**Original Research Article**

**Study of genetic variability for cane yield and its component characters in midlate clones of sugarcane (*Saccharum spp*.)**

**Abstract**

Seventeen sugarcane clones were evaluated in randomized block design with three replications at ARS, Perumallapalle, Tirupati, Andhra Pradesh to study the variability for cane yield and its component traits. The analysis included key agronomic and quality traits such as germination rate at 30 DAP, tillers at 120 DAP, shoot count at 240 DAP, number of millable canes, number of nodes per cane, cane length, cane diameter, single cane weight, fibre percentage, top leaf weight, juice extraction percentage, brix, sucrose, purity, commercial cane sugar (CCS), reducing sugars, and cane yield at harvest. The analysis of variance (ANOVA) revealed significant differences for mean sum of squares for all the characters**.** The PCV is greater than GCV for most of the traits under study. The characters tillers at 120 DAP, number of nodes per cane, cane length, single cane weight, top leaf weight, juice extraction %, CCS yield, cane yield showed high heritability coupled with high GAM indicating presence of additive gene action and selection would be effective for these traits. Hence, these traits can be utilized for further selection and genetic improvement of midlate clones.

**Keywords:** Genetic advance, heritability, genetic variability and midlate clones of sugarcane.

**Introduction**

Sugarcane (*Saccharum spp*. hybrids) is major commercial crop grown in India after cotton. Sugarcane originated from the New Guinea. It belongs to the family Poaceae, subfamily Panicoideae, tribe Andropogoneae, sub-tribe Saccharineae, and genus *Saccharum*. Sugarcane varieties in commercial cultivation are complex polyploids and their chromosome number varies from 2n=80-120. Cultivated sugarcane had developed through the inter-specific hybridization between three species *Saccharum officinarum* (noble cane) and the wild species, *S. spontaneum* (native to subtropical to tropical Africa, Asia, and Australasia)and *S. robustum* (native only to the island of New Guinea) resistant to biotic and abiotic stresses. Backcrosses were made between the inter-specific hybrids and *S. officinarum* cultivars to disrupt linkage drag of undesirable genes from *S. spontaneum* and to keep the desirable genes conferring high sucrose producing ability of *S. officinarum.* It is an important cash crop accounting for 62% of world sugar production. India has become the world’s largest producer and consumer of sugar and the 2nd largest exporter after Brazil. It is cultivated in an area of 5.47 Million hectares with 457.8 Million tonnes production and 84 tonnes per hectare productivity. Overall, 21% of India’s agricultural land is dedicated to sugarcane production. In Andhra Pradesh, sugarcane is cultivated on 0.047 million hectares with a productivity of 77.66 tonnes per hectare (Directorate of Economics and Statistics, MOA 2022-23)[5].

Variety is the “chip” of sugarcane industry. According to the International Society of Sugarcane Technologists (ISSCT), the contribution of improved variety is as high as 60% (Chen *et al*., 2011) [4]. **Sugarcane productivity is mostly dependent on the cultivars from various maturity groups, prevailing agro-climatic conditions of the region and other cultural practices**. Information of variability and heritability are important to the breeder for effective selection among the clones. Appropriate selection strategies help in genetic improvement of sugarcane. Therefore, the present investigation is aimed at assessing the variability among mid-late sugarcane clones for various traits.

**Material and Methods**

The material of the present investigation comprised of seventeen midlate clones. All these clones were planted in a Randomized Block Design with three replications during 2023-24 at ARS, Perumallapalle, Tirupati, Andhra Pradesh following all the packages of practices to raise good sugarcane crop in order to study the genetic parameters. Four three-budded sets were planted per metre row length with an inter row spacing of 90 cm. Observations were recorded by selecting five canes of each clone from each replication for component traits of cane yield and quality parameters viz., germination per cent at 30 DAP, tillers at 120 DAP ('000 ha-1), shoots count at 240 DAP ('000 ha-1), number of millable canes ('000 ha-1), cane yield (t ha-1). Some of the observations were recorded on ten randomly selected canes per genotype in each replication for characters *viz*., single cane weight (kg), cane length (cm), cane diameter (cm), number of nodes per cane, top leaf weight (kg), fibre %, juice extraction %, brix %, sucrose %, purity %, CCS %, and reducing sugars and CCS yield (t ha-1 ) at harvest.

The genetic parameters i.e. phenotypic coefficient of variance (PCV) and genotypic coefficient of variance (GCV), heritability (h2) in broad sense and genetic advance as percent of mean were calculated as suggested by Burton and Devane (1952) [3] and Johnson *et al*. (1955) [8]. The data analysis was carried out with INDOSTAT software.

**Results and Discussions**

Out of seventeen clones studied, 2014 A 224 recorded superior performance for six important yield components *i.e.* percentage og germinationat 30 DAP, number of nodes per cane, single cane weight, top leaf weight, percentage of brix, and percentage of sucrose content. The next promising clone identified is 2013 T 39 with superior performance for six traits *i.e.* tillers at 120 DAP, shoots at 240 DAP, number of millable canes, cane diameter, brix % and sucrose%. The performance of another clone, 2014 T 39 is also promising for six traits *i.e.* number of nodes per cane, weight of single cane, percentage of fibre, top leaf weight, percentage of brix, and cane yield per hectare. The mean performance of clones for quality and yield characters are presented in Table 3 & 4 respectively. The success of any breeding programme depends on the amount of genetic variability within the population. A broad range of genetic variability aids in selecting desirable genotypes. In genetic studies, traits with a high genotypic coefficient of variation suggest a strong potential for effective selection. Heritability indicates the extent to which a genetic trait can be passed on to successive generations. By combining heritability estimates with genetic advance, the effectiveness of selecting the best individuals can be accurately predicted. As per overview in the Table 1 it clearly indicates the significant differences for all the characters among the clones under study. Hiremath and Nagaraja (2016), Agrawal and Kumar *et al.* (2017) [9]and kumari *et al.* (2020) [11] registered similar findings which supports present results. In the present investigation phenotypic coefficient of variation is higher than genotypic coefficient variation for all the characters which indicates the influence of non-genetic factors on expression of these traits. These results are in accordance with the findings of Negi *et al*. (2017) [13], Patil *et al.* (2023) [15].

Moderate PCV and GCV valuesobserved for tillers at 120 DAP followed by number of millable canes, number of nodes per cane, cane length, juice extraction %, reducing sugars %, CCS yield and cane yield**.** Similar kind of variation were obtained by Kumar*et al.* (2018) [10], Triveni*et al.*(2016) [17] *.* High heritability coupled with low GAM were observed for percentage of fibre and purity.The selection for these traits is not effective because presence of both additive and non-additive gene action genetic improvement for these traits is possible through heterosis breeding. These results are in accordance with the findings of Ahmed*et al.* (2012).[1] High heritability coupled with high GAM were observed for traits i.e. tillers at 120 DAP, single cane weight, cane length, number of nodes per cane, top leaf weight, percentage of fibre and juice extraction, CCS yield and cane yield indicates that the selection for these traits would be effective as gene action is additive. Similar kind of gene action was reported by Gowda *et al.* (2016) [7] and Kumari *et al.* (2020) [11]**.** Hence, direct selection can be done through these characters for selection of clones for higher cane and sugar yield in midlate group in sugarcane.

Table 1 Analysis of Variance for cane yield, yield attributing and quality characters in midlate clones of sugarcane (*Saccharum* spp*.)*

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **S.No.** | **Character** | **Mean Sum of Squares** | | |
| **Replication (df:2)** | **Treatments (df:16)** | **Error (df:32)** |
| 1 | Germination % at 30 DAP | 6.53 | 24.75 \*\* | 5.49 |
| 2 | Tillers at 120DAP ('000/ha) | 41.21 | 1932.36 \*\* | 71.05 |
| 3 | Shoot Count at 240DAP ('000/ha) | 152.85 | 364.28 \*\* | 56.31 |
| 4 | No.of Millable canes ('000/ha) | 11.5 | 367.6 \*\* | 29.8 |
| 5 | No.of nodes per cane | 25.49 | 75.39 \*\* | 7.93 |
| 6 | Cane Length (cm) | 305.88 | 3812.25 \*\* | 177.24 |
| 7 | Cane Diameter (cm) | 0.004 | 0.11 \*\* | 0.014 |
| 8 | Single Cane Weight (Kg) | 0.13 | 0.26 \*\* | 0.01 |
| 9 | Fibre % | 0.005 | 0.70 \*\* | 0.08 |
| 10 | Top leaf weight (kg) | 0.003 | 0.075 \*\* | 0.004 |
| 11 | Juice Extraction % | 16.60 | 175.44 \*\* | 12.45 |
| 12 | Brix % | 1.33 | 7.56 \*\* | 0.52 |
| 13 | Sucrose % | 0.30 | 2.68\*\* | 0.20 |
| 14 | Purity % | 16.4 | 93.1 \*\* | 15.5 |
| 15 | Reducing Sugars % | 0.09 | 0.17 \*\* | 0.03 |
| 16 | Commercial Cane Sugar % | 0.19 | 1.63\*\* | 0.21 |
| 17 | Commercial Cane Sugar yield (t/ha) | 0.09 | 26.44 \*\* | 2.41 |
| 18 | Cane yield (t/ha) | 28.38 | 1999.74 \*\* | 153.16 |

\*,\*\* Significant at 5% and 1 %, respectively.

Table 2 Mean, range, coefficient of variation, heritability (broad sense), genetic advance and genetic advance as percent of mean for cane yield and quality characters in midlate clones of sugarcane (*Saccharum* spp*.)*

|  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **S.No.** | **Characters** | **Mean** | **Range** | | **Variance** | | **Co- efficient of variation** | | **Heritability** | **Genetic Advance** | **Genetic advance as % of mean** |
| **Min.** | **Max.** | **Genotypic** | **Phenotypic** | **Genotypic (%)** | **Phenotypic (%)** |
| 1 | Germination % at 30 DAP | 60 | 50.93 | 66.93 | 6.42 | 11.92 | 4.21 | 5.74 | 53.87 | 3.83 | 6.37 |
| 2 | Tillers at 120 DAP ('000/ha) | 162.07 | 119.4 | 209.8 | 620.44 | 691.49 | 15.37 | 16.22 | 89.72 | 48.60 | 29.99 |
| 3 | Shoot at 240 DAP ('000/ha) | 119.84 | 101.8 | 151.2 | 102.66 | 158.97 | 8.45 | 10.52 | 64.58 | 16.77 | 14.00 |
| 4 | Number of millable Canes ('000/ha) | 102.8 | 77 | 133.7 | 112.6 | 142.4 | 10.3 | 11.6 | 79.1 | 19.4 | 18.9 |
| 5 | No.of nodes per cane | 34 | 11 | 13 | 22.49 | 30.42 | 13.96 | 16.23 | 73.94 | 8.40 | 24.72 |
| 6 | Cane length (cm) | 271.17 | 216.66 | 353 | 1211.7 | 1388.9 | 12.84 | 13.74 | 87.24 | 66.98 | 24.70 |
| 7 | Cane diameter (cm) | 3.05 | 2.80 | 3.40 | 0.03 | 0.05 | 5.96 | 0.05 | 70.44 | 0.31 | 10.31 |
| 8 | Single cane weight (kg) | 1.48 | 1.04 | 2.09 | 0.07 | 0.12 | 18.34 | 23.15 | 62.78 | 0.44 | 29.92 |
| 9 | Fibre % | 11.89 | 11.64 | 12.91 | 0.20 | 0.29 | 3.83 | 0.29 | 70.95 | 0.79 | 6.65 |
| 10 | Top weight (kg/ha) | 0.41 | 0.13 | 0.74 | 0.023 | 0.027 | 37.53 | 40.56 | 85.61 | 0.29 | 71.53 |
| 11 | Juice Extraction % | 57.12 | 46.17 | 71.91 | 54.33 | 66.78 | 12.9 | 14.30 | 81.36 | 13.70 | 23.97 |
| 12 | Brix % | 18.35 | 16.16 | 21.26 | 2.35 | 2.87 | 8.35 | 9.23 | 81.74 | 2.85 | 15.54 |
| 13 | Sucrose % | 15.85 | 14.37 | 17.19 | 0.82 | 1.02 | 5.73 | 6.39 | 80.53 | 1.68 | 10.6 |
| 14 | Purity % | 86.79 | 79.01 | 91.02 | 25.86 | 41.38 | 5.86 | 7.41 | 62.49 | 8.28 | 9.59 |
| 15 | Reducing sugars % | 1.54 | 1.72 | 2.32 | 0.04 | 0.07 | 11.23 | 13.98 | 64.50 | 0.36 | 18.58 |
| 16 | Commercial cane Sugar % | 10.88 | 9.69 | 12.0 | 0.47 | 0.68 | 6.30 | 7.61 | 69.15 | 1.18 | 10.84 |
| 17 | Commercial cane sugar yield (t/ha) | 16.45 | 9.61 | 20.80 | 8.01 | 10.42 | 17.20 | 19.62 | 76.87 | 5.11 | 31.07 |
| 18 | Cane yield (t/ha) | 146.94 | 97.4 | 176.19 | 615.53 | 768.68 | 16.48 | 18.42 | 80.08 | 45.73 | 30.38 |

**Fig 1 Heritability and Genetic advance as percent of mean for cane yield and its component characters**

**Fig 2 GCV and PCV for cane yield and component characters**

**Table 3 Mean performance for quality characters in midlate clones of sugarcane (*Saccharum spp.)***

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **S.No** | **Clone** | **Juice extrn %** | **Br %** | **Su%** | **Pu %** | **Red.sugars %** | **CCS%** | **CCSY (kg/ha)** |
| 1 | 2013 T 39 | 59.17 | 19.7 | 16.7 | 84.9 | 1.72 | 11.4 | 18.59 |
| 2 | 2013 V 46 | 49.74 | 20.9 | 16.5 | 79.0 | 2.32 | 10.8 | 19.11 |
| 3 | 2013 T 106 | 71.91 | 16.2 | 14.4 | 89.1 | 1.92 | 10.0 | 9.61 |
| 4 | 2014 T 39 | 46.17 | 19.9 | 16.1 | 80.6 | 1.91 | 10.6 | 18.79 |
| 5 | 2014 A 224 | 50.29 | 19.8 | 16.6 | 83.5 | 2.08 | 11.2 | 18.88 |
| 6 | 2018 T 163 | 57.78 | 18.8 | 17.0 | 90.8 | 1.82 | 12.0 | 18.77 |
| 7 | 2018 T194 | 50.71 | 16.7 | 14.6 | 87.3 | 1.75 | 10.0 | 10.94 |
| 8 | 2018 T 235 | 50.70 | 19.7 | 15.9 | 80.8 | 1.82 | 10.6 | 15.27 |
| 9 | 2018 T 321 | 53.71 | 16.8 | 16.5 | 91.0 | 1.92 | 12.0 | 15.27 |
| 10 | 2018 T 359 | 52.96 | 21.3 | 17.2 | 80.8 | 2.09 | 11.4 | 20.80 |
| 11 | 2018 T 364 | 63.44 | 17.1 | 16.3 | 89.0 | 1.76 | 11.7 | 14.91 |
| 12 | 2018 T 414 | 67.97 | 17.2 | 14.4 | 83.9 | 2.19 | 9.7 | 16.42 |
| 13 | 2018 T 439 | 55.92 | 17.2 | 14.4 | 83.6 | 2.15 | 9.7 | 16.25 |
| 14 | 2018 T 541 | 54.73 | 17.5 | 15.6 | 88.8 | 2.50 | 10.8 | 16.74 |
| 15 | 83 V 15 © | 55.43 | 17.5 | 16.4 | 90.5 | 1.76 | 11.7 | 14.40 |
| 16 | CO 86249 © | 58.84 | 18.4 | 15.7 | 85.1 | 1.58 | 10.7 | 19.06 |
| 17 | CO 86032 © | 71.59 | 17.3 | 15.3 | 89.1 | 1.87 | 10.7 | 15.84 |
|  | **Mean** | **57.12** | **18.3** | **15.8** | **86.79** | **1.95** | **10.9** | **16.45** |
|  | **S.E (m)** | **2.03** | **0.4** | **0.2** | **2.27** | **0.09** | **0.2** | **0.89** |
|  | **C.D. 5%** | **5.86** | **1.2** | **0.7** | **6.55s** | **0.27** | **0.7** | **2.58** |
|  | **C.V %** | **6.17** | **3.94** | **2.8** | **4.5** | **8.33** | **4.2** | **9.43** |

|  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **S.No** | **Clone** | **G % at 30 DAP** | **T- 120 DAP**  **('000/ha)** | **S- 240 DAP**  **('000/ha)** | **NMC**  **('000/ha)** | **Nodes** | **C L**  **(cm)** | **CD**  **(cm)** | **SCW**  **(kg)** | **TLW (kg)** | **F %** | **CY**  **(t/ha)** |
| 1 | 2013 T 39 | 62.19 | 199.15 | 145.45 | 131.03 | 36 | 268.3 | 3.06 | 1.25 | 0.24 | 11.7 | 164.90 |
| 2 | 2013 V 46 | 61.88 | 194.52 | 138.87 | 109.01 | 35 | 268.3 | 3.03 | 1.60 | 0.59 | 11.5 | 174.86 |
| 3 | 2013 T 106 | 56.40 | 140.07 | 111.09 | 94.51 | 36 | 256.6 | 2.80 | 1.03 | 0.26 | 11.4 | 97.44 |
| 4 | 2014 T 39 | 6119 | 203.66 | 116.13 | 106.47 | 42 | 291.6 | 2.96 | 1.65 | 0.42 | 12.9 | 176.19 |
| 5 | 2014 A 224 | 64.04 | 165.13 | 126.52 | 105.75 | 41 | 343.3 | 2.96 | 1.61 | 0.35 | 12.4 | 170.32 |
| 6 | 2018 T 163 | 59.11 | 160.19 | 120.35 | 112.85 | 38 | 228.3 | 3.03 | 1.38 | 0.33 | 11.2 | 156.03 |
| 7 | 2018 T 194 | 63.35 | 143.40 | 113.77 | 97.34 | 38 | 216.6 | 3.06 | 1.10 | 0.25 | 12.6 | 107.74 |
| 8 | 2018 T 235 | 56.71 | 151.62 | 118.91 | 99.57 | 28 | 276.6 | 3.30 | 1.44 | 0.47 | 12.3 | 143.30 |
| 9 | 2018 T 321 | 56.79 | 162.32 | 123.13 | 97.85 | 37 | 250.0 | 2.90 | 1.29 | 0.53 | 12.6 | 126.57 |
| 10 | 2018 T 359 | 59.88 | 194.13 | 111.09 | 92.36 | 32 | 280.0 | 3.40 | 1.33 | 0.41 | 11.6 | 120.90 |
| 11 | 2018 T 364 | 64.28 | 144.00 | 115.10 | 101.22 | 25 | 228.3 | 3.40 | 1.27 | 0.51 | 11.3 | 128.58 |
| 12 | 2018 T 414 | 56.94 | 122.92 | 109.03 | 80.44 | 32 | 266.6 | 3.23 | 2.09 | 0.60 | 11.8 | 168.49 |
| 13 | 2018 T 439 | 57.95 | 141.03 | 108.73 | 99.37 | 38 | 271.6 | 3.16 | 1.66 | 0.74 | 11.6 | 165.68 |
| 14 | 2018 T 541 | 56.94 | 142.24 | 104.92 | 94.02 | 32 | 260.0 | 2.76 | 1.64 | 0.50 | 11.9 | 155.08 |
| 15 | 83V15 © | 59.03 | 143.27 | 118.19 | 112.74 | 30 | 261.6 | 2.96 | 1.08 | 0.13 | 12.0 | 122.00 |
| 16 | CO 86249 © | 61.88 | 194.42 | 132.69 | 111.10 | 35 | 288.3 | 2.80 | 1.57 | 0.29 | 11.4 | 175.09 |
| 17 | CO 86032 © | 63.81 | 152.75 | 123.23 | 102.25 | 37 | 353.3 | 3.03 | 1.41 | 0.30 | 11.6 | 144.79 |
|  | **Mean** | **60.0** | **162.7** | **119.84** | **102.8** | **34** | **271.1** | **3.05** | **1.47** | **0.41** | **11.8** | **146.94** |
|  | **S.E (m)** | **1.35** | **4.86** | **4.33** | **3.15** | **1.41** | **7.6** | **0.06** | **0.12** | **0.03** | **0.16** | **6.40** |
|  | **C.D. 5%** | **3.9** | **14.02** | **12.48** | **9.07** | **4.07** | **22.1** | **0.19** | **0.34** | **0.10** | **0.48** | **18.43** |
|  | **C.V %** | **3.89** | **5.2** | **6.26** | **5.30** | **7.01** | **4.9** | **3.86** | **14.11** | **15.38** | **2.45** | **7.54** |

**Table 4 Mean performance for cane yield and yield components in midlate clones of sugarcane (*Saccharum* spp*.)***

**Note: G-%:**Germination % at 30 Days After Planting, **T-120** : Tillers at 120 Days after Planting: **S-240**: Shoots at 240 Days after Planting: **NMC:** Number of millable Canes ;**Nodes :**No.of nodes per cane **SCW:** Single cane weight; **TLW** : Top Leaf weight. **Br%** : Brix %: **Su %** : Sucrose %; **Pu%** :Purity Percentage ; **CCS %** : Commercial cane sugar %; **F %** : Fibre %; **CY**: Cane yield ; **CCSY** : Commercial cane sugar yield: **Red su %** : Reducing sugars %;

**Conclusion**

The results of Analysis of variance (ANOVA) revealed that significant difference for mean sum of squares of all the characters under the study indicates the presence of ample variability among all the clones. High heritability and genetic advance as per cent of mean recorded for traits *viz.,* tillers at 120 DAP, number of nodes per cane, cane length, single cane weight, top leaf weigh, juice extraction %, CCS yield and cane yield indicating the prevalence of additive gene action hence crop improvement could be achieved by simple selection of these traits.

**COMPETING INTERESTS DISCLAIMER:**

Authors have declared that they have no known competing financial interests OR non-financial interests OR personal relationships that could have appeared to influence the work reported in this paper.

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