

Journal of Pharmacognosy and Phytochemistry

Available online at www.phytojournal.com



E-ISSN: 2278-4136 P-ISSN: 2349-8234 JPP 2020; 9(1): 833-836 Received: 19-11-2019 Accepted: 21-12-2019

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Estimation of genetic diversity for yield parameters in yellow pericarp sorghum germplasm lines [(Sorghum bicolor L.) Moench]

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Abstract

Forty germplasm lines of yellow pericarp sorghum having different geographical origins were evaluated at ARS, Madhira during early *rabi* 2015-16 for genetic divergence using D^2 analysis. The analysis of variance showed highly significant differences among the accessions for all the characters. Principal component analysis revealed that PC I, PC II and PC III explained 70.95, 11.50 and 7.46 % of total variance. The 40 germplasm lines were grouped into six clusters. Among them, Cluster 1 is the largest and had the maximum number (30) of genotypes followed by cluster 5 with 4 genotypes, cluster 2 with 3 genotypes and cluster 3, cluster 4 and cluster 6 with single genotype each. Percent contribution towards genetic divergence showed that plant height contributed the most (37.31%) followed by straw weight (26.92%) and grain yield per plant (22.69%).

Keywords: sorghum, genetic divergence, yield

Introduction

Sorghum is the third most important cereal crop cultivated extensively in India after wheat and rice in semi arid regions under rainfed situations. Sorghum grown in *rabi* season is characterized by its excellent grain quality, exclusively utilized for human consumption and hence fetches higher market price as compared to *kharif* sorghum. Yield is a complex trait influenced by many factors and is polygenically inherited. Utilization of heterosis to enhance yield depends on the choice of suitable parents with wide genetic divergence for crossing purpose. For such species, the parents with more genetic divergence are expected to yield heterotic hybrids in addition to generating a broad spectrum of variability in segregating generations. Grouping of the available germplasm into different clusters based on genetic distances is an important criterion for parental selection for crossing. D² statistic is a useful multivariate statistical tool for effective discrimination among various genotypes on the basis of genetic divergence. Hence, an attempt has been made to study the genetic divergence in available germplasm of yellow pericarp sorghum lines for grain yield and its components to provide a basis for selection of parents for hybridization to generate heterotic hybrids.

Materials and Methods

The experimental material consisted of forty yellow pericarp yellow sorghum germplasm lines of different geographical origins obtained from ICRISAT. The germplasm lines were evaluated in a randomized block design with two replications at ARS, Madhira during early *rabi* 2015-16. Each entry was planted in 2 rows of 5m length with 45 and 15 cm spacing between and within rows. Observations on agro morphological traits *viz*. plant height, number of leaves per plant, leaf length, leaf width, ear length, straw weight, 100 seed weight and grain yield per plant were recorded on randomly selected five plants per replication. Data on days to 50% flowering and days to maturity was noted on plot basis and the data was subjected to statistical analysis.

Divergence was estimated by the multivariate analysis using Mahalanobis's (1936) ^[2] and D² statistic as described by Rao (1952) ^[4]. On the basis of D² values obtained, the variables were grouped into different clusters by employing Tocher's method (Rao, 1952) ^[4]. The percent contribution of each character to the total divergence was calculated by ranking each character on the basis of transformed uncorrelated values. Finally, the percent contribution for each character was calculated by taking total number of ranks of all the characters to hundred. The data were analyzed statistically using the software WINDOSTAT, developed by INDOSTAT services Ltd. Hyderabad, India.

Results and Discussion

The analysis of variance showed highly significant differences among the accessions for all the characters studied indicating the presence of considerable variability in the experimental material.

Principal component analysis

Partitioning of total variance through principle component analysis showed that three principal components viz PC I, PC II and PC III contributed about 89.91% of total variance for the germplasm lines studied. These three PCs i.e. PC I, PC II and PC III contributed 70.95, 11.50 and 7.46 % of total variance (Fig 1). The results obtained from PCA were further corroborated by cluster analysis using UPGMC (Unweighted Paired Group Method using Centroids). The forty yellow sorghum germplasm lines were grouped into six distinct clusters (Fig. 1). Cluster 1 is the largest with a maximum number (30) of genotypes followed by cluster 5 with 4 genotypes, cluster 2 with 3 genotypes and cluster 3, cluster 4 and cluster 6 with single genotype each (Fig 2). The results of D^2 analysis helped to identify diverse accessions from the available germplasm lines for use in crop improvement programmes.

Cluster distances and cluster means

The genetic divergence among the genotypes as indicated by

intra and inter cluster distances for six different clusters are presented in Table 2. Highest intra cluster distance of 7.13 was recorded for cluster 5 followed by cluster 2 (6.20) and cluster 1 (5.78). The inter cluster distances ranged from 23.39 (between cluster 2 and 4), followed by 23.26 (between cluster 2 and 6), 15.38 (between cluster 2 and 3), 14.94 (between cluster 2 and 5), 11.26 (between cluster 4 and 5), 10.28 (between cluster 3 and 6), 9.30 (between cluster 1 and 5), 7.83 (between cluster 1 and 6), 7.36 (between cluster 1 and 3), 6.04 (between cluster 3 and 5) and 5.74 (between cluster 4 and 6). Clusters 3, 4 and 6 are solitary clusters with inter cluster distance of 0.00. The maximum amount of heterosis is expected from the crosses with parents belonging to the most divergent clusters ie., between cluster 2 and 4 followed by parents in clusters of 2 and 6. These results are in agreement with earlier reports of Singh et al. (2001), Yadav et al. (2004), Jain and Patel (2016), More et al., (2018) and Nishant et al. (2018) ^[7, 9, 5, 3, 6]. The progenies derived from such crosses are expected to show wide variability, providing greater scope for isolating transgressive segregants in the advanced generations which can be used for selecting desirable genotypes for yield improvement in sorghum. The cluster means for various traits included in the present study are shown in Table 3.

Table 1: Principal component analysis in yellow sorghum germplasm lines for ten morphological characters

		1 Vector	2 Vector	3 Vector
	Eigene value (Root)	1396.44400	226.47800	146.92250
	% Var. Exp.	70.95946	11.50834	7.46578
	Cum. Var. Exp.	70.95946	82.46780	89.93356
1	Plant height	0.85211	0.01048	0.40698
2	Days to 50% flowering	0.09749	0.06791	0.09299
3	Days to maturity	-0.11995	-0.01509	-0.16085
4	No. of leaves per plant	-0.03772	0.05304	0.00592
5	Leaf length	0.16341	-0.00289	0.10569
6	Leaf width	-0.01838	0.04671	-0.02197
7	Ear length	0.12561	-0.02581	-0.05489
8	Straw weight	0.05676	0.97760	-0.11277
9	100 seed weight	0.14570	-0.15127	-0.03698
10	Grain yield per plant	0.42582	-0.10391	-0.87810

Table 2: Intra and inter cluster distances for ten characters in yellow pericarp sorghum germplasm lines

	Cluster 1	Cluster 2	Cluster 3	Cluster 4	Cluster 5	Cluster 6
Cluster 1	5.78	21.31	7.36	7.25	9.30	7.83
Cluster 2	21.31	6.20	15.38	23.39	14.94	23.26
Cluster 3	7.36	15.38	0.00	10.31	6.04	10.28
Cluster 4	7.25	23.39	10.31	0.00	11.26	5.74
Cluster 5	9.30	14.94	6.04	11.26	7.13	12.31
Cluster 6	7.83	23.26	10.28	5.74	12.31	0.00

Table 3: Cluster means for	ten characters i	in vellow r	pericarp sorgh	um germplasm lines

	Plant height	Days to 50% flowering	Days to maturity	No. of leaves per plant	Leaf length	Leaf width	Ear length	Straw weight	100 seed weight	Grain yield per plant
Cluster 1	371.42	79.70	109.34	12.38	60.88	7.05	16.47	543.54	2.67	35.48
Cluster 2	100.07	75.33	105.00	8.47	53.52	6.27	17.41	400.00	2.14	13.72
Cluster 3	286.60	78.00	101.00	11.20	61.00	7.00	14.00	400.00	2.92	35.50
Cluster 4	384.80	79.00	112.00	12.60	59.40	8.00	23.17	800.00	1.38	56.30
Cluster 5	288.90	80.75	106.50	11.56	59.38	7.58	16.61	625.00	2.05	20.59
Cluster 6	367.60	75.00	116.00	13.00	58.60	7.00	35.00	500.00	2.81	62.41

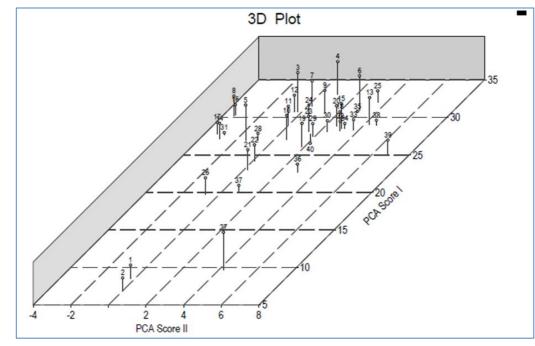


Fig 1: Principal component analysis diagram for yellow pericarp sorghum germplasm lines

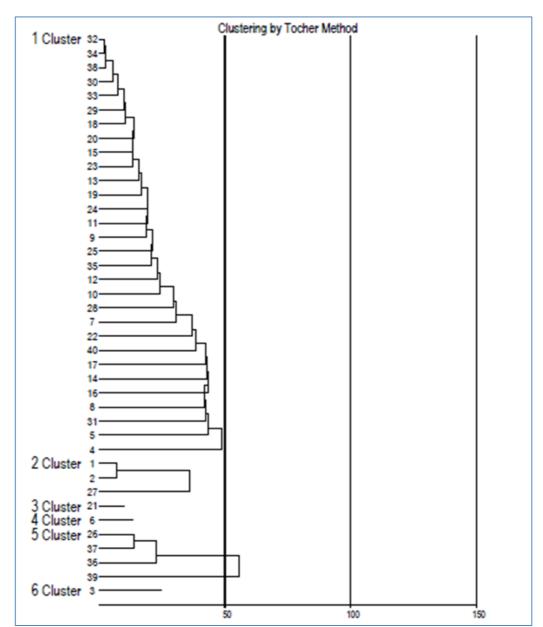


Fig 2: Dendrogram showing clustering of yellow pericarp sorghum germplasm lines

Percent contribution towards genetic divergence

The relative contribution of different traits included in the present study towards genetic divergence is shown in Table 4. Plant height contributed the most (37.31%) followed by straw weight (26.92%), grain yield per plant (22.69%), ear length (3.72%), 100 seed weight (3.59%), days to maturity (2.82%), leaf length (1.54%), days to 50% flowering (1.15%) and number of leaves per plant (0.26%). The grouping of germplasm lines based upon their genetic divergence into different clusters is shown in Table 5. The genotypes belonging to divergent clusters may be selected as parents in hybrid development programmes for yield improvement in sorgum. Similar results were earlier reported by Umakanth et al. (2003), Elangovan and Babu (2015) and Nishant et al. (2018)^[8, 1, 6]. This information can also be used to assess the genetic divergence among the genotypes for framing an effective breeding programme for selection of parents for yield gain in yellow pericarp sorghum germplasm lines under study.

 Table 4: Percent contribution of ten traits towards genetic divergence in yellow pericarp sorghum germplasm lines

Source	Times ranked 1st	Contribution %
Plant height	291	37.31
Days to 50% flowering	9	1.15
Days to maturity	22	2.82
No. of leaves per plant	2	0.26
Leaf length	12	1.54
Leaf width	0	0.00
Ear length	29	3.72
Straw weight	210	26.92
100 seed weight	28	3.59
Grain yield per plant	177	22.69

 Table 5: Clustering pattern of yellow pericarp sorghum germplasm

 lines

Cluster	No. of accessions	Genotypes			
Ι	30	NSJB-6572, NSJB-6566, NSJB-6590, NSJB- 6657, NSJB-6648, NSJB-6581, NSJB-6678, NSJB-6887, NSJB-6601, NSJB-6662, NSJB- 6565, NSJB-6590, NSJB-6587, NSJB-6685, NSJB-6579, NSJB-6574, NSJB-6595, NSJB- 6661, NSJB-6568, NSJB-6677, NSJB-6599, NSJB-6692, NSJB-6648, NSJB-6676, NSJB- 6679, NSJB-6674, NSJB-6597, NSJB-6672, NSJB-6571, NSJB-6547,			
II	3	IS-10529, IS-21821, NSJB-6575			
III	1	NSJB-6682			
IV	1	NSJB-6671			
V	4	NSJB-6580, NSJB-6565, NSJB-6566, NSJB- 6683			
VI	1	NSJB-6628			

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