Forage Res., **42** (3) : pp. 176-179 (2016) **http://forageresearch.in**

GENETIC DIVERGENCE IN FODDER SORGHUM (*SORGHUM BICOLOR* (L.) MOENCH)

VISHWANATH MEENA*, A. K. MEHTA AND MONIKA JYOTI KHUJUR

Department of Plant Breeding & Genetics
Jawaharlal Nehru Krishi Vishva Vidyalaya,
Jabalpur-482 004 (M. P.), India
**(e-mail : vishwanathmeeena@555gmail.com)*

(Received : 18 October 2016; Accepted : 24 December 2016)

SUMMARY

Sixty-two sorghum genotypes were analyzed for genetic divergence which resulted in 10 clusters having maximum inter-cluster distance between clusters II and IX and least between clusters VI and VIII. Maximum intra-cluster distance was exhibited by cluster IX followed by cluster VII. Putative lines selected were from cluster IX (E 169, GGUB 41, GGUB 59 and ICSR 93025) for leaf : stem ratio, green fodder yield per plant, green fodder yield per plant per day, dry matter yield per plant, dry matter yield per plant per day, crude protein yield per plant, plant height and internodal length; cluster IV (E 219 and ELG 24) for green fodder yield per plant, dry matter yield per plant, crude protein yield per plant, brix's value and plant height. These lines can be used as patents in different hybridization programmes to obtain maximum variation for further selection.

Key words : Genetic divergence, fodder yield, protein, sorghum

Sorghum [*Sorghum bicolor* (L.) Moench] is one of the five major millet crops in the world. It is native of Africa and potentially rich in genetic variability. Early introduction in Asia led to further diversity. It is cultivated in more than 100 countries, out of which 59 per cent of world sorghum area is in Africa and 25 per cent in Asia. Asia alone contributes 45 per cent of world sorghum production (Iqbal *et al.*, 2010).

Genetic variability in the "*sine quanon*" of crop improvement programme. Selection is said to be effective in populations having large heritability. It is the genetic fraction of the observed variation that provides a measure of transmissibility of variation under study and response to selection (Jain and Patil, 2012). Breeding programme primarily aims at improving the yield components and the pre-requisite for its success is the knowledge of nature and degree of divergence in the existing germplasm (Jain and Patil, 2016). Hence, information on genetic diversity is used to identify putative genotypes, which may be used as parents in various breeding strategies.

MATERIALS AND METHODS

The experiment was laid out in randomized complete block design with three replications having plot size 2 x 1.6 m^2 and keeping row to row distance 40 cm. The experiment was conducted at Seed Breeding Farm, Department of Plant Breeding & Genetics, JNKVV, Jabalpur (M. P.), India. The soil of experimental field was heavy black, clayey, uniform in its topography and free from waterlogged condition. It is deep, well drained alluvial in origin and has fairly good moisture holding capacity. The germplasm consisted of 62 genotypes. At 50 per cent flowering, five competitive plants were tagged from each replication of each germplasm and data were recorded for days to 50 per cent flowering, plant height (cm), number of leaves per plant, internodal length, penultimate leaf area (cm^2), stem girth (cm), leaf : stem ratio, tillers per plant, green fodder yield per plant (g), green fodder yield per plant per day (g), dry fodder yield per plant (g), dry fodder yield per plant per day (g), crude protein yield per plant (g), crude protein yield per plant per day (g) and Brix's value (%). Estimation of degree of divergence was analyzed by Mahalanobis (1936) D^2 statistics among different pairs of statistics. While method suggested by Rao (1952) was followed for computing D^2 values and for determining group constellations.

RESULTS AND DISCUSSION

The analysis of variance showed highly

significant differences within the population for all the 15 characters studied. This suggested that the genotypes under investigation consisted of sufficient amount of diversity and also indicated that this material was appropriate for estimation of further analysis. On the basis of D^2 values, the 62 genotypes were grouped into 10 clusters following Tocher's method. The clusters I & II, the largest clusters, were polygenotypic (12 genotypes) followed by cluster III with nine genotypes, clusters IV, VII and IX with five genotypes and clusters VI, VII and X with each have (monogenotypic) 1 genotype. Significant amount of variability can be inferred from the pattern of group constellation (Table 1). This revealed that pattern of clustering of genotypes did not depend upon its geographical origin. It means the genotypes from same geographical origin do not group together i.e. genetic constituent of the genotypes is dominant. Clustering between genetic diversity and geographical diversity is in agreement with that of Roquib and Das (1995), Singh *et al.* (1999) and Basavaprabhu *et al.* (2013).

The inter- and intra-average distance among 10 clusters were computed and presented in Table 2. The highest inter-cluster divergence was observed among genotypes of clusters II and IX (D^2=2527.38) followed by clusters V and IX (D^2=1597.49), clusters VII and IX (D^2=1516.78), clusters II and III (D^2=1297.73), whereas least inter-clusters divergence was observed among genotypes of clusters VI and VIII (D^2=30.83).

The intra-cluster distance was highest in the cluster IX (130.86) followed by cluster VII (128.75). It can be observed that the intra-cluster distance was much less than the inter-cluster distance, indicating homogeneity within the clusters and heterogeneity between the clusters.

Analysis of cluster mean (Table 3) revealed that cluster IX had highest mean value for green fodder yield per plant (438.45 g), plant height (165.55 cm), dry matter yield per plant (87.53), crude protein yield per plant (7.31 g), green fodder yield per plant per day (4.31 g) and crude protein yield per plant per day (0.063 g). Whereas number of leaves per plant, leaf : stem ratio, tillers per plant and Brix's value were highest in cluster X. Cluster

TABLE 1
Cluster composition based on D^2 statistics in fodder sorghum genotypes

Cluster	No. of genotypes	Name of genotypes
I	12	E 202, EG 90, ICSV 12015, E 189, E 246, E 233, GGUB 63, Raj 20, ELG 13, GGUB 51, NLC 56, GGUB 3
II	12	E 252, ELG 2, GGUB 13, EG 241, E 20, EG 53, Raj 36, GGUB 43, E 242, MP Chari, ICSV 25306, ICSR 93022
III	9	E 248, ER 9, EG 20, GGUB 11, ICS 28001, GGUB 68, E 195, Raj 34, GGUB 30
IV	5	E 219, ELG 24,ICSV 12008, ICSV 12018, ICS 14002
V	11	ICSR 14006, SSG 59-3, E 207, GGUB 55, NLC 62, E 234, ICSV 25316, E 210, Raj 21, E 219, ICSV 93046
VI	1	ICSV 12012
VII	5	S 35, E 223, ICSR 93034, NTJ 2, ICSV 12006
VIII	1	ICSV 12013
IX	5	E 169, GGUB 41, GGUB 59, ICSR 93025, ICSR 93026
X	1	ICSV 25308

TABLE 2
Average intra (diagonal and bold) and inter-cluster distance (D^2) values in fodder sorghum

Cluster	I	II	III	IV	V	VI	VII	VIII	IX	X
I	**51.19**									
II	468.57	**67.16**								
III	330.71	1297.73	**78.50**							
IV	270.79	1220.51	312.59	**91.52**						
V	156.75	207.68	726.04	586.98	**95.50**					
VI	160.68	756.56	132.22	385.82	393.21	**0.00**				
VII	369.43	499.23	553.15	961.76	415.78	229.58	**128.75**			
VIII	288.11	975.22	137.41	512.17	581.03	30.83	276.25	**0.00**		
IX	943.29	2537.58	346.37	470.46	1597.49	698.55	1516.78	669.59	**130.86**	
X	122.63	580.62	544.20	224.94	208.04	375.97	718.78	548.48	1060.18	**0.00**

TABLE 3
Cluster mean for yield and its component traits of 62 genotypes in fodder sorghum

Clusters	Days to 50% flowering	Plant height	No. of leaves/ plant	Internodal length	Penultimate leaf area	Stem girth	Leaf : stem ratio	Tillers/ plant	Green fodder yield/ plant	Green fodder yield/ plant/ day	Dry matter yield/ plant	Dry matter yield/ plant/ day	Crude protein yield/ plant	Crude protein yield/ plant/ day	Brix's value
I	74.92	149.41	9.39	24.34	272.15	1.36	0.47	3.50	314.53	3.39	60.64	0.78	4.79	0.053	15.80
II	71.72	162.35	7.94	24.05	264.97	1.53	0.40	4.17	222.41	2.74	41.39	0.58	3.33	0.050	15.97
III	81.33	162.19	9.07	24.62	304.31	1.43	0.44	4.44	359.12	3.86	69.59	0.87	5.51	0.057	17.33
IV	74.13	132.21	9.07	22.76	287.33	1.64	0.39	4.07	384.19	4.29	76.00	0.93	5.53	0.062	18.13
V	72.58	160.68	9.33	22.23	316.78	1.48	0.39	4.00	277.02	3.04	52.73	0.67	4.23	0.049	17.34
VI	80.00	125.40	8.67	16.17	372.00	1.80	0.53	5.00	315.10	3.44	64.00	0.84	4.93	0.063	17.83
VII	80.93	140.63	9.47	22.03	308.43	1.77	0.34	3.47	253.37	3.07	45.60	0.57	3.77	0.040	16.70
VIII	82.00	137.47	10.3	15.33	393.22	1.83	0.78	3.00	316.15	3.67	72.00	0.84	5.82	0.063	17.00
IX	81.93	165.55	10.7	24.01	334.00	1.48	0.45	4.60	438.45	4.31	87.53	0.85	7.31	0.063	17.10
X	71.00	113.80	11.3	16.22	307.14	1.57	0.79	6.00	332.56	3.50	63.00	0.83	3.82	0.043	19.30

TABLE 4
Percentage contribution of characters towards divergence in fodder sorghum

S. No.	Characters	No. of times ranked first	Percentage contribution towards divergence
1.	Days to 50% flowering	599	31.68
2.	Plant height	11	0.58
3.	Np. of leaves/plant	0	0
4.	Internodal length	10	0.53
5.	Penultimate leaf area	2	0.11
6.	Stem girth	0	0
7.	Leaf : stem ratio	39	2.06
8.	Tillers/plant	2	0.11
9.	Green fodder yield/plant	1202	63.56
10.	Green fodder yield/plant/day	3	0.16
11.	Dry matter yield/plant	0	0
12.	Dry matter yield/plant/day	1	0.05
13.	Crude protein yield/plant	0	0
14.	Crude protein yield/plant/day	17	0.9
15.	Brix 's value	5	0.26

VIII had highest mean value for days to 50 per cent flowering, penultimate leaf area and stem girth. Cluster III had maximum internodal length (24.62 cm) and cluster IV had maximum dry matter yield per plant per day (0.93 g). Difference in relative contribution of different characters (Table 4) for genetic divergence (D^2) was highest for green fodder yield per plant (63.56%) followed by days to 50 per cent flowering (31.68%), leaf : stem ratio (2.06%), plant height (0.58%), internodal length (0.53%), Brix's value (0.26%), green fodder yield per plant per day (0.16%), penultimate leaf area and tillers per plant (0.11%), crude protein yield per plant per day (0.9%) and dry matter yield per plant per day (0.05%). Number of leaves per plant,stem girth, dry matter yield per plant and crude protein yield per plant had no contribution towards divergence.

From the present investigation, it can be concluded that parent lines selected from cluster IX (E 169, GGUB 41, GGUB 59 and ICSR 93025) for leaf : stem ratio, green fodder yield per plant, green fodder yield per plant per day, dry matter yield per plant, dry matter yield per plant per day, crude protein yield per plant, plant height and internodal length; cluster IV (E 219 and ELG 24) for green fodder yield per plant, dry matter yield per plant, crude protein yield per plant, Brix's value and plant height could be used to achieve desired segregants for the crossing programme and broaden the genetic base of future genotypes.

REFERENCES

Basavaprabhu, N. M., Niranjana, Murthy, M. Asif, K. T. Venkatesha, and K. V. Vijay Kumar. 2013 : Genetic divergence analysis in ricebean, *Vigna umbellata* (L.). *Internat. J. Plant Sci.,* **8** : 166-168.

Jain, S. K. and P. R. Patel. 2012 : Genetic variability in land races of forage sorghum [*Sorghum bicolor* (L.) Moench] collected from different geographical orgin of India. *Int. J. Agri. Sci.* **4** : 182-165.

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

Iqbal, A., B. Sadia, A. I. Khan, F. S. Awan, R. A. Kainth, and H. A. Sadaqat. 2010 : Biodiversity in the sorghum [*Sorghum bicolor* (L.) Moench] germplasm of Pakistan. *Genet. Mole. Resistance,* **9** : 756-764.

Mahalanobis, P. C. 1936 : On the generalized distance in statistics. *Proc. Nat. Acad. Sci. : Indian,* **12** : 49-55.

Rao, C. R. 1952 : D^2 analysis. In : *Advanced Statistical Methods in Biometrical Research.* John Wiley and Sons Inc., New York. pp. 357-363.

Roquib, M. A. and M. Das. 1995 : Genetic divergence in rice bean (*Vigna umbellata*). *Advances in Plant Sciences,* **8** : 312-318.

Singh, M. R. K., P. R. Sharma, and L. I. Singh. 1999 : Genetic divergence among rice bean (*Vigna umbellata* (Thumb) Owhi and Ohashi) cultivars of Manipur hills. *Indian J. Genet. and Plant Breed.,* **59** : 221-225.