GENETIC DIVERSITY STUDY FOR IDENTIFICATION OF DUAL PURPOSE SORGHUM

SU MON THANT[1]*, PUMMY KUMARI[2], ARPIT GUAR[2] AND S. K. PAHUJA[2]

[1]Department of Agriculture Research, Yezin, Nay Pyi Taw, Myanmar
[2]Department of Genetics and Plant Breeding,
CCS Haryana Agricultural University, Hisar-125 004 (Haryana), India
(e-mail : sumonthantdarrice@gmail.com)

SUMMARY

The present investigation was carried out to assess genetic diversity in 30 sorghum genotypes based on nineteen agro-morphological and biochemical parameters during *kharif* 2019. Analysis of variance showed highly significant variations for 19 quantitative parameters in the study. Further the genetic diversity was assessed with the help of D^2 statistics and the genotypes under study were clustered into five distinct clusters. Among those clusters, Cluster-IV was the largest followed by Cluster-I and Cluster-III, each having 8, 7 and 6 genotypes, respectively. The maximum inter-cluster distance found between clusters IV and V (506.77) followed by distance between cluster III and IV (395.29). Genotypes mainly HJ 541, S 713, HJ 513, CSV 21F in these clusters are most suitable for their use as parents for development of dual purpose type genotypes in hybridization based breeding programme.

Sorghum (*Sorghum bicolor* (L.) Moench) is the fifth most important grain crop in the world. Sorghum is originated in Africa and belongs to family Poaceae and genus Sorghum. It is a diploid crop having some perennial ancestors and often cross-pollinated in nature. Cultivated sorghum is diploid with chromosome number is 20 with genome size approx. 730-megabase (Paterson. *et al.*, 2009). Being a drought tolerant crop, it is an important cereal crop in the semi-arid tropics. Beside this, it is also a moderately salt tolerant crop (Devi *et al.,* 2018). It is mainly useful for human food with grain and for animal as fodder crop with good nutritional composition (Dehinwal *et al.,* 2017). Sorghum has high nutritional value with high levels of unsaturated fats, proteins, fiber and minerals like potassium, phosphorus, calcium and iron. Sorghum is grown in more than 86 countries in area of 38 million ha in annual production and grain production of sorghum is about 58 million tones. Sorghum production in the world is about 1.5 tonnes/ha (FAO, 2018). India is an agricultural country and has the largest livestock population in the world. Availability of green fodder plays an important role in livestock security. India supports 20% of the livestock population of the world on 2.3% geographical area only (20th Livestock Census, 2019). Andhra Pradesh, Maharashtra, Karnataka, Tamil Nadu and Gujarat are major sorghum growing states of country. It is a good choice of fodder for farming community due to its high green biomass yield, wide adaption potential, fast growing nature, good ratoonability, palatability, digestibility and drought tolerance & having various potential uses like green fodder, dry roughage, hay and silage. The dual purpose sorghum includes all those sorghum genotypes which produce sufficient quality grains for human consumption and fodder for animal feed. Sorghum is utilized by animals for providing milk and meat for nourishment of human.

Sorghum has rich genetic diversity having large number of landraces and various wild relatives (Vijaylaxmi *et al.*, 2019a). Many of plant genetic resources can be utilized to produce new varieties with desired characteristics by plant breeders and which contains breeder's selectable traits like pests and diseases resistance and photosensitivity and includes yield potential and large seed size as farmer-preferred traits (Govindaraj *et al.* 2015). Forage sorghum varieties/hybrids having good quality, high fodder yield and other yield attributing traits suitable to wide range of environment is in great demand to obtain higher grain/biomass yield coupled with good quality traits.

Genetic improvement for the quantitative traits depends on the natural selection and amount of genetic variability (Choudhary *et al.,* 2015). Dual purpose sorghum also includes high green fodder yield, more stem sugar content and high grain yield. For this reasons, a good knowledge about usage of genetic resource of sorghum accessions for improving crop yield and quality

must be required. Keeping above points in view, the study was undertaken with the following objectives- to estimate genetic diversity in sorghum germplasm using agro-morphological and biochemical traits for dual purpose type.

MATERIALS AND METHODS

The experimental material consists of 30 diverse genotypes of sorghum (Table 1). The seeds of following genotypes were collected from Forage Section, Department of Genetics and Plant Breeding CCS HAU, Hisar. The field experiment was conducted in research area of Forage Section, Department of Genetics and Plant Breeding, CCS Haryana Agricultural University, Hisar during *kharif* 2019. It is situated in semi-arid sub-tropical region at $29^0=10^0$N latitude and 75^0-46^0E longitude with elevation of 215.52 m above mean sea level and weather conditions and rainfall received during *kharif* 2019 presented in Fig. 1. All the recommended agronomical practices for sorghum were followed to raise a good crop during the season. Observation were taken on five randomly selected competitive plants of each genotype in each plot for nineteen different agro-morphological and biochemical traits *viz.,* days to 50% flowering, days to maturing, plant height (cm), number of leaves/plant, no. of tillers/plant, leaf length (cm), leaf breadth (cm), leaf: stem ratio, stem diameter, green fodder yield q/ha, stover yield q/ha, dry fodder yield q/ha, grain yield q/ha, 100 grain wt. and panicle length.

Among biochemical traits, HCN content (μg/g on fresh wt. basis) using Gilchrist *et al.,* 1967 and crude protein content (%) by Micro-Kjeldhal's method were estimated and crude protein was converted into protein yield q/ha. Total soluble solids (TSS) content was estimated using refractometer. Analysis of variance (ANOVA) for the observations recorded on different characteristics was carried out as per the standard described by Panse and Sukhatme (1967). The hierarchical clustering of genotypes was performed on the Euclidean distance matrix utilizing Ward's linkage method. These analyses were done using statistical software packages of SAS 9.2 software.

RESULTS AND DISCUSSION

Analysis of variance : ANOVA has revealed that among all the genotypes under study huge genetic diversity was present. On the basis of mean performance, the highest green fodder yield and dry fodder yield was recorded for the genotypes HJ 541 and S 713, respectively. Regarding nutritional quality, lowest amount of HCN and high TSS was recorded in
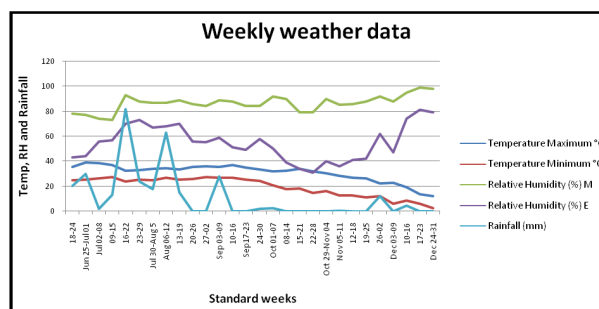

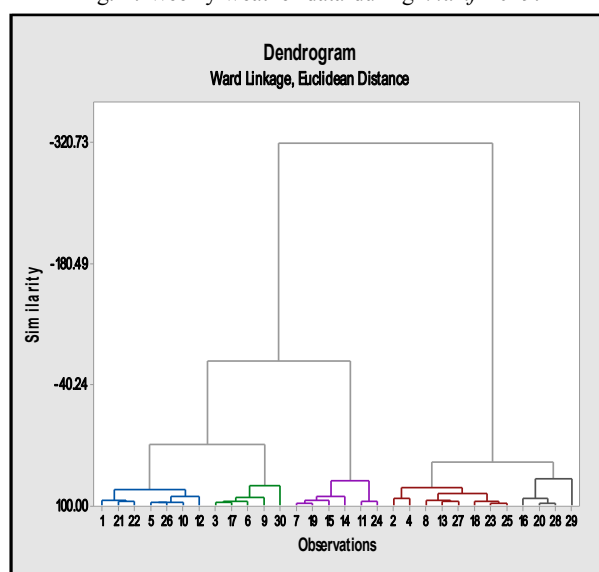Fig. 1. Weekly weather data during *kharif* 2019.

Fig. 2. Dendrogram showing the clustering pattern of different sorghum genotypes.

PC 1080 and CSV 32F, respectively. The highest amount of crude protein and crude protein yield was recorded for S 652 and HJ 541 respectively. Therefore, presence of substantial genetic diversity among the lines screened in the present study indicate that this material may serve as good source for selecting the diverse parents for dual purpose hybridization programme aimed for isolating desirable segregates (Diwakar *et al.,* 2017) in developing high grain and fodder yielding dual purpose varieties of sorghum.

Inter and Intra Cluster distance : To estimate the genetic divergence among the studied sorghum genotypes Mahalanobis D^2 distance matrix was calculated and a dendrogram was developed using Euclidean method of clustering (Fig. 2). The results revealed a substantial level of genetic divergence among the studied sorghum genotypes. The cluster analysis grouped all 30 genotypes in five different clusters (Table 2). The diagonal values represent the intra cluster distances and off-diagonal values represent the inter-cluster distances. Cluster-IV was reported to be the largest with 8 genotypes followed by Cluster-I (7),

TABLE 1
List of genotype use in study

S. No.	Genotype	S. No.	Genotype
1.	HC 136	16	CSV 15
2.	PC 3	17	PC 1080
3.	ICSV 700	18	G 46
4.	PC 7	19	S 713
5.	PC 5	20	SH 1591
6.	IS 651	21	SH 1562
7.	CSV 21F	22	CSV 32F
8.	S 722	23	SH 1574
9.	HC 171	24	CSV 30F
10.	S 652	25	IS 2205
11.	HC 308	26	HC 260
12.	GFS 5	27	SH 1532
13.	SPV 2451	28	PC 4
14.	HJ 513	29	SH 1485
15.	HJ 541	30	UTMC 1539

Cluster-III (6), cluster II (5) and cluster V(4). Intra and inter-cluster distance was calculated for different cluster as described in the Table 3. The maximum cluster distance found between clusters IV and V (506.71) followed by cluster II and IV (395.29). However, the minimum inter cluster distance was recorded between cluster II and V (114.77). Similar clustering pattern was reported by Vijaylaxmi *et al.,* 2019a among forage sorghum germplasm study.

Cluster Means : The mean values (Table 4) of all traits under study varied significantly between clusters. In cluster I maximum mean values were recorded for 100 grain weight (3.10), TSS (7.77), and protein content (8.12). In cluster II maximum mean values were recorded for HCN (43.50). The maximum mean values for no. of tillers/plant (1.689), no. of leaves/plant (20.578) and L/S ratio (0.255) was recorded in Cluster III. Cluster IV showed maximum mean value for plant height (266.56), leaf length (77.54), leaf breadth (7.8), green fodder yield (730.38), stover yield (657.61), stem diameter (13.86), dry fodder yield (172.4), grain yield (15.65), panicle length (22.80) and protein yield (13.53). Maximum values for days to 50% flowering (84.167) and days to maturity was reported in (126.66) cluster V.

The minimum mean value for plant height (213.73) was reported in Cluster I and for panicle length (20.287) was reported in cluster II. Cluster III showed minimum mean value for stem diameter (11.70) and 100 grain weight (2.66). The lowest value for days to 50% flowering (82.11) and days to maturity (124.11) and HCN (19.23) was recorded in cluster IV. The minimum value of no. of tillers/plant (1.33), no. of leaves/plant (18.03), leaf length (72.18), leaf breadth (6.845), L/S ratio (0.236), GFY (365.917), SY(318.833), DFY (88.26), TSS (6.522), PC (7.41%) and PY (6.54q/ha) in Cluster V.

The average cluster means for different characters showed that cluster IV comprised genotypes

TABLE 2
Distribution of thirty sorghum genotypes in different clusters

Cluster	No. of Genotypes	Name of Genotypes
I	7	HC 136, SH 1562, CSV 21F, PC 5, HC 260, S 652, GFS 5
II	5	ICSV 700, PC 1080, IS 651, HC 171, UTMC 1539
III	6	CSV 21F, S 713, HJ 541, HJ 513, HC 308, CSV 30F,
IV	8	PC 3, PC 7, S 722, SPV 2451, SH 1532, G 46, SH 1574, IS 2205
V	4	CSV 15, SH 1591, PC 4, SH 1485

TABLE 3
Inter and intra-cluster distance matrix of 30 sorghum genotypes

		Cluster				
		1	2	3	4	5
Cluster	1	0.00				
	2	239.86	0.00			
	3	116.67	128.89	0.00		
	4	161.61	**395.29**	267.54	98.72	
	5	352.84	114.77	239.62	**506.77**	0.00

with high green fodder yield, plant height, leaf length, leaf breadth, stem diameter, stover yield, dry fodder yield, grain yield, panicle length and protein yield and low HCN (low value is desirable) so these genotypes can be utilized as a parent in crossing programme towards breeding of genotype with more dry matter, high grain yield and good quality with low HCN content which is an important fodder quality parameter or we can say dual purpose genotypes breeding having early maturity. High crude protein content, 100 grain weight and high TSS content was reported in cluster I. Number of tillers/plant and number of leaves/plant were maximum in the cluster III.

The crosses between the genotypes belonging to distantly located clusters IV and V are likely to produce good transgressive segregants and genotypes with better mean values. They can be selected among all the genotypes to suit the dual purpose sorghum genotype 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 Yadav *et al.,* 2003, Damor *et al.,* 2018, Doijad *et al.* (2016), Jain and Patel (2016) and Vijaylaxmi *et al.,* 2019b.

CONCLUSION

The maximum inter-cluster distance found between clusters IV and V (506.77) having genotypes

TABLE 4
Cluster means for nineteen traits of sorghum genotypes

Variables	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V
Days to 50% flowering	82.476	83.958	83.133	**82.111**	**84.167**
Days to maturity	124.143	126.417	125.400	**124.111**	**126.667**
Plant height	**213.735**	214.640	239.704	266.563	223.142
No of tillers/plant	1.476	1.417	**1.689**	1.407	**1.333**
No of leaves/plant	19.683	19.208	**20.578**	19.056	**18.083**
Leaf length	75.235	75.786	73.860	**77.546**	**72.186**
Leaf breadth	7.385	7.425	7.126	**7.859**	**6.845**
Stem diameter	12.924	12.158	**11.709**	**13.860**	11.871
L/S ratio	0.250	0.253	**0.255**	0.254	**0.236**
Green fodder yield	613.524	446.175	532.667	**730.378**	**365.917**
Stover yield	561.586	396.846	484.533	**657.617**	**318.833**
Dry fodder yield	151.857	108.099	131.208	**172.415**	**88.260**
Grain yield	13.522	12.344	12.615	**15.650**	**12.177**
Panicle length	20.724	**20.287**	20.871	**22.807**	21.247
100 grain wt.	**3.103**	2.827	**2.660**	3.049	2.741
TSS Content	**7.775**	7.340	6.796	7.259	**6.522**
HCN content	22.401	**43.509**	27.056	**19.231**	30.803
Protein content	**8.128**	7.692	7.460	7.847	**7.415**
Protein yield	12.349	8.318	9.789	**13.531**	**6.546**

in both clusters PC 3, PC 7, G 46, IS 2205, CSV 15, PC 4 etc. followed by distance between cluster III and IV (395.29) having genotypes CSV 21F, S 713, HJ 541, HJ 513, HC 308, CSV 30F, PC 3, PC 7, G 46, IS 2205 in both clusters. In combination breeding programmes genotypes of cluster IV and III can be tested for developing high grain yielding genotypes high green biomass yield.

ACKNOWLEDGEMENT

REFERENCES

20th Livestock Census, 2019 : http://dahd.nic.in/about-us/divisions/statistics.

Choudhary, Sunita, P. Singh, B. K. Hooda and R. K. Arya, 2015 : Multivariate analysis of pearl millet data to delineate genetic variation. *Forage Res.,* **40** : 201-208.

Damor, H. I., H. P. Parmar, D. P. Gohil, and A.A. Patel, 2018 : Genetic variability, character association, path coefficient in forage sorghum (*Sorghum bicolour* L. Moench). *Green Farming*, **9** : 218-233.

Dehinwal, A. K., S. K. Pahuja, M. Shafiqurrahaman and Anil Kumar, 2017 : Assessment of quality components in multicut forage sorghum in different environments. *Forage Res.,* **43** : 151-155.

Devi, S., Satpal, H. S. Talwar, Ramprakash and V. Goyal, 2018 : Performance of sorghum [*Sorghum bicolor* (L.) Moench] under salt stress. *Forage Res.,* **44** : 209-212.

Diwakar, A., B.R. Ranwah, P. Diwaker, Namrata and P. Bisen, 2017 : Genetic Divergence Study in Forage Sorghum [Sorghum bicolor (L.) Moench]. *Indian Journal of Ecology* Special Issue, **44** : 834-837.

Doijad, S. B., A. B. Bagade and A.W. More, 2016 : Evaluation of sorghum germplasm for genetic diversity using D² statistics. *Electronic J. Plant Breed.* **7** : 934-938.

FAO, 2018. Web:http://www.fao.org/faostat/en/data / QC.

Gilchrist, D. G., W. E. Lueschen and C. N. Hittle, 1967 : Revised Method for the Preparation of Standards in the Sodium Picrate Assay of HCN 1. *Crop Science*, **7** : 267-268.

Govindaraj. M., M. Vertiventhan and M. Srinivasan, 2015 : Importance of genetic assessment in crop plants and its recent advance: an overview of its analysis perspectives. *Genetics Research Int.* Volume 2015, Article ID 431487.

Jain, S. K and P. R. Patel, 2016 : Principal component and cluster analysis in sorghum (*Sorghum bicolor* (L.) Moench). *Forage Res.* **42** : 90-95.

Panse, V. G. and P. V. Sukhatme, 1967 : Statistical methods for agricultural workers 2nd enlarge edition ICAR New Delhi.

Paterson, A. H., J. E. Bowers, R. Bruggmann, I. Dubchak, J. Grimwood, H. Gundlach and J. Schmutz, 2009 : The Sorghum bicolor genome and the diversification of grasses. *Nature*, **457** : 551-556.

Vijaylaxmi, S. K. Pahuja and P. Kumari and U. N. Joshi, 2019a : Genetic divergence studies for agro-morphological, insect pest and quality parameters in mini core collection of forage sorghum. *Forage Res.* **44** : 237-241.

Vijaylaxmi, S. K. Pahuja and P. Kumari, 2019b : Identification of New Sources for Good Quality High Biomass Yield and other Promising Traits in Mini Core Collection of Forage Sorghum. *Ind. J. Plant Genetic Resources*, **32** : 150-157.

Yadav, R., S. K. Pahuja and R. P. S. Grewal, 2003 : Evaluation of phenotypic variability in forage sorghum genotypes collected from western Uttar Pradesh using multivariate analysis. *Forage Res.* **29** : 123-128.