Pak. J. Agri. Sci., Vol. 53(1), 121-128; 2016
ISSN (Print) 0552-9034, ISSN (Online) 2076-0906
DOI: 10.21162/PAKJAS/16.4823
http://www.pakjas.com.pk

CHARACTERIZATION OF LOCAL AND EXOTIC SUGARCANE GENOTYPES ON THE BASIS OF MORPHOLOGICAL AND QUALITY RELATED ATTRIBUTES

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The current breeding program of sugarcane in Pakistan does not fulfill the variety evolution of desired characters. It mostly depends on import of exotic fuzz-seed of sugarcane varieties, without keeping varietal characters in view. So, it is the dire need of the time to characterize the sugarcane germplasm not only for saving resources but also for finding genetic relationships among breeding materials for overall sugarcane crop improvement. In the present study 60 genotypes of sugarcane, belonged to 3 research stations two of Pakistan and one from Sri Lanka, were characterized using Principal Component Analysis (PCA) and Cluster Analysis. At maturity data were analyzed for 19 traits and analyzed. PCA showed seven principal components (PCs) having eigen value more than one and exhibited 72.1% variability in the genotypes. Four groups of PCA were formed for the traits. Cluster analysis placed genotypes in seven groups. Groups were not formed according to origins of genotypes which might be due to resemblance in their progenitors. Each cluster was also marked for specific trait improvement related to that cluster based upon maximum mean value of that trait, either through selection or hybridization. Four traits were found better in Sugarcane Research Institute, Faisalabad (SRI, FSD) genotypes, five in Shakarganj Sugarcane Research Institute (SSRI), Jhang genotypes and three in Sugarcane Research Institute (SRI), Udawalawae, Sri Lankan genotypes, on the basis of mean values. Thus more emphasis could be given on these traits related to specific station for use in variety selection program for improvement of target trait. Another interesting conclusion drawn from the study was that clusters were not formed according to genotypes of a specific research station because these local and exotic sugarcane genotypes are allopolyploid (with aneuploidy) hybrids, and can be traced back to founder clones (*S. officinarum* × *S. spontaneum*).
Keywords: Sugarcane, breeding, morphology, PCA, clustering, genetic diversity.

INTRODUCTION

Sugarcane (*Saccharum* spp. hybrids) is grown in many countries of the world like other agricultural crops for different purposes. Human and animal needs such as food, feed and fuel are being satisfied by this crop (D'Hont *et al.,* 1998). Sugar and its by-products like ethanol, molasses, bagasse, press mud and wax etc. are derived from this non cereal grass which is widely cultivated in tropical and subtropical regions of the world. It recently has attained particular consideration as a second generation energy crop for cellulosic ethanol due to its high-biomass (Pinto *et al.,* 2010; Suman *et al.,* 2011). It is an important cash crop of Pakistan, mainly grown for sugar and sugar-related products like *Gur* and *Shakr* . Keeping in view the prominent position of sugarcane in the agricultural industry, strenuous efforts are being made for the improvement of this crop for sustainable and better agronomic traits (Nawaz *et al.,* 2013). So, for fulfilling the needs of ever increasing population it is crucial to increase sugar yield of this crop.

Sugar yield is a quantitative character and depends upon cane yield and sugar recovery. Considering the constraints (latitude, diurnal temperature, humidity and photo period), for true seed (fuzz) production of sugarcane in the country the chances of genetic improvement through conventional breeding only are very low. Assessment of genetic diversity is very important for the improvement of sugarcane because diverse parents could be crossed by breeders for producing viable superiors (Hamrick 2004). Sugarcane breeding has thrived all over the world largely by intercrossing the original inter-specific hybrids and their derived progenies. Genetic diversity in cultivated sugarcane is alarmingly narrow (Berding and Roach, 1987) because only a few clones were involved in the original crosses (Irvine 1999). In Pakistan new varieties of sugarcane are mostly evolved through selection. The selection procedure can be strengthen to many folds if the scientists are well aware with the genetic makeup of parentage used. Mostafa *et al.* (2011) described that an understanding of genetic diversity for finding genetic associations among

populations, makes the heterogeneous groups of specific lines.

Different statistical techniques have been used including Principal Component Analysis (PCA) and Cluster Analysis by Ward's method for characterization of genotypes and same were successfully practiced in sugarcane (Olaoye 1999; Luo *et al.,* 2005; Ilyas, 2011; Klomsa *et al.,* 2013; Brasileiro *et al.,* 2013; Tahir *et al.,* 2013; You *et al.,* 2013), rice (Ogunbayo *et al.,* 2005), cotton (Rana *et al.,* 2005) and bread wheat (Khodadadi *et al.,* 2011; Fahim 2014).

Therefore, the present study was undertaken for grouping of parents and various traits in order to use in future breeding program keeping in view the region-wise specific traits of genotypes.

MATERIALS AND METHODS

The germplasm used in the present study were obtained from SRI, FSD having 31 genotypes including series: Canal Point (CP), Sao Paulo (SP), Hawaii (H) and Barbados (B); SSRI, Jhang having 15 genotypes including series: Sao Paulo (SP), Canal Point (CP), CSIRO, Australia (CS) and Hauma (Ho) and SRI, Udawalawae, Sri Lanka having 14 genotypes including series: Philippine (PH), Coimbatore (Co), Mauritius (M) and North Carolina (NC) in their progenitors (Table 1).

Double budded setts of 60 sugarcane genotypes were planted to raise the crop at experimental field, at latitude 30-35° to 31-47° North and 72-80° to 73-40° East longitude, of Sugarcane Research Institute, Ayub Agricultural Research Institute (AARI), Faisalabad-Pakistan, on loamy soil having pH of 7.8, EC (0.36 dsm-1) and organic matter of 0.90 (%). Sixty genotypes were planted in randomized complete block design with 3 replications. Three rows (5 meters long) for each genotype were maintained with a row to row distance of 60cm and plant to plant 25cm. The crop was given 168-112-112kg NPK/ha as urea, single super phosphate and potash (MOP), respectively. The crop was planted in February 2013 and harvested in early January 2014. Meteorological data for growing periods of the crop were collected from the Observatory of Plant Physiology, Agronomic Research Institute, Ayub Agricultural Research Institute, Faisalabad, Pakistan (Fig.1). All other agronomic practices and plant protection measures were applied uniformly when required during crop season. At maturity data were recorded for cane thickness (cm), cane length (cm), leaf area (cm^2), number of leaves per plant, number of tillers per plant, inter-nodal length (cm), leaf margins, inter-node shape, growth habit, bud type, cane shape, trashing, cane color, Brix (%), pol (%), purity (%), fiber (%), commercial cane sugar (CCS%) and sugar recovery (%).

The data were analyzed using Ward's linkage cluster analysis and principle component analysis (Ogunbayo *et al.,* 2005). Widow operated SPSS version 12.0 was used for cluster analysis and for PCA "R language" was used. To group all studied genotypes and determine their genetic affinity, cluster analysis was performed using the squared Euclidean and Ward's method (Kumar *et al.,* 2009). Average standardized data were used for cluster analysis, whereas, diagnosis function was used for separating the clusters of dendrogram. Cluster analysis identified variables which were further clustered into main group and subgroups. Principal component analysis simplified the complex data by transforming number of correlated variables into a smaller number of variables called principal components. The first principal component accounted for maximum variability in the data as compared to each succeeding component. Scatter diagram was plotted to show the variation pattern. Mean value of each variable was standardized prior to cluster and PCA to avoid the effects due to difference in scale.

Table 1. Pedigree of 60 sugarcane genotypes.

Sr.	Varieties/Clones	Female	Male	ID
1	CPF 247	CP-87-1628	CP84-1198	1-F
2	SPF 245	G 6888	-	2-F
3	S2003–US-618	CP -87-1628	CP 84-1198	3-F
4	S2002-US-628	US-90-1090	CP72-1210	4-F
5	S2003-US-247	CP89-879	CP88-764	5-F
6	HSF 240	CP-43-33	CP84-1198	6-F
7	CPF 237	86P-19	CP 70-1133	7-F
8	SPF 234	SP- 71-8210	SP -71-6180	8-F
9	S2003-US-718	CP -87-1628	CP- 84-1198	9-F
10	S2003-US-778	CP -43-33	CP -89-879	10-F
11	S2003-US-165	CP -89-879	CP-90-956	11-F
12	S2002-US-312	CL-75-0853	CP-86-1180	12-F
13	HSF 242	SPHS- 89-2085	CP -89-879	13-F
14	CP -77-400	Introduction	-	14-F
15	CP 72-2086	CP 62-374	CP 63-558	15-F
16	CPF 246	US -90-1093	CP- 81-1425	16-F
17	SPF 213	SP -70-1006	-	17-F
18	S2003-US-694	CP87-1628	CP84-1198	18-F
19	S2003-US-633	CP87-1628	CP84-1198	19-F
20	S2003-US-127	CP89-879	CP90-956	20-F
21	S2003-US-410	US90-25	HoCP85-845	21-F
22	S2003-US-114	CP89-879	CP90-956	22-F
23	S2002-US-133	CP88-1561	CP85-1491	23-F
24	S96-SP-302	Co.1148	BL-4	24-F
25	S2005-US-54	CP92-1167	CP93-1634	25-F
26	CPF 235	86P-30	CP 70-1133	26-F
27	BF 162	Co 1001	-	27-F
28	S2002-US-312	CL75-0853	CP86-1180	28-F
29	CP 43-33	Introduction	-	29-F
30	BL 4	PoJ 2878	-	30-F
31	SPF 238	Polly cross	CP49-34	31-F

Cont. Table 1

Sr.	Varieties/Clones	Female	Male	ID
32	SPSG 79	N5679	SP70-1143	32-J
33	SPSG 26	SP73-5358	SP70-1143	33-J
34	NSG 311	N19	Mo/F	34-J
35	SPSG 394	N5679	SP70-1143	35-J
36	HoSG 1296	CP90-956	RSB90-12	36-J
37	NSG 59	87F2007	77Fo790	37-J
38	CPSG 3481	CP85-1308	CP81-1238	38-J
39	CPSG 2923	CP93-1309	HoCP94-822	39-J
40	CSSG 668	81-N289	CP74-2005	40-J
41	CSSG 676	ROC-01	CP74-2005	41-J
42	CPSG 2875	CP93-1309	HoCP94-822	42-J
43	CPSG 437	CP92-1320	CP92-1167	43-J
44	HoSG 1257	CP88-702	CP86-1747	44-J
45	HoSG 315	CP90-956	CP89-879	45-J
46	CSSG 2476	MG87-1215	86A-3626	46-J
47	SL 92-5588	CP 56 59	Poly cross	47-SL
48	SL 95-4443	PH 85 296	Co 775	48-SL
49	SL 96-771	Co 1148	SL 85 18	49-SL
50	SL 89-1673	CP 63 306	NCO 339	50-SL
51	SL 92-4997	SL 7229	Selfed	51-SL
52	SL 94-3325	CP 77-414	SLC 91-8	52-SL
53	SL 96-328	Co 1148	Co 527	53-SL
54	SL 96-128	Co 775	CP 77 414	54-SL
55	SL 92-4918	CP 64 103	selfed	55-SL
56	SL 95-4432	Co 775	PHIL 56 59	56-SL
57	SL 71-03	Co 775	SL 63 01	57-SL
58	SL 96-278	SLC 91 01	CP 70 300	58-SL
59	SL 93 945	CP 48 103	selfed	59-SL
60	SL 95 4033	LF 75 10045	PH 83 1164	60-SL

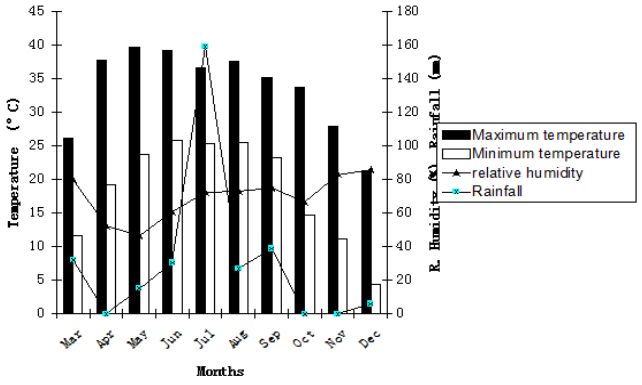

Figure 1. Meteorological data at AARI, Faisalabad, Pakistan-2013.

Data matrix of 60 × 19 were prepared and averages were analyzed using Ward's linkage cluster analysis (WLCA) and principal component analysis. Out of 19, 7 PCs exhibited eigen value more than one (Table 2a) and accounted about 72.1% of variability and were given due importance for further explanation.

The PC_1 accounted for 19.3%, PC_2 12.2%, PC_3 10.9%, PC_4 9.6%, PC_5 8%, PC_6 6.6% and PC_7 showed 5.6% variability among genotypes for traits under study (Table 2a). The most effective traits in first component PC_1 were: sugar recovery, polarity, purity and CCS while number of leaves/plant, leaf area and internode length in PC_2. PC_1 was mostly related to quality parameters while PC_2 morphological traits related to foliage. Brix was an effective trait in third component (PC_3) while cane diameter, bud type and trashing values showed greatest effective influence on PC_4. Brix is quality controlling factor while PC_4 parameters mostly related to morphological traits related to variety identification characters. PC_5 was mostly related with leaf margins, growth habit and cane shape (morphological traits related to variety identification) while in PC_6 most genotypes were related to cane length, tillers/plant and fiber. Overall, PC_6 was closely related to yield traits. The PC_7 was good in internodal shape and cane color (morphological traits related to variety identification) (Table 1b). From first seven PCs it was clear that among all the 19 variables, cane length had highest weight-age value (Table 2b).

***Scree plot*:** Scree plot explained the percentage variance associated with each principal component, obtained from the graph between eigen values and principal component numbers. The PC_1 showed 19.3% variability with eigen value of 3.67 in the germplasm and gradually decreased (Table 2a). It tends to straight after 7th PC, subsequent to little variance was observed in each PC. It ends at 5.3 % at 7th PC with eigen value 1.005. The graph showed 72% variation is present in first seven PCs (Fig. 2).

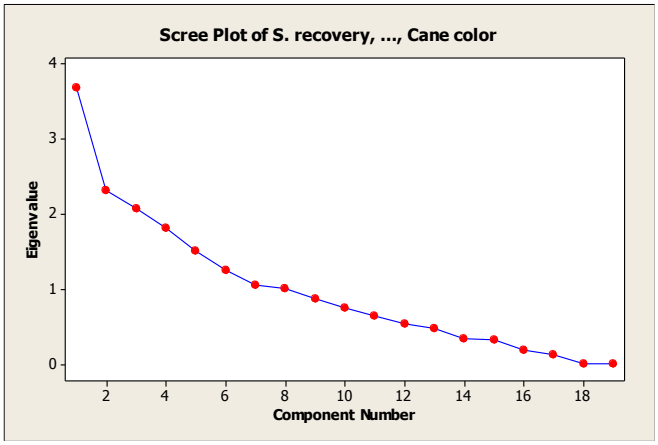

Figure 2. Scree plot analysis between eigen values and number of principal components using principal component analysis.

Table 2b. Principal components of 60 sugarcane genotypes for 19 characters.

Variable	PC_1	PC_2	PC_3	PC_4	PC_5	PC_6	PC_7
SR	-0.492	-0.116	0.006	-0.027	0.117	-0.051	0.056
LM	-0.046	-0.076	0.303	0.319	-0.433	0.162	-0.070
NL/P	0.200	-0.406	0.023	-0.149	0.199	0.141	-0.069
LA	0.060	-0.442	-0.220	0.128	-0.280	-0.144	0.260
CL	0.051	-0.065	0.124	0.203	0.065	-0.597	0.273
CD	0.021	-0.198	-0.012	-0.398	0.194	-0.260	0.244
IL	0.147	-0.457	-0.119	0.199	-0.165	0.259	0.154
T/P	0.007	0.213	-0.127	0.370	0.028	-0.431	-0.213
B	0.142	0.131	0.574	-0.133	0.071	-0.045	0.157
POL	-0.389	-0.099	0.302	-0.112	0.096	0.057	0.093
PU	-0.402	-0.114	-0.382	0.070	0.039	0.015	-0.072
F	0.170	-0.320	0.073	-0.017	-0.043	-0.376	-0.246
CCS	-0.492	-0.116	0.006	-0.027	0.117	-0.050	0.056
IS	0.093	0.257	-0.348	-0.126	-0.067	-0.126	0.431
GH	0.179	-0.112	-0.153	0.037	0.451	-0.003	-0.381
BT	0.116	0.027	-0.183	-0.362	0.035	0.053	-0.182
CS	-0.144	0.126	-0.095	-0.182	-0.425	-0.170	-0.401
T	-0.016	0.011	0.041	0.500	0.430	0.098	-0.006
CC	0.095	0.269	-0.227	0.123	0.070	0.217	0.298

SR=Sugar recovery, IL=Internodal length, IS=Internode shape, CC=Cane color, CCS= Commercial Cane Sugar, B=Brix, GH=Growth habit, L/P= Number of leave per plant, POL=Polarity, BT=Bud type, LA=Leaf area, PU=Purity, CS=Cane shape, CL=Cane length, F=Fiber, T=Trashing, CD=Cane diameter, T/P=Tiller per plant, LM=Leaf margins.

***Score plot*:** The character loading was used to calculate the accession component scores. The first two components were extracted for two dimensional ordinations of genotypes (Fig. 3). Principle component score or scatter plot depicted that the accessions that were close together, supposed to be similar when rated on the 19 variables. While accessions which were farther apart might be different from each other.

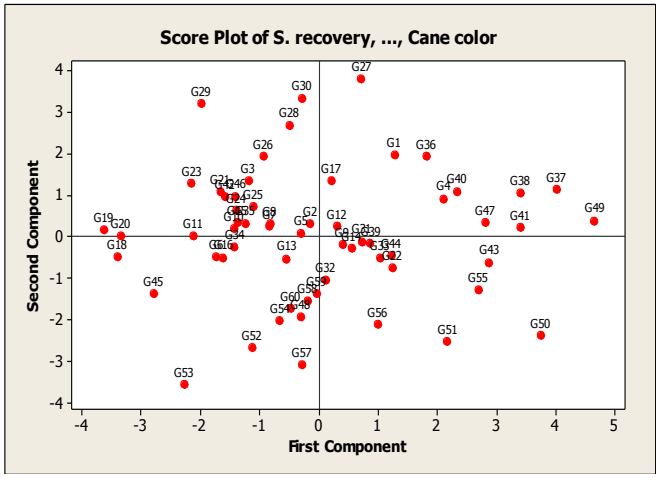

Figure 3. Two dimensional ordinations using principal component axis I and II for 60 genotypes of sugarcane.

The accessions 10-15-35, 7-8, 21-42, 33-44, 31-39, 9-14 and 4-40 were very close to each other on score plot. The accessions 27 and 53, 29 and 50, 49 and 45 were at opposite axis to each other. The accessions 52, 57, 56, 51, 55, 43 were spread on score plot at distance. The present results showed that Pakistani's genotypes were at opposite axis to Sri Lankan's on score plot (in score plot genotypes 1-31 represents the codes of SRI, FSD genotypes while 47-60 of SRI, Sri Lanka).

***Loading plot*:** The projection traits on PC_1 and PC_2 revealed that length of 4 vectors (CCS, sugar recovery, number of leaves/plant and internode length) were greater than others, followed by leaf area, polarity and purity (Fig. 4).

While minimum length of vector related to leaf margins. Cane shape and growth habit were opposite to each other, and negatively correlated. Similarly, internodal shape and cane color were at opposite axis to leaf margins and showed negative association with each other (Figure 4). It may be concluded from the results of principal component analysis that characters could be grouped in 4 categories, namely: "quality related traits", "morphological traits related to foliage", "yield traits" and "morphological traits related to variety identification characters".

The results from cluster analysis were placed in 7 groups. All genotypes based on minimum variance method.

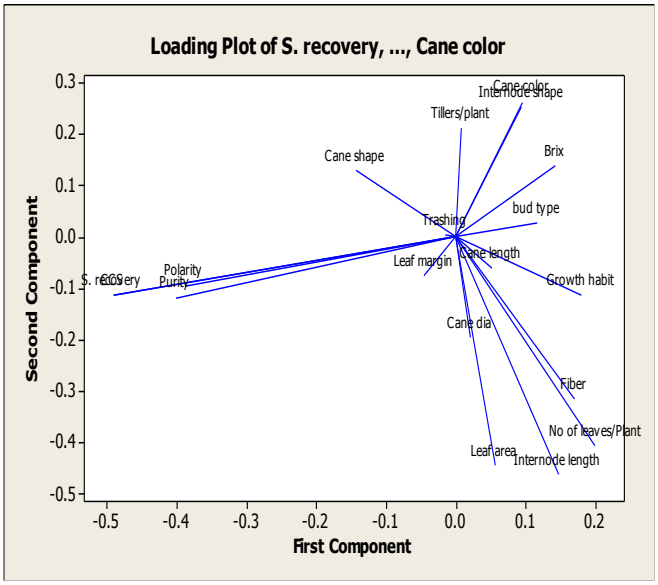

Figure 4. Loading Plot of 60 genotypes of sugarcane on Principal Component axis I and II.

Cluster I had 13 genotypes (Fig. 5) which were further divided into 3 sub-clusters (1a, 1b, 1c) on the basis of similarities. This cluster belonged to genotypes from all the three stations. Accessions grouped in cluster I had highest cane diameter but lower in polarity and majority of genotypes related to ovate typed bud.

Cluster II contained 2 sub-clusters (2a, 2b) which also had 13 genotypes (Fig. 5). This cluster contained genotypes mostly belonged to SRI, FSD. Accessions grouped in cluster II had higher tillers/plant, cane length, sugar recovery, fiber and CCS. While majority of genotypes were having serrated leaf margins, medium trashing, straight cane shape and round buds.

Cluster III had 6 genotypes (Fig. 5) in 2 sub-clusters (3a, 3b) and almost all belonged to SRI, Sri Lanka. Accessions grouped in cluster III were higher in number of leaves/plant and internodal length. While majority of genotypes were bearing cylindrical shaped internodes, erect type of growth habit, medium trashing type and whitish green cane color.

Clusters IV included 6 genotypes (Fig. 5) with 2 sub-clusters (4a, 4b). 5 of them belonged to SRI, Sri Lanka. Accessions grouped in cluster IV had highest leaf area and purity but lower in Brix. Majority of genotypes were having light green cane color with semi erect growth habit.

Cluster V contained 3 sub-clusters (5a, 5b, 5c) consisting of 8 genotypes (Fig. 5) belonged to SRI, FSD and SSRI, Jhang. Accessions grouped in cluster V had highest polarity and Brix while leaf margins were found to be serrated in majority of genotypes.

Cluster VI had 2 sub-clusters (6a, 6b) which contained 11 genotypes (Fig. 5) among which 6 genotypes were from SRI, FSD while 5 genotypes were from SSRI, Jhang.

Cluster VII contained 2 sub-clusters (7a, 7b) with 3 genotypes (Fig. 5) which all belonged to SRI, FSD.

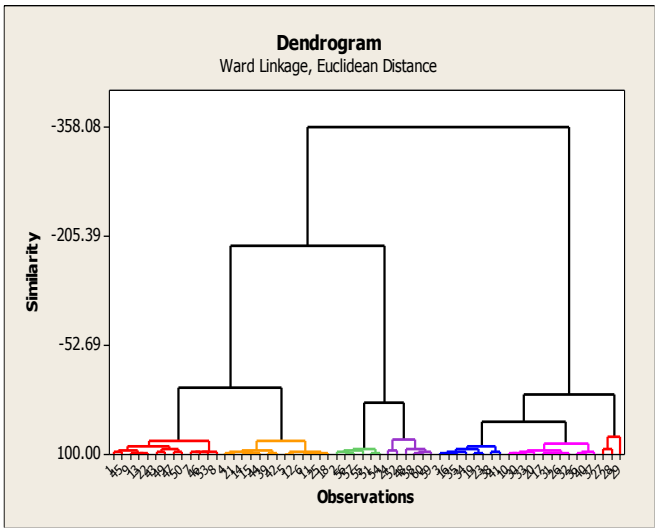

Figure 5. Dendrogram of 60 genotypes of sugarcane for 19 studied variables using Ward's Linkage method.

The germplasm contained CP, Ho, CS, SL, B, SP and N series genotypes and were grouped in same cluster irrespective of their geographical origins. Furthermore, genotypes from three stations (SRI-FSD, SSRI-Jhang and SRI-Sri Lanka) did not fall in separate clusters, rather almost each cluster was mixed with genotypes of all stations. The means and standard errors for all the clusters are given in Table 3.

From the table of mean values and standard deviations of clusters (Table 3) it was concluded that selection of genotypes for high cane diameter could be from cluster I. Similarly for sugar recovery, cane length, tillers/plant, fiber and CCS cluster II genotypes could be preferable. For number of leaves/plant and internodal length cluster III, for leaf area and purity cluster IV and for high Brix and polarity cluster V genotypes could be selected. Maximum differences for traits were observed among clusters II and III while maximum similarity observed among clusters number. IV and VI. Mean values were also calculated of each station genotypes for each trait. Like means of all 31 genotypes of SRI, FSD for cane diameter were combined and similar was done for other two station genotypes and then trait with maximum value in particular station was written in front of that station (Table 4). So on the basis of this calculation it was concluded that SRI, FSD genotypes were higher for number of tillers per plant,

Table 3. Means and standard errors of all seven clusters.

Variable	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI	ClusterVII
SR	11.13±1.43	11.91±0.51	11.09±0.97	11.67±1.33	11.61±0.77	11.03±1.69	11.02±0.77
NL/P	13.33±1.30	12.28±1.42	14.33±1.22	12.81±2.19	13.62±1.37	12.61±1.41	10.30±0.90
LA	574.74±15.16	527.21±25.9	629.18±11.26	700.82±7.92	455.73±9.07	489.68±9.92	372.41±70.15
CL	2.41±0.33	2.73±0.43	2.57±0.48	2.33±0.28	2.46±0.33	2.21±0.37	2.03±0.50
CD	2.68±0.21	2.54±0.31	2.57±0.09	2.52±0.23	2.51±0.15	2.55±0.15	2.36±0.20
IL	16.55±5.17	13.52±6.20	23.38±1.16	21.23±0.83	13.61±5.38	13.13±1.37	12.87±1.70
T/P	2.23±0.50	2.53±0.21	2.11±0.35	2.33±0.34	2.07±0.17	2.24±0.23	2.44±0.50
B	19.48±1.90	20.44±1.28	18.18±2.09	17.75±2.49	21.13±2.01	20.31±2.86	18.76±0.90
POL	16.45±1.36	17.43±0.69	16.58±1.23	17.26±0.98	17.81±0.34	16.87±1.14	16.58±1.13
PU	84.58±8.00	85.67±2.48	87.25±5.28	89.01±9.05	82.73±6.67	83.20±10.57	88.24±4.08
F	13.82±1.18	14.16±0.36	14.12±0.92	13.45±1.22	13.03±0.96	13.84±0.85	11.91±0.09
CCS	11.84±1.53	12.67±0.54	11.79±1.03	12.42±1.41	12.34±0.81	11.74±1.81	11.72±0.82
IS	Conidial	Cylindrical	Cylindrical	Conidial	Cylindrical	Cylindrical	Conidial
GH	Erect	Erect	Erect	Erect	Erect	Erect	Erect
BT	Ovate	Round	Round	Round	Round	Round	Round
CS	Straight	Straight	Straight	Straight	Zigzag	Straight	Straight
T	Loose	Medium	Medium	Loose	Loose	Loose	Medium
CC	Light purple	Light purple	Whitish green	Light green	Whitish	Greenish white	Greenish purple
LM	Serrated	Serrated	Serrated	Serrated	Serrated	Serrated	Serrated

SR=Suger recovery, IL=Internodal length, IS=Internode shape, CC=Cane color, CCS= Commercial Cane Sugar, B=Brix, GH=Growth habit, L/P= Number of leave per plant, POL=Polarity, BT=Bud type, LA=Leaf area, PU=Purity, CS=Cane shape, CL=Cane length, F=Fiber, T=Trashing, CD=Cane diameter, T/P=Tiller per plant, LM=Leaf margins.

sugar recovery, purity and CCS. SSRI, Jhang genotypes were higher for number of leaves per plant, cane length, cane diameter, Brix and polarity while SRI, Sri Lanka genotypes were higher for leaf area, internodal length and fiber.

Table 4. Character selection from each station of the basis of mean values of a particular station genotypes.

Sr. No.	Characters	Region
1	Number of tillers per plant	SRI, FSD
2	Sugar recovery	
3	Purity	
4	CCS	
5	Number of leaves per plant	SSRI, Jhang
6	Cane length	
7	Cane diameter	
8	Brix	
9	Polarity	
10	Leaf area	SRI, Sri Lanka
11	Internodal length	
12	Fiber	

DISCUSSION

Popular genetic materials could form the breeder's initial material for developing cultivars. Characterization and accurate estimation of genetic diversity is very important in crop breeding as it helps in the selection of desirable genotypes, identifying diverse parental combination for further improvement through selection in the segregating populations (Mohammadi and Prasanna, 2003). This study evaluated the breeding worth of sugarcane source material.

The use of multivariate statistical analysis like PCA has potential to increase the comprehension of relationship among variable and could be helpful in understanding the nature of traits (Al-Sayed *et al.*, 2012). The conducted PCA allowed the reduction of 19 primary characteristics to 7 PCs. The new trait's groups were named: quality related traits, morphological traits related to foliage, yield traits and morphological traits related to variety identification characters. Means for improvement of quality related traits, consideration could be made via traits: sugar recovery, purity, polarity, CCS and Brix for specific trait improvement or on all traits at a time for overall quality upgrading. Similar is for other 3 concluded groups. Traits fall under one variable/group could be selected for the improvement of that specific variable/group. Tahir *et al.* (2013) categorized the components into two groups named “Vigor, and “Quality. Deepak *et al.* (2012) came up with similar findings like ours and found quality traits (Brix, Pol) in first two principal components. Al-Sayed *et al.* (2012) found yield parameters in first 3 PCs contributing 85.3% variability contrary to our

results which showed yield traits in 6th PC. In present study first 7 PCs exhibited 72% variation. Contrary to our results Muyco (2000) found 4 principal components giving rise to 76% variation in the data. The results of loading plot/biplot indicated that sugar recovery and CCS had positive and high association with both polarity and purity and cane diameter with tillers/plant as angle between these vectors was very small (Acute, <90°). These results contrasted to Smiullah *et al.* (2013) where they found that cane diameter had higher association with number of nodes. Sugarcane genotypes from Pakistan were at opposite axis on score plot to Srilankan genotypes. Similar results were obtained by Gulnaz *et al.* (2012) in wheat where they found Pakistani varieties were at opposite axis to CIMMYT varieties.

Cluster analysis showed that on the basis of geographical origins, there was no correspondence between clustering of genotypes. The germplasm contained genotypes of three regions and were grouped in same cluster irrespective of their geographical origin. Tahir *et al.* (2013) found similar findings but opposite results were found by Olaoye 1999 who found two groups of genotypes on the basis of region. This suggested that the genotypes of different regions have genetic similarity and could have been derived of same genetic material. The formation of groups is important in progenitor choice in breeding programs, since the new hybrid populations should be established on the basis of the magnitude of their dissimilarities and on the "*per se*" potential of the progenitors. The Ward's clustering method has permitted the formation of groups in the studies of various crops, like; sugarcane (Tahir *et al.,* 2013; You *et al.,* 2013; Luo *et al.,* 2005; Ilyas *et al.,* 2005), wheat (Khodadadi *et al.,* 2011) and *Brassica rapa* (Mahmud *et al.,* 2011). The clustering pattern of the genotypes revealed that varieties/lines originating from the same places did not form a single cluster because of direct selection pressure. This indicates that geographic diversity has not related to genetic diversity that may be due to continuous exchange of genetic materials among countries of the world. Same results had been reported by Anand and Rawat (1984) in brown mustard. Higher estimate of inter-cluster between cluster II and IV was observed which indicated wider genetic diversity between these two groups. Thus, genotypes with high index for specific character that fall into different clusters could be inter-crossed to have maximum hybrid vigor and good number of useful segregants. Hybridization of these two groups may result in transgressive recombinants for important biometric traits.

***Conclusion*:** The findings of this study suggested 4 groups for 19 variables using PCA, named quality related traits, morphological traits related to foliage, yield traits and morphological traits related to variety identification. Cluster analysis grouped genotypes in seven groups. Group I and II contained 13 genotypes each; similarly group III and IV contained 6 genotypes each. Group V had 8, group VI 11 while group VII had 3 genotypes. Two conclusions were drawn through cluster analysis. First is genotypes falling in respective cluster could be selected for trait improvement mentioned with that specific cluster either through selection or hybridization. This was separately concluded for five clusters. Second conclusion was trait improvement for future breeding on the basis of mean values from studied genotypes for all the three mentioned stations. Four mentioned traits could be improved by selection in SRI, FSD genotypes, five in SSRI, Jhang and three in SRI, Sri Lankan genotypes.

***Acknowledgments*:** This work was supported by Sugarcane Research Institute, AARI, Faisalabad and Shakarganj Sugar Research Institute, Jhang-Pakistan.

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