Integrated stability analysis of compact cotton genotypes for yield and plant architecture under rainfed conditions using AMMI, GGE biplot, WAAS, BLUP, and MTSI

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Research Article

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Integrated stability analysis of compact cotton genotypes for yield and plant architecture under rainfed conditions using AMMI, GGE biplot, WAAS, BLUP, and MTSI

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Abstract

Background The development of high-yielding stable cotton genotypes with compact plant architecture is critical for improving productivity and sustainability in rainfed ecosystems of India. This study evaluated 22 compact to semi-compact genotypes, including two check varieties (ARBC1651, CSH3075), across three distinct environments in Tamil Nadu during Kharif 2024.

Results Genotypic performance was analyzed using a suite of stability assessment tools including AMMI, GGE biplot, WAAS, BLUP, and MTSI. Joint ANOVA revealed highly significant ($p \leq 0.001$) genotype, environment, and GEI effects for most traits, with genetic variance contributing up to 72% of phenotypic variation in seed cotton yield (SCY). The first two IPCs of AMMI and GGE biplots explained >75% of GEI variation and consistently identified Suraksha, Subiksha, and Suraj as stable, high-yielding genotypes. Whereas RS2818, CO17, and Nano represented compact types with plant height <90 cm, reduced internode length (~5.7 cm), and sympodial branching (~18.8 cm), aligning with ideotypes suitable for high-density planting and mechanized harvesting. BLUP analysis showed high heritability for SCY (h^2mg = 0.91), with strong genotypic variance (71.99%) and high selection accuracy (0.95). It confirmed AMMI and GGE biplots results, identifying Suraksha, Subiksha, and Suraj as superior yielders, while CO17, Nano, and TVH002 promising compact types with high predictive accuracy. WAAS/WAASBY indices confirmed Suraksha and Subiksha as the most stable and productive genotypes, whereas MTSI ranked Suraj (MTSI = 2.16), Subiksha, F2383, and RS2818 as top multi-trait stable performers. Compact plant traits were found to be negatively correlated with excessive vegetative growth but positively associated with yield stability under rainfed conditions. Among the test environments, Veppanthattai (E3) effectively discriminated genotypes, while Coimbatore (E1) and Srivilliputhur (E2) were representative for selecting compact and stable high-yielding types.

Conclusion This integrated stability models enabled precise identification of compact, high-yielding genotypes, supporting breeding of rainfed-adapted and machine-harvestable genotypes.

Keywords: Compact plant architecture, AMMI, GGE biplot, WAAS, BLUP, MTSI, yield stability, rainfed cotton

Introduction

Cotton is one of the most important fiber crops in India, and the country is among the largest producers and users of cotton in the world. Nearly 82% of the cotton area in the country is cultivated under rainfed conditions, primarily in central and southern states (Madhu et al., 2023), where farmers face challenges of erratic rainfall, fluctuating yields, and high production costs. Harvesting is usually done by hand, but this practice is becoming less sustainable because of rising labor costs, shortage of workers during the picking season, and inefficiencies in completing harvests on time (Venugopalan et al., 2011). Manual picking increases production expenses, delays harvesting, and often reduces both yield and lint quality. Given that over 95% of Indian cotton is composed of long-duration Bt hybrids, which are typically tall and possess monopodial branching with extended boll-opening duration, which requires multiple hand pickings (Sivakumar et al., 2024). These traits require several rounds of hand-picking and make the crop unsuitable for machine harvesting; it suggests that urgent need for architectural and agronomic improvements.

In contrast, compact cotton plants with shorter height, reduced internodes, absence of monopodia, shorter fruiting branches, and uniform boll maturity are more suitable for modern farming. Such plants allow high-density planting, better use of light, improved boll retention, easier crop management, and mechanical harvesting (Venugopalan et al., 2011; Yan et al., 2019; Gunasekaran et al., 2020). For machine harvesting, ideal plant height is less than 120 cm for spindle pickers and less than 80 cm for stripper pickers (Williford et al., 1994; Van der Sluijs 2015; Madhu et al., 2023). Plant types with the first fruiting branch appearing higher on the stem and a uniform canopy also improve harvest efficiency (Van der Sluijs, 2015). However, while plant architecture is important, high seed cotton yield is the main target in breeding. Both yield and plant architecture are strongly affected by the interaction between genotype and environment (GEI), which makes it necessary to test genotypes in multi-environment trials (METs) to assess their performance, adaptability, and stability (Sheeba et al., 2025; Shahzad et al., 2019; Sivakumar et al., 2024).

Past studies have shown that the environment plays a major role in yield variation and contributes more than 80% of the total variance (Meredith et al., 2012). Still, GEI can also affect specific traits. For example, a study with 82 germplasm lines showed that GEI explained 46% of the variation in boll weight (Campbell et al., 2012). Evidence suggests that for traits like branch height and number, the effects of genotype and GEI are stronger than the environment (Madhu et al., 2023, Sivakumar et al., 2024). Since yield and architecture are complex traits controlled by many genes and affected by environmental conditions. GEI reduces the relationship between the genetic and observed values of traits (Yan and Tinker, 2006), making stability analysis essential to find genotypes that perform well across locations and years (Vaezi et al., 2019).

Several statistical models are used to study GEI and stability. The Additive Main Effects and Multiplicative Interaction (AMMI) model is widely applied in many crops (Gauch, 1988). It combines variance analysis with principal component analysis (PCA) to explain GEI and create biplots to show genotype performance. Another improvement is the WAAS index, which considers all significant components and gives a more detailed picture of genotype stability (Olivoto et al., 2019a). Along with AMMI, the genotype plus genotype-by-environment interaction (GGE) biplot is also popular. It helps compare test locations, identify mega-environments, and select winning genotypes (Yan, 2001; Yan et al., 2007; Yan, 2024). Apart from AMMI, the Best Linear Unbiased Prediction (BLUP) method is also used in stability analysis, as it provides accurate estimates of genetic values (Smith et al., 2005). Unlike AMMI, which treat genotypes as random effect, BLUP uses linear mixed models to separate effects (Piepho 1994, Gauch 2013). To combine the strengths of both methods, weighted average of absolute scores (WAAS) and WAAS from BLUP and yield (WAASBY) indices were developed, which link stability and mean yield in genotype evaluation (Olivoto et al., 2019a; Smith et al., 2005). Selecting superior genotypes for cotton cannot be based on yield alone, as yield depends on several growth and physiological traits. Improving compact plant architecture together with yield is important for developing varieties suitable for modern farming. However, selection of multiple traits at time is difficult because of negative correlations among them (Elsamman et al., 2024). To tackle this, the Multi-Trait Stability Index (MTSI) was introduced (Olivoto et al., 2019b). MTSI uses factor analysis to measure the distance of each genotype from an "ideal" genotype and allows simultaneous selection of multiple traits based on performance and stability.

In this background, the present study aims to evaluate cotton genotypes that combine compact architecture with high yield using different stability assessment tools such as AMMI, GGE,WAAS, BLUP and MTSI, tested across three environments. This integrated approach can help identify promising cotton lines with desirable plant type and stable yield, improving the profitability and sustainability of cotton cultivation in rainfed areas of India.

Materials and Methods

Plant material selection

A total of twenty-two elite compact to semi-compact cotton genotypes were sourced from ICAR-CICR Regional Station and the Department of Cotton, TNAU, Coimbatore. Two widely cultivated check varieties, ARBC1651 and CSH3075, known for their high yield and zero monopodial compact plant architecture suitable for rainfed regions, were included for comparison is given in Table 1.

Experimental sites and setup

Field trials were conducted during the Kharif season of 2024 across three distinct agro-climatic zones in Tamil Nadu, India. The first site (E1) was at Coimbatore characterized by red clay and laterite soils under semi-arid climate. The second site (E2) at Veppanthattai featured very deep, calcareous clay soils with moderate drainage and low hydraulic conductivity. The third site (E3) was Srivilliputhur, comprised of vertisols with clay loam texture over canker nodules. These locations represent the Western, Cauvery Delta, and Southern agro-climatic zones of Tamil Nadu, respectively. Fig. 1 shows the geographical locations of experimental sites and their agroclimatic characteristics. A randomized complete block design (RCBD) with three replications was used for the experiments. Each plot measured 4 meters in length, consisting of six rows per genotype, with row and plant spacing set at 90 cm and 30 cm, respectively.

Crop management practices

During August 2024, three fuzzy cotton seeds were sown per hill at a depth of 3-5 cm. Three weeks of post-sowing thinning was performed to retain a single healthy plant per hill. Fertilizer was applied at a recommended rate of 16:16:8 kg/ha (NPK) as a basal dose during sowing, followed by a top dressing of 16:0:8 kg/ha at 40-45 days after sowing. Pendimethalin 30% EC (3.3 l/ha) was applied as a pre-emergence herbicide three days after sowing, and manual weeding was carried out twice during the crop growth period. Pest and disease management followed standard agronomic practices. Irrigation was supplied artificially at critical stages to avoid drought stress, ensuring uniform growth and reliable data.

Data collection and trait measurement

At harvest, five plants were randomly selected from the inner rows of each plot in every replication. The following traits were recorded: plant height (PH, cm), first sympodial branch height from ground (FSB, cm), main stem internode length (MIL, cm), and sympodial branch length (SBL, cm). Plant height was measured from the cotyledonary node to shoot apex using a tape. The methods described by (Madhu et al., 2023) were followed for MIL and SBL measurements. The number of monopodial (NMB) and sympodial branches (NSB) were counted per plant. Boll count per plant (BP) was recorded, and five randomly selected bolls per plant were weighed to determine average boll weight (BW, g). Seed cotton yield (SCY, g per plant) was calculated by hand-picking bolls during the first fortnight of December.

Statistical analysis approach

All analysis were conducted using R Studio v.4.0 (R-Studio Team, 2020) and the “metan” package (Olivoto and Lúcio, 2020). Bartlett’s test (Bartlett, 1937) used to verify homogeneity of error variances across locations before performing joint ANOVA. The joint RCBD ANOVA and AMMI analysis (Bradu and Gabriel, 1978) were used to to evaluate the additive mean effects of genotypes and locations. PCA was then used to identify non-additive interaction effects within the experimental setup (Zobel et al., 1988). AMMI biplots were constructed to illustrate the relationship between genotype means and the first two principal components (PC1 and PC2), following Gauch (1988). GGE biplots (Yan, 2024) were employed to visualize genotype performance and stability. The environment-centered data and symmetrical singular value partitioning (SVP) with row metric preservation method enabled consistent comparison across environments (Yan, 2002; Yan, 2024). The WAAS method involved singular value decomposition (SVD) of the GEI matrix from AMMI ANOVA, providing stability measures based on the first IPC (Olivoto et al., 2019a). BLUP analysis was applied using a linear mixed model with genotypes as random effects to predict genotypic performance across environments (Olivoto et al., 2019a). Variance components were estimated through restricted maximum likelihood, with the likelihood ratio test used for random effects significance. WAAS values derived from BLUP (WAASB) were calculated by applying SVD to the BLUP-based GEI matrix. The WAASBY index (Olivoto et al., 2019a) integrated yield and stability for comprehensive genotype selection. The MTSI was calculated from the Euclidean distance between each genotype and an ideotype, based on on scores obtained through factor analysis with varimax rotation (Olivoto et al., 2019b). MTSI was estimated to use all yield and plant architecture traits, whereas boll count per plant was excluded as it showed no significant correlation with yield components.

Results and discussion

Additive main effects and multiplicative interaction (AMMI)

Considering the homogeneity of error variance across locations, a joint ANOVA based on RCBD and AMMI's additive model was performed for plant architecture, yield, and yield-related traits are given in Table 2. The environment (E) had a highly significant effect on all traits, indicating substantial variation between test locations. The genotype (G) effect was also highly significant ($p \leq 0.001$) for all traits, except for BP, reflecting strong genetic differences among the tested genotypes due to their diverse backgrounds and performance under contrasting environments (Ali et al., 2018; Madhu et al., 2023). In addition, the GEI was highly significant ($p \leq 0.001$) for all traits, causing differential genotype ranking across environments and revealing the complex nature of genotype adaptability (Sheeba, et al., 2025). These findings agree with earlier cotton multi-location studies (Orawu et al., 2017; Shahzad et al., 2019; Sivakumar et al., 2024).

The evaluation of genotypes across three environments (E1, E2, and E3) for nine traits showed notable differences in trait distribution and variability, as illustrated the violin plots in Fig. 2 and mean values are presented in Supplementary Table 1. Plant height (PH) ranged from 87.99 cm (E2) to 92.29 cm (E3), with E2 showing a narrower distribution and lower median, indicating conditions favoring shorter plant growth. The number of monopodial branches (NMB) was lowest in E2 (0.61) and highest in E3 (0.79), while the first sympodial branch height (FSB) varied from 21.37 cm (E2) to 22.04 cm (E3). Sympodial branch number (NSB) ranged from 20.13 (E2) to 21.11 (E3), and sympodial branch length (SBL) ranged from 18.27 cm (E2) to 19.67 cm (E3). Mainstem internode length (MIL) was lowest in E2 (5.51 cm) and highest in E3 (5.90 cm). The number of bolls per plant (BP) remained stable across environments (21.47 to 21.89), while boll weight (BW) was lowest in E2 (4.88 g) and highest in E1 (5.03 g). Seed cotton yield (SCY) was highest in E3 (116.30 g) and lowest in E1 (114.90 g). The violin plots revealed that E3 consistently exhibited broader trait distributions and higher medians, indicating a more favorable environment for trait expression and higher yield, whereas E1 and E2 provided favorable conditions for developing a compact plant type with narrower distributions and lower trait values. These results align with previous multi-environment cotton studies reporting the significant influence of environment on yield and architectural traits (Gul et al., 2016; Ali et al., 2018; Sivakumar et al., 2024).

The partitioning of phenotypic variance among the studied traits revealed differential contributions from genotype, environment, and GEI is depicted in Fig. 3. Genetic variance contributed the highest proportion for most traits, ranging from 42.22% (SBL) to 78.98% (SCY), with SCY showing the strongest genetic control, followed by PH, and FSB. This indicates that these traits are largely heritable and can be efficiently improved through selection. In contrast, NSB was predominantly influenced by the environment, accounting for 83.73% of the total variance, making it the most environmentally driven trait. BP showed the strongest GEI effect (53.07%), while other traits also exhibited substantial GEI influence, indicating their sensitivity to environmental changes. Except for NSB, the genetic-to-environmental variance ratio was higher across traits, suggesting more reliable genotype selection under diverse conditions (Ali et al., 2018). Overall, most traits were mainly controlled by genetics, with moderate to high GEI effects, aiding the selection of suitable genotypes for specific environments (Madhu et al., 2023).Whereas, NSB was almost entirely shaped by environmental variation, and BP was largely driven by GEI, both contributing to yield variation across environments (Sivakumar et al., 2024). These findings differ from earlier studies (Shahzad et al., 2019; Ali et al., 2018; Gul et al., 2016; Farias et al., 2016), which reported environmental dominance in controlling SCY, BW, and BP, while (Ali et al., 2017) found genotype as the major source of yield variation, reflecting significant genetic diversity.

Investigating GEI is essential for identifying stable and high-yielding compact cotton genotypes across specific or diverse environments using AMMI analysis. The first two principal components (PC1 and PC2) significantly explained the GEI for all traits, with the AMMI model using two significant IPCs identified as the most reliable for stability analysis (Zobel et al., 1988). PC1 explained the majority of GEI variation, ranging from 76.2% (SCY) to 96.2% (NSB), while PC2 contributed between 3.8% and 23.8%, offering additional clarification. Specifically, traits such as NSB (96.2%), SBL (92.2%), BP (92.3%), NMB (90.8%), and FSB (86.4%) were predominantly explained by PC1. PH (76.8%) and SCY (76.2%) showed a relatively higher contribution of PC2 (23.2% and 23.8%, respectively), indicating its moderate influence. MIL (83.4%) and BW (86.2%) also displayed a strong PC1 effect with some contribution from PC2 (16.6% and 13.8%). These results suggest that PC1 is the most informative axis for assessing genotype adaptability and stability across environments, while PC2 provides useful but minor additional insight into GEI. Our findings align with previous studies (Sheeba et al., 2025; Sivakumar et al., 2024; Shahzad et al., 2019; Ali et al., 2018), which similarly reported that PC1 explains a greater portion of GEI variation than PC2.

Genotype plus genotype-by-environment interaction (GGE) biplot

Mean vs. stability biplot

A two-dimensional biplot was constructed based on the first two PCs using the row metric preservation method to assess genotype mean performance and stability (Yan, 2002; Yan, 2024; Memon et al., 2023). From the average environment coordination (AEC) perspective, the AEC line, represented by a single arrow passing through the origin, indicated the direction of increasing mean performance, whereas short perpendicular projections (dotted lines) from the AEC axis identified genotypes with greater stability. Fig. 4 shows the GGE biplots for plant height (Fig. 4A), sympodial branch length (Fig. 4B), mainstem internode length (Fig. 4C), and seed cotton yield (Fig. 4D) were explained by PC1 and PC2, accounting for 91.80%, 96.59%, 93.43%, and 96.42% of the total GGE variation, respectively (PH: PC1 = 69.34%, PC2 = 22.46%; SBL: PC1 = 74.38%, PC2 = 22.21%; MIL: PC1 = 64.47%, PC2 = 28.96%; SCY: PC1 = 84.46%, PC2 = 11.96%). It indicating that PC1 predominantly captured the mean trait performance across genotypes, while PC2 reflected the GEI and stability.

Genotypes showed significant variation in mean performance and stability for studied traits. Anjali, ARBC19, ARBC1651, and PKV-081 Bt exhibited higher mean plant height, but their stability differed, with Anjali showing greater stability due to shorter projections from the AEC axis. In contrast, Nano, Rajat-Bt, and CO17 were shorter but less stable, while Suraj, Subiksha, Roja, F2383, RS2818, and Bt/C-62 showed stable performance with average or below-average PH. For SBL, PKV-081Bt and Bt/C-63 recorded longer branches with high stability, whereas Nano and HC-54 had shorter branches and less stability. Genotypes CO17, Suraj, Subiksha, F2383, and Anjali were positioned closer to the origin, indicating greater stability with average to below-average SBL. MIL varied widely, with Anjali showing the longest and RS2818 the shortest internode length. Nano, Rajat Bt, and H C-54 had shorter internodes but lower stability, while CO15, Suraj, Bt/C-62, CO17, and F2383 showed short and stable internodes. Roja, Subiksha, Bt/C-61, and F2381 exhibited moderate internode length with stable performance. Suraksha, Suraj, and Subiksha demonstrated the highest mean SCY and stability, indicating wide adaptability under rainfed conditions, whereas CO17 showed strong GEI, indicating specific adaptation. ARBC1601, PKV-081Bt, and Bt/C-63 had lower mean yield and stability. Among environments, Veppanthattai (E3) was most discriminative for trait expression, while Coimbatore (E1) and Srivilliputtur (E2) were more representative, making them suitable for selecting high-yielding, compact, and stable genotypes. Similar studies by Ali et al. (2018), Verma et al. (2022), and McPherson (2022) used GGE biplot to identify high-yielding stable genotypes, and Sivakumar et al. (2023) applied it for selecting compact, high-yield cotton genotypes under multi-environment trials.

Which-won-where biplot

The which-won-where GGE biplot helps identify the best genotype for each environment (Aditi Rani et al., 2023; Yan, 2024). It forms a polygon by connecting the top-performing genotypes, with dotted lines (rays) originating from the biplot center and extend perpendicularly to the sides of the polygon, dividing the plot into sectors called mega-environments (Yan, 2024). The genotype at a vertex performs best in the environments within its sector, showing specific adaptation. Genotypes near the origin are more stable across environments, while those at the vertices are highly interactive (Yan and Tinker, 2006).

Fig. 5A shows the plant height (PH) biplot revealed three distinct mega-environments. Anjali and ARBC19 exhibited the tallest PH at E1 and E2, while PKV-081Bt performed best at E3. Vertex genotypes such as Nano, Rajat-Bt, RS2818, and HC54, which did not fall into any environment sector, were associated with shorter PH across the sites. Genotypes located near the origin (e.g., Subiksha, Roja, Bt/C-61, F2383, Suraj) showed more stable and below average PH. Fig. 5B shows the biplot for sympodial branch length, two mega-environments were identified: E1 and E2 formed one, while E3 was distinct. ARBC1651, Bt/C-63, and HC54 were high performers in E1 and E2, whereas PKV-081Bt and Suraksha excelled in E3. Other vertex genotypes (Nano, Suraksha, Subiksha, RS2818) showed shorter branch length responses in specific environments. Genotypes near the origin, including Roja, Bt/C-61, CSH3075, F2381, and CO15, were stable across locations but lacked superior performance in any single environment. Fig. 5C shows the biplot for mainstem internodal length (MIL) biplot, three separate mega-environments were formed by E1, E2, and E3. Anjali and ARBC19 were top performers in E1; PKV-081Bt excelled in E2; no genotype showed superiority in E3. Vertex genotypes such as Nano, Rajat-Bt, RS2818, and CO17 were linked to shorter MIL under certain conditions. Genotypes near the origin (ARBC1051, Subiksha, DSC1651) demonstrated stable and below average MIL across environments. Fig. 5D shows the biplot for seed cotton yield, the three environments constituted a single common mega-environment, with Suraksha as the high-yielding vertex genotype. Other vertex genotypes without associated environments in their sector indicated lower yields across sites. Genotypes located near the origin (Suraj, Subiksha, F2383, RS2818, Nano) were stable and showed no significant interaction with the environments. However, these genotypes were not positioned at the vertices and exhibited very poor yield performance across the tested environments (Ali et al., 2017). Our findings agree with previous studies showing that the environment divides cotton-growing sites into distinct mega-environments (Abro et al., 2022; Verma et al., 2022).

Weighted average of absolute scores (WAAS)

The WAAS biplot, which assesses the mean performance (Y) against WAAS and provides a comprehensive stability evaluation by incorporating all scores of IPCs, unlike the AMMI model that considers only the first IPC. This approach captures the total variance of GEI when identifying stable genotypes (Olivoto et al., 2019a). In the WAAS biplot, the vertical axis represents the average mean of traits such as PH (Fig. 6A), SBL (Fig. 6B), MIL (Fig. 6C) and SCY (Fig. 6D) across environments, with genotypes or environments placed to the right of this line performing above average, and those on the left performing below average. The horizontal axis indicates mean WAAS values, and its intersection with the vertical axis divides the plot into four quadrants, each representing groups of genotypes with distinct adaptability and stability patterns for studied environments. Genotypes positioned in the first quadrant of the biplot, including Nano and Rajat-Bt for PH in environments E1-Coimbatore and E2-Srivilliputtur, Nano, ARBC19, TVH002, and Rajat-Bt for SBL in E1 and E2, Nano, Rajat-Bt, and HC-54 for MIL in E2, and ARBC1601, Bt/C-62, CO15, RS2818, and ARBC19 for SCY in E1 and E2, recorded high WAAS values but below-mean performance. This reflects their instability and inconsistent response across environments and making them generally unsuitable for cultivation. However, genotypes expressing lower PH, SBL, and MIL values are desirable for developing compact plant types and thus recommended for cultivation where reduced plant height, internode and branch length are advantageous. Genotypes such as TCHB213, ARBC19, HC-54, and PKV-081Bt were placed in the second quadrant of the PH biplot under environment E3-Veppanthattai. Similarly, HC-54, ARBC1651, Suraksha, and F2381 for SBL in E3, while Suraksha, TCHB213, ARBC19, CSH3075, and PKV-081Bt for MIL under E1 and E3. For SCY, CO17, Roja, Bt/C-61, and TCHB213 occupied the second quadrant in E3. These genotypes showed high WAAS values combined with performance above the average mean, indicating strong adaptability to favorable environments. Environment E3 for PH, SBL, and SCY, while both E1 and E3 for MIL served as effective discriminators for genotypes. Under favorable environmental conditions, these genotypes are likely to achieve high yield potential and can be recommended for cultivation in regions suited to cotton growth and development.

Genotypes CO17, RS2818, Suraksha, Suraj, F2383, Bt/C-62, CO15, and DSC1651 were clustered in the third quadrant of the PH biplot, whereas Suraksha, RS2818, Suraj, CO17, Bt/C-62, and CO15 for SBL. Similarly genotypes RS2818, CO17, Suraj, TVH002, F2383, Bt/C-62, CO15 and DSC1651 for MIL and CSH3075, PKV-081Bt, Bt/C-63, F2381, ARBC1651, Anjali, Rajat-Bt and DSC1651 SCY. These genotypes exhibited lower WAAS values, indicating greater stability and minimal environmental influence. However, they also showed lower mean performance for the evaluated traits. The genotypes associated with PH, SBL, and MIL traits represent the most desirable compact types, characterized by shorter plant height, reduced internode length, and shorter sympodial branches, making them well-suited for cultivation in rainfed ecosystems than for yield maximization. Genotypes Anjali, ARBC1651, Subiksha, Roja, Bt/C-63, Bt/C-61, ARBC1601, F2381, and CSH3075 were positioned in the fourth quadrant of the PH biplot; PKV-081Bt, Roja, Bt/C-63, Anjali, ARBC1601, Bt/C-61, F2383, TCHB213, CSH3075, and DSC1651 in the SBL biplot; Anjali, Bt/C-63, Roja, ARBC1601, Suraksha, Bt/C-61, F2381, and ARBC1651 in the MIL biplot; and Suraksha, Suraj, Subiksha, Nano, F2383, TVH002, and HC-54 in the SCY biplot. These genotypes exhibited low WAAS values and above-average performance, indicating they are stable with minimal environmental sensitivity while maintaining optimal trait expression. Such genotypes are ideal for cultivation due to their consistent performance across varying conditions. In general, genotypes with WAAS values close to zero are considered the most stable. Accordingly, Anjali, Subiksha, F2383, Suraj, and ARBC1651 for PH; PKV-081Bt, Anjali, Roja, CO17, and ARBC1601 for SBL; Anjali, Roja, Bt/C-62, Suraj, and CO15 for MIL; and Suraksha, CSH3075, Subiksha, Suraj, Nano, and PKV-081Bt for SCY exhibited low GEI and high stability. However, ideal genotypes not only have low WAAS values but also performance above the average mean. Therefore, Anjali, Subiksha, and ARBC1651 (PH), PKV-081Bt, Anjali, and Roja (SBL), Anjali, Roja, Subiksha, and Bt/C-63 (MIL), and Suraksha, Subiksha, Suraj, Nano, and F2383 (SCY) were identified as stable genotypes with superior performance. The genotypes with high mean SCY performance are most desirable for yield, whereas low values in PH, SBL, and MIL contribute to a more compact plant type, advantageous for agronomic adaptability. Despite various yield stability methods, WAAS biplot from AMMI analysis provides valuable insight for accurate stability assessment (Vineeth et al., 2022; Taleghani et al., 2023; Mostafavi and Saremirad 2021; Sharifi et al 2017).

Weighted average of absolute scores from BLUP and yield (WAASBY)

The simultaneous ranking and selection of genotypes based on trait performance and stability were performed using the WAASBY index, which combines the WAASB stability measure with the trait mean (Olivoto et al., 2019a). Blue circles represent genotypes with WAASBY values above the mean, while red circles indicate those below the mean. For plant height (PH), among 12 high-performing genotypes (blue circle), Anjali showed a WAASBY index above the mean, while ARBC1651 and Subiksha also exhibited relatively high stability and lengthier plant height compared to others (Fig. 7A). In the case of SBL, PKV-081Bt, Bt/C-63, and Roja had the highest WAASBY indices among 11 genotypes exceeding the mean branch length (Fig. 7B). For trait

MIL, Anjali again displayed the highest WAASBY index among 15 above mean internodal length genotypes, making it the top-performing and most stable genotype (Fig. 7C). For SCY (Fig. 7D), eight genotypes showed high WAASBY values, with Suraksha surpassing the mean WAASBY index, and it identified as most stable and highest-yielding genotype, followed by Subiksha and Suraj. These results confirm that the WAASBY index efficiently identifies genotypes combining high trait performance and stability (Olivoto et al., 2019a), which is essential for breeding programs targeting consistent performance across varied rainfed ecosystems.

Considering the advantage of WAASB approach, it is possible to customize the magnitude of this stability index in relation to trait performance for identifying desirable genotypes (Olivoto et al., 2019a). Therefore, WAASB values were plotted against the responsible variable (WAASBY) across several weights of WAASB for each trait (Fig. 8A). Accordingly, variation in genotype rankings was recorded based on the weighted contribution of traits PH (Fig. 4A), SBL (Fig. 8B), MIL (Fig. 8C), SCY (Fig. 8D), and their stability index (WAASB). The WAASB/GY heatmap was partitioned into two columns, first on left side of heatmap and second on right side on 50/50 WAASB weights. In the first column, where genotypes rankings were determined exclusively by the WAASB index (0/100). It revealed, Subiksha < ARBC1651 < Anjali was identified as stable genotypes with lengthier PH; Roja < Anjali < PKV-081Bt as stable genotypes with longer SBL; Bt/C-63 < Roja < Anjali as stable genotypes with longer MIL; and Suraj < Subiksha < CSH3075 < Suraksha as stable genotypes with higher SCY. In the second column, when ranking was based only on WAASB index (100/0), genotypes Anjali > ARBC19 > ARBC1651 were identified superior for PH, PKV-081Bt > Bt/C-63 > ARBC1601 for SBL, Anjali > PKV-081Bt > ARBC1601 for MIL, and Suraksha >

Suraj > Subiksha for SCY, and it highlighting that these genotypes are most superior and stable with desirable trait expression. The ranking of genotypes based on equal weights (50/50) is assigned to stability and the respective trait. Under this criterion, Anjali > ARBC1651 > Subiksha was identified as the most promising genotypes for PH, PKV-081Bt > Bt/C-63 > Roja for SBL, Anjali > Bt/C-63 > ARBC1601 for MIL, and Suraksha > Subiksha > Suraj for SCY. The WAASBY method effectively integrates trait performance and stability with WAASB analysis (Olivoto et al., 2019a), enabling the selection of cotton genotypes with consistent yield across variable environments. This approach helps breeders develop high-yielding, stable, and adaptable cultivars for diverse climates and farming practices. While most cotton yield stability studies have applied GGE biplot (Sivakumar et al., 2024), non-parametric methods (Baraki et al., 2024), and AMMI (Shahzad et al., 2019), the WAASB method-derived from AMMI and BLUP techniques-offers a powerful tool for identifying compact plant types in cotton genotypes adapted to rainfed conditions.

Best linear unbiased prediction (BLUP)

AMMI ANOVA applies a fixed-effects model treating genotype and environment as fixed factors, while LMM treat genotypic effects as random, providing a more realistic estimation of GEI (Piepho, 1994; Olivoto et al., 2019). In this study, LMM with genotype as a random effect was used, and BLUPs enabled accurate prediction of genotypic performance, especially with incomplete data (Smith et al., 2005). Variance component analysis confirmed significant effects of genotype and GEI for all traits except boll per plant (BP), which showed non-significant genotypic variance and was excluded from MTSI analysis. SCY had the highest genotypic variance proportion (71.99%), followed by BW and PH, indicating strong genetic control (Table 3). In contrast, NSB exhibited low genotypic variance (22.74%) and high environmental influence. GEI variance was highest for NSB (52.20%) and SBL (50.70%), while SCY showed the lowest (19.26%), reflecting greater yield stability. Heritability (h^2) ranged from 0.23 (NSB) to 0.72 (SCY), with moderate estimates for PH, NMB, FSB, and MIL. Genotypic mean heritability (h^2mg) was high for SCY (0.91), BW (0.77), and PH, NMB, FSB (0.71 each), confirming reliable selection based on multi-environment performance. Selection accuracy (A_S) was highest for SCY (0.95), followed by BW (0.88) and PH, NMB, FSB (0.84 each), demonstrating model robustness. The GEI coefficient of determination (GEIr^2) ranged from 0.19 (SCY) to 0.52 (NSB), indicating stronger GEI influence on branch-related traits, while SCY showed greater stability. The low GEIr^2 for SCY and moderate values for PH, NMB, and FSB suggested higher residual variation in the interaction component compared with AMMI ANOVA which explained most of the GEI through the first two IPCAs (Koundinya et al., 2021).

The correlation of genotypic values across environments (rge) was highest for PH (0.76) and lowest for BW (0.47), with most traits showing rge > 0.66, aiding stable genotype selection (Table 3). Genotypic coefficient of variation (CVg) was highest for NMB (26.26%) and moderate for SCY (6.42%), while residual variation (CVr) ranged from 2.24% (SCY) to 19.39% (NMB). The CV ratio exceeded unity for most traits, especially SCY (2.87), indicating strong selection potential, whereas NSB and SBL showed greater environmental masking. BLUP-predicted mean values (Fig. 9) showed 13 genotypes above average for PH, with Anjali and ARBC 19 as tallest, and RS 2818, CO 17, Rajat Bt, Suraksha, and Nano as most compact (Fig. 9A). For SBL, 14 genotypes performed above average, led by PKV-081 Bt and Bt C-63, whereas Subiksha, RS 2818, and Nano had the shortest SBL (Fig. 9B). Similarly, 13 genotypes showed above-average predicted mean for MIL, with Anjali and PKV-081 Bt recording the longest internodes, and RS 2818, CO 17, and Rajat Bt having the shortest (Fig. 9C). For SCY, 11 genotypes exceeded the average, with Suraksha, Suraj, and Subiksha showing the highest predicted means (Fig. 9D). Additionally, 14 genotypes exhibited above-average predicted means for NSB, 13 for FSB, 11 for NMB, and 13 for boll weight (BW) (Supplementary Fig. 1). Overall, Suraksha, Suraj, and Subiksha emerged as superior yield performers, while RS 2818, CO 17, Rajat Bt, and Nano represented compact types with lower PH, SBL, and MIL. These results highlight substantial genetic variability, supporting selection for both vigorous and compact types depending on breeding goals. The BLUP method proved effective for multi-environment prediction, consistent with previous studies in crops such as cowpea (Sousa, et al., 2019), cotton under saline conditions (Vineeth et al., 2022), cassava (Koundinya et al., 2021), and olive (Li et al., 2025).

Multi-trait stability index (MTSI)

MTSI is an advanced tool designed to overcome the limitations of traditional stability models that assess single traits independently (Memon et al., 2023). Traditional stability models focus on mean performance, regression, and deviations but fail to fully capture genotype stability or key trait strengths and weaknesses (Bhering et al., 2012; Yue et al., 2022). MTSI overcomes these limitations by analyzing multiple traits simultaneously, helping breeders identify superior and stable genotypes more effectively (Olivoto et al., 2019). In this study, MTSI was applied to evaluate the performance and stability of cotton genotypes for multiple yield and plant architecture traits across environments. Factor analysis (PCA with Varimax rotation) grouped eight traits into three factors explaining 70.78% of the total variation (Table 4, Table 5). FA1 (eigenvalue 2.84, 35.50% variance) was associated with PH, SBL, and MIL; FA2 (eigenvalue 1.48, 18.45%) related to BW and SCY; and FA3 (eigenvalue 1.35, 16.83%) involved NMB, FSB, and NSB. Mean communality of 0.72 indicated a good representation of trait variation.

The MTSI ranked genotypes from lowest (most desirable) to highest values (Fig. 10a), with Suraj (MTSI = 2.16), Subiksha (2.53), F2383 (2.54), and RS2818 (3.08) identified as the most promising under a 15% selection intensity (Supplementary Table 2). The red dot in (Fig. 10A) marks the cut-off MTSI value (3.08), highlighting genotypes for future evaluation. Selected genotypes showed favorable selection differentials (SDp), ranging from –8.48% (SBL) to +5.50% (BW), and high heritability for SCY (0.91) and BW (0.77). However, negative selection gains were observed for PH, SBL, MIL, NMB, FSB, and NSB. The radar plot (Fig. 10B) illustrated the strengths and weaknesses of selected genotypes, with RS2818 driven mainly by FA1, F2383 by FA3, Subiksha by FA2, and Suraj showing balanced contributions from FA2 and FA3. These results suggest that Suraj and F2383 are stable and widely adaptable compact genotypes, while Subiksha offers intermediate stability, and RS2818 is suited for targeted trait improvement. Similar successful applications of MTSI have been reported in Cotton (DS Raj et al., 2024; Elsamman et al., 2024), cassava (Koundinya et al., 2021), rice (Sharifi et al., 2021), and pearl millet (Yadav et al., 2022), confirming its efficiency in identifying superior and stable genotypes, consistent with the findings of this study.

Trait correlation patterns

The scatterplot matrix (Fig. 11) revealed clear patterns of association among plant architecture and yield-related traits in cotton. PH showed a moderate positive correlations with NMB, SBL, and NSB, indicating that taller plants tended to have more and longer branches (Madhu et al., 2023). PH was also strongly correlated with MIL, confirming that longer internodes contribute to greater plant height. However, excessive vegetative growth can hinder crop management (Venugopalan et al., 2011; Kerby et al., 2010). In contrast, shorter MIL and SBL were associated with compact plant architecture, which improves resource allocation to reproductive growth, enhances boll retention, and suits high-density planting (Gunasekaran et al., 2020; Yan et al., 2019; Sivakumar et al., 2024). NMB and FSB showed weak correlations with yield traits, suggesting limited impact on yield improvement (Van der Sluijs, 2015). SCY was primarily driven by BP and BW, while PH, SBL, MIL, and NSB showed negative correlations with SCY. These findings suggest that excessive vegetative growth does not enhance yield, contradicting several earlier studies that reported positive associations (Meredith et al., 2012; Ali et al., 2017; Ul-Allah et al., 2017; Ali et al., 2018) but aligning with studies that found negative correlations (Pujer et al., 2014; Yan et al., 2019; Sivakumar et al., 2024; Madhu et al., 2023). The results highlight the importance of selecting compact plant types that improve reproductive efficiency, supporting the goals of ideotype breeding in cotton.

Conclusion

This METs identified cotton genotypes combining compact plant architecture with stable high yield, suitable for rainfed systems in Tamil Nadu. Yield variation was largely governed by genetic factors with moderate GEI, whereas branch number and boll count were predominantly influenced by environmental conditions. Suraksha emerged as the most stable and highest-yielding genotype, while Suraj, Subiksha, and F2383 exhibited a favorable balance of compact growth and adaptability across environments. Genotypes RS2818, Nano, and CO17, characterized by reduced plant height and internode length, represent valuable donors for compact plant traits. The integration of AMMI, GGE, WAAS, BLUP, WAASBY, and MTSI analyses provided complementary insights into genotype evaluation, underscoring the importance of multi-trait and multi-location testing in cotton ideotype breeding. For practical applications, these selected genotypes offer potential as parental lines for developing compact, high-density, and machine-harvestable cotton hybrids. These findings form a strong basis for breeding programs targeting compact architecture and sustainable yield under rainfed conditions in India.

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Author’s contribution

All the authors contributed to the study conception and design. Banoth M executed the experiment, analysed the data, results interpreted and written original draft. All authors critically revised the manuscript for important intellectual contents and approved the final manuscript.

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Data availability

Data will be made available on request.

Declarations

Ethics approval and consent to participate

Not applicable.

Consent for publication

Not applicable.

Competing interests

Authors declare that they don’t have competing interests.

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Table 1 List of twenty-two elite cotton genotypes used in the study

Genotypes	Released Institute	Year	Source	Genotypes	Released Institute	Year	Source
CO15	TNAU, Coimbatore	2018	Dept. of Cotton, TNAU, Coimbatore	Bt/C-61	ICAR-CICR, Coimbatore	2022	ICAR-CICR, Coimbatore
CO17	TNAU, Coimbatore	2020	-do-	Bt/C-62	-do-	2022	-do-
TCHB213	TNAU, Srivilliputhur	2020	-do-	Bt/C-63	-do-	2022	-do-
TVH002	TNAU, Veppanthattai	2023	-do-	Subiksha	-do-	2018	-do-
F2381	PAU, Faridkot	2016	-do-	PKV-081Bt	-do-	2017	-do-
F2383	PAU, Faridkot	2016	-do-	Nano	-do-	2023	-do-
ARBC1601	UAS, Dharwad	2020	-do-	Anjali	-do-	1992	-do-
ARBC1651*	UAS, Dharwad	2020	-do-	Rajat-Bt	-do-	2017	-do-
ARBC19	UAS, Dharwad	2016	-do-	Suraj	-do-	2008	-do-
DSC1651	UAS, Dharwad	2020	-do-	Suraksha	-do-	2018	-do-
RS2818	SKRAU, Sriganganagar	2020	-do-	HC-54	-do-	2002	-do-
CSH3075*	ICAR-CICR, Sirsa	2017	ICAR-CICR, Coimbatore	Roja	-do-	2011	-do-

*Checks included

Table 2 Combined analysis of variance, principal components and their contributions as per AMMI model for GEI of yield and plant architecture traits in cotton

Traits	Joint RCBD + AMMI ANOVA mean squares					PC1 (df: 24)		PC2 (df: 22)		CV (%)	Bartlett's K-squared (df: 2)	Mean over Environments
	Environment (E) (df: 2)	Genotype (G) (df:23)	Replication within (E) (df: 6)	GEI (df: 46)	Residual (df: 138)	Mean Square	Contribution (%)	Mean Square	Contribution (%)			
PH	361.76***	326.44***	1.95	93.61***	8.89	137.88***	76.8	45.32**	23.2	10.78	1.34	89.77
NMB	0.70***	0.46***	0.01	0.23***	0.01	0.23***	90.8	0.03*	9.2	14.62	0.33	0.72
FSB	7.97***	13.22***	0.59	3.80***	0.49	6.30***	86.4	1.08**	13.6	8.99	0.33	21.70
NSB	18.10***	9.51***	0.57	4.48***	0.62	8.25***	96.2	0.36*	3.8	10.35	1.80	20.56
SBL	40.67***	20.42***	1.15	8.65***	1.13	15.30***	92.2	1.40*	7.8	13.63	1.80	18.81
MIL	2.68***	1.20***	0.01	0.42***	0.04	0.68***	83.4	0.15***	16.6	11.40	4.41	5.71
BP	3.71*	7.47***	1.70	7.74***	0.91	13.70***	92.3	1.24*	7.7	12.80	1.51	21.73
BW	0.49***	0.68***	0.02	0.16***	0.04	0.28***	86.2	0.04*	13.8	7.93	0.72	4.98
SCY	35.80**	546.88***	2.04	50.93***	6.69	74.42***	76.2	25.30***	23.8	6.18	1.68	115.57

*, **, *** represents significant at p-value ≤ 0.001, ≤ 0.01, and ≤ 0.05, respectively. PH Plant-height, NMB Number of monopodial branches, FSB Height of first sympodial branch origin from ground, NSB Number of sympodial branches, SBL Sympodial branches length, MIL Mainstem internodes length, BP Bolls per plant, BW Boll weight, SCY Seed cotton yield

Table 3 Estimation of variance components from LMM for nine studied traits in cotton

Variance components	**PH**	**NMB**	**FSB**	**NSB**	**SBL**	**MIL**	**BP**	**BW**	**SCY**
GEN	25.87**	0.04***	1.05***	0.56*	1.31*	0.09**	0.00	0.06***	55.11***
GEN:ENV	28.24***	0.04***	1.11***	1.29***	2.51***	0.13***	2.25***	0.04***	14.75***
Residual	8.89	0.02	0.49	0.62	1.13	0.04	0.91	0.04	6.69
% GV in PV	41.06	38.30	39.65	22.74	26.43	33.51	0	42.12	71.99
%IV in PV	44.83	40.81	41.89	52.20	50.70	49.03	71.23	27.27	19.26
%EV in PV	14.11	20.89	18.46	25.06	22.87	17.46	28.77	30.60	8.74
Phenotypic variance (PV)	63.00	0.09	2.64	2.46	4.95	0.26	3.15	0.14	76.55
Heritability	0.41	0.38	0.40	0.23	0.26	0.34	0.00	0.42	0.72
$GEIr^2$	0.45	0.41	0.42	0.52	0.51	0.49	0.71	0.27	0.19
h^2_{mg}	0.71	0.71	0.71	0.53	0.58	0.65	0.00	0.77	0.91
Accuracy of selection (A_S)	0.84	0.84	0.84	0.73	0.76	0.80	0.00	0.88	0.95
r_{ge}	0.76	0.66	0.69	0.68	0.69	0.74	0.71	0.47	0.69
CV_g	5.67	26.26	4.71	3.64	6.08	5.14	0.00	4.85	6.42
CV_r	3.32	19.39	3.22	3.82	5.65	3.71	4.38	4.14	2.24
CV ratio	1.71	1.35	1.47	0.95	1.08	1.39	0.00	1.17	2.87

GV Genotypic variation, IV Interaction variance, EV Environment variation, h^2_{mg} heritability of genotypic mean, $GEIr^2$ GEI coefficient of determination, r_{ge} correlation between genotypic value across environments, CV_g genotypic coefficient of variation (%), CV_r residual coefficient of variation (%), CV ratio between the coefficients of genotypic and residual variations (%)

Table 4 Factor loadings derived through varimax rotation and communalities obtained from factor analysis

Factor components	**FA1**	**FA2**	**FA3**	**Communality**	**Uniquenesses**
Eigenvalues	2.84	1.48	1.35		
Variance (%)	35.50	18.45	16.83		
Cum. variance (%)	35.50	53.95	70.78		
PH	-0.85	0.28	0.00	0.80	0.20
NMB	-0.30	0.40	0.63	0.65	0.35
FSB	0.22	0.26	-0.85	0.84	0.16
NSB	-0.19	-0.21	-0.52	0.35	0.65
SBL	-0.77	0.04	0.19	0.63	0.37
MIL	-0.93	0.00	-0.03	0.86	0.14
BW	-0.28	0.87	-0.11	0.85	0.15
SCY	0.03	0.79	0.25	0.68	0.32
Mean				0.71	0.29

Table 5 Assessment of traits and selection differential in cotton genotypes using the WAASBY index derived from MTSI

Traits	**Factor**	**Xo**	**Xs**	**SD**	**SD_P (%)**	**h2**	**SG**	**SG_P (%)**	**Sense**
PH	FA 1	89.77	85.54	-4.23	-4.71	0.71	-3.02	-3.36	Decrease
SBL	FA 1	18.81	17.22	-1.60	-8.48	0.58	-0.92	-4.89	Decrease
MIL	FA 1	5.71	5.44	-0.27	-4.76	0.65	-0.18	-3.08	Decrease
BW	FA 2	4.98	5.25	0.27	5.50	0.77	0.21	4.24	Increase
SCY	FA 2	115.57	121.59	6.02	5.21	0.91	5.46	4.73	Increase
NMB	FA 3	0.72	0.69	-0.03	-3.54	0.71	-0.02	-2.50	Decrease
FSB	FA 3	21.70	21.09	-0.61	-2.81	0.71	-0.43	-2.00	Increase
NSB	FA 3	20.56	20.54	-0.03	-0.13	0.53	-0.01	-0.07	Increase

Xo Original genotypes mean, Xs Selected genotypes mean, SD Selection differential, SD_P selection differential percent, h2 heritability; SG Selection gain, SG_P selection gain percent.

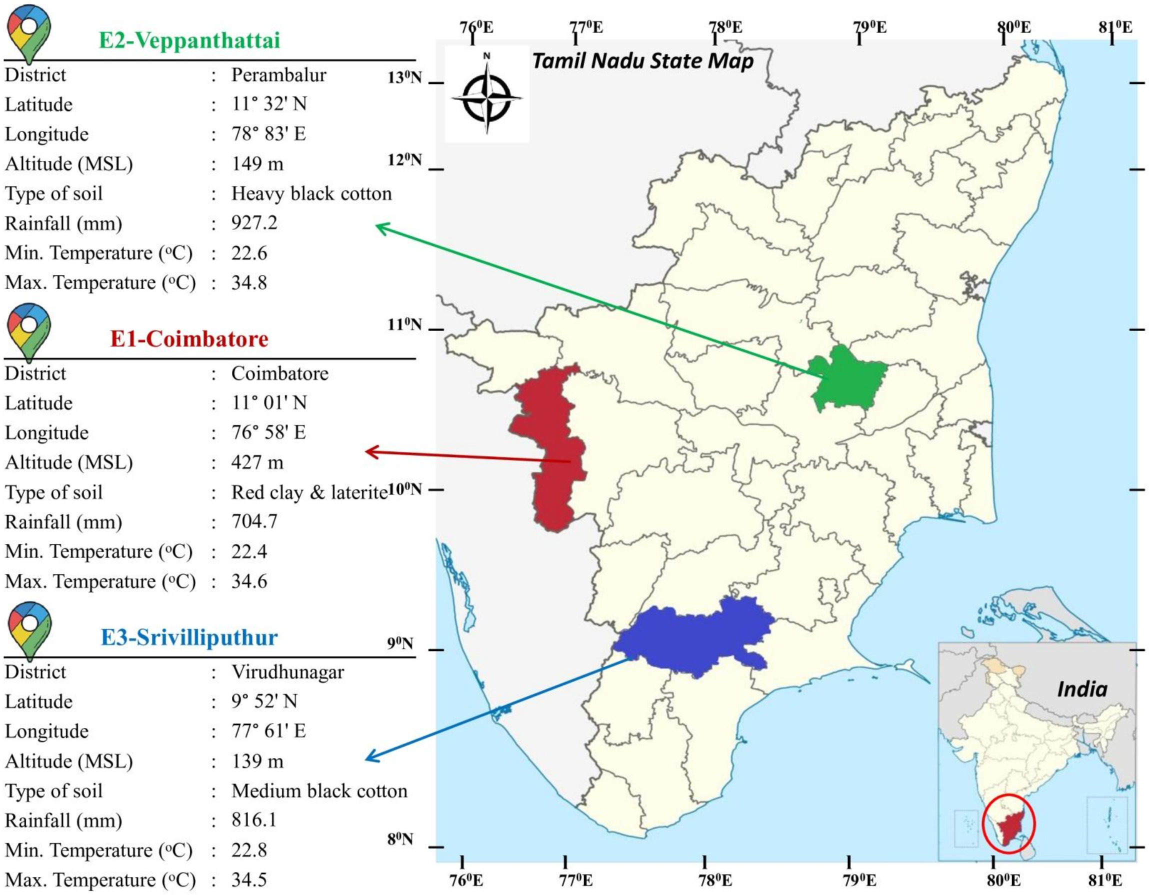

Fig. 1 Geographical locations of experimental sites in Tamil Nadu, India with their agro-climatic characteristics, where the study was conducted under rainfed conditions during Kharif 2024 in cotton

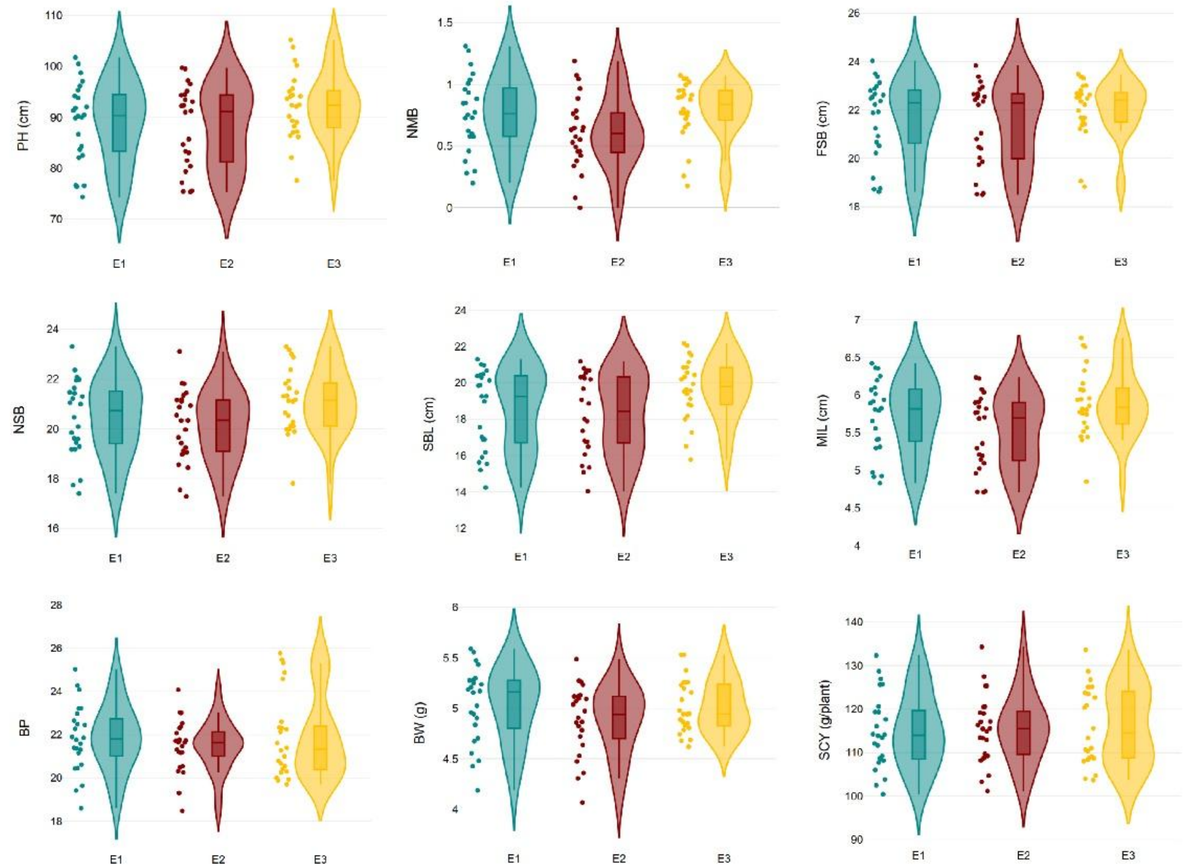

Fig. 2 Violin plots depicting the mean performance of nine traits evaluated in 24 cotton genotypes across three environments under rainfed conditions during Kharif 2024. PH Plant-height, NMB Number of monopodial branches, FSB Height of first sympodial branch origin from ground, NSB Number of sympodial branches, SBL Sympodial branches length, MIL Mainstem internodes length, BP Bolls per plant, BW Boll weight, SCY Seed cotton yield

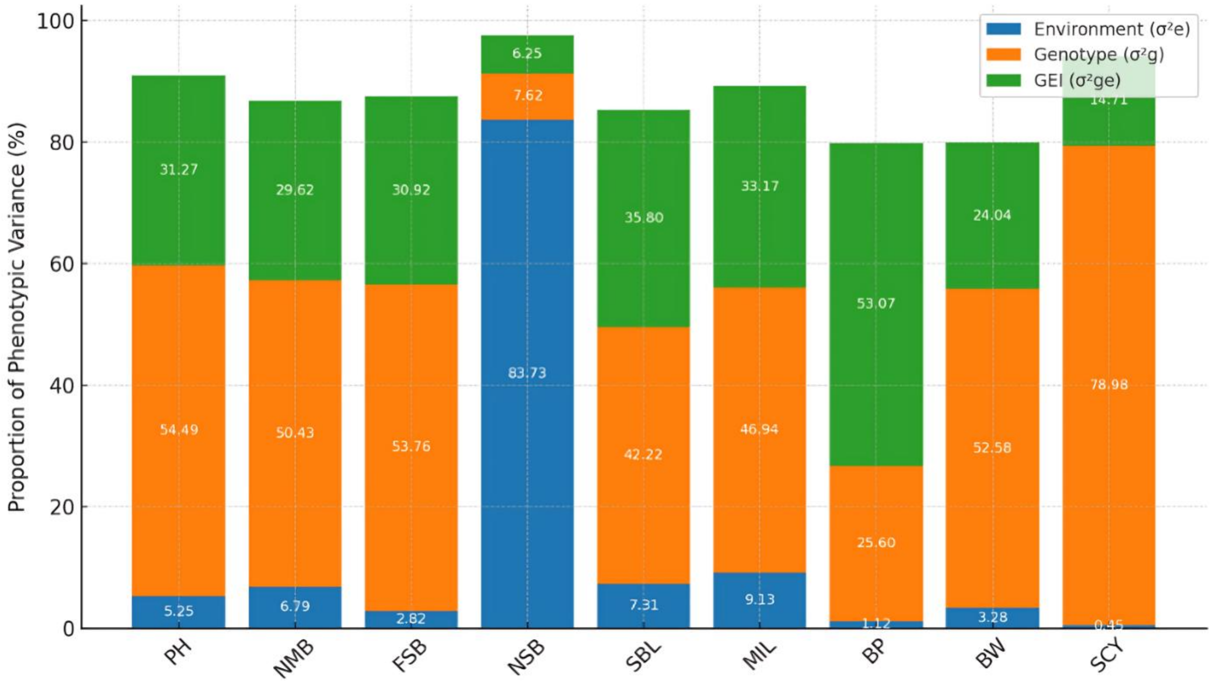

Fig. 3 Proportion of phenotypic variance for nine traits in 24 cotton genotypes evaluated under rainfed conditions during Kharif 2024. PH Plant-height, NMB Number of monopodial branches, FSB Height of first sympodial branch origin from ground, NSB Number of sympodial branches, SBL Sympodial branches length, MIL Mainstem internodes length, BP Bolls per plant, BW Boll weight, SCY Seed cotton yield

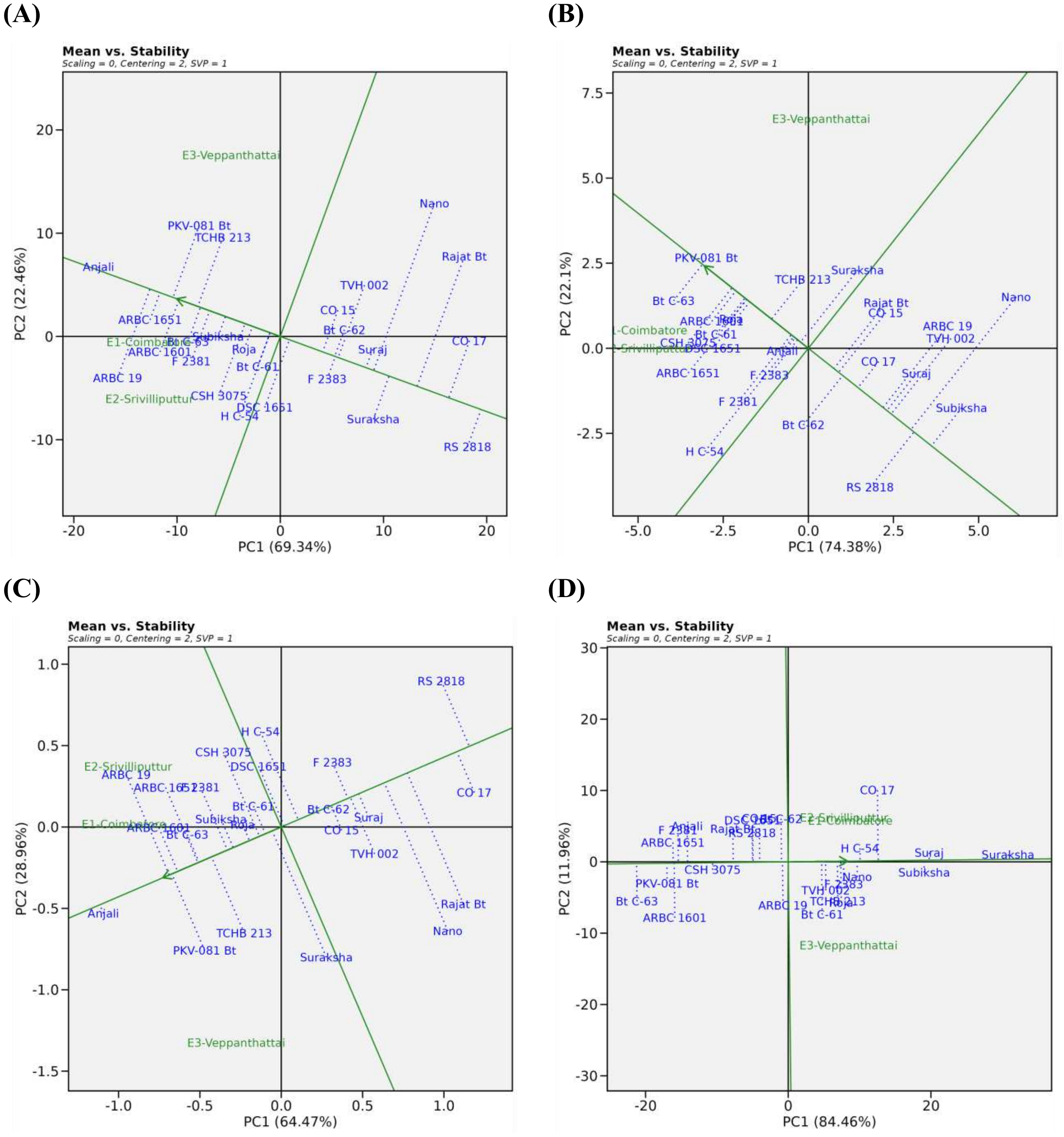

Fig. 4 The mean vs. stability GGE biplot of **(A)** plant height, **(B)** sympodial branch length, **(C)** mainstem internode length, and **(D)** seed cotton yield across three environments

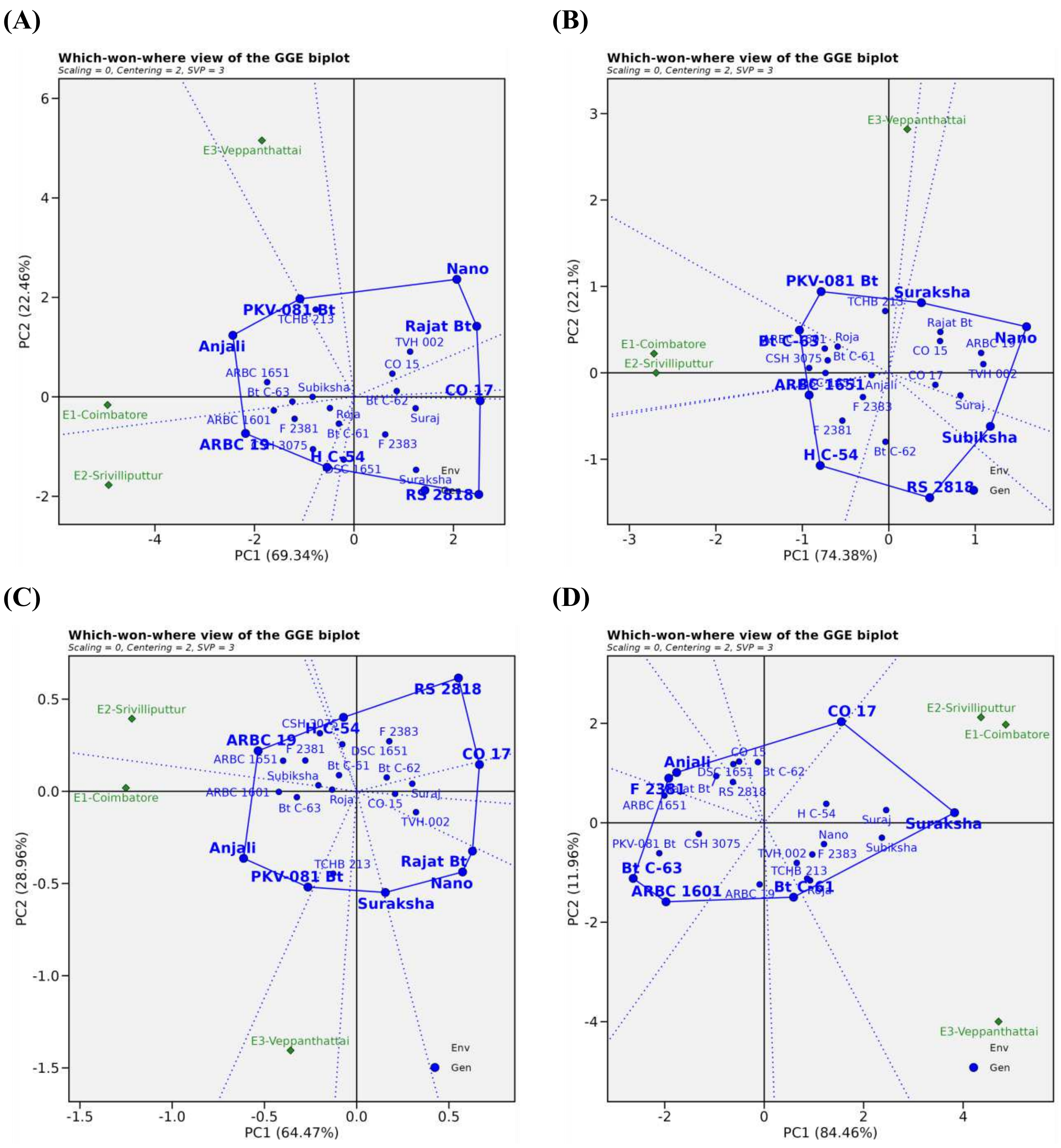

Fig. 5 The Which-Won-Where GGE biplot of **(A)** plant height, **(B)** sympodial branch length, **(C)** mainstem internode length, and **(D)** seed cotton yield across three environments

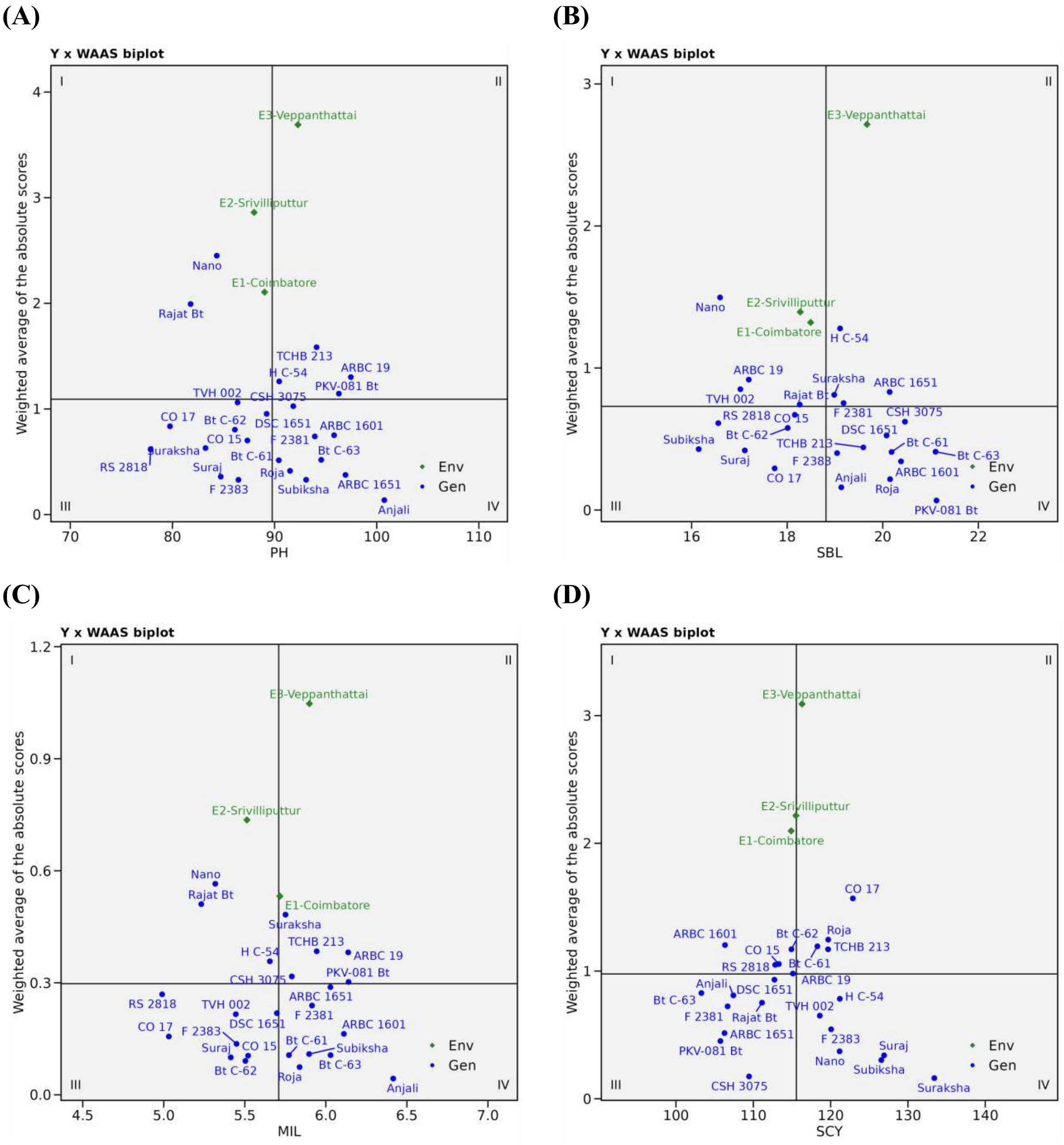

Fig. 6 Mean performance vs. WAAS biplot derived from the AMMI model for **(A)** plant height, **(B)** sympodial branch length, **(C)** mainstem internode length, and **(D)** seed cotton yield across three environments. The x-axis represents the arithmetic mean of each trait across environments, while the y-axis indicates the WAAS index

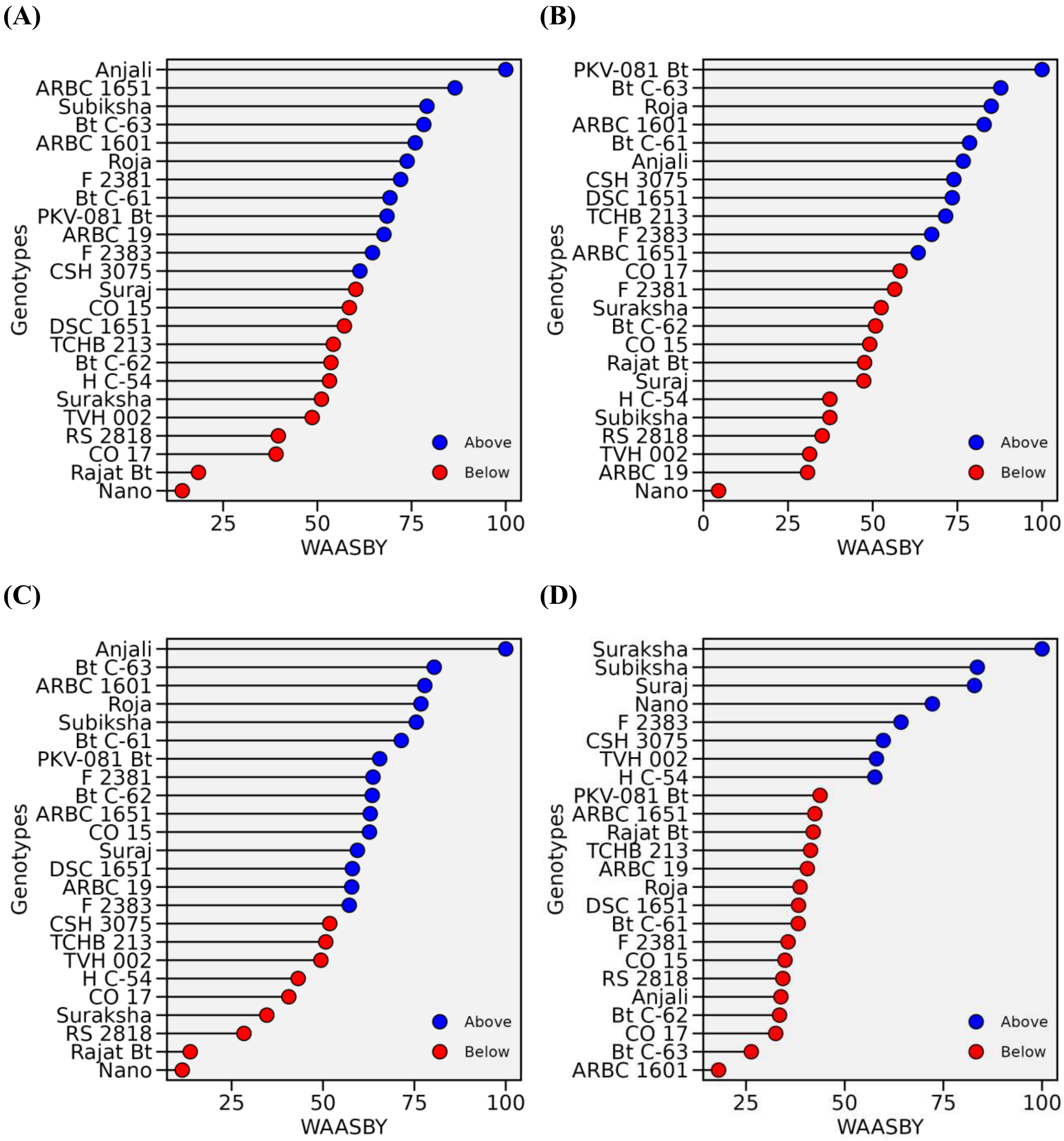

Fig. 7 Estimated WAASBY index values for **(A)** plant height, **(B)** sympodial branch length, **(C)** mainstem internode length, and **(D)** seed cotton yield in cotton genotypes, calculated by assigning equal weights (50:50) to mean performance and stability

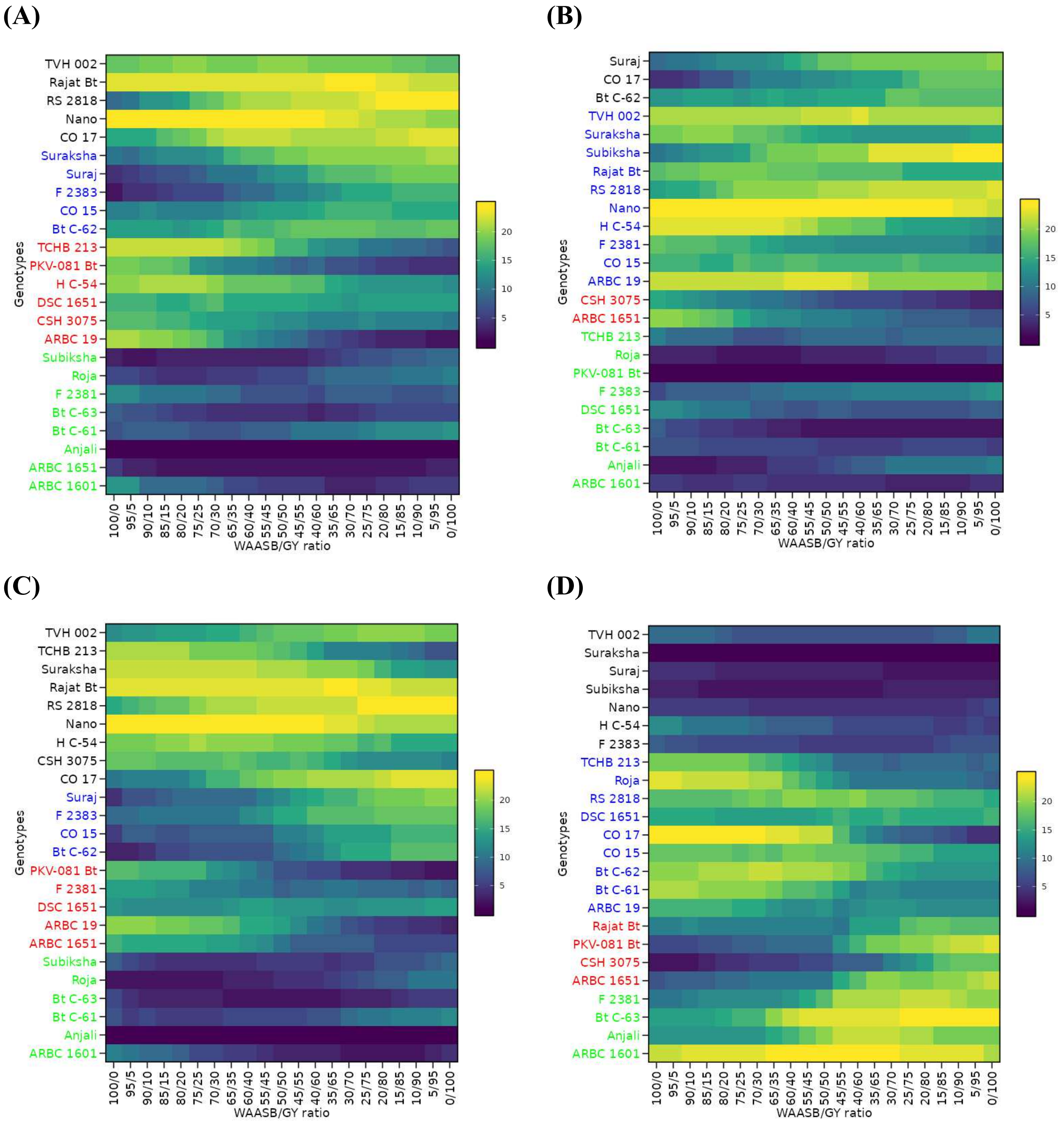

Fig. 8 WAASB/GY heatmap showing the ranking of 24 cotton genotypes based on different weight combinations of trait mean performance and WAASB stability index. Relative genotype rankings are represented by color intensity, where darker shades indicate higher ranks and lighter shades indicate lower ranks. Results are presented for **(A)** plant height, **(B)** sympodial branch length, **(C)** mainstem internode length, and **(D)** seed cotton yield

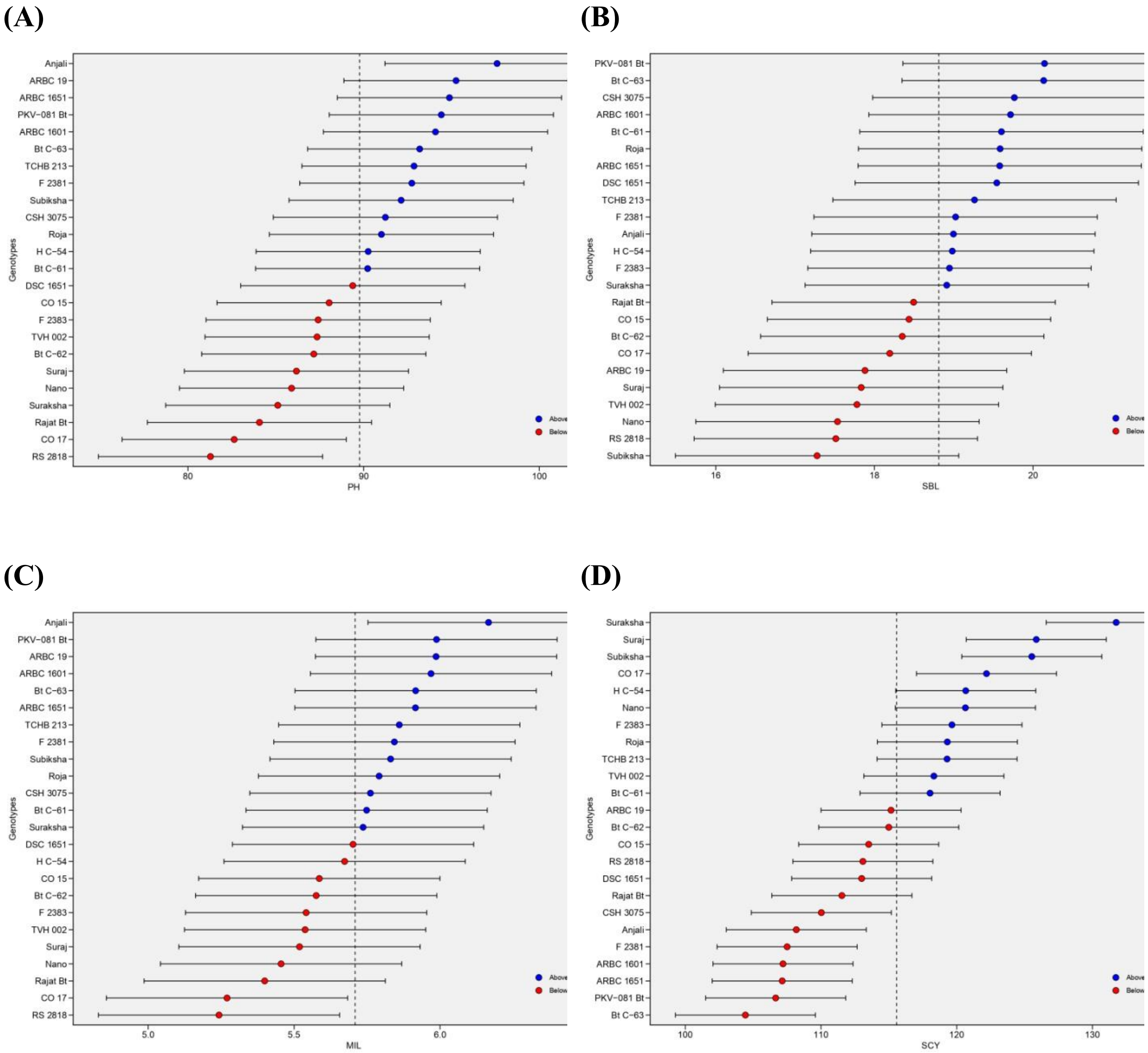

Fig. 9 BLUP mean values for **(A)** plant height, **(B)** sympodial branch length, **(C)** mainstem internode length, and **(D)** seed cotton yield in 24 cotton genotypes evaluated across three environments

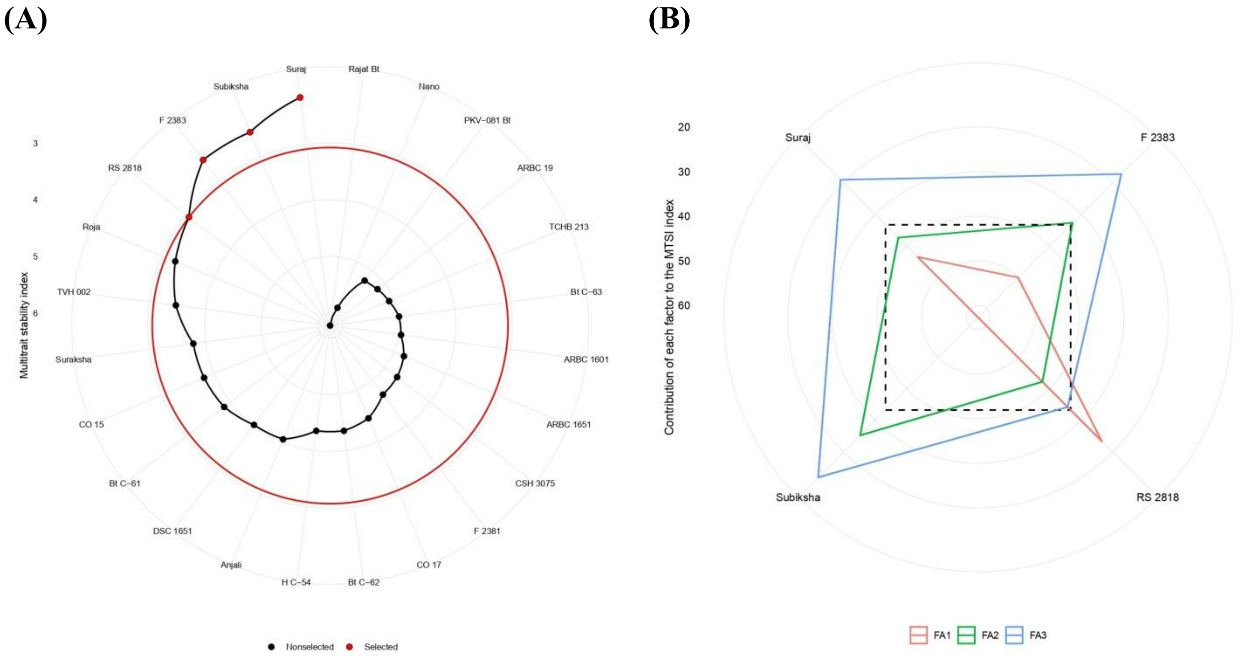

Fig. 10 (A) Ranking of cotton genotypes in ascending order based on MTSI score, with selected genotypes are highlighted in red. The radar plot scale represents the MTSI score. **(B)** The strengths and weaknesses of selected genotypes are presented as the proportional contribution of each factor to the computed MTSI score

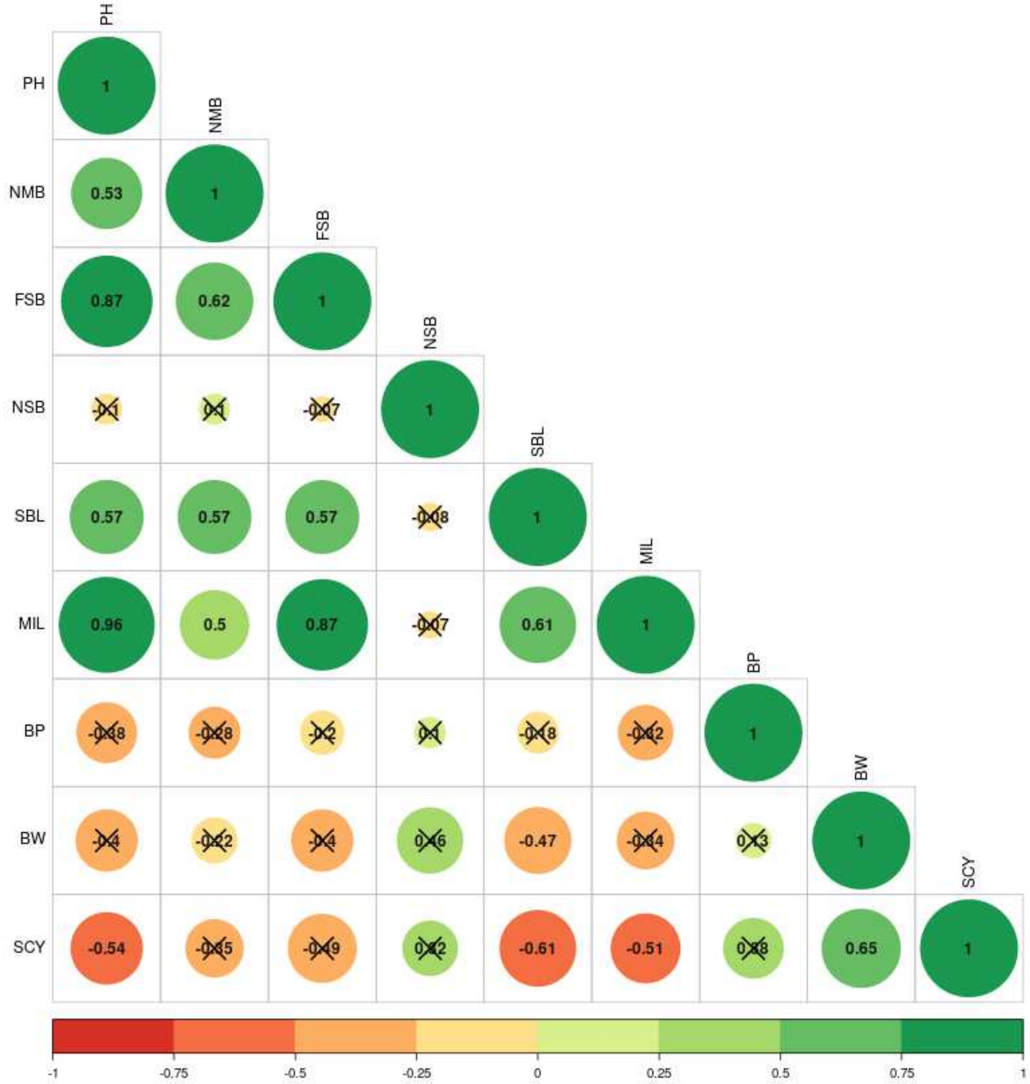

Fig. 11 Correlogram of plant architecture and yield traits across three environments. Every correlation coefficient (r) which matches two traits was calculated with Pearson method. Numbers ranges from -1 to 1 are Pearson rank of traits on horizontal and vertical axes. Color depth and size of the circle diagrams indicates the correlation strength

Supplementary Files

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- Supplementaryfile.docx