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# GENETIC DIVERSITY ANALYSIS IN COMMERCIAL SUGARCANE (*SACCHARUM OFFICINARUM*L.) GENOTYPES

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## ABSTRACT

The present research was carried out to analyze the genetic diversity of commercial sugarcane varieties for various quantitative and qualitative traits including plant height (cm), tillers plant$^{-1}$, internodes plant$^{-1}$, internodes length (cm), cane girth (cm), weight stool$^{-1}$, brix (%), sucrose (%), fiber (%), commercial cane sugar (%), sugar recovery (%) and purity (%). In total, six genotypes of sugarcane were evaluated using analysis of variance, principal component analysis, cluster analysis and coefficient of parentage. Results displayed that sugarcane genotypes differed highly significantly for all the studied traits, registering the significant genetic diversity among the genotypes for further evaluation. With regards to genetic distance, out of the 15 pairs of comparisons, a good number of pairs exposed greater genetic distance; consequently, these pairs can further be utilized in sugarcane breeding for getting useful clone with great hybrid vigor. In cluster analysis, all genotypes divided into three clusters, indicating the existence of wider genetic diversity among the tested sugarcane genotypes. From PCA analysis, three components were isolated from twelve studied characters. The first, second and third components attributed 54.10, 26.70 and 13.10 % of total variation, respectively. The cumulative percent of variance accounted for 93.90% in the first three components, demonstrating a considerably high variability that can be exploited for further breeding programs in sugarcane breeding.

**Keywords:** Sugarcane, genetic diversity, genetic distance, cluster analysis

## INTRODUCTION

Sugarcane (*Saccharum*spp. complex) is an important industrial crop, it is being grown mainly in tropical and subtropical regions of the world and is grown in about 90 countries around the world for its great amount of sugar and currently ethanol is also produced as a source of bio-fuel (Andreoli and Souza, 2007). Present day sugarcane varieties are complex hybrids obtained through crossing between different species involving *Saccharum officenarum* L. and *S. spontaneum* L. species (Srivastava and Gupta, 2008). Sugarcane is the major source of raw materials on which sugar industry is based; cane juice is being utilized for the manufacturing of various products, including gur, shaker and sugar while tops of the cane are used for animal feed as fodder (Sanghera *et al.,* 2015). The by-products of the sugar industry are also very economical and being used extensively such as baggas, molasses, filter-cake, wax etc. (Kang *et al.,* 2013). The sucrose percentage differs from 12-18% depending on cane variety, time of maturity, soil conditions, environmental conditions and cultural practices applied by the farmers (Singh and Singh 2002). Evaluation of genetic diversity is an important practice for the improvement of sugarcane genotypes since parents with diverse genetic materials could be hybridized by breeders for developing viable superior progenies (Hamrick, 2004). Sugar cane breeding has flourished throughout the world mostly by inter-mating the inter-specific hybrids and their resultant progenies. The most important complication in sugarcane breeding is that the parents tend to possess narrow genetic base, that is, the greater frequency of common ancestors in their linkage which lead to a large amount of progeny inbreeding and decreases genetic variability. In respect to boost up advancement in sugarcane breeding programs, the new hybridization programs are suggested, including assessment of exploitable variability. This can be achieved by conducting various experiments regarding genetic divergence (Peixota *et al.,* 1984). Genetic divergence studies by means of one or more multivariate technique, such as principal component and cluster analysis have been used over the last 40 years for several crops and with different breeding objectives. These techniques help to quantify the amount of variability available in used genetic materials and also indicate groups of crop plants with similar or dissimilar genetic makeup (Ahmed and Obeid, 2010). Moreover, various researchers (Mangrio *et al.,* 2014; Solangi *et al.,* 2014; Solangi *et al.,* 2016) also explored variations in sugarcane genotypes at tissue culture level. The current study was designed

to explore the genetic diversity among the comercial sugarcane genotypes of Pakistan.

## MATERIALS AND METHODS

In this study, six sugarcane genotypes were sown at experimental farm, Nuclear Institute of Agriculture, Tando Jam during the growing season of 2015. The experiment was carried out in a randomized complete block design with three replications, keeping 30 cm plant to plant and 1 meter row to row distance. At maturity, 10 randomly selected plants were tagged for field and laboratory observations. All agronomic and plant protection practices were applied as recommended. The sugarcane genotypes were included NIA-2004, NIA-2010, NIA-2011, NIA-2012, NIA-1198 and Thatta-10. The observations were taken on plant height (cm), tillers plant$^{-1}$, internodes plant$^{-1}$, internodes length (cm), cane girth (cm), weight stool$^{-1}$(kg), brix (%), sucrose (%), fiber (%), commercial cane sugar (%), sugar recovery (%) and purity (%). The data obtainned was subjected to statistical computer package (Statistix Ver. 8.1) for analysis of variance and LSD test so as to compare the means between the genotypes. Co-efficient of parentage, cluster analysis and principal component analysis was carried out with the help of SPSS v. 21 computer software.

## RESULTS AND DISCUSSION

To carry on crop improvement program, it is very necessary to identify the germplasm, which tend to have hidden potential to be utilized. High yielding species with better environmental sustain-ability and phenotypically required characters could be rightly utilized for usual growing. Further-more, use of improved high yielding varieties to facilitate production efforts is the almost requirement for any important crop. It is significant to portray germplasm because its knowledge will help in the selection of superior genotypes (Arrey and Mih, 2016). The analysis of variance for all characters is given in Table 1. The obtained results revealed that genotypes differed significantly at P ≤0.01 probability level for plant height (cm), tillers plant$^{-1}$, internodes plant$^{-1}$, internodes length (cm), cane girth (cm), weight stool$^{-1}$(kg), brix (%), sucrose (%), fiber (%), commercial cane sugar (%), sugar recovery (%) and purity (%). This suggests that observed materials possess useful genetic resources for variety of traits, thus can extensively be utilized for next breeding program. Khan *et al.,* (2013) observed highly significant differences among cultivars, environment and interaction of cultivars x environments by factorial analysis of variance. Genetic composition and dissimilarity in their origin suggests differences in the genotype (Thippeswamy *et al*., 2003). Similar to our findings, Chaudhary and Joshi (2005) also reported a considerable difference among the tested sugarcane genotypes for different characters and attributed to the fact that used clones were developed from diverse parents with different genetic and geographic backgrounds.

Table-1: Mean squares from analysis for various quantitative and qualitative traits in sugarcane genotypes

| Characters | Replications D.F.=2 | Genotypes D.F.=5 | Error D.F.=10 |
|---|---|---|---|
| Plant height | 13.7 | 14456.1** | 138.8 |
| Tillers plant$^{-1}$ | 0.05 | 1.95** | 0.38 |
| Internodes plant$^{-1}$ | 7.05 | 46.88** | 2.32 |
| Internodes length | 0.74 | 3.71** | 0.56 |
| Cane girth | 0.00389 | 0.063** | 0.008 |
| Weight stool$^{-1}$ | 2.09 | 5.25** | 0.69 |
| Brix (%) | 0.18 | 2.17** | 0.03 |
| Sucrose (%) | 0.09 | 6.72** | 0.14 |
| Fiber (%) | 0.01 | 10.63** | 0.10 |
| Commercial cane sugar (%) | 0.14 | 10.53** | 0.21 |
| Sugar recovery (%) | 0.13 | 9.30** | 0.18 |
| Purity (%) | 6.57 | 121.77** | 14.05 |

**= Significant at 1% of probability level

Principal component analysis appears to be efficient in deciding which agromorphic characters of crop species contribute most to economic production (Jan Mohammadi *et al.,* 2014). It also provides a chance for exploitation of suitable germplasm in crop improvement for particular plant traits (Pecetti *et al.,* 1996). In the current study, PCAs were carried out based on correlation for all studies traits, the first, second and third components showed variance percentage of 54.10, 26.70 and 13.10, respectively; the contribution of first three components for sugarcane genotypes was 93.90% of variance. Contrary to our results, Al-Sayed *et al.,* (2012) and Shahzad *et al.,* (2016) observed less genetic variances in the set of sugarcane genotypes in first three components, having 85.3 and 42.4%, respectively. The results of pervious authors reflect that their evaluated sugarcane genotypes did not possess a variety of diverse gene and were closer in their phenotypic expression. Coefficients of first PCA were greatly associated with fiber percentage (0.384%), followed by commercial cane sugar percentage (0.373%), sugar recovery (0.373%), internodes length (0.320%) and purity percentage (0.318%); however, sucrose percentage also highly associated with $PC_1$ but in negative direction (-0.377%). While, cane girth (0.492%), internodes plant$^{-1}$ (0.406%), tillers plant$^{-1}$ (0.391%), birx percentage (0.388%) and plant height (0.381%) had great contribution with $PC_2$. However, $PC_3$ had larger contribution for weight stool$^{-1}$ (0.649%). These characters contributed substantially towards

genetic divergence in commercial varieties of sugarcane. It indicated that these characters may be preferred to exploit genetic variation in sugarcane genotypes. Shahzad *et al.,* (2016) reported that out of 19, 7 PCs exhibited Eigen value more than one and accounted about 72.1% of variability. 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 sugarcane cultivars for different attributes. The most effective traits in first component $PC_1$ were: sugar recovery, sucrose, purity and CCS while number of leaves$plant^{-1}$, leaf area and internodes 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 $PC_4$.

Table-2: The variables of morpho-yield traits with their contribution to the first three principal components of commercial sugarcane genotypes

| Variables | Components | | |
|---|---|---|---|
| | PC1 | PC2 | PC3 |
| Plant height (cm) | 0.220 | 0.381 | 0.340 |
| Tillers $plant^{-1}$ | 0.120 | 0.391 | -0.379 |
| Internodes$plant^{-1}$ | 0.230 | 0.406 | 0.271 |
| Internodes length (cm) | 0.320 | 0.143 | 0.351 |
| Cane girth (cm) | 0.109 | 0.492 | 0.095 |
| Weight $stool^{-1}$ | 0.219 | 0.039 | 0.649 |
| Brix (%) | 0.225 | 0.388 | 0.215 |
| Sucrose (%) | -0.377 | 0.045 | 0.174 |
| Fiber (%) | 0.384 | 0.045 | 0.014 |
| Commercial cane sugar (%) | 0.373 | 0.121 | 0.110 |
| Sugar recovery (%) | 0.373 | 0.121 | 0.111 |
| Purity (%) | 0.318 | 0.293 | 0.099 |
| Percent of variance | 54.1 | 26.7 | 13.1 |
| Cumulative percent of variance | 54.1 | 80.8 | 93.9 |

The problem with breeding projects, which are done through hybridization, is to assess the relationship between parental lines before attempting the crosses. Euclidean distance can provide the extent of genetic similarity or dissimilarity between parents so as transgressive segregates can be exploited (Hoque and Rahman, 2006). Evaluation of genetic variability is helpful in plant breeding and hence more efficient plant species may be isolated for the cultivation under different conditions. The data matrix of tested characters formed the basis of Euclidean genetic distance calculations. Genetic distance values for all 15 pair wise comparisons of the 6 sugarcane genotypes are presented Table 6. The greater genetic distance of 195.291 was found between NIA-2012 and NIA-2011, followed by NIA-1198 and NIA-2011 (171.448), NIA-2011 and NIA-2004 (163.628), NIA-2011 and Thatta-10 (131.261), and NIA-2010 and NIA-2011 (117.951). Furthermore, the moderate genetic distance of 80.572 was found between NIA-10 and NIA-2012, followed by Thatta-10 and NIA-2012 (65.631) and NIA-2010 and NIA-1198 (56.921). However, the minimum distance between genotypes was found between NIA-1198 and NIA-2004 (8.578), followed by NIA-2010 and Thatta-10 (15.754), NIA-1198 and NIA-2012 (24.291), NIA-2004 and NIA-2012 (32.103), Thatta-10 and NIA-2004 (34.047), Thatta-10 and NIA-1198 (41.963) and NIA-2010 and NIA-2004 (48.978) respectively.

Table-3: Assessment of genetic distance between commercial sugarcane genotypes based on various quantitative and qualitative traits

| Genotypes | NIA-2010 | NIA-1198 | NIA-2011 | Thatta-10 | NIA-2004 |
|---|---|---|---|---|---|
| NIA-2010 | 000 | | | | |
| NIA-1198 | 56.921 | 000 | | | |
| NIA-2011 | 117.951 | 171.448 | 000 | | |
| Thatta-10 | 15.754 | 41.963 | 131.261 | 000 | |
| NIA-2004 | 48.978 | 8.578 | 163.628 | 34.047 | 000 |
| NIA-2012 | 80.572 | 24.291 | 195.291 | 65.631 | 32.103 |

Cluster analysis is one of the most important statistical analyses, which helps group genotypes based on genetic variability which exists for various traits. Dendrogram was obtained from cluster analysis of six genotypes of sugarcane based on thirteen morphological traits as shown in Figure 1. According to grouping under study, sugarcane genotypes divided into three main clusters. Cluster one composed of three sugarcane genotypes such as, NIA-1198, NIA-2004 and NIA-2012; cluster two comprised of two sugarcane genotypes including, NIA-10 and Thatta-10: cluster three only contained one genotype (NIA-2011). Clustering patterns designated genotypes divided into different groups possess different morphological features, which indicates great genetic divergence. Genotypes belonging to sub-clusters could have greater genetic divergence and intermating between genotypes belonging to them would provide vigorous sugarcane genotypes in future breeding programmed would give more transgressive in advanced generations.

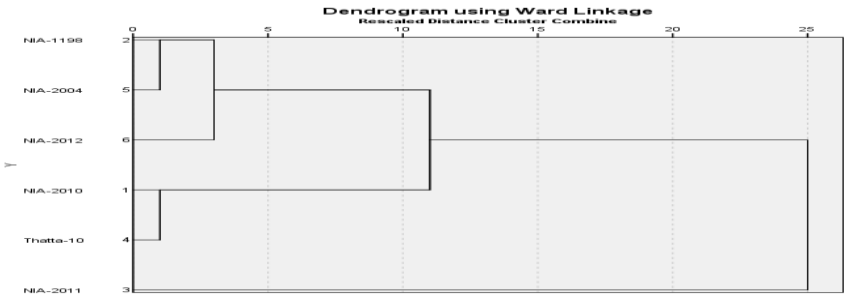


Figure-1: Dendogram of 6 sugarcane genotypes based on qualitative as well as quantitative characters

## CONCLUSIONS

The results obtained through different statistical approaches, including analysis of variance, genetic distance, cluster analysis and principal component analysis, all analysis registered the presence of considerably high genetic diversity among the evaluated sugarcane genotypes. This refers that used materials tend to possess a great amount of genetic variations, hence can further be exploited for various breeding programs so as to improve sugarcane genotypes. It is also concluded that diverse parents of this experiment can be used for hybriddization program in order to get useful genotypes.

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