S. Afr. J. Agric. Ext. Mekonnen, Azene & Tessema
Vol. 52 No. 2, 2024: 145-158
10.17159/2413-3221/2024/v52n2a15988 (License: CC BY 4.0)

Yield and Multivariate Analysis among Twelve Sugarcane (*Saccharum Officinarum* L*)* Genotypes at Mankusa, North Western, Ethiopia

Mekonnen, S.A.[1], Azene, T.F.[1] and Tessema, W.M.

Corresponding Author: S.A. Mekonnen. Correspondence Email: Shitahun_alemu@dmu.edu.et

ABSTRACT

Smallholders cultivated sugarcane for household consumption, immediate cash, and feeding livestock in Ethiopia. However, its production and productivity are constrained by a lack of improved varieties. Sugarcane germplasm was collected from Districts of West Gojjam, Ethiopia, to evaluate yield and its contributing characters and quantify the phenotypic diversity at Mankusa, Jabitehnan, Ethiopia. The experiment was conducted using a randomised complete block design with three replications for two crop cycles, from April 2020 to March 2023. Data were recorded for the number of tillers, internode length, sellable stalks, plant height, stalk diameter, cane yield and biomass yield from twelve genotypes collected. The data recorded were subjected to analysis of variance, and means were separated using the Duncan Multiple Range Test at a 5% significance level. Variance and multivariate analysis indicated the existence of high phenotypic diversity between genotypes in all quantitative traits studied. Acc 7/20 and Acc 5/20 genotypes produced the highest number of tillers and longest internodes, while Acc 6/20 produced the highest number of sellable stalks. The genotype Acc 4/20 was the longest, and the thickest genotype, which could be elite donors for it respected quality traits through crossing. The highest cane yield was recorded from Acc 4/20 (178.04 t/ha), Acc 7/20 (151.41 t/ha), Acc 8/20 (134.1 t/ha) and Acc 12/20 (132 t/ha), producing 58, 34, 19 and 17% advantageous from the overall genotypes mean, respectively. Cluster analysis grouped the twelve sugarcane genotypes into four clusters, indicating the possibility of broadening the genetic basis by crossing genotypes in the different clusters. It also indicated that a cross between cluster II and III genotypes could create the thickest canes with many sellable stalks. Therefore, genotypes Acc 04/20, Acc 07/20, Acc 8/20 and Acc 12/20 have been recommended and must be evaluated in

[1] Debre Markos University Burie Campus, Department of Plant Sciences, Burie, Ethiopia. Corresponding Author Email: Shitahun_alemu@dmu.edu.et. Orcid id: [1*] https://orcid.org/0000-0003-4910-863X

Vol. 52 No. 2, 2024: 145-158
10.17159/2413-3221/2024/v52n2a15988

other sugarcane growing areas to exploit their potential.

Keywords*:* Cluster Analysis, PCA, Sugarcane, Variability, Yield

1. INTRODUCTION

Sugarcane is an important crop cultivated in tropical and subtropical climatic regions for chewing, animal feed and sugar production (Ochami & Ochieng, 2020).The most preferred natural sweetener and energy source worldwide. Sugarcane (*Saccharum*) is a genus characterised by high ploidy levels with chromosome numbers ranging from 2n= 80 to 2n= 130. The high ploidy nature of sugarcane complexes improves practices for the crop as it is highly influenced by changes in the environment and favoured specific adaptations. Globally, sugarcane breeders develop better-adapted and high-yielding varieties to meet the requirements of the smallholder farmers and sugar industry (Govindaraj *et al.*, 2016).

Sugarcane is an important crop widely cultivated for multiple purposes by smallholder farmers in sub–Saharan Africa (SSA), including Ethiopia. It has been cultivated in Ethiopia since the 16th century and preceded the commercial sector, and commercial sugarcane production has a history of six decades (Esayas *et al*., 2018). A report by the Central Statistics Agency (CSA, 2019) of Ethiopia showed that 998,749 households grew sugarcane in about 27,826.98 hectares of land with a production of 12,940,81t/year and productivity of 46.5t/ha. However, sugarcane production and productivity under smallholder farming systems are constrained by biotic, abiotic, and socioeconomic factors (Tena *et al.,* 2016). The low yield of sugarcane genotypes and production technologies are the major causes of the hampering of sugarcane yield in Ethiopia. Promising varieties and suitable technologies are solutions to improve growers' cane yield. These constraints can be resolved by evaluating locally collected sugarcane landraces by identifying preferred genes for breeding purposes. Information about genetic diversity is a prerequisite for any breeding program. New avenues and sources of genetic diversity enable breeders to develop cultivars that can tolerate changing environments, diseases, pests and climatic conditions. Sufficient genetic diversity enables species to resist diseases and adapt to new climatic conditions.

In Ethiopia, the smallholder sugarcane production sector for chewing is under-researched, with no industrial link or support. There is a limited effort to collect and characterise sugarcane varieties locally. However, they have long agricultural values, adaptation, and co-evolution with prevailing pests and diseases across different agroecological regions of the country. They can also serve as a rich source of novel genes desired for farmer's preferred traits. In addition, sugarcane production declined from 30 296 to 27 827 ha and the number of growers reduced from 1,270,627 to 998,749 households (CSA, 2015 and CSA, 2019).

Developing high-yielding and stable varieties requires a continuous supply of new germplasm as a source of desirable genes. One of these germplasm sources is local sugarcane landraces, which could be sources of desirable genes that adapt and coevolve with the country's agroecologies and growing conditions. The addition of desirable genes and knowledge of phenotypic and genetic diversity is crucial in any crop improvement programs and gene introgression. Multivariate analysis allows the estimation of the contribution of variations in different traits to the total variability in a germplasm collection (Karakoy *et al.*, 2013). Cluster and principal component analysis are the major multivariate analysing tools used to provide information for the existing genetic variability and the trend of character association, which help to identify donor genotypes for important sugarcane traits (Karakoy *et al.*, 2013). Cluster analysis (CA) is important in grouping genotypes with multi-desirable characters. Principal component analysis (PCA) is a valuable method of determining the inter-relationship among variables (Brown *et al.*, 2000).

Therefore, this study was initiated to collect and screen the best local sugarcane genotypes cultivated across West Gojjam in Ethiopia. The study's specific objectives were 1) to screen the best sugarcane genotypes for yield and their contributing characteristics and 2) to quantify the genetic diversity of collected sugarcane genotypes for sources of genes to farmers' preferred traits based on cluster and principal component analyses.

2. MATERIALS AND METHODS

The study was conducted at Mankusa (10^0 70′ N 37º18′ E) in the Jabi Tehinan district, which is 397 km away from Addis Ababa during the 2020/21 growing season using irrigation. The experimental site is at 1,917 m above sea level with an average annual rainfall of 1,450 mm and

minimum and maximum temperatures of 10 ^{0}C and 23 ^{0}C, respectively. The soil type is nitosols, with a pH ranging from 5.3 to 6.

Twelve sugarcane genotypes (Acc 1/20, Acc 2/20, Acc 3/20, Acc 4/20, Acc 5/20, Acc 6/20, Acc 7/20, Acc 8/20, Acc 9/20, Acc 10/20, Acc 11/20 and Acc 12/20) were collected in April 2020 across West Gojjam, Ethiopia, from farmers' fields and local markets. The districts and sub-districts were selected based on the long agricultural history and relatively wide areas allocated to sugarcane production. Moreover, purposive sampling was also employed based on information supplied by key informants on the uniqueness and quality of sugarcane types grown in these areas. Sugarcane clones were collected following the methods proposed by Hawkes (1980). Information on the sampled sugarcane germplasm was recorded, and passport data was collected following the Biodiversity International method (Hawkes, 1983).

The collected genotypes were tagged and planted in April 2020 at Mankusa, grown with the supplementary use of irrigation until March 2023. The experiment was a completely randomised block design with three replications. An equal number of two-budded sets was planted using the end-to-end planting method for each genotype. Cultural practices such as tillage operations, fertilisation, moulding, irrigation, weed, pest and disease control were done uniformly to all entries as per the farmers' practice.

Data was collected from the two central rows for the tillers, sellable stalk, stalk length, internode length, stalk girth, single stalk weight, cane yield, and biomass yield. The quantitative data recorded was subjected to variance analysis using the SAS software (SAS, 2002). Duncan Multiple Range Test comparison method at 5% level of significance was used to separate the treatment means. Clustering of genotypes based on all yield and yield contributing traits was done using the PROC clustering strategy of SAS 9.0, and principal component analysis was computed using statistical analysis software.

3. RESULT AND DISCUSSION

3.1. Phenotypic Characterisation

Analysis of variance revealed that the variation among the twelve sugarcane genotypes was significant for all traits studied (Table 1), declaring that the performance of sugarcane genotypes

10.17159/2413-3221/2024/v52n2a15988

could be significantly affected by environmental conditions. These results coincide with those of Alam *et al.* (2018), Darika *et al.* (2021) and Panhwar *et al.* (2022), who found significant differences among sugarcane genotypes for all the traits examined. This is important for the sugarcane improvement through selection from the diversity of genes attributed to different characters.

The performances of the genotypes for eight important phenotypic traits over the two ratoon cycles are presented in Table 2. The results showed a wide range of variation in different traits; number of tillers (278 – 644), internode length (5 – 16 cm), number of sellable stalks (166 – 453), single stalk weights (1.04 – 2.21 kg), stalk girth (2.27 – 3.11 cm), stalk length (1.84 – 2.75m), cane yield (64.91 – 178.04 t/ha) and biomass yield (87.85 – 244.70 t/ha). This indicates a wide range of genetic variability for studied characters and highlights the potential for genetic improvement. Arain *et al*. (2011) also found significant differences among sugarcane genotypes in these traits.

TABLE 1: Mean Squares of Sugarcane Characters at Mankusa for Twelve Genotypes

Sources of Variation	DF	Tiller Count	Internode Length (cm)	Stalk Length (m)	Stalk Girth (cm)	Single stalk Wt (kg)	Sellable Stalk Count	Cane Yield (t/ha)	Biomass Yield (t/ha)
Genotypes	11	69252*	34.3*	0.42*	0.34*	0.65*	32532*	6737*	9208*
Replication	2	65704*	13.33 ns	0.20ns	0.03ns	0.20 ns	24382*	8571*	11714*
Error	22	7465	1.92	0.19	0.05	0.10	2010	413	564
Mean		456	10	2.32	2.71	1.36	293	112.68	153.67
CV		18.95	13.86	18.79	8.25	23.25	15.30	18.04	15.5

* indicates significance at 0.05 probability, and ns indicates non-significance at 0.05 probability

The genotypes Acc 6/20 and Acc 7/20 produced the highest significant number of tillers compared to the genotypes. The Acc 7/20, Acc 4/20, and Acc 5/20 genotypes had long

Vol. 52 No. 2, 2024: 145-158
10.17159/2413-3221/2024/v52n2a15988

internodes, with 60%, 40%, and 14.2% lengths higher than the overall genotypes mean (10cm). Those genotypes could be elite donors for internode length and number of tillers in sugarcane (Table 2).

Significant differences were detected for stalk length among tested genotypes. The top four genotypes that exceeded the overall stalk length mean (2.32m) by more than 10% were Acc 4/20(18.5%), Acc 8/20 (15.1%) and Acc 6/20 (11.6%). Genotypes Acc 2/20 (1.84m) and Acc 11/20 (2.05m) recorded the shortest plants with 20.7% and 11.6% less than the overall genotype mean. Significant differences were also detected in the number of sellable stalks. The genotype Acc 6/20 had significantly the highest number of sellable stalks (453), while the accession Acc 1/20 had significantly the lowest sellable stalking numbers. The genotypes Acc 4/20 (3.11cm) and Acc 1/20 (3.07cm) had the highest significant cane thickness and more than 13% advantageous from the overall stalk girth performances of the collected sugarcane genotypes. Acc 6/20 (2.27cm) was recorded significantly as the thinnest sugarcane genotype (Table 2).

Five genotypes (Acc 4/20, Acc 7/20, Acc 8/20, Acc 12/20 and Acc 9/20) yielded up to 62.5% more single stalk weights than overall genotypes mean. The genotype Acc 4/20 (2.21 kg) produced the highest single stalk weights. The highest cane yield-producing genotypes were Acc 4/20 (178.04 t/ha), Acc 7/20 (151.41 t/ha) and Acc 8/20 (134.1 t/ha), with 58, 34 and 19 % more yields than the overall genotype mean. These genotypes also had the highest biomass yield than the overall genotype mean (Table 2). Muhammad *et al.* (2020), Rao *et al.* (2022), and Shitahun and Tesfaw (2022) have also reported variability in different yield and yield-related traits of sugarcane. The inherent genetic constitution of the sugarcane genotypes might have resulted in higher and lower cane yields. Ali *et al*. (2020) and Nishad and Kumar (2020) have also reported higher differences for different yield and yield-related traits among sugarcane genotypes.

10.17159/2413-3221/2024/v52n2a15988

TABLE 2: Mean Performances of Twelve Collected Sugarcane Genotypes at Mankusa

Accessions	Number of Tillers	Internode Length (cm)	Number of Sellable Stalks	Single Stalk Weights (kg)	Stalk Girth (cm)	Stalk Length (m)	Cane Yield (t/ha)	Biomass Yield (t/ha)
Acc 1/20	278 d	10.67 bc	166 e	1.35 bcde	3.07 a	2.18 cd	64.91 d	87.85 de
Acc 2/20	463 b	5.00 d	238 d	1.07 ef	2.76 b	1.84 e	70.96 d	96.13 cd
Acc 3/20	474 b	7.00 cd	290 cd	1.12 ef	2.50 d	2.10 d	89.65 cd	122.71 cd
Acc 4/20	408 bc	14 a	277 cd	2.21 a	3.11 a	2.75 a	178.04 a	244.70 a
Acc 5/20	504b	11.42 ab	374 b	1.05 f	2.49 d	2.30 cd	111.68bcd	153.84 bcd
Acc 6/20	644a	11 ab	453 a	1.04 f	2.27 e	2.59 ab	130.63bc	179.81 bc
Acc 7/20	636a	16a	339 bc	1.55 b	2.81 b	2.26 cd	151.41ab	206.25 ab
Acc 8/20	481b	11 ab	305 bcd	1.52 bc	2.76 b	2.67 ab	134.1abc	184.56 abc
Acc 9/20	320 cd	9.00 bcd	229 de	1.42 bcd	2.80 b	2.23 cd	97.22 cd	131.07 cd
Acc 10/20	421 bc	8.58 bcd	281 cd	1.26 cdef	2.55 cd	2.43 bc	101.32 cd	136.89 cd
Acc 11/20	425 bc	6.33 bcd	256 d	1.21 def	2.70 bc	2.05 de	90.24 cd	121.52 cd
Acc 12/20	419 bc	10 bc	307 bcd	1.50 bc	2.73 b	2.42 bc	132 bc	178.68 bc
LSD	106	4.552	69	0.26	0.15	0.23	42.23	57.80
Mean	456	10		1.36	2.71	2.32	112.68	153.67

10.17159/2413-3221/2024/v52n2a15988

3.2. Cluster Analysis

Cluster analysis isolates genotypes into clusters, which have demonstrated closer similarities and dissimilarities between clusters. Cluster analysis revealed that the twelve sugarcane genotypes were grouped into four clusters based on the tillers, internode length, sellable stalks, stalk length, cane girth, single stalk weights, cane yield and biomass yield. Alemu *et al.* (2022) also classified twenty-two sugarcane genotypes into four clusters. Seven genotypes (Acc 2/20, Acc 3/20, Acc 4/20, Acc 8/20, Acc 10/20, Acc 11/20 and Acc 12/20) were grouped into cluster I (58.33%), two genotypes (Acc 1/20 and Acc 9/20) in cluster II (16.67%), two genotypes (Acc 6/20 and Acc 7/20) in cluster III (16.67%) and one genotype (Acc 1/20) in cluster IV (8.33%) (Figure 1). This indicates the presence of high genetic variability among genotypes and the possibility to broaden the genetic basis through the crossing of genotypes in the different clusters.

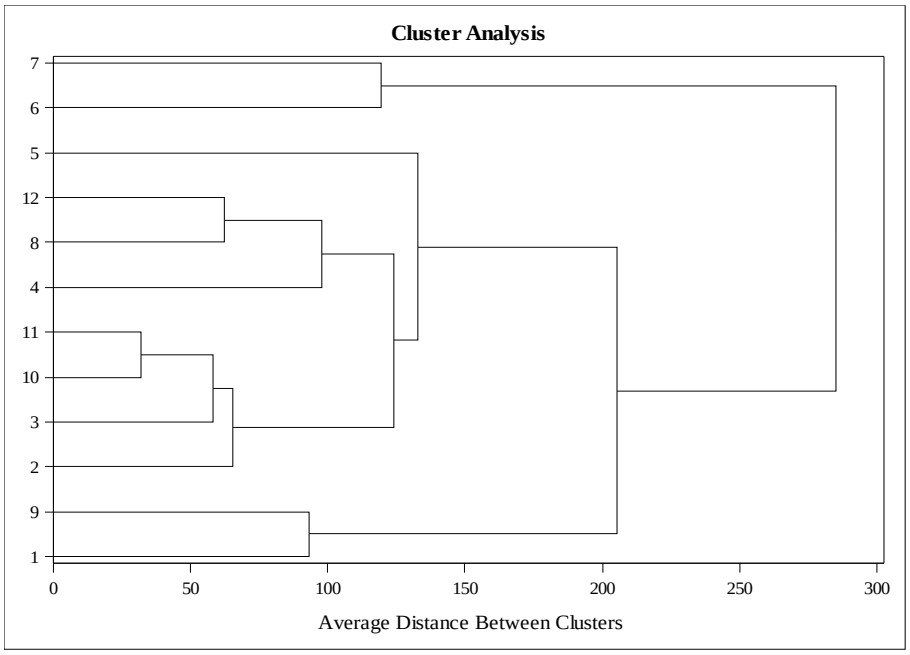

FIGURE 1: Diagram of Twelve Sugarcane Accessions Based on Different Yield and its Related Characters

Genotypes in cluster I are characterised by average performances regarding the number of tillers and sellable stalks, whereas genotypes in cluster III had the highest number of tillers and sellable stalks. Genotypes grouped in cluster II had the lowest number of tillers and sellable stalks but were the thickest canes. The average rates for the number of tillers (640), internode length

(13.5cm), sellable stalk count (396), stalk length (2.43m), cane yield (141.02 t/ha) and cane yield (193.03 t/ha) were the highest in cluster III(Table 3). In this group, Acc 6/20 and Acc 7/20 were superior in their yield and yield-related traits and might be taken into account as a potential to further the breeding program. The cluster analysis indicated the existence of genetic variability among the tested genotypes and showed the possibility of increasing the genetic basis through the crossing of genotypes in the different clusters. For example, genotypes in cluster II are characterised by thicker canes but have a low number of sellable stalks, whereas genotypes in cluster III have the highest number of sellable stalks. A cross made between selected genotypes in those clusters could possibly create the thickest canes with a high number of sellable stalks. Ajmal *et al.* (2013) argued that cluster analysis makes the isolation procedure simple by considering genotypes recorded higher values yield attributes traits and grouped in a single cluster.

TABLE 3: Cluster Mean Values for Eight Morphological Characters of Twelve Sugarcane Germplasm

Characters	Cluster Name			
	I	II	III	IV
Number of tillers	442	299	**640**	504
Internode Length (cm)	8.84	9.84	**13.5**	11.42
Sellable Stalk Count	279	198	**396**	374
Single stalk Weight (kg)	**1.41**	1.39	1.3	1.05
Stalk Girth (cm)	2.73	**2.94**	2.54	2.49
Stalk Length (m)	2.32	2.21	**2.43**	2.3
Cane Yield (t/ha)	113.76	81.07	**141.02**	111.68
Biomass Yield (t/ha)	155.03	109.46	**193.03**	153.84

3.3. Principal Component Analysis

A principal component analysis (PCA) was carried out to describe and better understand the sources of variance among sugarcane genotypes. Four principal components (PC1 to PC4) were extracted from the original data and accounted for 96% of the total variation. Muhammad *et al.* (2018) also reported 85.7% of the total variation in the tested breeding material from the first

four principal components. The first principal component had high positive component loading from cane yield, biomass, stalk height and internode length. The second principal component had high positive component loading from stalk girth and single stalk weight and negative component loading from stalk count and the number of tillers, indicating the existence of a positive and negative correlation between the components and the character (Table 4). The characters with a high positive or negative loading contributed more to the genetic diversity, and they became important in representing the clusters.

TABLE 4: Percent Variation Explained by the Major Four Principle Components

Traits	Prin1	Prin2	Prin3	Prin4
Number of Tillers	0.24	-0.45	-0.28	0.44
Internode Length	0.40	0.12	-0.28	0.16
Stalk Count	0.28	-0.48	-0.07	-0.11
Single Stalk Wt	0.31	0.45	0.05	0.07
Stalk Girth	0.02	0.58	-0.12	0.28
Stalk Length	0.40	0.05	0.15	-0.74
Cane Yield	0.47	0.04	0.03	0.11
Biomass Yield	0.47	0.03	0.01	0.09
Eigenvalue	4.416	2.732	1.065	0.431
Proportion Variance	0.491	0.304	0.118	0.048
% Cumulative	0.491	0.794	0.913	0.960

4. CONCLUSIONS AND RECOMMENDATIONS

The variances and multivariate analysis confirmed the existence of significant variability among studied genotypes for the number of internodes, cane length, stalk girth, single stalk weight, stalk count and cane yield. The highest cane yield was recorded from Acc 4/20 (178.04 t/ha), Acc 7/20 (151.41 t/ha), Acc 8/20 (134.1 t/ha) and Acc 12/20 (132 t/ha), producing 58, 34, 19 and 17% advantageous from the overall genotypes mean, respectively. Cluster analysis grouped the twelve sugarcane genotypes into four clusters, indicating the possibility of broadening the genetic basis by crossing genotypes in the different clusters.

Therefore, genotypes Acc 04/20, Acc 07/20, Acc 8/20 and Acc 12/20 had been recommended and must be evaluated in other sugarcane growing areas to exploit their potential.

ACKNOWLEDGEMENT

The authors are grateful for the financial grant from Debre Markos University.

Vol. 52 No. 2, 2024: 145-158
10.17159/2413-3221/2024/v52n2a15988

REFERENCES

AAMER, M., RIZWAN, M., MUSTAFA, G. & SOHAI, M., 2018. Principal component analysis of some morphological and quality traits in sugarcane. *J. Nsc. R.*, 8(14).

AJMAL, S.U., MINHAS, N.M., HAMDANI, A., SHAKIR, A., ZUBAIR, M. & AHMAD, Z., 2013. Multivariate analysis of genetic divergence in wheat germplasm. *Pak. J. Bot*., 45(5): 1643-1648.

ALAM, K.S., HOSSAIN, G.M.A., ISLAM, M.S. ALAM, K.M., 2018. Performance of chewing sugarcane varieties in a saline prone area. *Eco-friendly Agril. J.*, 11(03): 33-37.

ALEMU, S., FETENE, T. & TADESSE, F., 2022. Morphological diversity and principal component analysis of sugarcane (Saccharum officinarum L) genotypes at Finchaa Sugar Estate, Ethiopia. *Ratar. Povrt.*, 59(1): 9-15.

ALI, M.A., HASSAN, M.S., MOHAMED, B.D. & ALI, M.A., 2020. Performance and stability analysis of some sugarcane genotypes across different environments. *SVU-Int. J. Agric. Sci.*, 2(2): 192-213.

ARAIN, M.Y., PANHWAR, R.N., GUJAR, N., CHOHAN, M., RAJPUT, M.A., SOOMRO, A.F. & JUNEJO, S., 2011. Evaluation of new candidate sugarcane varieties for some qualitative and quantitative traits under Thatta agro-climatic conditions. *The J. Anim. & Plant Sci.*, 21(2): 226-230.

BLACKBURN, F., 1984. *Sugarcane*. New York: Longman Inc.

BROWN G.L., THOMPSON, J.A., NELSON, R.L. & WARBURTON, M.L., 2000. Evaluation of genetic diversity of soybean introductions and North American ancestors using RAPD and SSR markers. *Cr. Sc*., 40: 815-823.

CENTRAL STATISTICAL AGENCY., 2015. *Area and production of major crops*. Addis Ababa, Ethiopia: Federal Democratic Republic of Ethiopia Central Statistical Agency.

CENTRAL STATISTICAL AGENCY., 2019. *Area and Production of Major Crops*. Addis

Ababa, Ethiopia: Federal Democratic Republic of Ethiopia Central Statistical Agency.

CORDEIRO, G.M., TAYLOR, G.O. & HENRY, R.J., 2000. Characterization of microsatellite markers from sugarcane (*Saccharum* sp.), a highly polyploid species. *P.Sc.*, 155(2): 161-8.

DARIKA, B. & RUCHUON, W.G., 2021. Evaluation 16 elite sugarcane lines for ethanol yield and yield related traits under rainfed conditions. *Aust. J. Crop Sci.,* 15(07): 1020-1028.

GASHAW, E.T., MEKBIB, F. & AYANA, A., 2018. Sugarcane landraces of Ethiopia: Germplasm collection and analysis of regional diversity and distribution. *Adv. Agric*., 2018(6): 1-18.

GOVINDARAJ, P., KARTHIGEYAN, S. & PAZHANY, A.S., 2016. Exploration and genetic diversity analysis of *Saccharum spontaneum* in Maharashtra state. *India. J Sugarcane Res*., 6(2): 72-84.

HAWKES, J.G., 1980. *Crop genetic resources field collection manual*. Wagnningen, Netherland: Pudoc.

HAWKES, J.G., 1983. *The diversity of crop plants*. London, England: Harvard University Press.

KARAKÖY, T., BALOCH, F.S., TOKLU, F. & ÖZKAN, H., 2013. Variation for selected morphological and quality-related traits among 178 faba bean landraces collected from Turkey. *Plant Genet. Resour., 12*: 5–13.

KHURSHID, M.R., AHMAD, N., MAJEED, A., ZUBAIR, M., QAMAR, H…, 2020. Evaluation of New Promising Sugarcane Clones under Agro-Ecological Conditions of Faisalabad, Pakistan. *Life Sci J.*, 17(6): 84-88.

LANDON, J.R., 1991. *Booker Tropical soil manual: A handbook for soil survey and agricultural land evaluation in the tropics and subtropics*. London: Routledge.

NISHAD, H.K. & KUMAR, B., 2020. Genetic divergence in early maturing sugarcane clones for the cane yield and yield attributing traits. *Int. J. Sci. Res. Publ.,* 10(2): 548-564.

OCHAMI, F. & OCHIENG, N., 2020. Evaluation of some new sugarcane varieties for yield and yield components under coastal climatic conditions. *Int. J. Adv. St. Res*., 3(8): 2581-5997.

PANHWAR, R.N., SOOMRO, A.F., CHOHAN, M., BHATTI, I.B., MARI, A.H., ARAIN, S. & AHMAD, S., 2022. Assessment of variation in newly developed sugarcane genotypes for morphological and quality associated parameters. *Pakistan J.A.R.,* 35(3): 533-540.

RAO, P.S., MUKUNDA, R.C., SREEDEVI, P., BHARATHALAKSHMI, M. & JAMUNA, P., 2022. Evaluation of sugarcane clones for quality cane juice used for beverage. *Biological Forum – An Int.J*., 14(1): 290-293.

SAS INSTITUTE., 2003. *SAS System for Windows.*

SHITAHUN, A. & TESFAW, F., 2022. Phenotypic evaluation of ten sugarcane (*Saccharum officinarum* L.) genotypes at Finchaa Sugar Estate, Ethiopia. *Ratar. Povrt*., 59(2).

TENA, E., MEKBIB, F. & AYANA, A., 2016. Genetic diversity of quantitative traits of sugarcane genotypes in Ethiopia. *American J. Plsc.,* 7: 1498-1520.