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Assessment of genotype × environment interaction for cane yield and sucrose content in sugarcane using GGE biplot analysis

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Abstract

Identification of sugarcane genotypes with consistent performance across diverse environments remains a major challenge in varietal improvement because the expression of economically important traits is strongly influenced by genotype × environment interaction. The present study evaluated genotype × environment interaction and ratoon ability of sugarcane genotypes across the East Coast Zone, North West Zone, and Peninsular Zone using GGE biplot analysis for cane yield, CCS yield and sucrose content. Ratoon ability analysis revealed sucrose content exhibited comparatively better retention under ratoon conditions irrespective of zone, whereas cane yield and CCS yield showed relatively larger reductions. The GGE biplot analysis revealed substantial genotype × environment interaction for cane yield, CCS yield, and sucrose content across the three sugarcane production zones. In the ECZ, Co 09004 for CCS yield, CoA 20321 for cane yield, and Co 11015 for sucrose content were identified as superior and stable genotypes. In the NWZ, CoS 19231 was identified as the ideal genotype for CCS yield, cane yield, and sucrose content. In the PZ, Co 18003 was identified as the desirable genotype for CCS yield and cane yield, whereas CoC 671 was identified as the ideal genotype for sucrose content. Among the test environments, Vuyyuru in ECZ, Muzaffarnagar & Shahjahanpur in NWZ, and Pune & Sameerwadi in PZ were identified as highly informative and representative environments. The identified genotypes and representative environments can be effectively utilized in future breeding programmes and zone-specific cultivar recommendation.

Introduction

Sugarcane (*Saccharum* spp.) is a highly important industrial crop cultivated extensively under tropical and subtropical regions. Besides being the principal raw material for sugar production, it also supports several allied industries including ethanol, cogeneration, paper and other by-products, thereby contributing significantly to agricultural income and industrial development (Eggleston and Lima, 2015; Malik et al., 2019). In India, sugarcane forms an integral component of the farming system and plays a major role in supporting the livelihood of growers, sugar industries, and associated rural economies (Solomon, 2016). Sustained improvement in both cane productivity and sugar recovery is therefore a major priority in sugarcane improvement programmes (Singh et al., 2019).

The development of superior sugarcane varieties is challenging because genotype performance is often influenced by environment. Differences in climatic conditions, soil characteristics, management practices and other location-specific factors can alter the expression of important economic traits such as cane yield and commercial cane sugar (Zhou and Gwata 2015). Due to strong significant genotype × environment interactions genotypes frequently exhibit inconsistent performance across testing locations. Such interactions can reduce the effectiveness of selection and make varietal recommendation difficult if genotype evaluation is based on limited environments (Elias et al., 2016).

Evaluation of advance breeding materials across multiple environments is therefore essential to identify genotypes with either broad adaptation or specific adaptation to particular production zones. In multi-location trials, a suitable analytical approach is required not only to quantify genotype × environment interaction but also to understand the response pattern of genotypes across environments. Among the available analytical methods, genotype main effect plus genotype × environment interaction (GGE) biplot analysis provides an effective graphical approach for studying genotype performance, environmental discrimination, and adaptation patterns (Mullualem, et al., 2024). This method enables visualization of genotype superiority in specific environments, identification of representative testing locations, and classification of environments into distinct mega-environments, thereby supporting more precise selection decisions (Yan and Tinker, 2006; Sadaiah et al., 2026; Thomas et al., 2026; Olanrewaju et al., 2021).

Sugarcane cultivation in India extends across diverse agro-ecological regions, and varietal evaluation is commonly undertaken in different zonal testing systems such as the East Coast Zone (ECZ), North Central and North Eastern Zone (NC&NEZ), North West Zone (NWZ) and Peninsular Zone (PZ). These zones differ markedly in temperature regime, rainfall distribution, soil conditions, and crop management practices, which may influence genotype performance. Therefore, understanding genotype responses across these production zones is essential for identifying high-performing and adaptable clones. In addition to plant crop productivity, ratooning ability is an important breeding objective in sugarcane because ratoon crops contribute substantially to total cane production and profitability (Garbiate et al., 2016). Ratoon cropping reduces cultivation cost and shortens crop

duration, thereby increasing economic returns to farmers (Srithawong et al., 2026). However, the performance of genotypes under ratoon conditions is often affected by environmental factors and their interaction with genotype, resulting in differential ratooning ability among cultivars (Xu et al., 2021). Therefore, identification of genotypes capable of maintaining higher cane yield, sugar yield and sucrose content in ratoon crop is essential for developing stable and economically viable varieties suitable for commercial cultivation.

Keeping this in view, the present analysis was undertaken to ascertain genotype × environment interaction among promising sugarcane genotypes for cane yield and commercial cane sugar across diverse testing environments representing major sugarcane-growing zones of India using GGE biplot analysis. The study also aimed to evaluate ratooning ability of the genotypes for cane yield, CCS yield, and sucrose content under different production zones.

Materials and Methods

Experiment location

The study was conducted under the All India Coordinated Research Project (AICRP) on Sugarcane across three major agro-climatic zones of India, namely the ECZ, NWZ, and PZ. Multi-environment trials were conducted at different research stations in each zone. Genotypes were evaluated across five locations in the ECZ, nine locations in the NWZ, and sixteen locations in the PZ, with details presented in Fig. 1.

Plant materials:

Plant materials and experimental design

Zone-specific sugarcane genotypes comprising improved sugarcane clones evolved at different sugarcane research stations in India (called test entries) and standards were evaluated across the three zones, with nine genotypes in ECZ, seven genotypes in NWZ and fourteen genotypes in PZ, as detailed in Table 1. The trials at all locations were laid out in a Randomized Complete Block Design (RCBD) with three replications. Each genotype was planted in plots consisting of eight rows of 6 m length each, following the recommended agronomic package of practices for the respective zones. The experimental material was evaluated over two plant crops and one ratoon crop. The first plant crop was established in February 2023, followed by the second plant crop in February 2024. After harvesting the first plant crop, ratoon crop management practices were undertaken to record ratoon performance.

Table 1
Zone-wise list of sugarcane genotypes evaluated under ECZ, NWZ, and PZ during 2023-24 to 2024-25 seasons

No.	Zone	Genotypes evaluated
01	ECZ	Co 11015, Co 09004, Co 14002, CoA 20321, CoA 20322, CoC 20336, CoA 92081*, CoC 01061* and CoA 11321*
02	NWZ	CoLk 19201, CoLk 19202, CoPb 19212, CoS 19231, CoJ 64* Co 0238* and Co 05009*
03	PZ	Co 18001, Co 18002, Co 18003, Co 18009, Co 18012, Co 18013, Co 18024, CoVC 18061, CoN 18071, CoN 18072, CoVSI 18121, Co 86032*, CoC 671* and Co 09004*
Genotypes marked with * represent standards		

Phenotypic evaluation:

Observations were recorded at harvest for economically important yield and quality traits, including sucrose percentage (SUC), number of millable canes (NMC), and single cane weight. Sucrose content was determined by polarimetry using a Micronal-Saccharomat polarimeter as previously described by (Carneiro et al., 2022). The genotypes evaluated in the NWZ and ECZ

belonged to the early-maturing group, and SUC, NMC, CY, and CCSY were measured at 10 months after planting. In contrast, the genotypes evaluated in the PZ were assessed at 12 months after planting. Derived traits were calculated as follows:

Cane Yield (t/ha) = NMC per hectare × Single Cane Weight

Commercial cane sugar yield (t/ha) = Cane Yield (t/ha) x CCS%/100

Data analysis:

Trait observations were recorded from five plants in the first plant crop, second plant crop, and ratoon crop, and the mean values were calculated for each genotype across replications. The replication pooled mean values were used for Genotype × environment interaction analysis. Genotype × environment interaction analysis was performed using the GGE biplot methodology. The analysis was carried out using the R package GGEBiplotGUI in R version 4.4.2 (RStudio Team, 2020). Ratoon ability (RA) was estimated as the percentage of the trait value in the ratoon crop relative to the corresponding trait value in the plant crop and expressed in percentage.

RA= (Ratoon yield / Plant crop yield) x 100

Results and Discussion

Ratooning ability of genotypes

Considerable variation was observed among genotypes within and across zones, indicating differential ratooning potential under diverse agro-climatic conditions (Table 2). In the PZ, ratooning ability for CCSY ranged from 76.51% to 90.73%, with higher values recorded in Co 18009, Co 86032, Co 18012, and CoC 671. Ratooning ability for cane yield varied from 76.15% to 87.30%, while that for sucrose (%) remained relatively stable (99.96–102.88%), indicating good maintenance of sucrose content under ratoon conditions. In the NWZ, CCSY ratoon ability ranged from 84.51% to 93.35%, and cane yield from 85.74% to 93.67%. Genotypes CoJ 64, Co 05009, Co 0238, and CoLk 19202 exhibited superior ratooning performance. Sucrose ratoon ability ranged from 97.20% to 100.75%, reflecting stable sucrose retention in the ratoon crop. In the ECZ, wider variability was observed, with CCSY ratoon ability ranging from 63.18% to 88.21% and cane yield from 66.14% to 98.75%. CoC 01061, CoA 20321, CoA 92081, and Co 14002 showed comparatively better ratooning ability. Ratoon ability for sucrose varied between 90.26% and 100.85%, with most genotypes maintaining values close to 100%.

Table 2
Ratoon ability (%) of sugarcane genotypes for cane yield, commercial cane sugar yield, and sucrose content across ECZ, NWZ, and PZ

PZ (in %)				NWZ (in %)				ECZ (in %)			
GENOTYPE	**CCSY RA**	**CY RA**	**SUC RA**	**GENOTYPE**	**CCSY RA**	**CY RA**	**SUC RA**	**Genotype**	**CCSY RA**	**CY RA**	**SUC RA**
Co 09004	80.41	77.65	102.88	CoLk 19201	86.02	87.73	98.17	Co 11015	67.86	71.67	94.27
Co 18001	76.51	76.15	100.89	CoLk 19202	88.40	90.59	97.20	Co 09004	76.78	75.22	100.85
Co 18002	81.25	80.49	99.96	CoPb 19212	84.51	85.74	99.47	Co 14002	85.20	93.78	91.32
Co 18003	84.52	82.49	100.59	CoS 19231	88.05	87.10	100.75	CoA 20321	86.46	90.96	95.93
Co 18009	90.73	87.30	102.23	CoJ 64	93.35	93.67	100.01	CoA 20322	83.96	93.44	90.26
Co 18012	88.28	86.51	102.86	Co 0238	88.56	91.07	97.46	CoC 20336	63.18	66.14	96.37
Co 18013	78.05	77.33	100.57	Co 05009	91.81	93.55	98.70	CoA 92081	86.31	89.67	95.35
Co 18024	78.41	78.09	100.42					CoC 01061	88.21	98.75	91.70
Co 86032	88.52	85.73	101.99					CoA 11321	80.13	90.42	100.22
CoC 671	86.12	84.67	101.52								
CoN 18071	85.42	85.18	101.56								
CoN 18072	85.39	83.71	102.06								
CoVC 18061	82.89	81.93	101.39								
CoVSI 18121	77.34	76.99	101.25								
Mean	83.13	81.73	101.44	Mean	88.67	89.92	98.82	Mean	79.79	85.56	95.14

In the NWZ, CCSY ratoon ability ranged from 84.51% to 93.35%, and cane yield from 85.74% to 93.67%. Genotypes CoJ 64, Co 05009, Co 0238, and CoLk 19202 exhibited superior ratooning performance. Sucrose ratoon ability ranged from 97.20% to 100.75%, reflecting stable sucrose retention in ratoon crop. In the ECZ, wider variability was observed, with CCSY ratoon ability ranging from 63.18% to 88.21% and cane yield from 66.14% to 98.75%. CoC 01061, CoA 20321, CoA 92081, and Co 14002 showed comparatively better ratooning ability. Ratoon ability for sucrose varied between 90.26% and 100.85%, with most genotypes maintaining values close to 100%.

GGE biplot analysis of commercial cane sugar yield, cane yield and sucrose content

The GGE biplot adequately captured genotype performance and G×E interaction for CCSY, cane yield, and sucrose content across the three zones (Figs. 2 and 3). For CCSY, PC1 and PC2 explained 65.28 and 20.96% of the variation in ECZ (86.24% cumulative), 48.61 and 29.54% in NWZ (78.15%), and 45.89 and 14.26% in PZ (60.15%), respectively. For cane yield, the corresponding values were 60.53 and 28.94% in ECZ (89.47%), 50.12 and 31.40% in NWZ (81.52%), and 44.08 and 15.61% in PZ (59.69%). For sucrose content, PC1 and PC2 explained 78.68 and 12.08% in ECZ (90.76%), 46.80 and 24.25% in NWZ (71.05%), and 53.48 and 15.83% in PZ (69.31%), respectively. The relatively high cumulative variation explained by the first two principal

components across the zones indicated that the GGE biplot provided an adequate representation of genotype performance and G×E interaction for the three traits.

Mean performance and stability of genotypes

The mean versus stability view of the GGE biplot, based on the average environment coordination (AEC) method, was used to simultaneously assess genotype mean performance and stability (Fig. 2). Genotypes projecting farther in the direction of the AEC abscissa showed higher mean performance, whereas shorter perpendicular projections indicated greater stability. Thus, genotypes with high mean performance and minimal deviation from the AEC abscissa were considered desirable. For CCSY in ECZ, Co 09004 (14.60 t/ha) exhibited the highest mean performance, followed by CoA 20322 (14.18 t/ha) and CoA 20321 (13.75 t/ha), whereas Co 09004 and CoA 11321 demonstrated greater stability across environments. Considering both mean performance and stability, Co 09004 was identified as the most desirable genotype for ECZ. In NWZ, CoS 19231 (11.68 t/ha) and CoPb 19212 (10.57 t/ha) exhibited both high mean performance and greater stability and were therefore considered desirable genotypes. In PZ, Co 18003 (16.64 t/ha), followed by CoVC 18061 (16.26 t/ha) and Co 86032 (16.17 t/ha), exhibited superior mean performance, whereas CoC 671, Co 18009, and Co 18012 showed greater stability.

For cane yield, CoA 20322 (116.90 t/ha), followed by CoA 20321(115.57 t/ha) and Co 09004 (111.30 t/ha), exhibited higher mean performance in ECZ, while CoA 20321 and CoA 11321 showed greater stability. CoA 20321, which was positioned close to the direction of the AEC abscissa with the least perpendicular distance, was identified as the most desirable genotype. In NWZ, CoS 19231 (91.07 t/ha), followed by CoPb 19212 (87.93 t/ha) and Co 0238 (85.85 t/ha), exhibited higher mean performance, while CoS 19231 showed the highest stability across environments and was therefore identified as the most desirable genotype. In PZ, CoVC 18061 (120.71 t/ha), followed by Co 86032 (117.69 t/ha) and Co 18003 (117.43 t/ha), exhibited higher mean performance, whereas Co 18009, Co 18013, and CoC 671 showed greater stability.

For sucrose content, Co 11015 (18.71%) and Co 09004 (18.70%) exhibited higher mean performance in ECZ, while CoC 01061, followed by Co 11015, showed greater stability across environments. Considering both mean performance and stability, Co 11015 emerged as the most desirable genotype for this zone. In NWZ, CoS 19231 (18.41%) and CoLk 19201 (18.25%) were identified as high mean-performing genotypes, whereas CoPb 19212 and Co 05009 exhibited greater stability. In PZ, CoC 671 (20.52%) and Co 09004 (20.28%) recorded higher mean performance, while Co 18009 and CoC 671 exhibited greater stability. Considering both performance and stability, CoC 671 was identified as the most desirable genotype. The high-yielding but relatively less stable performance of some genotypes, such as CoVC 18061, Co 18003 in PZ, indicates that high mean performance alone may not ensure consistent performance across locations. Therefore, further examination of crossover G×E interaction through mega-environment analysis is important for identifying genotypes with specific adaptation.

“Which-won-where” pattern and mega-environment delineation

The polygon view of the GGE biplot revealed distinct mega-environments and identified winning genotypes for CCSY across the three zones (Fig. 3). In ECZ, the five environments formed two mega-environments. Nayagarh, Vuyyuru, and Nellikuppam constituted the first group, with Co 09004 as the vertex genotype, whereas Anakapalle and Cuddalore formed the second group, with CoA 20322 as the winning genotype (Fig. 3A). In NWZ, nine environments were grouped into three mega-environments: Sriganganagar, Kota, Kapurthala, Shahjahanpur, Muzaffarnagar, Uchani, and Pantnagar were dominated by CoS 19231; Faridkot was represented by Co 05009; and Lucknow was dominated by CoLk 19202 (Fig. 3B). In PZ, sixteen environments were grouped into three mega-environments, with CoVC 18061 superior in Sankeshwar, Mandya, Coimbatore, Padegaon, Belagavi, and Thiruvalla; Co 18003 performing best in Pune, Sameerwadi, Rudrur, Pugalur, Tharsa, Basmathnagar, Kawardha, and Kolhapur; and CoVSI 18121 winning in Powarkheda and Navsari (Fig. 3C).

For cane yield, ECZ formed two mega-environments, where CoA 20322 performed best in Anakapalle, Cuddalore, Nayagarh, and Vuyyuru, while CoA 20321 was superior at Nellikuppam (Fig. 3D). In NWZ, four mega-environments were identified: Sriganganagar, Kota, and Kapurthala with CoPb 19212 as the winner; Muzaffarnagar, Shahjahanpur, and Uchani with CoS 19231; Lucknow with CoLk 19202; and Pantnagar and Faridkot with Co 05009 as the best performer (Fig. 3E). In PZ, three mega-environments were observed, where CoVC 18061 dominated Sankeshwar, Mandya, Coimbatore, Padegaon, Navsari, Pune, and

Thiruvalla; Co 18003 was superior in Belagavi, Sameerwadi, Rudrur, Tharsa, Basmathnagar, Kawardha, and Kolhapur; and CoVSI 18121 performed best in Powarkheda and Pugalur (Fig. 3F).

For sucrose content, ECZ formed two mega-environments, with Vuyyuru, Anakapalle, and Cuddalore dominated by Co 09004, while Nayagarh and Nellikuppam were led by Co 11015 (Fig. 3G). In NWZ, four mega-environments were identified: Kota, Shahjahanpur, Muzaffarnagar, Uchani, and Lucknow with CoS 19231 as the winner; Sriganganagar and Faridkot with CoLk 19201; Pantnagar with CoPb 19212; and Kapurthala with CoJ 64 (Fig. 3H). In PZ, four mega-environments were formed, with Mandya, Coimbatore, Padegaon, Belagavi, Pune, Navsari, and Tharsa dominated by CoC 671; Sankeshwar, Sameerwadi, and Rudrur by Co 18003; Powarkheda, Pugalur, Kawardha, and Kolhapur by Co 86032; and Thiruvalla by Co 18024 (Fig. 3I).

Discriminativeness and representativeness of test environments

The discriminativeness versus representativeness view of the GGE biplot was used to evaluate the suitability of test environments for genotype assessment (Fig. 4). Discriminating ability is indicated by the length of the environmental vector from the biplot origin, with longer vectors indicating greater ability to differentiate among genotypes. Representativeness is assessed by the angle between the environmental vector and the AEC abscissa, where a smaller acute angle indicates greater representativeness. For CCSY in ECZ, Nellikuppam and Anakapalle exhibited relatively longer vectors, indicating greater discriminating ability, whereas Nayagarh and Vuyyuru were positioned closer to the AEC abscissa, indicating greater representativeness. Vuyyuru, with an appreciable vector length and close proximity to the AEC abscissa, combined both discriminating ability and representativeness and was therefore considered an ideal testing location. In NWZ, Sriganganagar, Faridkot, Pantnagar, and Muzaffarnagar exhibited strong discriminating ability. Among these, Muzaffarnagar was located closer to the AEC with a relatively long vector, suggesting that it was the most suitable environment for genotype evaluation. In PZ, Tharsa exhibited the longest vector, indicating high discriminating ability, whereas Pune and Sameerwadi were positioned closer to the AEC with moderate vector lengths.

A similar pattern was observed for cane yield. In ECZ, Nellikuppam and Anakapalle were highly discriminating, whereas Nayagarh and Vuyyuru were more representative. In NWZ, Sriganganagar, Faridkot, Pantnagar, Muzaffarnagar, and Lucknow exhibited greater discriminating ability, with Muzaffarnagar showing the best combination of discriminating ability and representativeness. In PZ, Tharsa exhibited the highest discriminating ability, while Belagavi and Kawardha were relatively representative test environments.

For sucrose content, Nellikuppam, Vuyyuru, Anakapalle, and Cuddalore exhibited strong discriminating ability in ECZ. Among these, Vuyyuru was located closer to the AEC with a comparatively longer vector, indicating that it was both highly discriminating and representative. In NWZ, Kota, Sriganganagar, Faridkot, and Shahjahanpur exhibited strong discriminating ability, while Uchani appeared to be the most representative environment. In PZ, Powarkheda exhibited strong discriminating ability, whereas Tharsa and Belagavi, being located close to the AEC with moderate vector lengths, exhibited both discriminating ability and representativeness.

Discussion

Under changing climatic conditions and rising cultivation costs, the identification of genotypes capable of consistently maintaining stable cane yield and CCSY across plant and ratoon crops is essential for enhancing farm productivity and sustainable sugarcane cultivation (Jaganur, 2013; Yadawad et al., 2022). Sustaining productivity in ratoon crops has become increasingly important in modern sugarcane cultivation because ratooning determines the long-term profitability and resource-use efficiency of the crop production system (Singh et al., 2015; Sharma et al., 2026). In the present study, ratoon ability differed considerably among the sugarcane-growing zones, with NWZ recording the highest ratoon ability for cane yield (89.92) followed by ECZ (85.56), whereas genotypes evaluated in PZ exhibited comparatively lower ratoon performance for CY (81.73). The decrease in yield under ratoon was also reported by Mehareb et al., 2015 and Resende et al., 2025. The comparatively lower ratoon efficiency observed in PZ genotypes, particularly for cane yield, suggests the need for greater breeding emphasis on ratoon yield stability in peninsular zone. Sucrose content remained relatively stable under ratoon conditions in all the zones ranging from 95.14% (ECZ) to 101.44% (PZ), indicating lesser environmental influence on juice quality traits compared with yield

traits. Previous studies by Dlamini et al. (2024) and Mehareb and Galal (2017) also confirmed that sucrose content remains relatively stable. The ratoon ability of CCSY was relatively lower in ECZ than in PZ and NWZ, which could be attributed to the lower cane yield, sucrose content besides nature of genotypes and climatic factors.

Commercial cane sugar yield is the ultimate dependent traits looked by end user or sugar factories. The present study revealed substantial genotype × environment interaction for CCSY, cane yield, and sucrose content across the major sugarcane-growing zones of India, emphasizing the importance of multi-environment evaluation for identifying stable and high-performing genotypes (Dlamini et al., 2024; Durai et al., 2025). In ECZ, Co 09004 was identified as the best genotype for CCSY. This has performed well across all environments in the zone. However, specific genotype like Co 11015 for Nellikuppam and CoA 20322 for Cuddalore may be promoted as they have shown specific adaptability to the respective location. The clone CoA 20322 exhibited high cane yield, while CoA 20321 showed high stability for cane yield. For sucrose content, Co 11015 demonstrated superior performance along with high stability. In NWZ, CoS 19231 consistently exhibited stable and high cane yield, sugar yield and sucrose content across all locations in the zone Therefore, this genotype may be given emphasis for widespread cultivation in the zone, subject to release and notification. In the zone Lucknow and Faridkot acted as most discriminating environment. In PZ, Co 18003 emerged as the high mean for CCSY and cane yield, whereas CoC 671 exhibited high and stable sucrose content across environments. The mean vs. stability (AEC) view of the GGE biplot simultaneously evaluates the average performance and stability of genotypes across test environments and facilitates the identification of genotypes suitable for general cultivation within a zone (Menzir et al., 2025; Daemo et al., 2024). However, some high-yielding genotypes, such as Co 18003, exhibited lower stability, indicating that their performance may not be consistently reproduced across different locations within the zone. Therefore, to account for crossover genotype × environment interaction and identify genotypes with specific adaptation, the test environments were grouped into mega-environments using the which-won-where analysis. This approach enabled the identification of the winning genotype for each mega-environment, thereby facilitating location-specific genotype recommendations.

The Which-Won-Where analysis revealed the existence of broad and specifically adapted genotypes across the locations of three zones (Yan et al., 2023; Eskezia et al., 2026). For CCSY, CoS 19231 in NWZ, CoVC 18061 and Co 18003 in PZ, and Co 09004 in ECZ exhibited broad adaptation across multiple locations, whereas Co 05009 (Faridkot), CoLk 19202 (Lucknow), and CoVSI 18121 (Powarkheda and Navsari) showed location-specific adaptation. Similar trends were observed for cane yield, where CoA 20322 in ECZ, CoS 19231 in NWZ, and CoVC 18061 and Co 18003 in PZ demonstrated broad adaptation, while CoA 20321 (Nellikuppam), Co 19202 (Lucknow), and Co 05009 (Pantnagar and Faridkot) showed specific adaptation. For sucrose content, CoS 19231 in NWZ, CoC 671 in PZ, and Co 09004 in ECZ exhibited wider adaptation, whereas CoPb 19212 (Pantnagar), CoJ 64 (Kapurthala), and Co 18024 (Thiruvalla) performed better under specific environments. These findings demonstrate the usefulness of mega-environment analysis in identifying both widely adapted and location-specific genotypes for targeted varietal deployment (Kachapur et al., 2023; Fonseca et al., 2022).

The discriminativeness vs. representativeness view of the GGE biplot is used to identify ideal test environments for genotype evaluation. Highly discriminating environments, such as Tharsa, Nellikuppam, and Sriganganagar, are useful for effectively distinguishing superior and inferior genotypes and can therefore be prioritized for genotype evaluation in breeding programmes. In contrast, representative environments, such as Muzaffarnagar, Vuyyuru, and Uchani, closely reflect the average conditions of their respective target production regions and are valuable for identifying genotypes with broad adaptation. Locations combining both high discriminating ability and representativeness, particularly Muzaffarnagar and Vuyyuru, are considered ideal test environments because they effectively differentiate genotypes while accurately representing the target production region. The identification of such environments is valuable for future multilocation testing programmes, as representative and discriminating test locations improve selection efficiency and facilitate the identification and recommendation of stable, widely adapted genotypes (Aboye and Edo, 2024; Bilate Daemo et al., 2023).

Conclusion

The GGE biplot analysis effectively explained genotype performance, environmental discrimination, and adaptation patterns, enabling clear identification of superior genotypes across the ECZ, NWZ and PZ. The analysis revealed the presence of distinct

mega-environments, indicating differential genotype responses under varying production conditions and emphasizing the need for location specific recommendation. Based on mean performance and adaptability, genotypes CoA 20321 and Co 09004 were identified as promising entries in ECZ, CoS 19231 emerged as a superior and broadly adapted genotype in NWZ, while Co 18003 showed desirable performance and adaptability in PZ for cane yield and commercial cane sugar. For sucrose content, Co 11015 in ECZ, CoS 19231 in NWZ, and CoC 671 in PZ were identified as stable and high-performing genotypes with desirable adaptation across environments. Among test locations, Vuyyuru in ECZ, Muzaffarnagar and Shahjahanpur in NWZ, and Pune and Sameerwadi in PZ were identified as informative and representative environments for genotype evaluation. The superior genotypes and ideal testing locations identified in the present study can be effectively utilized in varietal advancement, region-specific cultivar recommendation, and future breeding programmes aimed at improving productivity and sugar recovery in Indian sugarcane cultivation.

Declarations

Author contributions

SK and KKM conceptualized the study and edited the manuscript. SK, KKM, NKKR and IN conducted the investigation and prepared the original draft of the manuscript. SK, NKKR and IN generated the phenotypic data. KKM and NKKR performed the statistical analyses. All authors contributed to the article and approved the submitted version of the manuscript.

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Conflict of interest

The authors declare that there is no conflict of interest regarding the publication of this manuscript.

Data Availability statement

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

Ethics and consent to participate

Plant materials was used in accordance with applicable national guidelines for agricultural research

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Figures

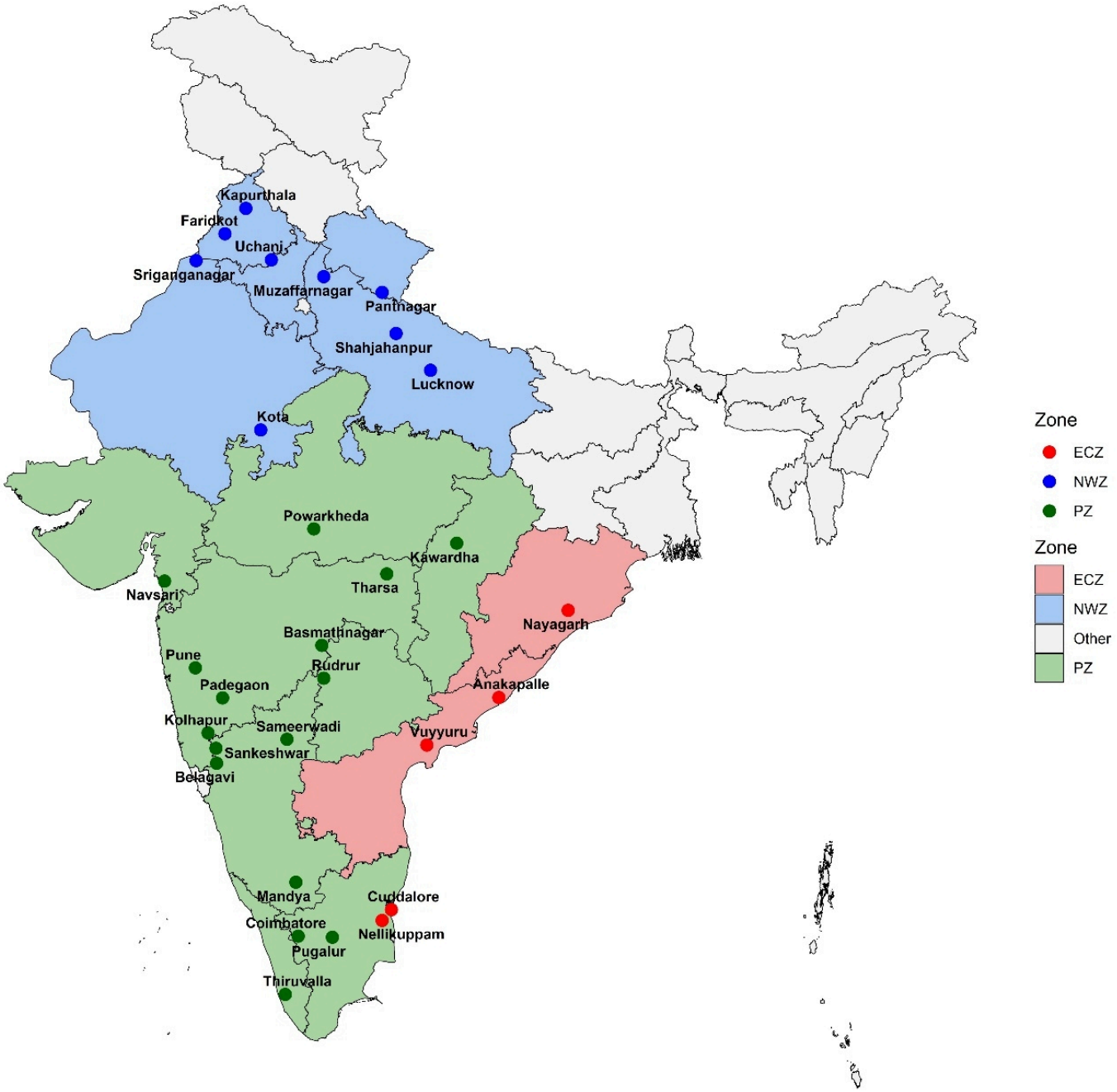


Figure 1

Geographical distribution of test locations across the East Coast Zone (ECZ), North West Zone (NWZ), and Peninsular Zone (PZ) for multi-location evaluation of sugarcane genotypes in India.

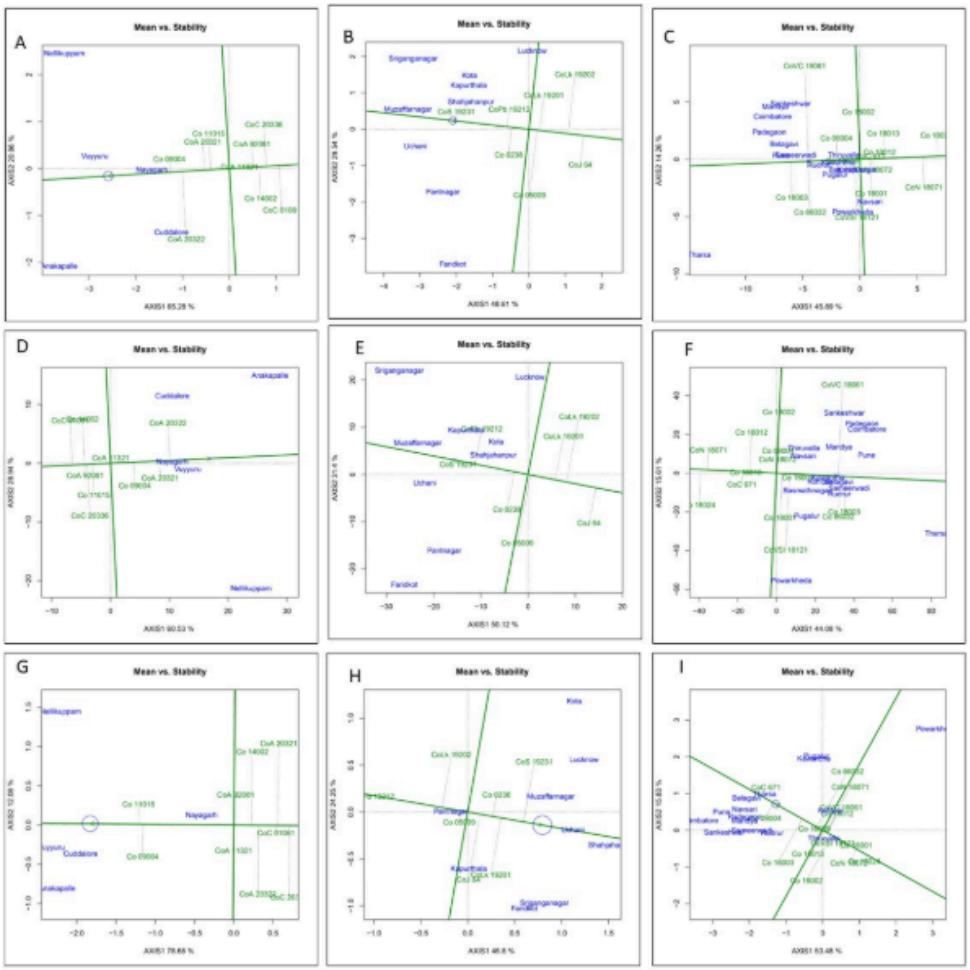


Figure 2

Mean performance and stability assessment of genotypes for CCSY, CY, and SUC in ECZ, NWZ and PZ. Panels A, B, and C represent CCSY in the ECZ, NWZ and PZ, respectively; panels D, E, and F represent CY in ECZ, NWZ, and PZ, respectively; and panels G, H, and I represent SUC in ECZ, NWZ, and PZ, respectively.

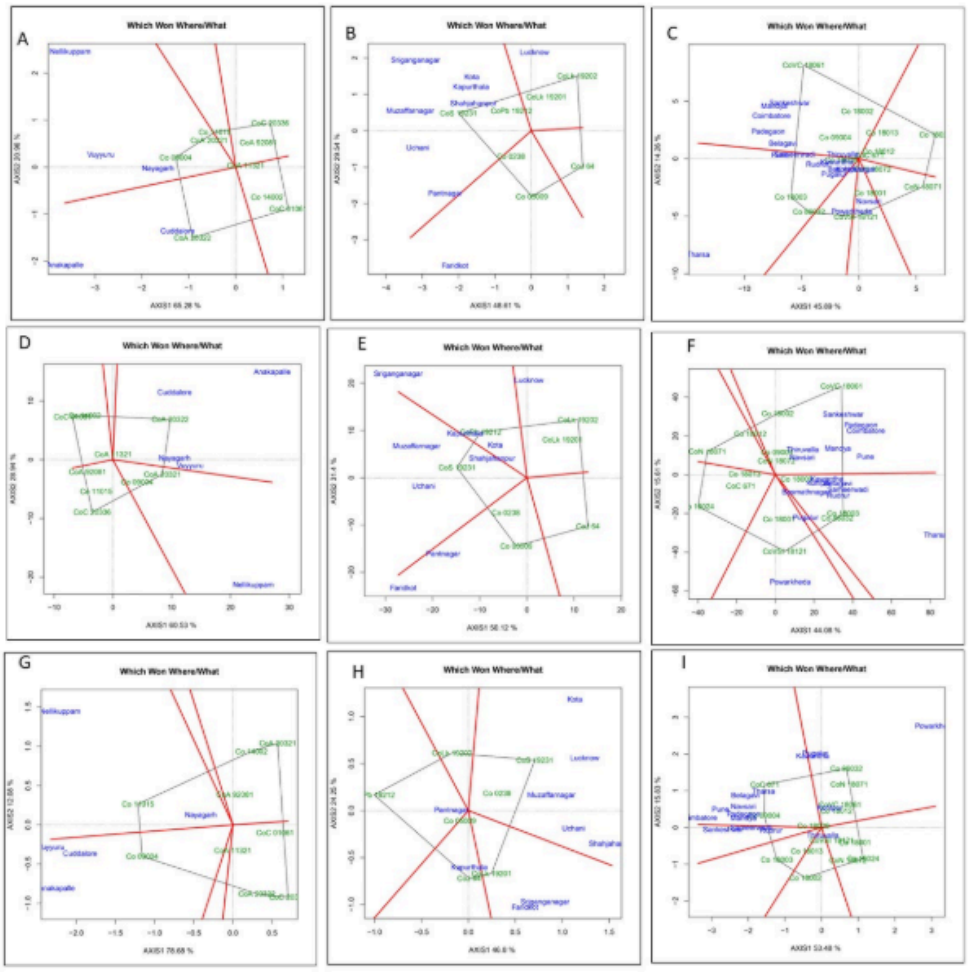


Figure 3

Which-won-where patterns and mega-environment delineation for CCSY, CY, and SUC in ECZ, NWZ and PZ. Panels A, B, and C represent CCSY in the ECZ, NWZ and PZ, respectively; panels D, E, and F represent CY in ECZ, NWZ, and PZ, respectively; and panels G, H, and I represent SUC in ECZ, NWZ, and PZ, respectively.

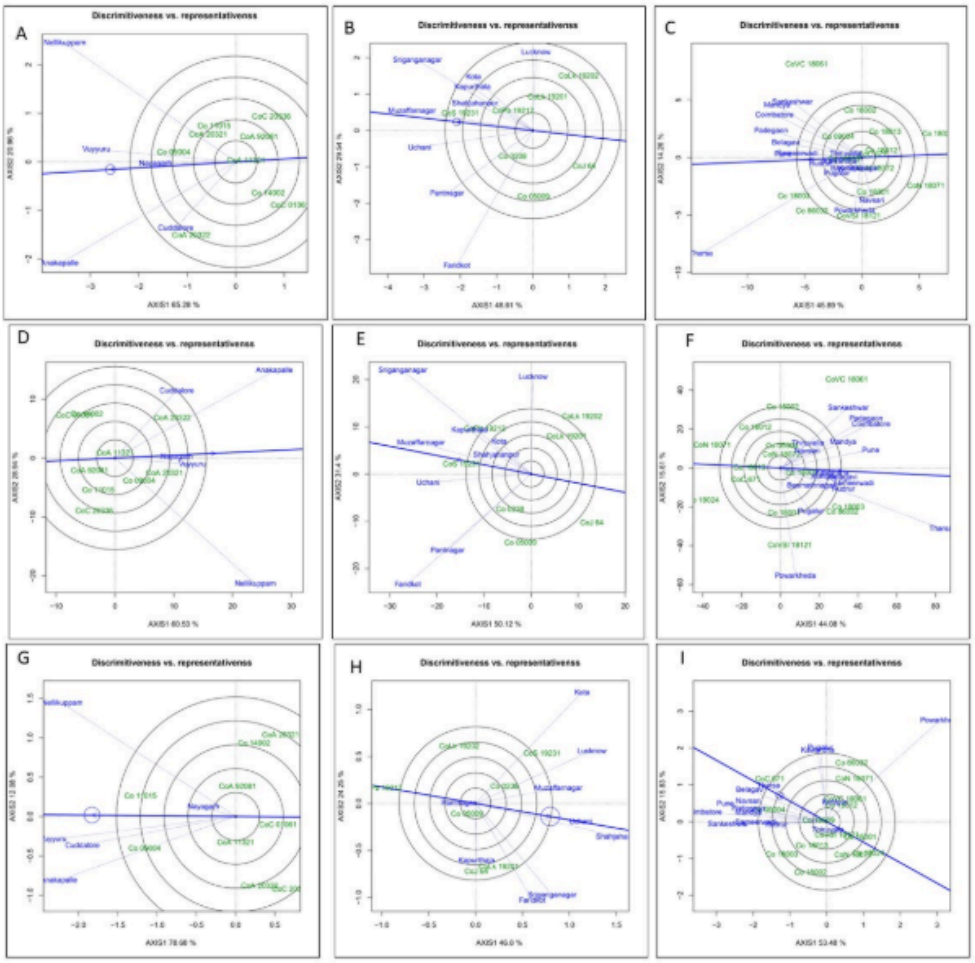


Figure 4

Discriminativeness and representativeness of test locations revealed through GGE biplot analysis. Panels A, B, and C represent CCSY in the ECZ, NWZ and PZ, respectively; panels D, E, and F represent CY in ECZ, NWZ, and PZ, respectively; and panels G, H, and I represent SUC in ECZ, NWZ, and PZ, respectively.