

Drought Tolerance and Multi-Environment Adaptation of Saccharum- and Erianthus- Derived Sugarcane Clones

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Abstract

Drought is one of the most important constraints limiting sugarcane productivity worldwide, necessitating the identification of climate-resilient germplasm with stable performance across diverse environments. In the present study, 18 interspecific (*Saccharum* spp.) and intergeneric (*Erianthus* × *Saccharum*) sugarcane clones were evaluated under contrasting water regimes across four agro-climatic locations in India to identify drought-tolerant and broadly adapted genotypes. Agronomic, yield and juice quality traits were assessed together with seven widely used drought tolerance indices. To improve genotype discrimination, a variance-weighted adaptation of the multivariate genotype–ideotype distance analysis (VW-MGIDI) framework was employed by integrating factor analysis with multiple drought tolerance indices. Genotype × environment interaction for commercial cane sugar yield was further investigated using GGE biplot analysis. Drought stress significantly reduced tiller number, cane height, cane weight, leaf area, cane yield and CCSY, with average reductions of 15.59%, 14.06%, 15.14%, 26.99%, 25.83% and 25.43%, respectively, whereas most juice quality traits remained comparatively stable. VW-MGIDI effectively identified location-specific superior genotypes, with IGH 829, ISH 548, ISH 590 and ISH 502 ranking highest at Karnal, Lucknow, Pune and Sankeshwar, respectively. GGE biplot analysis identified ISH 512 as the closest to the ideal genotype under drought, combining high commercial cane sugar yield with superior stability. Sankeshwar was the most discriminating environment for drought evaluation, whereas Pune was the most representative test location. The superior performance of selected *Saccharum spontaneum*- and *Erianthus*-derived clones highlights the potential value of wild-relative-derived germplasm for improving drought adaptation in sugarcane, although the specific contribution of wild-species ancestry requires further genetic validation.

Introduction

Sugarcane (*Saccharum* spp. hybrid complex) is one of the most important commercial crops of the tropical and subtropical regions, serving as a major source of sugar, ethanol, bioenergy and several value-added products (Pérez-Contreras et al., 2025). India is among the world's leading sugarcane-producing countries, with 454.61 million tonnes of sugarcane produced during 2024–25 (Ministry of Agriculture and Farmers Welfare, 2025). Uttar Pradesh, Maharashtra and Karnataka are the major sugarcane-producing states, accounting for approximately 85% of national sugarcane production in 2024–25. The crop therefore has considerable importance for the agricultural economy, rural livelihoods and the sugar-based bioeconomy of the country.

Despite its economic importance, sugarcane is a relatively water-demanding crop, and water availability is one of the major factors determining cane growth and productivity (Malee et al., 2026). The crop has a prolonged growth cycle and produces a large amount of biomass, resulting in substantial water requirements, particularly during the grand growth phase (Raheja et al., 2024). Under Indian production conditions, the total water requirement of sugarcane can be very high and varies with genotype, crop duration, climate, soil type and production system. Water requirement is also influenced by the method of planting and soil characteristics (Tayade et al., 2023). Field studies in subtropical India have also

demonstrated considerable variation in water use and water-use efficiency according to soil type and irrigation regime (Singh et al. 2007; Kumar et al., 2014). The magnitude of water demand makes sugarcane particularly vulnerable in regions where irrigation water is limited or rainfall is erratic (Ngcobo et al., 2024). Depending on cultivar, crop duration and environmental conditions, sugarcane may require approximately 160–350 cm of water during the crop cycle (Shukla et al., 2022). In addition to rainfall, with longer-duration and high-biomass canes generally requiring greater water availability. Consequently, increasing the productivity of sugarcane per unit of water has become an important objective for sustainable production.

Drought is one of the major abiotic stresses limiting sugarcane productivity, particularly when water shortage occurs during active vegetative growth (Ferreira, et al., 2017). Water deficit can reduce leaf area, photosynthetic activity, stalk growth, biomass accumulation and ultimately cane and sugar yield (Sajid et al., 2023). Importantly, genotypes differ considerably in their response to water limitation, indicating the existence of exploitable genetic variation for drought adaptation (Talabi et al., 2026; Meena et al., 2013). Research on sugarcane grown under contrasting water regimes has demonstrated substantial genotypic variation in yield response and physiological traits, while increased rooting depth, intrinsic water-use efficiency and improved root water supply have been identified as important attributes for adaptation to water-limited environments (Inman-Bamber et al., 2012; Takaragawa et al., 2025; Khonghintaisong et al., 2024). Therefore, the development and identification of drought-tolerant genotypes represent an important component of climate-resilient sugarcane breeding.

The genetic resources within the *Saccharum* and related genera offer valuable opportunities to broaden the genetic base of cultivated sugarcane. *Saccharum spontaneum* is particularly important owing to its vigorous root system, strong ratooning ability, wide ecological adaptation and contribution to stress tolerance (da Silva, 2017). Its incorporation into sugarcane breeding has contributed to improved adaptation and resistance to several stresses. Among allied genera, *Erianthus* has attracted attention as a potential source of drought tolerance (Jackson & Henry, 2011), owing to its deep and vigorous root system and high intrinsic water-use efficiency under water-limited conditions (Shiotsu et al., 2015). Recent studies have further demonstrated greater intrinsic water-use efficiency in *E. arundinaceus* than in cultivated sugarcane under both well-watered and water-deficit conditions (Takaragawa et al., 2025). Intergeneric hybrids involving *E. arundinaceus* have also exhibited deeper root systems, supporting its value for drought adaptation (Fukuhara et al., 2013). Thus, *E. arundinaceus* and wild *Saccharum* species represent valuable reservoirs of genes for drought tolerance, biomass production, ratooning ability, disease resistance and environmental adaptation. Interspecific (ISH) and intergeneric (IGH) hybridization provides an effective means of transferring these desirable attributes and generating novel genetic combinations. However, drought tolerance is complex and strongly influenced by environment, necessitating evaluation of promising clones across contrasting agroclimatic conditions to identify reliably adapted genotypes.

Accordingly, the present study aimed to evaluate the drought response and environmental adaptation of interspecific and intergeneric sugarcane clones across contrasting agroclimatic environments.

Genotypic performance under drought and non-drought conditions was assessed using a multivariate approach integrating multiple drought tolerance indices to identify genotypes combining high productivity and drought tolerance. Associations among morphological and yield traits were examined to identify traits contributing to drought adaptation. Furthermore, genotype × environment interaction across four drought-testing locations was assessed using GGE biplot analysis to identify stable and specifically adapted clones.

Materials and Methods

Plant material

The plant material comprised 18 sugarcane clones, of which four were intergeneric hybrids (IGHs) derived from crosses between *Erianthus* and *Saccharum* spp., while the remaining 14 were interspecific hybrids (ISHs) derived from crosses between *Saccharum* spp.. The details of the intergeneric and interspecific hybrids, along with their pedigree information are provided in Supplementary Table 1. Initially, 138 progenies were selected from the C₀ Population derived from interspecific and intergeneric hybridization. Based on their growth and quality attributes, the progenies were subsequently evaluated and selected, resulting in a final set of 18 promising clones for the present study.

Experimental locations and design

The selected clones were evaluated for two years at four locations, representing subtropical and tropical agro-climatic conditions. The experiments were conducted at the ICAR–Indian Sugarcane Research Institute, Lucknow, and the ICAR- SBI, Regional centre, Karnal, representing the subtropical zone, and at the Vasantdada Sugar Institute, Pune, and Agriculture Research Institute, Sankeshwar representing the tropical zone. The details of the locations has been given in Supplementary table 2. The experiments were conducted using an alpha-lattice design with two replications at each location.

Treatment details

The experiments were conducted under two contrasting water regimes: control (well-watered) and water-limited (drought stress) conditions. Under the drought-stress treatment only 2 irrigations were given, irrigation was withheld during the period from 60 to 150 days after planting. This period corresponds to the formative phase and grand growth phase of sugarcane, during which the crop has a high-water requirement. Under control conditions, all 6 irrigations were given according to the recommended package of practices to ensure adequate water availability throughout the crop growth period.

Phenotypic evaluation

Data were recorded for the following traits: number of tillers at 90 days (NOT9), number of millable canes at 360 days (NOT36), cane height (CH), cane diameter (CD), single cane weight (CW), number of internodes (NOI), brix (BRIX), sucrose content (SUC), extraction percentage (EXT), fibre content (FIB), cane yield (CY), leaf area (LA), commercial cane sugar content (CCS), and commercial cane sugar yield (CCSY). Fibre content was determined from wet bagasse using the Tanimoto method, and sucrose content was determined by polarimetry using a Micronal-Saccharomat polarimeter as previously described by (Carneiro et al., 2022).

Drought tolerance indices and multivariate analysis

Seven drought tolerance indices, namely stress tolerance (TOL), geometric mean productivity (GMP), stress susceptibility index (SSI), stress tolerance index (STI), harmonic mean (HM), yield susceptibility index (YSI), and yield index (YI), were calculated based on CCS yield under control and water-limited conditions following established methodologies (Fischer and Maurer, 1978; Rosielle and Hamblin, 1981; Fernandez, 1992). For genotype (i), the drought tolerance indices were calculated as follows:

- Stress Tolerance (TOL): $TOL = Y_{opt} - Y_{drt}$
- Geometric Mean Productivity (GMP): $GMP = \sqrt{Y_{opt} \times Y_{drt}}$
- Stress Susceptibility Index (SSI): $SSI = [1 - (Y_{opt} / Y_{opt})] / [1 - (Y_{drt} / Y_{opt})]$
- Stress Tolerance Index (STI): $STI = (Y_{opt} \times Y_{drt}) / (Y_{opt})^2$
- Harmonic Mean (HM): $HM = [2 \times (Y_{opt} \times Y_{drt})] / (Y_{opt} + Y_{drt})$
- Yield Susceptibility Index (YSI): $YSI = Y_{opt} / Y_{drt}$
- Yield Index (YI): $YI = Y_{drt} / Y_{opt}$

Y_{opt} = The crop yield of a specific genotype grown under optimal conditions

Y_{drt} = The crop yield of that same genotype grown under moisture-stress conditions.

$\bar{Y}_{opt}$ = The average yield calculated across all genotypes under optimal conditions.

$\bar{Y}_{drt}$ = The average yield calculated across all genotypes under drought conditions.

Because the indices differ in their scales and directions of desirability, their values were rescaled to a common 0–100 scale before multivariate analysis. For indices in which higher values indicate greater drought tolerance (GMP, STI, HM, YSI and YI), the standardized value for genotype (i) was calculated as:

For indices where higher values are desirable (GMP, STI, HAM, YI and YSI):

$$Z_{\{ij\}} = \left(\frac{X_{ij} - X_{\{j.min\}}}{X_{\{j,max\}} - X_{\{j.min\}}} \right) \times 100$$

The lower values are desirable (TOL and SSI):

$$Z_{\{ij\}} = \left(\frac{X_{\{j,max\}} - X_{\{ij\}}}{X_{\{j,max\}} - X_{\{j,min\}}} \right) \times 100$$

- X_{ij} = original value of genotype i for drought index j
- $X_{j,min}$ = minimum value of index j
- $X_{j,max}$ = maximum value of index j
- Z_{ij} = standardized value ranging from 0 to 100

Pearson's correlation analysis was performed among the standardized drought tolerance indices separately for each location. Factor analysis was subsequently conducted using the correlation matrix, with factors having eigenvalues > 1 retained according to the Kaiser criterion (Kaiser, 1960), followed by Varimax rotation (Kaiser, 1958). Factor scores were obtained for each genotype, and the retained factors were interpreted according to their factor-loading patterns.

The multivariate genotype–ideotype distance analysis followed the general framework of the Multi-Trait Genotype-Ideotype Distance Index (MGIDI) proposed by Olivoto and Nardino (2021), including the rescaling of variables according to their desired direction, factor analysis, estimation of factor scores, definition of a multivariate ideotype, and distance-based ranking of genotypes. However, the framework was modified by assigning variance-based weights to the retained factors according to their respective proportions of explained variance, rather than giving equal weight to each factor. This variance-weighted adaptation of the multivariate genotype–ideotype distance analysis was termed the Variance-Weighted Multivariate Genotype-Ideotype Distance Index (VW-MGIDI).

For (f) retained factors, the weight assigned to factor (j) was calculated from its proportion of explained variance as:

$$w_j = \frac{P_j}{\sum_{j=1}^f p_j}$$

P_j = Proportion of variance explained by factor j

The modified multivariate genotype–ideotype distance for genotype (i) was calculated as:

$$VW - MGIDI_i = \sqrt{\sum_{j=1}^f w_j (f_{ij} - f_{Ij})^2}$$

where F_{ij} is the factor score of genotypes (i) for factor (j), F_{Ij} is the corresponding ideal factor score, and (w_j) is the variance-explained weight assigned to factor (j). Lower distance values indicate greater proximity to the multivariate ideotype and, consequently, greater overall desirability across the drought-response dimensions. Statistical analyses were performed using R software, with the *psych*, *tidyverse*, and *ggplot2* packages.

Correlation and GGE biplot analysis

Correlation analyses were performed using Rstudio v4.4.2 using the “corr” package (RStudio Team, 2020). Genotype × environment interaction for commercial cane sugar yield (CCSY) was examined separately under drought and control conditions using the GGE biplot methodology. The GGE biplot simultaneously considers genotype main effects and genotype × environment interaction, while the environmental main effect is excluded because it is common to all genotypes within a given environment. The first two principal components (PC1 and PC2) were used to construct the biplots. The resulting biplots were interpreted using four complementary views: (i) mean performance and stability, (ii) ranking of genotypes relative to the ideal genotype, (iii) which-won-where analysis to identify specifically adapted genotypes and potential mega-environment patterns, and (iv) discriminativeness and representativeness of the test environments. The analysis was performed using the GGEBiplotGUI package in R version 4.4.2.

Results

Response of Agronomic, Yield and Quality Traits to Drought Stress

The number of tillers at 90 days decreased from 142.65 under control to 120.10 under drought, representing a 15.59% significant reduction ($p < 0.001$). Similarly, the number of millable canes at 360 days declined from 112.84 to 93.52 (17.11%), while cane height decreased from 240.92 to 207.33 (14.06%). Cane weight decreased from 0.93 to 0.79 (15.14%), and the number of internodes declined from 19.84 to 17.52 (11.58%), all the reductions being significant ($p < 0.001$). Cane diameter showed only a marginal reduction from 2.23 to 2.20 (0.96%), which was non-significant.

Among the juice quality traits, brix increased marginally from 18.96 under control to 19.01 under drought (– 0.41%), while sucrose content increased from 16.34 to 16.39 (– 0.49%); neither change was significant. Juice extraction decreased slightly from 44.23 to 43.63 (1.13%), and this reduction was also non-significant. In contrast, fibre content declined significantly from 19.82 to 15.95 (17.67%; $p < 0.001$). Cane yield decreased from 99.41 to 73.80 (25.83%; $p < 0.001$), while leaf area declined from 3646.21 to 2615.03 (26.99%; $p < 0.001$). CCSP showed a negligible increase from 11.17 to 11.21 (– 0.56%), whereas CCSY declined markedly from 11.16 to 8.27 (25.43%; $p < 0.001$) (Table 1).

Table 1

Effect of drought stress on agronomic, yield and juice quality traits across 18 sugarcane genotypes

Agronomic and yield traits				Quality traits			
Trait	Control	Drought	Percent change	Trait	Control	Drought	Percent change
NOT9	142.65	120.10	15.59***	°Brix	18.96	19.01	-0.41
NOT36	112.84	93.52	17.11***	SUC (%)	16.34	16.39	-0.49
CH (cm)	240.92	207.33	14.06***	EXT (%)	44.23	43.63	1.13
CD (cm)	2.23	2.20	0.96	FIB (%)	19.82	15.95	17.67***
CW (kg)	0.93	0.79	15.14***	CCSP (%)	11.17	11.21	-0.56
NOI	19.84	17.52	11.58***				
CY (t/ha)	99.41	73.80	25.83***				
LA (cm)	3646.21	2615.03	26.99***				
CCSY (t/ha)	11.16	8.27	25.43***				

Correlation among morphological and yield traits under control and drought conditions

Under control conditions, CCSY exhibited significant positive correlations with CD ($r = 0.73^{***}$), CW ($r = 0.92^{***}$), BRIX ($r = 0.75^{***}$), SUC ($r = 0.76^{***}$), EXTR ($r = 0.70^{**}$), CY ($r = 0.81^{***}$) and CCSP ($r = 0.76^{***}$), whereas a significant negative correlation was observed with fibre ($r = -0.57^*$). SUC was positively correlated with CD ($r = 0.86^{***}$), CW ($r = 0.81^{***}$) and BRIX ($r = 0.98^{***}$), but negatively correlated with fibre ($r = -0.60^{***}$). Under drought conditions, CCSY showed positive associations with CD ($r = 0.57^*$), CW ($r = 0.75^{**}$), BRIX ($r = 0.52^*$), SUC ($r = 0.54^*$), EXTR ($r = 0.55^*$), CY ($r = 0.81^{***}$) and CCSP ($r = 0.54$), while showing a significant negative correlation with fibre ($r = -0.70^{***}$). Similarly, SUC exhibited positive correlations with CD ($r = 0.86^*$), CW ($r = 0.70^{***}$) and BRIX ($r = 0.99^{***}$), whereas its association with fibre was negative ($r = -0.70^{***}$). The detailed correlation coefficients and their significance levels are presented in Fig. 1.

Interrelationships and factor structure of drought tolerance indices

The seven drought tolerance indices calculated for the 18 genotypes across the four locations are presented in Supplementary File 2. The correlation pattern among the drought tolerance indices varied across locations (Fig. 2). TOL, SSI and YSI exhibited perfect positive correlations ($r = 1.000$) at Karnal, Lucknow and Sankeshwar, indicating complete redundancy among these three indices at these

environments. GMP, STI, HAM and YI showed strong positive interrelationships across all four locations, with correlation coefficients ranging from 0.973–0.999 at Karnal, 0.932–0.993 at Lucknow, 0.938–0.996 at Pune and 0.951–1.000 at Sankeshwar. In contrast, the associations of these indices with TOL, SSI and YSI were moderate and positive at Karnal ($r = 0.441$ – 0.626) and Lucknow ($r = 0.225$ – 0.558), negative at Pune ($r = -0.333$ to -0.261), and weakly positive at Sankeshwar ($r = 0.168$ – 0.431).

Factor analysis based on the eigenvalue > 1 criterion retained two dominant factors at all four locations (Table 2). At Karnal, the first and second factors had eigenvalues of 5.299 and 1.691, explaining 54.84 and 45.02% of the total variation, respectively, whereas at Lucknow, their eigenvalues were 4.726 and 2.261, accounting for 55.05 and 44.76% of the variation. At Pune, the two factors explained 55.56 and 44.19%, while at Sankeshwar they accounted for 55.68 and 44.08% of the total variation. Thus, the two retained factors collectively explained approximately 99.8–100% of the variation in drought tolerance indices across the four environments. The first factor consistently contributed slightly more to the total variation, with weights ranging from 0.549 to 0.558, compared with 0.442–0.451 for the second factor. The factor-loading pattern was remarkably consistent across locations. Factor 1 was predominantly represented by GMP, STI, HM and YI, and was therefore interpreted as a productivity–drought tolerance dimension, whereas Factor 2 was primarily associated with TOL, SSI and YSI and represented a drought susceptibility dimension. The consistency of this factor structure across locations indicates that the major dimensions underlying variation in drought response remained relatively stable despite differences in growing environments.

Table 2

Eigenvalues, variance explained and factor weights of drought tolerance indices across four locations

Location	RC1 eigenvalue	RC2 eigenvalue	RC1 variance (%)	RC2 variance (%)	RC1 weight	RC2 weight
Karnal	5.299	1.691	54.84	45.02	0.549	0.451
Lucknow	4.726	2.261	55.05	44.76	0.552	0.448
Pune	4.410	2.573	55.56	44.19	0.557	0.443
Sankeshwar	4.469	2.514	55.68	44.08	0.558	0.442

Genotype ranking based on VW-MGIDI

The weighted multivariate ideotype distance index effectively discriminated the 18 genotypes based on their combined performance across drought tolerance dimensions (Fig. 3). Lower VW-MGIDI values indicated a shorter distance from the multivariate ideotype and, consequently, greater overall desirability. The ranking of the top five genotypes differed among locations, demonstrating environmental effects on the expression of drought tolerance. At Karnal, IGH 829 ranked first, followed by ISH 501, ISH 534, ISH 502 and ISH 536. At Lucknow, ISH 548, ISH 502, ISH 501, ISH 590 and ISH 512 occupied the first five positions. At Pune, ISH 590, IGH 829, ISH 519, IGH 833 and ISH 502 were the top-ranked genotypes, whereas ISH 502, ISH 534, ISH 524, IGH 829 and IGH 823 ranked highest at Sankeshwar.

Comparison of VW-MGIDI rankings across locations further revealed differential genotype responses to the testing environments. ISH 502 showed the most consistent performance, ranking 4th at Karnal, 2nd at Lucknow, 5th at Pune and 1st at Sankeshwar. IGH 829 also exhibited favourable performance, ranking 1st, 10th, 2nd and 4th at Karnal, Lucknow, Pune and Sankeshwar, respectively. In contrast, ISH 534 performed particularly well at Karnal and Sankeshwar, while ISH 590 ranked first at Pune but showed comparatively poor performance at Sankeshwar. These results revealed differences in the consistency and environmental specificity of drought response.

GGE biplot analysis for CCSY

GGE biplot analysis was performed to assess genotype $\times$ environment interaction and identify stable and specifically adapted genotypes for CCSY under drought and control conditions. Under drought, PC1 and PC2 accounted for 64.17% and 16.81% of the total variation, respectively. In the mean performance versus stability view, the average environment coordination (AEC) abscissa was used to compare genotype mean performance, whereas the projection of a genotype onto the AEC ordinate was interpreted as an indication of its instability across environments. The mean performance versus stability view indicated that ISH 502 had the highest mean CCSY, followed by IGH 829 and ISH 534, while IGH 833, IGH 823, ISH 501 and ISH 512 showed comparatively smaller projections onto the AEC ordinate and therefore lower variation in performance across the test environments (Fig. 4a). In the ranking view, genotypes located closer to the ideal genotype were considered to have a more favourable combination of high mean CCSY and greater stability. Based on the distance from the ideal genotype, ISH 512 was positioned closest to the ideal genotype, indicating the most desirable combination of high CCSY and stability (Fig. 4b). The which-won-where view was used to identify environments in which particular genotypes performed relatively better and to delineate possible mega-environments. The which-won-where analysis indicated three distinct response sectors under drought. Karnal formed one sector, with IGH 829 as the vertex genotype, whereas Pune and Sankeshwar formed another sector with ISH 502 as the winning genotype. Lucknow constituted a third sector, with ISH 548 as the winning genotype. These patterns indicate differential genotype responses among locations rather than uniform superiority of a single genotype across all environments. (Fig. 4c). The discriminativeness versus representativeness view was used to assess the usefulness of each test location for differentiating genotypes and its representativeness of the overall target environment. The discriminativeness versus representativeness view identified Sankeshwar as the most discriminating environment, indicating a relatively high capacity to differentiate the genotypes for CCSY. Pune was positioned as the most representative environment among the four test locations under drought, suggesting that genotype performance at Pune was more closely associated with the average response across the tested environments (Fig. 4d).

Under control conditions, PC1 and PC2 explained 72.20% and 13.28% of the total variation, respectively. The mean performance versus stability analysis identified ISH 512 as the highest-performing genotype, followed by IGH 502 and ISH 501. IGH 829, ISH 548 and IGH 834 showed smaller projections onto the AEC ordinate, indicating comparatively greater stability across environments (Fig. 5a). The ranking based on distance from the ideal genotype placed ISH 512 closest to the ideal genotype, followed by IGH 829

and ISH 548, indicating their favourable combination of high CCSY and stability (Fig. 5b). The “which-won-where” analysis again delineated three mega-environments. Pune constituted the first mega-environment, with IGH 519 as the winning genotype, while Karnal and Sankeshwar comprised the second mega-environment. Lucknow constituted the third mega-environment, where ISH 502 was the winning genotype (Fig. 5c). The discriminativeness versus representativeness analysis identified Sankeshwar as the most discriminating environment and Karnal as the most representative environment under control conditions (Fig. 5d).

Discussion

Drought stress during the formative and grand growth phase had a pronounced adverse effect on the agronomic and yield attributes of sugarcane, whereas most juice quality traits remained comparatively stable (Dinh et al., 2018). Cane yield exhibited a substantial reduction under drought stress, ranging from 12.37% to 39.63% among the genotypes, with a mean reduction of 25.83%. Similar reductions in cane yield under drought stress have also been reported in previous studies (Hemaprabha et al., 2004; Tippayawat et al., 2025). The marked decline in cane yield was associated with reductions in major growth and yield-contributing traits, particularly the number of tillers at 90 days, number of millable canes at 360 days, cane height, cane weight, number of internodes, and leaf area. Reduced tillering under water-limited conditions can directly decrease the number of harvestable canes, while reductions in cane height, individual cane weight and internode development can further constrain biomass accumulation (Botha et al., 2023). The substantial decline in leaf area may have additionally restricted the photosynthetic surface and, consequently, assimilate production and biomass accumulation during the grand growth phase (Zhao et al., 2013). In contrast, cane diameter showed negligible change under drought, suggesting that this trait was comparatively less sensitive to water limitation and may have contributed less to the observed variation in cane yield reduction.

In contrast to the strong effects on growth and yield attributes, drought stress caused limited changes in most juice quality traits. brix, sucrose content, juice extraction, and commercial cane sugar percentage did not differ significantly between control and drought conditions, indicating relative stability of these quality parameters under water stress. Similar findings were also reported by Abou-gabal et al., 2023. Fibre content was the notable exception, showing a significant reduction of 17.67% under drought. The relative stability of BRIX and sucrose content despite substantial losses in cane yield may be attributed to the developmental timing of sucrose accumulation in sugarcane. Drought stress during the grand growth phase primarily restricts vegetative growth and biomass accumulation, whereas substantial sucrose accumulation occurs predominantly during the subsequent maturity phase. Thus, the stress imposed during the grand growth phase had a greater impact on cane biomass and yield than on sucrose accumulation and juice quality (Ahmed et al., 2024). The reduction in commercial cane sugar yield by 25.43% further demonstrates the substantial impact of drought on the economic productivity of the crop. This reduction was largely associated with the decline in cane yield, as the commercial sugar concentration remained statistically unchanged under drought. Thus, the loss in CCSY appears to have resulted predominantly from reduced cane biomass rather than deterioration in sugar concentration.

Correlation analysis showed that CCSY was positively associated with cane weight, cane yield, cane diameter, BRIX, sucrose content, juice extraction and commercial cane sugar percentage under control conditions, while fibre showed a negative association (Adilakshmi et al., 2026; Thippeswamy et al., 2003). Under drought, these relationships were largely maintained, although the strength of several associations declined. Cane yield remained strongly associated with CCSY under both conditions, highlighting its importance as a major contributor to sugar productivity (Silva et al., 2008; Silva et al., 2014). The stronger negative association of fibre with CCSY under drought further suggests its adverse effect on sugar yield under water stress. The relationship of sucrose content with other traits was highly consistent across both moisture regimes. BRIX, cane diameter and cane weight showed positive associations with sucrose content, whereas fibre content was negatively associated with sucrose. The strong and stable relationship between BRIX and sucrose content under both conditions suggests that BRIX can serve as a useful indicator of sucrose accumulation (Pistón et al., 2016; Appunu et al., 2024). The negative relationship between fibre and sucrose under drought further suggests that increased fibre content may be unfavourable for sugar accumulation under water stress (Gravois and Milligan, 1992).

Drought tolerance indices provide complementary measures of yield potential, yield loss and relative performance under water-limited conditions, making them useful for screening genotypes for drought adaptation (Azrai et al., 2025). The strong associations among GMP, STI, HAM and YI indicated a common productivity–tolerance dimension, whereas TOL, SSI and YSI largely represented a drought susceptibility dimension, with their relationships varying across environments (EYNI et al., 2020). Factor analysis consistently separated these two dimensions across locations, confirming that drought response is multidimensional. The contrasting rankings of genotypes across individual indices further demonstrate that selection based on a single index may be misleading, as productivity-oriented indices may favour high-yielding genotypes, whereas susceptibility-oriented indices may favour genotypes with lower yield loss but limited yield potential. Therefore, simultaneous consideration of multiple drought-response dimensions is essential for reliable genotype selection (Ghazvini et al., 2024). The weighted multivariate ideotype distance index integrated the information from all seven indices and provided a unified criterion for ranking genotypes according to their combined productivity and drought response. The location-specific rankings confirmed substantial environmental influence on drought tolerance, with IGH 829, ISH 548, ISH 590 and ISH 502 identified as the most desirable genotypes at Karnal, Lucknow, Pune and Sankeshwar, respectively. The clone IGH 829 is derived from Co 62195 X IK 76–91 (*E.arundinaceus*). Th *E.arundinaceus* is known for high biomass yield, deep root systems, and strong resistance to environmental stresses (Terajima et al., 2023; Meena, et al., 2024). The genotype ISH 548, developed from the cross CoC 671 × (PIO 91–488 × SIP 93–397), traces part of its ancestry to *Saccharum spontaneum*. Its favourable performance under drought conditions suggests a potential association between *S. spontaneum*-derived genetic variation and drought adaptation, consistent with previous reports on the potential role of *S. spontaneum* in drought-response traits (Vinu et al., 2025). Among these, ISH 502 showed the most consistent performance, ranking within the top five across all four locations, indicating broader adaptation to drought-prone environments.

The GGE biplot analysis demonstrated substantial genotype $\times$ environment interaction for CCSY, with genotype performance and stability varying between drought and control conditions. Under drought, ISH 502 expressed high mean CCSY, while ISH 512 was closest to the ideal genotype, indicating a favourable balance between productivity and stability. The genotype ISH 512 was developed from the pedigree Co 7201///28 NG 121/SES 515-7//Co 775////CoA 7602. As its pedigree includes *Saccharum spontaneum* (SES 515-7), a wild sugarcane species recognized as a valuable source of abiotic stress tolerance, ISH 512 is expected to possess enhanced drought tolerance (Vinu et al., 2025). The identification of distinct mega-environments further revealed differential adaptation, with IGH 829, ISH 502 and ISH 548 performing best in Karnal, Pune–Sankeshwar and Lucknow, respectively. The greater discriminating ability of Sankeshwar suggests that it was particularly effective in differentiating genotypic responses to drought, whereas the high representativeness of Pune makes it useful for assessing broader drought adaptation.

Under control conditions, ISH 512 showed the highest mean CCSY and was also closest to the ideal genotype, indicating superior productivity with favourable stability under non-stress conditions. The distinct mega-environments identified under control conditions, with IGH 519 winning at Pune and ISH 502 at Lucknow, further confirmed environment-specific genotype performance. Interestingly, Sankeshwar remained the most discriminating environment under both moisture regimes, suggesting its strong capacity to differentiate genotypes, whereas the most representative environment shifted from Pune under drought to Karnal under control, reflecting changes in environmental relevance with moisture regime. Genotypes such as ISH 502 and ISH 512, which exhibited favourable performance across environments and/or moisture regimes, represent promising material for breeding programmes targeting stable CCSY under variable water availability.

Conclusion

This study demonstrates that drought stress imposed during the formative and grand growth phase substantially reduced cane yield and commercial cane sugar yield, primarily through its adverse effects on vegetative growth and biomass accumulation, while most juice quality traits remained relatively stable. Integrating multiple drought tolerance indices through the VW-MGIDI provided a more comprehensive and reliable assessment of drought tolerance than individual indices alone by simultaneously capturing productivity and drought susceptibility. Among the evaluated clones, ISH 502 emerged as the most consistently drought-tolerant genotype across environments, whereas ISH 512 combined high commercial cane sugar yield with excellent stability and was identified as the ideal genotype under drought conditions. The superior performance of ISH 512 and ISH 548, both possessing *Saccharum spontaneum* ancestry, and IGH 829, derived from *Erianthus arundinaceus*, suggests a potential association between wild-relative-derived genetic variation and drought adaptation in cultivated sugarcane. However, these observations are based on phenotypic performance and further genomic characterization and validation across diverse environments and genetic backgrounds are required to confirm the contribution of *S. spontaneum*- and *Erianthus*-derived genetic variation to drought adaptation. GGE biplot analysis further identified Sankeshwar as the most discriminating environment and Pune as

the most representative location for drought evaluation, providing valuable guidance for future multi-environment testing.

Declarations

Conflict of Interest

The authors declare that they have no conflicts of interest related to this work.

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Author Contribution

S.K. and K.K.M. conceived and designed the study and critically revised the manuscript. S.K. and K.K.M. conducted the investigation and prepared the initial draft of the manuscript. S.K., N.K.K.R., and I.N. generated the phenotypic data. K.K.M. performed the statistical analyses. All authors reviewed, contributed to, and approved the final version of the manuscript.

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Data Availability

The datasets generated and/or analyzed during the current study are available from the corresponding author upon reasonable request.

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Figures

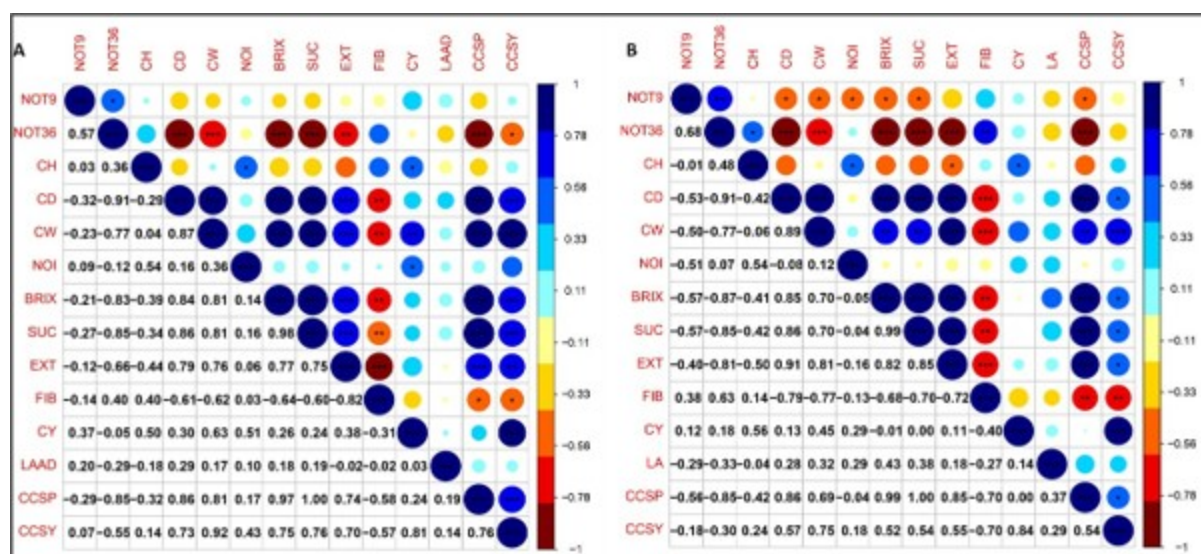


Figure 1

Footnote:(A) Control and (B) drought conditions. Blue and red colors indicate positive and negative Pearson's correlation coefficients, respectively, with color intensity proportional to the magnitude of the correlation. $P < 0.05$ (*), $P < 0.01$ (**), and $P < 0.001$ (***). Abbreviations: NOT9, number of tillers at 90 days; NOT36, number of tillers at 360 days; CH, cane height; CD, cane diameter; CW, single cane weight; NOI, number of internodes; BRIX, total soluble solids ($^{\circ}$ Brix); SUC, sucrose content (%); EXT, commercial cane sugar extraction (%); FIB, fibre content (%); CY, cane yield; LA, leaf area; CCS, commercial cane sugar content (%); CCSY, commercial cane sugar yield (t ha^{-1}).

Figure 1. Pearson's correlation matrices among agronomic, juice quality, and sugar yield traits in sugarcane under (A) control and (B) drought conditions.

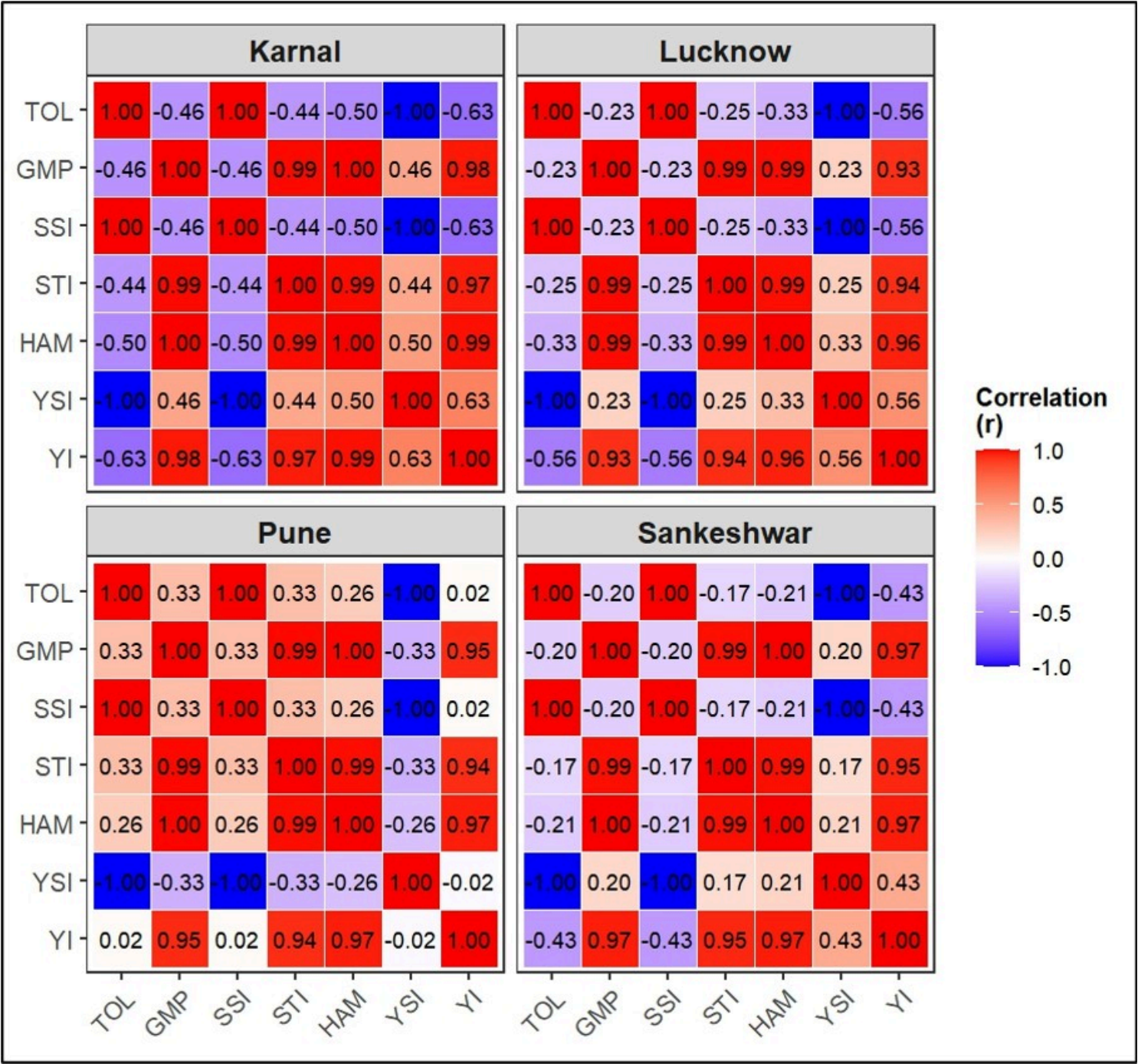


Figure 2
Heatmaps showing Pearson's correlation coefficients among drought tolerance indices at (A) Karnal, (B) Lucknow, (C) Pune, and (D) Sankeshwar.

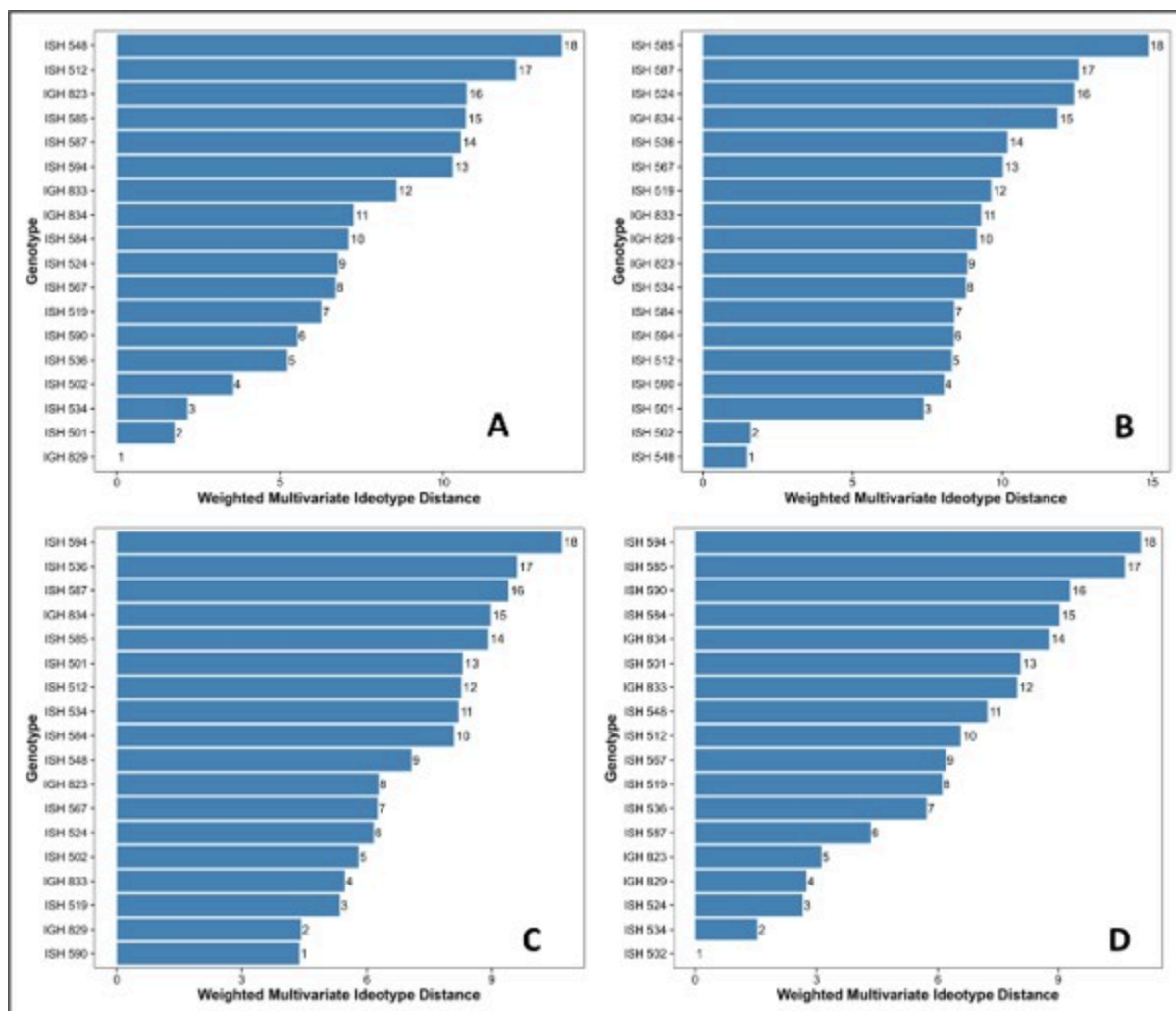


Figure 3

Weighted Multivariate Ideotype Distance Index of 18 sugarcane clones for drought tolerance across four test locations: (A) Karnal, (B) Lucknow, (C) Pune, and (D) Sankeshwar.

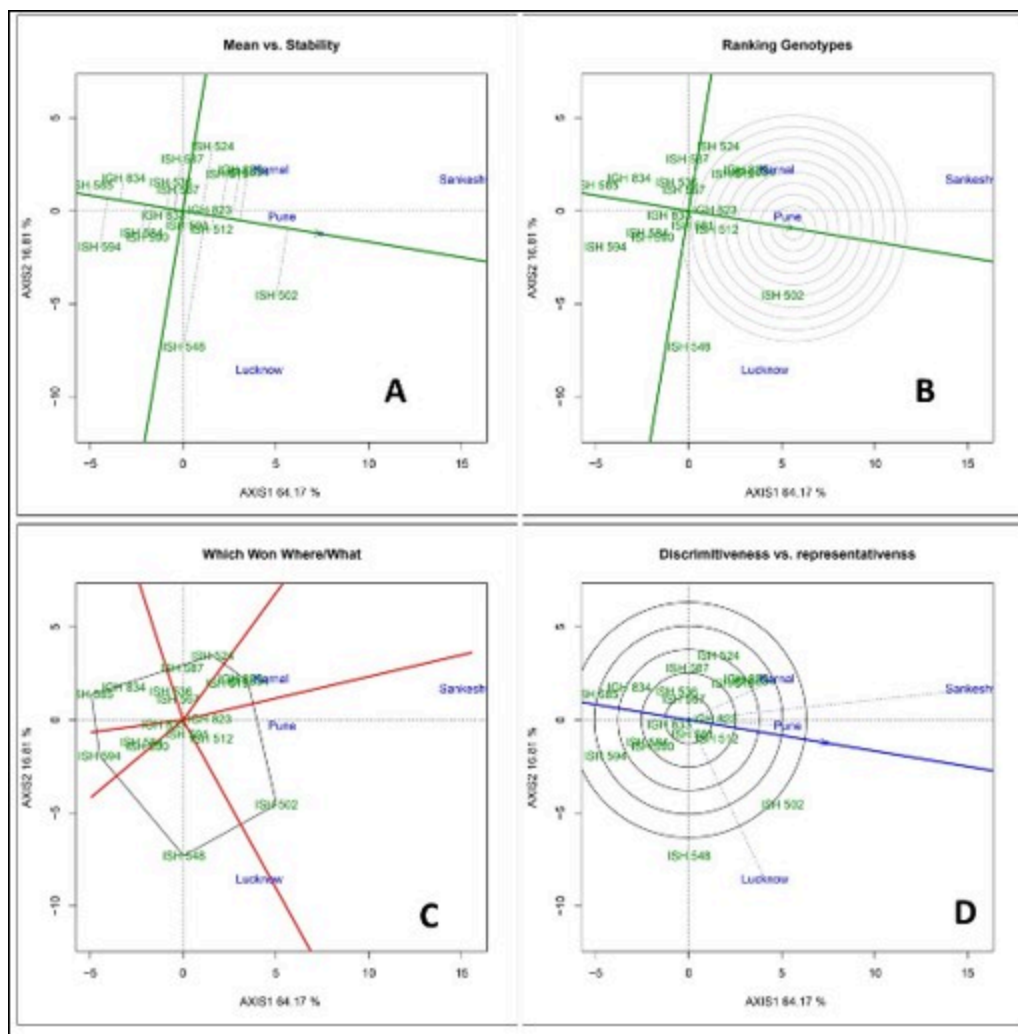


Figure 4

GGE biplot analysis of commercial cane sugar yield (CCSY) under drought conditions showing (A) mean performance versus stability of genotypes, (B) ranking of genotypes relative to the ideal genotype, (C) "which-won-where" pattern and (D) discriminativeness versus representativeness of the test environments.

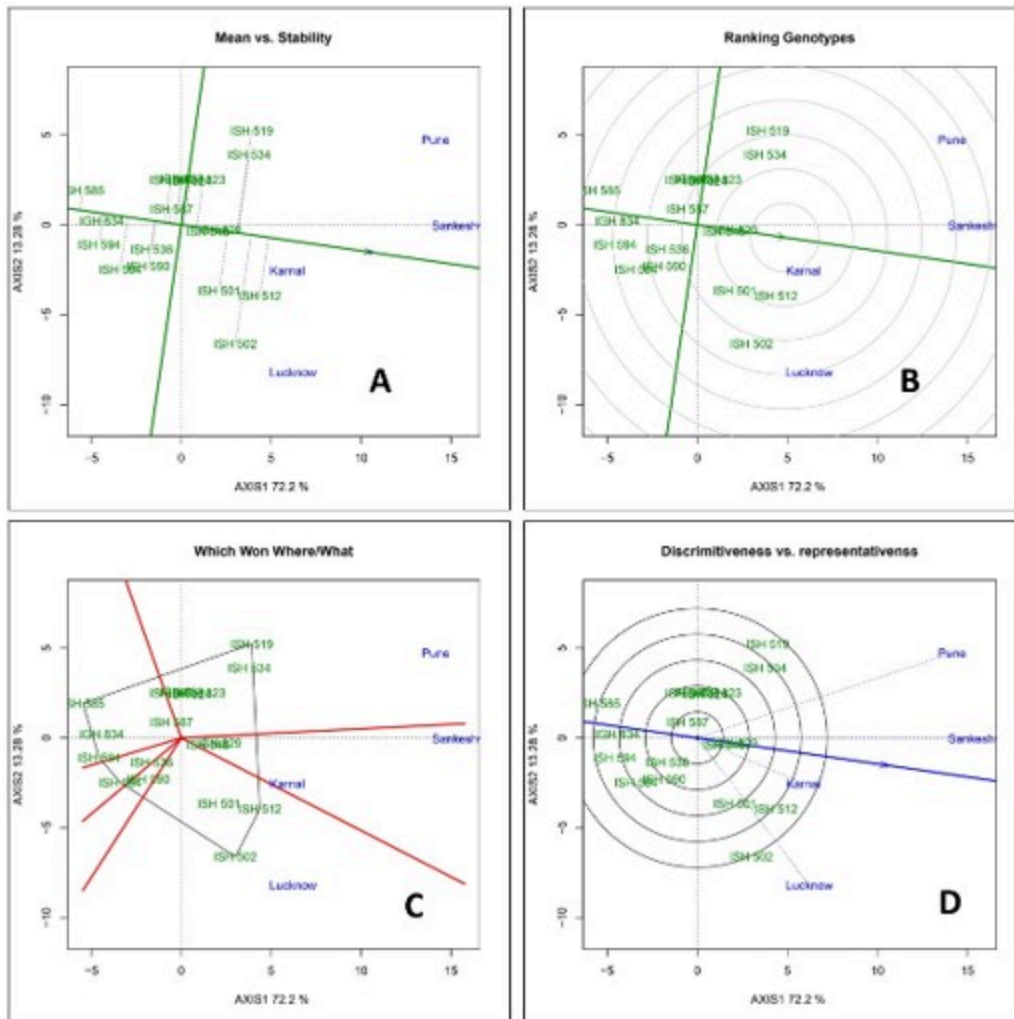


Figure 5

GGE biplot analysis of commercial cane sugar yield (CCSY) under control conditions showing (A) mean performance versus stability of genotypes, (B) ranking of genotypes relative to the ideal genotype, (C) "which-won-where" pattern and (D) discriminativeness versus representativeness of the test environments.

Supplementary Files

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