



P-ISSN: 2349-8528

E-ISSN: 2321-4902

[www.chemijournal.com](http://www.chemijournal.com)

IJCS 2021; 9(4): 387-389

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Received: 18-05-2021

Accepted: 27-06-2021

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## Genetic diversity studies in *Rabi* sorghum (*Sorghum bicolor* (L.) Moench) genotypes

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**Abstract**

Forty-four *Rabi* sorghum genotypes (*Sorghum bicolor* L. Moench) collected from different geographical region were assessed for their genetic divergence based on twelve characters during *Rabi*, 2019-20 at Sorghum Improvement Project, MPKV, Rahuri. The genotypes were grouped into 7 clusters which indicating high genetic diversity among them. It indicated that genetic diversity and geographic diversity are not related. From inter cluster distance and cluster mean for various yield contributing traits, it could be concluded that cluster I, II and III were most divergent from all other clusters. The present study revealed that plant height contributed maximum (26.85%) for divergence followed by 1000 grain weight (26.11%) and panicle weight (18.60%). Based on inter-cluster distance, intra-cluster distance and per se performance the genotypes *viz.*, RSLG-2419, RSLG-2421, RSLG-2423, RSLG-2430, RSLG-2458, RSLG-2461 and Phule Suchitra are suggested to utilize for future breeding programme.

**Keywords:** Sorghum, genetic diversity, clusters, grain yield

**Introduction**

Sorghum (*Sorghum bicolor* (L.) Moench) is one of the world's most significant cereal grain crop. In India, it is grown during both kharif (rainy season from June-October) and *Rabi* (post-rainy season from October-January) seasons for multiple uses as a food, feed, fodder and fuel crop. Due to different agro-climatic conditions, the cultivar requirements for these two seasons are silent diverse [1]. Maharashtra, the country's leading sorghum producer, with a total area of 21.90 lakh hectares. The total area under cultivation, with an annual production of 18.09 lakh tonnes and a productivity of 826 kg per hectare. In kharif, 2.80 lakh hectares are planted, with an annual production of 1.77 lakh tonnes and a productivity of 630 kg per hectare. It is grown on 19.09 lakh hectares during the *Rabi* season, with an annual production of 16.33 lakh tonnes and a productivity of 855 kg per hectare [2].

The nature and magnitude of genetic divergence in a population is essential for selection of diverse parents, which upon hybridization leads to a wide spectrum of gene recombination for quantitatively inherited traits. Multivariate analysis is a powerful tool in quantifying the degree of divergence in germplasm collection of crop plants. In present study, genetic divergence among forty-four genotypes of *Rabi* sorghum was quantitatively assessed by adopting Mahalanobis D<sup>2</sup> statistics based on grain yield and yield attributes [3]. The present study involved to assess the extent of genetic diversity in 44 *Rabi* sorghum genotypes collected from different geographical region.

**Material and Methods**

The field experiment was carried out at Sorghum Improvement Project, MPKV, Rahuri during *Rabi* 2019-20 in RBD design with two replication to study the genetic diversity among forty four *Rabi* sorghum genotypes including two checks *i.e.* Phule Anuradha and Phule Suchitra. Observation were recorded on five randomly selected plants for grain yield and yield contributing characters like days to 50% flowering, days to maturity, plant height (cm), number of internodes per plant, number of green leaves per plant at harvest, panicle length (cm), panicle width (cm), panicle weight (g), 1000 grain weight (g), dry fodder yield per plant (g), harvest index and grain yield per plant (g). Analysis of variance was estimated as per procedure proposed by Panse and Sukhatme (1995) [4]. Significant differences between genotypes based on the pooled effects of all the traits were tested by Wilk's 'λ' (Statistics) criterion (1932) [5].

Genetic divergence estimated by multivariate analysis using Mahalanobis  $D^2$  statistics (1936). The genotypes were grouped into different clusters as per Tocher's method as described by Rao (1952) [6].

### Result and Discussion

Genetic diversity is the base for survival of plants in nature and for crop improvement. Diversity in plant genetic resources provides opportunity for plant breeders to develop new and improved cultivars with desirable characteristics. The utility of  $D^2$  analysis, which is a potent tool to quantify the extent of divergence in biological populations at genetic level, is further enhanced by its applicability to estimate the relative contribution of the various plant characters to genetic divergence.

The analysis of variance showed highly significant difference among the genotypes for all the characters studied. Forty-four

genotypes were grouped into 7 clusters (Table 1) as per Tocher's method as described by Rao (1952). Cluster I was the largest with 33 genotypes, followed by cluster II with 4 genotypes, followed by cluster III with 3 genotypes. Cluster IV, V, VI and VII were monogenotypic. These four genotypes maintained separate identity and they were not included with any other cluster and exhibited high genetic diversity with most of the other clusters. Clustering pattern indicated that geographical and genetic distribution are not related. Earlier workers Umakanth *et al.* (2003) [7] grouped 44 *Rabi sorghum* genotypes into 14 clusters, Kumar *et al.* (2010) [8] grouped 54 genotypes into 8 clusters, Sujata and Pushpavalli (2015) [9] grouped 62 genotypes into 15 clusters, Swami *et al.* (2015) [10] grouped 61 genotypes into 14 clusters, Jain *et al.* (2016) [11] grouped 25 genotypes into 4 clusters and Girma *et al.* (2020) [12] grouped 366 landraces into 5 clusters.

**Table 1:** Distribution of 44 *Rabi sorghum* genotypes into different clusters based on  $D^2$  values

Clusters	Number of genotypes included	Genotypes
I	33	RSLG2434, RSLG2448, RSLG2433, RSLG2439, RSLG2435, RSLG2442, RSLG2425, RSLG2432, RSLG2454, RSLG2451, RSLG2446, RSLG2455, RSLG2436, RSLG2447, RSLG2428, RSLG2445, RSLG2431, RSLG2453, RSLG2422, RSLG2450, RSLG2427, RSLG2449, RSLG2456, RSLG2452, RSLG2440, RSLG2423, RSLG2457, RSLG2437, RSLG2438, RSLG2460, RSLG2441, RSLG2430, RSLG2420
II	4	RSLG2458, RSLG2459, RSLG2421, Phule Suchitra (C)
III	3	RSLG2424, RSLG2426, RSLG2429
IV	1	RSLG2461
V	1	RSLG2418
VI	1	RSLG2419
VII	1	Phule Anuradha (C)

The maximum intra cluster distance (Table 2) observed by cluster I (13.15) followed by cluster II (12.71), III (11.25), and rest of cluster had zero intra cluster distance as they have only one genotype (monogenic). The maximum inter cluster distance showed by cluster VII and cluster V (36.58) followed

by cluster VII and VI (30.82), cluster VI and III (30.19), cluster VII and I (28.73), cluster V and III (28.38), cluster IV and III (27.62) and cluster VI and II (27.34). The minimum  $D$  values observed between cluster IV and II (17.56) followed by cluster II and I (17.83) and cluster III and I (17.98).

**Table 2:** Average intra (bold) and inter cluster distance ( $D$ ) values for seven clusters in forty four *Rabi sorghum* genotypes

Clusters	I	II	III	IV	V	VI	VII
I	13.15	17.83	17.98	22.62	19.52	24.72	28.73
II		12.71	24.03	17.56	24.73	27.34	24.43
III			11.25	27.62	28.38	30.19	26.88
IV				0.00	27.19	27.00	23.95
V					0.00	18.86	36.58
VI						0.00	30.82
VII							0.00

Diagonal: Intra cluster and above diagonal: inter cluster  $D$  values

**Table 3:** Mean values of the seven clusters for twelve characters in forty-four *Rabi sorghum* genotypes

Cluster No.	Days to 50% flowering	Days to maturity	Plant height (cm)	No. of internodes /plant	No. of green leaves per plant at harvest	Panicle length (cm)	Panicle width (cm)	Panicle weight (g)	1000 grain weight (g)	Dry fodder yield/plant (g)	Harvest index (%)	Grain yield/plant (g)
CL-I	89.03	130.65	202.75	9.72	4.35	12.74	4.90	97.85	31.10	191.92	23.63	70.58
CL-II	81.88	123.50	246.79	9.62	5.41	18.14	7.17	160.00	37.01	230.88	32.00	125.88
CL-III	85.83	127.67	148.44	8.33	3.55	9.94	4.55	94.17	22.05	140.67	26.15	61.67
CL-IV	68.50	110.00	242.50	9.33	1.67	15.16	5.33	117.50	36.40	229.50	23.05	80.00
CL-V	87.50	133.00	180.30	9.67	4.50	12.83	6.00	64.50	43.50	171.00	15.95	37.50
CL-VI	88.50	130.00	164.98	9.17	2.33	14.83	4.66	102.50	48.10	132.50	35.05	82.50
CL-VII	71.00	111.50	204.00	7.00	6.50	17.41	5.00	115.00	29.50	152.50	25.85	69.00

Based on the cluster means of different characters (Table 3), the genotypes involved in cluster II had the outstanding mean performance for yield and yield contributing characters. Based on cluster mean, cluster II was identified for the earliness. The highest mean value for no. of internodes per

plant was scored by cluster I while, highest cluster mean for plant height, panicle length, panicle width, panicle weight, dry fodder yield per plant and grain yield per plant were scored by cluster II. So, genotypes which included in cluster I was suitable for improving grain yield.

The contribution of particular trait to genetic diversity was assessed by cluster mean which represent in Table 4. The present study revealed that plant height contributed maximum (26.85%) for divergence followed by 1000 grain weight (26.11%), panicle weight (18.60%), panicle length (8.77%) and days to maturity (7.51%). This result was in accordance with Swami *et al.* (2015) reported high contribution to the

divergence by plant height, high contribution due to seed yield was reported by Kumar *et al.* (2010)<sup>[8]</sup> and Sujata and Pushpavalli (2015)<sup>[9]</sup>. High contribution to the divergence due to days to 50% flowering was reported by Swamy *et al.* (2018)<sup>[13]</sup> while Nithiyananth (2005)<sup>[14]</sup> reported same for leaf width.

**Table 4:** Per cent contribution for divergence of twelve different characters of *Rabi* sorghum genotypes

Sr. No.	Source	Times ranked first	Contribution %
1	Days to 50 % flowering	21	2.22
2	Days to maturity	71	7.51
3	Plant height (cm)	254	26.85
4	Number of internodes/plant	2	0.21
5	Number of green leaves/plant at harvest	8	0.85
6	Panicle length (cm)	83	8.77
7	Panicle width (cm)	20	2.11
8	Panicle weight (g)	176	18.60
9	1000 grain weight (g)	247	26.11
10	Dry fodder yield /plant (g)	44	4.65
11	Harvest index (%)	1	0.11
12	Grain yield /plant (g)	19	2.01

Based on inter-cluster distance, intra-cluster distance and *per se* performance the genotypes *viz.*, RSLG-2419, RSLG-2421, RSLG-2423, RSLG-2430, RSLG-2458, RSLG-2461 and Phule Suchitra are suggested to utilize for future breeding programme

### Conclusion

Based on inter-cluster distance, cluster mean and *per se* performance the genotypes *viz.*, RSLG-2419, RSLG-2421, RSLG-2423, RSLG-2430, RSLG-2458, RSLG-2461 and Phule Suchitra are suggested to utilize for future breeding programme.

### Acknowledgment

This is a part of research work of M.Sc. thesis carried out by M.S. Nikam and submitted to Mahatma Phule Krishi Vidyapeeth, Rahuri. The authors are grateful to the Department of Agricultural Botany, M.P.K.V., Rahuri and Sorghum Improvement Project, M.P.K.V., Rahuri for facility provided and supply of seed material of *Rabi* sorghum genotypes for present study.

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