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Estimation of genetic correlation among morphological and quality traits in *Saccharum Officinarum* L.

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Abstract
Twenty two accessions of sugarcane were investigated for determining genetic variability and suitable combination of characters for maximizing cane yield and sucrose percentage based on twelve pivotal quantitative traits using correlation and principal component analysis. The analysis of variance revealed considerable range of variability for all the characters studied. Cane weight was positive and significantly correlated with plant height, cane height, leaf area, brix value, juice contents and bagasse weight. Bagasse weight, dry matter contents and brix value had positive significant correlation with sucrose percentage. Principal component analysis was applied and three components which caused more than 70 percent of total variance were considered important and all the traits were studied in accordance to these components. Results indicate that different sugarcane accessions can be exploited for yield contributing traits and for specific use high yielding can be developed.

Keywords: genetic diversity, sugarcane, morphological traits, correlation, principal component analysis

Introduction

Sugarcane is a genetically complex, heterozygous and economically important crop grown mainly in tropical and subtropical areas (Khan *et al*., 2012) [19]. It is derived from interspecific hybridization between *Saccharum officinarum* and *S. spontaneum*. A series of back crosses were made between *S. spontaneum* and *S. officinarum* to minimize the negative traits of *S. spontaneum* and maximizing the sucrose producing traits of *S. officinarum* that lead to “nobalization” of sugarcane (Sreenivasan *et al.*, 1987; Qamar *et al*., 2105, 2017) [32, 28, 29]. In Pakistan it is a valauable and economically important cash crop grown for sugar and sugar products. It shares 3.2% in value added in agriculture and 0.9 % in GDP. In Pakistan it is grown on an area of around one million hectares with total production of 52.8 million tonnes and per hectare yield of 55 ton along with sugar recovery of 8.74% compared to world average production of 63.7 tons per hectare and sugar recovery of 10.6% (Anonymous, 2012-13) [7]. Hence it is a dire need to change current synerio and develop new high yielding cultivars that not only boost provincial and national cane yields but also enhance the economy of Pakistan. Information about the contribution of various cane and quality characters to cane yield is vital for development of new high yielding sugarcane cultivars.

To get high sugarcane yield and sugar recovery percentage is main objective of sugarcane variety improvement program. Sugar per unit area is determined by the cane yield/unit area and sucrose percent in juice. These characters are mostly influenced by their component traits. Milligan *et al*., (1990) [25] reported the most important determinant of sugarcane yield is cane yield. So selection for high sucrose contents mainly include cane yield with focus on stalk number. It can be concluded that selection for high sugarcane yield and sugar recovery percentage will be more efficient if there is better understanding of correlation and association between cane yield contributing components. In recent years sugarcane yield has been increased by making improvement in cane yield rather than sugar yield (Jackson 2005) [17]. Due to high poloidy level with variable chromosome numbers in somatic cells in both cultivated and wild types the progress in breeding of sugarcane is slow (Awais *et al*., 2017, 2019; Garcia *et al.*, 2006) [8, 9, 13]. As the demand for white sugar is continuously increasing the cane productivity and sugar recovery has to be increased accordingly. In sugarcane, complex traits like sugar quality and cane yield are influenced by a number of traits. These traits directly and indirectly contribute to the yield and variety development is the most pivot and cheapest technology for boosting cane productivity and production through sugarcane varietal improvement programme and it proceeds via choosing parents having desire traits, determining association between those traits and making crosses (Ali *et al*., 2010, 2013, 2014; Kanwal *et al*., 2019; Mahmood *et al*., 2019; Mustafa *et al*., 2018; Tahir *et al*., 2013) [5, 19, 23, 26, 34]. Multivariate statistical techniques like

Principal Component Analysis (PCA) techniques could be used for estimating genetic divergence among sugarcane genotypes (Ali *et al*., 2010; Ali *et al*., 2016; 2017) [5, 6]. This analysis has been used successfully to study genetic diversity in crops like chickpea (Malik *et al.*, 2010) [24], sugarcane (Luo *et al.*, 2005; Ilyas 2011; Chen *et al.*, 2006) [22, 15, 11], groundnut (Sudhir *et al.*, 2010) [33], potato (Ali *et al*., 2019) [1]; cotton (Hafeez *et al*., 2019) [14] and other crops. Ram and Hemaprabha (1998) [30] reported that PCA may help in isolating progenies with higher sugar yield and yield contributing traits.

They concluded that information on sugar composition should assist breeders in selecting superior accessions for the relevant breeding program. Zhang *et al.*, (2006) [36] studied ninety four genotypes of S. spontaneum for principal component analysis based on seven yield related characters of *S. spontaneum*. The three principal components provided 82.47% cumulative variance. Based on these seven traits, the 94 genotypes were grouped into four clusters. The current study was planned to exploit the genetic potential of sugarcane accessions for cane yield and sugar yield related traits and evaluate the magnitude of genetic diversity as well to develop a selection criterion for further improvement of the crop.

Materials and methods

Twenty two sugarcane genotypes viz. CP77-400, CP-72, CPF-235, SGH-292, CoJ-84, HSF-240, CPF-234, L-118, SCP-237, SGH-297, NO.21-77, HSF-242, NO.10-72, NO.11-77, CP-43-33, CoJ-64, NO.41-77, NO.11-72, SPF-232, NO.61, SPSG-26 and BF-129 were grown at during the 2012-13, trireplicated using randomized complete block design (RCBD). Recommened 30 cm P×P and 70 cm R×R distance was maintained. Agronomic and plant protection practices were applied as per recommendations to raise healthy and vigorous crop. At maturity 10 guarded canes were randomly selected for quantitative parameter study of the following traits i-e Cane height (cm), Plant height (cm), No. of tillers /stool, Leaf area (cm^2), No. of leaves, Cane weight (g), Cane diameter (cm), Juice contents (%), Dry matter contents (g), Bagasse weight (g), Sucrose value and Brix value (%). The data collected was subjected to Fisher's (1958) [12] analysis of variance, correlation analysis outlined by Kown and Torrie (1964) [21] and principal component analysis (Yan, 2001) [35].

Results and discussion

From analysis of variance it was revealed that there were significant differences among all the traits of studied accessions. Correlation analysis figures out the intensity of relationship between the two traits. To estimate the genetic inter-relationship of the characters under study particularly their relationship with the "brix value", genotypic and phenotypic correlations were computed. Correlation of plant height with cane height was highly significant and positive at phenotypic level but at genotypic level it has significantly positive correlation with cane height, at the same time plant height had significantly negative phenotypic correlation with number of tillers and same is the situation with brix value and sucrose contents. However its correlation with juice contents, cane weight, leaf area and no. of leaves was significant and positive at phenotypic as well as genotypic level. Soomro *et al*., (2006) [31] concluded that there is positive correlation between cane weight and plant height. Association of cane height with plant height, cane weight, leaf area, no. of leaves, and juice content was significant and positive at genotypic but highly significant and positive at phenotypic level. Chaudhary and Joshi (2005) [10] reported a positively and highly significant correlation between cane height, cane diameter and cane weight. The correlation of no. of tillers per stool with no. of leaves per plant was non-significant and positive at phenotypic but significant and positive at genotypic level. Its association with leaf area was found to be significant and positive at genotypic but positive and highly significant at phenotypic level. It was also observed that that no. of tillers had positive and significant correlation with juice, bagasse weight, dry matter content and brix at genotypic level. The association of number of leaves with plant height, cane height was significant and positive genotypic but positive and highly significant at phenotypic level. It also had significant and positive correlation with no. of tillers at genotypic but non-significant at phenotypic level and same is the case with leaf area.

Table 1: genotypic and phenotypic correlations for different traits

Traits	Cane Height	No. of Tillers	No. of Leaves	Leaf Area	Cane Diameter	Cane Weight	Juice Contents	Bagasse Weight	Dry Matter	Brix Value	Sucrose Value
Plant height	0.64* 0.62**	-0.46 -0.41**	0.61* 0.59**	0.23* 0.21	0.16 0.14	0.62* 0.57**	0.37* 0.35**	0.38* 0.35**	0.29* 0.27*	-0.44 -0.42**	0.33* 0.31**
Cane Height		0.14* 0.09	0.82* 0.77**	0.45* 0.43**	0.001 0.011	0.61* 0.56**	0.34* 0.32**	0.29* 0.28*	0.22* 0.21	-0.71 -0.67**	-0.70 -0.67**
No. of tillers/Stool			0.12* 0.08	0.36* 0.32**	0.06 0.07	-0.05 -0.01	-0.15 -0.13	-0.06* -0.05	0.20* 0.17	0.14* 0.12	0.01 0.01
No. of Leaves				0.12* 0.11	-0.18 -0.16	0.32* 0.29*	0.49* 1.48**	-0.016 -0.019	-0.14 -0.14	-0.68 -0.66**	-0.70 -0.68**
Leaf Area					0.35* 0.35**	0.50* 0.48**	0.21* 0.21	0.25* 0.25*	0.38* 0.37**	-0.18 -0.18	-0.26 -0.26*
Cane Diameter						0.006 -0.001	-0.052 -0.051	0.0134* 0.0131	0.20* 0.19	0.23* 0.22	0.044 0.042
Cane Weight							0.31* 0.30*	0.68* 0.66**	0.64* 0.62**	-0.36 -0.35**	-0.25 -0.24*
Juice Contents								-0.385 -0.384**	-0.41 -0.42**	-0.53 -0.52**	-0.434 -0.432**
Bagasse Weight									0.94*0.93**	0.202*0.201	0.204*0.203
Dry Matter Contents										0.293*0.291*	0.282*0.281*
Brix Value											0.91* 0.90*

Table 2: Eigen values for first four components

Sr. No.	Eigen value	% Total variance	Cumulative Eigenvalue	Cumulative %
1	4.319453	35.99544	4.31945	35.9954
2	3.042459	25.35383	7.36191	61.3493
3	1.519547	12.66289	8.88146	74.0122
4	1.058500	8.82083	9.93996	82.8330

Correlation of leaf area with plant height and number of leaves was positive and significant at phenotypic level but non-significant at genotypic level. Leaf area was positively correlated with cane weight, cane dia and dry matter content and statistically highly significant at phenotypic level whereas significant at genotypic level. Ilyas and Khan (2010) [16] found that leaf area is positively correlated with sucrose value, number of leaves and cane diameter. Association of cane diameter with plant height and number of leaves was non-significant and negative at both phenotypic and genotypic level. It had also non-significant and negative correlation with juice content where as its correlation with dry matter content, bagasse weight and brix value was statistically non-significant at phenotypic but significant and positive at genotypic level. Khan *et al*. (2003) [20] Studied that cane diameter is significantly associated with cane height and cane weight. Association of cane weight with cane height, plant height and leaf area was significant and positive at genotypic level but highly significant at phenotypic level. It was also found that cane weight has positive and significant correlation with number of leaves and juice content at both genotypic and phenotypic level. Association of juice contents with bagasse weight, dry matter, brix value and sucrose value was significant at phenotypic level but non-significant at genotypic level. Bagasse weight had significant and positive correlation with number of tillers and cane weight at genotypic level whereas non-significant at phenotypic level. It also had positive and significant correlation with brix value and sucrose content at genotypic level but non-significant at phenotypic level. The association of dry matter contents with cane diameter and leaf area was positive and significant at genotypic level and highly significant at phenotypic level. With plant height it has positive and significant correlation at both genotypic and phenotypic level. Sucrose content and brix value also had positive and significant correlation with dry matter at both genotypic and phenotypic level. Correlation of brix value with cane diameter, number of tillers and bagasse weight were positive and significant at genotypic level where as at phenotypic level it was non-significant. Correlation of sucrose value was significantly and positively correlated with bagasse weight at genotypic level and non-significantly at phenotypic level. The correlation of sucrose value was positive and significant with dry matter content at both of the genotypic and phenotypic level. It was found to be correlated with brix value significantly and positively at genotypic level and highly significantly at phenotypic level. (Table: 1 shows genotypic and phenotypic correlations among different traits).

The eigenvalues presented in the Table: 2 were above 1 for component 1, 2, 3 and 4. The component 1, 2 and 3 accounted for 35.99%, 25.35 % and 12.66% of total variance whereas cumulative variance explained by these 3 components was 74 % which is within the range (70-80%) and hence is satisfactory. However Muyco (2000) on the contrary found 4 principal components giving rise to 76% variation in the data, with the first component comprising juice quality, yield and stalk diameter traits. Similarly, Deepak *et al* (2012) recorded quality traits (Brix, Pol %) loading on the first two principal components. Salient features observed from the first PC were the negative associations of brix value and sucrose content whereas for 2nd PC most of the characters have negative associations and only juice content and number of leaves had positive association (Fig. 1 and Fig. 2). In case of PC 3 number of tillers, cane diameter and leaf area had negative associations, juice content also had negative association but it had a small value so can be ignored (Fig. 3).

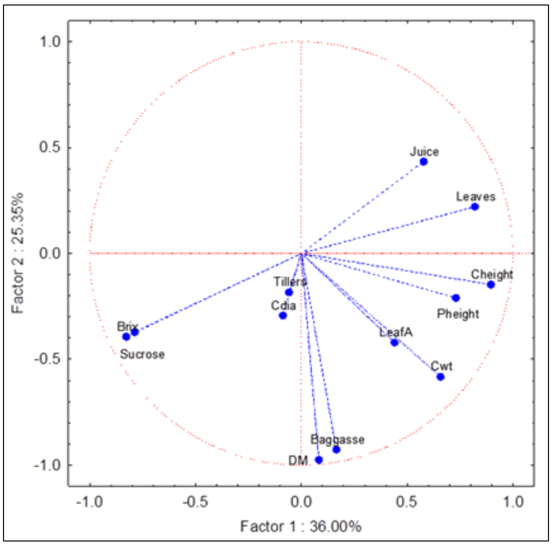

Fig 1: Projection of traits against factor 1*2

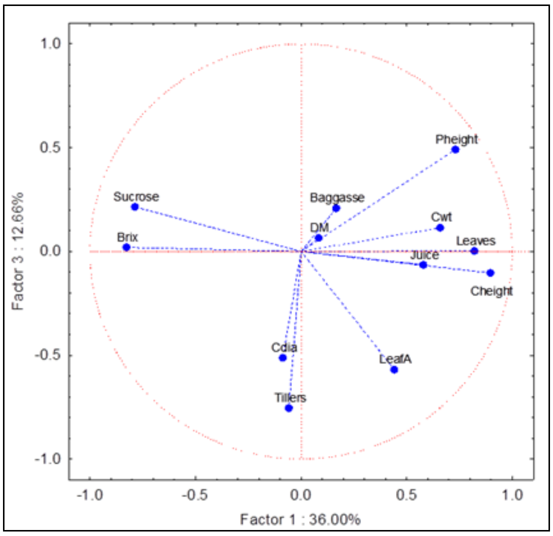

Fig 2: Projection of traits against factor 1*3

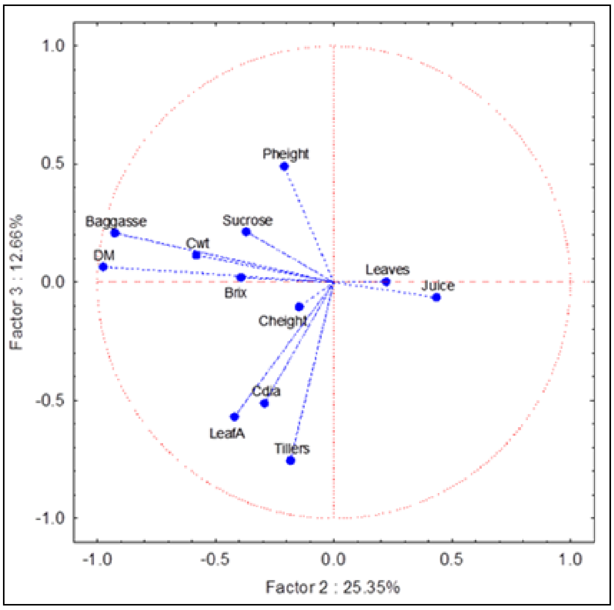

Fig 3: Projection of traits against factor 2*3

Conclusion

From all of the results above discussed it can be concluded that sugarcane accessions studied had a vast genetic diversity for morphological and quality traits and most of these are correlated with each other either positively or negatively. So it can be said that for the improvement of sugarcane cultivars for these parameters the genotypes studied can be exploited and good yielding varieties of sugarcane specific to their use can be developed.

References

1. Ali A, Ali Q, Iqbal M, Nasir I, Wang X. Fine screening for resistance to cold-induced sweetening in a wild potato population. Applied Ecology and Environmental Research. 2019; 17(4):7333-7344.
2. Ali F, Ahsan M, Ali Q, Kanwal N. Phenotypic stability of *Zea mays* grain yield and its attributing traits under drought stress. Frontiers in plant science. 2017; 8:1397.
3. Ali Q, Ahsan M, Ali F, Aslam M, Khan NH, Munzoor M *et al*. Heritability, heterosis and heterobeltiosis studies for morphological traits of maize (*Zea mays* L.) seedlings. Advancements in Life sciences. 2013; 1(1):52-63.
4. Ali Q, Ali A, Ahsan M, Nasir IA, Abbas HG, Ashraf MA. Line× Tester analysis for morpho-physiological traits of *Zea mays* L seedlings. Advancements in Life sciences. 2014; 1(4):242-53.
5. Ali Q, Abbas HG, Farooq J, Tahir MHN, Arshad S. Genetic analysis of some morphological traits of *Brassica napus* (Canola). Electronic Journal of Plant Breeding. 2010; 1(5):1309-1319.
6. Ali Q, Ahsan M, Kanwal N, Ali F, Ali A, Ahmed W *et al*., Screening for drought tolerance: comparison of maize hybrids under water deficit condition. Advancements in Life Sciences. 2016; 3(2):51-58.
7. Anonymous. Agricultural Statistics of Pakistan. Ministry of Food and Agricultural Division (Planning unit), Government of Pakistan, Islamabad, 2012-13.
8. Awais M, Tariq M, Ali A, Ali Q, Khan A, Tabassum B *et al*., Isolation, characterization and inter-relationship of phosphate solubilizing bacteria from the rhizosphere of sugarcane and rice. Biocatalysis and Agricultural Biotechnology. 2017; 11:312-321.
9. Awais M, Tariq M, Ali Q, Khan A, Ali A, Nasir IA *et al*., Isolation, characterization and association among phosphate solubilizing bacteria from sugarcane rhizosphere. Cytology and Genetics. 2019; 53(1):86-95.
10. Chaudhary RR, Joshi BK. Correlation and Path Coefficient Analysis in Sugarcane. Nepal Agric. Res. J, 2005, pp. 24-27.
11. Chen Y, Haihua D, Jinan L. Differences of physiological and biochemical characters among the progenies of Erianthus arundinaceus. Journal of Huazhong Agriculture University. 2006; 25(6):598-602.
12. Fisher RA. Statistical methods for research workers. 13th Ed. New York: Hafner, 1958.
13. Garcia AA, Kido EA, Meza AN, Souza HMB, Pinto LR, Pastina MM *et al*. Development of an integrated genetic map of a sugarcane (Saccharum spp.) commercial cross, based on maximum likelihood approach for estimation of linkage and linkage phases. Theor. Appl. Genet. 2006; 112:298-314.
14. Hafeez MN, Ahmad S, Mamoon-Ur-Rashid M, Ali A, Salman S, Bakhsh A *et al*., An overview of enhancing drought tolerance in cotton through manipulating stress resistance genes. Applied Ecology and Environmental Research. 2019; 17(3):7003-7025.
15. Ilyas MK. Genetic variability and contribution of some morphological traits in cane yield and sucrose recovery in (*Saccharum officinarum*). Available, 2011: http://agris.fao.org. AGRIS Record No. PK2004000303.
16. Ilyas MK, Khan FA. Determining sucrose recovery in *Saccharum officinarum* L. using regression and correlation analyses. African J Biotech. 2010; 9(20):2985-2988.
17. Jackson PA. Breeding for improved sugar content in sugarcane. Field crop res. 2005; 92:277-290.
18. Kanwal N, Ali F, Ali Q, Sadaqat HA. Phenotypic tendency of achene yield and oil contents in sunflower hybrids. Acta Agriculturae Scandinavica, Section B-Soil & Plant Science. 2019; 69(8):690-705.
19. Khan IA, Bibi S, Yasmin S, Khatri A, Seema N, Abro SA. Correlation studies of agronomic traits for higher sugar yield in sugarcane. Pak. J Bot. 2012; 44:969-971.
20. Khan MA, Khan KH, Salahuddin J, Noor PR, Muhammad AR, Muhammad MY *et al*. Evaluation of new sugarcane genotypes developed through fuzz correlation of cane yield and yield components. J Appl. Sci. 2003; 3(4):270-273.
21. Kown SH, Torrie JH. Heritability and inter-relationship among traits of two soybean populations. Crop Sci. 1964; 4:196-198.
22. Luo J, Hua Z, Liangnian X. Comparison and Cluster Analysis of Photosynthetic Characters of Different Sugarcane Varieties. Scientia Agricultura Sinica. 2005; 38(8):1562-1569.
23. Mahmood A, Ali Q, Ahmad S, Bakhsh A, Mahpara S, Kamaran S *et al*., genetic potential and association among morpho-physiological traits of petunia inbred lines. Applied Ecology and Environmental Research. 2019; 17(4):7311-7332.
24. Malik SR, Bakhsh A, Asif MA, Iqbal U, Iqbal SM. Assessment of genetic variability and interrelationship

among some agronomic traits in chickpea. Int. J Agric. Biol. 2010; 12:81-85.
25. Milligan SB, Gravois KA, Bischoff KP, Martin FA. Crop effects on genetic relationships among sugarcane traits. Crop Sci. 1990; 30:927-931.
26. Mustafa HSB, Mahmood T, Hameed A, Ali Q. Enhancing food security in arid areas of Pakistan through newly developed drought tolerant and short duration mustard (*Brassica juncea* L.) Canola. Genetika. 2018; 50(1):21-31.
27. Muyco RR. Genetic diversity in sugarcane (*Saccharum spp*. L.) from the active germplasm collection of Philsurin [Philippine Sugar Research Inst.,] based on coefficient of parentage, agro-morphological traits and DNA microsatellite markers. Available, 2011. http://agris.fao.org. AGRIS Record No. PH2003001327.
28. Qamar Z, Riaz S, Nasir IA, Ali Q, Husnain T. Transformation and transgenic expression studies of glyphosate tolerant and cane borer resistance genes in sugarcane (*Sccharum officinarum* L.). Molecular Plant Breeding, 2015, pp. 6.
29. Qamar Z, Riaz S, Nasir IA, Ali Q, Husnain T. Transformation and evaluation of different transgenic lines for Glyphosate tolerance and cane borer resistance genes in sugarcane (*Saccharum officinarum* L.). Cytology and genetics. 2017; 51(5):401-412.
30. Ram B, Hemaprabha G. Nature and pattern of genetic divergence of sugar yield and its components in the progenies of *Saccharum barberi*. Indian J Gen. Plant Breed. 1998; 58(2):193-199.
31. Soomro FA, Junejo S, Ahmed A, Aslam M. Evaluation of different promising sugarcane varieties for some quantitative and qualitative attributes under Thatta (Pakistan) conditions. Int. J Agri. Biol. 2006; 8(2):195-197.
32. Sreenivasan TV, Ahloowalia BS, Heinz DJ. Cytogenetics in: Heinz DJ. (ed), Sugarcane improvement through breeding. Elsevier, Amsterdam, 1987, pp. 211-253.
33. Sudhir IK, Govindraj M, Kumar VK. Estimation of Genetic Diversity of new advanced breeding lines of Groundnut (*Arachis hypogaea* L.). World J Agric. Sci. 2010; 6(5):547-557.
34. Tahir M, Rahman H, Gul R, Ali A, Khalid M. Genetic Divergence in Sugarcane Genotypes. American. J of Exp. Agric. 2013; 3(1):102-109.
35. Yan W. GGE Biplot a windows application for graphical analysis of multi environment trial data and other types of two way data. Agron J. 2001; 93(5):1111-1118.
36. Zhang G, Yang R, Liu H, Fang W. Principal component analysis for 7 quantitative traits and cluster analysis based on 7 quantitative traits of *Saccharum spontaneum* L. Southwest China J. Agric. Sci, 2006.