

## GENETIC ITEMIZATION OF EXOTIC SUGARCANE CLONES ON THE BASIS OF QUANTITATIVE AND QUALITATIVE PARAMETERS

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### Abstract

Sugarcane varietal development program in Pakistan primarily depends on evaluation of imported genotypes because of the unfavorable climatic conditions for sugarcane flowering and hybridization in the country. Performance of 41 exotic sugarcane clones was assessed in this study on the basis of seven quantitative (plant height, number of tillers, internode length, number of internode, cane girth, cane yield, and weight per stool) and six qualitative (sucrose %, brix %, CCS %, fiber %, sugar recovery % and sugar yield) attributes. Sugarcane clones comprised of fifteen genotypes from Canal Point (USA), eight from Homma (USA), and eighteen from Brazil. The clones exhibited statistically significant differences for tillers per plant, weight per stool, plant height, cane yield, brix%, sucrose%, fiber%, sugar recovery and sugar yield. Highest cane yield of 51.66 t/ha was observed for Canal Point clone CPNIA-240 while the lowest yield of 26.66 t/ha was recorded in Homma clone HoNIA-795. The highest sugar recovery (10.83 & 10.81) was exhibited by the clones SPNIA-396 and SPNIA-8 whereas the lowest (4.00) was observed in clone SPNIA-05. Moreover, maximum sugar yield was recorded in clone SPNIA-8 (5.37 tha<sup>-1</sup>) and minimum was observed in clone SPNIA-05 (0.91). Ward's linkage cluster analysis of the exotic clones placed the genotypes into six major groups in dendrogram. Genotypes appeared in the clusters irrespective of their geographical location. Cluster II, IV and V showed excellent qualitative, combination of quantitative and qualitative, and quantitative characters respectively. Clones from different clusters demonstrate genetic variations and thus can be subjected to selection and hybridization for further improvement. The accessions demonstrating excellent cane and sugar yield can serve as potential candidates for varietal development program in Pakistan.

**Key words:** Sugarcane, Cane yield, Sugar recovery, Exotic clones, Screening.

### Introduction

Sugarcane is one of the most important field crops. It accounts for approximately 75% of sugar production in the world (FAO Statistics, 2015). Modern sugarcane is an outstandingly complex aneuploid polyploid interspecific hybrid of *Saccharum officinarum* and *Saccharum spontaneum* (Irvine, 1999). Sugarcane also carries enormous importance in bio-energy (ethanol and electricity) production in many of the tropical and subtropical countries (Waclawovsky *et al.*, 2010; Khan *et al.*, 2017).

Sugarcane varietal development program in Pakistan, where the climatic conditions does not favor flowering of the crop, mostly depends upon the introduction of exotic fuzzi and genotypes from foreign sugarcane breeding centers. Nearly all varieties of this crop currently cultivated in Pakistan have been developed through direct introduction or selection of the exotic fuzzi (Khan *et al.*, 2015). Sugarcane yield and recovery may decline over time; therefore, it is essential to develop and select new genotypes having high yield potential. Evaluation of exotic sugarcane varieties in different ecological zones for agronomic performance is necessary before a variety is introduced for commercial cultivation.

It has been reported that yield of sugarcane can be improved by adopting superior genotypes and utilizing modern agricultural practices (Heinz, 1987). Cultivation of unapproved and inferior sugarcane genotypes is the major reason of low cane yield and sugar recovery (Mian, 2006). Quality of cane juice also depends upon many factors including genotypic potential, age of the crop, agronomic management, and the environmental conditions (Khan *et al.*, 2003). Resolution of the low sugar recovery and cane yield problems lies in the development and adoption of better cane genotypes (Chattha *et al.*, 2006). Thus, sugarcane researchers are

focusing to increase cane production through selection of improved varieties and better agricultural technology (Gill, 1995).

Assessment of genetic diversity is very important for the improvement of sugarcane as diverse parents could be crossed by the breeders for producing viable superiors (Hamrick, 2004). Genetic diversity of modern cane is very narrow (Berding & Roach, 1987) because of the fact that only a few sugarcane clones constituted the original crosses in the development of commercial cane (Irvine, 1999). In Pakistan, new varieties of sugarcane are mostly evolved through selection. Mostafa *et al.* (2011) reported that comprehensive information of genetic associations among populations made the parental selection easier and meaningful for future breeding programs. Selection of a suitable genotype for a particular agroclimatic zone is an essential requirement to explore yield and sugar recovery potential. Diverse genetic resources of a crop species provide the source for developing new varieties of crops thus making it possible to select the genotypes having better ability to strive and cope with the biotic and abiotic stresses of a particular area of cultivation (Sajjad & Khan, 2009).

Cluster analysis is used to investigate the nature of divergence among crop genotypes using different agronomic and quality characteristics (Nagatomi & Ohshiro, 1983). In present study, 41 accessions of sugarcane clones collected from three different sugarcane breeding centers viz., Canal Point (USA), Homma (USA), and Brazil were grown at the Nuclear Institute of Agriculture (NIA), Tando Jam, Pakistan during the spring cropping season. This is the first ever report of performance of these particular genotypes in agroclimatic conditions of Sindh province. An attempt is made to determine the genetic relationship within the 41 adapted sugarcane clones and evaluate the major qualitative and quantitative traits by

cluster analysis using ward's linkage method. Primary aim of the study was to investigate genetic diversity in a collection of exotic clones having contrasting traits under subtropical environment of Sindh, Pakistan. Sindh produces comparatively less yield in spite of its better suitability for the sugarcane crop regarding agroclimatic conditions of the province. Thus, there is a strong need to evaluate exotic germplasm for their adaptation in the province, and then hybridize the genotypes based on their genotypic and phenotypic dissection.

## Materials and Methods

To assess the genetic potential, a set of 41 promising clones were sown at Nuclear Institute of Agriculture (NIA) Tando Jam, Pakistan, during the spring cropping season of 2013-14 and 2014-15. The experiment was laid out in randomized complete block design (RCBD) with four replications. All the agronomic practices were carried out as described by Khan *et al.* (2015).

The analysis of variance (ANOVA) was performed using Statistix Computer Software v. 8.1 (Statistix, 2006). Data were also subjected to Ward's Linkage Cluster Analysis (Ogunbayo *et al.*, 2005). Statistical software SPSS (Statistical Package for Social Studies) version 21 was used for Ward's cluster analysis on windows operating system employing squared Euclidean distance method (Kumar *et al.*, 2009). Dendrogram of the data was developed to visualize and classify the results, and to get an insight into genetic and phenotypic affinity of the sugarcane clones. Considering the difference in scales of different variables, mean data were standardized to z-scores before subjecting it to cluster analysis. Finally, data were averaged for all the resulting clusters using Microsoft Office Excel version 2013.

## Results and Discussion

**Quantitative characters:** The analysis of data revealed significant differences among all the quantitative characters (Tables 1, 2 & 3). The highest plant height (268.0 & 254.33 cm) was observed in Brazil clones SPNIA-2875 and SPNIA-26 followed by Canal Point clone CPNIA-223 and Homma clone HoNIA-34 (241.67 & 233.67 cm respectively) while, the lowest height was recorded in Canal Point clone CPNIA-2923 (77.67cm). Maximum average cane thickness was recorded in Brazil clone SPNIA-12 and Canal Point clone CPNIA-223 (2.40 cm). The results revealed that the clone HoNIA-254 and CPNIA-223 remained on top regarding internodes per plant (21.33) followed by SPNIA-2713 (20.66) whereas; minimum internodes per plant were recorded in CPNIA-2923 (13.66). The maximum numbers of tillers per plant is a major parameter for enhancing the final yield of sugarcane. SPNIA-238, SPNIA-8, SPNIA-2875, SPNIA-05, and CPNIA-2875 were observed to have maximum numbers of tillers per plant (6.66) and minimum numbers of tillers (2.66) were recorded for clone SPNIA-12 (Table 3). The maximum germination and tillering with synchronized millable canes of average girth are important selection characters to assess the agronomic performance of sugarcane

varieties (Sharma & Agarwal, 1985). Habib *et al.* (1991) stated that number of stool and weight per stool per plot were major characters of cane yield. The Canal Point clone CPNIA-240 remained on top with maximum weight per stool (5.16 kg m<sup>-2</sup>) and cane yield (51.66 t ha<sup>-1</sup>). Whereas, the Homma clone HoNIA-795 produced lowest weight per stool (2.66 kg m<sup>-2</sup>) and average cane yield of 26.66 t ha<sup>-1</sup>. Nazir *et al.* (1997) proposed that superior cane yield was a role of high potential of a genotype. Javed *et al.* (2002) also suggested that cane yield depends upon number of stools per hectare and weight per stool. Similar results were also reported by Nadeem *et al.* (2011).

**Qualitative characteristics:** Statistical analysis of the data depicted highly significant differences at  $p \leq 0.05$  for all the qualitative parameters as well (Tables 4, 5 & 6). Commercial cane sugar percent (CCS%) is a major parameter of cane quality determined by the genotypic makeup of the variety and the environment. The maximum CCS% values were recorded for clones SPNIA-8 (11.50%) followed by CPNIA-718 and HoNIA-520 (10.33% & 10.00%, respectively). The maximum sucrose percent (16.23%) was recorded in clone SPNIA-8 followed by CPNIA-718 (14.85%) and the minimum sucrose % was shown by the clone SPNIA-05 (7.46%). The highest sugar recovery (10.83%) was exhibited by the clone SPNIA-396 whereas the minimum (4.00%) was recorded for the clone SPNIA-05 (Table 6). Earlier studies by Sarwar *et al.*, (2011) and Khalid *et al.* (2014) also reported similar results. The total fiber solids in the extracted cane juice are considered as brix contents. The highest brix percent (20.33%) was obtained in clone SPNIA-8, followed by CPNIA-718 and HoNIA-520 (19.00% & 18.66%). While, the minimum brix percent (11.66%) was observed in clone SPNIA-05. The maximum fiber percent (17.03%) was observed in clone SPNIA-238 followed by CPNIA-718 and HoNIA-520 (16.24% & 13.21%). Whereas the minimum fiber was recorded in SPNIA-571 (9.98). The maximum sugar yield was recorded in clone SPNIA-8 (5.37 tha<sup>-1</sup>) followed by HoNIA-05 and CPNIA-2875 (4.81 & 4.44 tha<sup>-1</sup>) and minimum was observed in clone SPNIA-05 (0.91 tha<sup>-1</sup>). Performance of sugarcane clones is determined by genetic make-up of the crop. Thus, genetically improved and artificially selected genotypes may have the capability to produce adequate results for per hectare yield and sugar percentage under certain agroclimatic conditions (EL-Geddway *et al.*, 2002).

**Cluster analysis:** Cluster analysis of the sugarcane genotypes resulted in six major groups (Fig. 1). Sugarcane clones appeared in same clusters regardless of their geographical backgrounds. Moreover, some of the genotypes (SPNIA-45321, SPNIA-05, and CPNIA-223) appeared to be distinctly unique from other clones in the major groups. All the clusters represented certain distinguishing unique features of the accessions they comprised of. Classification of accessions into different clusters is presented in Table 7, whereas means of the parameters for each cluster is presented in Table 8.

**Table 1. Quantitative traits of sugarcane genotypes from Homma, USA.**

Clones	Plant height (cm)	Girth (cm)	Number of internode/plant	Internode length (cm)	Tillers/plant	Weight/stool (kg m <sup>-2</sup> )	Cane yield (t/ha)
HoNIA-520	112.67d	2.20a	14.66e	7.66d	3.66d	3.83bc	38.33bc
HoNIA-05	190.33b	2.23a	19.66bc	9.66b	6.66a	4.83a	48.33a
HoNIA-795	162.00c	2.30a	18.66c	8.66c	4.66bc	2.66d	26.66d
HoNIA-750	111.33d	2.36a	16.66d	6.66e	4.66bc	3.66c	36.66c
HoNIA-254	177.67bc	2.30a	21.33a	8.33cd	4.66bc	4.16abc	41.66abc
HoNIA-552	118.00d	2.26a	18.66c	6.33e	4.33cd	3.50cd	35.00cd
HoNIA-34	233.67a	2.23a	20.00b	11.66a	5.33b	4.83a	48.33a
HoNIA-31	172.67bc	2.23a	20.33ab	8.33cd	4.66bc	4.66ab	46.66ab
SE ±	12.47	0.08	0.48	0.44	0.43	0.43	4.30
LSD (5%)	26.74	0.18	1.03	0.96	0.93	0.92	9.23

**Table 2. Quantitative traits of sugarcane genotypes from Canal Point, USA.**

Clones	Plant height (cm)	Girth (cm)	Number of internode/plant	Internode length (cm)	Tillers/plant	Weight/stool (kg m <sup>-2</sup> )	Cane yield (t/ha)
CPNIA-223	241.67a	2.40a	21.33a	11.33a	5.66ab	4.83ab	48.33ab
CPNIA-11	174.33b	2.33ab	18.66b	9.33bc	5.33bc	3.33de	33.33de
CPNIA-240	180.67b	2.30abc	18.66b	9.66b	5.33bc	5.16a	51.66a
CPNIA-319	177.00b	2.30abc	18.33b	9.66b	4.33cde	4.16bc	41.66bc
CPNIA-640	155.00c	2.30abc	16.00d	9.66b	5.66ab	3.33de	33.33de
CPNIA-718	122.67de	2.30abc	16.00d	7.66d	4.66bcd	3.33de	33.33de
CPNIA-437	136.00d	2.26abc	15.66de	8.66c	3.66de	3.33de	33.33de
CPNIA-5008	111.33e	2.26abc	16.66cd	6.66e	4.66bcd	2.83ef	28.33ef
CPNIA-212	135.33d	2.23bc	20.33a	6.66e	5.66ab	3.66cd	36.66cd
CPNIA-500	111.33e	2.23bc	16.66cd	6.66e	5.00bc	3.66cd	36.66cd
CPNIA-2086	136.00d	2.23bc	15.66de	8.66c	4.66bcd	2.66ef	26.66ef
CPNIA-2875	118.00e	2.23bc	17.66bc	6.66e	6.66a	4.83ab	48.33ab
CPNIA-2923	77.67f	2.23bc	13.66f	5.66f	3.33e	2.33f	23.33f
CPNIA-3338	112.67e	2.20bc	14.66ef	7.66d	6.66a	4.66ab	46.66ab
CPNIA-32	155.33c	2.16c	16.66cd	9.33bc	5.66ab	4.16bc	41.66bc
SE±	8.40	0.07	0.53	0.39	0.49	0.39	3.92
LSD (5%)	17.21	0.15	1.08	0.79	1.00	0.80	8.03

**Table 3. Quantitative traits of sugarcane genotypes from Brazil.**

Clones	Plant height (cm)	Girth (cm)	Number of internode/plant	Internode length (cm)	Tillers/plant	Weight/stool (kg m <sup>-2</sup> )	Cane yield (t/ha)
SPNIA-238	134.67ghi	2.23bc	18.33c	6.33g	6.66a	4.33ab	43.33ab
SPNIA-1237	156.67efg	2.23bc	16.66d	8.66d	3.66de	3.33c	33.33c
SPNIA-45321	127.00i	2.13c	16.33d	6.66fg	3.66de	2.33de	23.33de
SPNIA-05	170.00cde	2.20bc	18.66c	8.66d	3.33ef	2.16e	21.66e
SPNIA-8	153.00efgh	2.30ab	19.66b	7.66e	6.66a	4.66a	46.66a
SPNIA-2875	268.00a	2.20bc	18.66c	13.66a	6.66a	4.66a	46.66a
SPNIA-12	160.67def	2.40a	18.66c	7.66e	2.66f	2.16e	21.66e
SPNIA-26	254.33a	2.30ab	20.00ab	10.66b	3.66de	2.33de	23.33de
SPNIA-449	133.33hi	2.30ab	16.66d	7.33ef	5.00bc	3.16cd	31.66cd
SPNIA-18	159.00ef	2.20bc	18.66c	7.00efg	4.33cd	3.66bc	36.66bc
SPNIA-2713	182.33bcd	2.23bc	20.66a	8.66d	4.66c	3.33c	33.33c
SPNIA-571	140.00fghi	2.20bc	16.66d	7.66e	3.66de	3.33c	33.33c
SPNIA-396	160.67def	2.16bc	16.66d	8.66d	3.66de	3.16cd	31.66cd
SPNIA-2004	203.67b	2.30ab	18.66c	9.66c	4.66c	3.66bc	36.66bc
SPNIA-18	159.67ef	2.26abc	16.66d	8.66d	4.66c	4.33ab	43.33ab
SPNIA-234	149.33efghi	2.16bc	18.66c	7.66e	5.66b	3.33c	33.33c
SPNIA-24	144.00fghi	2.13c	16.66d	8.66d	4.66c	3.66bc	36.66bc
SPNIA-27	186.33bc	2.16bc	18.66c	9.66c	5.66b	3.66bc	36.66bc
SE±	10.99	0.07	0.32	0.32	0.37	0.41	4.16
LSD (5%)	22.34	0.14	0.66	0.66	0.75	0.84	8.46

**Table 4. Qualitative traits of sugarcane genotypes from Homma, USA.**

Clones	CCS %	Sucrose %	Sugar recovery %	Brix %	Fiber %	Sugar yield (t/ha)
HoNIA-520	10.00a	14.51a	9.40a	18.66a	13.06a	3.81bc
HoNIA-05	9.95a	14.35a	9.35a	18.50a	12.45ab	4.81a
HoNIA-795	9.74a	14.18a	9.15a	18.33a	13.06a	2.58d
HoNIA-750	9.39ab	13.51ab	8.83ab	17.66ab	11.29abc	3.45bcd
HoNIA-254	8.62bc	12.85bc	8.10bc	17.00bc	13.21a	3.60bc
HoNIA-552	8.52bc	12.51bc	8.01bc	16.66bc	11.77abc	2.97cd
HoNIA-34	8.37cd	12.18cd	7.87cd	16.33cd	10.55bc	4.04ab
HoNIA-31	7.57d	11.18d	7.12d	15.33d	10.11c	3.54bc
SE±	0.43	0.59	0.40	0.58	0.91	0.42
LSD (5%)	0.92	1.27	0.87	1.26	1.97	0.90

**Table 5. Qualitative traits of sugarcane genotypes from Canal Point, USA.**

Clones	CCS %	Sucrose %	Sugar recovery %	Brix %	Fiber %	Sugar yield (t/ha)
CPNIA-223	6.37h	10.35f	5.98h	14.50f	16.24a	3.08cd
CPNIA-11	9.21bcd	13.18bcd	8.65bcd	17.33bcd	10.54g	3.09cd
CPNIA-240	7.30gh	11.35ef	6.87gh	15.50ef	14.54bc	3.77abc
CPNIA-319	8.39cdef	12.51cde	7.88cdef	16.66cde	13.06cde	3.48bcd
CPNIA-640	8.69cd	13.18bcd	8.17cd	17.33bcd	15.18ab	2.92cde
CPNIA-718	10.33a	14.85a	9.71a	19.00a	12.62def	3.44bcd
CPNIA-437	8.25cdefg	12.18de	7.75cdefg	16.33de	11.76defg	2.77def
CPNIA-5008	7.37fgh	11.51ef	6.93fgh	15.66ef	15.18ab	2.12ef
CPNIA-212	8.85bcd	13.51bc	8.32bcd	17.66bc	16.10ab	3.26cd
CPNIA-500	9.77ab	14.01ab	9.18ab	18.16ab	11.57efg	3.58abcd
CPNIA-2086	7.61efg	11.51ef	7.15efg	15.66ef	12.73def	2.04ef
CPNIA-2875	9.17bcd	13.51bc	8.62bcd	17.66bc	13.29cd	4.44a
CPNIA-2923	8.19defg	12.51cde	7.70defg	16.66cde	14.97ab	1.92f
CPNIA-3338	9.27bc	13.51bc	8.71bc	17.66bc	12.41def	4.34ab
CPNIA-32	8.57cde	12.51cde	8.05cde	16.66cde	11.29fg	3.56abcd
SE±	0.49	0.63	0.47	0.63	0.78	0.44
LSD (5%)	1.02	1.29	0.96	1.30	1.60	0.91

**Table 6. Qualitative traits of sugarcane genotypes from Brazil.**

Clones	CCS %	Sucrose %	Sugar recovery %	Brix %	Fiber %	Sugar yield (t/ha)
SPNIA-238	7.62i	12.10f	7.16i	16.33fg	17.03a	3.32defg
SPNIA-1237	8.38gh	12.46ef	7.88gh	16.66ef	12.47efg	2.78fg
SPNIA-45321	5.82j	9.44h	5.47j	13.66h	13.68cd	1.36ij
SPNIA-05	4.26k	7.46i	4.00k	11.66i	13.41cde	0.91j
SPNIA-8	11.50a	16.23a	10.81a	20.33a	12.44efg	5.37a
SPNIA-2875	10.26bc	14.50cd	9.65bc	18.66cd	10.81ijk	4.81ab
SPNIA-12	7.55i	11.99fg	7.10i	16.66ef	14.97b	1.64ij
SPNIA-26	8.23h	12.07f	7.73h	16.33fg	10.53jk	1.92hi
SPNIA-449	8.75fgh	13.05e	8.22fgh	17.33e	13.13def	2.77fg
SPNIA-18	7.34i	11.37g	6.90i	15.66g	13.68cd	2.68gh
SPNIA-2713	9.58de	14.32d	9.00de	18.50cd	15.18b	3.19defg
SPNIA-571	9.10ef	12.99e	8.55ef	17.16e	9.98k	3.04efg
SPNIA-396	11.53a	16.24a	10.83a	20.40a	12.20fgh	3.65de
SPNIA-2004	10.73b	15.16bc	10.09b	19.26bc	11.64ghi	3.93cd
SPNIA-18	10.45b	15.22b	9.82b	19.26bc	14.34bc	4.53bc
SPNIA-234	10.61b	15.31b	9.98b	19.73ab	12.44efg	3.54def
SPNIA-24	9.87cd	14.21d	9.28cd	18.26d	12.44efg	3.62de
SPNIA-27	8.79fg	12.92e	8.27fg	17.33e	11.29hij	3.22defg
SE±	0.25	0.32	0.24	0.39	0.51	0.41
LSD (5%)	0.52	0.66	0.49	0.79	1.04	0.83

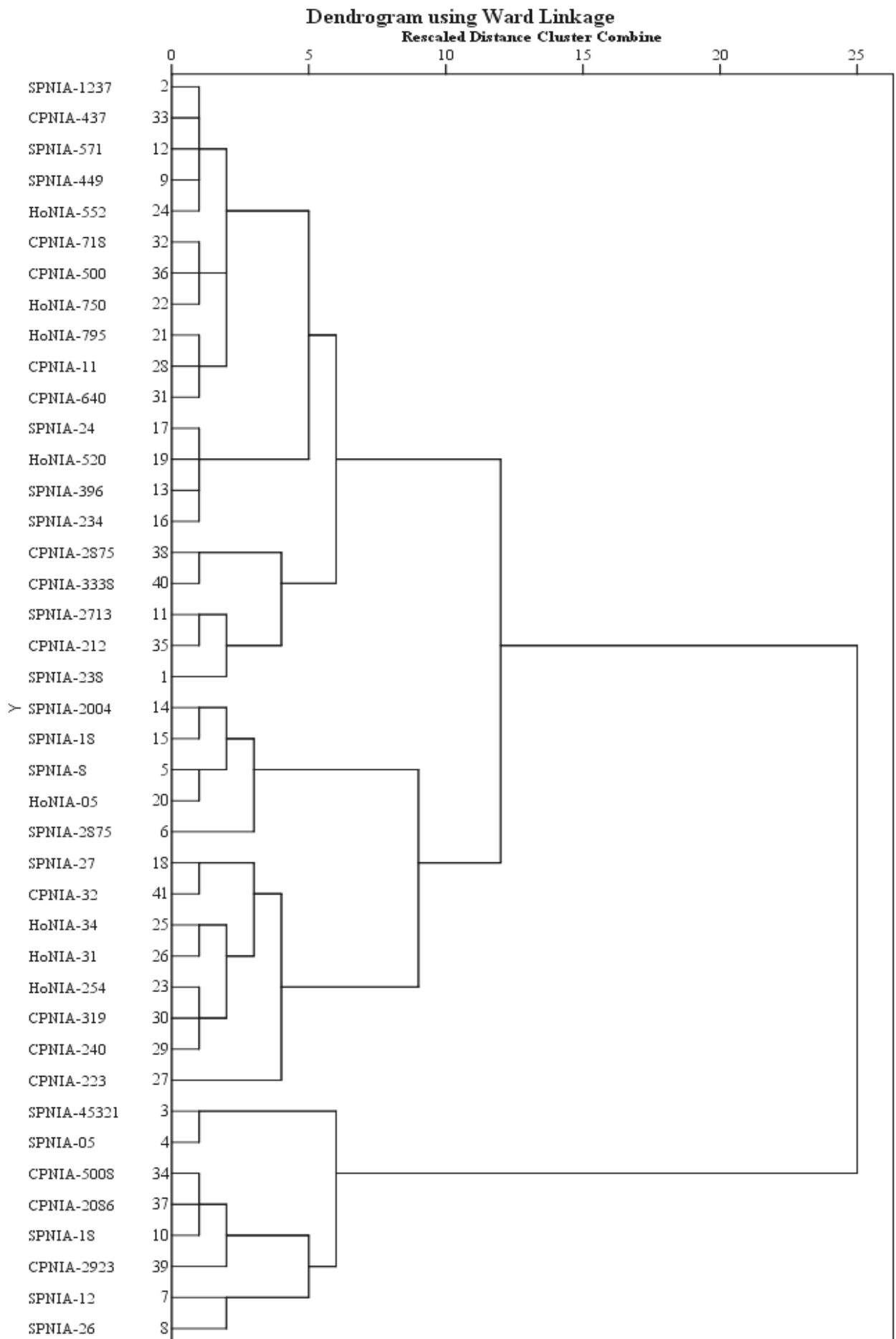


Fig. 1: Dendrogram of 41 exotic genotypes based on qualitative and quantitative characters of sugarcane clones (Ward's Linkage Method, Euclidian Distance).

**Table 7. Classification of exotic sugarcane genotypes into clusters based on Euclidean distance.**

Cluster	Accessions
Cluster I	SPNIA1237, SPNIA-449, SPNIA-571, HoNIA-795, HoNIA-750, HoNIA-552, CPNIA-11, CPNIA-640, CPNIA-718, CPNIA-437, CPNIA-500
Cluster II	SPNIA-396, SPNIA-234, SPNIA-24, HoNIA-520
Cluster III	SPNIA-238, SPNIA-2713, CPNIA-212, CPNIA-2875, CPNIA-3338
Cluster IV	SPNIA-8, SPNIA-2875, SPNIA-2004, SPNIA-18, SPNIA-05
Cluster V	SPNIA-27, HoNIA-254, HoNIA-34, Ho NIA-31, CPNIA-240, CPNIA-319, CPNIA-32
Cluster VI	SPNIA-12, SPNIA-26, SPNIA-18, CPNIA-5008, CPNIA-2086, CPNIA-2923

**Table 8. Means of parameters for accessions appearing in each cluster of the dendrogram based on Euclidean distance.**

Parameter	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI
Height	138.242	141.668	136.600	194.934	183.334	149.833
Girth	2.279	2.163	2.224	2.258	2.240	2.270
No. of internodes	16.995	16.660	18.328	18.660	19.139	17.217
Inter node length	7.934	8.160	7.194	9.860	9.519	7.717
Tillers	4.571	4.410	6.060	5.860	5.090	3.883
Weight/Stool	3.329	3.495	4.162	4.428	4.399	2.662
Cane yield	33.329	34.995	41.662	44.328	44.041	26.662
CCS	9.103	10.503	8.898	10.578	8.230	7.715
Sucrose	13.282	15.068	13.390	15.092	12.214	11.827
Sugar recovery	8.555	9.873	8.362	9.944	7.737	7.252
Brix	17.450	19.263	17.562	19.202	16.401	16.105
Fiber	12.125	12.535	14.802	12.336	12.007	13.677
Sugar yield	3.035	3.655	3.710	4.690	3.601	2.053

**Table 9. Traits selection from different clusters of the exotic genotypes.**

Cluster	Characters
Cluster I	Cane girth
Cluster II	CCS%, Sucrose %, Sugar recovery, Brix %
Cluster III	Fiber %, Tillers per plant
Cluster IV	Cane yield, Cane height, Internode length, Weight per stool, CCS%, Sucrose %, Sugar recovery, Brix %, Sugar yield.
Cluster V	Height, Number of internodes, Internode length, Weight per stool, Cane yield
Cluster VI	Average height and fiber %

Cluster I had three sub-clusters and it contained maximum number of cane genotypes i.e., 11. The cluster embraced accessions from all the three locations under study (Brazil, Homma USA, and Canal Point USA). It was observed to have accessions with distinguishing feature of high cane girth against any other cluster. However, height, and fiber % were seen to be low for this cluster. On the other hand, cluster II comprising of four accessions was characterized by high qualitative characters along with low quantitative traits. The clones possessed excellent CCS%, sucrose %, brix %, and sugar recovery values. This group contained accessions from Brazil, and Homma, USA whereas no clone from Canal Point, USA appeared in this group. Conversely, cluster III did not contain any clone from Homma, USA, while accessions from both of the remaining two locations were seen. Total number of accessions in this cluster was five and it had distinct parameters of high number of tillers per plant, and fiber % along with average number of internodes and weight per stool (Table 9).

Cluster IV showed most promising characters. The observations recorded for this group were excellent in terms of both qualitative as well as quantitative traits. This cluster contained one genotype from Homma, USA, and the rest from Brazil. None of the clones from Canal Point, USA fell into this group. This cluster was

distinguished by high internode length along with good height, tillers, weight per stool, cane yield, CCS %, sucrose %, sugar recovery %, brix % and sugar yield. This group clearly indicated that the sugarcane accessions from Brazil were more adaptive to the agroclimatic conditions they were exposed to, in this study.

Cluster V is characterized by high quantitative but low qualitative traits. Most of the quantitative records including height, number of internodes, weight per stool, and cane yield were excellent for this group. However, all of the qualitative characters were low. The group comprised of seven clones from all three locations while majority of the clones were from Canal Point. Cluster VI was observed to contain sugarcane accessions with low qualitative as well as quantitative parameters. This cluster included six accessions, all from Canal Point, and Brazil. The cluster was characterized by lowest number of tillers, weight per stool, cane yield, CCS%, sucrose %, sugar recovery, brix %, and sugar yield.

Our observations were in agreement with several previous studies. Shahzad *et al.* (2016) presented similar results when they exposed exotic germplasm to environmental conditions of Pakistan. They also reported that the clusters were not formed according to geographical origins of the accessions which could have been a result of resemblance in the progenitors. The study was also in

agreement to the report of Tahir *et al.* (2013) however, Olaoye (1999) observed that the genotypes were clustered as per their geographical locations into two groups in their study. These findings propose that the genotypes from different locations could have been derived from similar genetic material. The results are also consequence of continuous germplasm exchange between sugarcane breeding stations, and direct selection pressure in order to obtain certain traits in the progeny plants (Anand & Rawat, 1984). It has already been proposed that the characters constellation which should be related with a certain region in nature can lose the individuality because of human interference and selection pressure (Singh & Bains, 1986).

Formation of several groups in the cluster analysis showed that these genotypes could successfully serve the purpose of obtaining genetic diversity in progeny plants on hybridization. Ward's analysis has been employed in various earlier studies having similar results not only in sugarcane but also in other crops (Ilyas, 2011; Khodadadi *et al.*, 2011; You *et al.*, 2013). The genotypes falling in different clusters can be utilized for hybridization for crop improvement.

It was evident from the data that cluster IV could be selected for good combinations of qualitative and quantitative traits, cluster II for qualitative parameters, cluster V for quantitative traits, cluster I for cane girth, and cluster VI for obtaining genetic diversity in sugarcane crosses. The data depicted that it would be promising to cross the accessions appearing in cluster II with cluster V to achieve high quantitative and qualitative parameters in next generations. It was also apparent that accessions from cluster IV were promising in terms of numerous traits under study and they could be evaluated for further selection and adaptation in agroclimatic conditions of Sindh. Yadav & Singh (2010) also reported similar patterns in maize lines. Hybridization between distant genotypes have been employed in previous studies for different crops (Vivekananda & Subramanian, 1993). It is evident from our results that hybridization of accessions from distant clusters in this study can produce desired outcomes in terms of yield and sugar recovery in future.

## Conclusions

In this study, SPNIA-8, HoNIA-05 and CPNIA-2875 performed exceptionally well out yielding any other clone in sugar yield. Further, SPNIA-396, SPNIA-8, and SPNIA-2004 showed high potential in terms of sugar recovery. Whereas, Canal Point, USA clone CPNIA-240 showed highest cane yield. Cluster analysis of the sugarcane clones can be utilized for predicting the outcomes of future crosses and hybridization. The genotypes illustrating high qualitative and quantitative parameters can serve as potential candidates for utilization in sugarcane breeding and varietal development program in Pakistan.

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