



Multi-traits Stability Index Analysis for Yield Traits in Rice (*Oryza sativa* L.)

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ABSTRACT

Background: Global warming has a high significant effect on rice farming in India, where it lowers yields and in extreme situations cause crop failure which result in economic losses. The Multi-Trait Stability Index (MTSI) is a statistical method that assesses the stability of rice genotypes by analyzing multiple traits and environmental conditions using factor analysis of yield traits.

Methods: Varietal stability for cultivation throughout seasons are measured by genotype×environment (G×E) interaction and yield stability and AMMI analysis. The present study evaluated 29 diverse rice genotypes for yield stability across three seasons at a single location during 2020-21.

Result: Among the 29 genotypes analyzed, G12, G9, G7, G13, G6, G14 and G11 exhibited high yield and significant additive effects, reflected in their positive PC1 scores; However, G11 emerged as the most superior genotype overall. Therefore, it was determined that the genotype G11 (Alamani) was a culture that was specifically adapted to the environments listed and those environments were thought to be among the many conditions that this genotype would thrive in.

Key words: AMMI, GGE, MTSI, Rice genotypes, Stability.

Abbreviations: AMMI= Additive main effects and multiplicative interaction, FA= Factor, GGE= Genotype and genotype × environment, G×E= Genotype×environment, IPCA= Interaction principal component axis, MGIDI= Multi-trait genotype-ideotype index, MTSI= Multi-trait stability index, NRRI= National rice research institute, PC= Principal component, PCA= Principal component analysis, RBD= Randomized complete block design.

INTRODUCTION

Stability analysis in rice is a crucial area of research that encompasses the examination of various factors influencing the consistency of rice yield in different environmental conditions, particularly in the climate variability and agricultural practices. This analysis not only involves understanding the genetic stability of rice varieties but also requires a comprehensive assessment of agronomic practices, pest and disease management and soil health. By employing statistical models and field trials, plant breeders aim to identify the resilience of specific rice cultivars, which can significantly contribute to food security in regions heavily reliant on rice as a staple food source (Vanitha *et al.*, 2018). Furthermore, the integration of modern technologies, such as remote sensing and data analytics, has enhanced the ability to conduct in-depth stability analyses, allowing for more informed decision making regarding breeding programs and sustainable agricultural practices aimed at maximizing productivity while minimizing environmental impact. Rice breeding is very important because it helps to improve the yield, quality and resilience of rice, which is a major cereal staple food for many people around the world. When a group of genotypes is cultivated in different environments, they may not exhibit the same response across all conditions. The impact of location, seasonal variations and the interaction among them significantly affect the performance of genotypes and their yield potential. Thus, identifying stable genotypes across diverse environments presents a significant yet

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challenging work for breeders (Mahendran *et al.*, 2024). While plant breeders have noted genetic variations related to adaptability, they have not yet succeeded in fully utilizing these differences to breed for stable genotypes. This has primarily resulted from problems with identifying and measuring phenotypic stability. Numerous efforts were taken to analyze the responses of genotypes to different

environmental conditions. AMMI analysis determines stable genotypes for cultivation by integrating multiplicative components with the classical additive main effects model for genotype and environment interaction through a least squares analysis. The statistic could enhance AMMI and GGE in the selection of varieties that are well-suited to specific locations characterized by unique fluctuations in environmental indices (Nassir and Ariyo, 2011). Previously the analysis was done for the early duration rice varieties by Ponsiva *et al.*, 2024. Hence, this study aims to identify long duration rice genotypes that perform consistently across diverse environments and multiple traits. This helps

breeders to select stable varieties suitable for various growing conditions and yield-related challenges.

MATERIALS AND METHODS

The 29 rice genotypes were cultivated for three season's viz., Navarai, *Kharif* and Navarai at the same location in 2020 and 2021. The list of genotypes used in the present study are provided in Table 1.

Trials were conducted at Plant Breeding Farm, Annamalai University in randomized complete block design (RBD) with three replications and each plot consisted of 40 plants. The following 19 traits were observed: X1-Number of days to first flowering, X2-Number of days to 50% flowering, X3 - Number of days to maturity, X4 - Height of the plant at first flowering, X5-Height of the plant at maturity, X6-Number of leaves at first flowering, X7-Total number of tillers per plant, X8-Number of productive tillers per plant, X9-Length of primary panicle, X10-Total number of seeds per primary panicle, X11-Percentage of seed fertility, X12-Length of seeds, X13-Breadth of the seeds, X14-L/B ratio of seeds, X15-Weight of 100 seeds, X16 - Total dry matter production, X17-Harvest index, X18-Per day productivity and X19-Seed yield per plant. The Eberhat and Russell (1966) model was used for stability analysis.

RESULTS AND DISCUSSION

Based on the AMMI analysis of variance, genotypic main effects were the primary source of variation in yield, accounting for a substantial 92.31% of the total variance across the 27 genotypes evaluated in three environments. Environmental main effects explained a smaller portion (5.38%), while the genotype $\times$ environment (ENV $\times$ GEN) interaction contributed only 1.12% to the total variance (Table 2). In accordance with the findings of Misra *et al.*, 2009 and Fentie *et al.*, 2013, the study highlights that the variances due to environmental and ENV $\times$ GEN interactions were statistically significant.

The large sum of squares attributed to genotypes confirms significant inherent differences in yield potential among them. The AMMI model effectively captured the ENV $\times$ GEN interaction, as evidenced by the significance of the first three interaction principal component axes (Table 3). The first principal component (PC1) alone explained a

Table 1: The list of genotypes used for this study.

Genotype	Name	Geographical origin
G2	Durga	West Bengal
G3	CR 1014	NRRI, Cuttack
G9	CR dhan 601	NRRI, Cuttack
G11	Jalamani	NRRI, Cuttack
G12	CR dhan 501	NRRI, Cuttack
G16	CR dhan 408	NRRI, Cuttack
G17	CR dhan 307	NRRI, Cuttack
G19	Sumit	NRRI, Cuttack
G20	Tapaswini	NRRI, Cuttack
G21	Pooja	NRRI, Cuttack
G24	Improved lalat	NRRI, Cuttack
G25	Gayatri	NRRI, Cuttack
G26	Samalei	NRRI, Cuttack
G29	Savala	NRRI, Cuttack
G30	CR dhan 701	NRRI, Cuttack
G31	Swarna Sub 1	NRRI, Cuttack
G50	IC-377869	NRRI, Cuttack
G51	IC-379136	NRRI, Cuttack
G52	IC-611162	NRRI, Cuttack
G53	IC-386231	NRRI, Cuttack
G54	IC-ARC-11203	NRRI, Cuttack
G55	C-67725	NRRI, Cuttack
G56	IC-264987	NRRI, Cuttack
G57	C-518987	NRRI, Cuttack
G58	IC-ARC-7432	NRRI, Cuttack
G59	C-ARC-10595	NRRI, Cuttack
G68	CR 1009 (Sub 1)	NRRI, Cuttack

Table 2: AMMI Analysis of variance.

Source of variation	df	SS	MSS	Cal F	P Value	% Sum of square	G $\times$ E explained (%)
ENV	2	1726.00	863.00	1489.17	<0.01	5.38	
REP (ENV)	6	3.50	0.58	4.30	<0.01	0.01	
GEN	26	29604.50	1138.64	8449.79	<0.01	92.31	
ENV $\times$ GEN	52	358.40	6.89	51.15	<0.01	1.12	
PC1	27	271.72	10.06	74.68		0.85	75.8
PC2	25	86.68	3.47	25.73		0.27	24.2
Residuals	156	21.00	0.13			0.07	

considerable 75.8% of the interaction sum of squares, with the second principal component (PC2) accounting for an additional 24.2%. This indicates that the interaction between genotypes and the three environments can be largely predicted by the first two principal components of both genotypes and environments (Pandey *et al.*, 2020). In essence, while the overall contribution of the G×E interaction to the total variance was relatively small, its structure was well-defined and captured by the initial principal components of the AMMI analysis.

AMMI biplots

Biplot analysis is probably the most effective interpretative technique for AMMI models. The AMMI 1 biplot illustrates

Table 3: Eigen values, variance (%) and cumulative variance (%) of genotypes.

PC	Eigen values	Variance (%)	Cum. variance (%)
PC1	6.32	33.3	33.3
PC2	3.45	18.2	51.5
PC3	1.95	10.3	61.8
PC4	1.73	9.09	70.8
PC5	1.27	6.71	77.6
PC6	1.1	5.79	83.3
PC7	0.88	4.61	87.9
PC8	0.7	3.71	91.6
PC9	0.49	2.56	94.2
PC10	0.41	2.14	96.4
PC11	0.31	1.62	98
PC12	0.2	1.06	99
PC13	0.1	0.5	99.5
PC14	0.04	0.24	99.8
PC15	0.02	0.12	99.9
PC16	0.01	0.07	100
PC17	0	0.02	100
PC18	0	0.01	100

the primary effects and PC1 scores for both genotypes and environments in relation to each other, along with two additional basic AMMI biplots. The AMMI 2 biplot displays the scores for PC1 and PC2. Based on the average yield values of the genotypes across various environments, G13 exhibited the highest yield, while G19 showed the lowest yield.

AMMI 1 biplot

Biplot analysis acts as diagrams that illustrate the associations between genotypes and environments by plotting elements of both on the same axis. The AMMI 1 biplot is typically analyzed by observing that the movements along the vertical axis indicate differences in interaction effects, whereas deviations along the horizontal axis reflect variations in main (additive) effects. Environments that are grouped together exhibit a comparable influence on the genotypes, while genotypes that are combined demonstrate similar adaptations. The genotype exhibiting optimal adaptation is capable of strategizing for the future in relation to its environment. A genotype or environment is considered stable when the IPCA1 score is closer zero, signifying minimal interaction effects. An affirmative interaction takes place when both the genotype and environment align with the same sign on the PCA axis, while a negative interaction arises when they exhibit opposing signs. Utilizing the standard techniques outlined by Gauch and Zobel in 1997, the AMMI 1 biplot allows for the calculation of predicted yield for each genotype and environment as illustrated in (Fig 1).

The AMMI 1 biplot shows that genotypes and environments on the same line or coordinate have similar yields. Those on the right side of the center exhibit higher yields. Genotypes G12, G9, G7, G13, G6, G14 and G11 displayed high yield and positive PC1 scores, with G11 identified as the best overall and specifically adapted to certain environments. Since no environment had a PC1 score near zero, no habitat was universally suitable. Consequently, the high-yielding genotypes don't have universally favorable environments. Genotypes G2, G3, G24 and G16 had near-zero PC1 scores, indicating reliability across environments. Despite showing G × E interaction,

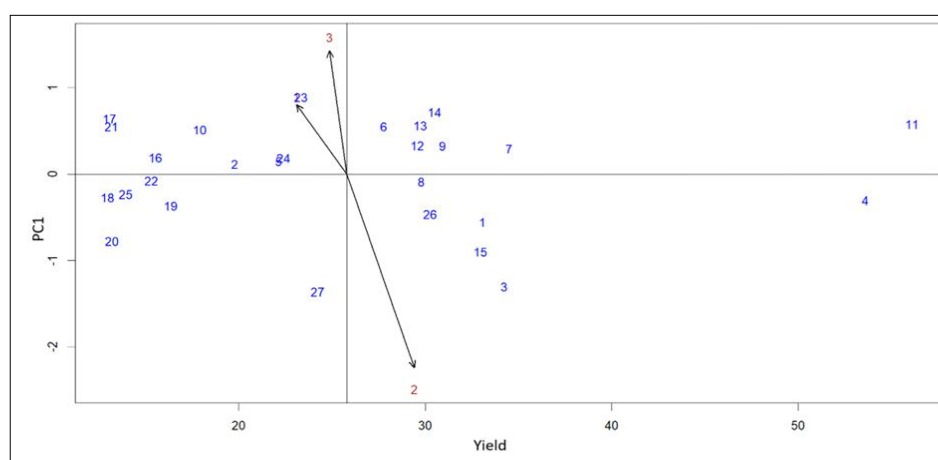


Fig 1: AMMI 1 biplot of predicted yield for each genotype and environment.

the high-yielding genotypes are expected to perform well in various environments.

AMMI 2 biplot

The environmental values are connected to the origin through lateral arrows in the AMMI 2 biplot. Strong interaction forces are exerted by sites with lengthy spokes (Fig 2), where the lines denoting environments 1, 2 and 3 are joined to the origin, provides an illustration of it. While genotypes that occur out of contour may have a varied pattern of response across the environments, genotypes that occur in the contour tend to generate identical responses in every environment. Because they were farther from the origin, G9, G16 and G21 were more sensitive in the current investigation. All genotypes, with the exception of G9, G16

and G21, were located near the origin, suggesting their stability and lack of susceptibility to the impacts of environmental interactions.

Eigen values were utilised as a key criterion to establish the proper amount of elements to keep. Six factors with eigenvalues larger than one were chosen from the group (Table 4). The attributes' cumulative variance was 83.30% explained by these six variables. As a result, only the data with strong explanatory power may be kept when the dimensionality of the data is reduced by about 17%. Sorting the 19 characteristics into these six variables was the following stage.

The best four genotypes-G11, G13, G4 and G5-were determined by ranking each genotype according to the required characteristic values using the MGIDI analysis

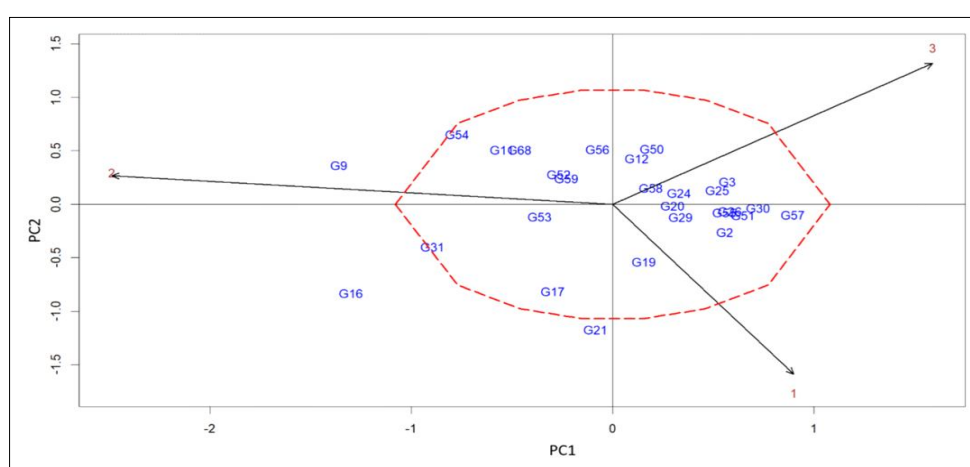


Fig 2: AMMI 2 biplot of environments 1, 2 and 3 to the origin.

Table 4: Factorial loadings, communalities and uniqueness derived from the multi-trait genotype-ideotype distance index.

Variables	FA1	FA2	FA3	FA4	FA5	FA6	Communality	Uniquenesses
X1	-0.12	-0.95	-0.1	0.06	0.05	0.17	0.96	0.04
X2	-0.1	-0.95	-0.1	0.05	0.05	0.15	0.96	0.04
X3	-0.1	-0.95	-0.06	0.05	0.05	0.18	0.95	0.05
X4	-0.63	-0.57	-0.04	0.22	0.02	-0.36	0.91	0.09
X5	-0.63	-0.58	-0.01	0.21	0.07	-0.29	0.87	0.13
X6	0.04	0.17	-0.07	-0.07	-0.86	0.1	0.78	0.22
X7	-0.75	-0.13	-0.47	0.06	0.03	-0.07	0.81	0.19
X8	-0.88	-0.19	-0.22	0.02	0.01	-0.04	0.85	0.15
X9	-0.03	-0.17	-0.1	-0.02	-0.15	0.73	0.59	0.41
X10	-0.63	-0.27	0.13	0.16	0.25	0.44	0.77	0.23
X11	-0.39	0.17	-0.28	0.3	0.6	0.24	0.77	0.23
X12	-0.1	0.02	-0.92	0.08	-0.1	0.09	0.87	0.13
X13	-0.29	0.53	0.2	0.38	-0.38	0.25	0.76	0.24
X14	0.08	-0.32	-0.87	-0.18	0.17	-0.01	0.92	0.08
X15	0.29	0.12	-0.01	0.22	-0.19	-0.44	0.38	0.62
X16	-0.74	0.01	0.02	-0.53	-0.05	0.26	0.9	0.1
X17	-0.11	-0.2	0.03	0.9	0.18	-0.1	0.91	0.09
X18	-0.9	0.23	0.16	0.06	0.07	0.2	0.94	0.06
X19	-0.91	-0.15	0.11	0.05	0.09	0.22	0.93	0.07

(Fig 3). The MGIDI study effectively estimated 19 features and predicted selection differentials (SD) ranging from 3.36% to 39.10% for various traits in selected genotypes, which all exhibited good trait values. Genotype G6's proximity to the selection boundary suggests it might possess unique characteristics. High heritability was observed for traits X1, X2, X3, X8, X10, X16, X17, X18 and X19, indicating strong potential for improvement through selective breeding. Traits X8, X10 and X19 showed both high heritability and high SD, highlighting them as key targets for breeding programs aimed at developing superior genotypes.

Strength and weakness of genotypes

Strengths and Weaknesses of Genotypes Based on MGIDI Factors: The strengths and weaknesses of several genotypes are shown in detail in (Fig 4), which is based on how each component contributes to the Multi-Trait Genotype-Ideotype Distance Index (MGIDI). G11 and G13, two genotypes linked to Factor 1 (FA1), exhibit distinct strengths in qualities including X4, X5, X7, X8, X10, X16, X18 and X19. Conversely, FA2-associated genotypes G5 and G4 exhibit strength in characteristics such as X1, X2,

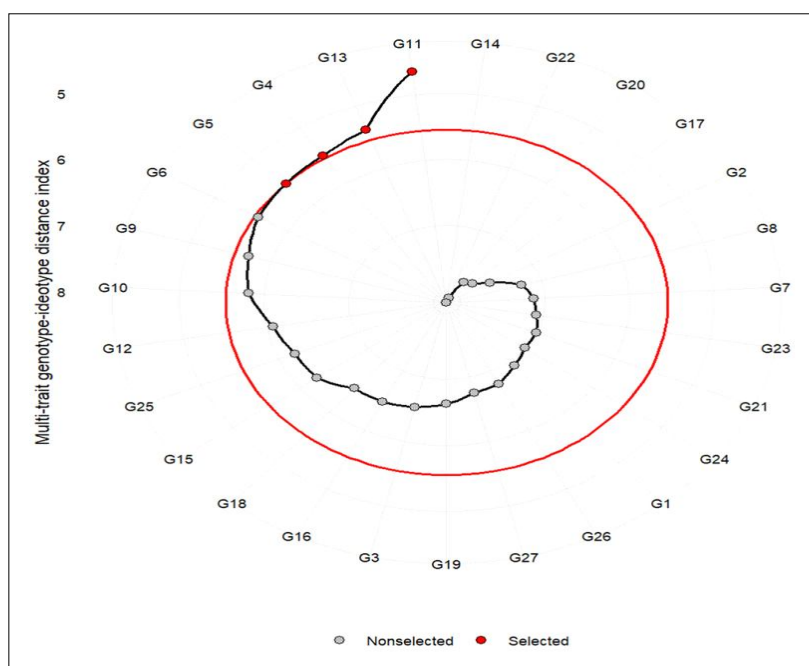


Fig 3: Genotypes rankings showing selected genotypes using the multi-trait genotype-ideotype index (MGIDI).

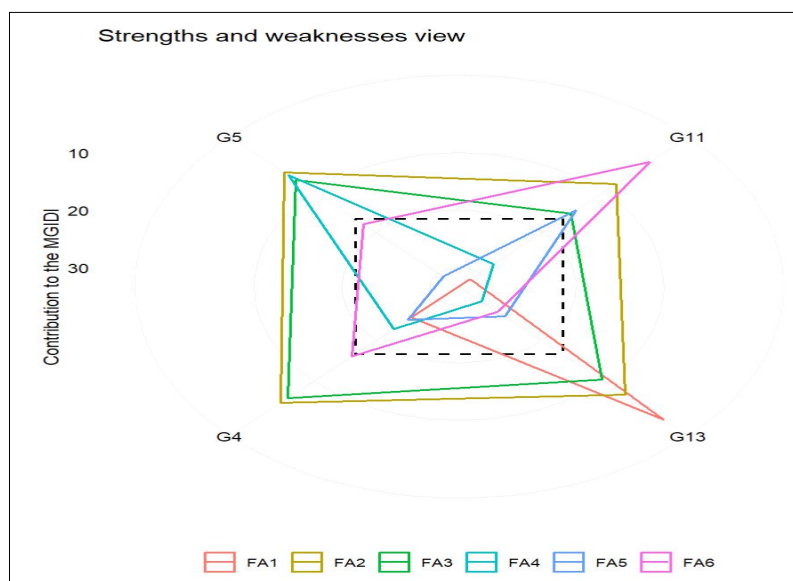


Fig 4: The strengths and weakness of selected genotypes are shown as the proportion of each factor on the computed multi-trait genotype-ideotype distance index.

Table 5: The correlated traits, selection differential, heritability and indicators interrelations.

Variables	Factor	Xo	Xs	SD	SD (%)	h2	SG	SGperc	Sense	Goal
X4	FA1	116	133	17.1	14.7	0.951	16.3	14	increase	100
X5	FA1	123	135	11.9	9.73	0.950	11.4	9.25	increase	100
X7	FA1	25.8	35.9	10.1	39.1	0.940	9.49	36.8	increase	100
X8	FA1	18.2	27.6	9.35	51.3	0.983	9.19	50.5	increase	100
X10	FA1	120	156	36	30.1	0.986	35.5	29.7	increase	100
X16	FA1	86.9	101	13.7	15.8	0.987	13.5	15.6	increase	100
X18	FA1	242	307	64.2	26.5	0.965	62	25.6	increase	100
X19	FA1	25.8	35.2	9.39	36.4	0.974	9.15	35.5	increase	100
X1	FA2	75.5	87.3	11.8	15.6	0.994	11.7	15.6	increase	100
X2	FA2	78.4	89.7	11.3	14.4	0.985	11.1	14.2	increase	100
X3	FA2	108	118	10.2	9.47	0.987	10	9.34	increase	100
X13	FA2	2.66	2.83	0.175	6.59	0.850	0.149	5.61	increase	100
X12	FA3	8.72	9.62	0.898	10.3	0.955	0.857	9.82	increase	100
X14	FA3	3.32	3.54	0.22	6.63	0.826	0.182	5.48	increase	100
X17	FA4	31.9	40.6	8.7	27.2	0.965	8.39	26.3	increase	100
X6	FA5	71.6	75.5	3.89	5.43	0.760	2.96	4.13	increase	100
X11	FA5	70.6	79.5	8.96	12.7	0.947	8.49	12	increase	100
X9	FA6	25	25.9	0.841	3.36	0.941	0.791	3.16	increase	100
X15	FA6	3.24	3.47	0.23	7.1	0.949	0.219	6.74	increase	100

Selected genotypes: G11, G13, G4, G5.

X3 and X13. Furthermore, features like X12 and X14 are stronger in genotypes G4 and G5, which are linked to FA3. Additionally, FA4-associated genotypes G5 and G11 show strength in characteristics like X6 and X11. Finally, both FA5 and FA6 were linked to genotypes G11 and G13, where FA6's X9, X15 related qualities and FA5's X6, X11 related characteristics (Table 5).

These understandings of genotype strengths and weaknesses can be very helpful in guiding the choice of parents for next breeding initiatives (Vanitha and Mahendran., 2018). The study conducted by Mamun *et al.* (2022) highlighted the importance of the optimum genotype found using MGIDI, highlighting its potential for better quantitative characteristics. The discovered genotypes-including some that are the focus of this study-prove to be the best for next breeding initiatives and are essential for improving crop quality in general. High-performing and strong varieties are developed as a result of this deliberate use of characteristics and variables (Saidaiah *et al.*, 2011).

More important influencing elements are located close to the middle of the strength and weakness plot, whereas smaller contributors are more distant out. This helps determine appropriate parentage for hybridisation projects. The radar graphic displays the characteristic influence hierarchy for each selected genotype by underlining the MGIDI participants. This helps to match characteristics to the ideotype, as seen by elements closer to the plot's edge (Ponsiva *et al.*, 2024). After a comprehensive evaluation of several features, genotype ranking revealed that G11 and G13 were the best-performing genotypes. This suggests that they have the ability to improve characteristics

associated with total yield. It is expected that the use of the MGIDI index for agricultural research would expand quickly. This index was used by Singamsetti *et al.*, 2023; Azrai *et al.*, 2024; and Zendrato *et al.*, 2024 to determine the optimal genotypes based on their strengths and weaknesses. Genotype ranking was made easier by the incorporation of yield in additional target criteria, underscoring the need of evaluating several features at once.

CONCLUSION

The AMMI 1 biplot revealed that genotypes G12, G9, G7, G13, G6, G14 and G11 exhibited high yield and additive effects, with G11 identified as the best overall. The AMMI 2 biplot further highlighted the environmental interaction, with G9, G16 and G21 being the most sensitive to environmental changes, while the remaining genotypes displayed stability. Analysis of genotype strengths and weaknesses based on MGIDI factors (FA1-FA6) provides valuable insights for parental selection in future breeding programs. G11 and G13 showed strengths in various yield-related traits (X4, X5, X7, X8, X10, X16, X18, X19), while G5 and G4 exhibited strengths in traits like X1, X2, X3, X12, X13 and X14. These findings, consistent with other research, underscore the utility of MGIDI in identifying superior genotypes with desirable quantitative characteristics for crop improvement. The study emphasizes the importance of evaluating multiple traits simultaneously for effective genotype ranking and the strategic use of identified strengths and weaknesses to guide hybridization efforts towards developing high-performing and resilient crop varieties.

Conflict of Interest

The authors declare no conflict of interest.

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