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Research Note

Characterization of sorghum genotypes for yield and other agronomic traits through genetic variability and diversity analysis

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Abstract
Studies on the genetic variability and diversity analysis were carried out with 39 sorghum genotypes for nine quantitative characters. The Shannon-Weaver diversity index (H'), a measure of dissimilarity was found to be highest for number of leaves per plant, plant height and leaf width and these characters had high heritability coupled with high genetic advance. Of the 36 correlations, 24 were significant at P=0.05 and 21 were significant at 0.01 and 14 were found to be of useful correlations (r>±0.500). Among the useful correlations, yield had significant correlation with days to 50% flowering, leaf length, leaf width and panicle weight. In path analysis, panicle weight had positive direct effect on single plant yield. First three principal components explained more than 70% of variation which reduced nine characters into seven characters and confirmed the correlation analysis. The highest diversity index (0.879) was observed between TNS598 and IS5030. Hierarchical clustering divided the genotypes into six clusters. Promising genotypes were identified for early flowering, plant height, number of leaves, leaf length and yield based on cluster mean values.

Key words:
Sorghum, REML, variability, Shannon-Weaver diversity index, PCA.

Sorghum [*Sorghum bicolor* (L.) Moench] is one of the most important cereals of the semi-arid tropics. Sorghum ranks 5th in the world in terms of area and production (FAO, 2009). The cultivated sorghum is classified as Bicolor, Caudatum, Durra, Guinea, and Kafir. All these races (except Kafir) are found in Ethiopia (Teshome *et al.* 1997), with broad agro-ecological variations, which have resulted in the accumulation of genetic diversity in this crop species. Progress in plant breeding depends on the extent of genetic variability present in a population. Therefore, the first step in any plant breeding program is to assess the magnitude of genetic variability present in the population. The genetic facts are inferred from phenotypic observations, which are the results of interactions of genotype and the environment. The variability available in breeding material is the prime requirement for the improvement and selection of elite genotypes. However, the quantitative characters are influenced by environment and necessitate the partitioning of overall variances as heritable and non-heritable components. The present investigation was carried out with the objective to estimate the extent of variability, heritability, genetic advance for various traits and phenotypic diversity of the genotypes and based on which agronomically superior and diverse accessions were identified.

The material used in the study consisted of 39 genotypes (Table 1) maintained at the Department of Millets, Centre for Plant Breeding and Genetics, Tamil Nadu Agricultural University, Coimbatore. The trial was conducted during summer (March to June, 2009) at Millets breeding station, TNAU, Coimbatore, Tamil Nadu. All the 39 genotypes were raised in a randomized block design with three replications and each accession was raised in two rows of 4m length. The rows were 75cm apart and 10 cm spacing was adopted between plants so as to accommodate 40 plants per row. Observations were recorded on nine quantitative characters *viz.*, days to 50 per cent flowering, plant height (cm), number of leaves per plant, leaf length (cm), leaf width (cm), stem width (cm), panicle length (cm), panicle weight (g) and single plant yield (g). The observations were recorded on five randomly selected plants from each genotype in each replication. The mean values of all the quantitative traits were subjected to statistical analysis using Residual Maximum likelihood (REML) method (Paterson and Thompson, 1971) considering genotypes as random using Genstat version12. The Shannon-Weaver diversity index (H') (Shannon-Weaver, 1949) was calculated for all the quantitative characters. Dissimilarity index was estimated using NTSYSpc 2.02i to find out the most diverse accessions and least diverse accessions. Principal Component analysis on all the quantitative characters was performed to determine character contributing to the polymorphism in the material. Data on quantitative characters was standardized with mean 0 and standard deviation of 1 was used to perform PCA using GENSTAT 12. Cluster analysis was performed using scores of the first three principal components following Ward (1963).

Residual maximum likelihood (REML) analysis for nine quantitative characters indicated that the variance due to genotypes were significant for all the characters (Table 2). The genotypes exhibited considerable amount of variability for all the nine

characters studied. Narrow differences observed between phenotypic and genotypic co-efficients of variation for all the characters indicating little influence of environment on the expression of these characters. Higher estimates of genotypic and phenotypic co-efficients of variation were observed for grain yield, panicle weight, panicle length and plant height (Table 3). The results are in accordance with the studies of Biswas *et al*., (2001), Aba *et al*., (2001) and Bello *et al*., (2007). A moderate values of phenotypic and genotypic co-efficient of variation were observed for all the other characters.

The Shannon Diversity index (H′) was calculated to compare phenotypic diversity for the characters used in the study. A low H′ indicates an extremely unbalanced frequency classes for an individual trait and lack of genetic diversity (Upadhyaya, 2010). The mean H′ of the characters under study was 0.55±0.005. The H′ of leaf length (0.53), stem width (0.54), panicle length (0.54), panicle weight (0.53) and single plant yield (0.54) were on par with the mean H′. The characters *viz.*, number of leaves per plant (0.59), leaf width (0.59) and plant height (0.57) were found to have H′ greater than the mean (table 3). This shows that these characters have high diversity. Moreover high heritability coupled with high genetic advance was observed for days to 50 % flowering, leaf width, plant height, stem width, panicle length, panicle weight and single plant yield (table 3). The heritability estimate and the Shannon Diversity index (H′) of the characters reflect its stability and range of variability. Hence the characters with high H′ and heritability can be used as a primary set of criteria for selection, both under favorable and stress environments. Similar results were obtained by Tariq *et al*., (2007) for single plant yield and Bello *et al.* (2007) for days to 50% flowering, number of leaves, plant height and panicle length.

Correlation studies**:** Although variability estimates provide information on the extent of improvement, they do not throw much light on the extent and nature of relationship which exists between the characters. This could be obtained from simple association analysis. Knowledge of the association of component characters with single plant yield may greatly help in making selection precise and accurate. The greater the magnitude of correlation coefficients, the stronger is the association. Any correlation with 37 degrees of freedom with a value more than 0.390 will be significant at P=0.05 and greater than 0.416 will be significant at P=0.01. Of the 36 correlations, 24 were significant at P=0.05 and 21 were significant at 0.01 (Table 4). The proportion of variation in one trait can be attributed to its linear relationship with a second trait and is indicated by the squares of the correlation coefficient (Snedecor and Cocharn, 1980). In the present study those correlations which are greater than ±0.500 are considered as useful correlation as at least 25 per cent of the variation in one trait is predicted by the other. Among the useful correlations, the yield had significant and meaningful correlation with days to 50% flowering, leaf length, leaf width and panicle weight.

Path co-efficient analysis provides an effective means of partitioning direct and indirect causes of association. It permits a critical look to recognize the specific forces acting to produce a given correlation and measures the relative importance of each causal factor. Among the characters correlated to the yield, leaf length and panicle weight had positive direct effect on single plant yield (Table 5). The maximum direct effect was recorded for panicle weight. Simple direct selection based on these traits would be rewarding. This information would be of greater value in selecting the useful traits and thus optimize the data recording by taking observations on a few related traits in the preliminary trails involving a large number of germplasm accessions (Upadhyaya, 2010).

This association between the characters and their contribution to the diversity can also 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. The results showed the importance of the first three Principal Components (PC) in discriminating the entire germplasm. The percentage of variation explained by these PCs was more than 70 per cent and it reduced the original nine characters into seven characters. The PC 1 is the most important component accounted for 52.07 per cent with five latent roots (Table 6). The PC1 separates the accessions on 5 traits *viz*., days to 50 per cent flowering, leaf length, leaf width, panicle width and single plant yield, which indicates the contribution of these characters towards the phenotypic variation of the genotypes under study. The most prominent relations revealed by the biplot (Fig 1.) was the strong positive association between panicle width and single plant yield. The correlation coefficient among any two indices is approximately the cosine of the angle between their vectors. Thus r = cos 180^o = -1, cos 0^o = 1 and cos 90^o = 0 (Yan and Rajcan, 2002). The results obtained from biplot graph confirmed correlation analysis. So character associated with the yield can be used for the indirect selection of accessions with high yield.

Phenotypic diversity**:** The grouping of similar genotypes based on the similarity and dissimilarity among them, can be determined by phenotypic diversity index. The highest diversity index was

found between TNS 598 and IS 5030 (0.879) and least dissimilarity was found between IS 4825 and EP 94 (0.038) with average diversity index of 0.323. The top five pair accessions with high dissimilarity index and top five pair of accessions with low dissimilarity index are given in the Table 7. The accessions with high dissimilarity can be utilized in the breeding

The hierarchical cluster analysis was conducted using the method of Ward (1963) on the first three PC accounting for 80 per cent of the total variation. The 39 genotypes were grouped into six clusters (Fig 2.). Among the six clusters, cluster IV was found to be largest with 10 accessions and followed by clusters II and III (nine accessions in each cluster) and the cluster I was found to be the smallest cluster with two accessions. Promising genotypes can be identified from the clusters based on the estimated cluster means recorded for each trait. Among the six clusters, accessions for early flowering and short plant can be selected from the cluster II because the cluster mean (Table 8) was low for days to 50 per cent flowering and plant height. Based on this the accessions IS 3436, IS 4283 for early flowering and IS 4789, IS 5030 for short plant type were selected. The cluster 5 and 6 can be used for selecting accessions with highest leaf number and leaf length which can be used for the forage sorghum breeding and so the accessions EP 57, IS 1055 of cluster 5 and IS 4337, IS 3573 of cluster 6 were selected for high leaf number and leaf length. Accessions from cluster 4 which is the largest, also had high cluster mean for yield would be promising for seed yield. Hence, the accessions EP 60, TNS 598, TNS 608, TNS 609 were identified for high yield. The mean data of the individual genotypes are given in the Table 9.

Conclusion**:** The results have implications in selecting parents for use in sorghum improvement program. Providing new sources of variation for agronomic traits can enhance genetic potential of sorghum. In the present study accessions TN598 and IS5030 were identified as highly diverse accessions. It is always expected that hybridization involving diverse parents have more chance to produce transgressive segregants for beneficial traits which occur due to reshuffling of alleles. While selecting germplasm lines for inclusion in breeding programs, it is important to consider the agronomic performance of the lines, as it may be useful in predicting their behavior in hybrid combinations with adopted genotypes. In the present study accessions for early flowering (IS3436, IS4283), short plant type (IS4789, IS 5030), high leaf number (EP57, IS 5055, IS4337, IS3573) and high yield (EP60, TN598, TNS608 and TN605) were identified. These identified accessions can be used as parental source for breeding programs with selective objective.

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Table 1. List of sorghum genotypes used in the study

S.No.	Accessions	S.No.	Accessions
1	IS 4337	21	IS 19560
2	EP 88	22	EP 94
3	IS 3436	23	IS 3585
4	IS 12447	24	IS 18551
5	IS 2195	25	IS 1124
6	IS 3573	26	IS 4789
7	IS 2122	27	IS 4085
8	IS 1130	28	IS 9552
9	IS4646	29	IS 1028
10	IS 4825	30	CO (s) 28
11	IS 4283	31	CO26
12	SPV 615	32	K8
13	EP 60	33	APK1
14	EP 57	34	TNS 598
15	IS 1055	35	TNS 599
16	IS 5622	36	TNS 603
17	IS 5826	37	TNS 607
18	IS 5030	38	TNS 608
19	IS 18303	39	TNS 609
20	IS 9664		

Table 2. Genotypic variance, mean and range for quantitative characters of sorghum genotypes used in the study.

Characters	Genotypic variance (σ_g)	Mean±SE	Range
Day to 50% flowering	35.99**	58.48±0.810	48.52-65.86
Number of leaves/plant	1.33**	10.59±0.502	8.22-12.55
Leaf length (cm)	56.98**	72.39±2.412	56.66-85.27
Leaf width (cm)	1.28**	8.25±0.366	6.13-10.74
Plant height (cm)	2504**	206.55±3.603	104.50-289.60
Stem width (cm)	0.09**	1.91±0.106	1.51-2.55
Panicle length (cm)	45.10**	26.90±0.890	12.75-48.28
Panicle weight (g)	2438**	92.26±2.215	20.48-216.62
Single plant yield (g)	1174**	57.22±2.997	13.93-152.43

Table 3. Variability parameters for quantitative characters of sorghum genotypes used in the study.

CHARACTERS	GV	PV	GCV %	PCV %	h^2_b	GA	H′
Day to 50% flowering	35.99	38	10.26	10.54	94.72	20.57	0.44
Number of leaves/plant	1.333	2.267	10.89	14.21	58.79	17.21	0.59
Leaf length (cm)	56.98	76.42	10.43	12.08	74.57	18.55	0.54
Leaf width (cm)	1.278	1.727	13.71	15.94	74.01	24.29	0.59
plant height (cm)	2504	2543	24.23	24.41	98.46	49.53	0.57
Stem width (cm)	0.09	0.13	15.61	18.70	69.67	26.84	0.54
Panicle length (cm)	45.1	47.51	24.97	25.63	94.92	50.11	0.54
Panicle weight (g)	2438	2453	53.52	53.68	99.4	54.96	0.53
Single plant yield (g)	1174	1201	59.86	60.55	97.74	60.98	0.54
Mean							0.55±0.005

GV- Genotypic variance, PV- Phenotypic variance, GCV% - Genotypic coefficient of Variation, PCV%- Phenotypic coefficient of variation, h^2_b – Heritability broad sense, GA- Genetic advance as per cent of mean, H′- Shannon-Weaver Diversity Index

Table 4. Correlation co-efficient for quantitative characters of sorghum genotypes used in the study.

	NL	LL	LW	PH	SW	PL	PW	SPY
DF	0.649**	0.714**	0.569**	0.458**	0.476**	0.133	0.649**	0.632**
NL		0.535**	0.487**	0.216	0.416**	-0.100	0.401*	0.421**
LL			0.680**	0.364*	0.498**	0.181	0.641**	0.686**
LW				0.218	0.508**	0.174	0.695**	0.581**
PH					0.489**	-0.140	0.285	0.239
SW						-0.054	0.516**	0.407*
PL							0.246	0.242
PW								0.916**

DF- Days to 50% flowering, NL- Number of leaves per plant, LL-Leaf length (cm), LW-Leaf width (cm), PH-Plant height (cm), SW- Stem width (cm), PL-Panicle length (cm), PW-Panicle weight (g), SPY- Single plant yield (g)

Table 5. Direct (diagonal) and indirect effects of yield components with single plant yield

	DF	NL	LL	LW	PH	SW	PL	PW	r_g
DF	**-0.127**	0.090	0.286	-0.182	-0.014	-0.055	0.000	0.639	0.616**
NL	-0.093	**0.123**	0.222	-0.160	-0.007	-0.050	0.000	0.434	0.408*
LL	-0.097	0.073	**0.375**	-0.217	-0.012	-0.057	0.001	0.660	0.683**
LW	-0.078	0.066	0.275	**-0.296**	-0.007	-0.062	0.001	0.717	0.571**
PH	-0.059	0.029	0.144	-0.069	**-0.030**	-0.055	0.000	0.279	0.228
SW	-0.066	0.057	0.201	-0.171	-0.016	**-0.107**	0.000	0.538	0.390*
PL	-0.018	-0.014	0.074	-0.055	0.004	0.008	**0.003**	0.242	0.247
PW	-0.083	0.055	0.253	-0.218	-0.009	-0.059	0.001	**0.976**	0.900**

Residual effect = 0.303; r_g = Genotypic correlation, **, *significant at 1 and 5% respectively
DF- Days to 50% flowering, NL- Number of leaves per plant, LL-Leaf length (cm), LW-Leaf width (cm), PH-Plant height (cm), SW- Stem width (cm), PL-Panicle length (cm), PW-Panicle weight (g), SPY- Single plant yield (g)

Table 6. Shannon diversity index (H′), vector loadings and percentage of variation explained by the first five principal components of sorghum genotypes.

Characters	Principal components		
	1	2	3
Variation explained (%)	52.07	15.00	9.19
Latent root	4.687	1.35	0.827
Days to 50% flowering	0.393	-0.073	0.079
Number of leaves/plant	0.397	0.045	0.049
Leaf length (cm)	0.369	0.109	0.146
Leaf width (cm)	0.307	-0.226	0.613
plant height (cm)	0.221	-0.483	-0.636
Stem width (cm)	0.082	0.694	-0.340
Panicle length (cm)	0.400	0.218	-0.092
Panicle weight (g)	0.314	-0.312	-0.257
Single plant yield (g)	0.380	0.264	-0.017

Table 7. Least similar (First five accessions) and most similar (First five accessions) accessions based on dissimilarity index

Most diverse accession	Dissimilarity Index	Most similar accessions	Dissimilarity index.
TNS598 and IS5030	0.879	IS4825 and EP94	0.038
IS5038 and EP60	0.848	IS4085 and EP94	0.039
IS5038 and CO(S)28	0.807	IS8303 and EP94	0.039
TNS598 and IS 2122	0.748	IS9664 and IS1055	0.042
IS5826 and IS5030	0.744	IS 4825 and IS1124	0.052

Table 8. Means of each cluster for the quantitative characters

Cluster No.	Accessions	DF	NL	LL	LW	PH	SW	PL	PW	SYP
I	IS12447, IS2122	52.94	8.90	66.88	7.31	244.25	1.58	40.02	47.22	24.31
II	IS1130, IS18551, IS3436, IS4283, IS4646, IS4789, IS5030, IS9552, SPV615	52.30	9.96	65.39	7.46	134.81	1.68	27.27	54.02	35.31
III	EP88, EP94, IS1124, IS18303, IS2195, IS3585, IS4085, IS4825, IS9664	54.81	10.29	68.77	7.50	235.98	1.91	19.94	64.06	36.12
IV	CO(s)28, CO26, EP60, IS5622, IS5826, K8, TNS598, TNS607, TNS608, TNS609	63.74	11.14	79.50	9.31	215.32	2.15	31.41	160.73	103.03
V	EP57, IS1028, IS1055	63.79	11.55	76.99	9.15	273.87	2.32	22.39	93.78	61.99
VI	APK1, IS19560, IS3573, IS4337, TNS599, TNS603	63.68	11.19	76.03	8.64	209.18	1.77	27.14	92.06	54.00

DF- Days to 50% flowering, NL- Number of leaves per plant, LL-Leaf length (cm), LW-Leaf width (cm), PH-Plant height (cm), SW- Stem width (cm), PL-Panicle length (cm), PW-Panicle weight (g), SPY- Single plant yield (g)

Table 9. Mean value of nine agronomic traits for the sorghum genotypes used in the study.

Genotypes	DF	NL	LL	LW	PH	SW	PL	PW	SPY
IS 4337	65.67	11.67	71.63	9.11	236.73	1.81	21.33	99.00*	34.53
EP 88	58.00*	9.33	67.77	8.09	262.73	1.80	22.33	76.17	23.37
IS 3436	48.33*	7.67	54.87	7.17	142.27*	1.57	31.83*	48.83	20.63
IS 12447	49.67*	8.00	65.83	6.61	232.55	1.58	48.67*	53.97	23.20
IS 2195	52.67*	10.33	77.20	8.44	247.33	1.74	24.67	91.30	29.37
IS 3573	63.33	12.33*	80.17*	8.67	200.47	1.88	26.67	62.40	29.27
IS 2122	56.00*	9.00	66.67	7.78	256.37	1.49	31.83*	40.30	19.43
IS 1130	54.00*	11.00	66.83	6.89	140.93*	1.62	28.67	80.90	37.20
IS4646	54.33*	11.67	66.87	7.11	112.77*	1.46	29.83*	65.93	31.07
IS 4825	50.00*	10.00	60.10	7.44	213.30	1.97	21.17	44.33	21.93
IS 4283	48.67*	9.33	68.30	8.67	136.07*	1.76	28.50	38.37	19.00
SPV 615	50.67*	8.33	64.53	7.28	137.27*	1.80	24.83	64.13	28.17
EP 60	62.33	11.67	75.87	11.03*	231.07	2.45*	27.33	216.87*	92.00*
EP 57	63.67	11.67	75.20	10.22*	265.30	2.34*	24.50	91.53	45.00
IS 1055	64.67	13.00*	86.67*	9.44*	290.00	2.49*	23.43	86.17	36.90
IS 5622	66.00	10.00	76.17	7.72	238.97	2.49*	42.50*	123.63*	69.57*
IS 5826	64.67	10.00	86.73*	10.44*	254.97	2.64*	32.33*	196.40*	87.03*
IS 5030	54.00*	9.00	70.10	7.72	105.87*	1.59	23.33	20.33	13.60
IS 18303	55.33*	10.33	68.20	6.72	205.47	1.87	12.50	42.97	20.53
IS 9664	52.00*	10.67	71.07	7.89	222.63	1.90	23.83	68.47	22.03
IS 19560	62.33	11.33	79.20	7.94	198.20	1.82	29.00	81.23	32.40
EP 94	55.67*	9.67	69.87	7.00	232.40	1.97	15.17	47.07	21.17
IS 3585	55.67*	10.00	67.63	6.94	249.00	1.73	18.33	109.17*	66.80*
IS 18551	55.00*	12.33*	56.97	7.78	160.53*	1.67	29.17	48.40	18.57
IS 1124	65.00	11.33	64.97	5.89	278.53	2.07	22.00	48.20	25.73
IS 4789	49.67*	9.33	63.44	7.22	103.97*	1.64	25.00	49.23	23.23
IS 4085	48.33*	10.33	68.44	8.24	213.73	2.18	18.33	48.37	20.40
IS 9552	55.00*	9.67	69.44	6.51	170.20*	1.72	24.33	69.30	57.00*
IS 1028	63.33	10.67	70.67	8.11	267.30	2.33*	19.00	103.67*	64.27*
CO (s) 28	62.67	12.00	70.78	9.34*	190.50*	2.32*	29.67*	174.77*	92.43*
CO26	62.67	12.00	85.78*	8.94	258.10	2.04	30.33*	113.47*	68.90*
K8	63.67	11.00	83.56*	9.89*	157.30*	1.89	39.00*	126.10*	92.97*
APK1	64.67	10.33	73.11	8.83	193.70*	1.51	27.83	96.80	34.93
TNS 598	65.00	10.67	79.67*	9.00	220.30	1.54	29.67*	194.47*	96.60*
TNS 599	64.00	11.00	78.22	8.95	213.73	1.65	28.33	117.77*	58.90*
TNS 603	62.67	11.33	76.33	8.61	212.30	1.82	29.67*	95.17	63.10*
TNS 607	65.33	12.67*	80.67*	9.94*	153.87*	2.15	31.00*	129.80*	79.47*
TNS 608	64.33	12.00	85.67*	8.66	213.20	2.39*	27.33	182.07*	86.33*
TNS 609	61.67	10.67	78.22	9.36*	235.43	1.95	25.67	151.10*	81.07*
MEAN	58.48	10.60	72.40	8.25	206.55	1.91	26.90	92.26	45.85
CD 5%	2.30	1.57	7.17	1.08	10.18	0.32	2.41	6.24	2.85

DF- Days to 50% flowering, NL- Number of leaves per plant, LL-Leaf length (cm), LW-Leaf width (cm), PH-Plant height (cm), SW- Stem width (cm), PL-Panicle length (cm), PW-Panicle weight (g), SPY- Single plant yield (g)