Journal of Pharmacognosy and Phytochemistry

Swamy N
Ph.D Scholor, Dept. of Genetics and Plant Breeding, College of Agriculture Raichur, University of Agricultural Sciences, Raichur, Karnataka, India

Biradar BD
Dept. of Genetics and Plant Breeding, University of Agricultural Sciences, Dharwad, Karnataka, India

Muttappa Hosamani
Ph.D Scholar, Dept. of Genetics and Plant Breeding, College of Agriculture Raichur, University of Agricultural Sciences, Raichur, Karnataka, India

Sajjanar GM
All India Coordinated Sorghum Improvement Project, RARS, Vijayapur, UAS, Dharwad, Karnataka, India

Ashwathama VH
All India Coordinated Sorghum Improvement Project, RARS, Vijayapur, UAS, Dharwad, Karnataka, India

Sajjan AS
Dept. of Seed Science and Technology, College of Agriculture, Vijayapur, UAS, Dharwad, Karnataka, India

Biradar AP
All India Coordinated Sorghum Improvement Project, RARS, Vijayapur, UAS, Dharwad, Karnataka, India

Genetic diversity analysis for productivity traits in *rabi* sorghum [*Sorghum bicolor* (L.) Moench]

Swamy N, Biradar BD, Muttappa Hosamani, Sajjanar GM, Ashwathama VH, Sajjan AS and Biradar AP

Abstract
A field experiment was conducted in Regional Agricultural Research Station, Bijapur, Karnataka using 122 *rabi* sorghum genotypes to assess the genetic diversity. The analysis of variance revealed significant differences among the genotypes for all the traits studied. Mahalanobis D^2 statistics was applied to assess the divergence among genotypes. Among the 11 quantitative characters studied, days to 50% flowering contributed maximum (34.53%) to the total divergence. All the genotypes were grouped into nine clusters and cluster I was largest with 88 genotypes, followed by cluster IV, II and V (17, 10 and 2 genotypes respectively) and remaining clusters (III, VI, VII, VIII and IX) were solitary in nature. Maximum intra cluster distance was shown by cluster II (4.46) and maximum inter cluster distance (11.32) was noticed between the clusters V and IX indicating that the crosses between genotypes of these different clusters could manifest heterosis and better recombinants after hybridization.

Keywords: *rabi* sorghum, productivity traits, D^2 analysis, genetic diversity

Introduction

Sorghum [*Sorghum bicolor* (L.) Moench] (2n=2x=20) is the fifth most important cereal crop in the world after wheat, rice, maize and barley in terms of production and utilization. In India, it is grown in both *kharif* and *rabi* seasons as a dual purpose crop serving both grain and fodder requirements of the farming community. The total sorghum production in India is around 4.238 m t from an area of 6.077 m ha with an productivity of 697 kg/ha (Anon., 2016) [1]. However, the productivity in *kharif* is higher compared to *rabi*. This gap is mainly due to the large-scale cultivation of highly heterotic hybrids in *kharif* while in *rabi* the stable and high yielding varieties suited to residual moisture stress situations are not available. Over decades, hybridization techniques for development of high yielding varieties and hybrids has increased the yield levels of sorghum for which genetic diversity among selected parents is an essential pre requisite. Diverse parents are expected to yield hybrids that exhibit more heterotic expression in addition to generating a broad spectrum of variability in segregating generations. Mahalanobis's generalized distance occupy a unique place and is an efficient method to know the extent of genetic diversity among genotypes. The present study is an attempt to assess the genetic divergence in selected genotypes of *rabi* sorghum using D^2 statistics.

Materials and Methods

The present investigation was carried out during *rabi* season 2013-14 at Regional Agricultural Research Station (RARS), Bijapur, Karnataka. A total of 122 genotypes (IS lines, selected B and R lines and released varieties) along with checks collected from All India Co-ordinated Sorghum Improvement Project, RARS, Bijapur were used for the study. The design adopted was randomized block design with two replications. Observations on various yield and its component characters were recorded. The data was subjected to statistical analysis using D^2 statistics (Mahalanobis, 1936) [2] and Tocher's method as described by Rao (1952) [3] for determining group constellation. Average inter and intra cluster distances were estimated as per the procedure outlined by Singh and Choudhary (1977) [4].

Results and Discussion

The mean sum of squares of different characters pertaining to yield and yield components were highly significant for all the 11 characters studied indicating greater distinctness among 122 *rabi* sorghum genotypes (Table 1). Genetic divergence (D^2) is the basis of variability and helps to craft the designed genotypes as per the requirement. The present study aims at analyzing the genetic diversity among 122 genotypes. Among the 11 productivity traits studied, the days to 50 percent flowering contributed maximum (34.53%) to the total divergence (Table 2).

Correspondence
Swamy N
Ph.D Scholar, Dept. of Genetics and Plant Breeding, College of Agriculture Raichur, University of Agricultural Sciences, Raichur, Karnataka, India

This was followed by panicle length (15%), stover weight (11.54%), panicle girth (11.37%), panicle weight (6.60%), plant height (5.41%), grain yield (5%), days to physiological maturity (3.96%) and 1000-grain weight (3.92%). The character SPAD at flowering and maturity did not contribute significantly to the total divergence. Similar instances for contribution of characters towards the divergence were recorded by Ganesamurthy *et al.* (2010) [5], Mahajan *et al.* (2010) [6] and Jain and Patel (2013) [7].

Table 1: Mean sum of squares for yield and yield components in 122 *rabi* sorghum genotypes at Bijapur during 2013-14

Traits	Replication	Genotypes	Error	S.Em.±	CD 5%
Degrees of freedom	1	121	121		
		Mean squares			
Days to 50% flowering	5.31	134.26**	7.79	1.97	5.53
Days to physiological maturity	36.99	51.89**	9.49	2.17	6.10
SPAD at flowering	0.10	59.19**	36.48	4.25	11.96
SPAD at physiological maturity	0.36	33.21*	22.67	3.35	9.43
Plant height (cm)	2149.39	1794.87**	624.45	17.60	49.47
Panicle length (cm)	6.86	33.99**	4.12	1.43	4.02
Panicle girth (cm)	1.08	9.21**	3.18	1.26	3.53
Panicle weight per plant (g)	494.96	610.52**	127.88	7.96	22.39
Stover weight per plant (g)	490.95	3581.77**	706.88	18.72	52.64
Grain yield per plant (g)	215.37	330.72**	73.86	6.05	17.02
1000-grain weight (g)	8.58	89.64**	27.21	3.67	10.33

* - Significant at 5%, ** - Significant at 1%

Table 2: Per cent contribution of yield and yield components towards divergence in 122 *rabi* sorghum genotypes.

Sl. No.	Traits	Times ranked	% contribution
1.	Days to 50% flowering	2549	34.53
2.	Days to physiological maturity	292	3.96
3.	SPAD reading at flowering	154	2.09
4.	SPAD reading at physiological maturity	44	0.60
5.	Plant height (cm)	399	5.41
6.	Panicle length (cm)	1107	15.00
7.	Panicle girth (cm)	839	11.37
8.	Panicle weight per plant (g)	487	6.60
9.	Stover weight per plant (g)	852	11.54
10.	Grain yield per plant (g)	369	5.00
11.	1000-grain weight (g)	289	3.92
	Total	7381	100.00

The distribution pattern (Table 3) of 122 genotypes into 9 clusters revealed that, among the 9 clusters, cluster I was the largest with 88 genotypes, followed by cluster IV (17 genotypes), cluster II (10 genotypes) and cluster V (2 genotypes). The remaining clusters, *viz.*, cluster III, VI, VII, VIII and IX were solitary in nature. The study indicated that the genotypes from different origins may be grouped into single cluster. The genotype of solitary clusters may be of distinct and unique in many respects and therefore can be extensively used in future breeding programme.

Table 3: Distribution of 122 *rabi* sorghum genotypes into 9 clusters for yield and yield components at Bijapur during 2013-14.

Cluster No.	No. of genotypes	Name of the genotypes
I	88	RL – 3, RL – 9, RL – 7, RL – 8, EP 61, RL – 6, RL – 15, RL – 1, IS 40791, RL – 14, M-35-1 (2), M 35-1 (6), RL – 4, M -35-1 (7), RL – 26, RL – 12, DSV – 5, RL – 13, RL – 5, IS 6351, RL – 11, BL – 1, IS 33756, BJV - 44, BL – 12, BL – 10, BL – 2, IS 40799, IS 40798, IS 40824, IS 33845, IS 40778, BL – 3, BL – 11, BL – 9, IS 40820, 5-4-1, BL – 8, RL – 10, RL – 18, RL – 17, BL – 6, RL – 24, CSV - 22 (5), CSV - 29R, BL – 13, RL – 21, M-35-1 (3), Phule Anuradha -3, Br-33, RL – 25, RL – 22, IS 5919, BL – 5, IS 40772, IS 25732, IS 2872, BL – 4, IS 40245, BL – 14, RL – 16, RL – 20, RL – 19, IS 30443, CSV 22 (2), IS 4698, LG 48, PEC 7, IS 5295, IS 2902, IS 40209, BL – 7, BL – 19, M 35-1 (5), IS 27912, Phule Anuradha -1, M 35-1 (1), LG 11, IS 40180, IS 30508, IS 40805, M 35-1 (4), Phule Maulee -3, IS 26025, IS 4576, CSV 22 (1), IS 29654, IS 30451
II	10	IS 13549, IS 7679, Phule Maulee -2, CSV 22 (4), IS 22720, Phule Anuradha -2, IS 16151, IS 9314, CSV 22 (3), IS 21863
III	1	EP 59
IV	17	EP 94, LG 33, EP 117, LG 47, IS 4578, IS 40251, IS 40182, IS 33853, IS 40752, IS 5676, IS 33763, LG 34, NIC 12, EP 87, LG 1, IS 36377, EP 97
V	2	IS 3121, Phule Anuradha -4
VI	1	IS 4951
VII	1	IS 29914
VIII	1	Phule Maulee -1
IX	1	IS 40813

The average D² values of intra and inter cluster distances (Table 4) revealed that the inter cluster distances are higher than the intra cluster distances indicating the presence of wider genetic diversity between the clusters rather than within the clusters. The intra cluster distances varied from 0.00 (cluster III, VI, VII, VIII and IX) to 4.46 (cluster II) revealing presence of divergent genotypes within different clusters. Maximum distance among the genotypes within the same clusters (intra cluster) was shown by cluster II (4.46) followed by cluster IV (4.32), cluster I (4.11) and cluster V (3.19). The maximum inter cluster distance (11.32) was noticed between the clusters V and IX. The lowest inter cluster distance was recorded between clusters III and IV (3.99). The genotypes belonging to the clusters having maximum inter cluster distance (cluster V vs IX, VII vs IX and VII vs VIII) needs to be chosen for further crossing programme and are likely to give heterotic hybrids or transgressive segregants in F₂.

Table 4: Average D² values of intra and inter cluster distances among 122 *rabi* sorghum genotypes.

Cluster	I	II	III	IV	V	VI	VII	VIII	IX
I	4.11	7.68	6.01	6.69	6.47	5.50	6.27	9.21	8.84
II		4.46	9.49	9.85	6.42	8.53	10.56	8.96	9.05
III			0.00	3.99	10.05	6.93	8.46	7.36	6.64
IV				4.32	9.92	7.72	8.75	6.63	7.49
V					3.19	7.71	8.56	10.63	11.32
VI						0.00	7.52	9.55	9.84
VII							0.00	11.27	11.29
VIII								0.00	8.60
IX									0.00

Diagonal values indicates intra cluster distances and off diagonal indicates inter cluster distances.

The cluster mean values estimated across genotypes for eleven characters are presented in Table 5. Minimum cluster mean values for days to fifty per cent flowering and days to physiological maturity was recorded in cluster IX. It reveals that genotypes included in these clusters can be exploited in breeding programme for earliness. Similar results were reported by Kadam *et al.* (2001) [8] and Patankar *et al.* (2005) [9].

The highest mean values for grain yield, panicle weight, panicle girth, 1000-grain weight, plant height and stover weight were scored by solitary cluster VII. Similarly, the cluster IV had the higher mean values for panicle girth, stover weight, grain yield and 1000-grain weight, the cluster I had next best mean values for panicle girth, panicle weight and grain yield. Therefore the results suggest that the genotypes belonging to the clusters VII, cluster IV and cluster I were most useful and can be further evaluated for their stability across environments and used for future breeding programme. The cluster VII with 1 genotype (IS 29914) ranked first and this genotype appears to be most potential one (Table 5). This genotype can be tested across years and locations and if found stable and high yielding can be released as new variety. In addition, the cluster I (88 genotype), VIII (Phule Maulee -1) and IV (17 genotype), which ranked 2ⁿᵈ, 3ʳᵈ, and 4ᵗʰ respectively were also most promising and these genotypes could be considered for further improvement programme.

In view of considerable genetic diversity found in the present study, there is sufficient scope for genetic improvement through hybridization between the genotypes belonging to divergent clusters.

Table 5: Cluster mean values of 9 clusters in 122 *rabi* sorghum genotypes for yield and yield components.

Character → Cluster ↓	Days to 50% flowering	Days to physiological maturity	SPAD reading at flowering	SPAD reading at maturity	Plant height (cm)	Panicle length (cm)	Panicle girth (cm)	Panicle weight/ plant (g)	Stover weight/ plant (g)	Grain yield/plant (g)	1000-grain weight (g)	Overall Score	Rank
I	81.14 (5)	124.34 (4)	44.27 (5)	25.41 (2)	165.72 (5)	14.22 (6)	13.46 (3)	56.45 (2)	122.55 (4)	43.11 (2)	35.90 (4)	42	2
II	83.10 (8)	126.10 (7)	49.50 (3)	24.50 (4)	165.22 (7)	24.40 (1)	9.59 (8)	31.17 (8)	51.26 (7)	28.57 (7)	25.10 (7)	67	7
III	68.00 (4)	121.00 (2)	37.40 (9)	13.17 (9)	117.67 (8)	10.17 (8)	12.87 (5)	39.59 (6)	82.75 (5)	34.10 (5)	40.14 (2)	63	6
IV	63.32 (3)	121.59 (3)	43.98 (6)	18.43 (8)	165.59 (6)	11.85 (7)	13.52 (2)	51.84 (4)	135.87 (3)	39.56 (3)	38.79 (3)	48	4
V	90.00 (9)	133.00 (9)	53.29 (1)	24.34 (5)	179.63 (3)	20.83 (2)	10.55 (7)	50.04 (5)	158.38 (2)	33.27 (6)	18.49 (8)	57	5
VI	83.00 (7)	126.00 (6)	42.54 (8)	24.30 (6)	172.67 (4)	8.84 (9)	13.02 (4)	39.00 (7)	40.75 (8)	25.85 (8)	17.77 (9)	76	9
VII	82.00 (6)	125.00 (5)	43.72 (7)	25.57 (1)	219.50 (1)	17.00 (4)	17.14 (1)	136.00 (1)	167.59 (1)	76.28 (1)	43.35 (1)	29	1
VIII	59.00 (2)	131.50 (8)	51.24 (2)	24.70 (3)	184.34 (2)	18.50 (3)	12.02 (6)	53.67 (3)	75.00 (6)	36.09 (4)	34.11 (5)	44	3
IX	58.50 (1)	101.50 (1)	44.37 (4)	22.84 (7)	101.83 (9)	16.17 (5)	7.67 (9)	24.00 (9)	23.58 (9)	21.35 (9)	25.48 (6)	69	8

Figures in the parenthesis, indicate the ranks/grade based on cluster mean. For days to 50% flowering & days to physiological maturity grade given smallest to largest, while for the rest largest to smallest. Overall score is the summation of rank numbers for 11 characters. Hence, the cluster which gets lowest score will get 1ˢᵗ rank.

References
1. Anonymous. (Indiastat.com), 2016. https://www.indiastat.com/table/agriculture/2/jowargreat millet/17197/7266/data.aspx
2. Mahalanobis PC. On the generalized distance in statistics. In: Proceed. Nat. Acad. Sci., India. 1936; 2:49-55.
3. Rao CR. Advanced Statistical Methods in Biometrical Research, John Wiley and Sons, New York, 1952.
4. Singh RK, Chaudhary BD. Biometrical Methods in Quantitative Genetic Analysis, Kalyani Publishers, New Delhi, 1977.

5. Ganesamurthy K, Punitha D, Elangovan, M. Genetic diversity among the land races of sorghum collected in Tamil Nadu. Electronic J Plant Breed. 2010; 1(6):1375-1379.
6. Mahajan RC, Wadikar PB, Pole SP. Genetic diversity studies in sorghum (*Sorghum bicolor* L. Moench). Res. J Agri. Sci. 2010; 1(4):332-334.
7. Jain SK, Patel PR. Multivariate analysis in sorghum [*Sorghum bicolor* L.) moench] for fodder yield and their attributes. Agri. Sci. Digest - A Research Journal. 2013; 33(3)-215-218.
8. Kadam DE, Patil FB, Bhor TJ, Harer PN. Genetic diversity studies in sweet sorghum. J Maharashtra Agri. Univ. 2001; 26(2):140-143.
9. Patankar AB, Sonone AH, Patil JV, Sarode ND. Genetic divergence in sweet sorghum. J Maharashtra Agri. Univ. 2005; 30(2):175-177.