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GENETIC DIVERGENCE STUDIES FOR AGRO-MORPHOLOGICAL, INSECT PEST AND QUALITY PARAMETERS IN MINI CORE COLLECTION OF FORAGE SORGHUM

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SUMMARY

Sorghum is the important cereal crop with multiple uses like food, feed, fodder, fuel and medicines etc. Hence exploration of existing variability in sorghum and its proper utilization for trait specific breeding is essential for sorghum improvement. In the present investigation, sixty one mini core of sorghum were screened for genetic diversity for 30 traits including quantitative and qualitative, out of which except leaf breadth all traits were contributing to variability were selected for genetic diversity analysis. By using hierarchical cluster analysis, the 40 accessions were grouped under 6 clusters. Cluster I contained maximum number of accessions and cluster VI contained the minimum. The maximum inter-cluster distance was observed between cluster VI and cluster IV. Cluster III had the highest mean value for hundred-seed weight and yield. Thus the selection of parents must be based on the wider inter-cluster distance and superior mean performance for yield and yield attributing traits. Therefore present investigation was planned to exploit the existence of a wide genetic diversity present in quantitative and qualitative traits in sorghum accessions which can be further used for sorghum genetic improvement.

Key Words : Minicore, cluster, diversity and sorghum

Sorghum is fifth most important food security crop globally and is the dietary staple of more than 500 million people living in arid and semi-arid tropics (Kumar *et al.*, 2011). Its small genome size (730 Mb) makes sorghum an attractive model for functional genomics of C_4 grasses. Heat and drought resistance with a fairly high green fodder yield makes sorghum especially important in dry regions such as northeast Africa (its center of diversity), India and the southern plains of the United States.

Sorghum has rich genetic diversity including landraces and wild relatives. Collection and conservation of sorghum germplasm has been accelerated in the past four decades to prevent the extinction of landraces and wild relatives of cultivated sorghum (Rosenow and Dahlberg 2000).

Landraces, wild and weedy relatives are rich sources of resistance to diseases, insect pests and other stresses such as high temperature and drought. They are also sources of traits to improve food and fodder quality, animal feed and industrial products. However, this natural genetic diversity is under threat due to the destruction of habitats, commercial agricultural practices, industrial and infrastructural activities, and large-scale adoption of improved cultivars. Scientists are using a very small proportion of the large germplasm collection. This is because of the lack of information on traits of economic importance, which often show genotype x environment interactions and require replicated multi locations evaluation. Knowing the genotype value for the accessions is helpful in using them in plant breeding programs, but this is a very costly and resource-demanding task owing to the large size of the collection. To overcome this problem, ICRISAT's germplasm research was focused on studying the diversity of the germplasm collection and developing "core collections", following the concept of Brown (1989).

At present, ICRISAT is a major repository for world sorghum germplasm with a total of 37,904 accessions from 91 countries. The collection is estimated to represent about 80% of the variability present in sorghum (Eberhart *et al.*, 1997). A core collection of 2247 accessions was developed in 2001 to enable researchers to have access to a smaller set of germplasm. However, this core collection was found to be too large. To overcome this, a sorghum mini core (10 % accessions of the core or 1 % of the entire collection) was developed and is being maintained at ICRISAT, Patancheru, India (Grenier *et al.*, 2001). This

consists of approximately 10% of the total landrace collection, but represents the entire genetic and geographical spectrum of the collection (Eberhart *et al.* 1997). So keeping this in view the present study was undertaken to characterize and assess genetic diversity in sorghum mini core accession on the basis on quality and biotic resistance.

MATERIALS AND METHODS

The field experiment was conducted at research area of Forage Section, Department of Genetics and Plant Breeding, CCS Haryana Agricultural University, Hisar. It is situated in semi-arid sub-tropical region at $29^0 10'$N latitude and $75^0 46'$E longitude with elevation of 215.52 m above mean sea level. The soil of the experimental field was sandy loam in texture, slightly alkaline in reaction (pH 8.0). Sixty one sorghum genotypes were used in the present study. The experiment was laid out in randomized block design in three replications of two rows of 4m each with inter-row distance of 60 cm intra-row plant distance of 15cm. All the recommended agronomical practices for sorghum cultivation were followed to raise a good crop. Data was recorded from five plants in every replication for below mentioned traits

I. Morphological traits : Observations were recorded for various morphological traits like plant height, leaf length, leaves per plant, tillers per plant, leaf breadth, stem girth, green fodder yield and dry fodder yield.

II. Quality Parameters : For quality estimation, 500 gm samples of green fodder was collected from the field and dried to constant weight at 60°C for dry matter determination. Then dried was passed through a small chopper, mixed thoroughly and sampled for dry matter determination and laboratory analyses. Neutral deteraent fibre (NDF) (%), acid detergent fibre (ADF) (%), Cellulose (%), Lignin (%) estimated using a method suggested by (Goering and Van Soest (1970);Total phenol (mg/g DM) by Swain and Hillis (1959); Tannin (mg/g DM) estimated using a method suggested by Bruns(1971); Mineral content : Zn, Fe, Cu, Mn, Na, K (µg/g DM) by Atomic Absorption Spectrophotometer; HCN content (mg/100g fresh matter basis) estimated using a method suggested by Gilchrist *et al.*, 1967; Crude Protein (%) by Micro-Kjeldhal's method; IVDMD (%)estimated using a method suggested by Tilley and Terry (1963); Total soluble sugar (%) by Dubois *et al.*, (1956); DDM (Digestible dry matter) (q/ha) by IVDMD (%) x DFY/ 100 and º Brix by Refractometer were estimated as per the standard procedure.

III. Foliar disease : Data for grey leaf spot (*Crecospora sorghi*), zonate leaf spot (*Gloeocercospora sorghi*) and sooty stripe (*Ramulispora sorghi*) at 35 and 55 days after sowing. Scoring for foliar diseases was done using visual standards adopting the following scale:

1= no symptoms;
3= few scattered lesions/spots;
5= typical lesion developed on leaves covering up to 25% leaf area.; 7= coalescing spots covering about 26-40% leaf area, and 9= symptoms severe covering more than 40% of leaf area
And the disease intensity was computed using the formula,

$$\text{Disease intensity} = \frac{\text{Sum of all numerical ratings}}{\text{Total number of leaves observed x highest rating}} \times 100$$

IV. Insect Pest Observations : Experimental genotypes were also evaluated for insect pest attack and observation were recorded for shoot fly (*Atherigona soccata*) and stem borer (*Chilo partellus*) attack as prescribed by Mathur (1991). For shoot fly data were collected at 14 and 28 days after germination and per cent dead hearts were calculated using the following formula :

$$\% \text{ Dead heart} = \frac{\text{Number of dead heart/ plot}}{\text{Number of plants/plot}} \times 100$$

Statistical analysis : The data were statistically analyzed for grouping of mini core genotypes in various clusters using UPGMA (Unweighted Pair group Method using Arithmetic averages) to find out the patterns of variability among genotypes and characters using statistical software packages of SAS 9.2 software.

RESULTS AND DISCUSSION

Variability studies : The mean sum of squares due to genotype were recorded to be highly significant for all the 30 characters studied, except for leaf breadth. This indicated prevalence of high level

TABLE 1
Cluster membership and number of genotypes in each cluster of sorghum

Cluster No.	Genotypes	No. of Genotypes
I	S 437-1, G 46, ICSV 700, COFS 29, HJ 513, HJ 541, IS 28614, SSG 59-3	9
II	S 540-1	1
III	S 540-2, IS 2205, GFS-5, SGL 87, HC308, HC 136, HC 171, S 490, IS 26749, IS 12804, IS 16151, IS 27887, IS 22720, IS 228, IS 5304, IS 1004, IS 5301, IS 29689, IS 23514, IS 31714, IS 22799, IS 12735, IS 5094, IS 29468, IS 4372, IS 19262, IS 2426, IS 2379, IS 2382, IS 30079, IS 13294, IS 29304, IS 1212, IS 29687, IS 19859, IS 4613, IS 30079, IS 473, IS 29714, IS 30383, IS 30040, IS 23992, IS 29269, IS 608, IS 12965, IS 20679, IS 1233, IS 19389	48
IV	IS 23890	1
V	IS 651	1
VI	IS 21512	1
Total		61

of genetic diversity among the sorghum accessions under study for selection and improvement of genotypes. This also indicated its suitability for further statistical analysis for all the characters studied. Mean, median, mode and range of 30 characters of mini core genotypes indicates that existence of sufficient variability among the sorghum genotypes.

Cluster analysis : The hierarchical cluster analysis led to the formation of six clusters containing one to sixty one genotypes (Table 1). Cluster III had the maximum number of genotypes i.e. 48 and the clusters II, IV, V and VI had the minimum i.e. one each and cluster I comprised of 9 genotypes. Cluster-wise means for all the traits studied are presented in Table 2.

The mean performance of different clusters revealed wide range of variation among these with respect to different traits. The perusal of the data reveals that cluster I comprised tallest genotypes with high green fodder yield, dry fodder yield, plant height, crude protein, DDM, K and low zonate leaf spot intensity. Cluster II which comprised only one genotype (S 540-1) was characterized with high IVDMD, low ADF, low cellulose, low lignin, low GLS, low ZLS and high DDM, Fe, Zn, K, Brix. The genotypes of cluster III had more number of tillers, more stem girth, higher crude protein, K, and low cellulose. High total soluble sugar, low tannin, lignin, HCN, sooty stripe incidence, ZLS, GLS and high Na, K, were observed in cluster IV which comprised only one genotype, cluster V with only one genotype was characterized with more leaf length, plant height, number of tillers, number of leaves, GFY, DDM, total soluble sugar, Mn and Cu and low total phenol, lignin, ZLS and sooty stripe. One genotype was grouped in cluster VI which had wide stem girth, low NDF, low cellulose, more K, less incidence of shoot fly and stem borer.

The intra and inter-cluster distances were calculated using city block distances and are presented in Table 3. The diagonal values represent the intra-cluster distances and off-diagonal values represent the inter-cluster distances. The maximum intra-cluster distance was observed in the cluster III (407.70) followed by in cluster I (360.73). Intra-cluster distances were zero in cluster II, cluster IV, cluster V and cluster VI due to grouping of only one genotype in these clusters which were unique in characteristics. Inter-cluster distance was maximum between clusters IV and VI (1645.26) followed by between clusters III and V (1630.68) and V and VI (1453.42), whereas, the minimum inter-cluster distance was observed between clusters II and VI (625.61).

Findings of present investigation is in close conformating the findings of Yadav and Pahuja (2011) They classified 90 genotypes of sorghum and reported that members of clusters III and II were found to be having maximum plant height and number of leaves/ plant. Leaf breadth and stem girth were maximum in the genotypes of cluster IV. Number of tillers/plant and number of leaves/plant were maximum in the cluster VIII. Similar results were reported by Singh *et al.,* (2010) and Diwakar *et al.,* 2017 who classified genotypes on the basis of D^2 analysis.

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TABLE 2
Cluster means for different characters in sorghum genotypes

S. No.	Characters	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI
1.	Plant height (cm)	256.9	222.3	189.8	212.2	257.8	129.3
2.	Leaf length (cm)	70.32	65.00	58.69	71.20	75.70	46.20
3.	Number of tillers/plant	2.00	2.00	3.00	2.00	3.00	2.00
4.	Number of leaves/plant	28.67	23.00	28.98	24.00	33.00	23.00
5.	Stem girth (cm)	2.71	2.55	2.98	2.22	2.44	3.13
6.	Green fodder yield (q/ha)	468.10	390.50	289.70	325.30	465.00	150.50
7.	Dry fodder yield (q/ha)	102.97	89.80	66.32	65.10	93.00	34.60
8.	Crude protein (%)	8.04	7.63	8.30	7.01	7.84	7.84
9.	IVDMD (%)	50.30	59.10	48.60	54.90	54.49	38.19
10.	Total Phenol (mg/g DM)	5.09	4.19	5.32	4.46	3.53	5.03
11.	Total soluble Sugar (%)	8.10	8.60	7.14	8.60	8.80	5.50
12.	Tannin (mg/g DM)	8.71	6.93	14.63	5.50	10.84	16.72
13.	NDF (%)	69.52	68.14	68.26	71.38	68.56	63.64
14.	ADF (%)	40.10	37.90	40.62	39.40	41.70	42.80
15.	Cellulose (%)	33.11	32.20	32.87	33.00	33.00	32.90
16.	Lignin (%)	5.67	4.63	5.72	4.19	4.10	6.69
17.	DDM (q/ha)	51.36	51.37	32.23	36.8	52.07	14.07
18.	Fe (µg/g DM)	486.02	916.50	417.56	518.10	870.90	862.90
19.	Mn (µg/g DM)	64.26	54.60	47.78	62.00	67.70	51.00
20.	Zn (µg/g DM)	60.46	91.40	64.43	55.10	70.60	57.50
21.	Cu (µg/g DM)	39.83	39.90	33.92	65.20	102.40	36.10
22.	Na (µg/g DM)	138	185	156	990	860	125
23.	K (%)	1.10	0.90	1.14	1.00	1.00	1.00
24.	Brix (%)	9.20	15.50	8.90	13.50	14.50	5.80
25.	HCN (µg/100 g DM)	33.05	45.41	52.17	14.71	30.30	56.55
26.	Shoot fly incidence (%)	12.61	14.85	16.33	15.35	27.05	8.30
27.	Stem borer incidence (%)	20.51	21.00	18.34	15.35	25.00	11.75
28.	Grey leaf spot (%)	3.40	0.05	14.00	0.07	10.95	25.60
29.	Zonate leaf spot (%)	6.12	6.65	10.89	6.68	5.60	24.85
30.	Sooty stripe (%)	11.54	17.85	7.21	0.05	0.43	4.45

followed by clusters III and V (1630.68) and V and VI (1453.42), whereas, the minimum inter-cluster distance was observed between clusters II and VI (625.61). The crosses between the genotypes belonging to distantly located clusters are likely to produce good transgressive segregants and genotypes with better mean values and can be selected among all the genotypes to suit the breeding programme. Large inter-cluster distance signifies that genotypes grouped in these clusters were different from the genotypes of other clusters for one or more traits which made them so divergent from others. Results obtained in the present study are in line with those reported by Singh *et al.*, (2010), Yadav and Pahuja (2013) and Ahalawat *et al*., (2018) indicated presence of enough variability for various characters in forage sorghum conforming to the result of the present study.

The association among different genotypes is presented in the form of dendrogram (Fig.1) prepared using rescaled distances. The genotypes which are lying nearer to each other in the dendrogram are more similar to one another than those lying apart. The resemblance co-efficient between the two genotypes is the value at which their branches join. The dendrogram also showed the relative magnitude of resemblance among the genotypes in different clusters.

CONCLUSION

The result of the present study can be used as a stepping stone for evolving well defined approach in various breeding programme with specific objective for forage sorghum improvement like quality, insect pest etc. This mini core collection can usefully be utilized in combination breeding programmes for developing transgressive segregants for desirable characters along with high green and dry fodder yield.

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TABLE 3
Inter and intra-cluster distances in sorghum genotypes

	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI
Cluster I	360.73	746.66	626.89	1308.60	1325.59	1085.23
Cluster II		0.00	846.46	1431.25	974.04	625.61
Cluster III			407.70	1209.06	1630.68	819.80
Cluster IV				0.00	806.89	1645.26
Cluster V					0.00	1453.42
Cluster VI						0.00

Diagonal-Intra-cluster distances Off-diagonal - Inter-cluster distances.

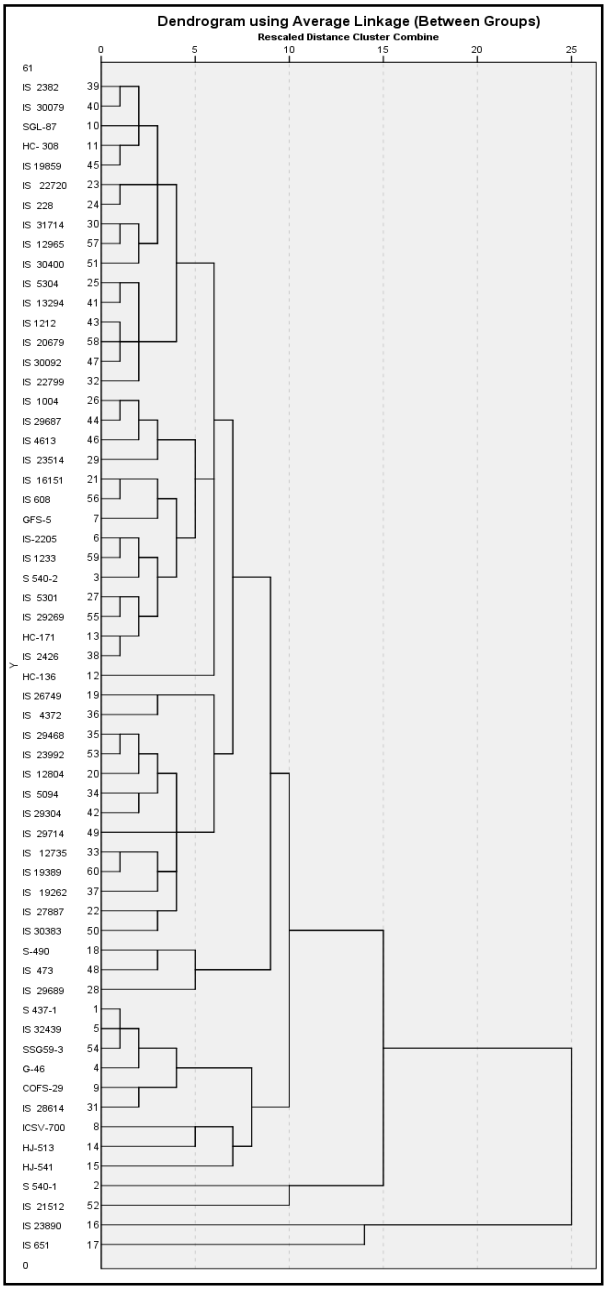

Fig. 1. Dendrogram showing the clustering pattern of different sorghum genotypes.

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