# Estimation of genetic components in clonally propagated sugarcane genotypes for cane yield and related attributes under the agro-ecological conditions of Mardan-Pakistan

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The present experiment comprised of 14 clonally propagated sugarcane genotypes and two check cultivars which were sown and assessed at the experimental fields of Sugar Crops Research Institute (SCRI), Mardan-Pakistan for two successive spring crop seasons of 2016-17and 2017-18. Significant variations (p≤0.05) among all the genotypes were observed for attributes. The interaction results of C×G were also significant (p≤0.05) for all the attributes except germination. Mean results presented maximum cane yield and sugar yield of 88.98 t/ha and 9.96 t/ha, respectively for genotype MS.99HO.317 followed by genotype RS.97N.45 which displayed cane and sugar yield of 75.13 t/ha and 8.90 t/ha, respectively. Both genotypes showed superior performance than the two check cultivars. Estimates for Genotypic Co-efficient of Variation (GCV) were lower than Phenotypic Co-efficient of Variation (PCV) for all attributes suggested that apparent variability was the combination of both genetic and environmental factors. High PCV and GCV were displayed by % germination, tillers and leaf area, moderate were recorded for weight of five stripped canes, cane yield, inter node length, and sugar yield while low was recorded for weight of five un-stripped canes and number of nodes per canes. The values of G.A as % of mean for all attributes were recorded from 0.30 to 355.80. The highest G.A as % of mean (355.80) was registered for sugar yield while the lowest (0.30) was recorded for number of nodes per cane. Similarly, highest heritability ($h^2$) was recorded for tillers (89.55%) and weight of five stripped canes (80.82%). High heritability was recorded for germination (68.39%), leaf area (76.40%), number of nodes per cane (73.11%), inter node length (77.78%), weight of five unstrapped canes (70.43%) and cane yield (65.98%). Moderate heritability was recorded for sugar yield (53.67%) only. High $h^2$ combined with high G.A as % of mean was recorded for tillers, leaf area, weight of five un-stripped canes and weight of five stripped canes which showed the presence of more additive gene effect and a simple selection procedure regarding these attributes might lead to improvement in sugar yield and cane yield.

**Keywords: Sugarcane clones, heritability, PCV, GCV, G.A as % of mean.**

## INTRODUCTION

Sugarcane (*Saccharum officinarum* L.) is

cultivated extensively as an important and major cash crop all over the world (Tiawari et al. 2011). It holds the position of second major cash crop in Pakistan and provides raw material for the manufacturing of a number of products (Khan et al. 2010). According to plant breeding view point, the extent of genetic variation existing in the genetic material of sugarcane is significant to initiate any effective selection program.

In plant breeding, selection procedure maintains the best genotypes and eliminates the undesirable ones, is an important strategy for the improvement of one or more plant attributes. Selection as random for quantitative attributes alters genotypic and gene frequencies and these alterations could be exploited to proceed the selected genotypes to the advance generations (Chopra, 2000; Idahosa et al. 2010). Any criterion to best exploit the selection process should be linked with high estimates of GCV and $h^2$, as $h^2$ magnitude and other genetic parameters for a trait would change from season to season and location to location (Ramachandran et al. 1982).

Due to high heterozygous nature coupled with high polyploidy level, breeding in sugarcane crop is extremely a complex and technical process. This heterozygosity and polyploidy nature, made this crop a very genetically diverse. For the genetic improvement in any plant attribute PCV, GCV along with $h^2$ and G.A are very useful tools because these parameters reflect a true picture to breeders whether or not the desired objectives can be accomplished from the material (Tyagi and Singh, 1998). In sugarcane breeding, for the expression of a specific attribute, heritability is important to provide information's of the magnitude of genetic control (Chopra, 2000). Heritability of a trait also provides guide lines to the breeders regarding the reliability of phenotypic variations in the selection program which reflects the success of any breeding program (Hamdi, 1992). However, to predict the resulting effect of selecting the desirable individuals, $h^2$ estimates coupled with G.A are more significant than $h^2$ alone (Johnson et al. 1955).

The purpose of the current research investigations are to assess the variability based on heritability, genetic advance as % of mean, GCV and PCV of sugar yield and cane yield and their associated component attributes in sugarcane's genotypes to furnish essential information that may be exploited in sugarcane breeding programs.

## MATERIALS AND METHODS

### Sugarcane Genotypes

Sixteen sugarcane genotypes were used as planting material in the present studies. These genotypes were introduced from international sugarcane breeding centers. The detail of genotypes and their origin has been illustrated in Table-1.

### Experimental site, statistical designand analysis

This trial was undertaken at SCRI, Mardan-Pakistan during the cropping season of spring 2016-17 and 2017-18. The clones were planted in Randomized Complete Block Design (RCBD) replicated four times. Three budded cuttings from each matured cane genotype were used as sowing material. Individual genotype cuttings were allotted to a block of seven rows. One hundred and fifty (150) buds were assigned to the middle row. Recommended standard dose of NPK (150 kg/ ha), (100kg/ ha) and (100 kg/ ha), respectively was applied at sowing time. Additional dose of nitrogen fertilizers were applied @ 125 kg/ha during earthing up operation.

### Data recording

Five randomly selected cane genotypes were tagged for data collection from each middle row of each plot. Nine morphological quantitative attributes were considered for data collection i.e., leaf area, germination percentage, number of tillers, inter node length, number of nodes per plant, weight of five un-stripped canes, cane yield, weight of five stripped canes and sugar yield.

Two seasonal data were compiled and subjected to statistically analysis through Fisher's developed combined Analysis Of Variance (ANOVA) technique using SAS (Ver. 9.1) statistical software to ascertain variability among the genotypes. Steel and Torrie (1997) procedure was utilized for means comparison test LSD (Least Significant Difference) of genotypes. According to Farshadfar et al. (2013) estimates, PCV, GCV, $h^2$ (b.s) and genetic advance (G.A) were computed from components of variance as follows:

$$V_E = MS_e$$

$$V_G = MS_g - MS_e/r$$

$$V_P = V_G + V_E$$

$$PCV = 100 \sqrt{\sigma_p^2}/\bar{X}$$

GCV = 100 $\sqrt{\sigma_g^2}/\tilde{X}$

ECV = 100 $\sqrt{\sigma_E^2}/\tilde{X}$

$h^2 = \sigma_g^2/\sigma_p^2$

G.A = (k. $h^2 \sqrt{\sigma_p^2}$)

G. A (Percent of trait mean) = (G.A/trait mean) x 100

## RESULTS AND DISCUSSION

### Germination percentage:

The most crucial physiological phase in the life cycle of herbs and shrubs including sugarcane is their germination or sprouting because there will be no plant without germination (Khalid et al. 2014).

In this research work, the analysis of variance combined over two seasons exhibited significant (p≤0.05) variability for germination among all genotypes (Table-2). Chaudhary, 2001; Khalid et al. 2014; Sangera et al. (2015) and Khalid et al. (2016) also quoted uniform results. The mean results showed that germination ranged from 23.33 to 57.67%. The highest plant germination (57.67%) was recorded for genotype MS.92CP.979 while the lowest (23.33%) was exhibited by the genotype S.96SP.1215 as shown in Figure 1.

### Number of tillers

The number of tiller is very important attribute that directly proportional to cane yield. The analysis of variance combined over both seasons exhibited significant (p≤0.01) variability for number of tillers among all clonal genotypes (Table-2). Similar results were also quoted by Sanghera et al. (2015) who conducted trial to detect diversity among 13 sugarcane clones. The C x G interaction results also revealed significant (p≤0.05) differences for tillers suggesting that both season crops performed differently for this trait. Number of tillers ranged from 140 to 355.50. The maximum numbers of tillers (355.50) were recorded for genotype MS.91CP.238 while the minimum (140) were displayed by Hoth.127 as shown in Figure 2.

### Cane Leaf area (cm²)

The ANOVA results combined over both seasons exhibited significant (p≤0.05) variability for leaf area among all genotypes (Table-2). Tena et al. (2016) also quote uniform findings in their trail conducted on sugarcane genotypes in Ethiopia to find out correlation and path coefficient analysis. The CxG interactions were also

significantly different for leaf area which suggested that both crops performance was different regarding this attribute. The mean results showed that leaf area ranged from 286.84 to 435.96 cm². The highest leaf area (435.96 cm²) was recorded for genotype MS.91CP.238 while the lowest (286.84cm) was displayed by genotype MS.99HO.93 as shown in Figure. 3.

### Number of nodes plant[-1]

Mean square analysis combined over two seasons exhibited significant (p≤0.05) variability for this attribute among all genotypes (Table-2). In support to our findings Jamoza et al. (2014) undertook studies on estimation of heritability (b.s) and correlation in Western Kenya and reported significant results for the same attribute. The CxG interactions were also significantly different for this parameter. The maximum numbers of nodes (23.72) were displayed by Hoth.127 while the lowest (17.16) were recorded for the genotype MS.99HO.675 (Fig- 4).

### Internode length

Combined mean square results exhibited significantly high (p≤0.01) variations for inter node length among the clones (Table-2). These findings are in close agreement to the results got by Tiawari et al. (2011) in their research work "GxE interactions and stability analysis in sugarcane". The interaction results of CxG were also significantly different for this parameter which suggested that both crops performed differently. The mean results showed that number of inter node length ranged from 12.53 cm to 18.33 cm. The highest inter node length (18.83cm) was recorded for genotype MS.94CP.15 while the lowest (12.53cm) was displayed by Hoth.127 (Fig-5).
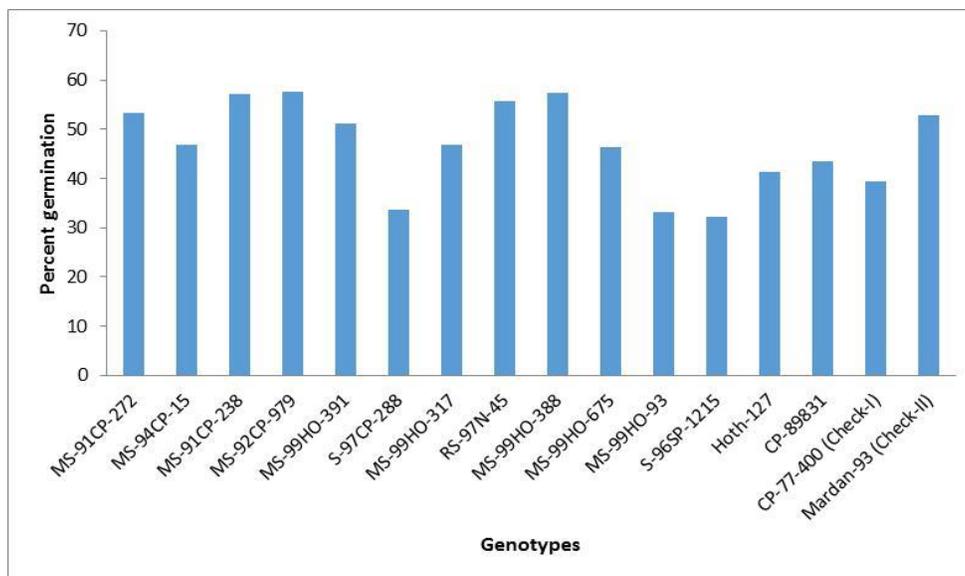
### Weight of five un-stripped canes (WFUSC)

Combined mean square results displayed significantly high (p≤0.01) variations for this attributes among all clones (Table-2). In support, Khalid et al. (2016) displayed uniform results in a trial conducted on sugarcane's qualitative and quantitative attributes under field conditions. The CxG interactions were also significantly different which indicated that both crops performance was different. The mean results showed that weight of five unstrapped canes ranged from 6.40 kg to 8.87 kg. The highest weight of five unstrapped canes (8.87kg) was shown by clone MS.99HO.317 while the minimum (6.40kg) was displayed by clone MS.91CP.272 (Fig-6).

**Table-1: Sixteen sugarcane clonal genotypes and their source information used for estimation of genetic components for cane yield and associated**

| S. No | Genotypes | Source |
|-------|-----------|--------|
| 1 | MS.91CP.272 | Uni. Stat.Deptt.of Agri. -Agri. Res. Serv. Stations, Canal Point, FL,USA |
| 2 | MS.94CP.15 | Uni. Stat. Deptt. of Agri. -Agri. Res. Serv. Stations, Canal Point, FL,USA |
| 3 | MS.91CP.238 | Uni. Stat. Deptt. of Agri. -Agri. Res. Serv. Stations, Canal Point, FL,USA |
| 4 | MS.92CP.979 | Uni. Stat. Deptt. of Agri. -Agri. Res. Serv. Stations, Canal Point, FL,USA |
| 5 | MS.99HO.391 | Uni. Stat. Deptt. of Agri. -Agri. Res. Serv. Stations, Houma, Louisiana, USA |
| 6 | S.97CP.288 | Uni. Stat. Deptt. of Agri. -Agri. Res. Serv. Stations, Canal Point, FL,USA |
| 7 | MS.99HO.317 | USDA-ARS stations, Houma, Louisiana, USA |
| 8 | RS.97N.45 | S. African Res. Instt.Natal (S. Africa) |
| 9 | MS.99HO.388 | Uni. Stat. Deptt. of Agri. -Agri. Res. Serv. Stations, Houma, Louisiana, USA |
| 10 | MS.99HO.675 | Uni. Stat. Deptt. of Agri. -Agri. Res. Serv. Stations, Houma, Louisiana, USA |
| 11 | MS.99HO.93 | Uni. Stat. Deptt. of Agri. -Agri. Res. Serv. Stations, Houma, Louisiana, USA |
| 12 | S.96SP.1215 | Brazil (São Paulo) |
| 13 | Hoth.127 | Uni. Stat. Deptt. of Agri. -Agri. Res. Serv. Stations,Houma, Louisiana, USA and Sugarcane Res. Instt. Thatta-Pakistan |
| 14 | CP.89831 | Uni. Stat. Dettp. of Agri. -Agri. Res. Serv. Stations, Canal Point, FL,USA |
| 15 | CP.77.400 (Ch-I) | Uni. Stat. Deptt. of Agri. -Agri. Res. Serv. Stations, Canal Point, FL,USA |
| 16 | Mardan.93 (Ch-II) | Uni. Stat. Deptt. of Agri. -Agri. Res. Serv. Stations, Canal Point, FL,USA |

Hoth: Houma-Thatta, SP: São Paulo, MS: Mardan Selection, N: Natal,Ho: Houma,



**Figure1: Mean comparisons of percent germination of 16 sugarcane genotypes.**

**Table 2 : Mean squares for germination%, Tillering, Leaf area (LA), Number of nodes per plant (NNPC), Inter node length (IL), Weight of five un-stripped canes (WFUSC), Weight of five stripped canes (WFSC), Cane yield (CY) and Sugar yield (SY) for 16 sugarcane genotypes.**

| SOV | D. F | Germination% | Tillering | LA | NNPC | IL | WFUSC | WFSC | CY(t ha$^{-1}$) | SY(t ha$^{-1}$) |
|---|---|---|---|---|---|---|---|---|---|---|
| Crop | 1 | 4638.57 | 1.26 | 1375127.99 | 327.82 | 233.13 | 55.66 | 35.53 | 24500.22 | 215.97 |
| CxR | 4 | 878.70 | 2024.76 | 6198.52 | 7.05 | 2.18 | 1.00 | 0.95 | 229.16 | 0.89 |
| G | 15 | 472.44** | 16960.98** | 12371.55** | 19.86** | 15.39** | 3.45** | 3.18** | 281.71** | 3.54* |
| CxG | 15 | 255.54$^{Ns}$ | 3410.55* | 9560.40** | 16.29** | 6.81* | 3.16** | 2.10** | 265.16** | 3.78* |
| Error | 60 | 149.33 | 1772.41 | 2919.24 | 5.34 | 3.42 | 1.02 | 0.61 | 95.84 | 1.64 |
| R$^2$ | | 0.68 | 0.75 | 0.91 | 0.74 | 0.74 | 0.72 | 0.76 | 0.85 | 0.77 |
| C.V | | 26.12 | 18.59 | 14.94 | 11.76 | 11.88 | 13.57 | 13.49 | 14.24 | 17.07 |

*Significant at 5% level of probability, ** Significant at 1% level of probability
Ns= Non-significant, D.F: Degrees of freedom, C.V= Coefficient of variation

**Table 3: Genetic components estimated for morphological attributes of 16 sugarcane genotypes.**

| Traits | MSG | Vg | Vp | Trait ave. | GVC | PVC | EVC | $h^2$ (%) | Genetic Advance | GAM |
|---|---|---|---|---|---|---|---|---|---|---|
| Germination% | 472.44 | 107.70 | 157.48 | 46.80 | 22.18 | 26.81 | 26.11 | 68.39 | 13.34 | 80.72 |
| Tillering | 16960.98 | 5062.86 | 5653.66 | 226.43 | 31.42 | 33.21 | 18.59 | 89.55 | 104.64 | 27.05 |
| LA | 12371.55 | 3150.77 | 4123.85 | 165.23 | 33.97 | 38.87 | 32.70 | 76.40 | 76.25 | 37.02 |
| NNPC | 19.86 | 4.84 | 6.62 | 361.76 | 0.61 | 0.71 | 0.64 | 73.11 | 2.92 | 0.30 |
| IL | 15.39 | 3.99 | 5.13 | 19.60 | 10.19 | 11.56 | 9.44 | 77.78 | 2.74 | 94.46 |
| WFUSC | 3.45 | 0.81 | 1.15 | 15.59 | 5.77 | 6.88 | 6.48 | 70.43 | 1.17 | 64.02 |
| WFSC | 3.18 | 0.86 | 1.06 | 7.42 | 12.47 | 13.88 | 10.53 | 80.82 | 1.29 | 311.33 |
| C.Y(t ha$^{-1}$) | 281.71 | 61.96 | 93.90 | 68.71 | 11.46 | 14.10 | 14.25 | 65.98 | 9.94 | 27.90 |
| S.Y(t ha$^{-1}$) | 3.54 | 0.63 | 1.18 | 5.81 | 13.70 | 18.70 | 22.04 | 53.67 | 0.91 | 355.80 |
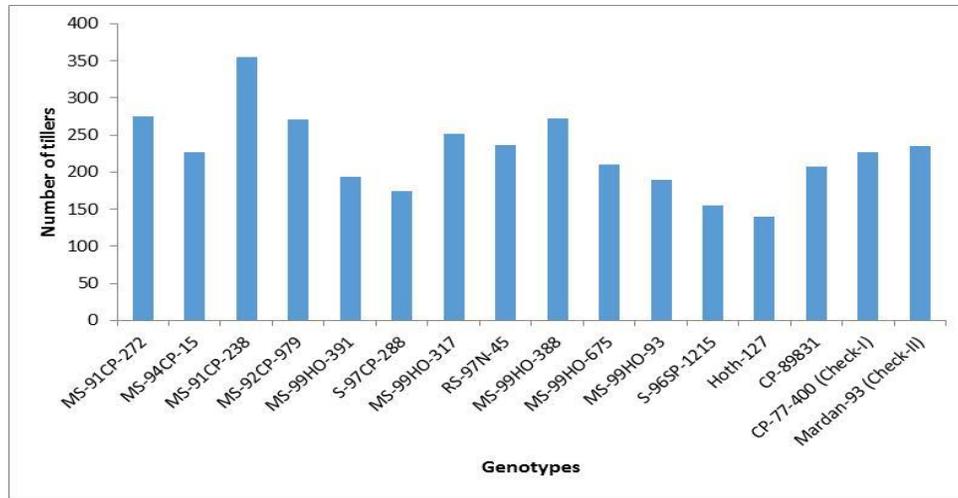
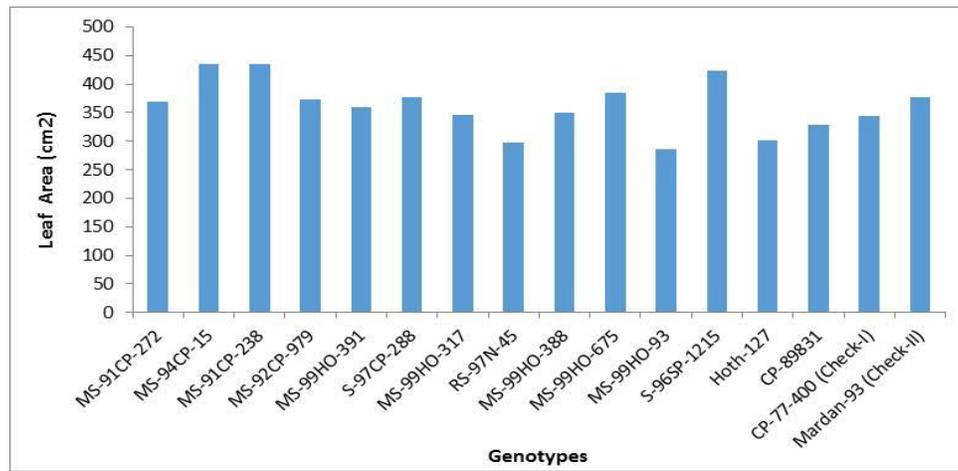**Figure 2: Mean comparisons of number of tillers of 16 sugarcane genotypes.**



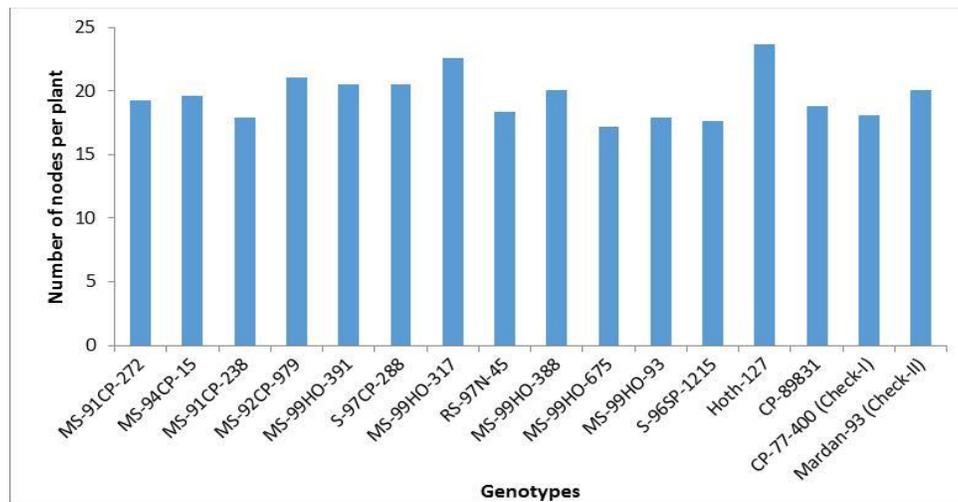**Figure 3: Mean comparisons of leaf area (cm$^2$) of 16 sugarcane genotypes.**



**Figure 4. Mean comparisons of no. of nodes per plant of 16 sugarcane genotypes.**
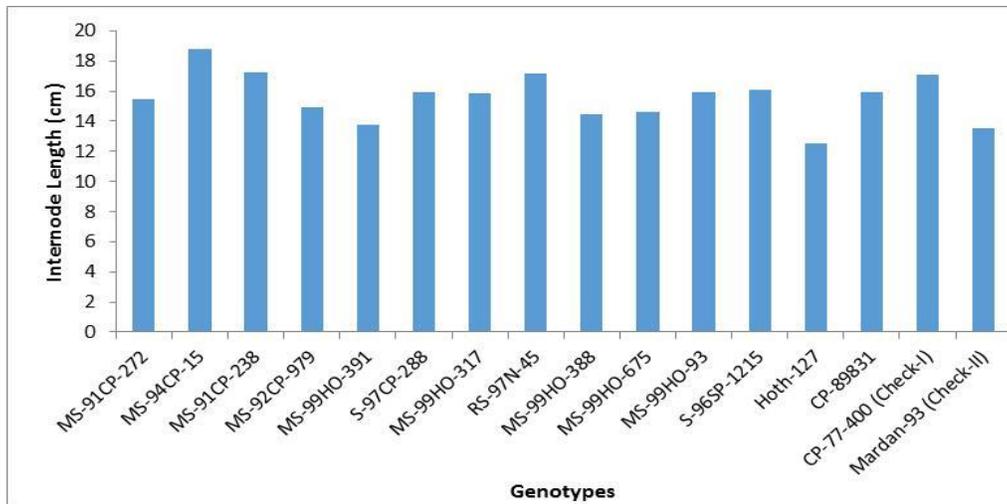
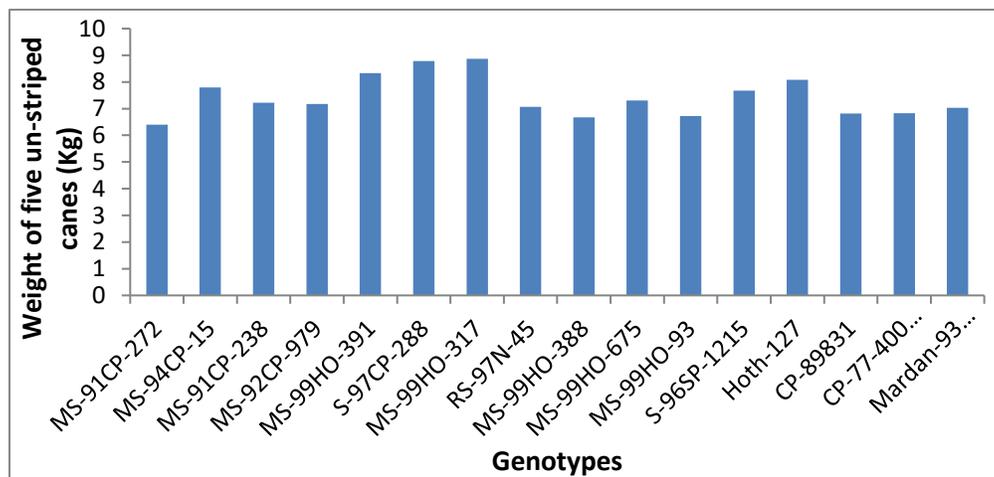**Figure 5: Mean comparisons of internodes length (cm) of 16 sugarcane genotypes.**



**Figure 6: Mean comparisons of weight of five un-stripped canes (Kg) of 16 sugarcane genotypes.**
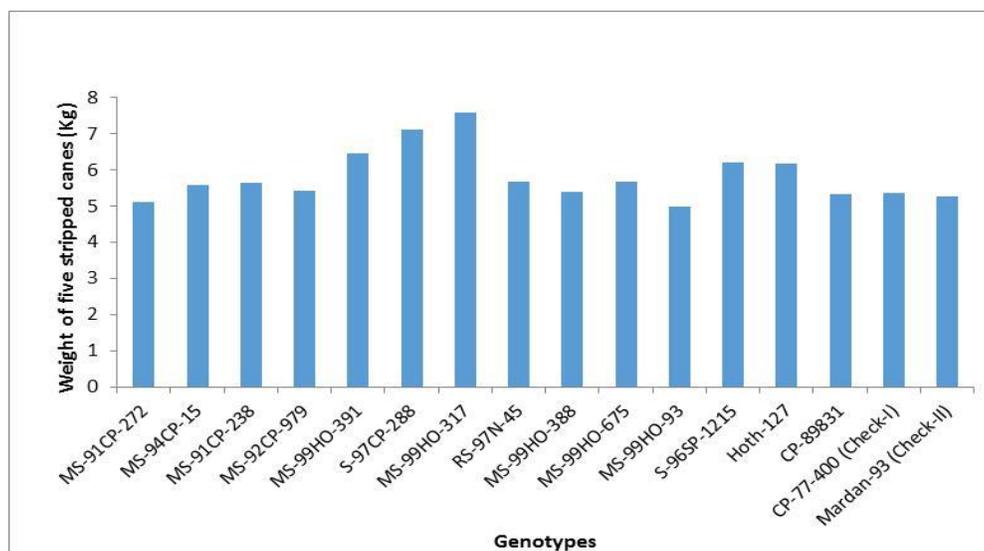


**Figure 7: Mean comparisons of weight of five stripped canes (Kg) of 16 sugarcane genotypes.**
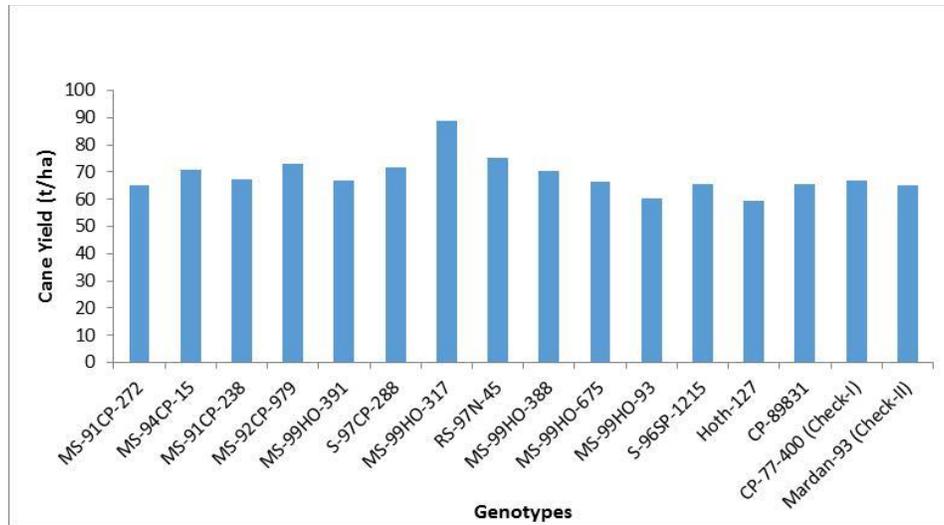
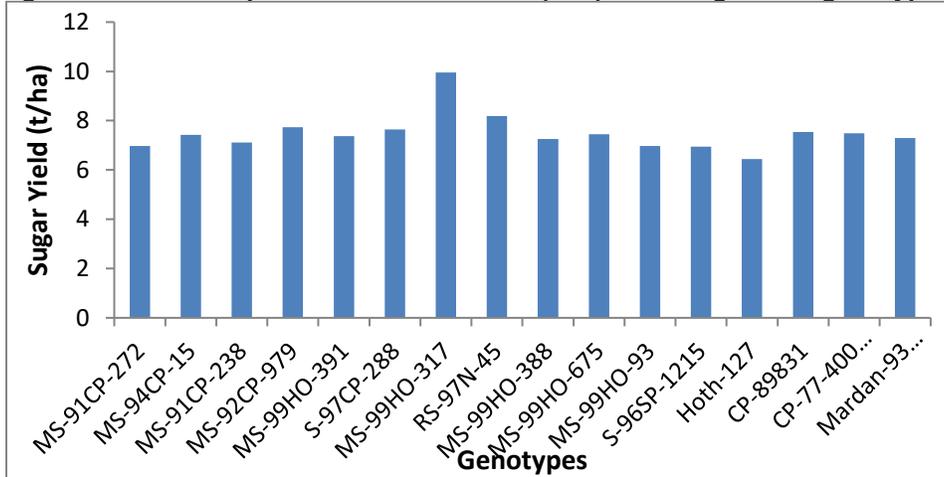**Figure 8: Mean comparisons of Cane Yield (t/ha) of 16 sugarcane genotypes.**



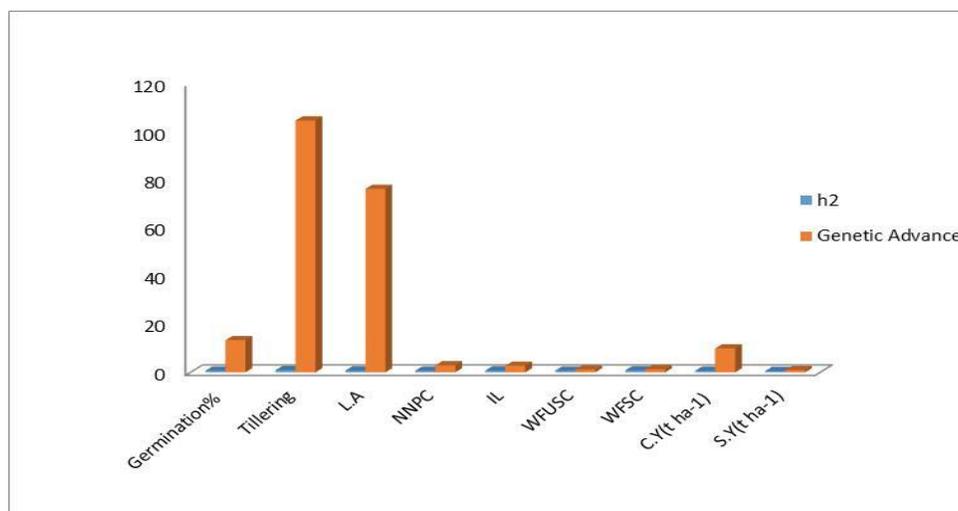**Figure 9: Mean comparisons of Sugar Yield (t/ha) of 16 sugarcane genotypes.**



**Figure 10: Heritability and genetic advance of 16 sugarcane genotype**

### Weight of five stripped canes (WFSC)

Mean square results revealed highly significant (p≤0.01) variations for this attribute among all clonal genotypes (Table-2). Again, our results are supported by the findings of Khalid et al. (2016). They evaluated sugarcane clones for qualitative and quantitative attributes under field conditions and got highly significant results for the same attribute. The interactions of C x G were also significantly different which suggested that both crops performance was different. The mean results showed that weight of five stripped canes ranged from 4.98 kg to 7.60 kg. The highest weight of five stripped canes (7.60kg) was displayed by clone MS.99HO.317 while the lowest (4.98kg) by clone MS.99HO.93 (Fig-7).

### Cane Yield

The means square results displayed significantly high (p≤0.01) variations for cane yield among all clones (Table 2). These results are in line to the results of Khalid et al. (2016) and Sanghera et al. (2015) who studied variations in sugarcane clones and got uniform results. The results of CxG interactions were also significantly different which indicated that both crops performance was different. The mean results exhibited that cane yield ranged from 59.20 kg to 88.98 kg. The maximum cane yield (88.98kg) was exhibited by clone MS.99HO.317 while the minimum (59.20kg) by clone Hoth.127 (Fig-8).

### Sugar Yield

The means square table displayed significant (p≤0.05) variations for sugar yield among the clones (Table-2). Khalid et al. (2016) got uniform results for the same attribute that studied variations in sugarcane clones and got uniform results. The interaction results of CxG were also significantly different which suggested that both crops performance was different. The mean results exhibited that sugar yield ranged from 6.44 kg to 9.96 kg. The highest sugar yield (9.96kg) was exhibited by clone MS.99HO.317 while the lowest (6.44 kg) by clone Hoth.127 (Fig-9).

### Estimation of Genotypic and Phenotypic Coefficient of Variation (GCV and PCV), Heritability (h2) and Genetic advance as % of mean.

In a random population of plants another measure of relative genetic variation of a trait is GCV (Ram and Hemaprabha, 1992). After partitioning phenotypic variance, it was observed that estimates for GCV was lower than PCV for all attributes which suggested that the ostensible variation was the combine effect of genetics and environment. In support to present studies, Alemu and Tadesse (2016) reported similar results while conducted studies on 11 newly introduced sugarcane genotypes. Singh and Singh (1999) also reported maximum PCV value than GCV for stalk diameter, cane yield and single cane weight. Chaudhary (2001); Tena). 2016); Ebid et al. (2015) also reported high magnitude of phenotypic variance than genotypic one for germination, number of tillers, leaf area, number of nodes plant$^{-1}$, cane diameter, sugar yield, inter node length and cane yield. These findings suggested that the effects of environment had a considerable role in the traits inheritance. Shivasubramanian and Menon (1973) and Deshmukh et al. (1986) reported that the GCV and PCV values are ranked as low (0 to 10%), medium (10 to 20%) and high (>20%).

In present research work, maximum GCV and PCV values were recorded for germination% (22.18, 26.81) number of tillers (31.42, 33.21), leaf area (33.97, 38.87), respectively. Tena et al. (2016) conducted studies on 400 sugarcane accessions and reported high GCV for germination, no. of tillers and leaf area while high PCV for germination, no. of tillers and moderate for leaf area. Bora et al. (2014) also observed high GCV for germination while moderate for number of tillers. Hiremath and Nagaraja (2016) reported higher magnitude of PCV and GCV for tillers in an experiment conducted on 35 sugarcane clones. Maximum values of PCV and GCV for tillers were also reported by Sanghera et al. (2015). Moderate values of GCV and PCV were observed for inter node length (10.19, 11.56), wt. of five stripped canes (12.47, 13.88), cane yield (11.46, 14.10) and sugar yield (13.70, 18.70), respectively. In support to this study, Chaudhary et al. (2001); Sanghera et al. (2015) and Alemu and Tedsse (2016) also reported moderate GCV and PCV values for sugar yield and cane yield. Moderate PCV and GCV for inter node length were also observed by Hiremath and Nagaraja (2016). Low magnitude of GCV and PCV were calculated for no. of nodes plant$^{-1}$(0.61, 0.71) and weight of five un-stripped canes (5.77, 6.88). Tadesse et al. (2014) and Jamoza et al. (2013) also observed low magnitude of PCV and GCV for number of nodes plant$^{-1}$.

The components of variance were used to work out heritability ($h^2$) estimates as shown in Table-3. Information regarding variation and $h^2$ of

a plant attribute is important for recognizing those genotypes which are acquiescent to genetic improvement through process of selection (Vidya et al. 2002). Singh (2001) reported that $h^2$ magnitudes higher than 80% were categorized as very high, magnitudes falls from 60–79% were categorized as moderately high, magnitudes from 40–59% were categorized as medium and magnitudes of $h^2$ minimum than 40% were categorized as low. Robinson et al. (1949) also stated that magnitudes of $h^2$ (60% and above) categorized as high, (30-60%) were categorized as moderate and (0-30%) were as low.

In this research investigation, high $h^2$ magnitude was observed for no. of tillers (89.55%) and weight of five unstrapped canes (80.82%). The results suggested that a greater extent of the total variability is heritable and a simple selection process would be effective for the advancement of these attributes (Nair et al. (1980) and Singh et al. (1994)). Viradiya and Patel (2013) also reported moderately high $h^2$ for germination, cane yield and no. of nodes cane[-1] in a study conducted on 39 sugarcane genotypes to find out genetic variability, correlation coefficient, path analysis and D$_2$ analysis. Moderately high heritability was recorded for germination (68.39%), leaf area (76.40%), inter node length (77.78%), number of nodes cane[-1] (73.11%), weight of five unstrapped canes (70.43%) and cane yield (65.98%). This suggested that a greater extent of the total variability is heritable and a simple selection process would be effective for the advancement of these attributes. Bora et al. (2014) also observed high $h^2$ for number of tillers and single cane weight. Chaudhary et al. (2001); Tadesse et al. (2014) and Ebid et al. (2015) also reported moderately high $h^2$ for cane yield. Ahmed and Obeid (2012) conducted research on twelve exotic sugarcane clones to investigate the variability, broad sensed heritability and genetic advance and reported moderately high heritability for sugar yield and cane yield. Hiremath and Nagaraja (2016) also reported moderately high $h^2$ (b.s) for inter node length and number of nodes cane[-1]. Tina et al. (2016) also observed medium broad sense heritability estimates for tiller count 4 months after sowing, number of internodes and leaf area.

Medium $h^2$ (b.s) was recorded for sugar yield (53.67%). In contrary, Tadeese et al. (2014) reported high $h^2$ for sugar yield. It might be due to the fact that heritability of an attribute varies in a specific population under a specific environment or conditions. Tadeese and Dilnesaw (2014)

reported high heritability for cane yield and moderate heritability for inter node length and sugar yield. The results extracted from this study illustrated that utilization of attributes with high $h^2$ as criteria for selection associated with sugar yield and cane yield could lead to the genetic improvement in these attributes. In sugarcane crop under the present research circumstances attributes such as number of tillers, no. of nodes cane[-1], germination%, weight of five unstrapped canes, leaf area, sugar yield, inter node length, weight of five stripped canes and cane yield were some of the reliable selection parameters.

**Genetic advance and genetic gain**

Any effective selection program depends on heritability associated with genetic advance (Butterfield et al. 2002). Johnson et al. (1955) reported that estimates of heritability ($h^2$) associated with genetic advance are more crucial than heritability alone to select the desire population. Johnson et al. (1955) stated that genetic advance as percent of mean (GAM) was categorized as low (0-10), moderate (10-20) and high (>20%).

In present investigation, high G.A as % of mean of a trait was registered for sugar yield (355.80%) and weight of five stripped canes (311.33%), followed by inter node length (94.46%), germination (80.72%), weight of five unstrapped canes (64.02), leaf area (37.02), cane yield (27.90) and number of tillers (27.05). These results indicated the scope of improvement of sugar yield and cane yield to an appreciable level through adoption of an appropriate breeding procedure. Low genetic advance coupled with high broad sense $h^2$ was observed for number of nodes cane[-1] that displayed the existence of non-additive gene action and a little scope in the improvement of this trait as shown in Table-2. In support to these results, Chaudhary et al. (2001) also observed high G.A as % of mean for cane yield and single stalk weight. Bakshi (2005) stated that high genetic advance of an attribute was the effect of high broad sense $h^2$ and high GCV. Similarly, high $h^2$ associated with high G.A was detected by Hiremath and Nagaraja (2016) for single cane weight, number of tillers, number of nodes plant[-1] and cane yield. These findings suggested that these attributes are under the control of additive genetic effects and display the expediency of the selection process based on appearance of an attribute (Gravois and Milligan, 1992). Tina et al. (2016) also observed high $h^2$ coupled with high genetic advance for cane

yield, leaf area and sugar yield. Bora et al. (2014) also quoted uniform findings for germination%, cane yield, number of tillers and single cane weight. Jamoza et al. (2014) got moderate genetic advance for no. of nodes cane$^{-1}$ in a study conducted on 13 sugarcane genotypes to determine correlation and $h^2$ (b.s) estimates for yield and agronomic attributes among sugarcane (*Saccharum* spp. hybrids). Similarly, opposite results were also observed by Hiremath and Nagaraja (2016). The possible reason for this contradiction could be the use of more diverse genotypes in their studies. The same trends of attributes for heritability and genetic advance have graphically shown in Fig-10.

## CONCLUSION

The results of this research investigation manifested that yield in sugarcane is associated in various magnitudes to its components phenotypically and genetically. All the genotypes are significantly different from each other based on germination, number of tillers, leaf area, number of nodes canes$^{-1}$, weight of five unstrapped canes, cane yield, inter node length, weight of five stripped canes, and sugar yield. The interaction results of genotypes and crop seasons also showed significant differences for all traits except germination%. Mean results revealed maximum sugar yield (9.96 t/ha) and cane yield (88.98 t/ha) for genotype MS.99HO.317 followed 75.13 t/ha and 8.90 t/ha for cane yield and sugar yield, respectively for genotype RS.97N.45. Both genotypes showed superior performance than the two check cultivars and can be released to the end users. The rest of the genotypes also performed well and can be used in future breeding programs for some more years to get more authentic results regarding their performance. The results also revealed highest GCV and PCV for germination%, no. of tillers and leaf area, moderate were recorded for weight of five stripped canes, internode length, sugar yield and cane yield and low was recorded for no. of nodes canes$^{-1}$ and weight of five unstrapped canes. Similarly, highest $h^2$ was recorded for no. of tillers and wt. of five stripped canes. High heritability was recorded for germination, No. of nodes cane$^{-1}$, leaf area, weight of five unstrapped canes, internode length, and cane yield. Moderate heritability was recorded for sugar yield only. High $h^2$ and high genetic advance as percent of mean was recorded for no. of tillers, weight of five un-stripped canes, weight of five stripped canes and leaf area, which showed the presence of more

additive gene action and a simple selection process based on these attributes might lead to the improvement in sugar yield and cane yield.

## CONFLICT OF INTEREST

The authors declared that present study was performed in absence of any conflict of interest.

## AUTHOR CONTRIBUTIONS

MK designed, performed and analyzed the experiment. IUK, RK, N, RMK, BA and MAQ helped with data analysis. AB and SAAS supervised the research process and provided critical feedback. RA wrote the manuscript. FS and TI reviewed the manuscript. Finally, every author read and approved the final version.

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