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RESEARCH ARTICLE

Selection of high-yielding stable forage sorghum genotypes using WAASB and MGIDI methods

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Abstract

Forage sorghum is a versatile and sustainable crop that is less demanding on inputs, produces significant biomass, and is tolerant of drought**.** In the present study, a set of 30 forage sorghum genotypes, including 21 B lines and nine varieties or fertility restorer lines, were evaluated under five different environments in Assam and Hyderabad during *kharif*, *rabi,* and summer 2020-2021 for 12 forage yield-related traits. Phenotypic stability was analyzed using multivariate techniques, including the weighted average absolute scores of BLUPs (WAASB) stability index and the multi-trait genotype ideotype distance index (MGIDI). A WAASBY, Y x WAASB bi-plot analysis revealed that genotypes G24 (348B), G25 (424B), and G30 (SSG-59-3) exhibited excellent stability with higher mean performance. MGIDI identified four genotypes, viz., G30 (SSG-59-3), G7 (NSS11B), G19 (327B) and G24 (348B), with higher mean performance and stability for all the 12 studied traits. These selected genotypes exhibited high heritability and genetic gain for green forage yield, indicating their stability and desirability. The strength-weakness plot showed that all selected genotypes were weak contributors to the MGIDI for all traits. This indicates that these genotypes are stable and closer to the ideotype, making them ideal candidates for breeding programs aimed at improving these traits.

Keywords: Forage sorghum, GEI, MGIDI, stability, WAASB

Introduction

Sorghum [*Sorghum bicolor* (L.) Moench] is a multipurpose crop, grown for grain, sweet stem, fodder, and broomcorn (Ananda et al. 2020). Forage sorghum is a nutrient-rich and cost-effective feed source for livestock and poultry (Getachew et al. 2016; Iqbal and Iqbal 2015). It plays a pivotal role in sustaining animal husbandry systems and supporting livestock productivity. However, the successful performance of forage sorghum is profoundly influenced by the intricate Genotype x Environment Interactions (GEIs) (Enyew et al. 2021). Variation in temperature, precipitation, soil fertility, and other factors leads to considerable differences in the crop's yield and quality (Druille et al. 2020). Genotypes with broad adaptability and stability across multiple locations and seasons are essential for crop improvement (Zakir 2018). Multi-Environmental Trials (METs) are a robust and reliable approach to identifying these genotypes (Eberhart and Russell 1966). Northeast India relies heavily on traditional crops, including forage sorghum, as a feed source for livestock. Stability analysis is a valuable tool for assessing genotype performance in METs and identifying genotypes that consistently exhibit high yield and adaptability across diverse environments (Finlay and Wilkinson 1963). Identifying and introducing stable forage sorghum hybrids is crucial for agricultural productivity, sustainability, and resilience in diverse environmental and socio-economic challenges. Studying the stability of A (male sterile), B (maintainer), and R (fertility restorer) forage sorghum lines helps predict performance, understand genotype-environment interactions, optimize resources, reduce risk, ensure commercial viability, and develop hybrids that adapt to diverse environments.

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The Best Linear Unbiased Prediction (BLUP)-based approaches, WAASB (Weighted Average Scores based on BLUPs), WAASBY (WAASB plus Years), BLUP, and MTSI (Modified Stability Index), demonstrated clear advantages over traditional methods among the various stability analysis. This was demonstrated in a study by Olivoto et al. (2019a, 2019b). BLUP-based stability analysis is becoming increasingly popular in agricultural research and breeding programs because it can provide reliable and precise estimates of genotypic performance (Piepho et al. 2008). These techniques use mixed-effect models to account for the variability associated with each factor, taking into account both the fixed and random effects of genotypes and environments (Yue et al. 2022; Olivoto et al. 2019). Moreover, these techniques can handle unbalanced data and missing values more effectively, which is common in field trials (Hartung and Piepho 2021). BLUP-based methods represent a significant advancement in stability analysis for researchers and breeders because they provide a more thorough and statistically sound approach to understanding the complex interplay between genotypes and environments.

Plant breeders often aim to combine a specific set of desirable traits into a single genotype, known as an ideotype, to achieve superior performance. Crop yield is a multifaceted trait that is closely linked to the performance of various traits, such as disease resistance, drought tolerance, and nutrient use efficiency. Plant breeders conduct research on genetic variability, heritability, genetic advance, and other genetic parameters to gain insights into the inheritance of these traits and devise breeding techniques to enhance crop yield. However, plant breeders often face challenges in identifying genotypes that possess a combination of multiple yield-related attributes. Additionally, they must make difficult choices when it comes to expressing the economic worth of traits and translating them into practical economic values (Bizari et al. 2017). 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 the Smith-Hazel (SH) index in identifying superior genotypes using information from multiple traits (Olivoto and Nardino, 2020). Olivoto et al. (2019b) proposed a unique selection procedure that considers multiple traits and their positive or negative selection differences for improving stability and mean performance. This procedure can help breeders achieve sustainable progress in primary traits, such as forage yield, while also preserving genetic advancements in secondary traits. These genotypes allow plant breeders to recommend stable and high-yielding forage genotypes that are reliable for specific regions. The current study used WAASB, WAASBY, and MGIDI to identify stable and superior genotypes for forage yield in sorghum.

Materials and methods

Planting material and experimental design

A total of 30 forage sorghum genotypes were used in this study (Table 1). The field experiment was conducted at two different locations viz., Assam Agricultural University (AAU), Jorhat and Indian Institute of Millet Research (IIMR), Hyderabad in 2020-21 in *rabi,* summer *kharif* seasons. Among both locations, Hyderabad is a suitable forage sorghum growing areas, while Assam is a non-conventional forage sorghum cultivation area. The in-depth description of five test environments (E1 to E5) are given in Supplementary Table S1.

The experiment was performed in a completely randomized block design with three replications at each location. Genotypes were sown at 45 × 20 cm spacing with two rows of 3 m length of plot having 15 plants of each genotype. Standard agronomic practices and protection measures were adopted during the experiment.

Trait phenotyping

A total of 12 morphological traits, namely, days to 50% flowering (FDF), plant height at 50% flowering (PH, in cm), number of leaves per plant (NLP), leaf length (LFL, in cm), leaf width (LFW, in cm), leaf area index (LAI), leaf to stem ratio (LSR), stem girth (SGT, in mm), number of nodes per plant (NNP), inter-nodal distance (IL, in cm), panicle length (PL, in cm) and green fodder yield per plant (GFYP, in g) were recorded on five randomly selected competitive plants of each genotype in each replication.

Statistical analysis

The green forage yield data and its related traits were analyzed using pooled analysis of variance across five test environments. The stability of the matrix of BLUPS was measured using singular value decomposition. The WAASB index is used to assess genotype stability by combining the AMMI model and BLUP approaches (Olivoto et al. 2019). This calculation is described by Olivoto et al. (2019a).

$$WAASBi = \sum_{k=1}^{p} IPCA_{ik} \, x \, EP_k \, v \sum_{k=1}^{p} EP_k$$

where WAASBi is the weighted average of absolute scores of the i_{th} genotype or environment, IPCAik is the score of the i_{th} genotype (or environment) in the k_{th} IPCA, and EP_k is the amount of the variance explained by the k_{th} IPCA.

This biplot with four quadrants was constructed with green forage yield on the x-axis and WAASB values on the y-axis. The forage yield was assigned a weight of 65, while the WAASB score was assigned a weight of 35.

The MGIDI was computed using the methodology of Olivoto and Nardino (2020) as follows;

Table 1. List of forage sorghum genotypes included in the present study

S. No.	Genotype code	Genotype Name	Type	Pedigree Information
1	G1	403B	B Line	(NSSB 1003 X NSSB 26)-3-1
2	G2	301B	B Line	(NSSB 2 X 2219B)-3-1
3	G3	412B	B Line	(NSSB 1002 x NSSB 1005)-3-5-3
4	G4	354B	B Line	(ICSB 342 x ICSB 687)-1-3-2
5	G5	ICS56B	B Line	(Serere elite x IS 9530)-2
6	G6	429B	B Line	(ICSB 342 x ICSB 687)-1-3-2
7	G7	NSS11B	B Line	Pedigree not available
8	G8	402B	B Line	(NSSB 1003 X NSSB 26)-2-2
9	G9	428B	B Line	(ICSB 342 x ICSB 467)-10-2-2
10	G10	CSV33MF	Variety	EMS mutant of CO FS 29
11	G11	384B	B Line	(NSSB 5 X 2219B)-5-1
12	G12	308B	B Line	(NSSB 5 X 2219B)-4-2
13	G13	370B (Black)	B Line	(90001B x NSSB 1005)-4-1-2
14	G14	CSV27	Variety	(GJ 38 x Indore 12) - 2 - 1 - 2 - 1 GJ 38 = GJ 35 x E 35 - 1
15	G15	382B	B Line	(NSSB 2 X 2219B)-3-2
16	G16	RS29	Restorer	Pedigree not available
17	G17	467B	B Line	[(ICSB 11 × ICSV 700) × PS 19349B) × ICSB 13]4-1
18	G18	Red B	B Line	Pedigree not available
19	G19	327B	B Line	(NSSB 1003 X NSSB 26)-2-2
20	G20	CSV33MF	Variety/ Restorer	Derived from COFS29
21	G21	CSV32F	Variety/ Restorer	HC 260 x B 35
22	G22	CSV21F	Variety/ Restorer	GSSV 148 x SR 897
23	G23	UPMC503	Restorer	Selection from IS 5977
24	G24	348B	B Line	(ICSB 342 x ICSB 467)-2-3-3
25	G25	424B	B Line	(ICSB 342 x ICSB 467)-2-3-3
26	G26	314B	B Line	(NSSB 15 X 296B)-2-1
27	G27	PCD-8-1-2	Restorer	Not Available
28	G28	307B	B Line	(NSSB 5 X 2219B)-4-1
29	G29	409B	B Line	(27B X NSSB 1002)-8-2
30	G30	SSG-59-3	Restorer	Non sweet Sudan grass × IS-263

$$MGIDI_i = \sqrt{\sum_{j=1}^{f}(F_{ij} - F_j)^2}$$

where, MGIDIis the multi-trait genotype-ideotype distance index for i_{th} genotype, γ_{ij} is the j_{th} score of the i_{th} genotype, and γ_j is the j_{th} score of ideotype (i = 1, 2, .. t; j = 1, 2, .., f), being t and f the number of genotypes and traits.

The strength and weakness of genotypes were assessed by calculating the proportion of the MGIDI of the i_{th} genotype explained by the j^{th} trait (ω_{ij}) as follows;

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

where, $D_{ij}$is the distance between the i_{th} genotype and ideal genotype for the j_{th} trait. A trait with low contribution indicates that the genotypes within such trait are close to the ideal genotype.

The analyses were performed in R Studio (Posit Team, 2022) using R version 4.1.2 (R Core Team 2021). The metan package (Olivoto and Lucio 2020) and ggplot2 package version 3.3.4 (Wickham 2016) were used to carry out stability analysis on various models with different parameters.

Results and discussion

Analysis of variance (ANOVA) and mean performances for forage yield

Genotype-by-environment interactions (GEI) can substantially impact selection efficiency and the development of adapted varieties, especially for complex traits such as forage yield (Rao et al. 2011). Prediction models play a crucial role in analyzing and interpreting multi-environment trials (Gauch and Zobel 1988). The pooled analysis of variance for forage yield is presented in Table 2. The pooled ANOVA results reveal significant genotype, environment, and genotype-environment interaction (GEI) effects. These results can be used to estimate G x E interaction, stability, and genotypic response parameters across various environments. Patel et al. (2019) observed significant genotypic and GEI effects on yield of green fodder per plant. Consistent findings had been documented earlier by multiple plant breeders. The mean performances of 30 forage sorghum genotypes over the five growing environments at two different locations for forage yield is presented in Table 3 and Fig. 1. The genotypes G24 (348B) and G10 (CSV33MF) exhibited the highest and lowest green forage yield per plant, respectively, with values of 391.7 and 108.16 g with the average of 255.14. The highest and lowest values were recorded in environments E1 (272.79 g) and E3 (225.75 g). The winning genotypes in individual environments had a maximum value of 436.72 g [G3 (412B) in E2] and a minimum value of 65.91 g [G10 (CSV33MF) in E4]. The genotypes G24 (348B), G30 (SSG-59-3), G21 (CSV32F), and G25 (424B) were considered the most desirable. Assessing the agronomic traits of germplasm resources is essential for identifying genotypes with beneficial traits that may thrive in various environments. These genotypes can be used in breeding programmes to develop superior varieties.

BLUP-based genetic parameter analysis using linear mixed-effect model

The BLUP model, which includes genotypic and interaction effects (GEI) as random factors, is superior to other models in accurately predicting random effects and genotype mean values. Genetic variability plays a vital role in enhancing agronomic traits during the plant breeding selection process. Understanding heritability is helpful for plant breeders because it enables them to determine the best strategy for improving a trait, calculate the advantages of selection, and evaluate the significance of genetic effects. The variance components for forage yield in forage sorghum genotypes over the five environments, as estimated by BLUP (Table 3). The likelihood ratio test against the *Chi*-square value showed that genotype and genotype x environment interactions significantly affected sorghum forage yield ($p < 0.001$). The BLUP-based heritability estimates mean heritability and selection accuracy demonstrate high effectiveness in selecting forage yield based on higher estimates of BLUP. The coefficient of determination for interaction effects (R^2_{ge}) suggested minimal residual variance in the G x E interaction component, which contributed significantly to the phenotypic variance. The genotypic correlation among environments was found to be high for green forage yield per plant, indicating a consistent trend across various environments. This finding is beneficial for identifying stable and superior genotypes. In a study conducted by Sousa et al. (2019), comparable findings were observed regarding the production of immature cowpea seeds. Similar results were observed in a study by Koundinya et al. (2021) in 25 cassava genotypes, while Yue et al. (2022) reported comparable findings in 28 maize genotypes.

Table 2. Combined ANOVA for green forage yield per plant in forage sorghum genotypes

Source	Df	Sum Sq	Mean Sq	F value	Pr (> F)
ENV	4	84361.56	21090.39**	45.52	1.01E-24
REP(ENV)	5	12357.49	2471.49	5.33	1.56E-04
GEN	29	1926083.65	66416.68***	143.35	2.29E-92
GEN:ENV	116	410314.35	3537.19**	7.63	9.59E-29
Residuals	145	67179.11	463.3		
CV (%)	8.436				

Notes: ** significant at $p < 0.01$; *** significant at $P < 0.001$

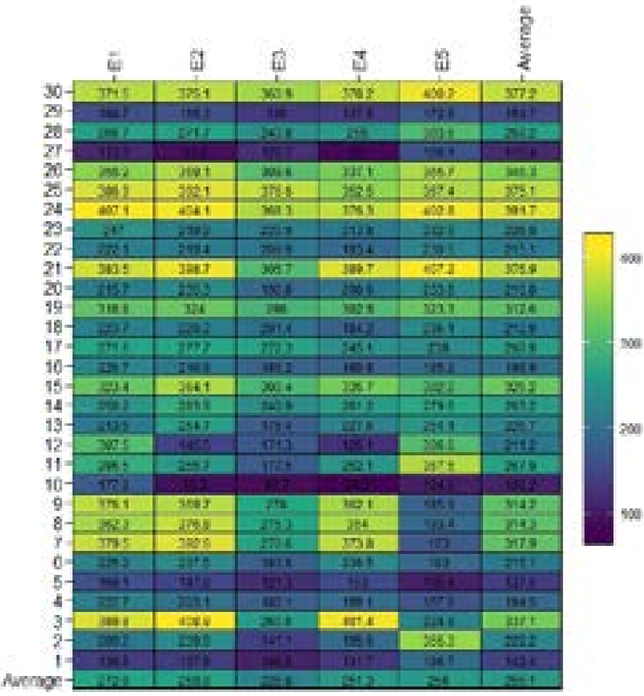

Fig. 1. Heat map of mean performances of 30 forage sorghum genotypes for green forage yield per plant in five different environments

Evaluation of forage sorghum genotypes using WAASB-based stability method

The selection of genotypes based on only stability using the WAASB index, whereas simultaneously selection of genotypes based on both desired mean yield and stability using the WAASBY index for forage yield is presented in Fig. 2 and Supplementary Table S2. Olivoto et al. (2019b) proposed examining the mean performance and stability of many desired agronomic attributes to improve varietal

Table 3. BLUP based genetic parameters for green forage yield per plant in forage sorghum genotypes

Parameters	GFYP	Parameters	GFYP
Mean	255.14	LRT_{ge}	122.66***
SE	5.28	Phenotypic variance	8288.067
SD	91.29	Heritability	75.866
CV	35.84	GEIr^2	18.544
Min	65.91 (G10 in E4)	h^2_{mg}	94.674
Max	436.72 (G3 in E2)	Accuracy	97.301
MinENV	E3 (225.75)	r_{ge}	0.768
MaxENV	E1 (272.79)	CV_g	31.079
MinGEN	G10 (108.16)	CV_r	8.436
MaxGEN	G24 (391.7)	CV ratio	3.684
LRT_g	134.81***		

***significant at $p < 0.001$, LRT significance test is conducted against the *Chi*-square value

LRT = Likelihood Ratio Test for the random effects; Heritability = Broad-sense heritability BLUP basis; R^2_{ge} = Coefficient of determination of the interction effects; h^2_{mg} = Heritability on the mean basis; Accuracy = Selective accuracy; rge = Genotype-environment correlation; CV_g = Genotypic coefficient of variation; CVr = Residual coefficient of variation; CV = Ratio between genotypic and residual coefficient of variation

selections and recommendations. In this study, G8 was identified as the genotype with the highest WAASB value for forage yield per plant, followed by G18 (Red B), G17 (467B), and G11 (384B). E2 was identified as the most stable environment. A higher WAASBY value indicates genotypes and environments with high yield and stability.G24 (348B) was identified as the genotype with the highest WAASBY value for forage yield per plant, followed by G25 (424B), G30 (SSG-59-3), and G21 (CSV32F). E1 was identified as the most stable environment. These genotypes and environments were identified as having both high yield and stability.

The genotypes and environments can be categorized into four groups in four quadrants in the Y x WAASB bi-plot, which allows for the joint interpretation of stability and mean performance in different environments (Fig. 3). The genotypes G24 (348B), G25 (424B), G30 (SSG-59-3), G21 (CSV32F) and G26 (314B) were included in the fourth quadrant; which indicates that they have both high yield and stability**.** These genotypes could be suggested to include in the varietal recommendation and high-yielding forage genotypes development programme. Sousa et al. (2019) found similar outcomes in the immature seed production of cowpea, while Koundinya et al. (2021) observed comparable results in 25 cassava genotypes and Yue et al. (2022) reported similar findings in 28 maize genotypes.

Evaluation of forage sorghum genotypes using MGIDI-based method

The genotype 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 traits under investigation. Genotypes with optimal yield and stability were chosen using a selection intensity of 15%. The selected and non-selected genotypes were shown graphically through the use of MGIDI scores plotted on a graph.

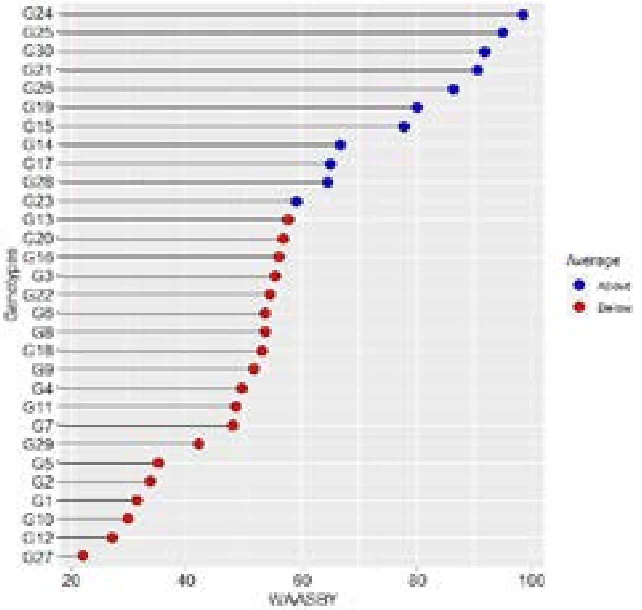

Fig. 2. WAASBY mean performances of 30 forage sorghum genotypes for green forage yield per plant across five different environments

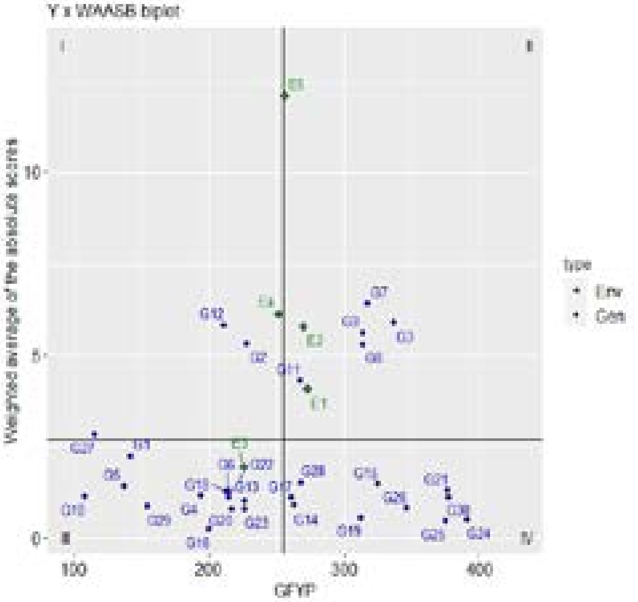

Fig. 3. Y X WAASB bi-plot mean performances of 30 forage sorghum genotypes for green forage yield per plant across five different environments

Loadings and factor description for MGIDI

The results of the factor analysis carried out on 12 adaptive traits in 30 forage sorghum genotypes were provided in Supplementary Table S3. This table includes the eigenvalues,

Table 4. MGIDI Scores of 30 forage sorghum genotypes

Rank	Genotype	MGIDI Value	Rank	Genotype	MGIDI Value
1	G30	3.03	16	G12	4.85
2	G7	3.10	17	G18	4.89
3	G19	3.36	18	G3	4.90
4	G24	3.44	19	G28	4.94
5	G25	3.50	20	G21	5.03
6	G8	3.68	21	G6	5.04
7	G2	3.70	22	G4	5.06
8	G9	3.76	23	G13	5.18
9	G26	3.78	24	G22	5.19
10	G14	4.10	25	G15	5.21
11	G20	4.19	26	G5	5.29
12	G17	4.21	27	G23	5.32
13	G10	4.27	28	G27	5.58
14	G11	4.28	29	G1	5.80
15	G16	4.50	30	G29	6.08

explained variance, factorial loadings after varimax rotation, and commonalities. The analysis revealed that four factors (FA1 to FA4) accounted for a substantial portion (82.98%) of the observed variation in the attributes and the WAASBY value of the BLUP estimates determined this. Thus, it was feasible to preserve strong explanatory power while decreasing data dimensionality. The average communality (h) after varimax rotation is 0.83. The maximum observed value for plant height was 0.927, whereas the minimum value was 0.635 for the number of leaves per plant. The communality's maximum value suggested that these factors could account for a substantial portion of the variance in each trait in factor analysis (FA). The traits under investigation were classified into four factors based on their communality value. In a recent study, Pour-Aboughadareh et al. (2021) discovered comparable findings in relation to the tolerance of barley towards salt. In a study conducted by Yue et al. (2022), similar results were observed in maize hybrids. Similarly, Olivoto and Nardino (2021) reported comparable findings in wheat, and Debsharma et al. (2023) found similar results in rice.

Selection of genotypes and predicted genetic gains under selection based on MGIDI analysis

Among the 30 forage sorghum genotypes, a total of 4 genotypes were chosen using a selection intensity of 15%. The genotype ranking, as determined by the MGIDI score and displayed in Table 4 and Fig. 4. Four genotypes, namely G30, G7, G19, and G24, were chosen based on their MTSI scores. Selected genotypes were utilised in order to compute selection differentials. The genotype G15 (382B) showcased a border point at the final red circle, as determined by the selection intensity, with an MGIDI score of 3.44. Genotype G25 (424B), situated in close proximity to the circle, may exhibit unique and favorable traits. Additional research is necessary to determine the genotypes at the cut point.

The predicted genetic gains and selection differentials for all traits were displayed in Table 5. The MGIDI Index effectively identified desired traits using WAASBY, achieving a 75% success rate. It achieved the desired selection differential (SD) for 9 out of 12 traits. Positive selection

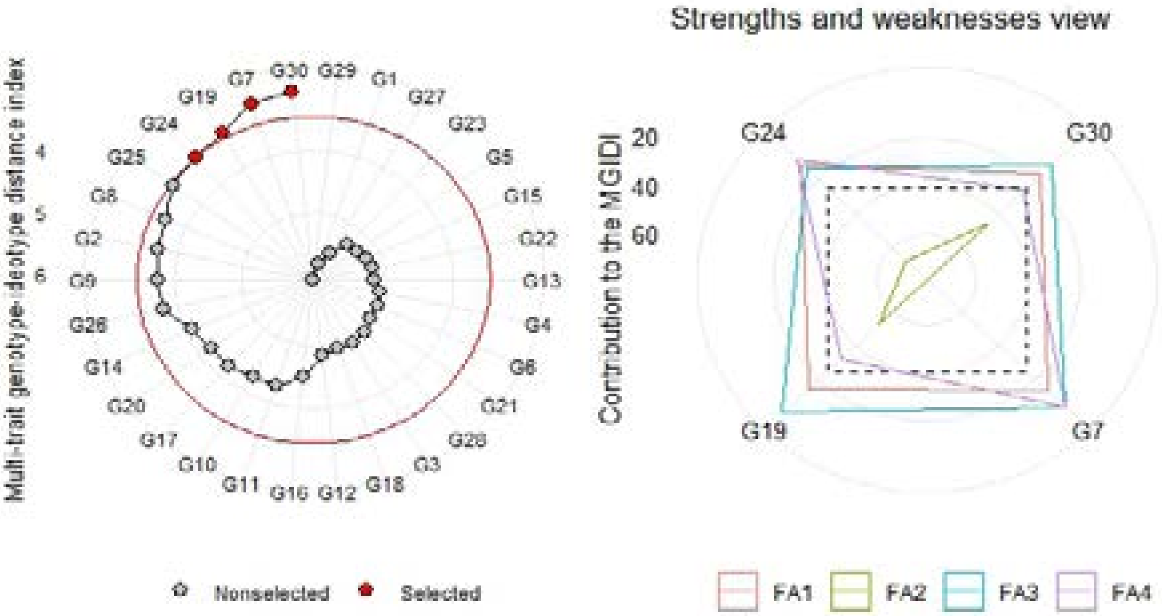

Fig. 4. Simultaneous selection and strength and weakness view of 30 forage sorghum genotype using MGIDI method considering a selection intensity of 15 per cent

Table 5. Selection gain for mean performance and stability across the environments based on the MGIDI values

Traits	Factor	Xo	Xs	SD	SDperc	h2	SG	SGperc
NLP	FA1	10.01	10.24	0.23	2.32	0.68	0.16	1.57
LFW	FA1	6.86	7.60	0.74	10.82	0.77	0.57	8.33
LAI	FA1	3.57	4.32	0.76	21.17	0.69	0.52	14.71
SGT	FA1	16.78	17.71	0.93	5.54	0.74	0.69	4.09
GFYP	FA1	255.14	287.58	32.44	12.71	0.86	27.84	10.91
PH	FA2	139.40	133.99	-5.42	-3.89	0.88	-4.75	-3.41
LFL	FA2	61.29	66.14	4.84	7.90	0.74	3.56	5.81
NNP	FA2	4.98	4.58	-0.40	-8.08	0.68	-0.27	-5.48
IL	FA2	12.39	13.39	1.00	8.10	0.94	0.94	7.61
FDF	FA3	73.85	81.26	7.41	10.03	0.82	6.09	8.25
LSR	FA3	0.21	0.24	0.03	12.46	0.87	0.02	10.83
PL	FA4	24.67	25.45	0.78	3.15	0.87	0.67	2.73

differentials were observed in all traits, except for two traits: the number of nodes per plant and plant height, suggesting undesired selection. However, days to 50% flowering exhibited a positive selection differential, which was also considered undesirable. The mean selection differential for this study was 6.8%, with the lowest selection differential observed for the number of leaves per plant and the highest selection differential observed for the leaf area index. The percent selection differential for green forage yield per plant is 12.71%. The average genetic gain under selection (SG %) is 5.49%, with the lowest value observed for the number of leaves per plant and the highest value observed for the leaf area index. The selection gain for green forage yield per plant, as measured by the WAASBY index, is 10.91%. According to the WAASBY index for these traits, this implies that the chosen genotypes showed greater stability. A higher positive selection differential (%) and genetic gain under selection (%) are advantageous as they indicate a greater desired value for the trait, thus suggesting the effectiveness of selection. The mentioned traits could be enhanced by directly selecting and incorporating the desired genotypes into the breeding programme. Olivoto and Nardino (2021) reported similar findings in wheat, while Yue et al. (2022) obtained comparable results in maize hybrids.

The strengths and weaknesses view

The strength and weakness plot was a graphical tool used to identify and select genotypes that possess desirable traits. Fig. 4 depicts the strengths and weaknesses of selected genotypes among 30 forage sorghum genotypes based on MGIDI scores. All the selected genotypes [G30 (SSG-59-3), G7 (NSS11B), G19 (327B) and G24 (348B)] were weak contributors to all the traits are included in FA1 to FA4. As their comparatively weak contributions indicated, these genotypes were stable and closer to the ideotype. They were selected and participated in breeding programmes aimed at improving these traits. Previous studies had found consistent findings across different crops. Olivoto et al. (2021) observed similar results in strawberries, Benakanahalli et al. (2021) in guar, and Debsharma et al. (2023) in rice.

The WAASB method provides a thorough and rigorous assessment of genotypic stability by including information from METs and combining it with advanced statistical modeling. The MGIDI method efficiently and simultaneously selects mean performance and stability, taking into account various attributes with different weights. The MGIDI index employed in this study proved to be effective in identifying high-yielding forage sorghum genotypes. The strengths and weaknesses of the selected genotypes in MGIDI highlight the significance of ideal genotypes that possess improved quantitative traits. This enables breeders and researchers to make informed judgments about selecting ideal genotypes and participating in potential breeding programs designed to improve forage sorghum, resulting in greater productivity, profitability, and sustainability in production.

Supplementary materials

Supplementary Tables S1 to S3 are provided, which can be accessed online www.isgpb.org

Authors' contribution

Conceptualization of research (RNS, AS, PPB); Designing of the experiments (RNS, AS); Contribution of experimental materials (AS, B V Bhatt); Execution of field/lab experiments and data collection (PPB); Analysis of data and interpretation (RNS, PPB); Preparation of the manuscript (PPB, RNS, AS).

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Supplementary Table S1. Description of test environments based on their location, growing season, and meteorological parameters

S. No	Particulars	E1	E2	E3	E4	E5
1	Environment Name	Rabi season, 2020	Rabi season, 2020	Summer Season, 2021	Kharif Season, 2021	Rabi Season, 2021
2	Date of Sowing	8-10-2020	14-10-2020	12-02-2021	25-05-2021	11-10-2021
3	Location	Research Field, IIMR, Hyderabad	ICR Farm, AAU, Jorhat	ICR Farm, AAU, Jorhat	ICR Farm, AAU, Jorhat	ICR Farm, AAU, Jorhat
4	Lattitude/Longitude/ Altitude	17°04'N, 75°54'E , 476.5M	26°44' N, 94°10'E, 91M	26°44' N, 94°10' E, 91M	26°44' N, 94°10' E, 91M	26°44' N,94°10'E, 91M
5	Soil Texture	Red clay & Red gravelly loam	Sandy loam	Sandy loam	Sandy loam	Sandy loam
6	Total Rainfall (mm)	27.70	13.23	16.35	50.27	8.91
7	BSSH (hr/day)	7.81	5.58	4.93	3.99	6.73
8	Mean Minimum Temperature (°C)	18.33	15.08	17.33	24.85	14.21
9	Mean Maximum Temperature (°C)	31.00	27.10	29.99	32.71	27.97
10	Mean Relative Humidity (%) (Morning)	98.50	97.84	93.16	93.39	97.03
11	Mean Relative Humidity (%) (Evening)	30.67	64.60	56.63	75.05	59.85

Supplementary Table S2. WAASB based stability parameters in forage sorghum genotypes for green forage yield per plant

Genotype	Y	r Y	WAASB	rWAASB	WAASBY	rWAASBY
G1	142.36	27	2.29	22	47.75	24
G2	228.23	16	1.13	12	70.89	17
G3	337.13	6	4.28	24	50.35	22
G4	194.53	25	5.84	29	15.81	30
G5	137.50	28	1.55	10	60.54	19
G6	215.12	20	0.94	8	71.41	15
G7	317.89	8	1.46	20	78.45	11
G8	314.33	9	0.31	1	90.45	2
G9	314.22	10	1.12	11	81.66	8
G10	108.16	30	1.37	18	53.54	21
G11	267.86	13	0.62	4	81.33	9
G12	211.21	23	5.32	26	23.57	26
G13	226.66	18	0.84	6	73.91	13
G14	263.15	14	1.28	17	73.65	14
G15	325.15	7	1.19	15	82.24	6
G16	199.95	24	0.89	7	70.09	18
G17	260.94	15	0.57	3	81.05	10
G18	212.93	22	0.48	2	76.08	12
G19	312.61	11	0.82	5	84.67	4
G20	216.83	19	2.94	23	50.00	23
G21	376.94	3	1.57	21	84.55	5
G22	215.06	21	0.95	9	71.22	16
G23	226.92	17	5.81	28	20.22	27
G24	391.70	1	1	13	90.90	1
G25	375.10	4	1.19	14	88.45	3

G26	346.34	5	1.44	19	82.16	7
G27	115.35	29	1.26	16	55.64	20
G28	268.18	12	6.32	30	19.75	28
G29	154.67	26	5.21	25	17.77	29
G30	377.17	2	5.59	27	41.07	25
E1	272.79	1	4.06	2	86.28	1
E2	269.81	2	5.79	3	73.16	2
E3	225.75	5	1.89	1	65.00	3
E4	251.32	4	6.16	4	57.05	4
E5	256.02	3	12.18	5	22.52	5

Supplementary Table S3. Loadings and factor descriptionthrough MGIDI analysis in 12 adaptive traits in 30 forage sorghum genotypes

VAR	FA1	FA2	FA3	FA4	Communality	Uniquenesses
FDF	-0.433	-0.104	0.631	-0.360	0.726	0.274
PH	-0.096	-0.933	0.186	-0.112	0.927	0.073
NLP	0.601	0.132	-0.296	0.409	0.635	0.365
LFL	0.211	-0.825	0.029	-0.360	0.856	0.144
LFW	0.924	0.089	0.112	-0.003	0.874	0.126
LAI	0.936	-0.217	-0.025	0.039	0.924	0.076
SGT	0.728	0.474	0.047	-0.053	0.760	0.240
LSR	-0.384	0.126	-0.816	0.063	0.834	0.166
NNP	0.246	-0.621	0.533	0.385	0.879	0.121
IL	-0.184	-0.889	0.057	-0.154	0.850	0.150
PL	-0.001	-0.309	0.107	-0.872	0.867	0.133
GFYP	0.872	-0.084	0.240	0.043	0.827	0.173
Eigenvalues	4.05	3.63	1.25	1.03		
Variance (%)	33.72	30.23	10.45	8.58		
Cum. variance (%)	33.72	63.95	74.40	82.98		