*Plant Archives* Vol. 26, No. 2, 2026 pp. 2708-2714 e-ISSN:2581-6063 (online), ISSN:0972-5210

Plant Archives

Journal homepage: http://www.plantarchives.org

DOI Url : https://doi.org/10.51470/PLANTARCHIVES.2026.v26.no.2.371

# ASSESSMENT OF GENETIC DIVERGENCE AMONG SUGARCANE (*Saccharum* spp. HYBRID) INTERSPECIFIC HYBRIDS USING MULTIVARIATE ANALYSIS UNDER HIGH RAINFALL CONDITIONS

**K.V. Sushir[1], S.S. Patil[2*], M.G. Pawar[2] and G.R. Sable[2]**

[1]Principal Scientist & Head (Plant Breeding), Vasantdada Sugar Institute, Pune, Maharashtra, India.

[2]Technical Officer, Plant Breeding Section, Vasantdada Sugar Institute, Pune, Maharashtra, India.

*Corresponding author E-mail: sp0316661@gmail.com

(Date of Receiving-07-08-2026; Date of Revision-14-10-2026; Date of Acceptance-19-10-2026)

**ABSTRACT**

Genetic diversity is an important prerequisite for the development of high-yielding and superior quality sugarcane cultivars. The present study was conducted to assess the genetic diversity among 122 Interspecific Hybrid (ISH) sugarcane genotypes under high rainfall conditions at the Sugarcane Breeding Centre, Amboli during 2024–25. The experiment was laid out in a randomized block design with three replications and observations were recorded on ten agronomic and juice quality traits. Mahalanobis' $D^2$ analysis grouped the genotypes into eight distinct clusters, indicating the presence of substantial genetic variability. Cluster II exhibited superior performance for cane yield, sucrose and commercial cane sugar, while Cluster V was the most genetically divergent, suggesting its potential use in hybridization programmes. Sucrose percentage (53.66%) and millable cane height (37.94%) were the major contributors to total genetic divergence. The study identified promising and genetically diverse parental lines that can be effectively utilized in future sugarcane breeding programmes for improving cane yield and sugar quality under high rainfall conditions.

***Key words :*** Sugarcane, Interspecific Hybrids, Genetic Diversity, Mahalanobis' $D^2$ Analysis, Genetic Divergence, Sugarcane Breeding.

## Introduction

Sugarcane (*Saccharum* spp. hybrid) is one of the most important commercial crop cultivated worldwide contributing significantly to sugar production, bioenergy generation and various agro-industrial products. India is the second-largest producer of sugarcane globally and plays a crucial role in the sugar industry, which supports the livelihood of millions of farmers and contributes substantially to the national economy. The increasing demand for sugar, ethanol and renewable energy necessitates the development of high-yielding, early maturing sugarcane varieties with improved quality, adaptability and resistance to biotic and abiotic stresses. The cultivated sugarcane varieties possess a narrow genetic base due to repeated utilization of a limited number of parental clones in breeding programmes. Such genetic uniformity restricts the scope for further genetic improvement and increases vulnerability to emerging pests, diseases and changing climatic conditions. Therefore, broadening the genetic base through the incorporation of diverse germplasm has become a major objective in modern sugarcane breeding (Ming *et al*., 2006 and Lu *et al*., 2024).

Interspecific hybridization has played a pivotal role in the evolution and improvement of modern sugarcane cultivars. The incorporation of genes from wild relatives, particularly (*Saccharum spontaneum*) into noble cane (*Saccharum officinarum*) has contributed to enhanced vigour, ratooning ability, disease resistance, adaptability and stress tolerance. Interspecific hybrids (ISH) represent a valuable reservoir of genetic variability and provide opportunities for the identification of superior genotypes possessing desirable agronomic and quality traits. Effective utilization of these hybrids in breeding programmes requires a comprehensive understanding of the extent and pattern of genetic diversity present among

them. Genetic diversity is a fundamental prerequisite for crop improvement, as it enables breeders to select genetically divergent parents capable of producing superior segregants and transgressive recombinants. Assessment of genetic divergence using multivariate statistical techniques such as Mahalanobis' $D^2$ analysis has been widely employed in plant breeding to classify genotypes into distinct clusters based on multiple traits simultaneously. Such analyses facilitate the identification of genetically diverse parental combinations for hybridization and help in the conservation and efficient utilization of genetic resources (Mahalanobis, 1936; Rao, 1952; Singh and Chaudhary, 1985).

Therefore, the present investigation was undertaken to assess the genetic diversity among interspecific hybrid (ISH) genotypes of sugarcane based on important germination, growth, yield and juice quality traits. The information generated from this study will aid in the identification of genetically diverse and agronomically superior genotypes, thereby contributing to the development of improved sugarcane varieties with enhanced productivity and adaptability.

## Materials and Methods

### Experimental site and Plant material

The present investigation was conducted at the Sugarcane Breeding Centre (SBC), Amboli, operated by the Vasantdada Sugar Institute (VSI), Pune, Maharashtra, India during the 2024-2025 crop season. Geographically, the centre is situated at approximately 14° N latitude and 73° E longitude, with an elevation of about 690 m above mean sea level. The centre is located in Sindhudurg district of Maharashtra in the Western Ghats region, a recognized hotspot for sugarcane flowering and hybridization activities. SBC Amboli was established to facilitate sugarcane breeding programmes owing to its favorable climatic conditions for flowering, pollen fertility and seed setting. The experimental material comprised 122 sugarcane genotypes of Interspecific Hybrid (ISH) developed under the sugarcane breeding programme.

### Experimental design and Crop establishment

The experiment was laid out in a Randomized Block Design (RBD) with three replications. Each genotype was planted in a single-row plot. The crop was planted during November 2024 using healthy two-eyed sugarcane setts as planting material. A total of 12 two-eyed setts were planted per row for each genotype. Rows were spaced 150 cm apart. Standard agronomic and crop management practices recommended for sugarcane cultivation in the region were followed uniformly throughout the crop growth period to ensure healthy crop establishment and development.

### Data recording

Observations were recorded on germination, growth, yield and juice quality parameters. Germination percentage was recorded at 45 days after planting (DAP). Tiller population was recorded at 120 DAP and expressed as thousand tillers per hectare. Number of millable canes (NMC) was recorded at harvest and expressed as thousand canes per hectare.

Five competitive plants were randomly selected from each plot in each replication for recording observations on growth and yield attributes. Data were recorded on millable cane height (cm), cane diameter (cm) and cane yield (t/ha). For quality analysis, representative cane samples were collected at harvest. Juice was extracted and analyzed for Brix (%), sucrose (%) and Commercial Cane Sugar (CCS %).

### Statistical analysis

The mean values of all recorded observations were subjected to statistical analysis. Analysis of variance (ANOVA) (Fisher *et al*., 1955). Statistical methods and scientific induction. *Journal of the Royal Statistical Society Series B: Statistical Methodology*, **17(1)**, 69-78. was performed to determine the significance of differences among genotypes. Genetic divergence among the 122 genotypes was estimated using Mahalanobis $D^2$ statistics and genotypes were grouped into different clusters following Tocher's method. Intra- and inter-cluster distances were computed to identify genetically diverse parents for future hybridization programmes. Cluster mean analysis was carried out to identify superior clusters for various agronomic and quality traits.

## Results and Discussion

### Clustering of interspecific hybrid (ISH) genotypes

Assessment of genetic divergence among the 122 Interspecific Hybrid (ISH) genotypes of sugarcane was carried out using Mahalanobis' $D^2$ statistics and the genotypes were grouped into eight distinct clusters following Rao's (1952) Tocher's method. The distribution pattern of genotypes among clusters indicated the existence of substantial genetic variability within the experimental material, suggesting the presence of diverse parental sources and broad genetic backgrounds. Such diversity is essential for the effective exploitation of heterosis and for selecting genetically divergent parents in sugarcane hybridization programmes.

The clustering pattern revealed that Cluster I was the largest comprising 32 genotypes, followed by Cluster IV (21 genotypes), Cluster VI (19 genotypes), Cluster

**Table 1 :** Cluster composition.

| Cluster | Number of Genotypes | Genotypes |
|---|---|---|
| I | 32 | ISH 107, ISH 110, ISH 111, ISH 112, ISH 119, ISH 131, ISH 135, ISH 154, ISH 184, ISH 201, ISH 229, ISH 234, ISH 263, ISH 267, ISH 27, ISH 28, ISH 295, ISH 301, ISH 305, ISH 31, ISH 345, ISH 37, ISH 41, ISH 43, ISH 45, ISH 48, ISH 519, ISH 52, ISH 576, ISH 6, ISH 62, ISH 71 |
| II | 6 | ISH 20, ISH 29, ISH 307, ISH 528, ISH 573, ISH 9 |
| III | 17 | ISH 105, ISH 134, ISH 139, ISH 148, ISH 157, ISH 188, ISH 244, ISH 257, ISH 281, ISH 288, ISH 5, ISH 501, ISH 513, ISH 524, ISH 526, ISH 57, ISH 60 |
| IV | 21 | ISH 1, ISH 100, ISH 147, ISH 151, ISH 163, ISH 165, ISH 177, ISH 189, ISH 2, ISH 209, ISH 210, ISH 265, ISH 296, ISH 297, ISH 302, ISH 314, ISH 512, ISH 548, ISH 584, ISH 590, ISH 7 |
| V | 4 | ISH 176, ISH 204, ISH 289, ISH 542 |
| VI | 19 | ISH 123, ISH 133, ISH 144, ISH 150, ISH 152, ISH 164, ISH 174, ISH 181, ISH 191, ISH 192, ISH 193, ISH 203, ISH 255, ISH 268, ISH 271, ISH 516, ISH 558, ISH 567, ISH186 |
| VII | 12 | ISH 11, ISH 115, ISH 129, ISH 137, ISH 18, ISH 218, ISH 269, ISH 535, ISH 545, ISH 554, ISH 61, ISH 63 |
| VIII | 11 | ISH 106, ISH 169, ISH 228, ISH 264, ISH 266, ISH 270, ISH 292, ISH 306, ISH 502, ISH 564, ISH 585 |

III (17 genotypes), Cluster VII (12 genotypes), Cluster VIII (11 genotypes), Cluster II (6 genotypes) and Cluster V (4 genotypes). The unequal distribution of genotypes among clusters indicates that the degree of genetic diversity among the evaluated ISH genotypes was not uniform.

The occurrence of a large number of genotypes in Cluster I suggests that these clones possess relatively similar genetic architecture with respect to the studied morphological, yield and quality traits. Such grouping generally occurs when genotypes have evolved from related parental combinations or possess similar gene complexes governing economically important traits. In contrast, Cluster V consisted of only four genotypes (ISH 176, ISH 204, ISH 289 and ISH 542) making it the smallest cluster. Small clusters generally represent genetically unique or distinct genotypes possessing uncommon combinations of alleles. Such genotypes are highly valuable in breeding programmes because they contribute novel genetic variation and broaden the breeding pool. Similar findings have been reported by Kumar *et al*. (2021), who suggested that solitary or small clusters generally contain elite and genetically divergent genotypes suitable for hybridization. The presence of intermediate-sized clusters such as Cluster III, IV, VI, VII and VIII further indicates that considerable diversity exists within the breeding population. This wide distribution of genotypes across eight clusters confirms that the ISH population possesses an appreciable level of genetic variability for yield and related traits.

Eight clusters were formed among 122 genotypes indicates that the breeding material has a relatively broad genetic base. Such broad genetic diversity is desirable because it increases the probability of obtaining superior recombinants through hybridization. Crossing genetically divergent parents generally enhances heterosis, increases transgressive segregation and improves the chances of recovering superior clones possessing desirable combinations of cane yield, juice quality and stress tolerance.

**Inter and Intra cluster distance**

The intra-cluster distances were consistently much lower than the inter-cluster distances, indicating that genotypes grouped within the same cluster were genetically similar, whereas those belonging to different clusters exhibited greater genetic divergence. This confirms the efficiency of Tocher's clustering method in grouping genetically homogeneous genotypes.

Among the eight clusters, Cluster V recorded the highest intra-cluster distance (10,746.49) followed by Cluster I (5,970.51), Cluster VIII (3,912.15), Cluster VII (3,904.40), Cluster II (3,452.67), Cluster VI (2,833.21), Cluster III (2,793.68) and Cluster IV (2,498.58). The relatively high intra-cluster distance observed in Cluster V indicates that although it contained only four genotypes, these genotypes were considerably diverse from one another. Such variation may have resulted from the accumulation of different favourable alleles inherited from diverse parental combinations. Similar observations have been reported by Singh *et al.* (2020), Mehareb *et al*. and Kumar *et al.* (2021), who reported that cluster size does not necessarily correspond to genetic homogeneity.

**Table 2 :** Average Inter- and Intra-Cluster Distances ($D^2$).

| | Cluster-I | Cluster-II | Cluster-III | Cluster-IV | Cluster-V | Cluster-VI | Cluster-VII | Cluster-VIII |
|---|---|---|---|---|---|---|---|---|
| Cluster-I | 5,970.51 | 43,851.78 | 25,812.63 | 60,943.59 | 612,696.20 | 367,941.68 | 133,703.72 | 235,009.65 |
| Cluster-II | | 3,452.67 | 121,279.76 | 192,931.50 | 957,707.14 | 643,922.04 | 313,128.70 | 461,796.35 |
| Cluster-III | | | 2,793.68 | 11,225.68 | 405,301.91 | 211,458.80 | 48,547.51 | 114,523.51 |
| Cluster-IV | | | | 2,498.58 | 297,508.48 | 135,817.50 | 17,932.29 | 61,992.24 |
| Cluster-V | | | | | 10,746.49 | 37,295.74 | 182,759.49 | 97,163.84 |
| Cluster-VI | | | | | | 2,833.21 | 63,082.93 | 19,245.32 |
| Cluster-VII | | | | | | | 3,904.40 | 18,659.73 |
| Cluster-VIII | | | | | | | | 3,912.15 |

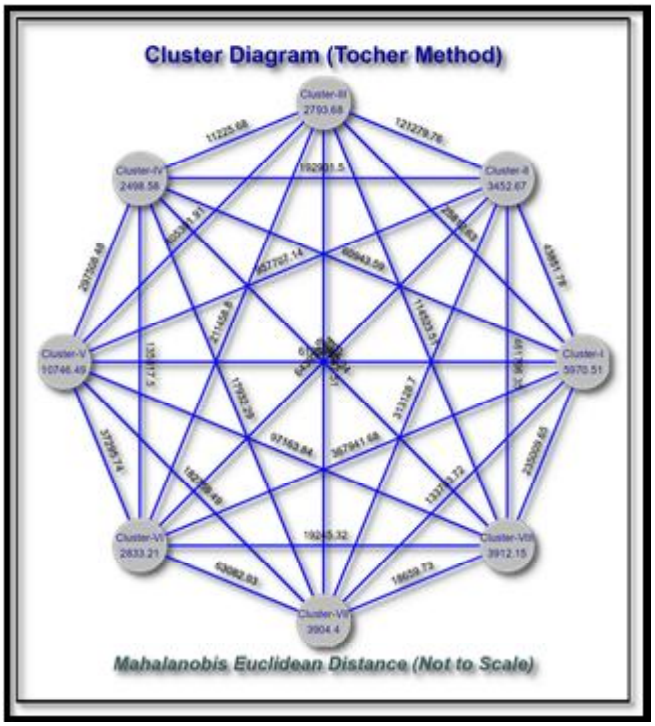



**Fig. 1 :** Cluster Diagram (Tocher Method).

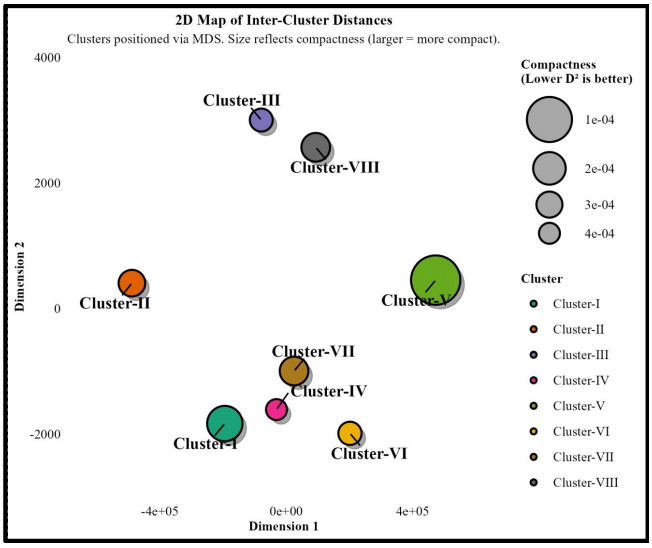



**Fig. 2 :** 2D Map of Inter- Cluster Distances.

The lowest intra-cluster distance was observed in Cluster IV (2,498.58), suggesting that the genotypes grouped within this cluster were highly similar genetically and probably shared a common breeding history or possessed similar gene complexes controlling yield and quality traits. A wide range of inter-cluster distances was observed, varying from 11,225.68 to 957,707.14.

The maximum inter-cluster distance was recorded between Cluster II and Cluster V (957,707.14) followed by Cluster I and Cluster V (612,696.20), Cluster II and Cluster VI (643,922.04), Cluster II and Cluster VIII (461,796.35) and Cluster III and Cluster V (405,301.91). Such exceptionally high genetic divergence indicates that the genotypes belonging to these clusters possess entirely different genetic constitutions and are likely to carry complementary alleles governing economically important characters. Hybridization between superior genotypes selected from Cluster II and Cluster V is therefore expected to produce maximum heterosis, broader segregation and a greater probability of recovering elite transgressive segregants. Likewise, crosses involving Cluster I × Cluster V, Cluster II × Cluster VI and Cluster III × Cluster were also expected to generate highly variable populations suitable for selecting superior clones.

Conversely, the minimum inter-cluster distance was observed between Cluster III and Cluster IV (11,225.68), followed by Cluster IV and Cluster VII (17,932.29), Cluster VII and Cluster VIII (18,659.73) and Cluster VI and Cluster VIII (19,245.32). These lower inter-cluster distances indicate that the genotypes belonging to these clusters are genetically more similar. Therefore, crosses between such clusters are less likely to generate substantial variability or high heterosis because of their close genetic relationship. The moderate inter-cluster distances observed among Cluster I, III and IV indicate the existence of intermediate genetic divergence.

From the present investigation, it can therefore be concluded that Cluster V, followed by Cluster II and Cluster VI, represents the most divergent genetic groups. Consequently, superior performing genotypes selected from these clusters should be preferred as parents in

**Table 3 :** Average Inter- and Intra-Cluster Distances (D Values).

| | **Cluster-I** | **Cluster-II** | **Cluster-III** | **Cluster-IV** | **Cluster-V** | **Cluster-VI** | **Cluster-VII** | **Cluster-VIII** |
|---|---|---|---|---|---|---|---|---|
| Cluster-I | **77.27** | 209.41 | 160.66 | 246.87 | 782.75 | 606.58 | 365.66 | 484.78 |
| Cluster-II | | **58.76** | 348.25 | 439.24 | 978.63 | 802.45 | 559.58 | 679.56 |
| Cluster-III | | | **52.86** | 105.95 | 636.63 | 459.85 | 220.33 | 338.41 |
| Cluster-IV | | | | **49.99** | 545.44 | 368.53 | 133.91 | 248.98 |
| Cluster-V | | | | | **103.67** | 193.12 | 427.50 | 311.71 |
| Cluster-VI | | | | | | **53.23** | 251.16 | 138.73 |
| Cluster-VII | | | | | | | **62.49** | 136.60 |
| Cluster-VIII | | | | | | | | **62.55** |

future hybridization programmes. However, parent selection should not be based solely on genetic distance. The mean performance of clusters for cane yield, sugar yield, sucrose percentage, CCS and other economically important traits must also be considered before finalizing crossing combinations.

**Cluster mean performance**

The mean performance of clusters provides valuable information for identifying genetically superior groups and facilitates the selection of appropriate parents for hybridization.

The highest germination percentage was observed in Cluster II (59.35%) followed by Cluster VIII (56.18%), Cluster III (54.26%), Cluster VII (51.32%) and Cluster I (51.15%). The lowest germination was recorded in Cluster V (42.39%). Cluster VIII recorded the highest number of tillers [181.96/ha (000)] considerably exceeding all other clusters. Cluster IV [149.21/ha (000)], Cluster I [146.80/ha (000)], Cluster II [145.76/ha (000)] and Cluster VII [145.45/ha (000)] also exhibited satisfactory tillering. The highest number of millable canes was observed in Cluster VIII [105.80/ha (000)] followed by Cluster II [86.73/ha (000)] and Cluster IV [85.22/ha (000)]. Cluster V exhibited the lowest value [68.14/ha (000)].

Maximum cane height was recorded in Cluster IV (266.43 cm) followed by Cluster I (260.89cm) and Cluster II (255.00 cm), whereas Cluster V recorded the shortest canes (222.92 cm). Cluster II exhibited the highest cane diameter (2.72 cm) followed by Cluster III (2.54 cm). Cluster VIII recorded the lowest cane diameter (2.30 cm).

Significant differences were observed among clusters for Brix, sucrose and CCS percentage. Cluster II recorded the highest Brix (22.00%), Sucrose (19.37%) and CCS percentage (13.56%), followed by Cluster I with 20.37% Brix, 17.92% sucrose and 12.54% CCS. The poorest juice quality was observed in Cluster V. The highest mean cane yield was recorded in Cluster II (99.45 t/ha) followed by Cluster VIII (86.58 t/ha), Cluster IV (83.18 t/ ha) and Cluster I (79.34 t/ha). Cluster V recorded the lowest yield (63.75 t/ha).

Commercial cane sugar yield represents the combined effect of cane yield and juice quality. The highest CCS yield was observed in Cluster II (13.38 t/ha) followed by Cluster I (9.85 t/ha), Cluster IV (9.16 t/ha), Cluster III (8.89 t/ha) and Cluster VIII (8.57 t/ha).

**Contribution towards Genetic divergence**

Among the ten characters studied, sucrose percentage (53.66%) contributed the highest proportion towards total genetic divergence, followed by millable cane height (37.94%), germination % (5.35%), cane diameter (1.54%), number of millable canes (0.76%), CCS percentage (0.61%), Brix (0.11%) and tillers per hectare (0.03%). In contrast, cane yield and CCS yield did not contribute to the observed divergence, each recording 0.00% contribution.

The dominance of sucrose percentage, which alone accounted for more than half (53.66%) of the total divergence, indicates that differences in sugar accumulation among the evaluated ISH genotypes were the principal source of genetic variability. Sucrose content is a complex quantitative trait influenced by multiple physiological and biochemical processes, including photosynthetic efficiency, assimilate partitioning, enzyme activity involved in sucrose synthesis and genetic regulation of sugar storage. The large variability observed for this trait suggests that the breeding material possesses substantial genetic potential for improving sugar recovery.

The second largest contributor was millable cane height (37.94%), indicating considerable variation in stalk elongation among the evaluated genotypes. Cane height is a major component of biomass production and is governed by both genetic and environmental factors. The substantial contribution of this trait reflects the diverse parentage of the interspecific hybrids and their contrasting growth habits. Together sucrose percentage and millable cane height accounted for 91.60% of the total genetic divergence, demonstrating that these two characters

**Table 4 :** Cluster means.

| Trait | Cluster-I | Cluster-II | Cluster-III | Cluster-IV | Cluster-V | Cluster-VI | Cluster-VII | Cluster-VIII |
|---|---|---|---|---|---|---|---|---|
| Germination % | 51.15 | 59.35 | 54.26 | 48.79 | 42.39 | 48.87 | 51.32 | 56.18 |
| Tillering | 146.80 | 145.76 | 141.65 | 149.21 | 133.23 | 139.78 | 145.45 | 181.96 |
| No. of millable cane | 80.37 | 86.73 | 78.62 | 85.22 | 68.14 | 79.00 | 81.37 | 105.80 |
| Mill. cane height | 260.89 | 255.00 | 246.67 | 266.43 | 222.92 | 237.46 | 226.67 | 239.39 |
| Cane diameter | 2.47 | 2.72 | 2.54 | 2.43 | 2.36 | 2.47 | 2.47 | 2.30 |
| Brix % | 20.37 | 22.00 | 19.27 | 18.23 | 14.88 | 15.86 | 18.15 | 16.67 |
| Sucrose % | 17.92 | 19.37 | 16.99 | 15.96 | 12.89 | 13.72 | 15.86 | 14.46 |
| CCS % | 12.54 | 13.56 | 11.90 | 11.14 | 8.95 | 9.52 | 11.06 | 10.04 |
| Cane Yield | 79.34 | 99.45 | 75.75 | 83.18 | 63.75 | 70.63 | 75.72 | 86.58 |
| CCS (t/ha) | 9.85 | 13.38 | 8.89 | 9.16 | 5.60 | 6.66 | 8.28 | 8.57 |

**Table 5 :** Contribution of Traits to Divergence.

| Trait | Contribution (%) | Times Ranked 1st |
|---|---|---|
| Sucrose % | 53.66 | 3,961 |
| Mill. Cane Height | 37.94 | 2,800 |
| Germination | 5.35 | 395 |
| Cane diameter | 1.54 | 114 |
| NMC | 0.76 | 56 |
| CCS % | 0.61 | 45 |
| Brix % | 0.11 | 8 |
| Tillering | 0.03 | 2 |
| Cane yield | 0.00 | 0 |
| CCS (t/ha) | 0.00 | 0 |

predominantly determined the grouping of genotypes into different clusters.

Germination% (5.35%) made the third highest contribution to genetic divergence. Although cane diameter (1.54%), number of millable canes (0.76%) and CCS percentage (0.61%) contributed comparatively less to the total divergence, these traits remain agronomically important because they directly influence cane weight, sugar recovery and overall productivity. The very low contribution of Brix (0.11%) and tillers per hectare (0.03%) indicates limited variability for these characters within the evaluated germplasm.

From a practical breeding standpoint, the present findings indicate that selection for sucrose percentage and millable cane height would be highly effective in exploiting the available genetic diversity. These traits should receive greater emphasis during parental selection because they are the major contributors to divergence and therefore provide maximum opportunity for generating genetically diverse and superior segregating populations.

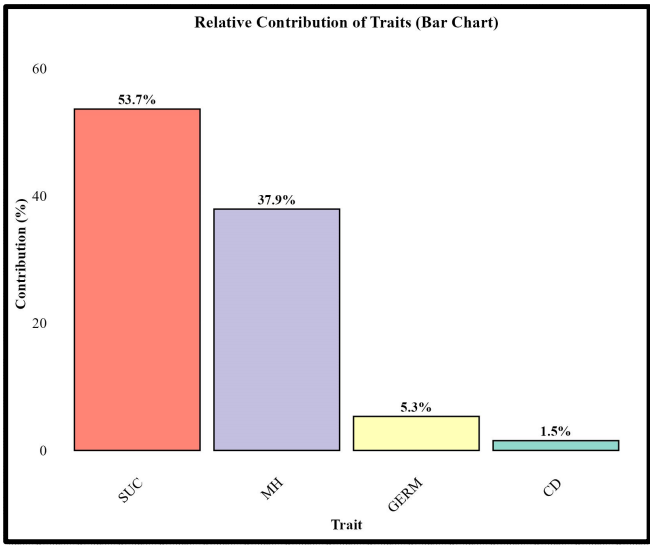



**Fig. 3 :** Relative contribution of Traits.

The present results also complement the cluster analysis. Cluster II recorded the highest mean sucrose percentage (19.37%), whereas Cluster IV recorded the tallest canes (266.43 cm). Furthermore, Cluster V exhibited the greatest genetic divergence from the remaining clusters. Consequently, crossing superior genotypes from Cluster II and Cluster IV with genetically distinct genotypes from Cluster V may provide an effective strategy for combining high sugar content, superior biomass, and broad genetic diversity in future sugarcane breeding programmes.

## Conclusion

Based on the combined evidence from cluster composition, inter-cluster distances, clustermean performance, andtrait contribution, the most promising breeding strategy is to use high-performing genotypes from Cluster II as one parent and genetically

divergentgenotypes from Cluster V as the other parent. Such crosses are expected to maximize heterosis and generate broad segregating populations with improved cane yield and sugar recovery. Because sucrose percentage and millable cane height were the primary contributors to divergence, these traits should receive the highest priority during parental selection and evaluation of progenies. The remaining traits can then be used to identify recombinants with balanced agronomic performance and commercial value.

## Acknowledgement

The authors express their gratitude to the, Director General of Vasantdada Sugar Institute, Pune for their encouragement, unwavering support throughout the research.

## References

Arunachalam, V. (1981). Genetic divergence in plant breeding. *Indian Journal of Genetics and Plant Breeding*, 41, 226–236.

Fisher, R. (1955). Statistical methods and scientific induction. *Journal of the Royal Statistical Society Series B: Statistical Methodology*, *17*(1), 69-78.

Johnson, H. W., Robinson, H. F., and Comstock, R. E. (1955). Estimates of genetic and environmental variability in soybeans. *Agronomy Journal*, 47, 314–318.

Kumar, N., Singh, P., and Sharma, M. (2021). Genetic divergence analysis in sugarcane germplasm using Mahalanobis $D^2$ statistics. *Sugar Tech*, 23, 1038–1048.

Lu, G., Liu, P., Wu, Q., Zhang, S., Zhao, P., Zhang, Y., & Que, Y. (2024). Sugarcane breeding: a fantastic past and promising future driven by technology and methods. *Frontiers in Plant Science*, *15*, 1375934.

Mehareb, E. M., Abazied, S. R., and El-Sayed, H. M. (2021). Assessment of genetic diversity among sugarcane genotypes using multivariate analysis. *Sugar Tech*, 23, 1015–1027.

Ming, R., Moore, P. H., Wu, K. K., D'Hont, A., Glaszmann, J. C., Tew, T. L., ... & Paterson, A. H. (2010). Sugarcane improvement through breeding and biotechnology. *Plant breeding reviews*, *27*, 15-118.

Ming, Y., Ramaswamy, V., Donner, L. J., & Phillips, V. T. (2006). A new parameterization of cloud droplet activation applicable to general circulation models. *Journal of the atmospheric sciences*, *63*(4), 1348-1356.

Mohammadi, S. A., andPrasanna, B. M. (2003). Analysis of genetic diversity in crop plants—salient statistical tools and considerations. *Crop Science*, 43, 1235–1248.

Rao, C. R. (1952). *Advanced Statistical Methods in Biometrical Research*. John Wiley and Sons, New York.

Singh, R. K., Singh, P. K., and Kumar, R. (2020). Genetic divergence studies in sugarcane for yield and quality traits. *Indian Journal of Genetics and Plant Breeding*, 80, 398–406.

Tena, E., Mekbib, F., andAyele, N. (2022). Multivariate analysis for assessment of genetic diversity in sugarcane germplasm. *Euphytica*, 218, 92.

Verma, R.S. and Srivastava S. (2020). Exploitation of genetic diversity in sugarcane breeding: Current perspectives. *Sugar Tech*, **22**, 785–797.