

## Research Article

# Assessment of Genetic Variability in Sugarcane (*Saccharum officinarum* L.) Genotypes for Better Yield, Quality and Sugarcane Mosaic Virus Resistance in Central Punjab, Pakistan

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**Abstract** | Sugarcane is the most valued sugar crop and main source of sucrose. Sugarcane is economic crop grown in tropical and subtropical areas world widely. It is also used for the production of biofuel and ethanol. Sugarcane yield is decreasing due to biotic and abiotic stresses. Among biotic factors, sugarcane mosaic virus (SCMV) is one of the most devastating factors that causes significant losses of sugarcane production. Here we are reporting the assessment of genetic variation among sugarcane accessions based on morphological parameters, SCMV severity, incidence and resistance/tolerance. The experiment was conducted in College of Agriculture, University of Sargodha, Sargodha, Pakistan using randomized complete design in triplicate. Different morphological parameters were calculated to observe sugarcane production and SCMV susceptibility by determining disease incidence and disease severity by using appropriate statistical software. Results revealed that all sugarcane genotypes performed well, showed significant variability for morphological characters and SCMV tolerance/susceptibility based on phenotypic scoring. Brix percentage is an important parameter as it is a yield contributing trait. Sugarcane accessions SC12 (23.03%) followed by SC11 (22.91%) attained maximum brix percentage while the least brix value 16% was observed in genotype SC31. SC4 displayed resistant to sugarcane mosaic virus but its yield was very poor as compared to others due to its genetic makeup. SC3 exhibited high disease incidence, having less brix percentage but showed maximum cane yield. Genotype SC7 revealed moderate susceptibility but exhibited high yield with maximum brix percentage. Evaluation of all agronomic traits and screening of superior genotypes would help in future sugarcane-breeding program to increase sugar production and development of SCMV resistant cultivars.

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## Introduction

Sugarcane is high valued cash crop in Pakistan. It contributes 80% in sugarcane production and 40% in fuel production (Aono *et al.*, 2021). It contributed 0.4% in GDP and 3.4% in agriculture and during 2020-2021, the total production of sugarcane was 81.009 million tones in Pakistan (Economic Survey of Pakistan, 2020-21). Pakistan ranked at 5<sup>th</sup> position worldwide in sugarcane production (FAO, 2021). After the textile industry sugarcane industry leading at second position in Pakistan (Khan *et al.*, 2021).

Sugarcane is a C4 ratoon crop (Lu *et al.*, 2021). It is the most efficient C4 grown on tropical and subtropical region of Pakistan (Yadav *et al.*, 2013). It belongs to oaceae family and genus *Saccharum*. Sugarcane has significant importance in manufacturing of different by products such as fuel, bioethanol and cane juice. It is a polyploidy and mainly cultivated for the source of sucrose (Menossiet *et al.*, 2008). It is a ratoon crop which is mainly cultivated by means of vegetative method, stalk-containing buds is used for germination purpose (Croft *et al.*, 2008).

There are many factors, which cause potential decrease in sugarcane production including biotic and abiotic factors. The important factors that badly effect the yield of sugarcane are use of improper irrigation method and cultural practices, lack of diseases and pests control and improper fertilizer application (Baloch *et al.*, 2020). Most of the existing sugarcane varieties in Pakistan are susceptible to different diseases like sugarcane mosaic virus, red rot, pokhoboeng, etc. Among diseases, sugarcane mosaic virus (SCMV) is one of the major diseases that causes 6-10% decrease in sugarcane yield (Haider *et al.*, 2011). Sugarcane mosaic virus causes yellowing of leaves, dark patches appear on leaves which causes paleness. It belongs to Potyviridae family and devastating for yield losses. Mosaic Virus affects the plant activities, reducing photosynthetic rate, plant metabolism and sugar percentage (Akbar *et al.*, 2021).

In Pakistan, fuzz (sugarcane seed) production is quite difficult because sugarcane is photothermal sensitive crop and it requires 25-33°C temperature for reproduction stage. In Pakistan, these conditions are available only in few places (Khan *et al.*, 2004). Due to limitation of fuzz production and lack of target-based sugarcane hybridization, the variety development is quite difficult (Khan *et al.*, 2012; Aamer *et al.*, 2018).

Regarding improvement of sugarcane genotypes, morphological markers play important role in breeding and selection of superior genotypes from germplasm accessions with high yield contributing traits proved significant in enhancing yield potential (Keerio, 2000). Therefore, to enhance sugarcane yield and quality, improvement should be made on yield contributing traits and diseases resistance of the plant (Khan *et al.*, 2012).

The aim of study was to evaluate sugarcane accessions for better yield in response to sugarcane mosaic virus. The objective of study was to investigate sugarcane mosaic virus resistant genotypes and to screen out superior genotypes from germplasm accessions on the basis of morphological traits for sugarcane improvement and future breeding programs.

## Materials and Methods

The experimental material comprised of 72 sugarcane genotypes (Table 1) planted on September 15, 2017 in research area of College of Agriculture, University of Sargodha in randomized complete block design having three replications. A loamy soil was selected and field was well prepared before planting and furrows were developed at a distance 75cm apart. Sugarcane setts having three eye buds were planted in two furrows per replication of plot size 1.5x5 m<sup>2</sup> and buried with shallow soil. Just after planting sugarcane genotypes, the field was irrigated with canal water. A total of 16 irrigations were applied during the whole year having 3 acre inches water per irrigation. Recommended cultural practices were applied round the year. At proper growth stage (at 7 months' age), sugarcane germplasm was phenotypically evaluated against sugarcane mosaic virus (SCMV) disease based on naturally appeared disease symptoms on leaves using scoring scale as suggested by Addy *et al.* (2017). Morphological data of different plant traits were also collected at 12 months' age to observe performance of sugarcane germplasm for yield contributing and quality traits. Five stools per genotype per replication were selected under natural field condition and data were collected for SCMV scoring to observe disease intensity and disease severity by using following formulae:

*Viral disease incidence (%)*

SCMV incidence was assessed by counting number of symptomatic plants per total observed plants of

each variety in each replication as suggested by Addy *et al.* (2017).

$$\text{Incidence (\%)} = \frac{\text{Number of symptomatic plants}}{\text{Total number of observed plants}} \times 100$$

**Table 1:** List of sugarcane genotypes used for morphological traits and SCMV.

S. No.	Code	Name of genotype	S. No.	Code	Name of genotype
1	SC1	SPCG24	37	SC37	CSSG676
2	SC2	SPSG28	38	SC38	US384
3	SC3	SPSG27	39	SC39	HSF240
4	SC4	SPSG26	40	SC40	CSSG2453
5	SC5	SSRI4	41	SC41	US133
6	SC6	SPSG25	42	SC42	CPS437
7	SC7	SSRI1	43	SC43	US127
8	SC8	SSRI7	44	SC44	CPPC247
9	SC9	SSRI6	45	SC45	CPPC246
10	SC10	US718	46	SC46	HSG315
11	SC11	SRRI3	47	SC47	CPF248
12	SC12	SPSG29	48	SC48	US633
13	SC13	India1	49	SC49	XT236
14	SC14	Thatha1312	50	SC50	CSSG2402
15	SC15	Co0283	51	SC51	CPSG2525
16	SC16	MSG502	52	SC52	FST19
17	SC17	CPSG2730	63	SC53	MSH2415
18	SC18	Aust 134	54	SC54	CP368
19	SC19	NIFA01	55	SC55	CPSG2718
20	SC20	CSSG33	56	SC56	CPSG3481
21	SC21	US832	57	SC57	Co239
22	SC22	CSSG23	58	SC58	Co240
23	SC23	SCCG32	59	SC59	Co241
24	SC24	SPSG27	60	SC60	CPSG2730
25	SC25	US272	61	SC61	XT910
26	SC26	YT53	62	SC62	SPPC213
27	SC27	CSSG25	63	SC63	SPPC220
28	SC28	US204	64	SC64	SPF234
29	SC29	YT210	65	SC65	SPPC237
30	SC30	SSRI2	66	SC66	HSPC240
31	SC31	India2	67	SC67	CP67-500
32	SC32	MSG1127	68	SC68	SPPC2038
33	SC33	XT55	69	SC69	Co 1148
34	SC34	US658	70	SC70	NSG59
35	SC35	WS130	71	SC71	Laliyan
36	SC36	US272	72	SC72	SPSG26

*Viral disease severity (%)*

SCMV severity was considered by estimating the percentage leaf area with mosaic symptoms using the following scoring system suggested by Addy *et al.*

Scoring scale	Leaf area showing symptoms rating
1	No symptoms Immune
2	0.1–2.5% Resistant
3	2.6–5% Resistant
4	5.1–10% Resistant
5	10.1–20% Moderately resistant
6	20.1–35% Moderately susceptible
7	35.1–50% Moderately susceptible
8	50.1–75% Susceptible
9	75.1–100% Highly susceptible

Growth and yield data were recorded for cane yield, cane height, cane diameter, leaf area, number of tillers per stool, single cane weight, weight per stool, brix percentage and lodging resistance. Analysis of variance was done by using mean data of all the parameters under study to observe significant differences among cultivars as described by Steel *et al.* (1997). Tuckey’s range test was used to check the data for similarities and range for each trait. It is also known as Tuckey’s HSD test (Honestly significance difference) it was used to check the genotypes whether they are similar to each other or not. Statistix 8.1 software (Microsoft 365) was used for statistical analysis of data.

**Results and Discussion**

*Evaluation of sugarcane genotypes for sugarcane mosaic virus (SCMV) intensity and severity*

Sugarcane mosaic virus (SCMV) is a complex disease of sugarcane and appears on leaves causes chlorosis and yellowing of leaves. Symptoms of disease depends upon the cultivar susceptibility and environment (Haider *et al.*, 2011; Akbar *et al.*, 2021).

*Viral disease incidence (%)*

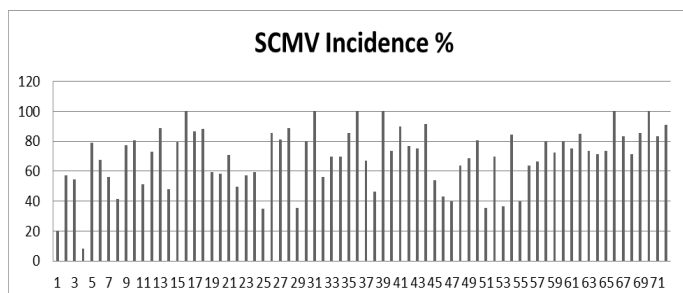
Viral tolerance/susceptibility in presented sugarcane genotypes was observed by disease scoring (%) to assess incidence and severity of sugarcane mosaic virus in natural field conditions (Table 3). Analysis of variance exposed highly significant differences among sugarcane genotypes for SCMV incidence (Table 2). This revealed that ample genetic variability was present among sugarcane genotypes for viral incidence. Viral disease scoring suggested that the genotypes SC-16, SC-30, SC 36, SC 44, SC-64, SC-66, SC-71 were found highly susceptible while genotypes SC1, SC-3, SC 4, SC-08, SC-07, SC-11,

SC-14, SC-25, SC-29, SC-38, SC-46, SC-51, SC-53 and SC-55 were observed as resistant/tolerant against SCMV. The highest incidence of SCMV was observed in genotype SC-16, SC-31, SC-36, SC-39, SC-66, SC-39, SC-66 and SC-70 while SC-4 was the least susceptible genotypes (Figure 1). Our results get support from the findings of Haider *et al.* (2011), Yasmin *et al.* (2011) and Addy *et al.* (2017) who reported similar variations for SCMV disease and other traits among different sugarcane genotypes.

**Table 2:** Analysis of variances of studied plant parameters in 72 sugarcane genotypes.

Variable analyzed	Sum of squares	Means squares	P value
SCMV incidence	81952.7	1154.26	0.000
SCMV severity	103117	1452.35	0.000
Emergence %	7057.4	99.40	0.000
Cane height	117525	1655.3	0.000
Cane diameter	46.1098	064943	0.000
Number of tillers per stool	286.292	4.0323	0.000
Single cane weight	4124190	6.26	0.000
Weight per stool	231.647	3.2626	0.000
Brix %	197.741	2.7851	0.000
Lodging %	40.862	0.5755	0.000

Note: Highly significant ( $P < 0.01$ ).

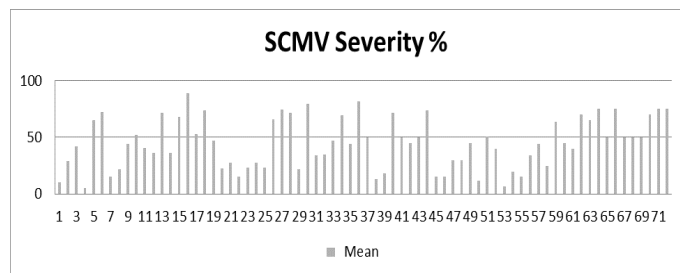


**Figure 1:** Means comparison of 72 sugarcane genotypes for SCMV incidence %.

*Viral disease severity (%)*

Regarding SCMV severity analysis of variance indicated that sugarcane genotypes under study differed significantly for viral severity % (Table 2). It showed that enough genetic variation was present among was present among sugarcane genotypes for SCMV severity. Statistical means comparison indicated that the genotype SC16 showed maximum severity. In other word the genotype SC16 was highly susceptible to the viral infection followed by SC 36 and SC-30 whereas genotype SC4 displayed least susceptibility to mosaic virus followed by SC 53 (Figure 2). This revealed that high level of genetic

variation prevailed in studied sugarcane genotypes for SCMV susceptibility and tolerance. The results are in accordance with findings of Addy *et al.* (2017).



**Figure 2:** Means comparison of 72 sugarcane genotypes for SCMV severity %.

**Table 3:** Sugarcane mosaic virus incidence and severity percentage in 72 sugarcane genotypes.

Geno- type	DI (%)	DS (%)	Geno- type	DI (%)	DS (%)	Geno- type	DI (%)	DS (%)
SC1	20.5	10.0	SC25	40	21	SC48	63.63	30
SC2	50	31	SC26	80	67	SC49	68.75	45
SC3	54.4	42.2	SC27	85.71	70	SC50	30	12
SC4	10	4.5	SC28	87.5	72	SC51	35.29	11
SC5	77.77	64	SC29	40	20	SC52	70	40
SC6	71.42	34	SC30	83.33	74	SC53	36.36	7
SC7	50	17	SC31	100	35	SC54	84.61	20
SC8	42.85	21	SC32	50	40	SC55	40	15
SC9	57.14	45	SC33	75	45	SC56	63.63	34
SC10	83.33	48	SC34	71.42	42	SC57	66.66	44
SC11	51.4	40.4	SC35	83.33	50	SC58	53.33	25
SC12	75	36	SC35	100	75	SC59	72.72	64
SC13	90	75	SC36	70	45	SC60	80	45
SC14	48.1	35.9	SC37	44.44	14	SC61	75	40
SC15	83.33	70	SC38	50	20	SC62	54.54	70
SC16	100	80	SC39	100	70	SC63	73.33	40
SC17	87.5	52	SC40	72.72	75	SC64	71.42	75
SC18	87.5	74	SC41	90	50	SC65	73.33	50
SC19	57.14	48	SC42	76.92	45	SC66	100	75
SC20	57.14	20	SC43	75	50	SC67	83.33	50
SC21	71.42	30	SC44	91.66	74	SC68	71.42	50
SC22	50	15	SC45	53.84	15	SC69	85.71	50
SC23	60	25	SC46	42.85	15	SC70	100	70
SC24	60	25	SC47	40	30	SC71	83.33	75
						SC72	90.90	75

Note: DI= disease intensity% and DS= disease severity %.

*Evaluation of sugarcane genotypes for yield contributing and quality traits*

**Emergence percentage:** Emergence is the first stage of plant initiation, which is the most delicate physiological plant stage. Good emergence percentage plays significant role in determining the production performance of sugarcane genotypes. The results

revealed that all genotypes displayed highly significant performance for emergence percentage (Table 2). Sugarcane accessions SC8 (79.00 %), SC1 (78.64%) and SC7 (78.00%) gained high mean emergence percentage than others (Figure 3). Similar findings were reported by Tena *et al.* (2016), and Khaliq *et al.* (2018).

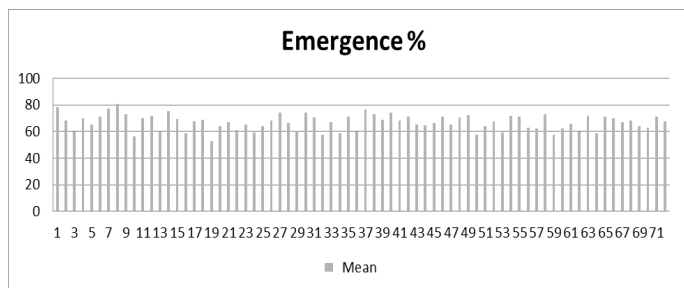


Figure 3: Means comparison of 72 sugarcane genotypes for emergence %.

**Cane height (cm):** Cane height is an important parameter as cane yield depends on it. Cane height was measured at maturing stage of plant. Analysis of variance showed that all accessions exhibited significant variation for cane height (Table 2). A good range was observed in sugarcane accessions for cane height as SC10 exhibited 210cm maximum mean value while SC33 gained 100.67 cm minimum cane height among all genotypes (Figure 4). Our results were similar as reported by Khalid *et al.* (2014).

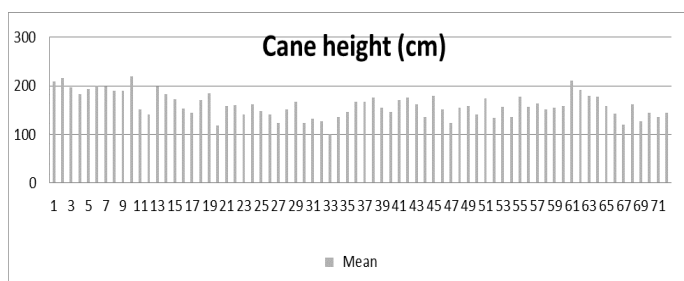


Figure 4: Means comparison of 72 sugarcane genotypes for cane height.

**Cane diameter (cm):** Cane diameter is an important indicator of cane yield as higher the cane diameter higher will be cane weight. The results of the experiments indicated that significant differences were present among studied sugarcane accessions for cane diameter which showed ample genetic variability for cane diameter (Table 2). Among maximum performance was observed in SC3 (4.43cm) while minimum performance was observed in SC8 i.e., 2.06cm (Figure 5), Alam *et al.* (2017) and Khan *et al.* (2018).

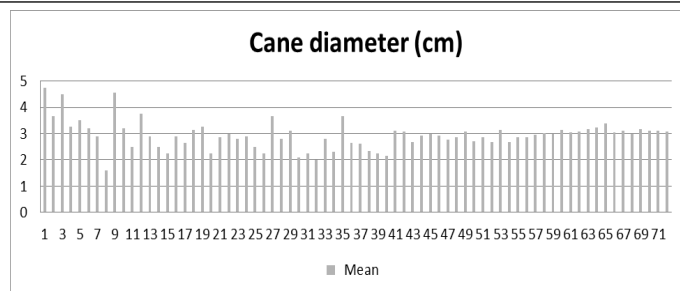


Figure 5: Means comparison of 72 sugarcane genotypes for cane diameter.

**Number of tillers per stool:** Number of tillers per stool is also an important trait for the yield of sugarcane. All genotypes showed variant results in exhibiting number of tillers per stool as it depended upon genotypic background of every genotypes (Table 2). The mean performance indicated that all genotypes performed well but maximum average performance was observed in SC3 while minimum performance was observed in SC12 (Figure 6). Our results agreed with the findings of Soomro *et al.* (2006), Mehrab and Abazied (2017) and Khan *et al.* (2018).

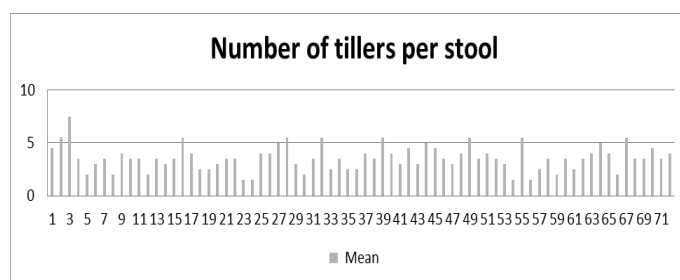


Figure 6: Means comparison of 72 sugarcane genotypes for number of tillers per stool.

**Single cane weight(g):** Single cane weight is also one of the most important yield contributing trait. Significant results were obtained after statistical analysis of studied sugarcane accessions (Table 2). Statistical means comparison revealed that SC1 gained maximum weight (1044g) while SC34 (578g) gained less weight than all other genotypes (Figure 7). Our results of analysis supported by the results of Khan *et al.* (2018) and Tripathi *et al.* (2017).

**Weight per stool (kg):** Weight per stool is one of the most important characters of sugarcane genotypes as it contributes directly towards cane yield. High stool population and more weight of sugarcane stool are indicator of increase in cane yield. ANOVA revealed significant differences among sugarcane genotypes for weight per stool were observed (Table 2). The mean comparisons displayed that the highest weight per stool 7.45Kg was gained by SC7 (Figure 8). Our

findings are in compliance with Khan et al. (2018).

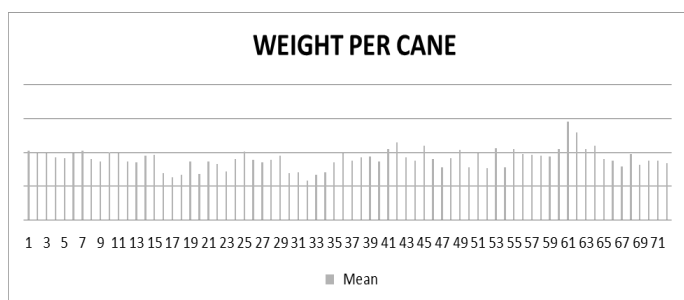


Figure 7: Means comparison of 72 sugarcane genotypes for number of single cane weight.

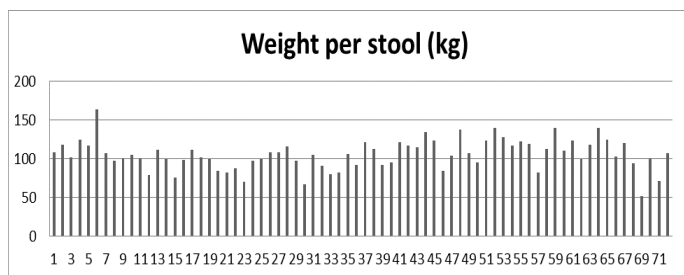


Figure 8: Means comparison of 72 sugarcane genotypes for weight per stool.

**Brix percentage:** Brix percentage plays significant role in quality of sugarcane. It is used to estimate the soluble solids present in juice of sugarcane. All genotypes exhibited significant genetic variation for brix percentage (Table 2). The highest value for brix percentage was observed in genotype SC12 (23.03%) followed by SC11 (22.91%) while the least brix value 16% was observed in genotype SC31 (Figure 9). Our findings are exactly in compliance with the results of Mehrab and Abazied (2017) and Khan et al. (2018).

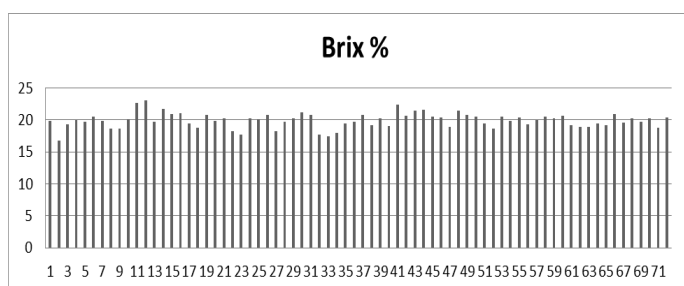


Figure 9: Means comparison of 72 sugarcane genotypes for brix percentage.

**Lodging resistance (%):** Lodging resistance is an important trait of sugarcane plant because it directly contributes to cane yield. ANOVA Table 2 represented that sugarcane genotypes did not show significant differences among themselves for lodging percentage. This indicated that all studied genotypes showed similar trend for lodging percentage. Mean comparisons showed that there were no statistical

differences among all sugarcane genotypes for lodging percentage (Figure 10). Our findings were in contrast with the results of Li et al. (2019).

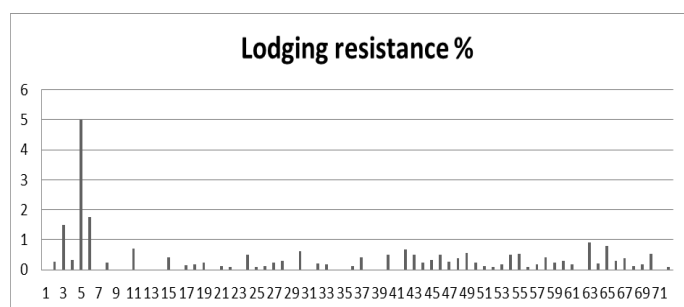


Figure 10: Means comparison of 72 sugarcane genotypes for lodging resistance (%).

### Conclusions and Recommendations

High level of genetic variation prevailed in studied sugarcane genotypes for morphological traits, sugar recovery and SCMV tolerance. Sugarcane genotypes SC-1, SC-3, SC-11, SC-14, SC-20, SC-24 and SC-40 were found excellent for sugar recovery and cane weight while sugarcane genotypes SC-1, SC-22, SC-04 and SC-38 were observed as resistance/tolerant against SCMV intensity and severity. Furthermore, SC-3, SC-4, SC-20 and SC-33 were found genetically diverse genotypes for studied morphological and quality traits and would be used in sugarcane breeding program to enhance sugar recovery, yield and viral resistance/tolerance in sugarcane cultivars.

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### Novelty Statement

Sugarcane mosaic virus is one of the most important disease of sugarcane. This study provides sufficient information about the screening of sugarcane genotypes against SCMV in the field which will be helpful in future for identification and utilization of SCMV free genotypes for in vitro micro-propagation and development of virus free sugarcane cultivars through conventional ways.

### Author's Contribution

**Naeem Akhtar:** Conducted experiment and wrote

manuscript.

**Sana Noureen:** Helped in data collection and did statistical analysis.

**Muhammad Asif:** Helped in manuscript write-up.

**Ahsan Aziz:** Helped in planning and conductance of research.

**Usman Saleem:** Helped in plagiarism report and proof reading.

**Talat Mahmood:** Improved language and writing style of the manuscript.

**Nadeem Raza:** Helped in provision of sugarcane genotypes.

**Waqas Raza:** Helped in write-up and submission of the revision.

#### *Conflict of interest*

The authors have declared no conflict of interest.

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