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Characterization of early maturing elite genotypes based on MTSI and MGIDI indexes: an illustration in upland cotton (*Gossypium hirsutum* L.)

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Abstract

Background Globally, the cultivation of cotton is constrained by its tendency for extended periods of growth. Early maturity plays a potential role in rainfed-based multiple cropping system especially in the current era of climate change. In the current study, a set of 20 diverse *Gossypium hirsutum* genotypes were evaluated in two crop seasons with three planting densities and assessed for 11 morphological traits related to early maturity. The study aimed to identify genotype(s) that mature rapidly and accomplish well under diverse environmental conditions based on the two robust multivariate techniques called multi-trait stability index (MTSI) and multi-trait genotype-ideotype distance index (MGIDI).

Results MTSI analysis revealed that out of the 20 genotypes, three genotypes, viz., NNDC-30, A-2, and S-32 accomplished well in terms of early maturity traits in two seasons. Furthermore, three genotypes were selected using MGIDI method for each planting densities with a selection intensity of 15%. The strengths and weaknesses of the genotypes selected based on MGIDI method highlighted that the breeders could focus on developing early-maturing genotypes with specific traits such as days to first flower and boll opening. The selected genotypes exhibited positive genetic gains for traits related to earliness and a successful harvest during the first and second pickings. However, there were negative gains for traits related to flowering and boll opening.

Conclusion The study identified three genotypes exhibiting early maturity and accomplished well under different planting densities. The multivariate methods (MTSI and MGIDI) serve as novel approaches for selecting desired genotypes in plant breeding programs, especially across various growing environments. These methods offer exclusive benefits and can easily construe and minimize multicollinearity issues.

Keywords Cotton, MTSI, MGIDI, Genotype environment interaction, Early maturity, Multi-trait, Multi-environment

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Background

Cotton, the most extensively relied-upon crop for textile fibers and one of the most lucrative cash crops, belongs to the genus *Gossypium*. According to Ulloa et al. (2005), *Gossypium* currently includes seven allotetraploid species and approximately 45 diploid species. Two allotetraploid species (*Gossypium hirsutum* L. and *G. barbadense* L.) and two diploid species (*G. herbaceum* L. and *G. arboreum* L.) were autonomously domesticated in the New and the Old Worlds, respectively (Renny-Byfield et al., 2016; Wendel et al., 2003). With 95% global production, upland cotton (*G. hirsutum*, $2n=4x=52$) has supplanted other categories and seized control as the preferred species (Tyagi et al., 2013). In India 33.723 million bales (170 kg per bale) of cotton was produced on 13.049 million hectares, with the productivity of 439 kg·ha^{-1} [ICAR-AICRP (cotton) annual report (2022-23), 2023].

The decision to devote land to other certain crops is driven by the more prolonged maturation time of cotton (Li et al., 2013), which usually results in an appreciation for cultivars with a short growing season. *G. hirsutum* was first domesticated at least 5 000 years ago (Smith et al., 1971). The whole growth period (WGP) of wild *G. hirsutum* is typically more than 180 days; in addition, the presence of photoperiod sensitivity makes its application in breeding programmes challenging (Zhu et al., 2014). Thus, early maturity in crops is an invaluable breeding strategy, as it offers a reformed tillage system and the improvement of multiple cropping indices, meanwhile curbing yield loss caused by harsh ecological circumstances. After thousands of years of direct selection, the early maturity of upland cotton has significantly improved; in particular, the WGP has significantly shortened to approximately 140 days, especially over the last ten years of directed breeding efforts.

The days to the first flower (DFF), days to the first boll opening (DFBO), flower to boll opening period (FBOP), the node number of the first fruiting branch (NNFFB), and height of the first fruiting branch (HFFB) constitute some of the scales used for determining early maturity in cotton, along with others such as Bartlett's index (BI), the proportion of primary and secondary pickings to the overall yield, earliness percentage (EP), mean maturity date (MMD), and production rate index (PRI). The most practical way to determine maturity is simply by juxtaposing the yield of early harvests with the total seed cotton yield harvested (Richmond et al., 1962). Notably, Ray et al. (1966) preferred that NNFFB is the most precise and advantageous over several morphological markers of early maturity in cotton.

Early maturity in cotton is a complex quantitative trait, characterized as being influenced by polygenes and the environment. Accordingly, it becomes important to comprehend how the genotypes work under a certain set of environmental conditions. This understanding can be achieved by exploring genotype-environment interactions (GEI) and stability analysis of target traits. Multivariate selection indices, such as the well-known Smith (1936) and Hazel (1943) indices, can be utilized for the selection of genotypes. However, Smith and Hazel indices were operated by inverting a multicollinearity-problematic phenotypic covariance matrix, which results in suboptimal selection of beneficial genetic characteristics pursuant to diverse environmental situations (Bizari et al., 2017; Rocha et al., 2018; Burdon et al., 2019). The multi-trait stability index (MTSI) (Olivoto et al., 2019b) and the multi-trait genotype-ideotype distance index (MGIDI) (Olivoto et al., 2021) were recently introduced indices that have arisen as innovative tools for selecting superior genotypes with enhanced performance under various environmental conditions, while maintaining stability for desirable traits. In light of this background, the current work provides a framework for determining ideal and early-maturing cotton genotypes under a range of microclimate conditions by using the MTSI and MGIDI indices for multi-trait stability analysis.

Materials and methods

Planting materials and field evaluation

The present investigation consisted of 20 *G. hirsutum* genotypes of diverse origins with different plant statures. The pedigree details, along with the special features of the genotypes are presented in Table S1. These genotypes were evaluated at the experimental fields of Agricultural Research Station, Dharwad, Karnataka, India, which aligns in the northern transitional zone (Zone 8) of Karnataka ($25^0$17' N, $71^0$46' E, and an altitude of 678 m above mean sea level) during rainy season in 2021 (season 1) and rainy season in 2022 (season 2) under three planting densities (Table 1). The experimental trial was carried out by adopting a completely randomized block design with two replications in each site. The seeds were hand dibbled as per different planting densities with varying plant-to-plant spacings of 15 cm, 30 cm, and 60 cm as described in Table 1. Each genotype was sown in 3 rows with a row-to-row spacing of 60 cm in a 4.2 m long bed, constituting a plot area of 7.56 m^2. The crop was raised as per the recommended package of practices to attain a good and healthy crop completely in rainfed conditions with the fertilizer dose of 40 kg N, 20 kg P_2O_5, and 20 kg K_2O per hectare. Alongside, meteorological parameters such as temperature, rainfall, and relative humidity were noted during both crop seasons. The maximum and minimum temperatures were 35.40 °C and 13.20 °C, respectively, and the average relative humidity was 66.40%

Table 1 Description of the planting densities in 2021 and 2022

Row and plant spaces /cm	Details of planting density	Plants per hectare	Designation of planting densities
60×15	High density cultivation situation	111 111	E1
60×30	Recommended cultivation situation	55 555	$E2_2$
60×60	Sparse density cultivation situation, where hybrids are grown in this geometry, usually	27 777	E3

across crop seasons. The annual rainfall was 1 052.30 mm and 1 101.64 mm during season 1 (2021) and season 2 (2022), respectively (Fig. S1).

Trait assessment

Various traits such as NNFFB and HFFB (cm) were documented for five randomly selected uniform plants at maturity. Phenological variables such as DFF, DFBO, the percent of crop harvest at the first pick (PCH-1), the percent of crop harvest at the first two picks (PCH-2; percentage of the seed cotton yield harvested in combined first and second pickings to total seed cotton yield harvested), the percent of crop harvest at the last pick (PCH-L; here indicated 5^{th} picking), BI (Bartlett, 1937), EP (Attiea, 2020), MMD (Christidis et al., 1955), and PRI ($g{\cdot}d^{-1}$) (Bilbro et al., 1973) were recorded on plot basis.

Statistical analysis

Pooled analysis and individual analysis for components of variance were computed in each environment using the "anova_joint" and "anova_ind" functions of the "metan" package (Olivoto et al., 2020) in R studio with R v.4.2.3 (R Core Team, 2021) to assess the significance of random effects. A likelihood ratio test (LRT) employing a two-tailed chi-square test with four degrees of freedom was conducted. Levene's test of homogeneity of variance (Levene, 1960) was conducted across planting densities using the 'car' package (Fox et al., 2019) in R studio with R v.4.2.3. Based on the significance or non-significance of Levene's test, the decision to combine the data of individual environments from both crop seasons was made. Best linear unbiased predictions (BLUP) were predicted to account for random effects across years using "multi environment trial analysis with R" (META-R) v6.04 statistical software (Alvarado et al., 2020). MTSI was employed to categorize genotypes that matured early and were stable for multiple traits. Within each test microclimate, MGIDI was applied to find the genotypes with early maturation under specific conditions, thereby capitalizing on narrow adaptation. Further, the stability analysis across three planting densities over two years was accomplished using the "metan" package v.1.18.0 (Olivoto et al., 2020). The mean performance of genotypes for various traits across seasons was depicted through box plots, which were elucidated using the "tidyverse v.2.0.0" package (Wickham et al., 2019) in R studio with R v.4.2.3.

Following ideotype perception, the MTSI/MGIDI involves rescaling of traits on a 0 to 100 scale. A value of 0 denotes the least valued trait, while 100 represents the most valuable and desired trait. This rescaling facilitated the definition of an ideotype, as proposed by Donald (1968).

Mean performance and stability of multiple traits

The preliminary phase was to perform a stability analysis and acquire the weighted average of absolute scores (WAASB) from the singular value decomposition (SVD) of the matrix of BLUP for the GEI effect (Olivoto et al., 2019a) for the individual genotypes. Subsequently, both the mean performance of early maturity indicators and the WAASB index stability values were rescaled to the range of 0 to 100, where 0 depicts the most undesirable value (e.g., the genotype with the most days to first flowering will have the lowest rescaled value of 0), and 100 for the most anticipated value (Olivoto et al., 2019a). The rescaled value of a given trait for the i^{th} genotype and the j^{th} trait for both mean performance (rY_i) and stability (rW_i) is given by Olivoto et al. (2019a). The genotype with a rescaling value of 100 for all the preferred traits represents the ideal genotype. For traits such as DFF, DFBO, NNFFB, HFFB, PCH-L, and MMD where negative gains are desired, we considered the original maximum and minimum values to be 0 and 100, respectively. However, for traits PCH-1, PCH-2, EP, BI, and PRI, where positive gains are desired, the original maximum and minimum values were considered to be 100 and 0, respectively.

The WAASB index

To determine the mean performance and stability of each trait, the WAASB index (Olivoto et al., 2019a) was calculated as per the formula.

$$WAASBY_i = \frac{(rY_i \times \theta_Y) + (rW_i \times \theta_W)}{\theta_Y + \theta_W}$$

where, $WAASBY_i$ is the superiority index for the i^{th} genotype; rY_i is the rescaled values (0 to 100) for the response trait (Y); rW_i is the rescaled values (0 to 100) for stability (WAASB); θ_Y is the weight of mean performance (e.g., days to first flowering); θ_W is the weight of stability (WAASB).

In the current analysis, we regarded higher weight for mean performance at the expense of stability. A two-way table comprising the WAASBY index of individual genotypes studied for each trait (rX_{ij}) was acquired and used to calculate the eigen values and vectors (Benakanahalli et al., 2021). The initial loadings were attained considering only the factors with eigen values > 1. Besides, varimax rotation criteria (Kaiser, 1958) was applied for determining the final loadings.

Ideotype prediction and MTSI index

The MTSI value (Olivoto et al., 2019b) was obtained using the equation given below:

$$MTSI_i = \left[\sum_{j=1}^{f} (F_{ij} - F_j)^2\right]^{0.5}$$

where, $MTSI_i$ is the multi-trait stability index of the i^{th} genotype; F_{ij} is the j^{th} score of the i^{th} genotype; F_j is the j^{th} score of the ideotype; and f is the number of factors. The genotype with the lowest MTSI value would be closer to the ideotype and portray higher mean performance and stability for the variables. The "*waasb*" and "*mtsi*" functions in "metan" package (Olivoto et al., 2020) were utilised to determine the MTSI index.

Multiple-trait mean performance within each planting densities

The genotypes with superior performance for the majority of the traits under each planting density were selected using MGIDI (Olivoto et al., 2021). The rescaled matrix used for factor analysis in the MGIDI was acquired with the BLUP for the mean performance of the genotype, in contrast to the WAASB (both mean performance and stability) in the MTSI. However, MGIDI and MTSI share the same mathematical foundations (trait rescaling, factor analysis computation, and the distance of each genotype to the ideotype). The genotype representing the desired values for all of the examined features within each environment is thus closest to the genotype with the minimal MGIDI. The MGIDI for the i^{th} genotype ($MGIDI_i$) was calculated as follows:

$$MGIDI_i = \left[\sum_{j=1}^{f} (\gamma_{ij} - \gamma_j)^2\right]^{0.5}$$

where, γ_{ij} is the score of the i^{th} genotype for the j^{th} factor ($i = 1, 2, \ldots, g$; $j = 1, 2, \ldots, f$); γ_j is the j^{th} score of the ideotype. The strengths and weaknesses of the genotypes within each environment were calculated as follows,

$$\omega_{ij} = \frac{\sqrt{D_{ij}^2}}{\sum_{j=1}^{f} \sqrt{D_{ij}^2}}$$

where, ω_{ij} is the MGIDI index of the i^{th} genotype explained by the j^{th} factor; and D^2_{ij} is the distance between the i^{th} genotype and ideotype for the j^{th} factor.

Traits approaching the ideotype were indicated by factors with low contributions. To calculate the MGIDI index, the "*gamem*" and "*mgidi*" functions in "metan" package (Olivoto et al., 2020) were used. The broad-sense heritability (h^2_{bs}) was estimated using the formula outlined by Allard et al. (1964). The broad-sense heritability based on genotypic mean performance (h^2_{mg}) was determined as follows:

$$h^2_{mg} = \frac{\sigma_g^2}{\sigma_g^2 + \frac{\sigma_i^2}{e} + \frac{\sigma_e^2}{eb}}$$

where, σ^2_g, σ^2_i and σ^2_e are the variances related to genotypes, genotype–environment interaction, and error terms, respectively; and e and b indicates the number of environments and blocks per environment, respectively.

The selection differential (ΔS) was calculated based on the mean of the selected parents (X_S) and the mean of the original population before selection (X_o) (Falconer et al., 1996).

$$\Delta S(\%) = [(X_s - X_\circ)/X_\circ] \times 100$$

Results

Mean performance and analysis of variance

The ANOVA results revealed that DFF, DFBO, PCH-1, PCH-2, PCH-L, BI, EP, and PRI were significantly different ($P < 0.05$) across planting densities (Table S2). The variation among the 20 genotypes for all traits under study is shown in Fig. 1. Regardless of environments and genotypes, DFF ranged from 65.33 to 83.67 days, and DFBO ranged from 120.00 to 137.67 days. The maximum variability was perceived for PCH-2 and EP among the genotypes, while the least variation was observed for BI and NNFFB. The highest coefficient of variation (CV) was PCH-L (105.04%)

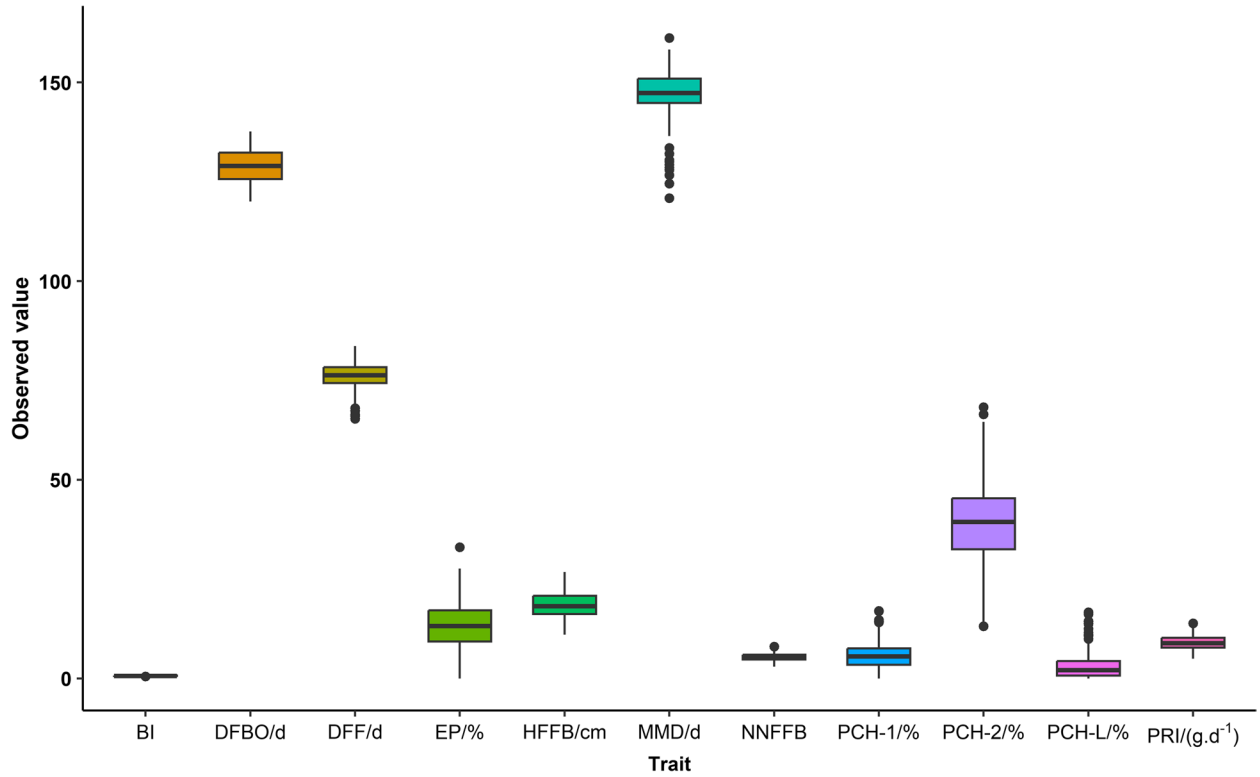

Fig. 1 Box plot depicting the variation for different traits of 20 cotton genotypes under three environments used in this study. BI: Bartlett's index, DFBO: Days to first boll opening (days), DFF: Days to first flower (days), EP: Earliness percentage, HFFB: Height of the first fruiting branch (cm), MMD: Mean maturity date, NNFFB: Node number of the first fruiting branch, PCH-1: Percent crop harvest at the first pick, PCH-2: Percent crop harvest at the first two picks, PCH-L: Percent crop harvest at the last pick, PRI: Production rate index ($g \cdot d^{-1}$)

with a range of 0.00 to 16.69%, followed by PCH-1 (55.38%), and EP (43.47%), while the least CV was evident in DFBO (3.01%) (Table 2). The results highlighted sufficient variation among genotypes for the diverse characters under the study. Further, the mean performance of each genotype in each environment was represented in Table S3-S8.

Variance components and likelihood ratio test

The LRT revealed significant effects due to GEI for DFF, PCH-1, PCH-L, BI, EP, and PRI. Across the traits, nearly 32% of the phenotypic variance was due to the genotypic variance. For traits such as DFF, DFBO, PCH-1, PCH-2, HFFB, and EP, the contribution from genotypic variance was higher than the GEI variance. Most traits exhibited medium heritability ($h^2_{bs} > 0.30$) except for NNFFB, HFFB, MMD, and PRI. The genotypic selection accuracy (AS) values ranged from 0.72 (HFFB) to 0.94 (DFF, DFBO, PCH-1, PCH-2, and EP). PCH-L recorded the highest genotypic coefficient of variation (CV_g). The GEI effects (R^2_{ge}) were relatively higher for DFF, PCH-1, PCH-L, and PRI, indicating the GEI as an important component of the phenotypic variance (Table 2).

Genotype selection across the test environments using MTSI

Correlation among traits

PCH-2, EP, and PCH-1 showed significant negative correlations with DFF, DFBO, PCH-L, and MMD. BI, PRI, DFBO, and NNFFB were negatively correlated with PCH-L and MMD. PCH-1, PCH-2, BI, EP, and PRI were positively correlated with each other. MMD and PCH-L displayed significant positive correlation ($r = 0.61$) (Fig. 2). The associations among the morphological traits in each environment were provided in Fig. S2.

Loadings, factor delineation, and selection gain

Factors with eigenvalues > 1 were retained. Eleven traits in this study with significant variation under each planting density were grouped into three factors, accounting for 72.48% of the total variation (Table 3). After proper varimax rotation, the mean communality was 0.72, indicating that the greater ratio of each trait variance was influenced by the three factors. FA1 clustered DFF, DFBO, PCH-2, PCH-L, BI, and MMD; FA2 grouped HFFB, NNFFB, and PRI; and FA3 grouped PCH-1 and EP (Tables 3 and 4). Three early maturing

Table 2 Likelihood ratio test, deviance analysis, genetic parameters, and variance components for 11 morphological traits evaluated in 20 cotton genotypes

Parameter	DFF	DFBO	PCH-1	PCH-2	PCH-L	BI	HFFB	NNFFB	EP	MMD	PRI
SE	0.21	0.25	0.21	0.67	0.21	0.00	0.20	0.06	0.38	0.38	0.11
CV/%	4.24	3.01	55.38	26.43	105.04	9.02	16.73	16.43	43.47	3.98	19.30
σ^2_p	7.63	5.09	9.14	71.16	5.03	0.00	5.36	0.52	30.16	19.39	1.57
σ^2_g	3.57	2.26	4.57	29.12	1.66	0.001	0.50	0.08	13.57	3.15	0.39
σ^2_{ge}	1.41	0.52	0.42	2.03	5.87	2.69	0.0002	0.72	0.01	3.48	0.50
h^2_{bs}	0.47	0.44	0.50	0.41	0.33	0.41	0.09	0.15	0.45	0.16	0.25
GEI R^2	0.19	0.10	0.22	0.08	0.54	0.12	0.14	0.03	0.12	0.03	0.36
h^2_{mg}	0.89	0.89	0.89	0.88	0.77	0.87	0.52	0.68	0.89	0.69	0.73
AS	0.94	0.94	0.94	0.94	0.88	0.93	0.72	0.82	0.94	0.83	0.85
R^2_{ge}	0.35	0.19	0.44	0.14	0.80	0.20	0.15	0.03	0.21	0.03	0.49
CV_g	2.48	1.17	36.81	13.77	41.74	3.99	3.84	5.24	27.54	1.21	6.96
CV_r	2.14	1.18	27.49	15.35	26.65	4.32	10.99	12.10	27.07	2.70	8.61
CV_g/CV_r	1.16	0.99	1.34	0.90	1.57	0.92	0.35	0.43	1.02	0.45	0.81
LRT_{ge}	13.71	3.67	23.34	2.06	111.45	4.10	2.36	0.10	4.73	0.10	28.79
***P*-value**	2.1×10^{-4}	5.55×10^{-2}	1.36×10^{-6}	1.51×10^{-1}	4.71×10^{-26}	4.28×10^{-2}	1.24×10^{-1}	7.56×10^{-1}	2.96×10^{-2}	7.53×10^{-1}	8.07×10^{-8}

SE Standard error, *CV* Coefficient of variation, σ^2_p Phenotypic variance, σ^2_g Genotypic variance, σ^2_{ge} GEI variance, h^2_{bs} Broad sense heritability, *GEI* R^2 GEI coefficient of determination, h^2_{mg} Heritability of genotypic mean, *AS* Accuracy of genotype selection, R^2_{ge} Association among genotypic values across environments, CV_g Genotypic coefficient of variation, CV_r Residual coefficient of variation, LRT_{ge} Likelihood ratio test for GE interaction, *P-value* Probability value, *DFF* Days to first flower, *DFBO* Days to first boll opening, *PCH-1* Percent crop harvest at the first pick, *PCH-2* Percent crop harvest at the first two picks, *PCH-L* Percent crop harvest at the last pick, *BI* Bartlett's index, *HFFB* Height of the first fruiting branch, *NNFFB* Node number of the first fruiting branch, *EP* Earliness percentage, *MMD* Mean maturity date, *PRI* Production rate index

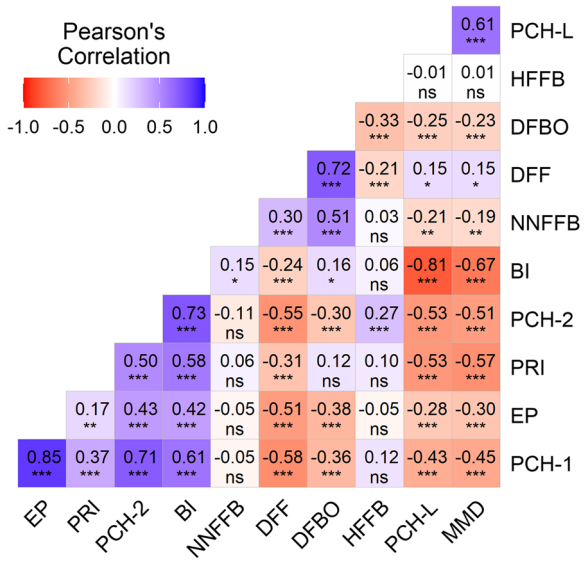

Fig. 2 Pearson's correlation between eleven early maturity related traits. DFF: Days to first flower, DFBO: Days to first boll opening, PCH-1: Percent crop harvest at the first pick, PCH-2: Percent crop harvest at the first two picks, BI: Bartlett's index, HFFB: Height of the first fruiting branch, NNFFB: Node number of the first fruiting branch, MMD: Mean maturity date, EP: Earliness percentage, PRI: Production rate index, PCH-L: Percent crop harvest at the last pick, *: $P<0.05$, **: $P<0.01$, ***: $P<0.001$, ns: $P\geq0.05$

Table 3 Factor loadings obtained using varimax rotation and communalities resulting from the factor analysis

Factor components	FA1	FA2	FA3	Communality	Uniqueness
Eigenvalues	4.92	1.73	1.32	-	-
Variance/%	44.71	15.76	12.01	-	-
Cumulative variance/%	44.71	60.47	72.48	-	-
DFF	-0.64	0.00	0.47	0.63	0.37
DFBO	-0.53	0.13	0.51	0.55	0.45
PCH-1	-0.34	-0.24	0.80	0.81	0.19
PCH-2	-0.94	-0.02	-0.11	0.89	0.11
PCH-L	-0.71	0.08	0.47	0.74	0.26
BI	-0.87	0.04	0.20	0.80	0.20
HFFB	-0.02	-0.85	-0.02	0.72	0.28
NNFFB	-0.05	-0.75	0.17	0.60	0.40
EP	-0.06	-0.02	0.93	0.86	0.14
MMD	-0.66	-0.25	0.46	0.71	0.29
PRI	-0.29	0.56	0.52	0.66	0.34

DFF Days to first flower, *DFBO* Days to first boll opening, *PCH-1* Percent crop harvest at the first pick, *PCH-2* Percent crop harvest at the first two picks, *PCH-L* Percent crop harvest at the last pick, *BI* Bartlett's index, *HFFB* Height of the first fruiting branch, *NNFFB* Node number of the first fruiting branch, *EP* Earliness percentage, *MMD* Mean maturity date, *PRI* Production rate index

cotton genotypes, namely, NNDC-30 (MTSI-2.20), A-2 (MTSI-2.31), and S-32 (MTSI-2.66) were selected based on the MTSI ranking (Table S13), presuming

Table 4 Traits measured and selection differential for the WAASBY index of 20 cotton genotypes using MTSI approach

Character	Factor	X_o	X_s	SD	PSD/%	SG	PSG/%	Indicators
DFF	FA 1	76.12	74.37	-1.75	-2.30	-1.55	-2.04	Decrease
DFBO	FA 1	128.95	127.39	-1.56	-1.21	-1.39	-1.08	Decrease
PCH-2	FA 1	39.18	44.42	5.24	13.38	4.61	11.77	Increase
PCH-L	FA 1	3.09	2.17	-0.91	-29.59	-0.70	-22.69	Decrease
BI	FA 1	0.66	0.69	0.03	4.60	0.03	4.02	Increase
MMD	FA 1	147.05	144.85	-2.20	-1.50	-1.53	-1.04	Decrease
HFFB	FA 2	18.49	18.26	-0.22	-1.20	-0.12	-0.63	Decrease
NNFFB	FA 2	5.41	5.17	-0.24	-4.45	-0.16	-2.98	Decrease
PRI	FA 2	9.02	9.31	0.29	3.22	0.21	2.35	Increase
PCH-1	FA 3	5.81	8.12	2.32	39.91	2.07	35.61	Increase
EP	FA 3	13.38	16.83	3.46	25.84	3.08	23.00	Increase

X_o Mean of the original population, X_s Mean of the selected genotypes, *SD* Selection differential, *PSD* Percent selection differential, *SG* Selection gain, *PSG* Percent selection gain, *DFF* Days to first flower, *DFBO* Days to first boll opening, *PCH-2* Percent crop harvest at the first two picks, *PCH-L* Percent crop harvest at the last pick, *BI* Bartlett's index, *MMD*: Mean maturity date, *HFFB* Height of the first fruiting branch, *NNFFB* Node number of the first fruiting branch, *PRI* Production rate index, *PCH-1* Percent crop harvest at the first pick, *EP* Earliness percentage

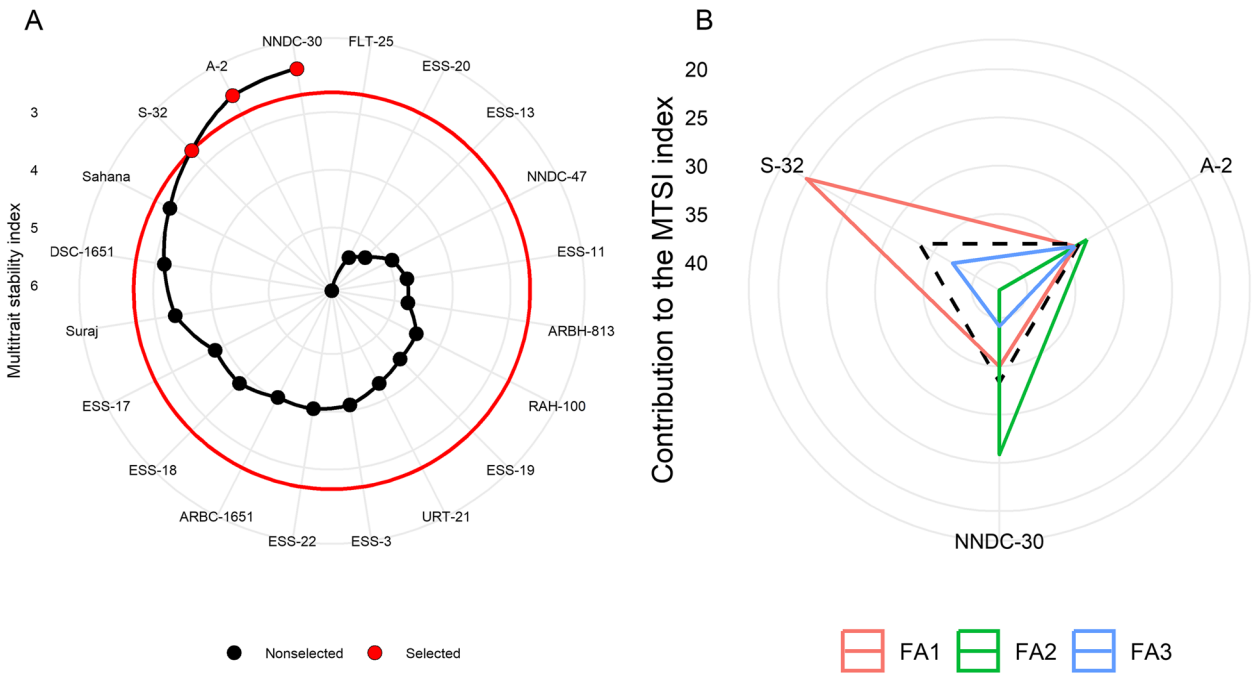

Fig. 3 **A** Genotype ranking based on the MTSI. Selected genotypes are highlighted in red. The scale in the radar plot represents the MTSI score. The red circle represents the threshold MTSI score, and inner circle next to the threshold circle represents the smallest value of the scale, and the innermost circle represents the highest value of the scale. **B** The strengths and weaknesses of genotypes are presented as the proportion of each factor on the computed MTSI. Scale represented in the strength and weaknesses plot depicts the contribution of factors. Immediate inner circle of the low contributing factor edge corresponds to the smallest scale value, and innermost circle corresponds to the highest scale value

15% selection intensity (Fig. 3). The MTSI value of 2.66 represented the cut-off point (Fig. 3A, red circle). Hence, in the forthcoming research, it would be desirable to explore the performance of these three genotypes nearer or closer to the basepoint. The percent selection differential (PSD) for the eleven traits ranged from − 29.59% (PCH-L) to 39.91% (PCH-1). The traits such as DFF, DFBO, PCH-1, and EP exhibited the highest heritability (89%), followed by PCH-2 (88%) (Table 2). The negative selection gains were displayed by DFF, DFBO, PCH-L, MMD, HFFB, and NNFFB (Table 4).

Interpretation of the strengths and weaknesses of the chosen genotypes

The radar plot (Fig. 3B) illustrated the strengths and weaknesses of the stable early maturing accessions predicted across the three planting densities. The factors that contributed the most were placed toward the centre, while those that contributed less were drawn near the plot edge. The strengths and weaknesses of the accessions showed that the first factor (FA1) had the highest contribution to accession NNDC-30, while FA2 had the highest contribution to accession S-32, and FA3 had the highest contribution to S-32 and NNDC-30. The weakness of S-32, however, was related to FA1.

Selection within the environment using MGIDI

Given that Levene's test of homogeneity revealed the non-significance for the majority of the studied traits in similar environments over two seasons (Table S9), further interpretations were proceeded using BLUP values. The genotype had a highly significant effect ($P < 0.05$) for some of the studied traits under E1, E2, and E3 (Table 5). The proportions of total variation explained by genotype, replication, and residuals under individual environments were shown in Table S10. The accuracy of genotype selection for the studied traits ranged from 0.20 (HFFB) to 0.93 (EP) in E1; 0.14 (HFFB) to 0.90 (DFF, DFBO, and PCH-1) in E2, and 0.22 (HFFB) to 0.91 (NNFFB) in E3. Several traits (DFF, DFBO, PCH-1, and EP) showed high heritability on a genetic mean basis ($h^2_{mg} > 0.50$) in the three planting densities.

Loadings and factor descriptions for MGIDI

According to the final loadings obtained from principal component analysis followed by exploratory factor analysis, two factors contributing 82.15% and 77.46% of the total variability were retained at 60 cm × 30 cm (E2) and 60 cm × 60 cm (E3) spacings, respectively. However, three factors with 84.80% of the total variability were retained under 60 cm × 15 cm spacing (E1) (Table S11). Among three factors retained in E1, FA1 included DFBO, PCH-1, PCH-2, PCH-L, BI, EP, and MMD; FA2 included NNFFB and HFFB; and FA3 included DFF and PRI. Under E2, all the traits were retained in FA1 except for NNFFB and PRI which belonged to FA2. Under E3, HFFB and NNFFB belonged to FA2, and the remaining nine traits belonged to FA1 (Table S12).

MGIDI and selection gains

Three genotypes were selected in each environment according to the MGIDI by assuming a selection index of 15%. ESS-20 (MGIDI = 1.67), ESS-3 (MGIDI = 1.69), and Sahana (MGIDI = 1.92) genotypes were selected in E1 (Fig. 4A); ESS-3 (MGIDI = 1.57), S-32 (MGIDI = 1.65), and DSC-1651 (MGIDI = 1.68) genotypes were selected in E2 (Fig. 4B); NNDC-30 (0.67), Sahana (0.87), and ESS-20 (0.95) genotypes were selected in E3 (Fig. 4C, Table S13).

The selected genotypes in each studied environment resulted in desired selection gains (SGs) for the mean performance of all the included traits, *i.e.,* negative SGs for DFF, DFBO, PCH-L, NNFFB, HFFB, and MMD, and positive gains for PCH-1, PCH-2, BI, EP, and PRI (Table S12). The contribution of each factor to the distance from MGIDI to the ideotype (ID) in all the environments was shown in Table S13.

Strength and weakness view of selected early maturing genotypes under each test environment

A view of strength and weakness under E1 revealed that FA1 had the highest contribution to Sahana, while FA2 had the highest contribution to ESS-20, and FA3 had the highest contribution to ESS-3 (Fig. 4D). In E2, the contribution of FA1 was the highest towards DSC-1651, and FA2 was the greatest towards S-32 (Fig. 4E). The selected genotype NNDC-30 in E3 had the highest contribution from FA1. FA2 had a greater contribution towards the selection of Sahana (Fig. 4F).

Discussion

This study focused on evaluating the performance of 20 upland cotton genotypes at various planting densities across two years in relation to 11 traits associated with early maturity. Specifically, this study focused on traits such as the number of days it took for the first flower and boll opening, the percentage of primary and secondary crop harvests, and other characteristics that contribute to early maturity. These assessments are crucial for identifying genotypes that exhibit early maturation and possess a favourable combination of traits suitable for various target environments. Such genotypes can be valuable for future cotton breeding programs. To develop cotton genotypes that consistently mature early in different environmental conditions (created by varied spacings here), it is important to thoroughly grasp how a genotype interacts with the environment. This understanding was emphasized by GEI (Comstock et al., 1963). In light of this, this study employed advanced multivariate techniques, specifically the MTSI and MGIDI.

Our findings indicated that both environment and GEI had significant effects on traits such as DFF, DFBO, PCH-1, PCH-L, EP, BI, and PRI. This variability in genotype mean performance across different environments can be attributed mainly to the diversity among genotypes. Such diversity offers a substantial amount of variation, which makes the selection process more manageable and effective. A non-significant interaction

Table 5 Likelihood ratio test and genetic parameters for eleven traits using 20 cotton genotypes studied in three environments

Trait	Genetic parameters									
	σ^2_g	σ^2_r	σ^2_p	h^2_{bs}	h^2_{mg}	AS	CV_g	CV_r	CV_g/CV_r	LRT_g
E1										
DFF	3.44	1.67	5.12	0.67	0.80	0.90	2.43	1.69	1.43	11.45**
DFBO	1.39	0.85	2.23	0.62	0.77	0.88	0.91	0.71	1.28	9.24**
PCH-1	2.71	1.18	3.89	0.70	0.82	0.91	33.33	22.05	1.51	12.56**
PCH-2	7.48	22.41	29.89	0.25	0.40	0.63	6.71	11.61	0.58	1.23
PCH-L	0.76	4.30	5.05	0.15	0.26	0.51	28.89	68.84	0.42	0.43
BI	0.00	0.00	0.00	0.54	0.70	0.84	3.69	3.42	1.08	6.48*
HFFB	0.01	0.45	0.46	0.02	0.04	0.20	0.48	3.36	0.14	0.01
NNFFB	0.01	0.02	0.03	0.41	0.58	0.76	1.94	2.34	0.83	3.47
EP	8.51	2.55	11.06	0.77	0.87	0.93	27.20	14.90	1.83	17.01**
MMD	0.70	1.69	2.40	0.29	0.45	0.67	0.58	0.89	0.64	1.71
PRI	0.49	0.52	1.01	0.48	0.65	0.81	7.28	7.51	0.97	5.09*
E2										
DFF	2.70	1.32	4.02	0.67	0.80	0.90	2.19	1.54	1.43	11.37**
DFBO	1.14	0.51	1.65	0.69	0.82	0.90	0.83	0.56	1.50	12.38**
PCH-1	5.71	2.83	8.55	0.67	0.80	0.90	34.66	24.41	1.42	11.24**
PCH-2	10.91	17.49	28.40	0.38	0.55	0.74	7.62	9.65	0.79	3.03
PCH-L	0.22	0.88	1.10	0.20	0.33	0.58	24.40	48.74	0.50	0.78
BI	0.00	0.00	0.00	0.62	0.77	0.88	2.61	2.04	1.28	9.25**
HFFB	0.00	0.10	0.10	0.01	0.02	0.14	0.16	1.64	0.10	0.00
NNFFB	0.00	0.09	0.09	0.01	0.03	0.16	0.64	5.59	0.12	0.00
EP	3.39	4.53	7.92	0.43	0.60	0.77	12.74	14.71	0.87	3.86*
MMD	0.17	1.53	1.71	0.10	0.18	0.43	0.28	0.84	0.33	0.19
PRI	0.18	0.71	0.89	0.20	0.34	0.58	4.38	8.71	0.50	0.79
E3										
DFF	1.12	1.76	2.87	0.39	0.56	0.75	1.37	1.72	0.80	3.11
DFBO	1.14	0.99	2.13	0.54	0.70	0.84	0.83	0.77	1.07	6.42*
PCH-1	2.04	2.45	4.49	0.45	0.63	0.79	25.60	28.03	0.91	4.40*
PCH-2	6.89	14.63	21.52	0.32	0.48	0.70	7.85	11.45	0.69	2.05
PCH-L	0.77	5.30	6.08	0.13	0.23	0.48	20.33	53.18	0.38	0.31
BI	0.00	0.01	0.01	0.09	0.17	0.42	0.46	1.42	0.32	0.17
HFFB	0.03	1.34	1.37	0.02	0.05	0.22	1.12	7.03	0.16	0.01
NNFFB	0.00	0.00	0.00	0.72	0.84	0.91	2.21	1.38	1.59	13.73**
EP	9.29	10.84	20.13	0.46	0.63	0.79	20.40	22.03	0.93	4.55*
MMD	0.51	1.28	1.79	0.29	0.44	0.67	0.48	0.76	0.63	1.61
PRI	0.07	0.27	0.34	0.21	0.35	0.59	3.43	6.64	0.52	0.86

σ^2_g Genotypic variance, σ^2_r Residual variance, σ^2_p Phenotypic variance, h^2_{bs} Broad sense heritability, h^2_{mg} Heritability of genotypic mean, *AS* Accuracy of genotype selection, CV_g Genotypic coefficient of variation, *CV*, Residual coefficient of variation, LRT_g Likelihood ratio test for genotypes, *DFF* Days to first flower, *DFBO* Days to first boll opening, *PCH-1* Percent crop harvest at the first pick, *PCH-2* Percent crop harvest at the first two picks, *PCH-L* Percent crop harvest at the last pick, *BI* Bartlett's index, *HFFB* Height of the first fruiting branch, *NNFFB* Node number of the first fruiting branch, *EP* Earliness percentage, *MMD* Mean maturity date, *PRI* Production rate index

** $P<0.01$, *$P<0.05$

effect on the earliness index under various environments has also been reported by earlier researchers (Dewdar, 2013; Stoilova et al., 2002; Mukoyi et al., 2015). We found a significant GEI for PCH-1 in this study, which was consistent with the results of Shah et al. (2005), Gibely et al. (2015), and Al-Obaidi et al. (2023). Further, Shah et al. (2005) evaluated cotton genotypes in 12 environments through three planting spacings (45, 30 and 15 cm between plants) and two sowing dates over two years to assess phenotypic stability for the earliness index based on the research of Eberhart et al. (1966).

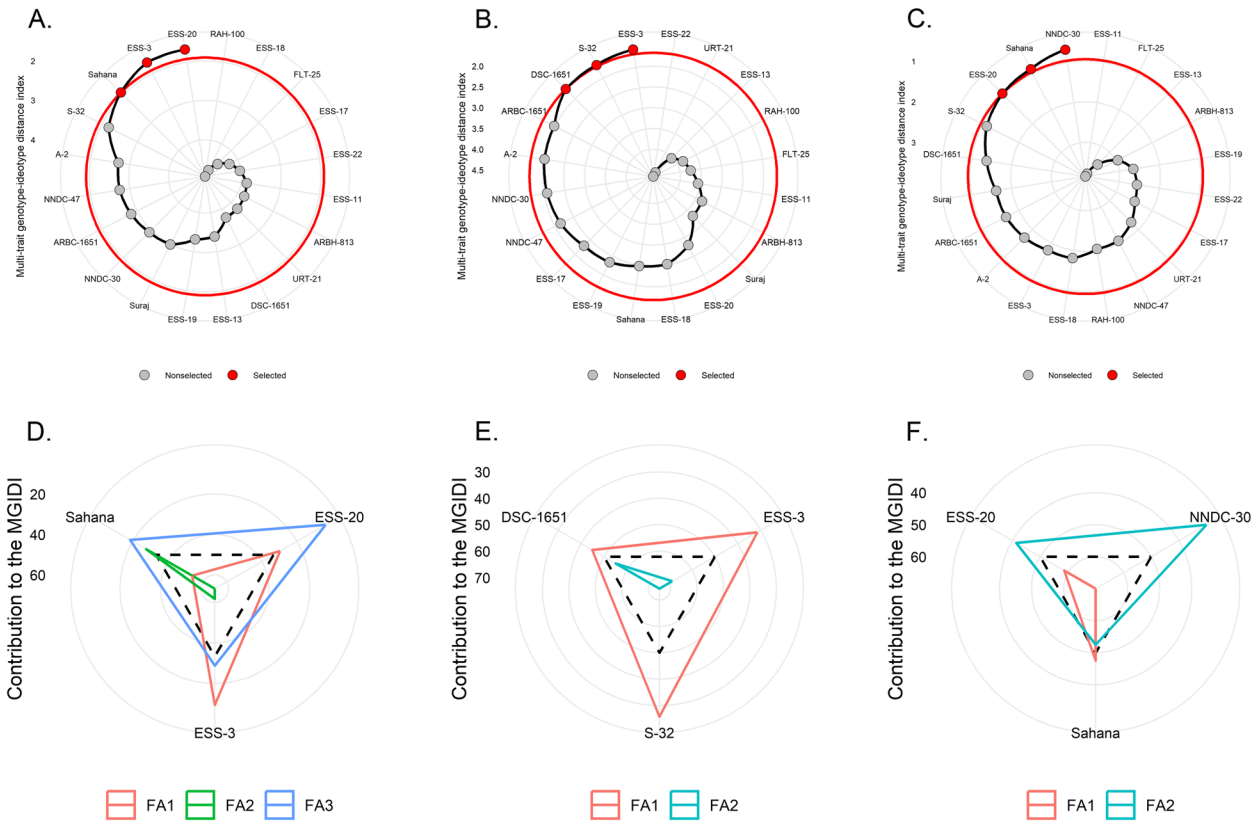

Fig. 4 Genotype ranking in ascending order for the MGIDI index tested under E1 (**A**)1, E2 (**B**) E2, and E3 (**C**), with selection intensity of 15% (red circle). Selected genotypes are highlighted in red. The scale in the radar plot represents the MGIDI score. The red circle represents the threshold MGIDI score, and inner circle next to the threshold circle represents the smallest value of the scale, and the innermost circle represents the highest value of the scale. Strength and weakness view of the stable genotypes identified across three environments, shown as the proportion of each factor on the computed MGIDI index under E1 (**D**), E2 (**E**), and E3 (**F**). Scale represented in the strength and weakness plot depicts the contribution of factors. Immediate inner circle of the low contributing factor edge corresponds to the smallest scale value, and innermost circle corresponds to the highest scale value

The influence of planting density on the expression of traits was evident from the average performance of these traits under various environments. Some of the outliers observed in the box plots representing the recorded traits were likely a result of interactions between genotypes and the microclimate conditions created. By comprehending the strength and direction of correlations among the traits studied and how these correlations change in conjunction with a variability parameter, breeders can enhance specific traits that lead to simultaneous improvement in other characteristics. Positive relationships among PCH-1, PCH-2, BI, EP, and PRI and their negative associations with DFF and DFBO were previously reported by Godoy et al. (1999), Imran et al. (2011), Song et al. (2012), Amna et al. (2013), and Valu (2021). Therefore, these traits can serve as key indicators for selecting genotypes with early maturity.

The majority of plant breeders have applied classic stability indices such as mean, regression, and deviation from regression parameters to choose stable genotypes. However, these statistical tools were insufficient for identifying strengths and weaknesses of genotypes and selecting those with the desired mean performance and stability (Bhering et al., 2012). Multiple trait selection indices, such as the MTSI and MGIDI evaluation systems, were found to be novel and unique techniques that have many practical applications in plant breeding practices (Abdelghany et al., 2021; Benakanahalli et al., 2021; Hadou el hadj et al., 2022; Yue et al., 2022a, b; Mezzomo et al., 2023; Singamsetti et al., 2023). Thus, the MTSI and MGIDI methods have proven to be robust tools for identifying genotypes with favoured average performance and desired specific traits, as well as for evaluating the strengths and weaknesses of selected and unselected genotypes without the issue of multicollinearity. This process maintains the original correlation structure of the data, while simultaneously identifying superior genotypes based on multiple traits (Olivoto et al., 2019b).

To carry out this rescaling technique, a specific selection direction is needed. All agronomic traits were adjusted to a scale ranging from 0 to 100. In this analysis, eleven traits were condensed into a few final latent variables (factors), with each variable having maximum trait loadings. This approach was used separately for different conditions, such as MTSI across three planting densities, and MGIDI in E1, E2, and E3. Based on the MTSI results, cotton genotypes NNDC-30, A-2, and S-32 were selected as early maturing ones because they exhibited the desired combination of mean performance and stability across several traits, including DFF, PCH-1, BI, PCH-2, MMD, and EP across three planting densities. According to MGIDI analysis, the chosen genotypes were ESS-20, ESS-3, and Sahana in E1; ESS-3, S-32, and DSC-1651 in E2; NNDC-30, ESS-20, and Sahana in E3, indicating their suitability for the respective planting conditions. Notably, NNDC-30 occupied a pivotal position with noteworthy characteristics that could be beneficial in future breeding programs with its wide adaptability to varied planting densities. Similarly, MTSI analysis has been successfully employed to identify sixteen stable lines with lower shoot fly damage in barnyard millet (Padmaja et al., 2022), drought tolerant wheat (Nardino et al., 2022; Pour-Aboughadareh et al., 2021) and chickpea lines (Hussain et al., 2021), drought- and salinity-tolerant soybean genotypes (Zuffo et al., 2020), and determination of quality traits in *Brassica* spp. (Bocianowski et al., 2019).

MGIDI, which offers a perspective on strengths and weaknesses, serves as a valuable graphical tool for discerning how tested genotypes perform in terms of traits that need improvement. For instance, under high-density planting conditions, the lower contribution of FA1 to Sahana indicated its high performance in terms of DFBO, PCH-1, PCH-2, and other traits retained in FA1. This inference can also be attributed to the greater contribution of FA1 to NNDC-30 in MTSI. A similar approach was used by Gabriel et al. (2019) and Olivoto et al. (2021) who studied the strength of 13 strawberry cultivars. In another study, Benakanahalli et al. (2021) proposed a framework to identify promising guar genotypes with productive traits such as gum and seed yield across three seasons, employing MGIDI. Similarly, Singamsetti et al. (2023) and Mezzomo et al. (2023) also proposed MGIDI as a powerful tool in developing better selection strategies for the development of climate-resilient maize hybrids and lines, respectively, by evaluating under various moisture and drought conditions. Notably, MGIDI-based analysis with varying plant spacings has already been demonstrated in quinoa by Ahmed et al. (2023). Our study represents an example of using MGIDI in upland cotton, providing a framework for identifying early-maturing ideotypes suitable for various planting densities.

Conclusion

The results from the present investigation suggested that the selection of early maturing cotton genotypes based on multi-factorial analysis is effective and that most potential and wide adaptive cotton genotypes are influenced by planting density, genetic factors, and their interactions (GEI). The multi-trait framework provided by MTSI suggested that three genotypes, namely NNDC-30, A-2, and S-32, exhibited good and stable performance with early maturation. The evaluation of a genotype's strengths and weaknesses within each environment using MGIDI identified genotypes suitable for a particular planting density. This technique highlights the significance of an ideal genotype characterized by enhanced morphological quantitative traits, such as days to the first flower and boll opening, crop yield harvested at the first, second, and last pick, Bartlett's index, earliness percentage, and production rate index. This approach not only optimizes the utilization of resources and time, but also contributes significantly to the sustainability of cotton breeding programs on a global scale.

Abbreviations

BI	Bartlett's index
DFBO	Days to first boll opening
DFF	Days to first flower
EP	Earliness percentage
GEI	Genotype-environment interaction
HFFB	Height of the first fruiting branch
LRT	Likelihood ratio test
MGIDI	Multi-trait genotype-ideotype distance index
MMD	Mean maturity date
MTSI	Multi-trait stability index
NNFFB	Node number of the first fruiting branch
PCH-1	Percent crop harvest at the first pick
PCH-2	Percent crop harvest at the first two picks
PCH-L	Percent crop harvest at the last pick
PRI	Production rate index

Supplementary Information

The online version contains supplementary material available at https://doi.org/10.1186/s42397-024-00187-w.

Supplementary Material 1:Table S1 List of genotypes used in this study. Table S2 Pooled analysis of variance for recorded traits in twenty cotton genotypes. Table S3 Mean performance for recorded traits of twenty cotton genotypes in E1 (kharif 2021). Table S4 Mean performance for recorded traits of twenty cotton genotypes in E2 (kharif 2021). Table S5 Mean performance for recorded traits of twenty cotton genotypes in E3 (kharif 2021). Table S6 Mean performance for recorded traits of twenty cotton genotypes in E1 (kharif 2022). Table S7 Mean performance for recorded traits of twenty cotton genotypes in E2 (kharif 2022). Table S8 Mean performance for recorded traits of twenty cotton genotypes in E3 (kharif 2022). Table S9 Levene's test of homogeneity for various early maturity traits studied across two years with varying planting density. Table S10 Mean sum of squares of various sources for three environments obtained from individual ANOVA. Table S11 Eigenvalues, explained variance,

cumulative variance, and final loadings of factors retained after superposition by exploratory factor analysis. Table S12 Traits measured and selection differential for the WAASBY index in twenty cotton genotypes using MGIDI index. Table S13 MTSI and MGIDI values of twenty cotton genotypes.

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Authors' contributions
Raj SDS: Conducting the experiment, data acquisition, writing and reviewing. Patil RS: Supervision, resources, validation and editing. Patil BR: Supervision and planning. Nayak SN: Supervision and resources. Pawar KN: Resources and planning.

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Availability of data and materials
The datasets used during this study can be provided upon reasonable request.

Declarations

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Not applicable.

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Competing interests
The authors declare that there are no conflicts of interest.

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