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Variability and divergence studies in sweet sorghum (*Sorghum bicolor* L.) for ethanol and its related traits

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Abstract
A field experiment was conducted during *Kharif*, 2017 at Agricultural College farm, Bapatla to assess genetic variability, heritability and diversity of 110 sweet sorghum genotypes. The observations were recorded for 13 quantitative traits. Estimates of PCV were narrowly higher than the corresponding GCV values for the characters days to 50% flowering, days to maturity and Stem girth. The number of nodes per plant, grain yield, fresh stalk yield, brix, T.S.S, juice yield and ethanol yield have moderate differences between PCV and GCV values while rest of the characters *viz.*, plant height, 1000 grain weight, panicle weight have shown a higher magnitude of difference between GCV and PCV. All characters studied have shown high heritability coupled with high genetic advance. Diversity analysis using Mahalanobis D^2 grouped 110 genotypes into eight clusters of which Cluster- I was possessing the highest number of genotypes (*i.e.*, 78) followed by Cluster-III with 15 genotypes, Cluster - II with 12 genotypes, Cluster-IV, V, VI, VII, VIII are solitary. The highest inter-cluster distance was observed between cluster II and VIII, followed by Cluster V recorded the highest value for brix% and total sugars estimation, Juice yield recorded the highest means in cluster – VII. Variability results indicates phenotypic selection is effective and based on the diversity, the genotypes from diverse clusters can be used in the hybridization program to generate wide range of transgressive segregants for genetic enhancement of sweet sorghum for ethanol related traits.

Keywords: Variability, diversity, sweet sorghum, ethanol

Introduction
Sorghum is a C_4 crop possessing different range of products like grain sorghum, forage sorghum, sweet sorghum. In India and Africa, it is used as food crop while in Europe and United states it is used as feed for livestock. Profuse alternative use of sorghum is not only as food and feed but also as a bioenergy crop which has rich amounts of sugars in stalks (10-20%) as in sugarcane (Hunter and Anderson, 1997) [1] terming it as sweet sorghum.

One of the important aspect in climate change is the air pollution, which is growing at an alarming rate, primary cause is the industries and secondary source is the exhaust from automobiles using petroleum products, crude oil, gasoline, diesel, *etc*.. as raw material. The dependency on fossil fuels is very high and they are depleting day by day, where there is need for other alternate sources like biofuels from plant based products like Sugarcane, Corn, Sweet sorghum (Reddy *et al.* 2005) [2] Sweet potato (Lareo *et al.* 2013) [3] and sugar beet (Duraisam *et al.* 2017) [4]. The countries *viz;* Brazil, The United States of America (USA) and China are the top ethanol producing countries respectively, while India stands in 4th position producing around 2000 million litres of ethanol, primarily from sugarcane molasses. (Prasad *et al*. 2018) [5]. When compared to sugarcane, the juice from sweet sorghum is possessing high amounts of reducing sugars which aids in the efficient fermentation, producing clear and potable ethanol with low aldehydes (Ratnavathi *et al.* 2003) [6].

The World ethanol production has increased from 13.6 billion gallons in 2007 to 22.3 billion gallons by 2012. (Satyanarayana and Rameshchandra, 2014) [7]. India has produced 530.09 million gallons of ethanol in 2019. (www.staista.com). In order to reduce carbon monoxide emission through automobiles, Indian government has mandated for blending of five per cent ethanol with petrol and diesel and could save nearly 80 million liter of petrol annually, if petrol is blended with ethanol by 10 per cent. (GAIN report 2013) [8]. The government has no stringent regulations for blending ethanol in petrol (gasoline) due to truncated production of sugarcane crop and it's byproduct in the past decade. The sweet sorghum can be a best alternative for ethanol production to meet up the demand of the country, by providing year the

round operations to molasses-based ethanol distilleries and provide an assured income to the farmers. In any breeding programme, there is need for knowing the available variability present. As yield is influenced by a number of yield contributing characters, which are controlled by polygenes and also influenced by environment. Cultivar development is, however, firstly based on the exploitation of genetic variability of the genotypes with the traits of interest (Makanda *et al.*, 2009). Genetic diversity is the basic requirement in any crop improvement programme. It provides a quantitative measure of association between geographic and genetic diversity based on generalized distance (Mahalanobis, 1936) [9]. Sorghum is endowed with high diversity due to its wide range of adaptation in tropical and temperate climates and free gene exchange among various races. In the D^2 statistics enables one to discriminate between different cultivars according to the diversity present in the genotypes and helps in the selection of genetically divergent parents for their exploitation in hybridization programme (Oliveira *et al.*, 2020) [10].

Materials and Methods

110 sweet sorghum genotypes were studied for assessing the variability, diversity in *kharif*, 2017 at Agricultural College, Bapatla. The experiment was conducted in a Randomized Block Design with three replications. Each entry was raised in five rows of 4 m length with 45 x 15 cm spacing. Recommended agronomic practices were followed throughout the crop season. The quantitative traits studied are Days to 50 per cent flowering, Days to Maturity, Plant height, Number of nodes per plant, Stem girth, Panicle weight, 1000 grain weight, Fresh Stalk Weight, Juice yield, Brix per cent, Total Soluble Sugars, Computed ethanol yield, Grain yield.

Results and Discussion

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 the study of genetic variability, which cannot be easily measured. The phenotypic variability in a given environment can be measured easily, but it reflects both non genetic as well as the genetic influence on the phenotypic expression. Genetic facts are inferred from phenotypic observations, which are the results of interactions of a genotype in a given environment. GCV and PCV is only an evidence of the presence of high degree of genetic variation; however, the amount of heritable portion of variation can only be determined with the help of estimates of heritability and genetic advance.

In the current study the estimates of phenotypic coefficients of variation were slightly higher than genotypic coefficient of variation for all characters studied. This indicated that variability for these characters was due to genetic factors and there was less influence of environmental factor in expression of these characters. High values of PCV and GCV indicates that variation in the traits are contributed markedly to the total variability (Biradar *et al.*, 1996) [11]. The estimates of variability parameters for 13 characters in sorghum are presented in table 1.

Moderate estimate of GCV and PCV were observed for days to 50% flowering, days to maturity, while for characters plant height, number of nodes per plant, 1000 grain weight the recorded GCV and PCV were moderate and high respectively. The rest of the traits stem girth, panicle weight, Fresh stalk yield, Juice yield, Total soluble sugars, ethanol and grain yield recorded high GCV and PCV. For characters days to 50% flowering, days to maturity, stem girth narrow difference observed between PCV and GCV indicate less influence of environment on this character. Therefore, phenotypic selection alone is effective for the improvement of these traits and selection based on phenotypic performance could be worth in achieving desired results. Bhagasara *et al.* (2017) [12], Badigannavar *et al*. (2017) [13] observed similar results. Plant height, Number of nodes per plant, stem girth, Brix%, Total soluble sugars indicate moderate influence while, panicle weight, 1000 grain weight, juice yield, ethanol yield and grain yield observed huge difference which indicates huge environmental influence on this character.

Likewise small difference between GCV and PCV observed indicated that there was very little environmental influence on these traits and cannot be improved by providing favourable environment. In general, high coefficient of variability shows scope of selection in favour of traits of interest and low coefficient of variability indicates the need for creation of variability and selection

The results of heritability act as a predictive tool in expressing the real potential of phenotypic value. Therefore, high heritability helps in predictive selection for a desirable character. Heritability in broad sense is the ratio of genotypic variance to the phenotypic variance and is expressed in percentage. In this current study, all 13 quantitative characters studied have shown high heritability which is clearly indicating, the scope for genetic improvement of these characters through phenotypic selection. If the value of heritability in broad sense is high, it indicates that though the character is least operative by the environmental effects, the selection for enhancement of such character at times may not be useful, because broad sense heritability is based on total genetic variance which includes both fixable (additive) and non- fixable (dominance and epistasis) variances.

On the other hand, if the estimates of genetic advance are high, it shows that the character is dominated by additive genes and hence selection shall be fruitful for the improvement of such trait. So high heritability guided with high genetic advance, indicates most likely the heritability is due to additive gene effect and selection may be rewarding.

In the present investigation, high heritability coupled with high genetic advance as percent of mean was observed for all the 13 characters studied Thus, these traits are predominantly under the control of additive gene action and hence these characters can be improved by selection. Tomar *et al.* (2012) [36, 14], Irradi *et al.* (2013) [15], Kalpande *et al*. (2014) [16], Sami *et al.* (2018) [17] and Wadikar *et al*. (2018) [18] have also reported results which are in accordance with above mentioned results.

Table 1: Estimation of Variability, Heritability and Genetic advance per cent of mean for 13 characters in Sorghum [*Sorghum bicolor* (L.) Moench]

S. No.	Character	GCV (%)	PCV (%)	h^2 (%)	GA	GA as% of mean (5%)
1.	Days to 50% Flowering (days)	19.22	19.52	97	31.69	38.97
2.	Days to maturity (days)	14.46	14.72	97	34.02	29.27
3.	Plant height (cm)	19.52	22.28	77	130.48	33.93
4.	Number of nodes per plant	19.01	21.00	82	4.97	35.41
5.	Stem girth (cm)	37.61	38.99	93	1.43	73.95
6.	Panicle weight (g)	28.90	32.12	81	19.89	53.02
7.	1000 grain weight (g)	17.41	20.62	71	8.73	30.25
8.	Fresh stalk yield (T ha^{-1})	37.50	39.09	92	38.17	73.73
9.	Juice yield (l ha^{-1})	40.95	43.38	89	7654.56	79.63
10.	Brix%	23.87	25.49	88	4.50	46.01
11.	Total soluble sugars	23.62	25.20	88	3.97	45.51
12.	Ethanol yield (l ha^{-1})	48.58	51.17	90	426.70	93.23
13.	Grain yield (T ha^{-1})	37.91	40.52	88	2.47	73.07

Divergence Analysis

In any crop improvement plan of action, the prior condition for hybridization programme is the availability of genetic diversity for the desired character. The involvement of genetically diverse lines as parents would result in the creation of superior recombinants (Shinde *et al*. 2013) [19]. An effort has been made in the present investigation to study the genetic diversity amongst the randomly acquired 110 genotypes of sorghum [*Sorghum bicolor* (L.) Moench] for thirteen characters. The results of the study thus obtained are presented and discussed below under the following heads.

The analysis of variance for dispersion had clearly indicated the significant pooled effect of all the characters between 110 studied genotypes. Hence, further studies were initiated to estimate D^2 analysis. The studied 110 genotypes were grouped into eight clusters indicating the presence of a wide range of genetic diversity. Cluster- I, among the 8 clusters was possessing the highest number of genotypes (*i.e.*, 78) indicating the genetic similarity among them and is followed by Cluster-III with 15 genotypes, Cluster - II with 12 genotypes, Cluster-IV, V, VI, VII, VIII are monogenotypic indicating the uniqueness of the genotypes included in those clusters when compared to other genotypes included in the study (Table: 2 and Fig: 1). The results obtained are collinear with the results of Mahajan and Wadikar (2012) [22]; Khadakabhavi *et al*. (2014) [21]; Sinha and Kumaravadivel (2016) [20].

Clustering pattern has also revealed that the genotype EC-23 (from A.P), EG-83 (from Tamil Nadu), PHULE VASUNDHARA (from MPKV, Rahuri), GGUB-62 (from Madhya Pradesh), IS-27072 (from Zimbabwe) are originating from different Agro climatic sources and yet were grouped into a single cluster (*i.e.* cluster -II). While genotypes of GGUB series (16 genotypes) are from one single source (*i.e*. M.P, India) were grouped into different clusters *viz.*, (cluster – I, II, III, VI). It denotes that cluster may accommodate the genotypes from different origins or genotypes from different origins may be grouped into single cluster. It confirms that geographic diversity is not fully reflected in genetic diversity. This also indicates there is a wide variability present among the genotypes though collected from a single source and the reason for variability could be introgression of alleles between the contrasting populations present in the same region. Harlan (1975) [23]. Murty and Arunachalam (1966) [24] have stated that genetic drift and selection in different environments could cause greater genetic diversity than geographical distance. Such unparallelism between geographic and genetic diversity was also reported by Kadam *et al.* (2001) [25]; Meena *et al.* (2016) [26]; Damor *et al.* (2017) [27]; More *et al.* (2018) [28]; Swamy *et al.* (2018) [29].

Contrary to the above quoted statement, 9 out of 10 entries of CJV series from same source were confined to cluster- I and the remaining one in cluster- II, NSJB series comprising total 6 genotypes from a single source (Khammam, India) and yet confined to cluster-II only, without any distribution. The possibility could be either attributed to the common ancestor of these genotypes having same pedigree or due to unidirectional selection pressure that could have been imposed on the genotypes. Further, the free exchange of seed material among different regions might have consequently caused character constellations because of human interference and material may lose its individuality. Such un-distribution of genotypes was also reported by Swamy *et al.* (2018) [29].

The average intra and inter-cluster values among the eight clusters are presented in Table 3. The intra-cluster distances were lower than the inter-cluster distances. Rohman *et al.* (2004) [31]; Sameerkumar *et al.* (2010) [30] obtained the same results as mentioned above. Thus the genotypes included within a cluster had less diversity among themselves. The maximum intra-cluster distance was observed in cluster III followed by cluster I, cluster II and Cluster IV, V, VI, VII, VIII.

Similar results are in accordance with Shinde *et al.* (2013) [19]. It indicated that these accessions were closely related in their evolutionary process and passed through similar evolutionary factors. The genotypes placed within the cluster were less divergent. This might be due to unidirectional selection practised in past that has resulted in uniformity and less divergence between these genotypes.

The highest inter-cluster distance was observed between cluster II and cluster VIII. Therefore crossing between divergent clusters could yield better segregants. This is closely followed by cluster V with cluster-VIII, cluster VII with cluster VIII, while the lowest inter cluster distance was observed between cluster IV and cluster VII. The genotypes belonging to these clusters were separated by high statistical distance and the genotypes having high *per se* performance should be used in hybridization programme for obtaining a wide spectrum of variation among the segregates. In this context, genotypes from cluster V, VI, VII, VIII can be selected in hybridization programme for yield improvement. These findings are in conformity with the findings of Bahadure *et al*. (2014) [32], Elangovan *et al.* (2014) [34], Doijad *et al*. (2016) [33], Prasad and Biradar (2017) [35].

The genotypes grouped into same cluster have displayed the lowest degree of divergence from one another, and in case

crosses are made between genotypes belonging to the same cluster, no transgressive segregant is expected from such combinations. Therefore, hybridization programmes should always be formulated in such a way that the parents belonging to different clusters with maximum divergence could be utilized to get desirable transgressive segregants.

The genotypes for hybridization may be chosen from widely separated clusters, as it is observed that there are single genotypes included in the crossing programme from widely separated clusters. Intercrossing of divergent groups would lead to wide genetic base in the base population and greater opportunities for crossing over to occur, which in turn may release the hidden variability by breaking close linkage. Results are collinear with results of Tomar and Sivakumar (2012) [17, 36] and Sameerkumar *et al*. (2010) [30].

The nearest and the farthest clusters were presented in Table 4. The cluster I was lined up with a huge heterogeneous populations. So, attempting crossing between genotypes of cluster I with cluster VIII genotype may result in early maturing, high biomass, ethanol yielding types, apart from the ethanol yielding, forage type sorghum varieties can also be developed.

Cluster II was very close to cluster V, while far from Cluster VIII, When cluster II genotypes were crossed with cluster V genotype there is less scope for transgressive segregants. Cluster III was nearer to cluster I, crossing among these could be less divergent resulting in segregating offspring, with little scope for improvement, while crossing with cluster II would yield intermediate types to both the parents.

The cluster means for different characters are presented in Table-5. The lowest means for days to 50% flowering and days to maturity are observed in cluster VIII respectively. Cluster means for number of nodes was highest in cluster II, followed by cluster VII and lowest in cluster VIII. The cluster II has recorded the highest mean for plant height, while the lowest in cluster VI. Fresh stalk yield recorded highest in cluster V followed by cluster- II, cluster-III, cluster-I and lowest in cluster-III.

Cluster means for character stem girth was highest in cluster-VI followed by cluster-V. Grain yield recorded maximum in cluster- II followed by cluster- III, cluster IV- cluster V and VII 1000 Grain weight recorded highest means in cluster- VI followed by cluster- IV while the lowest in cluster- I. The highest means for panicle weight was recorded in cluster- IV, V, II while the lowest in VI. Cluster V recorded the highest value for brix% and total sugars estimation followed by cluster- IV, VIII, VII. Juice yield recorded the highest means in cluster – VII followed by cluster- VI whereas the lowest in Cluster – II.

The character ethanol yield has recorded the highest value in cluster VII followed by cluster IV and cluster VI and cluster V whereas the lowest is recorded in cluster –II. All 110 genotypes were spread over 8 clusters and means were scored across the clusters for all the 13 characters, and this is given in Table 5. The highest cluster mean was given the first rank and next cluster is possessing next best means were given 2nd, 3rd and so on up to 8th rank for all the traits (usually for days to 50% flowering, days to maturity, plant height are ranked in ascending order i.e., lowest first rank and highest second rank, but in the present investigation the above mentioned characters has shown positive correlation with ethanol yield).

Finally, the clusters are ranked based on the overall score obtained from 13 characters. The lowest scoring cluster was given the first rank, and next cluster is possessing the score above the previous ones were given 2nd, 3rd and so on up to 8th rank. Figures in the parenthesis, indicate the ranks/grade based on cluster mean. The grade given the largest to the smallest.

The cluster IV ranked first with a score of 40 and cluster V, ranked second with a score of 48, Cluster VII in third position. The next best cluster was Cluster-II and Cluster–I. Cluster VI at next position followed by Cluster –III.

The clusters IV, V, VI, VII and VIII have recorded high mean performance for various characters. Hence the genotypes selected from these clusters can be used as parents in hybridization. Based on cluster means a wide range of variation was observed for ethanol yield and other traits in sweet sorghum. Therefore, it is suggested that lines from most diverse clusters may be used as parents in hybridization programme to develop high yielding hybrids or varieties.

It has been well established that the more genetically diverse parents used in hybridization programme, the greater will be the chances of obtaining high heterotic hybrids and broad spectrum of variability in segregating generations. It has also been observed that the most productive hybrids may come from high yielding parents with high genetic diversity. Similar type of results were given by Tomar and Sivakumar (2012) [17, 36] and Swamy *et al.* (2018) [29].

The contribution of each character towards total genetic diversity is presented in Table 6. Out of 13 characters studied, stem girth has contributed maximum to the genetic divergence followed by days to maturity, days to 50% flowering, Juice yield, brix% followed by fresh stalk weight, number of nodes, 1000 grain weight, plant height, ethanol yield, grain yield, panicle weight whereas total soluble sugars didn`t contribute to the divergence. Similar results are reported by Rohman *et al.* (2004) [31]; Tomar and Sivakumar (2012) [17, 36] and Elangovan *et al*. (2014) [34]. In the current study, these above mentioned characters were liable for genetic divergence in the ranking order. Selection of parents for hybridization programme on the basis of these characters stem girth, days to maturity, days to 50% flowering, juice yield, brix%, panicle weight, grain yield, ethanol yield, plant height. 1000 grain weight, number of nodes, stalk weight could yield better segregants.

Table 2: Grouping of 110 Sorghum [*Sorghum bicolor* (L.) Moench] genotypes into 8 clusters

Cluster	No of genotypes	Name ` of genotypes
1	78	CJV-07,CJV-16, CJV-17, CJV-18,CJV-19,CJV-21,CJV-24,CJV-25; DHBM-3; DHBM-5; E-40, E-63; EB-14, EB-15, EB-19, EB-20, EC-15, EC-20, EC-22, EC-25; EG-11, EG-19, EG-21, EG-22, EG-23, EG-24, EG-25, EG-39, EG-78, EG-81, EG-82, EG-84; EP-29, EP-61, EP-80, EP-84; GGUB-13, GGUB-27, GGUB-33, GGUB-43, GGUB-45, GGUB-50, GGUB-54, GGUB-61, GGUB-63, GGUB-64,GGUB-65, GGUB-67, GGUB-68; ICSSH-71; ICSV-12012, ICSV-25306, ICSV-25308, ICSV-25316; IS-1331, IS-2337, IS-27239, IS-2814, IS-3515, IS-1474; NSJB-6605; PV-22; RSSV-1381; SEVS-29, SEVS-04, SEVS-20, SEVS-29; SPV-2196, SPV-2328; SSS-10,SSS-14, SSS-15,SSS-23, SSS-46, SSS-62, SSS-65, SSV-74, SSV-84.
2	12	NSJB-6585, 6662,6657,6577,6648, 6629, EC-23, EG-83, EG-80, Phule Vasundhra, GGUB-62, IS-27072
3	15	EB-22, POP-15, CJV-26, IS-4599, IS-29469, IS-29650, RAJ-24, CSV-19 SS, SPV-2325, GGUB-29, IS-2834, CSV-24SS, PV-12, IS-30310, IS-6910
4	1	IS-29308
5	1	ICSV-15006
6	1	GGUB-28
7	1	SEVS-08
8	1	IS-3980

Table 3: Intra and inter cluster distances in 110 Sorghum [*Sorghum bicolor* (L.) Moench] genotypes tested

	Cluster 1	Cluster 2	Cluster 3	Cluster 4	Cluster 5	Cluster 6	Cluster 7	Cluster 8
Cluster 1	39.49	103.13	93.09	66.15	80.15	108.14	101.85	273.98
Cluster 2		26.98	255.74	115.67	98.58	248.44	134.60	596.33
Cluster 3			54.16	123.11	205.14	144.94	149.37	146.92
Cluster 4				0.00	87.44	141.91	50.54	326.11
Cluster 5					0.00	122.17	171.93	406.92
Cluster 6						0.00	192.45	193.69
Cluster 7							0.00	406.31
Cluster 8								0.00

Table 4: The nearest and farthest clusters from each cluster based on D^2 values in 110 Sorghum [*Sorghum bicolor* (L.) Moench] genotypes

S. No.	Cluster	Nearer Cluster	Farthest Cluster
1	I	IV (66.15)	VIII (273.98)
2	II	V (98.58)	VIII (596.33)
3	III	I (93.09)	II (255.74)
4	IV	VII (50.54)	VIII (326.11)
5	V	IV (87.44)	VIII (406.92)
6	VI	I (108.14)	II (248.44)
7	VII	IV (50.54)	VIII (406.31)
8	VIII	III (146.92)	V (406.92)

Table 5: Cluster means for 13 characters studied in 110 Sorghum [*Sorghum bicolor* (L.) Moench] genotypes

	DAF 50%	D.M	PH	N.N.S	SG	PW	1000 GW	FSTK	JY	BRIX	TSS	EY	GY	Score	Rank
++[T	80.78 (5)	115.84 (4)	373.83 (5)	13.86 (3)	2.03 (4)	33.86 (5)	28.33 (8)	54.28 (4)	9079.93 (6)	9.81 (5)	8.73 (5)	427.43 (6)	2.97 (3)	63	5
Cluster 2	111.56 (1)	114.50 (5)	435.30 (1)	18.78 (1)	2.54 (3)	35.45 (3)	29.29 (7)	71.00 (3)	8069.54 (8)	9.08 (7)	8.10 (7)	347.87 (8)	3.33 (1)	55	4
Cluster 3	66.40 (6)	100.00 (6)	317.14 (6)	11.29 (7)	0.80 (7)	32.17 (6)	30.84 (3)	22.30 (8)	10310.77 (4)	9.40 (6)	8.37 (6)	427.30 (7)	3.10 (2)	74	8
Cluster 4	95.00 (2)	116.33 (3)	389.13 (3)	13.33 (4)	1.73 (5)	44.17 (1)	33.08 (2)	41.53 (6)	16597.51 (3)	15.00 (2)	13.27 (2)	1173.29 (2)	2.60 (5)	40	1
Cluster 5	87.33 (4)	118.00 (2)	315.93 (7)	13.00 (5)	3.23 (2)	39.20 (2)	29.36 (6)	89.95 (1)	8548.14 (7)	17.33 (1)	15.31 (1)	695.53 (4)	2.53 (6)	48	2
Cluster 6	57.00 (7)	83.00 (7)	153.00 (8)	17.00 (2)	3.32 (1)	25.77 (8)	35.03 (1)	72.87 (2)	16730.85 (2)	9.00 (8)	8.02 (8)	718.07 (3)	2.03 (7)	64	6
Cluster 7	93.67 (3)	133.33 (1)	411.67 (2)	13.00 (5)	1.25 (6)	30.64 (7)	29.66 (4)	45.27 (5)	27022.20 (1)	10.00 (4)	8.90 (4)	1265.11 (1)	2.53 (6)	54	3
Cluster 8	26.33 (8)	53.00 (8)	387.67 (4)	12.00 (6)	0.73 (8)	35.15 (4)	29.47 (5)	29.25 (7)	9333.32 (5)	11.33 (3)	10.06 (3)	526.87 (5)	2.87 (4)	70	7

DAF 50%= Days to 50% flowering (Days), D.M= Days to maturity (Days), PH= Plant height (cm), N.N.S= Number of nodes per plant, SG= Stem girth (cm), PW= Panicle weight (g), 1000 GW= 1000 grain weight (g), FSTK= Fresh stalk yield (T ha^{-1}), JY= Juice yield (l ha^{-1}), Brix%, TSS = Total soluble sugars (%), EY= Ethanol yield (l ha^{-1}), GY = Grain yield (T ha^{-1}).

Table 6: Contribution of 13 quantitative characters to divergence studies in Sorghum [*Sorghum bicolor* (L.) Moench] genotypes

S. No.	Source	Contribution	% times ranked first
1	DAF	19.58%	1174
2	DM	22.2%	1331
3	PH	1.48%	89
4	N.N.S	2.42%	145
5	SG	22.49%	1348
6	PW	0.17%	10
7	1000 GW	2.22%	133
8	FSTK	7.02%	421
9	JY	10.39%	623
10	BRIX	9.89%	593
11	TSS	0.00%	--
12	EY	1.32%	79
13	GY	0.82%	49

DAF 50%= Days to 50% flowering (Days), D.M= Days to maturity (Days), PH= Plant height (cm), N.N.S= Number of nodes per plant, SG= Stem girth (cm), PW= Panicle weight (g), 1000 GW= 1000 grain weight (g), FSTK= Fresh stalk yield (T ha^{-1}), JY= Juice yield (l ha^{-1}), Brix%, TSS = Total soluble sugars (%), EY= Ethanol yield (l ha^{-1}), GY = Grain yield (T ha^{-1}).

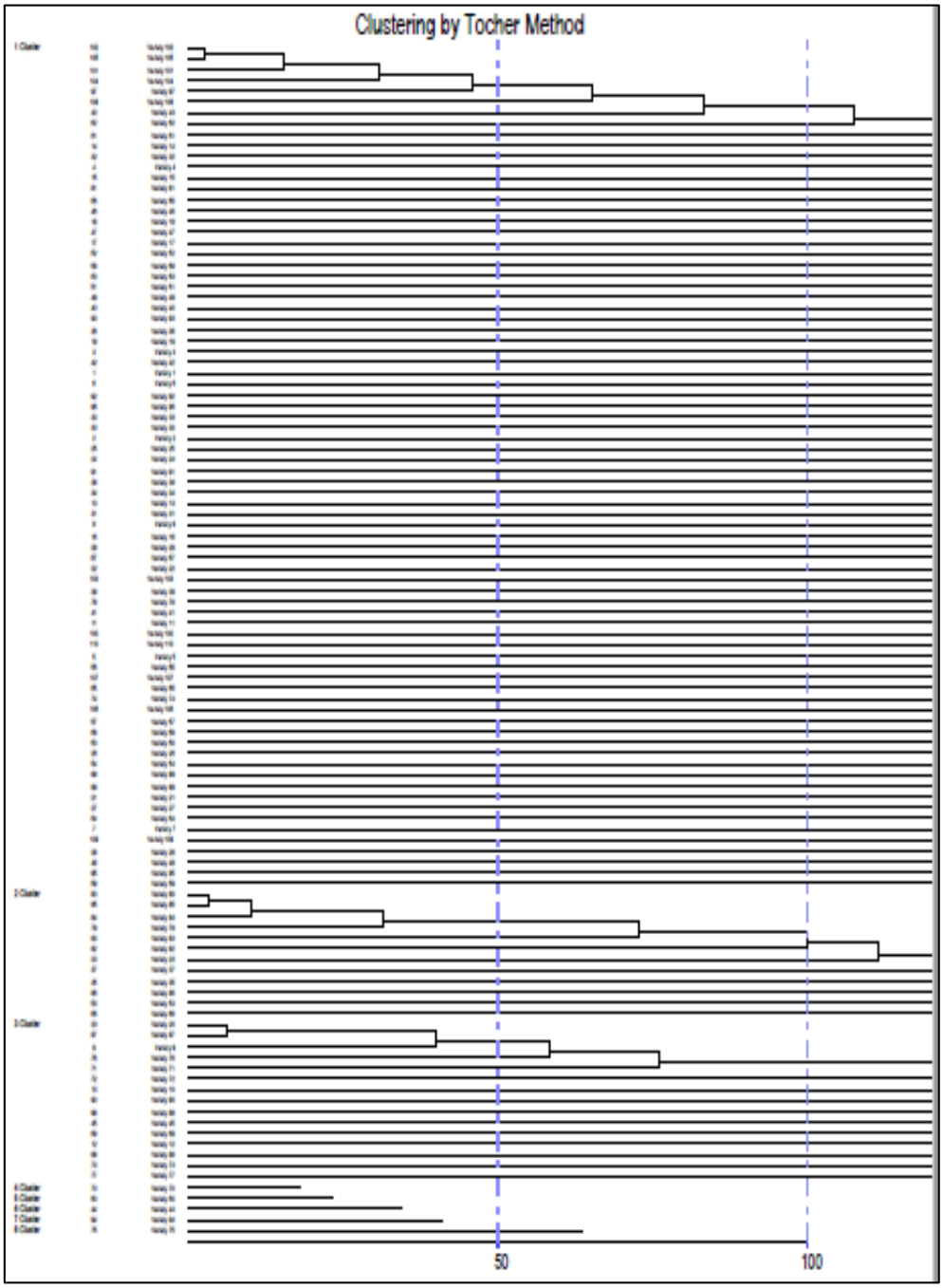

Fig 1: Grouping of 110 Sorghum genotypes into 8 clusters by Tocher`s method

Conclusions

For characters days to 50% flowering, days to maturity, stem girth narrow difference observed between PCV and GCV indicate less influence of environment on this character. Therefore, Selection based on phenotypic performance could be worth in achieving desired results. Plant height, Number of nodes per plant, stem girth, Brix%, Total soluble sugars indicate moderate influence while rest of the traits observed huge difference which indicates huge environmental influence on this character. High heritability guided with high genetic advance for 13 characters is predominantly under the control of additive gene action hence selection may be rewarding.

Based on inter-cluster distances, the most divergent clusters observed are cluster II and cluster VIII. This is closely followed by cluster V with cluster-VIII, cluster VII with cluster VIII. The genotypes belonging to these clusters were separated by high statistical distance and the genotypes having high *per se* performance should be used in hybridization programme for obtaining a wide spectrum of variation among the segregates. Based on cluster means, genotypes from cluster IV, V, VI, VII, VIII can be selected in hybridization programme for yield improvement.

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