VARIABILITY AND GENETIC DIVERGENCE AMONG THE *RABI* SORGHUM GERMPLASM ADAPTED TO DEEP SOIL SITUATIONS

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Abstract: Genetic variability and cluster analysis was used to assess the divergence among fifty *rabi* sorghum genotypes. The Analysis of variance revealed significant differences among the genotypes for all the 7 traits studied. Higher values of Phenotypic and Genotypic coefficient of variability were observed for grain yield, fodder yield, panicle length and test weight. High heritability coupled with high genetic advance over mean was obtained for the panicle length, test weight and fodder yield. Maximum inter cluster distance was observed between cluster III and cluster IV while minimum genetic distance was observed between cluster V and cluster VI. Based on the intercluster distances, cluster means and perse performance the advanced breeding lines RSV 1572, RSV 1620, RR 9826, SLV 218, RR 06-1, RR 06-3, EP 87 and PEC 15 can be deployed as potential parents in developing dual purpose *Rabi* sorghum types. Days to fifty percent flowering contributed maximum to the total genetic divergence (44.90%) followed by fodder yield (34.53 %) and Panicle length (10.53 %).

Key words: Heritability, Genetic Advance, Multivariate analysis, Principal components

Introduction: Sorghum is the third most important cereal crop cultivated extensively in India after wheat and rice. *Rabi* sorghum is highly valued as a food crop because of its excellent grain quality, nutritional status and low glycemic index. However the yields are lower (750 kg/ha) when compared to *kharif* sorghum (1100 kg/ha) as it is grown as a rainfed crop under residual soil moisture conditions under the influence of various biotic and abiotic stresses (Anonymous, 2006). Crop improvement efforts in the past have not made much impact on improving the productivity as the genetic diversity and phenotypic variability among the breeding lines is limited. All the *Rabi* sorghum types belong to a single race i.e. *durra* type (Reddy *et al.,* 2003). The parents with greater genetic divergence are expected to yield heterotic hybrids in addition to generating broad spectrum of variability in the segregating generations. The D^2 analysis is a multivariate statistical tool for effective discrimination of various genotypes on the basis of genetic divergence. In the present study estimation of variability parameters and cluster analysis through D^2 has been applied to assess the diversity among the 50 *rabi* sorghum genotypes and to identify divergent parents suitable for deep soils, to effect hybridization for the purpose of grain and fodder yield improvement

Material and methods: The material comprised of 50 *rabi* sorghum genotypes of which 31 are advanced breeding lines obtained from Centre for Rabi sorghum (CRS), Solapur, 15 elite varieties, 3 donors for drought tolerance and 1 donors for shoot fly resistance. The present study was carried out in *Rabi* 2015-16 at Agricultural research Station, Tandur. Each Genotype was sown in 4 rows of 5m length with a spacing of 45 cm between the rows and 15 cm within the row. The experiment was laid out in a randomized block design with 2 replications. Recommended package of practices were followed to raise a normal crop. In each genotype, ten plants were selected randomly and used for collecting data on seven characters namely Days to 50% flowering (DFF), Days to maturity (DM), Plant height (PH, cm), Panicle length (PL, cm), Test weight (TW, g) Grain yield (GY, Kg/ha) and Fodder yield (FY, Kg/ha). The data was subjected to analysis of variance and covariance (Panes and Sukhatme, 1954), genotypic and phenotypic coefficient of variation, heritability and genetic advance as per the method suggested by Johnson et al (1955).

The multivariate analysis of genetic divergence using D2 statistic (Mahalanobis, 1936) was carried out as described by Rao (1952). The data was analysed by INDOSTAT services Ltd (version 8.5), Hyderabad, India. The percent contribution of each character to the total divergence was calculated by ranking each character on the basis of transformed uncorrelated values. Rank 1 was given to the highest mean difference and for the lowest mean difference where n is the total number of characters. Finally the percent contribution for each character was calculated by taking total number of ranks of all the characters to hundred.

Results and discussion:

ANOVA: The analysis of variance revealed significant differences among the genotypes studied as the mean sum of squares (MSS) of the seven traits were found to be highly significant (Table 1). This variation provides ample scope for the plant breeder in selection of superior and genotypes for crop improvement

Variability: Effectiveness of selection depends on the magnitude of genetic variability for a particular trait. Hence, the coefficients of variation expressed in

percentage at phenotypic (PCV) and genotypic (GCV) levels have been used to compare the variability observed among the different characters. The PCV was higher than the GCV for all the traits which indicates that all traits were highly influenced by environment. High values of PCV and GCV were observed for grain yield, fodder yield, panicle length and test weight, indicating that variation in the triats contributed markedly to the total variability as reported by Biradar *et al* (1996). Low PCV and GCV were recorded for days to 50 per cent flowering, days to maturity and plant height in conformity with Nimbalkar *et al* (1988) and Mallinath *et al* (2004).

The effectiveness of selection for any character depends not only on the extent of genetic variability but also to the extent to which it is transferred from one generation to the next.

High heritability estimates were observed for fodder yield (92%) followed by days to 50% flowering (96%), days to maturity (94%), test weight (80%) and panicle length (80%).This indicates the major role of additive genes in governing these traits and lesser influence of environment. High heritability estimates for the above traits were also recorded by Nimbalkar *et al* (1988) and Biradar *et al* (1996). Lower heritability values were reported for plant height (51%) and grain yield (67%) indicating the role of non additive gene action and greater influence of environment in governing these traits.

Days to 50% flowering showed high heritability coupled with low genetic advance. Similar observations were also recorded by and Biradar *et al* (1996) indicating the presence of non-additive gene effects and high genotype and environment (G x E) interaction. This again reiterates the fact that it is difficult to make the progress in developing early maturing and high yielding genotypes

High heritability coupled with high genetic advance over mean was obtained for the panicle length, test weight, fodder yield. Hence, selection made through these characters would be effective as they are more predominantly controlled by additive gene effect. These results are in confirmation with the results of Nimbalkar *et al* (1988), Biradar *et al* (1996), Prabhakar (2001), Veerabadhiran and Kennedy (2001), Umakanth *et al* (2004), Deepalakshmi *et al* (2007).

Cluster analysis: Based on D^2 analysis, the 50 genotyps were grouped into 7 clusters with variable number of entries in each cluster (Table 2). Cluster I had maximum number of genotypes i.e. 27 followed by cluster II with 7 genotypes and cluster III and Cluster IV with 6 genotypes each. The remaining 2 clusters (Cluster V and Cluster VI) were represented by single genotypes which independently diverged from others. The formation of solitary clusters may be due to total isolation preventing the gene flow or intensive natural/human selection for diverse adaptive complexes. These genotypes may be very unique and useful in breeding point of view. Nine of fifteen elite varieties grouped under Cluster I indicating their proximity and narrow genetic base. The elite short duration variety suitable for shallow soils i.e. Phule Anuradha grouped in to a separate cluster along with 5 advanced breeding lines.

Average inter cluster D^2 values among 50 genotypes (Table 4) revealed maximum inter cluster distance values between cluster III and cluster IV (D=14.97) followed by cluster II and cluster VII (D=13.5) while minimum genetic distance was observed between cluster V and cluster VI (D=5.22). The data on cluster means (Table 5) revealed considerable differences among the clusters for the 7 traits studied. The cluster IV recorded the least value for days to 50% flowering and days to maturity and highest test weight. So the genotypes of IV cluster need to be crossed with genotypes of cluster III as these clusters recorded maximum inter cluster distance to develop high yielding short duration cultivars with bold grains. The genotype IS 18551 grouped with the advanced breeding line SLV 133 in the last cluster. It is a donor for resistance to shootfly and is agronomically inferior. It was included in the study to identify divergent parents so that crossing can be affected for the development of secondary donors which can be used in shootfly resistance breeding programmes. Based on the inter cluster distance values it should be crossed with genotypes of second cluster to obtain good segregants.

The genotypes of clusters I and II exhibited best agronomic performance with reference to higher cluster means for plant height, grain yield and fodder yield. Based on the data on inter cluster distances, cluster means and per se performance the advanced breeding lines RSV 1572 and RSV 1620 and the elite variety Phule Yashoda can be deployed for developing taller plant types under deep soil situations. The breeding lines RR 9826, SLV 218, RR 06-1, RR 06-3, EP 87 and PEC 15 can be deployed in enhancing grain yield in deep soils. The elite varieties CSV 18, Parbhani Moti, PKV Kranthi and the breeding line PEC 15 can be involved in crossing for developing fodder types. Classification of the germplasm in to divergent groups based on inter cluster distances, perse performance and selection of parents from diverse clusters was reported in several studies (Usha and rekha, 2016, Seetharam and K. Ganesamurthy, 2013). Intercrossing of divergent groups leads to wide genetic base in the base population and greater opportunities for crossing over to occur, which releases hidden variability by breaking the close linkages (Thoday, 1960).

Principal component analysis: The association between the various traits under study and their contribution to the total genetic divergence can be

confirmed by PCA analysis. The Principal Component Analysis (PCA) on the mean values of the genotypes provides a reduced dimension model that would indicate measured differences among the germplasm. Among the 7 traits studied (Table 6), days to 50% flowering contributed the most (44.9 %) to the total genetic divergence followed by fodder yield (34.53 %) and panicle length (10.538 %) while days to maturity recorded the least contribution (0.50 %). Principal component analysis divided the variance exhibited by these seven traits in to three components which cumulatively explained 90 % of the total variance (Table 7). The PC 1 is the most important component accounting to 50.8 per cent while PC 2 and PC3 explained 31.1% and 7.8% respectively. These results are in conformity with the findings of Sameer Kumar *et al* (2010) and Seetharam and Ganesamurthy (2013).

Conclusion: Based on the data on inter cluster distances, cluster means and per se performance, the study identified eight advanced breeding lines RSV 1572, RSV 1620, RR 9826, SLV 218, RR 06-1, RR 06-3, EP 87 and PEC 15 as potential parents in developing dual purpose rabi sorghum types suitable for deep soils. Selection based on the three traits, panicle length, test weight and fodder yield would be effective for deriving more genetic gain as they reported high heritability and genetic advance.

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Table 1: Analysis of variance (ANOVA) for the yield attributing traits

S. No.	Trait	Genotype mean sum of squares	Replication mean sum of squares	Error mean sum of squares	CD at 5%	CD at 1%
1	Plant height	482.1 **	156.2	157.5	25.2	33.6
2	Days to 50% flowering	45.3 **	1.44	0.8	1.8	2.4
3	Days to maturity	45.3 **	1.44	0.8	1.8	2.4
4	Panicle length	11.5 **	1.1	1.3	2.3	3.0
5	Test wt	0.6 **	0.04	0.06	0.5	0.7
6	Grain yield	222223.4 **	40844.4	43337.5	418.3	557.9
7	Fodder yield	6770065.4 **	1346760	282622.4	1068.3	1424.7

** 1% level of significance

Table 2: Variability parameters

Trait	Mean	Range (Min-Max)	GCV %	PCV %	% Heritability	GA		GA as % of mean	
						5%	1%	5%	1%
Plant height (cm)	170.8	125-212	7.45	10.47	50.7	18.69	23.95	10.94	14.02
Days to 50% flowering	71	56-82	6.64	6.76	96.3	9.53	12.21	13.42	17.21
Days to maturity	115	100-126	4.101	4.17	96.3	9.53	12.21	8.29	10.62
Panicle length (cm)	12.96	8-19	17.426	19.53	79.6	4.15	5.31	32.02	41.03
Test wt (g)	3.37	1-5	15.424	17.28	79.7	0.95	1.226	28.36	36.34
Grain yield (Kg/ha)	2111.37	1057-2772	14.165	17.25	67.4	505.64	648.01	23.94	30.69
Fodder yield (Kg/ha)	6539.15	2267-11350	27.54	28.71	92.0	3558.34	4560.21	54.41	69.73

Table 3: Clustering pattern of the germplasm based on D2 statistics

	Cluster1	Cluster2	Cluster3	Cluster4	Cluster5	Cluster6	Cluster7
Cluster1	4.39	6.7	7.87	9.18	5.46	6.08	9.50
Cluster 2		4.45	9.63	10.94	9.07	10.49	13.50
Cluster 3			4.57	14.97	9.53	7.38	11.97
Cluster 4				4.75	7.53	11.26	11.40
Cluster 5					0.00	5.22	7.76
Cluster 6						0.00	6.19
Cluster 7							4.70

Table 4: Average Intra and Inter cluster distances among 7 clusters of the germplasm

Cluster No.	No. of Genotypes	Genotypes
1	27	Phule Chitra, Phule Yashoda, Phule Suchitra, Phule Vasudha, CSV22R, CSV29R, DSV5, CSV26, M35-1, SLV103, CRS25, CRS18, CRS16, RR06-3, RR06-1, CRS15, EP57, EP87, BRJ343, RSV1620, RSV1544, RSV167, PVR930, BRJ229, RSV1572, BRJ341, CRS50
2	7	Phule Revathi, PKV Kranthi, CSV 18, Parbhani Moti, DSV 4, PEC 15, BRJ 235
3	6	SLV 200, SLV 210, SLV 218, DSV 5, SLV 222, SLV 207
4	6	CRS 18, CRS 20, SPV 570, BRJ 62, RR 2212, Phule Anuradha
5	1	RR 9826
6	1	BRJ 341
7	2	SLV 133, IS 18551

Table 5: Cluster means for seven yield and yield attributing traits in the *rabi* sorghum germplasm

Cluster	PH	DFF	DM	PL	TW	GY/ha	FY/ha
Cluster1	177.50	71.26	115.26	12.59	3.34	2142.72	6400.06
Cluster2	177.14	71.93	115.93	14.50	3.61	2212.21	9854.57

Cluster3	156.08	79.08	123.08	12.08	3.49	2145.92	5816.42
Cluster4	158.58	61.67	105.67	13.00	3.82	1975.83	5802.92
Cluster5	138.50	68.50	112.50	14.00	3.40	2678.00	5317.00
Cluster6	169.50	72.50	116.50	11.90	2.50	2218.00	3972.00
Cluster7	155.50	68.50	112.50	15.10	1.65	1301.50	3084.50

Table 6: Percent contribution of different traits to the total genetic divergence

S.No.	Source of variation	Times ranked first	% Contribution
1	Plant height (cm)	7	0.57
2	Days to 50% flowering	540	44.9
3	Days to maturity	10	0.5
4	Panicle length (cm)	129	10.53
5	Test wt (g)	75	6.12
6	Grain yield (Kg/ha)	41	3.35
7	Fodder yield (Kg/ha)	423	34.53

Table 7: Principal component analysis depicting the variance explained by the first three principal components

Particulars	PC1	PC 2	PC3
Eigen value (Root)	742.063	455.312	115.028
% variance explained	50.800	31.169	7.874
Cum. variance explained	50.800	81.969	89.844
Days to 50% flowering	0.010	0.101	0.264
Days to maturity	-0.948	0.055	0.097
Plant height (cm)	0.000	0.000	0.000
Panicle length (cm)	0.214	-0.014	0.845
Test wt (g)	0.223	0.293	-0.430
Grain yield (Kg/ha)	-0.068	0.109	-0.076
Fodder yield (Kg/ha)	-0.003	0.942	0.122

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