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BLUP-Based Multi-Trait Analysis for Identifying Climate-Resilient and High-Performing Mango Ginger (Curcuma amada Roxb.) Ideotypes

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Abstract

The mango ginger (*Curcuma amada* Roxb.) is an important rhizomatous group of spice crop with medicinal and industrial value. Despite strong industry demand, large-scale commercial cultivation has not been realized due to the lack of stable, high-yielding varieties; addressing this requires evaluating diverse genotypes across multiple environments. In the present study, 10 mango ginger genotypes, including the check Amba, were evaluated for fresh rhizome yield and yield-attributing traits in a randomised complete block design (RCBD) with three replications and were conducted over three years (2020–2022) in eight diverse environments. The multivariate techniques were used for the identification of the most stable genotypes in mangoginger. The genotype and genotype x environment interactions significantly affect the mango ginger fresh rhizome yield (FRY) and FRY attributing traits ($P < 0.001$), as determined by the likelihood ratio test against the Chi-square value. The mean heritability varied from 0.423% for number of tillers per clump (NTC) to 0.82% recorded for plant height (PH). It was observed that the selection accuracy (AS) of 10 mango ginger genotypes was lowest for NTC and highest for PH. A WAASBY biplot analysis identified *Acc* 265, Indira mango ginger-1 (IMG-1), and *Acc 347* as superior genotypes exhibiting consistent performance and enhanced stability for fresh rhizome yield. This work is the first to apply WAASB and multi-trait stability models to analyze genotype × environment interactions and stability in *Curcuma amada*.

Introduction

Curcuma amada Roxb. is commonly known as mango ginger, belongs to the genus *Curcuma* and the family Zingiberaceae, with its primary centre of origin in India (Syamkumar and Sasikumar, 2007; Wilson, 2016). The major cultivated species of the genus *Curcuma* include *Curcuma longa* (turmeric), *Curcuma amada* (mango-ginger), *Curcuma aromatica* (kasthuri turmeric) and *Curcuma zedoaria* (yellow zedoary). *Curcuma amada* is known for its characteristic mango-like taste and aroma in both leaves and rhizome (Wilson, 2016). The medicinal properties of mango ginger have been documented in Ayurveda and Unani systems of medicine, supporting its use in human and domestic animals. In culinary use, it is commonly used in pickles and chutneys, and as a flavouring agent in salads, curries, and other dishes to add a distinctive aroma and taste (Prakash et al., 2007).

Since mango ginger is clonally propagated, genetic improvement through conventional breeding is limited. Still, there is a considerable variability has been reported in flower colour, rhizome colour, odour, and taste among mango ginger genotypes. These variations influence the chemical composition of the genotype and its buffering capacity to changing environmental conditions (Raval et al., 2021). Earlier studies have reported that mango ginger fresh rhizome contains key bioactive compounds like β-Myrcene, epicurzeronone, squalene, α-acaridial, 2,6,11,15-Tetramethyl-hexadeca-2,6,8,10,14-pentaene and aromadandrene, β-pinene, (Policegoudra et al., 2000) as well as Amadannulen a novel compound (Policegoudra et al., 2007). The solvent extracts and essential oils of mango ginger possessed antimicrobial properties (Karthika et al., 2017). In addition to essential oil, it contains starch, fibre, reducing sugars, ash, and a significant amount of water (Policegoudra and Aradhya, 2007). These constituents contribute to its characteristic aroma, flavour, and medicinal properties. The importance of different species of turmeric in traditional medicine is ascribed due to presence of active bioactive compounds, including curcuminoids, phenolic acids, and essential oils (Prasath, 2018). Due to rising demand for mango ginger in food and pharmaceutical uses, its cultivation is expanding.

The performance of a genotype under diverse environmental conditions depends on inherent buffering capacity and latent adaptability to specific environmental conditions (Sawargaonkar et al., 2026). Evaluation of genotypes across diverse environments is essential for identifying high yielding and climate resilient mango ginger varieties. Breeding programmes that focus on high-yielding varieties play a key role in ensuring quality planting material for farmers. Variation in temperature, precipitations, soil fertility, and other factors exist in a specific location or year or combination leads to considerable differences in the crop's yield and quality (Druille et al 2020). Genotypes with wider adaptability and stable performance across locations and season are essential in genetic improvement programme of any crop (Zakir 2018). Traditionally, the Eberhart and Russell (1966) stability model uses three parameters—mean performance, regression coefficient, and deviation from regression—to identify stable genotypes. However, it is limited by its assumption of linear genotype × environment interaction, which restricts its ability to capture complex, non-linear stability patterns. Whereas, the modern approach of stability like the Best Linear Unbiased Prediction (BLUP)-based approaches, WAASB (Weighted Average Scores based on BLUPs), WAASBY (WAASB plus Years), and MTSI (Modified Stability Index), demonstrated clear advantages over traditional methods can handle complex and unbalanced data, accurately model random effects, and provide more reliable estimates of genotype performance across diverse environments (Yue et al 2022; Olivoto et al 2019). BLUP-based stability analysis is becoming increasingly popular in agricultural research and breeding programme because it can provide reliable and precise estimates of genotypic performance (Piepho et al. 2008) and have enhanced the efficiency of selecting genotypes with superior performance and stability across multiple traits evident from the studies in turmeric (Neeraja et al. 2026; Sampath et al. 2026) can be exercised in mango ginger.

The mango ginger (*Curcuma amada* Roxb.) is an important rhizomatous group of spice crop with medicinal and industrial value. Despite strong industry demand, large-scale commercial cultivation has not been realized due to the lack of stable, high-yielding varieties; addressing this requires evaluating diverse genotypes across multiple environments. To assess the stability of genotypes for yield and yield-attributing traits, plant breeders also need to estimate genetic parameters such as heritability, variability, and genetic advance. These provide insights into trait inheritance and support the application of appropriate breeding techniques to improve yield. In any plant breeding program, ideotype remains the ideal genotype, and achieving it is the main goal of researchers. The multi-trait genotype ideotype distance index (MGIDI) method has been developed as an innovative strategy to address the limitations of the classical selection index methods like Smith-Hazel (SH) index in identifying superior genotypes using information from multiple traits (Olivoto and Nardino, 2020). Current breeding program for mango gingers evaluates many genotypes in a variety of environments in order to identify high-yielding, climate-resilient variants by using WAASB, WAASBY and MGIDI. High-yielding mango ginger genotypes are essential to ensure a steady supply of raw material to meet industry demand.

Materials and methods

Plant material and test environments

A multilocational trial was conducted to evaluate the performance of mango ginger accessions across diverse agro-climatic conditions under ICAR-All India Coordinated Research Project on Spices (ICAR-AICRPS). The trial was conducted in a randomized complete block design (RCBD) with three replications over three years (2020–2022) across eight diverse environments, resulting in a total of 24 field trials. A total of 10 genotypes, including the check variety Amba, were evaluated. The trial was laid out in a net plot size of 3.0 × 1.0 m^2, maintaining a spacing of 25 cm between rows and 30 cm within rows. The experimental material comprised accessions sourced from multiple research organizations includes *Acc* 265 and *Acc* 347 from ICAR–IISR, Kozhikode, Kerala, India; NVMG 2, NVMG 9, and NVMG 10 from NAU, Navsari, Gujarat, India; CAM 2 and CAM 3 from OUAT, Pottangi, Odisha, India; RH 408 from Dholi, Bihar, India; and Indira Mango Ginger-1 (IMG-1) from CARS, Raigarh (IGKV), Chhattisgarh, India.

Prior to evaluation, planting material was multiplied during *Kharif* 2019 under non-replicated conditions at all test locations to ensure uniform and adequate seed rhizome availability. Field evaluations were conducted over three consecutive growing seasons (*Kharif* 2020, *Kharif* 2021 and *Kharif* 2022) across eight locations in India, namely Ambalavayal, Pottangi, Kozhikode, Dholi, Barapani, Pundibari, Raigarh, and Navsari, representing eight diverse environments. Geographic coordinates, altitude, soil type, and meteorological details of each location during the crop growth period are provided in supplementary Table 2.

Experimental design and crop management

Standard agronomic practices recommended for mango ginger cultivation were followed uniformly across all locations.

Trait measurement

Data were recorded on five randomly selected competitive plants per plot in each replication at physiological maturity. The traits evaluated included fresh rhizome yield (t ha^{-1}), plant height (cm), number of tillers per clump, and fresh weight of clump (g).

Data analysis and software

Variance component analysis

Variance components and genetic parameters were estimated using a best linear unbiased prediction (BLUP)-based mixed model, considering genotypes and genotype × environment interaction (GEI) as random effects, and environments and replications as fixed effects, following Olivoto *et al*. (2019) and Yang (2007). The analysis was performed using the gamem_met() function in the *metan* package. The significance of random effects was tested using the likelihood ratio test (LRT) based on a chi-square distribution. Genetic parameters including genotypic variance, GEI variance, residual variance, broad-sense heritability (h^2g), heritability of genotype means (h^2gm), selection accuracy, coefficient of determination of GEI (r^2i), genotype–environment correlation (rge), and coefficients of variation (CVg and CVr) were estimated as described by Olivoto and Lúcio (2020) and Olivoto et al. (2019).

Stability analysis (WAASB and WAASBY)

Stability was assessed using the Weighted Average of Absolute Scores from BLUP (WAASB), which integrates all principal components of GEI derived through singular value decomposition of the BLUP interaction matrix, as proposed by Olivoto et al. (2019a). Genotypes with lower WAASB values were considered more stable. The WAASBY index, combining yield performance and stability, was computed by assigning weights of 60% to yield and 40% to stability. Based on WAASB and yield performance, genotypes were classified into four groups using a biplot approach, where genotypes combining high yield and high stability were considered ideal.

Multi-trait stability and selection indices

Multi-trait selection was performed to identify superior genotypes considering both performance and stability across traits. Traits including fresh rhizome yield (FRY), plant height (PH), number of tillers per clump (NTC), and fresh weight of clump (FWC) were assigned a positive selection direction.

Multi-trait genotype-ideotype distance index (MGIDI)

The MGIDI was computed following the methodology of Olivoto and Nardino (2020) involving rescaling the traits, factor analysis, ideotype design and then calculating the MGIDI index. Genotypes with lower MGIDI values were considered closer to the ideal genotype.

Multi-trait stability index (MTSI) and multi-trait mean performance and stability

(*MTMPS) index*

The multi-trait stability index (MTSI) was estimated by integrating both mean performance and stability (WAASBY) through factor analysis, as described by Olivoto et al. (2019b). The multi-trait means performance and stability (MTMPS) index was also computed using Wricke's ecovalence, following Zuffo et al. (2020).

Multi-Trait Index Based on Factor Analysis and Genotype-Ideotype Distance (FAI-BLUP Index)

The factor analysis and ideotype-design based BLUP index (FAI-BLUP) was calculated to estimate the probability of each genotype being closest to the ideotype, following Rocha et al. (2018).

Smith - Hazel (SH) Index

The classical Smith-Hazel selection index was computed using phenotypic and genotypic variance-covariance matrices with assigned economic weights, following Smith (1936) and Hazel L. N. (1943).

Selection differential and genetic gain under selection

The genotypes were selected under different growing environments through MGIDI values by considering a selection intensity of ~ 20% and the selection differential in the percentage of population mean ($\Delta\ S\%$) was then computed for each trait as follows

$$\Delta\ S\% = \frac{(X_s - \ X_o)}{X_o}\ \mathrm{X}\ 100$$

Genetic gain percentage under selection $(\Delta\ G\%)$ is calculated as follows

$$\Delta\ G\% = \frac{(X_s - \ X_o)}{X_o}\ \mathrm{X}\ h\ \mathrm{X}\ 100$$

Where, Xo = mean for WAASBY index of the original population; Xs = mean for WAASBY index of the selected genotypes; ΔS: Selection differential; ΔG: Selection gains.

Software used for statistical analysis

All statistical analyses were conducted using R software (version 4.1.2) in the R Studio environment (R Core Team, 2021). The *metan* package (Olivoto and Lúcio, 2020) was used for mixed models, stability, and multi-trait indices, while graphical visualizations were generated using *ggplot2* (Wickham, 2016). The MGIDI index is calculated using the mgidi() function in metan. The mtsi() function is used for calculating the multi-trait stability index (MTSI), as suggested by Olivoto *et al*. (2019) in metan. The FAI-BLUP is a multi-trait index that utilises factor analysis and ideotype design. It can be calculated using the FAI-BLUP function, as described by Rocha et al. (2018). Smith - Hazel index was calculated by Smith (1936) and Hazel (1943) through using Smith-Hazel function. The coincidence indexe() function in the *metan* R package can calculate the coincidence index (CI) as defined by Hamblin and Zimmermann (1986), along with other multi-trait indexes.

Results

Mean performance:

The mean performance of 10 genotypes of mango ginger in eight different environments for four variables that contribute to FRY is given in Table 4. Genotype NVMG 9 (67.07 t ha^{-1}) had the maximum FRY in environment E 17, while RH 408 (6.6 t ha^{-1}) had the lowest FRY in environment E 5. For PH, CAM 2 (142.37 cm) reported the greater PH in environment E 13, whereas IMG-1 (45.6 cm) recorded the smaller PH in E 17. For NTC distinct genotype CAM 2 showed extreme values in E 16 and E 22. The highest FWC recorded by NVMG 2 (1086.2 g) in E 21 was significantly superior over the check Amba (54.1 g) which had lowest performing genotype in environment E 2.

The evaluation of different genotypes of mango ginger in 24 environments revealed that E 10 had the lowest mean FRY, suggesting unfavourable conditions for its growth, E 12 had the highest mean FRY, indicating favourable conditions for cultivation of mango ginger. E 2 had the lowest mean performance for FWC, NTC and PH, whereas E 8, E22, and E21 had the favourable environments for traits expression indicating its adequacy to respective environments for the traits.

The genotypes with the lowest mean genotypic performance values across all environments were CAM 2 for FRY, NVMG 9 for PH and FWC, and RH 408 for NTC respectively; while the genotypes with the highest mean performance were *Acc* 347 for FRY and PH, IMG-1 for NTC and NVMG 2 for FWC.

The first high-yielding genotype *Acc 347* (29.04 t ha^{-1}) for FRY also recorded the highest PH (111.2 cm), which was significantly better than check Amba (21.6 t ha^{-1} and 13.24 cm) followed by *Acc* 265 (26.4 t ha^{-1} and 111.57 cm) and IMG-1 (26.4 t ha^{-1} and 104.72 cm) respectively.

The pooled ANOVA indicated highly significant differences for genotypes, environments and GEI (P< 0.0001) for the all the studied traits (Table 3). The coefficient of variation values, which ranged from 0.08% for FWC to 8.25 for FRY, verified the existence of notable variations between treatments and the accuracy of the experimental measures in various locations under METs.

BLUP based analysis

The BLUP based variance components for four important morphological traits of ten genotypes of mango ginger over eight different environments is given in Table 4.

BLUP based genetic Parameters

The genotype and genotype x environment interactions significantly affect the mango ginger yield attributing traits ($P < 0.001$), as determined by the likelihood ratio test against the Chi-square value. The BLUP analysis revealed that highest phenotypic variance exhibited by FRY (77.52) and PH (665.53), while for NTC it was 1.42 and for FWC had 1531.48 as average value of all the genotypes. The highest BLUP-based heritability estimates recorded for the trait PH (0.165 %) followed by FWC (0.09) while lowest heritability observed for NTC (0.028 %). The mean heritability varied from 0.423% exhibited by NTC to 0.826 % for PH. The selection accuracy (AS) of ten mango ginger genotypes was lowest for NTC and highest for PH, FWC as well as FRY. The genotypic correlation among environments (rge) as well as the coefficient of determination for interaction effects (R^2ge) is high for all the four traits studied. The minimum genotypic coefficient of variation (CVg) recorded for traits NTC while higher CVg recorded for fresh weight of clump. Overall CVg recorded for all the genotypes evaluated in different multi-location trials showed acceptable values. The residual coefficient of variation (CVr) showed minimum values for FWC while maximum values for NTC. The ratio between genotypic and residual coefficient of variation (CV ratio) were high for FWC followed by PH and FRY while minimum was recorded for NTC.

BLUP based mean performances of mango ginger genotypes across environments

Predicted BLUP mean performance for 10 mango ginger genotypes for FRY was 2.38 while for PH reported 94.07 and NTC had 4.66 and 326.93 recorded for FWC. Blue and red circles represent the genotypes that had BLUP above and below of BLUP means, respectively (Fig 1, Table 4). Horizontal error bars represent the 95% confidence interval of prediction considering a two-tailed t test. BLUP based predicted mean for FRY revealed that total four genotypes showed above BLUP linear values. The highest BLUP value for FRY recorded by genotypes were *Acc 347*, *Acc 265*, IMG-1 and NVMG 10 respectively. Simillary for PH *Acc 347* and IMG-1 had showed highest BLUP predicted mean performance over the control variety Amba. For NTC high BLUP predicted mean showed by IMG-1 followed by *Acc 347* over the check Amba. For FWC genotype NVMG-2 had highest BLUP predicted mean followed by *Acc 347* and *Acc 265*. In the present study BLUP effects were close to normal as presented in QQ plots in Fig. 7 and highlights significance of *Acc* 265, IMG-1 and *Acc* 347.

Weighted average absolute scores based on BLUP (WAASB) based stability index

The stability of ten mango ginger genotypes was accessed across 24 different environments using Weighted Average of Absolute Scores (WAASB) for fresh rhizome yield (FRY), plant height (PH), number of tillers per clump (NTC), and fresh weight of clump (FWC) (Table 5; Fig. 2).

Stability analysis using WAASB

The WAASB analysis revealed that for FRY, the lowest WAASB values were recorded by Amba (0.96), followed by *Acc 265* (1.21) and NVMG 10 (1.70), indicating stable performance of genotypes across environments. For PH, NVMG 2 (3.12) and NVMG 10 (3.30) exhibited the lowest WAASB values. In the case of NTC, NVMG 10 (0.40), NVMG 2 (0.41), and Amba (0.44) showed greater stability while NVMG 9 and CAM 2 were poor performer for NTC confirmed by high WAASB values. For FWC, IMG-1 (5.02), *Acc 265* (5.56), and *Acc 347* (5.97) recorded the lowest WAASB values, while highest WAASB values recorded by NVMG 9, CAM 3 and NVMG 2. Overall, *Acc 265*, IMG-1, and NVMG 10 emerged as relatively stable genotypes across multiple traits.

Evaluation of mango ginger genotypes using WAASB based stability index

Yield–stability relationship using WAASBY

The results of WAASBY analysis from Table 6 revealed that for FRY genotype *Acc* 265 recorded first rank with the highest WAASBY value of 80.21, followed by *Acc* 347 (68.52, Rank 2) and IMG-1 (62.92, Rank 3) indicating genotypes above average performance and wider stability while CAM 3 showed the lowest WAASBY value (0.18, Rank 10), suggesting poor mean performance and high instability for FRY. For PH most desirable genotype was IMG-1 with a WAASBY value of 81.06 (Rank 1) followed by NVMG 2 (76.76, Rank 3) and NVMG 10 (71.55, Rank 4) while NVMG 9 had a WAASBY value of 20.00 (Rank 10), indicating it was the least stable/desirable for this trait. IMG-1 again performed strongly with a WAASBY value of 79.26 (Rank 2) for NTC, closely following *Acc* 347 (76.26, Rank 3) and *Acc* 265 (68.51, Rank 6) while minimum NTC showed by NVMG 9 (24.59, Rank 10). For FWC the top performer was *Acc* 265 with a WAASBY value of 96.37 (Rank 1), followed by *Acc* 347 (93.84, Rank 2) and IMG-1 (85.81, Rank 3) while least favourable genotype with WAASBY values and rank were NVMG 9 (30.00, Rank 10) and CAM 3 (34.36, Rank 8).

Genotype ranking depending on the weights for stability and performance (WAASBY)
Classification of genotypes based on Y × WAASB plot

The Y × WAASB plot classified ten mango ginger genotypes into four quadrants given in Table 7, figure 2 and 3. For FRY, *Acc 265*, *Acc 347*, IMG-1, and NVMG 10 were grouped in Quadrant IV, representing high-yielding and stable genotypes across the E2, E21, E11, E13, E19, E15, E4 and E7. This confirms their suitability for the cultivation across diverse environments. For PH, NVMG 2 and NVMG 10 were categorized as stable but poor yielding genotypes limits its cultivation in E9, E3 and E11 environments. In the case of NTC three genotypes Amba (check), IMG-1 and *Acc 347* were identified as high-yielding in all the environments except in E14 and E 3 environments. For FWC, IMG-1, *Acc 265*, and *Acc 347* were classified as highly stable and high yielding, highlighting their superiority for fresh rhizome yield production under E12, E20, E24, E16, E8 and E23.

Multi-trait indices analysis

The genotypes exhibiting the lowest MGIDI value demonstrated a strong alignment with the ideotype, resulting in consistently high performance and stability across various environments for all the trait under investigation. Genotypes with optimal yield and stability had chosen using a selection intensity of 20 %. The selected and non-selected genotypes were shown graphically through the use of MGIDI scores plotted on a graph (Table 8, Fig 4). The minimum MGIDI value recorded by *Acc* 265 which rank first for all the four traits studied followed by IMG-1 and NVMG 2 which ranked second and third with minimum MGIDI

score respectively. Similarly, for MTSI revealed from Table 8 that IMG-1 exhibited minimum MTSI score and rank 1 showed stability for all the traits studied while *Acc* 265 ranked second for MTSI score and *Acc* 347 had third rank for MTSI. The high MGIDI score recorded by RH 408 (rank 10) and CAM 2 (rank 9) while NVMG 9 and RH 408 had highest MTSI score and rank 10, 9 respectively which confirms its change in performance with the environments up and down. The higher value for SH index showed by genotype *Acc* 347 followed by *Acc* 265 and IMG-1 and obtained rank 1^{st}, 2^{nd} and 3^{rd} respectively indicating its higher adaptability while unstable and poor yielding genotypes were CAM 3, CAM 2 and RH 408 which exhibited minimum SH index and higher rank respectively.

Coincidence, common genotypes selected from different multi-traits-based stability models

Comparing the different multi-trait-based stability models, the coincidence index was higher between the two models, the coincidence was higher between the two models that have more common genotypes between them. The common genotypes and coincidence index were presented in Figure 5. The maximum coincidence index with common genotypes was observed between MGIDI, MTSI and FAI-BLUP by IMG-1 while *Acc 265* had common MGIDI, MTSI and SH index. The least common values recorded by *Acc 347* which showed common coincidence of FAI-BLUP and SH index only. This coincidence and selection of common stable genotype by MGIDI, MTSI and FAI identified IMG -1 as most desirable genotype followed by *Acc 265* and *Acc 347*.

FAI-BLUP

The results of the factor analysis carried out on four most important traits and ten mango ginger diverse genotypes were given in Table 9. This table includes eigenvalues, genotypic variance (%) explained, factorial loadings after varimax rotation and commonalities. The analysis revealed 76.76 % of the total variation by factor FA1 present among the attributes based on the WAASBY value of BLUP estimates determined this. Thus, it was feasible to preserve strong explanatory power while describing data dimensionality. In the present study all communalities' values were > 0.50 for all the traits which strongly indicating FA 1 successfully captures the major pattern across all four traits studied. The maximum communality observed value for FRY was 0.88 followed by for PH (0.84) and minimum communality value was 0.62 and 0.73 recorded for NTC and FWC respectively. The uniqueness for NTC had highest 0.38 which indicated 38 % of its variation is independent of FRY and PH followed by maximum uniqueness recorded by FWC (0.27) while FRY had lowest uniqueness (0.12).

Selection gain

The predicted genetic gains and selection differentials for all the traits were given in Table 10. In the present study MTSI index achieved a success rate of 75 % in selecting desired traits based on WAASBY index for yield contributing traits using MGIDI index with desired selection differential (SD) for three out of four traits studied. The positive selection differential observed for all the traits studied. The fresh weight of clump (FWC) recorded highest SD value of 24.87 % followed by PH (8.12 %) and FRY (1.89 %) while minimum selection differential of 0.13 % recorded by NTC. The WAASBY index showed a mean selection differential of 6.77 %, with PH recorded highest (8.64 %) and NTC (2.76 %) had lowest values for SD. The mean genetic gain under selection (SG %) was 2.47 % which was the highest genetic gain recorded for FWC (5.51 %) followed by PH (3.62 %), while for NTC no genetic gain was recorded. The heritability values ranged from 0.22 (FRY) to 0.32 % (PH) suggesting moderate genetic control.

Genetic correlations among the yield and its contributing traits

Correlation coefficient analysis is used in plant breeding to quantify the relationships between different plant traits and identify the component traits that can be used as a basis for genetic yield improvement. The Pearson's correlation coefficient of 10 mango ginger genotypes between FRY and other traits were presented in the figure 6. The mean values from the eight experimental sites were used to predict the relationship between the quantitative traits. In all the four quantitative traits studied six high positive and significant correlations were observed. FRY was found to be significantly and positively correlated with PH, NTC and FWC. The highest correlation (r = 0.68) was recorded between FRY and FWC, followed by PH with FWC (r = 0.65) and FRY (r = 0.64). The minimum significant positive Pearson's correlation (p > 0.05) recorded by NTC with FWC (0.15) and FRY (r =0.18).

Discussion

In the present investigation, the performance of mango ginger genotypes for rhizome yield and yield-attributing traits was evaluated across eight diverse environments over three consecutive years. This study is the first report of using WAASB and multi-trait stability model in understanding Genotype × Environment interactions and stability analysis in *curcuma amada*. The pooled ANOVA revealed highly significant differences due to genotypes, environments, and genotype × environment interaction (GEI), indicating appropriate site selection, substantial variability among the selected genotypes, and the precision of multi-location trials conducted across India. Similar findings were recently reported by Sawargaonkar et al. (2026). The present study shows that BLUP-based genetic parameters provide a statistical foundation for the superiority of specific genotypes identified using WAASBY, MGIDI, and MTSI. The highly significant GEI detected by LRTge and GEIr^2 > 0.83 for all traits explains the need for single-trait WAASBY analysis prior to multi-trait selection. The genotype NVMG 9 exhibited maximum FRY in E17 but had the lowest WAASBY rank, confirming that high mean performance without stability, as captured by its low h^2mg for NTC, leads to poor overall adaptability. This also highlights that genotypes with high performance but low heritability are suited to high-input environments and have limited wider adaptability. Similar results were reported by Mishra et al. (2015); Gupta et al. (2016); Aarthi et al. (2018) and Silaru et al. (2023). For any crop improvement programme high heritability taken in to consideration for identification of stable genotypes. The high h^2mg and selective accuracy for FRY (0.668, 0.817) and FWC (0.713, 0.844) validate the robustness of WAASBY ranks, as these traits showed both high heritability and high CV ratios (12.96 and 130.88, respectively), indicating strong genetic control and high potential for selection response. This explains why *Acc* 265, with WAASBY Rank 1 for both FRY and FWC, also emerged as the MGIDI ideotype with its superior performance in traits with high CVg/CVr and h^2mg resulted in minimal distance from the factor-derived ideotype. Similar results reported by Silaru et al. (2023) for number of tillers per clump in turmeric, Olivoto and Nardino (2021) in wheat, Yue et al., (2022) revealed in maize, and Behera et al. (2024) in forage sorghum. Similarly, the near-unity rge values (0.939–0.999) confirm that

crossover GEI was minimal, supporting the consistency of *Acc* 347 and IMG-1 across methods, their high genotypic means for FRY and PH coupled with high h^2mg translated into top ranks in SH and MTSI, respectively. The low CV ratio and high uniqueness for NTC bring into line with its low h^2mg, explaining why genotypes excelling only in NTC, like Amba (Check), could not dominate MGIDI despite Rank 1 in WAASBY for that trait. Thus, the genetic parameters confirm that MGIDI and MTSI effectively penalized instability and weighted traits according to their heritability and genetic variance, leading to the selection of *Acc* 265, *Acc* 347, and Indira Mango Ginger-1 as truly superior genotypes.

The highest value of communality indicated that these factors could account for a substantial portion of the variance in each trait in factor analysis (FA). In present study only one factor was responsible for the significance among all the traits studied. Similar results were reported by Pour-Aboughadareh et al. (2021) in barley, Yue et al. (2022) in maize hybrids, Oilvoto and Nardino (2021) in wheat and Debsharma et al. (2023) in rice while Behera et al. (2024) reported in forage sorghum using WAASB and MGIDI methods.

Multi-trait stability indices (MGIDI, MTSI, and SH)

In order to select mango ginger varieties that give higher yield and can perform for yield attributing traits together, a method called the Multi-Trait Genotype-Ideotype Distance Index (MGIDI) was used. This method helps select genotypes that come closest to the "ideal" plant high yielding and agronomical superiority among the tested. In the present study multi-trait stability analysis revealed clear superiority of certain genotypes. Based on MGIDI, *Acc 265* (Rank 1), IMG-1 (Rank 2) and NVMG 2 (Rank 3) were identified as the most desirable genotypes considering all traits simultaneously. The MTSI index ranked Indira Mango Ginger-1 first, followed by *Acc 265* and *Acc 347*, confirming their overall stability and adaptability. Similarly, the SH index further confirms the superiority of *Acc 347*, *Acc 265*, and IMG-1 over other accessed genotypes. The consistency across all three indices indicates that these genotypes possess high yielding ability, stability, and adaptability across environments. The rank 1 MTSI genotypes having Rank 2 MGIDI and rank 3 SH index confirms its genetic superiority overall the genotypes studied. The selection process raised the mean performance of yield-related traits (FRY and FWC) indicating effective genotype selection using MGIDI. In present study high heritability recorded for plant height showed larger percentage gains, implying selection is more effective for this character while low heritability for fresh rhizome yield suggests environmental effects are significant, requiring more intensive selection of environmental control.

In present study fresh rhizome yield considered as the dependent traits while plant height, number of tillers per clump and fresh weight of clump was independent traits. It was observed that for all the traits positive correlation were recorded. The highest positive correlation recorded between fresh rhizome yield with fresh weight of clump followed by plant height and number of tillers per clump. The results are in accordance with Das et al. 2026, Sampath et al. 2026; Neeraja et al. 2026; Silaru et al. 2023 in turmeric.

Conclusions

Multi-environment evaluation of 10 mango ginger genotypes across 24 environments revealed substantial genetic variability and strong genotype × environment interaction for all economic traits, necessitating stability-based selection. BLUP analysis confirmed moderate to high heritability on a mean basis and high selection accuracy, indicating that selection based on environmental means would be effective despite low plot-level heritability. CVg/CVr ratios > 10 for fresh rhizome yield, plant height, and fresh weight per clump indicated high prospects for genetic gain, particularly for fresh weight of clump. Integration of mean performance and stability through WAASBY identified *Acc* 265 as the most desirable genotype for yield traits, while MGIDI and MTSI provided concordant evidence that *Acc* 265, Indira Mango Ginger-1, and *Acc* 347 represent the ideotypes for multi-trait selection, combining high productivity with broad adaptation. The Smith-Hazel index further confirmed the superior weighted performance of *Acc* 347. Given their consistent superiority across all statistical models, Acc 265, Indira Mango Ginger-1, and Acc 347 may be recommended for wider cultivation.The high eigenvalue and variance explained by FA1 in MGIDI indicate that selection for a compact, high-tillering, high-yielding plant type will simultaneously improve multiple traits. Genotypes NVMG 9, CAM 3, and RH 408 performed consistently poorly across all indices and should be excluded from breeding programmes.In mango ginger, stability in rhizome yield and component traits is critical due to long crop duration, and strong influence of climatic and edaphic variability on rhizome development. The reduced genotype × environment interaction observed in the identified genotypes suggests a robust genetic architecture governing yield stability, making them particularly suitable for wide-area cultivation across heterogeneous agro-climatic zones. These genotypes also represent valuable genetic resources for use as parental lines in breeding programs aimed at developing high-yielding, stable, and climate-resilient mango ginger cultivars with consistent rhizome productivity.

Declarations

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Author contributions

All the authors directly involved in designing and conduct of experiments, data recording and documentation for individual environments respectively. Prasath Duraisamy contributed by guiding the main research frame work with role of Principal Collaborator between all the authors. Shrikant L. Sawargaonkar had compiled data and analysed and drafted the main manuscript.

Shrikant L. Sawargaonkar – Conceptualization, Writing- original draft; Formal analysis; Writing – review & editing; Data curation; **Ajit Kumar Singh**- Data curation; Resources; **Sarita Agrawal**- Supervision; **Jyoti Sahu**- Supervision; **Parshuram Sial**- Data curation; Supervision; **Asim Kumar Mishra**- Data curation;

Supervision; **Ritesh Patel**-Data curation; supervision; **Najeeb Naduthodi**- Data curation; Supervision; **Anamica Debnath**- Data curation; Supervision; **Ramkrishna Sarkar**- Data curation; Supervision; **Veerendra Verma**- Data curation; Supervision; **M.B. Devi**- Data curation; Supervision; **K.S. Krishnamurthy**- Supervision, Funding acquisition,, **Sharon Aravind**- Data curation; Supervision, **Souderarajan Aarthi**- Data curation; Supervision, **S. Mukesh Sankar**- Data curation; Supervision, Writing – review & editing, and **Duraisamy Prasath** – Conceptualization, Supervision, Funding acquisition, Writing – review & editing

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Data availability

Data will be made available on request.

Competing Interest

The authors confirm that they do not have any conflicts of interest.

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Tables

Table1 List of mango ginger genotypes included in the present study

Genotype code	Genotype Name	Characteristics	Pedigree Information
G1	*Acc 265*	High sprouting, more number of fingers / clump, high yielding	Clonal selection at ICAR-IISR, Kozhikoc
G2	*Acc 347*	Tall, more tillers /clump, high yielding	Clonal selection at ICAR-IISR, Kozhikoc
G3	CAM 2	Medium height, dark green and large leaves	Clonal selection at HARS, OUAT, Pottar
G4	CAM 3	Medium height, good germination, large leaves	Clonal selection at HARS, OUAT, Pottar
G5	Indira Mango Ginger-1 (IMG-1)	Tall, light-yellow colour, good fragrance, high oleoresin	Clonal selection at CARS, Raigarh, IGK
G6	NVMG 2	High yielding, medium height	Clonal selection at NAU, Navsari, Gujar
G7	NVMG 9	Tall, elongated leaves	Clonal selection at NAU, Navsari, Gujar
G8	NVMG 10	Tall, elongated leaves	Clonal selection at NAU, Navsari, Gujar
G9	RH 408	High yielding	Clonal selection at Dholi, Bihar
G10	Amba (Check)	High yielding, good fragrance	Identified variety at HARS, Pottangi

Table 2 Characterization of the growing environment based on location, growing season, and meteorological parameters

Particulars	Location	Lattitude/ Longitude/ Altitude	Soil Type	Planting season	Mean temperature (°C)		Total Rainfall (mm)
					Maximum	Minimum	
E1	Ambalavayal	11.62° N, 76.21° E, 900 m	Reddish brown	Rainy, 2020 to 2022	34.2	18.2	2300
E2	Pottangi,	18.56° N and 82.96° E, 914.4 m	Laterite Soils	Rainy, 2020 to	30.4	13.7	1520
E3	Kozhikode	11.25 N and 75.78^0 E, 34 m	Laterite Soils	Rainy, 2020 to 2022	32.3	28.4	3266
E4	Dholi	25.99^0 N and 85.59^0E, 170 m	Alluvial	Rainy, 2020 to 2022	31.5	21.8	1260
E5	Barapani	25.41^0 N and 91.63^0E, 952	Red loam / Hill soil	Rainy, 2020 to 2022	34	11.2	2390
E6	Pundibari	26.40^0 N and 89.38^0E, 43 m	Sandy loam to clay loam	Rainy, 2020 to 2022	32.2	08.1	2000
E7	Raigarh	21.9^0 N and 83.4^0E, 243.7 m	Yellow soil (Matasi/ Dorsa/Kanhar)	Rainy, 2020 to 2022	36.2	08.4	1484.7
E8	Navsari	20.95^0 N and 72.93^0E, 14 m	Clay loam	Rainy, 2020 to 2022	37.4	13.4	1564.4

Table 3 Pooled analysis of variance with mean sum of squares for yield and yield attributing traits in eight diverse environments

Source	Df	FRY	PH	NTC	FWC
ENV	23	2707.2**	30799.6**	509.3**	1084225.0**
REP (ENV)	48	4.7	11.2	11.2	11.5
GEN	9	645.4**	9603.5**	6.9**	145169.7**
GEN : ENV	207	214.6**	1665.7**	4.0**	41629.0**
Residuals	432	0.0	0.1	0.1	0.1
CV (%)	0.81	8.25	3.08	6.21	0.08
MSR+/MSR-	1.74	4.6	3.96	3.03	1.23
OV mean	23.38	20.4	94.06	4.66	326.92

Table 4 BLUP based genetic parameters for FRY, PH, NTC and FWC in mango ginger

Parameters	FRY	PH	NTC	FWC
LRTg	7.44***	23.36***	1.57***	10.06***
LRTge	3039.76***	3554.62***	974.51***	4944.97***
Phenotypic variance	77.52523	665.5369	1.424435	15314.48
Heritability	0.077187	0.165654	0.028691	0.093905
GEIr2	0.922354	0.83422	0.912367	0.90609
h2mg	0.667582	0.826558	0.427487	0.713245
Accuracy	0.817057	0.909153	0.653825	0.844538
rge	0.999502	0.999849	0.939317	0.999994
CVg	10.4611	11.16184	4.336332	11.59969
CVr	0.807163	0.308021	6.215258	0.088631
CV ratio	12.96032	36.2372	0.697691	130.8769
Mean	23.38	94.07	4.66	326.93
SE	0.47	1.48	0.16	8.21
Min	6.6 (RH 408 in E5)	45.6 (IMG-1 in E17)	1 (CAM-2 in E16)	54.1 (AMBA in E2)
Max	67.07 (NVMG 9 in E17)	142.37 (CAM 2 in E13)	18.53 (CAM 2 in E22)	1086.2 (NVMG 2 in E21)
MinENV	E10 (3.94)	E2 (35.55)	E2 (1.09)	E2 (24.81)
MaxENV	E12 (43.69)	E8 (131.92)	E22 (15.28)	E21 (726.15)
MinGEN	CAM 2 (20.2)	NVMG 9 (75.28)	RH 408 (4.2)	NVMG 9 (262.28)
MaxGEN	Acc 347 (29.04)	Acc 347 (111.2)	IMG-1 (5.24)	NVMG 2 (378.51)

Notes: *** significant at P < 0.001, LRT significance test is conducted against the Chi-square value

LRT - The Likelihood Ratio Test for the random effects; Phenotypic variance the phenotypic variance; Heritability the broad-sense heritability BLUP basis; R^2_{ge} the coefficient of determination of the interaction effects; h^2_{mg} the heritability on the mean basis; Accuracy the selective accuracy; rge the genotype-environment correlation; CV_g the genotypic coefficient of variation; CVr the residual coefficient of variation; CV ratio the ratio between genotypic and residual coefficient of variation; FRY-Fresh rhizome yield t ha^{-1}, PH =Plant height (cm), NTC = Number of tillers /plant, FWC = Fresh weight of clump

Table 5 Selection of stable mango ginger genotypes using WAASB score for fresh rhizome yield and FRY attributing traits

	WAASB VALUE				RANK			
GENOTYPES	FRY	PH	NTC	FWC	FRY	PH	NTC	FWC
Acc 265	1.21	4.81	0.54	5.56	2	9	4	2
Acc 347	2.53	4.47	0.60	5.97	7	5	5	4
CAM 2	2.41	4.47	1.09	5.86	6	6	9	3
CAM 3	3.44	4.65	0.94	10.50	10	8	7	9
IMG-1	1.96	3.48	0.95	5.02	5	3	8	1
NVMG 2	1.79	3.12	0.41	10.25	4	1	2	8
NVMG 9	3.32	4.96	1.73	12.88	9	10	10	10
NVMG 10	1.70	3.30	0.40	8.33	3	2	1	5
RH 408	2.89	4.49	0.80	9.72	8	7	6	7
Amba (Check)	0.96	3.56	0.44	9.35	1	4	3	6

Table 6 Selection of stable mango ginger genotypes using WAASBY value for fresh rhizome yield and FRY attributing traits

	WAASBY VALUE				WAASBY RANK			
GEN	FRY	PH	NTC	FWC	FRY	PH	NTC	FWC
Acc 265	80.21	42.63	68.51	96.37	1	6	6	1
Acc 347	68.52	63.25	76.26	93.84	2	5	3	2
CAM 2	20.89	27.07	33.18	54.32	7	7	9	6
CAM 3	0.18	25.43	33.46	34.36	10	8	8	8
IMG-1	62.92	81.06	79.26	85.81	3	1	2	3
NVMG 2	50.71	76.76	75.72	66.73	6	3	4	5
NVMG 9	12.03	0.00	24.59	0.00	9	10	10	10
NVMG 10	58.15	71.55	69.98	68.92	4	4	5	4
RH 408	15.50	21.79	35.05	31.38	8	9	7	9
Amba (Check)	57.69	77.04	79.67	34.93	5	2	1	7

Table 7 Classification of genotypes based on Y x WAASB plot for four traits in mango ginger genotypes

Trait	Quadrant No.	Category	Genotypes and Environments
FRY	Q4	Highly Yield and stable genotypes	ACC265, ACC347, IMG-1, NVMG 10, E2, E21, E11, E13, E19, E15, E4, E7
PH	Q3	Poor Yield and stable genotypes	NVMG2, NVMG10, E9, E3, E11
NTC	Q4	High yield but unstable genotypes	Amba (check), IMG-1, *ACC 347*, NVMG 2, E14, E3
FWC	Q4	Highly Yield and stable genotypes	IMG-1, *ACC 265*, *ACC 347*, E12, E20, E24, E16, E8, E23

* Q3 – includes poor yield and stable genotypes as lower height is desirable

Table 8 Different multi -trait stability index scores of 10 mango ginger genotypes

Genotype	MGIDI	Rank	Genotype	MTSI	Rank	Genotype	SH	Rank
Acc 265	0.003604	1	IMG-1	0.026876	1	*Acc 347*	466.4153	1
IMG-1	0.250864	2	*Acc 265*	0.314708	2	*Acc 265*	421.4662	2
0NVMG 2	0.504936	3	*Acc 347*	0.546342	3	IMG-1	415.2277	3
Acc 347	0.649425	4	NVMG 10	0.728867	4	NVMG 10	386.5888	4
NVMG 10	0.656576	5	NVMG 2	0.730726	5	NVMG 2	367.3525	5
Amba (Check)	0.905806	6	Amba (Check)	0.762082	6	NVMG 9	354.8233	6
CAM 3	1.820336	7	CAM 2	1.721522	7	Amba (Check)	335.6498	7
NVMG 9	1.886678	8	CAM 3	1.893646	8	RH 408	334.1002	8
CAM 2	1.929109	**9**	RH 408	1.992138	9	CAM 2	318.6803	9
RH 408	2.073762	10	NVMG 9	2.181808	10	CAM 3	317.3633	10

Table 9 Eigenvalues, explained variance and the community obtained after superposition by factor analysis in MGIDI

VAR	FA1	Communality	Uniqueness
FRY	0.94	0.88	0.12
PH	-0.92	0.84	0.16
NTC	0.79	0.62	0.38
FWC	0.85	0.73	0.27
Eigenvalues	3.07		
Variance (%)	76.76		
Cum. Variance (%)	76.76		

Table 10 Selection differential for mean performance and stability according to the WAASBY index for yield contributing traits using MGIDI index

MGIDI						Smith – Hazel Index						
VAR	Factor	Xo	Xs	SD	SD %	Xo	Xs	SD	SD %	h2	SG	SG%
FRY	FA1	23.38	25.28	1.90	8.11	23.38	26.77	3.39	14.49	0.22	0.77	3.31
PH	FA1	94.07	102.20	8.13	8.64	94.06	105.21	11.14	11.84	0.32	3.62	3.85
NTC	FA1	04.66	4.79	0.13	2.77	4.66	4.66	0.00	0.00	0.00	0.00	0.00
FWC	FA1	326.9	351.80	24.88	7.61	326.92	362.22	35.30	10.79	0.15	5.51	1.68

Xo = mean of the original population; Xs = mean of the selected genotypes; SD and SD %: The selection differential and selection differential in percentage, respectively; SG and SG %: The selection gains and selection gains in percentage, respectively

Figures

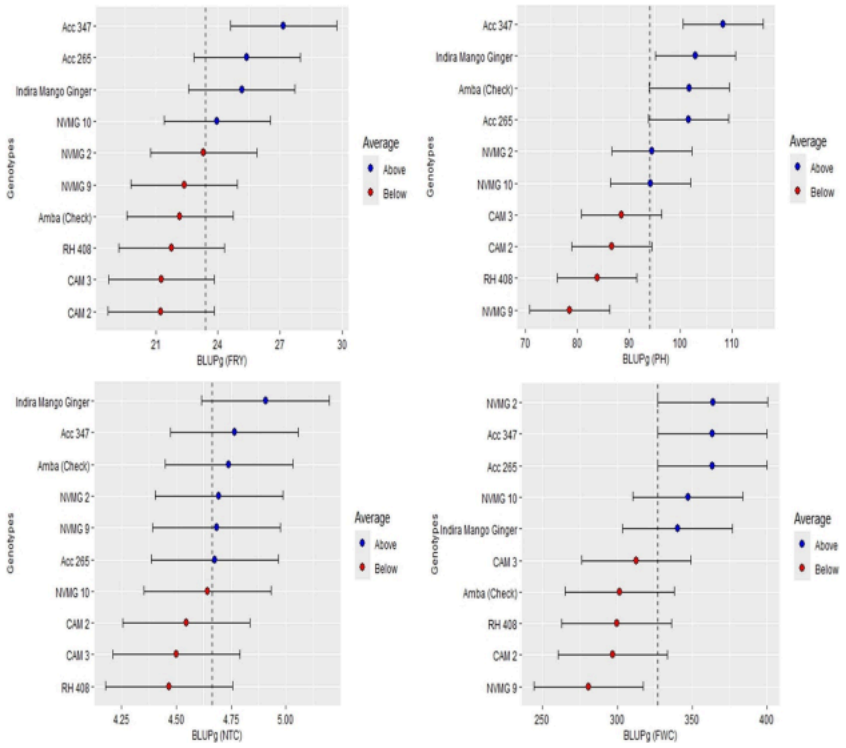


Figure 1

Predicted mean (best linear unbiased prediction, BLUP) for 10 Mango ginger genotypes. Blue and red circles represent the genotypes that had BLUP above and below of BLUP means, respectively. Horizontal error bars represent the 95% confidence interval of prediction considering a two-tailed t test.

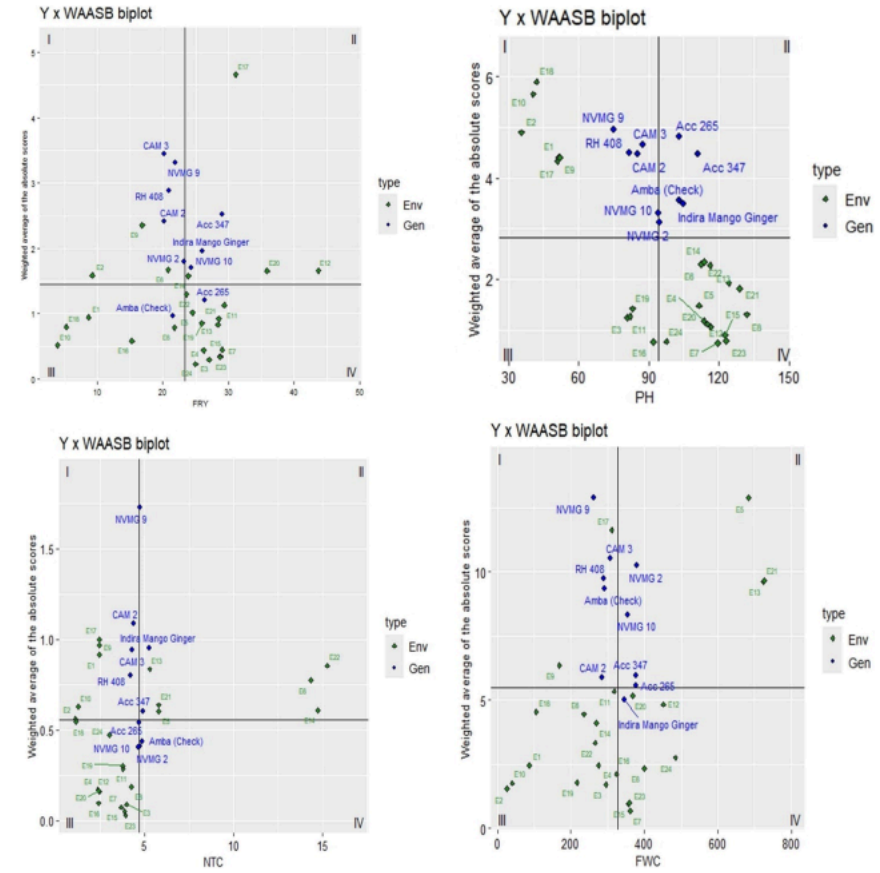


Figure 2

Biplot of the FRY, PH, NTC & FWC vs. weighted average of absolute scores for the best linear unbiased prediction s of the genotype- vs.-environment interaction (WAASB) of 10 Mango ginger genotypes evaluated in 24 environments.

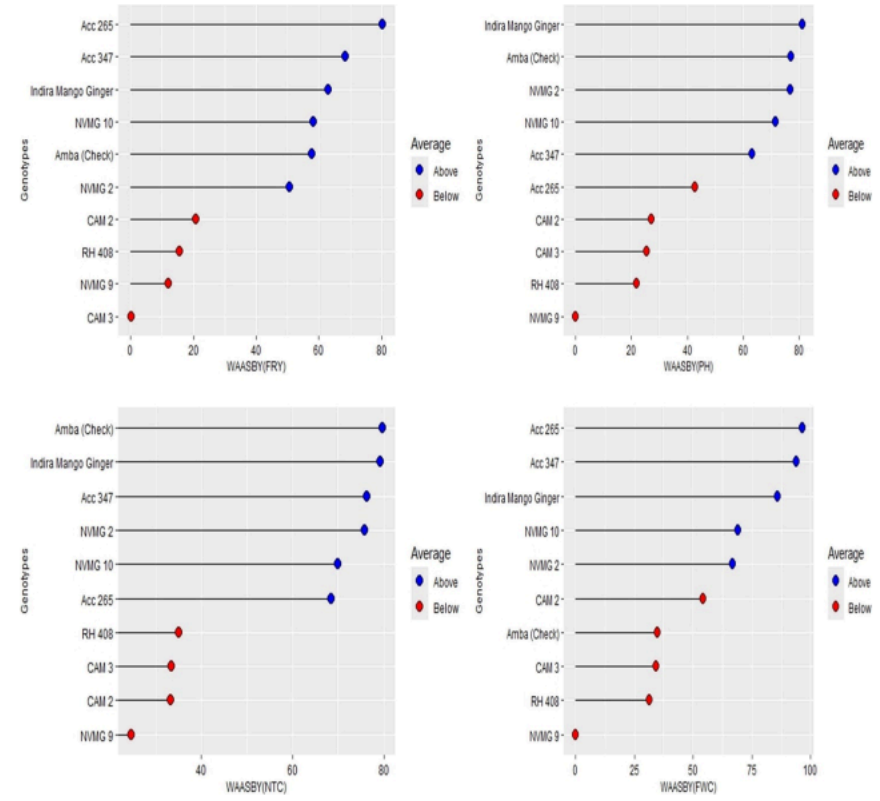


Figure 3

Estimatedvalues of weighted average of the stability (WAASB) and mean performance (Y) (WAASBY) for 10 mango ginger genotypes considering the weights of 65 and 35 for yielding and stability, respectively.

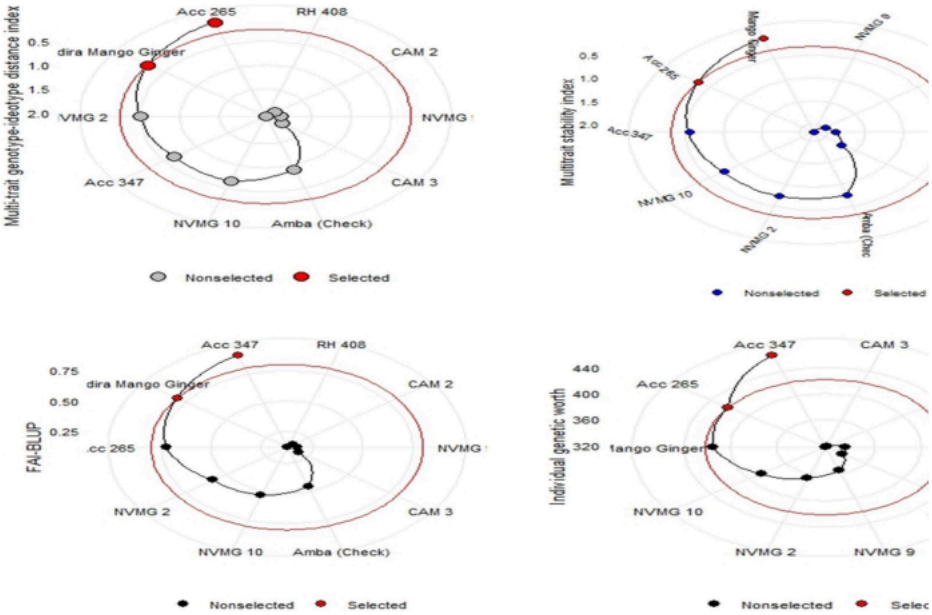


Figure 4

Selection of Mango ginger genotypes at 20% selection intensity through multi trait – based stability methods (Smith –Hazel index, FAI – BLUP index; MGIDI& MTSI)

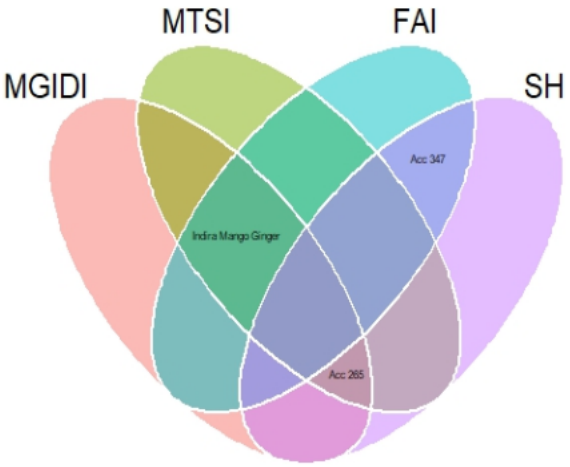


Figure 5

Comparing different multi trait based stability methods using Venn diagram plot in mango ginger genotype

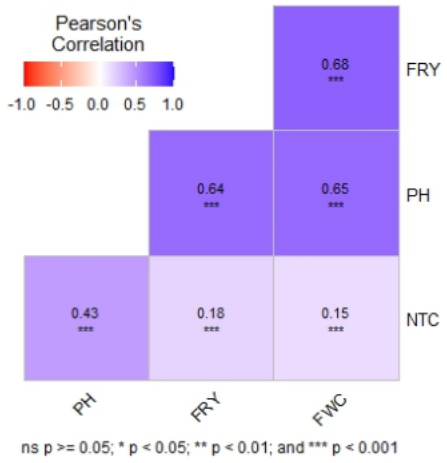


Figure 6

Correlation analysis in 10 mango ginger genotypes for fresh rhizome yield and attributing traits

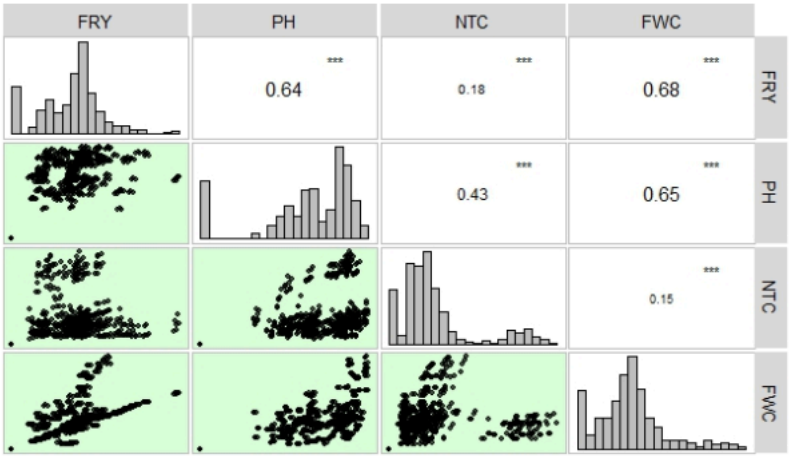


Figure 7

The correlation and frequency distributions of four agronomic traits among ten mango ginger genotypes