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Multi- trait genotype- ideotype distance index (MGIDI) for yield related traits to identify elite lines in foxtail millet (*Setaria italica* (L.) P. Beauv.) genotypes under foothills of Nagaland

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ABSTRACT

Foxtail millet (Setaria italica (L.) P. Beauv.) is a prominent crop that plays a significant role in the culture, rituals, and traditions of Naga tribes. Identifying superior genotypes that possess a combination of desirable agronomic traits is one of the major challenges faced by plant breeders. Therefore, this study evaluated the performance of 30 foxtail millet genotypes across four growing seasons in the foothills of Nagaland. We assessed mean yield, phenotypic stability, and the ideotype distance among genotypes using weighted average absolute scores of Best Linear Unbiased Predictors (BLUPs) stability index (WAASB) and the multi-trait genotype ideotype distance index (MGIDI).Genotypes viz., G25 (FOX4341), G8 (FOX 4403), G21 (FOX 4330), G18 (FOX 4489), G22 (ESD 75), and G23 (ESD 46)demonstrated stable yields across all four seasons, as shown by the WAASB biplot and WAASBY scores. Based on MGIDI index, genotypesviz., G25(FOX4341), G5(ERP82), G1(ELS20), and G22 (ESD75)wereidentified as high-yielding and stable performers across 14 agronomic traits.The strength-weakness design analysis indicated that all selected lines were weak contributors to their MGIDI for the 14 agronomic traits. Consequently, it is suggested that these candidate lines are close to the ideal plant type, making them superior elite lines for breeding programs.

Key words: Foxtail millet, MGIDI, BLUP, WAASB and WAASBY

INTRODUCTION

Foxtail millet (*Setaria italica* (L.) P. Beauv.), minor millet in the *Poaceae* family, originated in China and is used for both food and fodder. Foxtail millet is cultivated in 23 countries worldwide. In India, it spans approximately 80,000 hectares, with a production of around 60,000 metric tons. The primary cultivating states include Andhra Pradesh, Karnataka, Telangana, Rajasthan, Maharashtra, Tamil Nadu, and the North eastern states (Hariprasanna, 2023). It is a major source of dietary carbohydrates for a large section of the society. Additionally millets have enormous health benefits and also a good source of valuable micronutrients along with the major food components (Dholariyal *et al.* 2023). Millets have high degree of tolerance to drought and heat as well as high growth rate, tillering potential and water use efficiency (Rakesh Kumar *et al.* 2023). Genotype-by-environment interaction (GEI) plays major role in shaping complex traits like grain or seed yield in agricultural crops. Hence plant breeders should be carefully considering GEI interaction when introducing plant varieties or hybrids for either specific or general adoption on mega environments. However, GEI can aid plant breeders to identify stable varieties across test environments (Fasahat *et al.* 2016).Two approaches are used to analyze mega-environment data for predicting stability: univariate and multivariate methods (Olivoto *et al.* 2019). Among multivariate methods, the weighted average absolute scores of BLUPs (WAASB) and best linear unbiased predictors (BLUPs) are considered the most effective (Bizari *et al.* 2017). BLUPs are derived from linear mixed models, which incorporate both fixed and random effects. The fixed effects might represent overall mean of trait or environmental influences, while random effects typically represent genetic factors unique to each individual or family (Koundinya *et al.* 2021). WAASB combines WAAS stability scores with BLUP values, which estimate the genotypic performance across environments. This integration enables WAASB to provide a joint assessment of performance and stability, allowing breeders to identify genotypes that are both high-yielding and resilient to environmental

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variability. The WAASBY provides a metric that balances yield potential with stability, offering a comprehensive view of genotype adaptability (Yue *et al.* 2022).

Experienced breeders aim to create an ideal plant genotype, called the ideotype, by combining specific traits that lead to gives higher yield potential for a genotype. This involves selecting genotypes based on multiple traits simultaneously to enhance crop yield. The main challenge for plant breeder quickly develops the superior varieties to meet global food demands. Various linear selection indexes, such as the Smith-Hazel (SH) index, assist breeders in choosing superior genotypes (Cerón-Rojas and Crossa, 2018). The Smith-Hazel (SH) index uses phenotypic and genotypic variance-covariance matrices, along with economic weights, to maximize the correlation between genetic values and phenotypic values (Bizari *et al.* 2017). However, it can encounter limitations, particularly multicollinearity among traits, leading to unfair results (Burdon and Li, 2019). To address these challenges, some studies repeat with different economic weights to find the optimal set for identifying superior genotypes (Bizari *et al.* 2017). Additionally, advanced breeding programs depend onmulti-environment trials to account for environmental differences. Recent advances, like the multi-trait stability index, help select genotypes based on both performance and stability (Jahufer and Casler, 2015). In the face of the common use of the Smith-Hazel (SH) index in plant breeding, but evidence suggests it may not be optimal for plant breeding (Rocha *et al.* 2018). Despite their utility, a significant challenge lies in accurately defining the economic value of traits and translating these into practical economic weightings, which often constrains breeders in selecting optimal genotypes (Adilakshmi *et al.* 2025). To address these limitations recently a novel technique MGIDI has been proposed based on factor analysis and genotype-ideotype distance. This index focuses on selecting superior genotypes in breeding programs with multiple assessed traits. We validated the WAASBY and MGIDI indexes using data from an initial trial involving 30 foxtail millet genotypes evaluated across four cultivated seasons and assessed for 14 traits. This analysis enabled us to identify genotypes with stable performance across multiple desirable traits.

MATERIALS AND METHODS

Experiment location

The experiment was conducted from July 2022 to July 2023, covering four growing seasons: *Kharif, Rabi, Early summer, and Summer* (Table 1). Each season was designed to create a specific test environment for studying stability. Of the four seasons, Kharif, and Rabi were evaluated under rainfed conditions, while entire summer was assessed under irrigated conditions at weekly intervals. The entire experiment took place at the Research Farm of the School of Agricultural Sciences, Nagaland University, India. The coordinates of the research farm are “$25^0 45^0 35^0$ N and $95^0 25^0 45^0$ E,” with an altitude of 310 meters above mean sea level.

Table 1: Overview of experimental conditions across different growing seasons at Nagaland University Research Farm (July 2022 - July 2023)

Code	Season	Sowing date	Harvesting date	Latitude	Longitude	Altitude	Av. Temp		Av. Hum (%)		Rainfall (mm)	Year
							Max	Min	Max	Min		
E1	Kharif	20-05-2022	20-09-2022	25^0 45’ 15.95” N	93^0 51’ 44.71 E	310 MSL	31.66	22.30	91.75	69.64	51.92	2022
E2	Rabi	25-09-2022	20-01-2023	25^0 45’ 15.95” N	93^0 51’ 44.71 E	311 MSL	32.09	22.84	92.10	69.99	55.19	2023
E3	Early Summer	02-02-2023	21-05-2023	25^0 45’ 15.95” N	93^0 51’ 44.71 E	312 MSL	29.11	17.40	94.48	61.84	15.58	2023
E4	Summer	02-04-2023	30-07-2023	25^0 45’ 15.95” N	93^0 51’ 44.71 E	313 MSL	28.28	15.97	95.29	60.11	8.46	2023

Env=Environment, Av. Temp= Average temperature, Av. Hum=Average humidity

Plant materials and experimental design

A total of one hundred foxtail millet genotypes, including national and zonal check varieties, were collected from the Indian Institute of Millets Research (IIMR) in Hyderabad. These genotypes were evaluated during the Zaid season in 2022, in a consistent test environment. Based on the mean performance of grain yield per plant, the best 29 genotypes along with one national check variety were selected. The selected 30 genotypes were then used to conduct stability experiments in the foothills of Nagaland. The experiment was designed using a randomized complete block design (RCBD) with three replications across four seasons. Each replication consisted of 30 plots measuring 1 meter by 1 meter, with a plant and row spacing of 10 cm by 22.5 cm. Recommended agricultural practices were followed throughout the experiment. A list of the plant materials used in this experiment was presented in Table 2.

Table 2: List of plant materials used in the stability experiments

ACC. No	IC. No	Source	Code
ELS 20	IC 0621991	Andhra Pradesh	G1
FOX 4438	IC 0077702	West Bengal	G2
FOX 4394	IC0610541	Andhra Pradesh	G3
FOX 4339	IC 0597715	Andhra Pradesh	G4
ERP 82	IC 0622113	Tamil Nadu	G5
FOX 4384	IC 0610531	Andhra Pradesh	G6
FOX 4396	IC 0610543	Andhra Pradesh	G7
FOX 4403	IC 0610550	Andhra Pradesh	G8
FOX 4428	IC 0850064	Unknown	G9
ESD 79	IC 0618660	Maharashtra	G10
FOX 4336	IC 0597710	Andhra Pradesh	G11
FOX 4386	IC 0610533	Andhra Pradesh	G12
ERP 26	IC0622071	Tamil Nadu	G13
ESD 3	IC 0618597	Maharashtra	G14
ELS 40	IC 0622003	Andhra Pradesh	G15
ERP 90	IC 0622117	Tamil Nadu	G16
FOX 4478	IC 0078006	Uttar Pradesh	G17
FOX 4489	IC 0078200	Tamil Nadu	G18
FOX 4392	IC 0610539	Andhra Pradesh	G19
FOX 4390	IC 0610537	Andhra Pradesh	G20
FOX 4330	IC 0596783	Arunachal Pradesh	G21
ESD 75	IC 0618657	Maharashtra	G22
ESD 46	IC 0618634	Maharashtra	G23
ERP 57	IC 0622094	Tamil Nadu	G24
FOX 4341	IC 0597722	Andhra Pradesh	G25
FOX 4440	IC 0077761	Gujarat	G26
FOX 4420	IC 0613573	Andhra Pradesh	G27
ELS 36	IC 0621999	Andhra Pradesh	G28
ELS 34	IC 0621998	Andhra Pradesh	G29
Surya Nandi	Check	Andhra Pradesh	G30

Phenotyping of agronomic traits

Fourteen quantitative traits of foxtail millet *viz.,*days to 50% flowering (DF), days to maturity (DM), plant height (PH) (cm), panicle length (PL) (cm), flag leaf length (FL) (cm), flag leaf width (FW) (cm), peduncle length (PDL) (cm), total tiller numbers per plant (NT), panicle width (PW) (cm), biological yield (BY) (g), harvest index (HI) (%), test weight (g), fodder yield per plant (FY) (g) and Grain yield per plant (GY) (g). were taken into account during the process of data collection. The procedure for data collection for these traits was followed as per guidelines provided by PPV&FR's 2001 (DUS). In each genotype and plot with in replication, data from five randomly selected plants were collected. Days to flowering and maturity data were collected plot-wise.

Statistical analysis

Grain yield and yield per data of 30 foxtail millet genotypes variances were analyzed using a combined pooled analysis of variance across four seasons. The variance analysis was conducted by the metan package in R Studio (Posit Team, 2022) running R version 4.1.2 (R Core Team, 2021). Best Linear Unbiased Predictors (BLUPs), the Weighted Average of Absolute Scores (WAASB), The MGIDI index, and the WAASBY indexes were employed to assess genotype performance and stability. For stability analysis across various models and parameters, we utilized the metan package in R (Olivoto and Lucio, 2020).

RESULTS AND DISCUSSION

Estimation of thegenetic variance and mean performance

The mean squares from the combined analysis of variance for grain yield per plant among 30 genotypes are presented in Table 3. These results show significant effects ($P < 0.05$) related to genotypes, environments, and genotype-environment interactions. The significance of these findings indicates that the genotypes are effective for estimating genotype-environment interaction (GEI) and stability parameters. Similar conclusions have been drawn by Patel *et al.* (2019), Chala *et al.* (2019), and Nagesh Kumar *et al.* (2021). The mean yield

Table 3: Analysis of Variance for Grain Yield per Plant among 30 Genotypes

Source	Df	Sum Sq	Mean Sq	F value	Pr(>F)
ENV	3	1473.95	491.32	154.14	0.00
REP(ENV)	8	35.23	4.40	1.38	0.21
GEN	29	1758.61	60.64	19.02	0.00
GEN:ENV	87	1143.48	13.14	4.12	0.00
Residuals	232	739.51	3.19		
CV (%)	12.19				
MSR+/MSR-	1.98				
Overall mean	14.65				

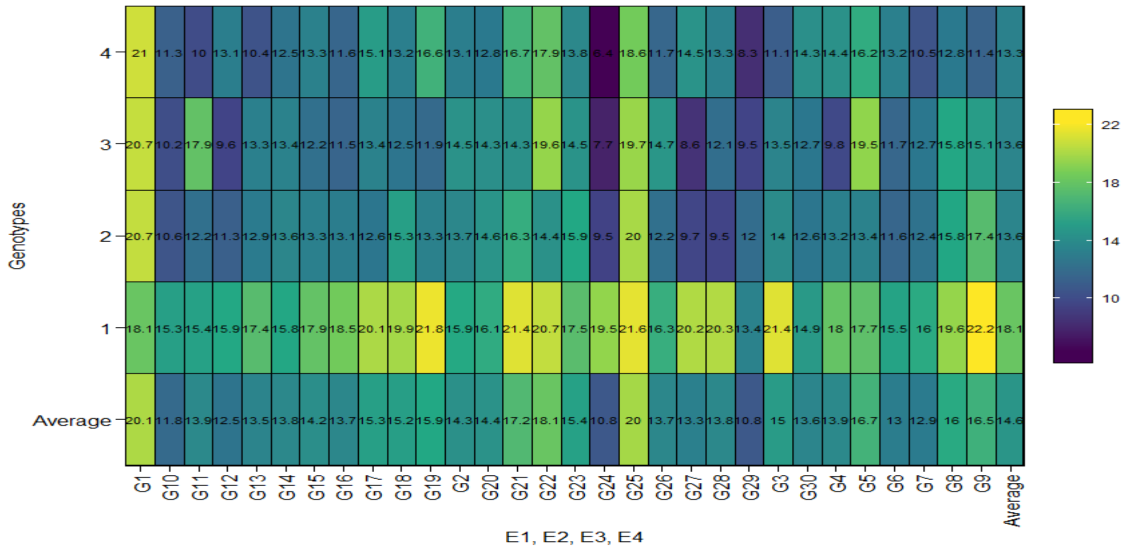

Fig1: Mean grain yield of 30 foxtail millet accessions across four seasons

of 30 foxtail millet accessions over four seasons is shown in Table 4 and Fig. 1. The average grain yield was 14.65 g per plant, with genotype G1 exhibiting the highest mean yield at 20.14 g per plant, while G24 recorded the lowest at 10.78 g per plant across the four seasons. The lowest mean yield occurred in the summer (E4) season (13.31 g per plant), whereas the highest was observed in the kharif season (18.15 g per plant). Genotype G9 was the top performer in the kharif season, with a mean yield of 26.4 g per plant, while G24 had the lowest mean yield during the summer (E4) season, at 5.0 g per plant.

Table 4: BLUP-Based Variance Components for Grain Yield per Plant across Four Growing Seasons

Parameters	GYPP	Parameters	GYPP
Mean	14.65	Phenotypic variance	10.46
SE	0.2	Heritability	0.38
SD	3.78	GEIr2	0.32
CV	25.86	h^2mg	0.78
Min	5 (G24 in E4)	Accuracy	0.89
Max	26.4 (G9 in E1)	r_{ge}	0.51
MinENV	E4 (13.31)	CV_g	13.58
MaxENV	E1 (18.15)	CV_r	12.19
MinGEN	G24 (10.78)	CV ratio	1.11
MaxGEN	G1 (20.14)		
LRT_g	30.32***		
LRT_{ge}	73.30***		

****significant at $p < 0.001$,LRT significance test is conducted against the Chi-square value; GYPP= Graian yield per plant; LRT = Likelihood Ratio Test for the random effects; Heritability = Broad-sense heritability BLUP basis; GEIr^2= Coefficient of determination for the genotype-vs-environment interaction effects; h^2 mg = Heritability on the mean basis; Accuracy = Selective accuracy; rge = Genotype X environment correlation; CVg = Genotypic coefficient of variation; CVr = Residual coefficient of variation; CV = Ratio between genotypic and residual coefficient of variation*

BLUP-based genetic parameter analysis

BLUPs (Best Linear Unbiased Predictions) are extensively utilized in livestock and crop breeding to estimate breeding values. They are generated by solving mixed-model equations (MME), which predict random effects by considering the relationships among genotypes, environments, and errors (Olivoto *et al.* 2019). Genetic variance refers to the variability in a trait resulting from genetic differences among individuals, while heritability indicates the proportion of phenotypic variance that can be attributed to genetic variance. A BLUP-based analysis calculates these parameters within a mixed-model framework, taking into account environmental factors that could otherwise skew the estimates (Silveira *et al.* 2022). Accurate heritability estimates are crucial for breeders as they help predict the effectiveness of trait improvement through selection. BLUP-based variance components for grain yield per plant across four growing seasons are presented in Table 4.

The likelihood ratio test against the Chi-square value revealed highly significant effects ($p < 0.05$) for both genotype and genotype-by-environment interaction (GEI) regarding grain yield per plant. This indicates that mean performances among genotypes varied significantly across different seasons or growing environments, providing sufficient genetic variation for effective selection (Yue *et al.* 2022). In this study, lower heritability was observed for grain yield, suggesting that a significant proportion of the variation in yield is due to environmental factors rather than genetic influences. The residual variance suppresses the genotypic variance for grain yield, consistent with the findings of Olivoto *et al.* (2021) and de Souza *et al.* (2019). This suggests that environmental variation had a limited impact on phenotypic variance, a conclusion supported by similar observations reported by Bennewitz *et al.* (2007). In the current study, high selection accuracy was noted for grain yield, indicating that the results of the experiment were reliable (de Souza *et al.* 2019). The genotypic correlation among seasons for grain yield per plant was found to be high, which indicates a consistent trend across various environments. Furthermore, the genotypic variance for grain yield was positive and significantly different from zero, highlighting the trait potential for genetic improvement. The relative coefficient of variation (CVr) for grain yield exceeded 1.0, further supporting its suitability for effective selection (Silveira *et al.* 2022).

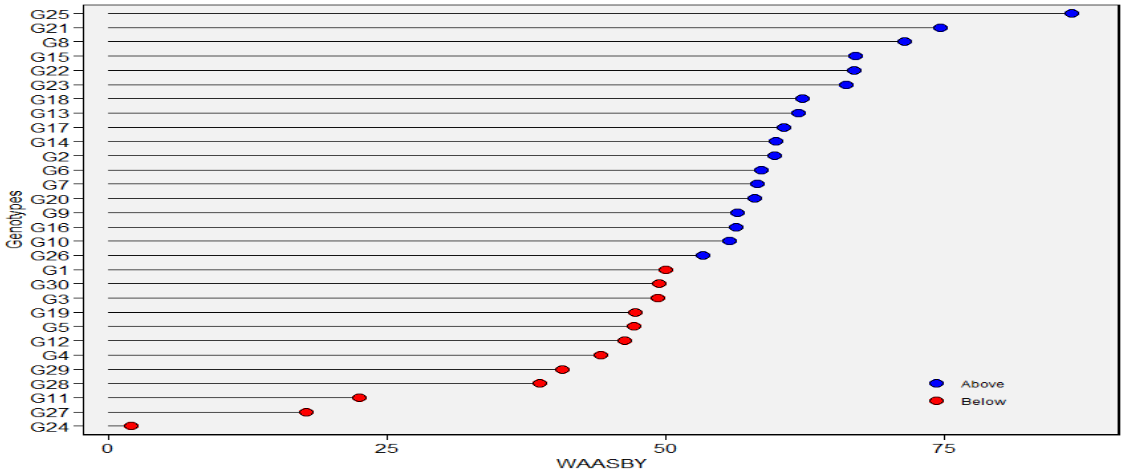

Fig 2: The WAASBY mean performances of 30 foxtail millet genotypes for grain yield per plant across four growing seasons

Evaluation of Foxtail Millet Genotypes Using the WAASB-Based Stability Method

The comparative analysis of the WAASB and WAASBY indices enhances the efficiency of selection. In this study, the WAASB and WAASBY scores are presented in Supplementary Table 1 and Fig 2. Based on the WAASB score, genotype G10 was identified as the most stable yielder across four seasons, followed by G15, G13, G6, and G7 (Supplementary Table 1.), which also demonstrated stable performance. The summer (E4) season was identified as the least productive environment. Notably, these genotypes had lower mean yields compared to the population mean grain yield, which means they are not recommended for cultivation or further breeding programs. However, based on the WAASBY index (Fig 2.), genotype G25 exhibited a higher mean yield with stable performance across the four seasons, followed by G21, G8, G23, and G22. The Kharif season was identified as the most productive environment. These genotypes and environments demonstrated both high yield and stability. The four cultivation seasons and 30 accessions can be categorized into four groups across the four quadrants of the Y × WAASB bi-plot, allowing for a combined assessment of stability and mean performance across environments (Fig 3.). Genotypes G25, G8, G21, G18, G22, G17, and G23 fall within the fourth quadrant, indicating both high yield and stability. These genotypes are promising candidates for varietal recommendations and programs aimed at developing higher grain yielding lines.

Table 5: MGIDI Scores of 30 foxtail millet genotypes

S. No	Genotype	MGIDI	S.No	Genotype	MGIDI
1	G25	2.12	16	G14	4.553
2	G5	2.50	17	G7	4.573
3	G1	2.51	18	G15	4.616
4	G22	2.92	19	G20	4.620
5	G21	3.00	20	G4	4.714
6	G2	3.22	21	G29	4.747
7	G28	3.43	22	G11	4.953
8	G18	3.53	23	G3	4.965
9	G9	3.74	24	G19	4.993
10	G8	3.90	25	G6	5.133
11	G23	4.07	26	G24	5.164
12	G17	4.31	27	G13	5.357
13	G26	4.34	28	G12	5.426
14	G16	4.35	29	G10	5.497
15	G27	4.46	30	G30	5.546

Selection of genotypes based on MGIDI index

Among the 30 foxtail millet genotypes evaluated, four were selected as ideotypes using a selection intensity of 15%. The ranking of the genotypes was determined based on their MGIDI scores (Table 5) and illustrated in Fig 4. The selected genotypes were G25, G5, G1, and G22, with G22 being close to the cut point indicated by the red circle. Based on the selection intensity, genotype G21, which is also near this cut point, may exhibit significant traits. Therefore, researchers should pay careful attention to investigating genotypes that are close to the cut point. These findings are consistent with the results reported by Olivoto *et al.* (2021).

Loadings and factor delineation

The results from the factor analysis carried out in 14 agronomic traits in 30 foxtail millet genotypes were summarized in Table 6.which includes eigenvalues and explained variance.Factor analysis is an effective technique for establishing an index with favourably selected traits, showing satisfactory selection gains for application in breeding programs (Bermudez and Pinheiro, 2020). The MGIDI index utilized factor analysis, similar to the FAI-BLUP, to address this correlation structure. Factor analysis provides orthogonal axes among final factors, enabling genotype scores free from multicollinearity. The Euclidean distance was used to compute the distance from a genotype to the ideotype (Bermudez and Pinheiro, 2020).

The factor analysis identified four eigenvalues greater than one, which together accounted for 68.65% of the overall variation observed in the yield attributes. Following varimax rotation, the average communality (h) was found to be 0.68, with minimum and maximum values recorded for the number of tillers per plant (0.43) and fodder yield (0.96), respectively. The yield and related traits under investigation were categorized into four distinct factors: FA1 is associated with yield traits, including grain yield, fodder yield, biological yield, and harvest index.FA2 relates to duration and plant-related traits, such as days to flowering, days to maturity, flag leaf width, and the number of tillers per plant. FA3 is linked to plant-related traits, including plant height, panicle length, and peduncle length. FA4 is connected to flag leaf length, panicle width, and test weight.

Predicted genetic gains under selection based on MGIDI

The selection differential and predicted genetic gains for yield and yield-related traits are shown in Table 7. The MGIDI Index successfully

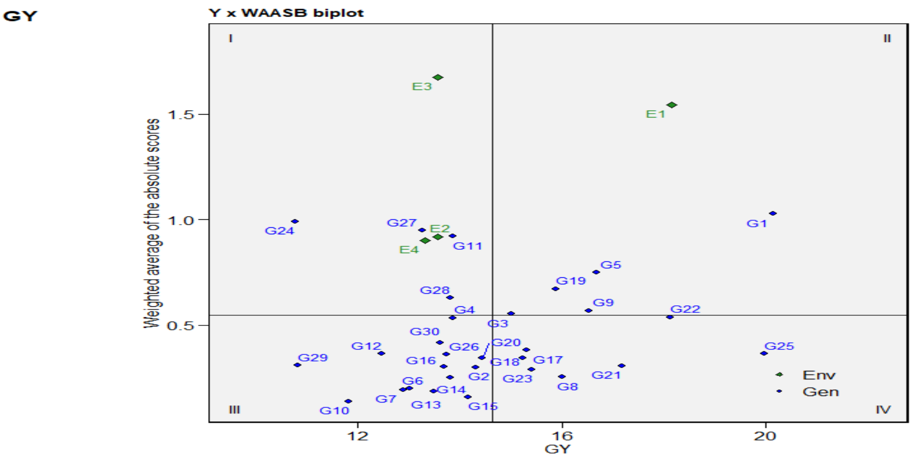

Fig 3: The Y X WAASB bi-plot mean performances of 30 foxtail millet genotypes for grain yield per plant across four growing seasons

Table 6: Factor analysis using MGIDI method for 14 yield traits in 30 foxtail millet

S.No	VAR	FA1	FA2	FA3	FA4	Communality	Uniquenesses
1	BY	**-0.94**	-0.14	0.22	0.02	0.95	0.05
2	HI	**0.62**	-0.21	0.55	0.02	0.73	0.27
3	FY	**-0.98**	-0.08	0.05	0.01	0.96	0.04
4	GY	**-0.79**	-0.22	0.43	0.03	0.85	0.15
5	DF	-0.23	**-0.83**	-0.08	-0.16	0.78	0.22
6	DM	-0.20	**-0.81**	-0.01	-0.13	0.71	0.29
7	FW	0.01	**0.64**	-0.02	0.15	0.44	0.56
8	NBT	-0.28	**0.52**	-0.05	-0.27	0.43	0.57
9	PH	-0.06	-0.15	**0.74**	0.13	0.59	0.41
10	PL	-0.17	0.13	**0.78**	0.22	0.70	0.30
11	PDL	-0.26	0.28	**0.61**	-0.36	0.64	0.36
12	FL	-0.11	0.08	0.50	**-0.60**	0.63	0.37
13	IW	-0.26	0.30	0.21	**0.66**	0.63	0.37
14	TW	-0.03	-0.16	-0.15	**-0.71**	0.55	0.45
	Eigenvalues	**3.62**	**2.56**	**1.93**	**1.49**		
	Variance (%)	25.86	18.32	13.79	10.68		
	Cum. variance (%)	25.86	44.18	57.97	68.65		

identified desirable traits using WAASBY, achieving a 75% success rate. A positive selection differential (SD) was observed for 13 out of 14 agronomic traits. All agronomic characters except for flag leaf width (-0.22) exhibited positive selection differentials, indicating an undesired selection for flag leaf width. Days to 50% flowering also showed a positive selection differential, even though its desirable outcome is associated with a negative selection differential. The percent selection differential for grain yield per plant was found to be 23.14%. The average genetic gain percentage (SG%) under selection was 5.50%, with the highest SG% observed for fodder yield (19.32%) and grain yield per plant (12.70%). The lowest SG% was for flag leaf width, which recorded -7.83%. Positive selection gains were noted for all agronomic traits except flag leaf width, indicating that the selected genotypes

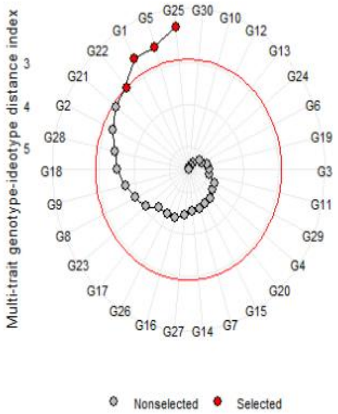

Fig 4: Ranking of 30 foxtail millet genotypes in ascending order based on MTSI index

Table 7: Evaluation of selection differential and genetic gains for 14 yield traits

S.No	VAR	Factor	Xo	Xs	SD	SDperc	h2	SG	SGperc	sense	goal
1	BY	FA1	32.65	40.59	7.94	24.32	0.74	5.86	17.96	increase	100
2	HI	FA1	44.91	45.18	0.27	0.59	0.27	0.07	0.16	increase	100
3	FY	FA1	18.02	22.32	4.30	23.85	0.81	3.48	19.32	increase	100
4	GY	FA1	14.65	18.04	3.39	23.14	0.55	1.86	12.70	increase	100
5	DF	FA2	71.88	73.19	1.31	1.82	0.72	0.94	1.31	increase	100
6	DM	FA2	111.11	113.65	2.54	2.28	0.74	1.88	1.69	increase	100
7	FW	FA2	1.88	1.66	-0.22	-11.61	0.67	-0.15	-7.83	increase	0
8	NBT	FA2	3.63	3.74	0.11	3.08	0.41	0.05	1.26	increase	100
9	PH	FA3	111.47	121.17	9.70	8.70	0.75	7.30	6.55	increase	100
10	PL	FA3	13.88	15.64	1.76	12.70	0.78	1.38	9.93	increase	100
11	PDL	FA3	20.41	22.64	2.23	10.94	0.71	1.58	7.76	increase	100
12	FL	FA4	21.40	22.92	1.51	7.08	0.65	0.98	4.58	increase	100
13	IW	FA4	1.80	1.84	0.04	2.22	0.66	0.03	1.46	increase	100
14	TW	FA4	2.78	2.79	0.01	0.25	0.88	0.01	0.22	increase	100
		sense	variable	min	mean	max	sum	sd			
		increase	SDperc	-11.611	7.811	24.318	109.351	10.400			
		increase	SGperc	-7.835	5.504	19.315	77.054	7.469			

Xo = mean for WAASBY index of the original population; Xs = mean for WAASBY index of the selected genotypes; SD and SD perc, The selection differential and selection differential in percentage; SG and SG perc, The selection gains and selection gains in percentage

performed stably across environments. Similar results were reported by Olivoto and Nardino (2022) in their study on wheat. A higher positive selection differential (%) and genetic gain under selection (%) are advantageous as they indicate a greater improvement in the trait, demonstrating effective selection. These traits can be enhanced by intentionally selecting and incorporating the desired genotypes into the breeding program.

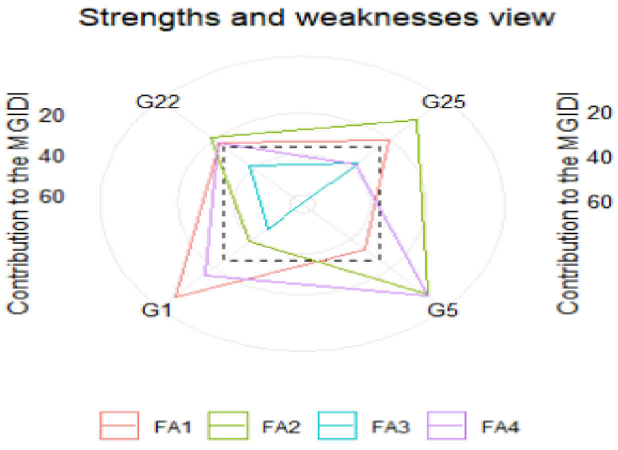

Fig 5: The strengths and weaknesses view of selected genotypes

The strengths and weaknesses view of selected genotypes

The Fig. 5 illustrates the strengths and weaknesses of selected genotypes among the 30 foxtail millet genotypes based on their MGIDI index. Fig 6 presents a comprehensive view of the strengths and weaknesses of all studied genotypes. Each component contributing to the MGIDI index is categorized into two groups: factors with the lowest contributions and those with the highest contributions. The highly significant contributing factors are shown at the center of the plot, while the lowest significant contributing factors are depicted at the edges.A dashed line represents the theoretical value, assuming all factors contribute equally (Olivoto and Nardino, 2202). In terms of FA1 (which includes grain yield, fodder yield, biological yield, and harvest index), all selected genotypes were identified as weak contributors; however, they exhibited positive selection gains and demonstrated higher productivity. For FA2 (comprising days to flowering, days to maturity, flag leaf width, and number of tillers per plant), all selected genotypes were again weak contributors. While duration traits showed positive selection gains, flag leaf width exhibited a negative selection gain. Regarding FA3 (which includes plant height, panicle length, and peduncle length), all selected genotypes were strong contributors, indicating that these genotypes possess a high stature. In FA4 (which includes flag leaf length, panicle width, and test weight), all genotypes except for G25 were weak contributors. Both FA3 and FA4 traits demonstrated positive selection gains. Overall, all selected genotypes were weak contributors for yield and yield-related traits across the four factor groups, suggesting that these genotypes are stable and close to the ideal plant type. Similar findings were reported by Benakanahalli *et al.* (2021) in guaran and Olivoto *et al.* (2021) in strawberry.

The WAASB assesses genotypic stability using multi-environment trial data, while the MGIDI method simultaneously selects the performance of genotypes and their stability in relation to multiple traits. This approach helps identify high-yielding genotypes with desirable trait combinations. Consequently, the MGIDI method aids plant breeders in making precise decisions to identify ideal plant genotypes with the desired traits, thereby supporting breeding programs designed to improve grain yield per unit area.

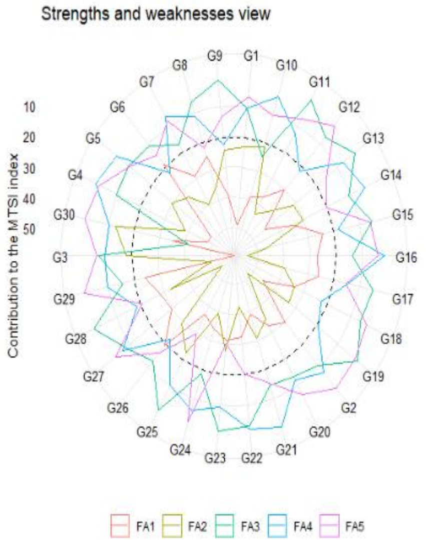

Fig 6: The strengths and weaknesses view of all studied genotypes

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