Indian J. Genet., 77(4): 531-539 (2017)
DOI: 10.5958/0975-6906.2017.00070.0

Morphological characterization and genetic diversity analysis of interspecific hybrids of sugarcane

E. Karpagam and S. Alarmelu*

Division of Crop Improvement, ICAR-Sugarcane Breeding Institute, Coimbatore 641 007

(Received: December 2016; Revised: September 2017; Accepted: October 2017)

Abstract

Interspecific hybrid derivatives involving *Saccharum spontaneum*, *S. robustum* and *S. barberi* were morphologically characterized with twenty two qualitative and six agronomic traits. Principal component analysis (PCA) of qualitative traits revealed that first nine principal components with eigen value > 1 accounted for a cumulative variance of 62.40 %. The traits *viz.*, ligule shape, auricle type, internode shape and its alignment, cane thickness, dewlap color, leaf blade width and curvature, leaf sheath hairiness, bud cushion and bud groove were identified as principal discriminatory characters which will be useful in preliminary screening and identification of interspecific hybrids. Cluster analysis of qualitative traits grouped hybrids into seven clusters. Maximum inter cluster distance was between cluster IV and VI followed by cluster I and III, III and VII and between VI and VII. Metroglyph analysis of agronomic traits categorized hybrids into ten groups. Groups III, IV, V, VIII and X with highest mean index scores were identified as genetically most distant. Thirty eight superior interspecific hybrids with high index score for agronomic traits (from metroglyph analysis) and wider inter cluster distance were identified as prebreeding stocks and utilized in further backcross programmes. BC_1 progenies of SBH 12-45 x Co 0303 and SRH 12-275 x Co 0240 were significantly superior for single cane weight and brix %. Elite recombinants from back crosses SSH 12-158 x Co 0209, SSH 12-409 x Co 09014 and SRH 12-119 x Co 94008 surpassed commercial check for cane yield and were on par for quality.

Key words: Sugarcane, morphology, principal component analysis, cluster analysis, metroglyph analysis

Introduction

Sugarcane is the most important crop cultivated in tropical and subtropical countries for sucrose and renewable energy. The commercial sugarcane cultivars are mostly hybrids of *S. officinarum* and *S. spontaneum* (Price 1967) and constitute the basic germplasm which represents only a few original progenitor clones (Roach 1989). The need of the hour is to utilize the unexploited genetic variation from wild species or related genera. Efforts to broaden the genetic base of sugarcane cultivars through hybridization with *S. spontaneum*, *S. barberi*, *Erianthus* and *Sorghum* were reported by Nair et al. (1999) and Bakshi Ram et al. (2007). When a population structure is not known, categorizing the accessions into morphologically identical or genetically similar groups is useful. Comparative morphology and agronomic traits were traditionally used to study genetic diversity in germplasm collection and pre-breeding population (Balakrishnan et al. 2000) and also in discriminating genotypes to form core/mini-core collection (Bhattacharjee et al. 2007); where the molecular methods or biochemical markers are not practical. Several efficient guidelines for morphological characterization of sugarcane were reported (Artschwager 1940; Skinner 1972; Wagih et al. 2004). Artschwager (1948) and Grassl (1956) suggested shape of vegetative organs; shape and arrangement of floret parts as valuable characters in identification of varieties. King et al. (1965) reported hair groups, bud and leaf sheath characters as reliable means of identification. Many authors have used morphological characters for characterization of germplasm collection (Chandran 2011; Govindaraj et al. 2014; Esayas Tena et al. 2016). Agronomic and morphological characters explained through methods of multivariate statistics were used to study genetic diversity in sugarcane hybrids and germplasm resources (Zhou et al. 2015; Ongala et al. 2016). The present study aimed to

---

*Corresponding author's e-mail: alarmelu.s@gmail.com

Published by the Indian Society of Genetics & Plant Breeding, F2, First Floor, NASC Complex, PB#11312, IARI, New Delhi 110 012
Online management by indianjournals.com; www.isgpb.com

investigate the extent of morphological diversity in interspecific hybrids of *S. spontaneum*, *S. robustum* and *S. barberi* based on qualitative traits through Principal Component Analysis (PCA) so as to identify the Principal Components (PC) that contributes to maximum variability. Cluster analysis with qualitative traits and metroglyph analysis based on quantitative traits were compared to identify distinct and potential genotypes for utilization in introgression studies.

Materials and methods

Plant material

Six interspecific crosses (CoC 671 x SES 90, Co 98003 x SIP-18, SIP 93-434 x Co 775, PIR 96-285 x Co 8371, PIR 00-1174 x Co 0303 and *S. barberi* x BO 91) were effected (flowering season, 2011) and seedlings were evaluated in two replications (2012). The experimental material (one hundred and twenty interspecific hybrid derivatives) with *S. spontaneum* base (67), derived from SES 90, SIP-18 and SIP 93-434 were named as SSH; hybrids with *S. robustum* base (31) of PIR 96-285, PIR 00-1174 named as SRH and *S. barberi* (Pathri) hybrids (22) named as SBH were evaluated in RBD in a plot size of 6 m x 0.9 m with two replications during two consecutive years (2013 and 2014) at Sugarcane Breeding Institute, Coimbatore. Normal package of practices and control measures were followed. Data on characters viz*.,* number of millable canes (NMC), cane thickness, cane height, single cane weight (SCW), clump yield, brix % and sucrose % were recorded at 300 days.

Morphological characteristics

Data on morphological characters were observed for two consecutive years (2013 and 2014) at 270 days after planting. The hybrids were characterized for 22 descriptors (qualitative characters) based on descriptors given by Artschwager (1940). The traits were studied on fully developed five primary canes from each replication in 120 genotypes. Plant growth habit (erect/semi-erect), adherence of leaf sheath (weak-self de-trashing, medium and strong), waxiness (light, medium and heavy), ligule shape (strap, deltoid, crescent and arch), internode alignment (straight/ zigzag), bud shape (ovate, obovate, oval, round, pentagonal, rhomboid, rectangular and triangular pointed), auricle type (incipient, deltoid, dentoid, unciform, calcariform, lanceolate and falcate) and leaf blade curvature (erect, curved tip and arched) were observed on group of canes/plant parts. Leaf width [narrow (< 3.0 cm), medium (3.0-5.0 cm) and broad (>5.0 cm)], leaf sheath hairiness (absent, dense and sparse), bud size, internode shape (cylindrical, tumescent, bobbin, conoidal, obconoidal and curved) and cane thickness [thin (<2.2 cm), medium (2.2 – 3.0 cm) and thick (>3.0 cm)] were measured from ten individual canes of each genotype. Node (bud groove, bud cushion, prominence of growth ring and root eye rows arrangement) and internode characters (growth crack and rind surface appearance) were recorded at mid height of fully developed canes. The Royal Horticultural Society (RHS) color chart was used to describe colors (dewlap and internode color). For each attribute state of a qualitative trait, numerical scores were given following the procedure given by Balakrishnan and Sanghvi (1968).

Principal component (PCA) and cluster analysis

Data for qualitative traits were used for PCA and cluster analysis using the statistical software MINITAB Version. 14. The cluster analysis was performed through complete linkage method based on euclidean distances.

Metroglyph analysis

Metroglyph analysis for six agronomic traits *viz*., NMC/ row, cane thickness, SCW, cane height, cane yield/ row and brix % was done using index score method (Anderson 1957).

Results and discussion

Morphological characterization

The qualitative characters *viz.*, leaf sheath hairiness, ligule shape, leaf blade curvature, leaf blade width, internode shape and cane thickness showed significant variation between the hybrids. Interspecific hybrids could be effectively differentiated with the extent of leaf sheath hairiness in this study, hairiness was dense and hard in SSH; medium to dense, soft hairs in SRH; either absent or sparsely present in SBH (Fig. 1). Deltoid shaped ligule was very specific to SSH, which can be effectively used to distinguish interspecific hybrids with *S. spontaneum* cytoplasm. Compact canopy with linear to lanceolate narrow erect leaves were very prominent in SSH, whereas SRH and SBH had medium to broad leaves with arched or curved tip (Fig. 1). The internode shape showed relatively high frequency for cylindrical followed by bobbin, which was very specific to SSH and conoidal shaped internodes found only in SRH (Fig. 1). Internode thickness in SSH ranged from 0.89 to 2.84 cm and maximum clones was thin types, whereas in SBH and SRH clones were

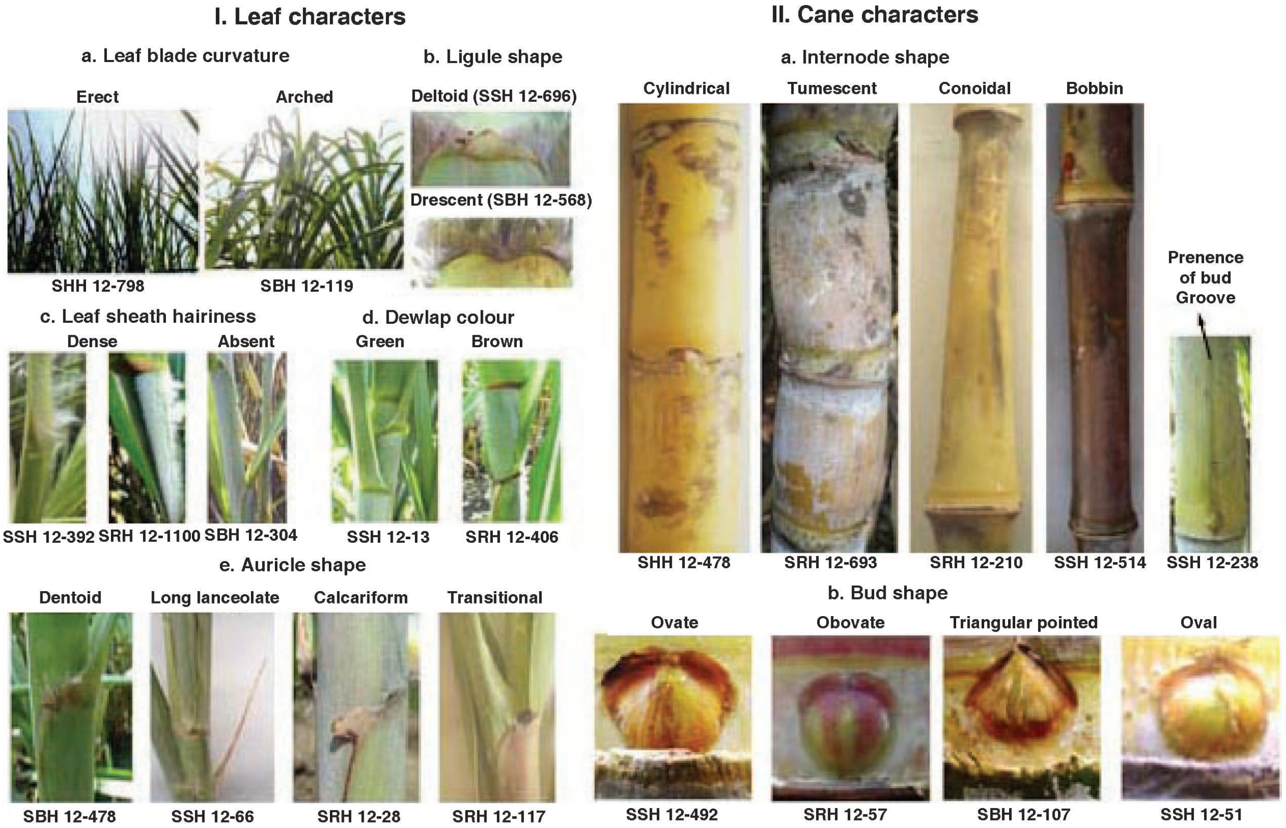

Fig. 1. Leaf and cane characteristics of *Saccharum* spp. interspecific hybrids

medium to thick types. The interspecific hybrids of SSH had hard spines, while *S. robustum* cytoplasmic base (SRH) hybrids had soft deciduous spines.

Five phenotypic classes were there for canopy structure of which open, erect and compact tip droopy were the most common ones. The most frequent shape of auricle was transitional (observed in 79.12% of genotypes) followed by calcariform, long lanceolate and dentoid shapes (Fig. 1). Five dewlap color classes *viz.*, yellow, green and greenish yellow was dominant with equal proportion and few clones had purple and brown colored dewlap. In all, 70.83% of genotypes had semi-clasping adherence of leaf sheath (allows easy detrashing) but few clones from SSH and SRH had tight clasping nature. Majority of clones were grouped under green yellow, yellow green and green group for internode color; few clones were purple and brown colored. Rind waxiness was prominent in clones derived from *S. spontaneum* and *S. robustum*. Internode alignment was predominantly straight except for few clones with zigzag alignment indicating the use of these clones in breeding for erect and non-lodging canes. Rind surface with corky patches and growth cracks were frequently noticed in SSH followed by SRH. Most of the hybrids from SBH had smooth surface with no wax. Bud size and bud characters also showed considerable variation among the clones studied.

Principal component analysis for qualitative traits

The results of this study indicated the wide distribution of phenotypic classes and a wide range of variability for the 22 qualitative traits studied. A total of 64 variables were detected which indicated the presence of genetically diverse and distinct genotypes in the population developed.

Thapa et al. (2009) reported that principal component analysis (PCA) is a useful technique in recognizing the best genotypes based on both quantitative and qualitative data. Gemin et al. (2006) obtained in *Saccharum spontaneum,* three principal components which explained 82.47% cumulative variance. In our study, PCA simplifies twenty two qualitative traits into nine PCs with eigen value > 1 and cumulative variance of 62.40%. It reduced morphological variables to eleven strong discriminative traits to facilitate the grouping of interspecific hybrids and selfs. PC_1 had high contributing factor loads from rind surface appearance, internode color,internode shape and bud size (Table 1). The effective traits in PC_2 were: leaf blade curvature, bud groove, adherence of leaf sheath, auricle shape and prominence of growth ring. In PC_3 the variations among the clones was mainly due to the characters *viz.,* bud cushion, growth habit, cane thickness, internode alignment and bud tip in relation to growth ring; where bud cushion had positive factor load. PC_4 explained the variability among genotypes with high positive factor loads from internode alignment, growth crack, bud shape and number of root eye rows and its arrangement. The eigen vectors of PC_5 showed large positive loads for ligule shape and number of root eye rows and its arrangement, also high negative loads for dewlap color and bud cushion. The PC_6 explained the diversity by ligule shape, waxiness, bud groove and bud tip in relation to growth ring. PC_7 had high factor loads from leaf sheath hairiness and leaf blade width. Traits separating the genotypes in eighth PC axis were dewlap color, ligule shape, internode color and leaf sheath hairiness. In PC_9 cane characters *viz.*, cane thickness, internode shape, bud size, bud groove and bud cushion contributed for variability with high negative loads.

Table 1. Eigen value, factor loads and contribution of first nine PC Axes for maximum variability in *Saccharum* interspecific hybrids

Variable	Eigen vectors								
	PC_1	PC_2	PC_3	PC_4	PC_5	PC_6	PC_7	PC_8	PC_9
Eigen value	1.9547	1.8849	1.8124	1.6335	1.4503	1.3714	1.2810	1.2183	1.1121
Cumulative percent of total variation	8.90	17.50	25.70	33.10	39.70	45.90	51.80	57.30	62.40
Growth habit	0.076	0.026	**–0.308**	–0.290	0.134	0.143	–0.196	0.282	0.104
Leaf sheath hairiness	–0.189	–0.164	–0.066	0.185	–0.186	–0.121	**0.417**	**–0.371**	0.008
Ligule shape	–0.014	–0.105	0.041	–0.146	**0.365**	**–0.437**	–0.032	**0.411**	–0.149
Auricle shape	0.229	**–0.307**	–0.023	0.157	–0.241	0.034	0.107	–0.029	–0.201
Dewlap colour	0.085	0.029	–0.210	–0.036	**–0.335**	0.004	0.255	**0.300**	0.004
Leaf blade curvature	0.021	**0.411**	0.089	0.087	–0.240	–0.036	0.276	0.056	0.145
Leaf blade width	0.106	–0.014	–0.299	–0.059	0.127	0.260	**0.398**	–0.282	–0.101
Adherence of leaf sheath	–0.089	**–0.399**	0.154	0.126	–0.206	–0.021	–0.123	0.050	–0.096
Internode colour	**0.437**	–0.004	0.250	–0.014	0.250	0.046	–0.083	**–0.382**	0.062
Cane thickness	0.169	–0.069	**–0.383**	–0.187	0.146	–0.082	0.176	–0.294	**–0.372**
Internode shape	**–0.336**	–0.196	0.021	–0.153	0.210	0.134	–0.078	0.080	**–0.408**
Internode alignment	–0.043	0.046	**–0.396**	**0.504**	–0.049	0.032	0.037	0.101	–0.000
Growth crack	–0.049	–0.172	0.016	**0.360**	0.177	–0.298	0.293	–0.092	–0.004
Rind surface appearance	**0.517**	0.150	–0.036	0.143	0.058	0.073	–-0.293	0.171	–0.251
Waxiness	0.159	–0.104	–0.157	–0.181	–0.207	**–0.340**	–0.220	–0.202	0.289
Bud shape	0.269	–0.175	0.030	**0.393**	0.071	0.242	–0.143	0.291	0.022
Bud size	**–0.315**	0.293	–0.070	0.190	–0.055	0.179	–0.202	–0.119	**–0.398**
Bud groove	0.207	**0.364**	0.118	0.083	–0.041	**–0.370**	–0.101	–0.047	**–0.374**
Bud tip in relation to growth ring	0.027	–0.219	**–0.324**	0.069	–0.059	**–0.390**	0.055	0.061	–0.025
Prominence of growth ring	0.116	**–0.339**	0.246	0.019	0.075	0.207	0.178	–0.003	–0.004
Number of root eye rows and its arrangement	–0.145	0.137	0.093	**0.318**	**0.458**	–0.153	0.130	–0.047	0.197
Bud cushion	0.020	–0.021	**0.383**	–0.092	**–0.302**	–0.142	0.266	0.055	**–0.304**

Bold text: Eigen vectors with highest factor loads

The projection of variables on PC axis revealed that dewlap color, leaf blade curvature, leaf blade width were placed at opposite axis with respect to ligule shape, auricle shape, adherence of leaf sheath and leaf sheath hairiness. Bud characters were negatively associated with bud shape, bud tip in relation to growth ring and prominence of growth ring. Internode alignment and rind surface appearance were negatively associated with internode color, internode shape, growth cracks, waxiness and cane thickness. Positive association of bud shape with adherence of leaf sheath and internode shape with cane thickness was similar to the findings of Sundas Shahzad et al. (2016).

The loading plot infers that rind surface appearance, bud size, internode shape, internode color followed by leaf blade curvature, bud groove, adherence of leaf sheath, auricle shape, bud shape and prominence of growth ring as a whole contributed maximum towards the variability in the hybrids. The traits *viz.*, ligule shape, auricle type, internode shape, cane thickness, leaf blade curvature, leaf sheath hairiness, bud cushion, bud groove, bud size and dewlap color were with maximum variability above 30% of variation factor. The other qualitative traits *viz*., leaf sheath hairiness, leaf blade curvature and leaf blade width also played an important role in identification of the hybrids and selfed progenies under study.

Information on genetic variability is a prerequisite in any selection program. Morphological descriptors are distinct for each variety and breeders have utilized them in easy discrimination of varieties under cultivation (Akthar et al. 2001). Key descriptors of sugarcane such as internode waxiness, leaf sheath wax, leaf sheath margin, leaf sheath hairiness, canopy arrangement, leaf length, leaf breadth, stooling habit are more stable and hence are reliable and can be used in precise identification of the clones and elimination of identical clones in selection process. Similar results were observed by Khalid et al. (2016) on characterization and identification of sugarcane genotypes using the stable characters. Agarwal (1969) indicated that physiological, chemical and morphological make-up of sugarcane clones has a great impact on resistance to various insect pests.

In this study, high amount of variation was observed for leaf hairiness among the hybrids, which can be exploited in identification of donor parents with tolerance to pests. Abubakar et al. (2013), suggested that presence of hairs can be also a control measure by resistant host plant (hypersensitive reaction) which could be used as phenotypic markers for biotic stress.

Cluster analysis for qualitative traits

Cluster analysis grouped the genotypes into seven clusters. The cluster size varied from 4 to 53 genotypes. Genotypes of SSH were grouped (Table 2) in cluster IV (53) followed by V (8), VII (5) and I (1). SRH were grouped in cluster II (13), VI (9), III (4), I (3) and VII (2). Clones from SBH were grouped to cluster II (7) and VII (15). Genotypes in cluster I had medium sized bud and bud cushion. Cluster II had genotypes common in attributes such as green yellowish dewlap, green internode color. Genotypes in cluster III commonly possessed zigzag internode alignment. 84.12% of genotypes in cluster IV possessed deltoid shaped ligule, heavy waxiness, thin canes, small sized bud, bud expansion below the growth ring and erect narrow leaves with dense leaf sheath hairiness. Bobbin shaped internode was the unique character in cluster V and conoidal shape was the distinct character of

Table 2. Distribution of 120 sugarcane interspecific hybrids on basis of hierarchical cluster analysis for qualitative characters

Cluster	No. of genotypes	Av. distance from centroid	Distance between cluster centroids
I	4	3.137	I and II (7.714); I and III (14.016); I and IV (9.079); I and V (8.890); I and VI (6.924); I and VII (11.867)
II	20	3.466	II and III (4.390); II and IV (4.167); II and V (11.002); II and VI (7.727); II and VII (9.800)
III	4	3.988	III and IV (7.895); III and V (10.286); III and VI (9.416); III and VII (13.943)
IV	53	3.941	IV and V (9.182);IV and VI (14.082);IV and VII (9.243)
V	8	4.371	V and VI (8.465); V and VII (5.748)
VI	9	4.311	VI and VII (12.435)
VII	22	3.809	-

genotypes grouped in cluster VI. Genotypes in cluster VII had thick canes, broad shaped leaves, self de-trashing leaf sheath, large ovate shaped buds, smooth canes with no splits and wax. Similar studies on cluster analysis and phenotypic diversity in Ethiopian sugarcane germplasm (exotic and local) indicated the use of descriptors in maintaining proper identity, conservation of germplasm (Esayas Tena et al. 2016) and the variability for the descriptors.

Maximum inter cluster distance was observed between the cluster IV and VI (14.082) followed by the cluster I and III (14.016), III and VII (13.943) and between VI and VII (12.435). This indicated high genetic divergence between the genotypes of clusters. Intercrossing of genotypes from these clusters will result in a wide array of variability for exercising effective selection. Inter cluster distance between clusters II and V (11.002), I and VII (11.867) and III and V (10.286) were moderate, suggesting crosses among these clusters for obtaining heterotic segregants. Minimum inter cluster distance was between clusters II and III (4.390), II and IV (4.167) and V and VII (5.748) which indicated the close relationship between these clusters; hence crosses involving the genotypes among the clusters may not be effective.

The cluster wise mean values for seven agronomic traits (Table 3) indicated substantial variation among the clusters. Nair et al. (1998) in his studies on sugarcane germplasm also observed that cane height contributed the highest to genetic divergence and cane weight was significantly added to genetic diversity among sugarcane genotypes. In the present study also maximum mean value for NMC, cane height and cane yield was in cluster IV followed by V and VI; which represents interspecific hybrids from SSH and SRH and the trait, cane height contributed to maximum divergence.

The genotypes in cluster IV had three of five yield component traits with mean values (NMC-101.5, cane height-258.55 cm and cane yield/row-88.71 Kg) greater than grand mean value considered over all other clusters. Cluster IV was further grouped in two sub clusters: IVa with 21 and IVb with 32 genotypes. Genotypes in sub cluster IVa had NMC > 90/row and 19 among 32 genotypes of sub cluster IVb had cane height above 300 cm. Genetic divergence studies by Kang et al. (2013) revealed that brix value had the highest contribution to genetic divergence (29.09%) followed by cane height and cane weight (16.36%) which was due to genetic dissimilarity among the genotypes for these traits. In this study, highest mean value for cane thickness was observed in cluster VII (2.72 cm) and I (2.46 cm), contributed mainly by the hybrids from SBH. SCW had maximum mean value in cluster VII (1.24 Kg) and II (1.08 Kg). High genetic divergence and highest mean value for juice quality was observed with genotypes in cluster VII (18.21 %) and with genetic divergence. Silva et al. (2005) also

Table 3. Cluster wise mean value with deviation percentage from total mean value for yield and quality characters

Cluster/ traits	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI	Cluster VII	Over all mean value of 120 genotypes
Number of millable canes/row	59.77 (–13.66)	54.17 (–21.75)	60.68 (–12.35)	101.5 (+46.61)	83.56 (+20.70)	72.02 (+4.03)	52.9 (–23.59)	69.23
Cane height (cm)	228.83 (+1.39)	181.38 (–19.64)	231.44 (+2.54)	258.55 (+14.55)	256.7 (+11.81)	252.35 (+13.74)	170.67 (–24.38)	225.7
Cane thickness (cm)	2.46 (+16.04)	2.21 (+4.25)	2.3 (+8.49)	1.53 (–27.83)	1.89 (–10.85)	1.74 (–17.92)	2.72 (+28.30)	2.12
Single cane weight (Kg)	0.9 (–5.26)	1.08 (+13.68)	0.88 (–7.37)	0.87 (–8.42)	0.75 (–21.05)	0.92 (–3.16)	1.24 (+30.53)	0.95
Brix %(300 days)	19 (+4.40)	18.38 (+0.99)	17.46 (–4.07)	15.73 (–13.57)	17.09 (–6.10)	18.89 (+3.79)	20.91 (+14.89)	18.20
Sucrose % (300 days)	17.23 (+7.15)	16.29 (+1.31)	15.27 (–5.04)	13.48 (–16.17)	15.62 (–2.86)	16.46 (+2.36)	18.21 (+13.25)	16.08
Cane yield/row (Kg)	63.19 (–12.47)	66.95 (–7.26)	60.47 (–16.23)	88.71 (+22.88)	79.21 (+9.72)	75.32 (+4.34)	71.48 (–0.98)	72.19

Deviation percentages from total mean value for different traits are in parentheses reported that brix value and juice contents contributed the highest in genetic divergence and were more favorable for genetic diversity study in sugarcane.

Among the clusters, cluster II was relatively characterized by low cluster mean value for traits *viz.*, NMC, cane height and cane yield/row than the grand mean value. Crossses involving genotypes of sub clusters IVa and IVb were effected in crop season 2015. Three crosses *viz.*, SSH 12-81 x SSH 12-33, SSH 12-331 x SSH 12-65 and SSH 12-79 x SSH 12-14 resulted in more number of transgressive recombinants for cane yield parameters (unpublished data).

Metroglyph analysis for quantitative traits

The metroglyph and index score analysis was carried out with six agronomic characters *viz.*, NMC/row, cane thickness, SCW, cane height, cane yield/row and brix % to categorize the genotypes. The most variable characters, cane height and NMC were used for construction of metroglyph pattern. Sanghera et al. (2015), assessed genetic diversity by cluster analysis and grouped them into five clusters with maximum genetic distance as much as 89 between two clusters. In our study, metroglyph chart (Fig. 2) grouped all the genotypes into ten distinct groups with specific differences. The mean index score of the groups varied from 8.6 to 16.2. Groups III, IV, V, VIII and X were identified with high mean index scores (Fig. 2). In group III and IV, four among the six traits (NMC, cane thickness, SCW and cane yield) contributed together for the highest mean index scores (Table 4) and hence identified as the most distant genetic groups. Genotypes in these groups had index scores (14 to 17) and so could be directly utilized in breeding programs. In group V, cane yield alone contributed for high index score. In group V, 22 SSH genotypes (high to moderate yielders) with individual index score above 11 were identified as elite clones for utilization in back cross breeding. Cane thickness and brix % were the contributory traits in groups VIII and X with high mean index scores. Similar line of research (Kang et al. 2013) partitioned sugarcane genotypes into eight clusters and their genetic divergence showed that brix value had the highest contribution to genetic divergence (29.09%) followed by cane height and cane weight (16.36%). In our findings also, the yield traits *viz.*, cane height, cane weight and the quality parameter brix % showed high divergence in the clusters for further exploitation. Zhou et al. (2015) from their multivariate studies also concluded that stalk height followed by stalk diameter and number of millable canes should be given more emphasis in sugarcane breeding. Group VI is a unique cluster as it

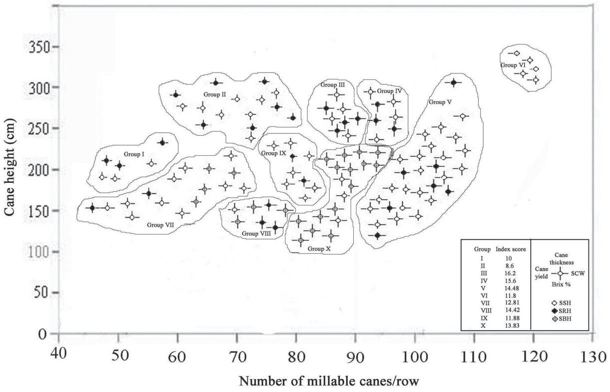

Fig. 2. Scatter diagram of metroglyph analysis representing 120 interspecific hybrids of *Saccharum* spp. on six agronomic characters

Table 4. Index score assigned and signs used for six quantitative characters in metroglyph analysis of *Saccharum* interspecific hybrids

Characters	Range	Score 1		Score 2		Score 3	
		Value (<)	Sign	range	sign	Value (>)	sign
NMC/row (X axis)	47-121	60	-	60-100	-	100	-
Cane height (cm) (Y axis)	125-345	175	-	175-275	-	275	-
Cane thickness (cm)	0.89-3.46	1.50	○	1.50-3.00	⬯	3.00	⬭
Single cane weight (Kg)	0.54-1.70	0.75	○	0.75-1.50	⬯	1.50	⬭
Brix % (300 days)	13.26-21.68	15.00	○	15.00-18.00	⬯	18.00	⬭
Cane yield/row (Kg)	53.45-118.2	85	○	85-105	⬯	105	⬭

Table 5. Promising genotypes for various traits grouped in clusters with wider inter cluster distance

Traits/ Cluster	NMC/row	Cane height (cm)	Cane thickness (cm)	SCW (kg)	Sucrose % (300 days)	Cane yield / row (Kg)
Cluster IV	SSH 12-331 (14), SSH 12-79 (17), SSH 12-33 (16), SSH 12-572 (12), SSH 12-390 (14), SSH 12-515 (15)	SSH 12-81 (16), SSH 12-65 (17), SSH 12-148 (17), SSH 12-14 (14), SSH 12-304 (17)	SSH 12-769(15)	SSH 12-223(14)	SSH 12-409(12)	SSH 12-158 (15), SSH 12-178 (13)
Cluster VI	SRH 12-108 (11), SRH 12-259 (16)	SRH 12-25 (12), SRH 12-102 (15)	SRH 12-275(14)	SRH 12-57(16), SRH 12-298(15)	SRH 12-128 (14)	SRH 12-119 (14)
Cluster VII	SSH 12-546 (13), SSH 12-66 (12)	SSH 12-590 (14)	SBH 12-568 (15), SBH 12-96 (13), SBH 12-45 (16)	SBH 12-392 (15)	SBH 12-304 (17), SRH 12-275 (16), SBH 12-442 (15)	SSH 12-496 (16)

Values in parentheses are individual index score obtained through metroglyph analysis

combines highest cane height with high NMC and can be further exploited in breeding programmes. The clones with highest index scores were found grouped in clusters IV, VI and VII (identified with maximum inter cluster distance in cluster analysis) in Table 5. Intermating between these genotypes will be highly beneficial for enhancement of both yield and quality traits. Group I, II, VII and IX have low genetic diversity and were near uniform and can be used as donors for hybridization with clones of other groups.

Authors' contribution

Conceptualization of research (SA, EK); Designing of the experiments (SA, EK); Contribution of experimental materials (SA); Execution of field/lab experiments and data collection (EK, SA); Analysis of data and interpretation (EK, SA); preparation of manuscript (EK, SA).

Declaration

The authors declare no conflict of interest.

Acknowledgements

The authors express gratitude to the Director, ICAR-Sugarcane Breeding Institute for providing necessary facilities to carry out this research work. The authors also gratefully acknowledge former Director Dr. N. Vijayan Nair for kindly providing the basic genetic material used in hybridization. Help of Shri P. Periyasamy is acknowledged for managing the field operations and data collection is duly acknowledged.

References

Abubakar L., Aliero A. A., Mohammed S. G., Mohammed S., Musa M. and Bubuche T. S. 2013. Preliminary evaluation of some qualitative traits of Sugarcane germplasm of North-Western Nigeria. Nig. J. Basic Appl. Sci., **21**(2): 116-121.

Agarwal R. A. 1969. Morphological characteristics of sugarcane and insect resistance. Entomol. Exp. Appl., **12**: 767-776.

Akhtar M., Elahi N. N. and Ashraf M. 2001. Evaluation of exotic sugarcane varieties for agronomic characters and productivity. Pak. J. Biol. Sci., **4**(1): 37-40.

Anderson E. 1957. A semigraphical method for the analysis of complex problems. Proc. Natl. Acad. Sci., Washington, **43**: 923-927.

Artschwagar E. 1940. Morphology of the vegetative organs of sugarcane. J. Agric Res., **60**: 503-549.

Artschwager E. 1948. Vegetative characters of some wild forms of *Saccharum* and related grass. U.S. Dept. Agric. Tech. Bull., 51-69.

Bakshi Ram., Nair N. V., Radhakrishnan C. M., Singh N. and Sahi B. K. 2007. Effect of cytoplasmic diversity on performance of sugarcane hybrids. Indian J. Genet., **67**: 229-231.

Balakrishnan R., Nair N. V. and Sreenivasan T. V. 2000. A method for establishing a core collection of *Saccharum officinarum* L. germplasm based on quantitative-morphological data. Genet. Res. Crop Evol., **47**: 1-9.

Balakrishnan V. and Sanghvi L. D. 1968. Distance between populations on the basis of attribute data. Biometrics, **24**: 859-865.

Bhattacharjee R., Khairwal I. S., Bramel P. J. and Reddy K. N. 2007. Establishment of a pearl millet

[*Pennisetum glaucum* (L.) R. Br.] core collection based on geographical distribution and quantitative traits. Euphytica, **155**: 35-45.

Chandran K. 2011. Characterization of exotic commercial hybrid clones of Sugarcane. Indian J. Plant Genet. Resour., **24**(3): 271-276.

Esayas Tena Gashaw, Firew Mekbib and Amsalu Ayana. 2016. Heritability and correlation among sugarcane (*Saccharum* spp) yield and some agronomic and sugar quality traits in Ethiopia. Am. J. Plant Sci., **7**: 1453-1477.

Gemin Z., Rongzhong Y., Haibin L. and Weikuan F. 2006. Principal component analysis for 7 quantitative traits and cluster analysis based on 7 quantitative traits of *Saccharum spontaneum* L. South west China. J. Agric. Sci., **19**(6): 1127-1131.

Govindaraj P., Amalraj V. A., Mohanraj K. and Nair N. V. 2014. Collection, characterization and phenotypic diversity of *Saccharum spontaneum* L. from arid and semi-arid zones of north western india. Sugar Tech., **16**: 36-43.

Grassl C. O. 1956. The morphology of grass spikelet with special reference to *Saccharum*. Proc. Int. Sugarcane. Tech., **9**: 764-780.

Kang. A., Muhammad Noor., Farooq A. Khan. and Farasat Saeed. 2013. Divergence analysis and association of some economical characters of sugarcane (*Saccharum officinarum* L.). J. Plant Breed. Genet., **1**: 01-06.

Khalid M. F., Khan L., Naz., Nayab D., Fayyaz H., Samad A., Gul F. and Khan R. N. 2016. Assessment of variability in sugarcane genotypes based on morphological traits. American-Eurasian J. Agric. & Environ. Sci., **16**(6): 1043-1050.

King N. J., Mungomery R. W. and Hughes C. G. 1965. *In*: Manual of cane growing. Augus & Robertson Ltd, Melbourne, Australia, **164-175**: 234-253.

Nair N. V., Balakrishnan R. and Sreenivasan T. V. 1998. Variability for quantitative traits in exotic hybrid germplasm of sugarcane. Gen. Res. Crop Evo., **45**(5): 459-463.

Nair N. V., Nair S., Sreenivasan T. V. and Mohan M. 1999. Analysis of genetic diversity and phylogeny in *Saccharum* and related genera using RAPD markers. Genet. Resour. Crop Evol., **46**: 73-79.

Ongala J., Mwanga D. and Nuani F. 2016. On the use of principal component analysis in sugarcane clone selection. J. Indian Soc. Agric. Stat., **70**(1): 33-39.

Price S. 1967. Interspecific hybridization in Sugarcane breeding. Proc. Int Soc Sugarcane Technol (eds. H. D. Cooper, C. Spillane and P. Hodgkin), **12**: 1021-1026.

Roach B. 1989. Origin and improvement of the genetic base of Sugarcane. Proc. Aust Soc Sugar Cane Technol (ed. B.T. Egan). Ferguson and Company, Salisbury, England: 34-47.

Sanghera G. S., Kumar R., Tyagi V., Thind K. S. and Sharma B. 2015. Genetic divergence among elite sugarcane clones (*Saccharum officinarum* L.) based on cane yield and quality traits from northern India. JEBAS, **3**(2): 184-190.

Silva C. M., Vidigal M. C. G., Filho P. S. V., Scapim C. A., Daros E. and Silverio L. 2005. Genetic diversity among sugarcane clones (*Saccharum* spp.). Acta Sci. Agron. Maringa, **27**(2): 315-319.

Skinner J. C. 1972. Description of sugarcane genotypes. *In*: Botanical description. Proc. ISSCT, **XIV**: 124-127.

Sundas Shahzad, Farooq Ahmad Khan, Muhammad Zafar Iqbal, Ihsan Khaliq and Nisar Ahmed, 2016. Characterization of local and exotic sugarcane genotypes on the basis of morphological and quality related attributes. Pak. J. Agri. Sci., **53**(1): 121-128.

Thapa D. B., Sharma R. C., Mudwari A., Ferrara G. O., Sharma S., Basnet R. K., Witcombe J. R., Virik D. S. and Joshi K. D. 2009. Identifying superior wheat cultivars in participatory research on resource poor farms. Field Crop Res., **12**: 124-130.

Wagih M. E., Musa Y. and Ala A. 2004. Fundamental botanical and agronomical characterization of sugarcane cultivars for clonal identification and monitoring genetic variations. Sugar Tech., **6**(3): 127-140.

Zhou H., Rong-Zhong Yang and Yang-Rui Li. 2015. Principal component and cluster analyses for quantitative traits in GT sugarcane germplasm (*Saccharum* spp. Hybrids). IJAIR, **3**(6): 1686-1690.