52
53	IS 9361	TNAU_Sor53
54	IS 9373	TNAU_Sor54
55	IS 9378	TNAU_Sor55
56	IS 9442	TNAU_Sor56
57	IS 9444	TNAU_Sor57
58	IS 9563	TNAU_Sor58
59	IS 9567	TNAU_Sor59
60	IS 9687	TNAU_Sor60
61	IS 9700	TNAU_Sor61
62	IS 9721	TNAU_Sor62
63	IS 9747	TNAU_Sor63
64	IS 9770	TNAU_Sor64
65	IS 9774	TNAU_Sor65
66	IS 9789	TNAU_Sor66
67	IS 9794	TNAU_Sor67
68	IS 9805	TNAU_Sor68
69	IS 9912	TNAU_Sor69
70	IS 9922	TNAU_Sor70
71	IS 9968	TNAU_Sor71
72	IS 9972	TNAU_Sor72
73	IS 9991	TNAU_Sor73
74	IS 10293	TNAU_Sor74
75	IS 10324	TNAU_Sor75
76	IS 10372	TNAU_Sor76
77	IS 10400	TNAU_Sor77
78	IS 10572	TNAU_Sor78
79	IS 10608	TNAU_Sor79
80	IS 10612	TNAU_Sor80
81	IS 10634	TNAU_Sor81
82	IS 10715	TNAU_Sor82
83	IS 10720	TNAU_Sor83
84	IS 10803	TNAU_Sor84
85	IS 10815	TNAU_Sor85
86	IS 10827	TNAU_Sor86
87	IS 10841	TNAU_Sor87
88	IS 10843	TNAU_Sor88
89	IS 10853	TNAU_Sor89
90	IS 10876	TNAU_Sor90
91	IS 10877	TNAU_Sor91

92	IS 10889	TNAU_Sor92	146	IS 12295	TNAU_Sor146
93	IS 10892	TNAU_Sor93	147	IS 12299	TNAU_Sor147
94	IS 10893	TNAU_Sor94	148	IS 12311	TNAU_Sor148
95	IS 10894	TNAU_Sor95	149	IS 12317	TNAU_Sor149
96	IS 10921	TNAU_Sor96	150	IS 12330	TNAU_Sor150
97	IS 10960	TNAU_Sor97	151	IS 12336	TNAU_Sor151
98	IS 10968	TNAU_Sor98	152	IS 12452	TNAU_Sor152
99	IS 10978	TNAU_Sor99	153	IS 12569	TNAU_Sor153
100	IS 10994	TNAU_Sor100	154	IS 12571	TNAU_Sor154
101	IS 11060	TNAU_Sor101	155	IS 12626	TNAU_Sor155
102	IS 11087	TNAU_Sor102	156	IS 12645	TNAU_Sor156
103	IS 11091	TNAU_Sor103	157	IS 12666	TNAU_Sor157
104	IS 11193	TNAU_Sor104	158	IS 14276	TNAU_Sor158
105	IS 11217	TNAU_Sor105	159	IS 14316	TNAU_Sor159
106	IS 11348	TNAU_Sor106	160	IS 14318	TNAU_Sor160
107	IS 11356	TNAU_Sor107	161	IS 14333	TNAU_Sor161
108	IS 11413	TNAU_Sor108	162	IS 14461	TNAU_Sor162
109	IS 11491	TNAU_Sor109	163	IS 14531	TNAU_Sor163
110	IS 11501	TNAU_Sor110	164	IS 14532	TNAU_Sor164
111	IS 11508	TNAU_Sor111	165	IS 14535	TNAU_Sor165
112	IS 11521	TNAU_Sor112	166	IS 14542	TNAU_Sor166
113	IS 11527	TNAU_Sor113	167	IS 14549	TNAU_Sor167
114	IS 11543	TNAU_Sor114	168	IS 14552	TNAU_Sor168
115	IS 11548	TNAU_Sor115	169	EC488361	TNAU_Sor169
116	IS 11550	TNAU_Sor116	170	IS 14775	TNAU_Sor170
117	IS 11818	TNAU_Sor117	171	IS 14798	TNAU_Sor171
118	IS 11902	TNAU_Sor118	172	IS 14813	TNAU_Sor172
119	IS 11911	TNAU_Sor119	173	IS 14816	TNAU_Sor173
120	IS 11912	TNAU_Sor120	174	IS 14817	TNAU_Sor174
121	IS 11929	TNAU_Sor121	175	IS 14819	TNAU_Sor175
122	IS 11944	TNAU_Sor122	176	IS 14820	TNAU_Sor176
123	IS 11955	TNAU_Sor123	177	IS 14826	TNAU_Sor177
124	IS 11958	TNAU_Sor124	178	IS 14842	TNAU_Sor178
125	IS 11962	TNAU_Sor125	179	IS 14861	TNAU_Sor179
126	IS 11967	TNAU_Sor126	180	IS 14875	TNAU_Sor180
127	IS 11971	TNAU_Sor127	181	IS 14929	TNAU_Sor181
128	IS 11980	TNAU_Sor128	182	IS 14932	TNAU_Sor182
129	IS 11986	TNAU_Sor129	183	IS 14941	TNAU_Sor183
130	IS 12006	TNAU_Sor130	184	IS 14991	TNAU_Sor184
131	IS 12024	TNAU_Sor131	185	IS 15005	TNAU_Sor185
132	IS 12150	TNAU_Sor132	186	IS 15033	TNAU_Sor186
133	IS 12166	TNAU_Sor133	187	IS 15042	TNAU_Sor187
134	IS 12175	TNAU_Sor134	188	IS 15045	TNAU_Sor188
135	IS 12176	TNAU_Sor135	189	IS 15061	TNAU_Sor189
136	IS 12183	TNAU_Sor136	190	IS 15076	TNAU_Sor190
137	IS 12198	TNAU_Sor137	191	IS 15088	TNAU_Sor191
138	IS 12203	TNAU_Sor138	192	IS 15094	TNAU_Sor192
139	IS 12230	TNAU_Sor139	193	IS 15096	TNAU_Sor193
140	IS 12267	TNAU_Sor140	194	IS 15098	TNAU_Sor194
141	IS 12284	TNAU_Sor141	195	IS 15144	TNAU_Sor195
142	IS 12285	TNAU_Sor142	196	IS 15144	TNAU_Sor196
143	IS 12286	TNAU_Sor143	197	IS 15146	TNAU_Sor197
144	IS 12289	TNAU_Sor144	198	IS 15150	TNAU_Sor198
145	IS 12294	TNAU_Sor145	199	IS 15191	TNAU_Sor199

200   IS 15122   TNAU_Sor200

RESULTS AND DISCUSSION

Sorghum has been considered a major important cereal in many developing countries due to its increasing animal feed value (fodder) and industrial (bio-ethanol) purposes over the years (Hariprasanna and Rakshit, 2016). In addition to fodder sorghum, farmers in India prefer dual purpose sorghum varieties as they tend to have fodder along with grains. Due to this increasing importance of fodder and dual purpose sorghum, this study was targeted to understand the genetic divergence of fodder contributing traits (plant height, days to flowering and fresh biomass) in 200 sorghum accessions using D^2 statistics and to identify the best genotypes for fodder improvement program by clustering.

D^2 statistics resulted that the fresh biomass contributed the highest (47.4%) to divergence followed by days to flowering (35.9%) and plant height (16.7%) (**Table 2**).

Table 2. Contribution of fodder component traits to divergence in sorghum

Traits	Number of First Rank	% Contribution
Plant Height	3332	16.7
Days to Flowering	7138	35.9
Fresh Biomass	9430	47.4
Total	19900	100

This study implies the importance of fresh biomass trait for selecting superior fodder yielding genotypes.
D^2 statistics analysis in this present study further grouped the accessions into 6 clusters (**Table 3**) of which Cluster II, III and V had the minimum number of accessions (2); Cluster I had the maximum number of accessions (108) followed by Cluster IV with 47 accessions and Cluster VI with 39 accessions. Doijad *et al.* (2016) performed clustering among 61 genotypes for 16 characters and observed 15 clusters from which most of the accessions (47) were confined to a single cluster indicating a less divergence than this present study. Subramanian *et al.* (2019) clustered 31 sorghum landraces into six clusters using eight characters but the present study clustered 200 accessions into 6 clusters indicating the richness of

Table 3. Clustering of sorghum genotypes

Clusters	Number of genotypes	Accession list
Cluster I	108	TNAU_Sor # 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 141, 142
Cluster II	2	TNAU_Sor # 171, 172
Cluster III	2	TNAU_Sor # 161, 198
Cluster IV	47	TNAU_Sor # 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 118, 119, 120, 121, 122, 123, 124, 125, 126, 127, 128, 129, 130, 131, 132, 133, 134, 135, 136, 137, 138, 139, 140, 143, 144, 145, 146, 147, 148 , 149, 150, 151, 152, 153, 154, 169
Cluster V	2	TNAU_Sor # 160, 183
Cluster VI	39	TNAU_Sor # 155, 156, 157, 158, 159, 162, 163, 164, 165, 166, 167, 168, 170, 173, 174, 175, 176, 177, 178, 179, 180, 181, 182, 184, 185, 186, 187, 188, 189, 190, 191, 192, 193, 194, 195, 196, 197, 199, 200

population size and genetic divergence observed in this present study.
The present study observed the highest inter cluster D^2 value (108.73) and inter cluster distance (10.43) between Cluster I & IV; highest intra cluster D^2 value (112.67) and intra cluster distance (10.61) among Cluster I (**Table 4 & 5**). The least inter cluster D^2 value (2.83) and distances (1.68) was observed between Cluster III & V; least intra cluster D^2 (0.17) and distance (0.41) was observed among Cluster II. Observing divergence between and among clusters is a good measure of selecting genotypes for breeding programs (Sinha and Kumaravadivel, 2016). The overall inter and intra cluster distance analysis from this present study indicates the superiority of accessions from

Cluster I as they showed high genetic distance among themselves and also between Cluster IV which indicates them as the best choice for hybridization programs. Several attempts were done to measure intra and inter clusters distances for selecting superior genotypes in the clusters (Gerrano *et al.,* 2014, Sinha and Kumaravadivel 2016, Ayush *et al.,* 2017, Subramanian *et al.,* 2019). Sinha and Kumaravadivel (2016) clustered 40 accessions into 6 clusters and observed the highest inter cluster distance of 5.148 which was lesser than the distance observed in

Table 4. Intra and inter Cluster D square values in the study population

Clusters	I	II	III	IV	V	VI
I	112.67	91.86	68.11	108.73	65.18	100.79
II		0.17	8.48	81.31	13.54	95.34
III			0.38	62.18	2.83	66.58
IV				105.92	57.83	96.22
V					0.57	55.82
VI						80.05

Table 5. Intra and inter cluster distances in the study population

Clusters	I	II	III	IV	V	VI
I	10.61	9.59	8.25	10.43	8.07	10.04
II		0.41	2.91	9.02	3.68	9.76
III			0.62	7.89	1.68	8.16
IV				10.29	7.61	9.81
V					0.76	7.47
VI						8.95

this present study.

Cluster means for all traits were calculated in this present study (**Table 6**). Cluster VI had the highest cluster mean for plant height (250.65 cm), days to flowering (60 days) and fresh biomass (361.24 g). Cluster I had the least cluster mean for plant height (213.83 cm), Cluster II with the least cluster mean flowering (49 days) and Cluster III had the least cluster mean for fresh biomass (188.33 g). Typical fodder sorghum would maintain a height range above 200 cm (Kumar, 2016). Cluster mean

of Cluster II had the plant height (215 cm) exhibiting typical fodder sorghum and also had the least cluster mean for a short duration for flowering (49 days) which indicates the importance of using this cluster on sorghum fodder improvement program. For providing the best fodder sorghum, most breeders prefer selecting sorghum having a medium duration as they can provide a better fodder yield than short duration sorghums and can save time and money (Kumar, 2016). Cluster IV had the cluster mean with medium duration for flowering and high fresh biomass (g) which can be used for sorghum breeding

Table 6. Mean values for fodder component traits

Clusters	Plant height (cm)	Days to flowering	Fresh biomass (g)
I	213.83	58.31	290.00
II	215.67	49.33	224.17
III	217.00	53.67	188.33
IV	224.51	57.11	322.34
V	241.50	54.33	240.83
VI	250.65	59.65	361.24

programs.

The present study was performed to understand the divergence on fodder component traits within the assembled 200 sorghum accessions. Further analysis from this study identified superior genotypes for all observed

fodder component traits. TNAU_Sor155 was observed to be the tallest (423 cm) with late flowering (76 days) and TNAU_Sor79 to be shortest (54 cm); TNAU_Sor138 had the shortest duration (38 days); TNAU_Sor107 had the highest fresh biomass (1058 g) and TNAU_Sor158 with the least fresh biomass (68 g). These observations imply

the importance of these superior genotypes for fodder improvement programs in sorghum.

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