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RESEARCH ARTICLE

Dissection of genotype × environment interaction for selection of elite stable genotypes of cumin (*Cuminum cyminum* L.)

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Abstract

Cumin (*Cuminum cyminum* L.) is a versatile seed spice containing 2-4% essential oil with a distinctive aroma and flavor. About 21 diverse cumin genotypes were evaluated for their stability under field conditions over three consecutive years in the *rabi* seasons. The phenotypic stability of cumin genotypes for seed yield was analyzed using multivariate analysis through AMMI and GGE biplots. Which-won-where biplot identified MCU-6 as a high-yielding vertex genotype for E1 environment, while MCU-73 and MCU-105 were suitable for E2 and E3. The multi-trait stability index identified three genotypes, namely MCU-73, MCU-105, and MCU-25, with higher phenotypic stability and mean performance across all the traits studied. The identified genotypes may be recommended for cultivation.

Keywords: Cumin, AMMI, GGE biplot, MTSI, stability

Introduction

Cumin (*Cuminum cyminum* L.), a diploid with somatic chromosome number 14, is a versatile seed spice plant belonging to the Apiaceae family. It can be cultivated as an annual or biennial crop and is renowned for its aromatic seeds. Cumin is characterized by its adaptability to a wide range of climatic conditions. It is a widely distributed plant found in regions ranging from tropical and subtropical climates to temperate zones, but it is preferably grown in arid and semi-arid regions due to its tolerance to drought. Cumin seeds are a valuable source of essential oils, containing approximately 2 to 4% essential oil with a distinctive aroma and flavor and also valued for their medicinal properties, including digestive benefits (Allaq et al. 2020; Reyes-Calderón et al. 2023; Mohammed et al. 2024). Cumin is also used for culinary purposes. India is a larger producer and exporter of cumin seeds, with the states of Gujarat and Rajasthan being major cultivation areas. It is also cultivated in several other countries, including Iran, Turkey, and Syria, making it a globally important spice and oilseed crop (Singhet al. 2023).

The yield of cumin seeds is a crucial consideration for farmers, as it directly impacts their economic returns. However, cumin seed yield is a complex trait influenced by various genetic and environmental factors, such as temperature, rainfall, and soil quality, which determine cumin crop yields. Understanding these factors is crucial for enhancing cumin production and ensuring the consistent availability of this essential spice. The use of stable cumin genotypes can contribute significantly to enhancing seed yield and essential oil content across different environmental conditions (Merah et al. 2020; Mehriya et al. 2023). It is, therefore, important to study genotype-environment interaction (GEI), which is a critical factor in introducing new cumin varieties to different cumin-growing regions. Several methodologies have been proposed for evaluating the stability of various crops, such as Roemer's method, which uses variation across different environments as an

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indicator of yield stability (Roemer1917); Wricke's concept of ecovalence assesses the stability of each cumin genotype (Wricke 1962); Shukla's recommendation of using variance components across different environments helps evaluate phenotypic stability (Shukla 1972). Furthermore, joint regression analysis, a widely used method for assessing stability, enables the estimation of cumin genotype characteristics in response to environmental variations (Finlay and Wilkinson 1963; Eberhart and Russell 1966). Similarly, among the various stability parameters discussed, the Additive Main Effect and Multiplicative Interaction (AMMI) model and the Genotype × Environment (GGE) biplot technique have proven highly efficient for processing multi-environmental data facilitating cumin cultivation. The AMMI model provides valuable information about main and interaction effects, including biplots. However, the AMMI model alone may not effectively identify the close relationship between high mean performance and stability in cumin crops. This issue is addressed by the GGE biplot method, which incorporates both genotype main effects and GEI effects into the analysis (Gauch 1988; Yan 2001; Gauch et al. 2008). Consequently, the GGE biplot model is employed to identify optimal cumin genotypes and test locations for cultivation (Ebdon and Gauch 2002). The multi-trait selection index (MTSI) has also emerged as a unique technique for selecting superior genotypes of crops with both high-yield stability and desirable traits across varied environmental conditions (Rahimi et al. 2023; Mousa et al. 2023; Ghasemi et al. 2019).

Despite the significance of cumin, breeding progress has been relatively slow as compared to other crops. Although cumin varieties have been developed in various countries, including India, there is still a need to accelerate cumin breeding globally by identifying high-yielding and stable genotypes. To address this gap and generate essential information, the current experiment was conducted to evaluate the performance of cumin germplasm at multiple locations, thereby analyzing its stability. There is limited information available on biplots, AMMI, and MTSI in the context of cumin. Therefore, the present study was conducted using the aforementioned methods to identify highly stable and high-performing cumin genotypes suitable for cultivation in various locations and seasons.

Materials and methods

Material, sight and the experimental design

A total of 21 diverse cumin genotypes, namely, GC-4 (C) from SDAU, Sarsarkrushi Nagar, Dantiwada (Gujarat) and MCU-105, MCU-116, MCU-117, MCU-121, MCU-153, MCU-2, MCU-21, MCU-25, MCU-300, MCU-31, MCU-32, MCU-34, MCU-36, MCU-4, MCU-53, MCU-6, MCU-71, MCU-73, MCU-78 and MCU-9 (C) from Agriculture Regional Station, Mandor, Jodhpur (Rajasthan) were taken for the present study. The field experiment was conducted over three subsequent years, i.e., 2019-20 (E3), 2020-21 (E2), and 2021-22 (E1), in the rabi season at the Agricultural Research Station, Mandor, Jodhpur. This center is located in highly hostile climatic conditions, with annual rainfall ranging from 150 mm in the west to 370 mm in the east from July to September. However, the *rabi* season is generally rainy. The experiment was laid down in a Randomized Complete Block Design (RCBD) with three replications each year. Each genotype was grown in a 10-row plot of 4 m length with a 30 cm distance between rows and 5 to 10 cm between plants. The crop was successfully raised by following the necessary agronomical and plant protection methods.

Observations recorded

Ten yield and yield attributing traits, namely, days to 50% flowering (DF), days to maturity (DM), plant height (PH, in cm), numbers of umbels per plant (UMPP), numbers of umbellate per umbel (UMUM), numbers of seed per umbel (SUM), numbers of branches per plant (NB), 1000 seeds weight (TW, in g), biomass (BM, kg/ha), and seed yield (YLD, kg/ha) were recorded from ten competitive plants per genotype per replication, whereas DF, DM, BM and YLD on whole plot basis as earlier used. For 1000-seed weight, the harvested seeds were threshed and manually cleaned. The weight of 1,000 seeds from each entry was recorded in grams and used in the statistical analysis.

Statistical analysis

The data on seed yield and its related traits under three test environments were analyzed through a pooled analysis of variance, where genotypes were assumed as fixed and test environments as random factors (Peterson 1938). AMMI analysis, including ASV, YSI, GGE biplots, and MTSI, was calculated using RStudio, R version 4.0.3, with the 'agricolae' and 'metan' R packages.

AMMI analysis

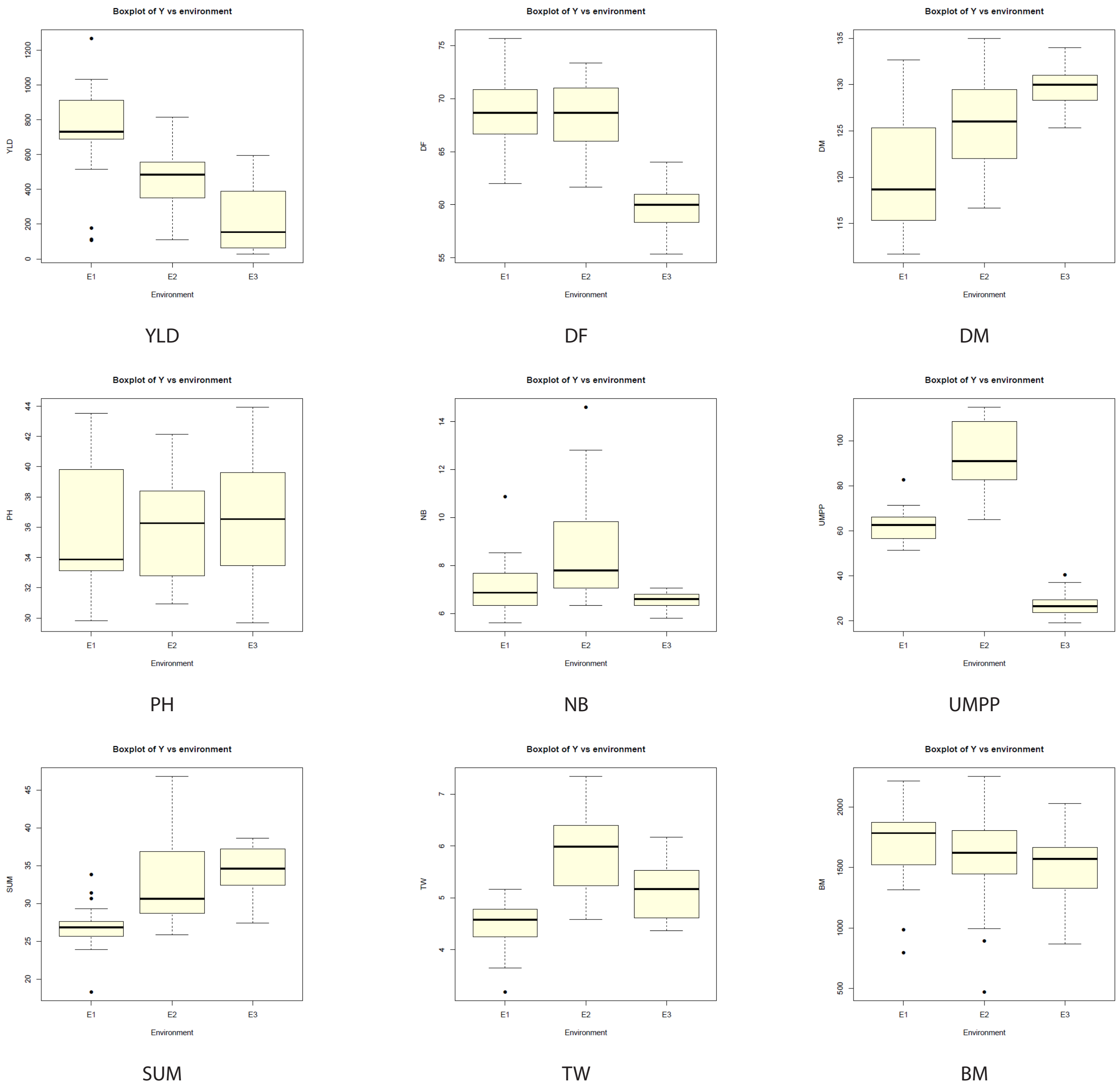
The data on seed yield per plant were subjected to AMMI analysis (Bradu and Gabriel, 1978; Gauch Jr. 1988). Regular ANOVA explained the additive main effects of genotype and environments, while PCA revealed a non-additive portion. The location-wise stable genotypes identified by AMMI analysis were assessed for significance using the Gollob, 1968 F-test approach (Vargas M. and Crossa J. 2000). The main effect of means vs the first principal component axis (PCA I) and between the first two principal component axes were used to create AMMI biplots. The AMMI stability values (ASV) and yield stability index (YSI) were also used to rank genotypes (Farshadfar, 2008; Atta et al. 2009).

GGE biplots

The site regression genotype-genotype environment interaction (GGEI) biplot models are regarded as a potent tool for successful analysis and interpretation of multi-environment data structures in plant breeding (Zobel et al. 1988). The GGE study revealed that the first two components, which are the best match for creating GGE biplots, explain most of the variance. All of the biplots in the research were constructed using environment-centered data and the symmetrical technique of the singular value partitioning (SVP) method. Mean versus stability biplot created with SVP's row metric preservation approach.

Multi-trait Stability Index (MTSI)

To measure the stability of each genotype, SVD (Singular Value Decomposition) of the matrix of Basic Linear Unbiased Predictions (BLUP) for the GE interaction effects was created using a linear mixed model (LMM). The stability of each genotype was determined by calculating the Weighted Average of Absolute Scores (WAAS) from the singular value decomposition of the matrix of best linear unbiased predictions for the GEI effects derived by a linear mixed-effect model and concurrent selection for mean performance and stability were accomplished by employing the WAASBY index (Olivotoet al. 2019). The genotype with the lowest MTSI score is more similar to the ideotype and, therefore, exhibits high mean performance and stability across all environments for all traits under study. The most desirable genotypes, with the best production and stability, were selected using a 15% selection intensity. MTSI scores were plotted to demonstrate these selected and non-selected genotypes. By generating a Y × WAAS biplot, the genotypes were categorized into four distinct groups,



YLD DF DM

PH NB UMPP

SUM TW BM

Fig. 1. Box plots showing mean performance of the studied traits across all three environments

Table 1. Combined analysis of variance for all the traits studied along with their contribution towards total variation among 21 cumin genotypes in three environments

Source of variation	Environment (df=2)		Genotype (df=20)		GEI (df=40)		Residuals (df=120)
Traits	Mean Sq	% (G+E+GEI)	MS	% (G+E+GEI)	MS	% (G+E+GEI)	MS
DF	1698.01**	65.50	49.01**	18.91	20.21**	15.59	8.45
DM	1216.4**	35.67	128.82**	37.77	45.28**	26.56	7.05
PH	5.58	0.43	93.81**	72.15	17.82**	27.42	7.16
NB	71.69**	27.52	10.94**	41.99	3.97**	30.49	0.46
UMPP	70789.44**	87.88	435.49	5.41	270.35**	6.71	46.95
SUM	959.75**	39.23	76.41**	31.23	36.12**	29.53	6.58
TW	33.09**	48.08	2.45**	35.54	0.56**	16.38	0.15
BM	433326.73**	3.61	775451.62**	64.57	191113.74**	31.83	24918.16
YLD	3504042.51**	40.72	283727.78**	32.98	113143.24**	26.30	4686.20

enabling the combined interpretation of stability and mean performance across varied contexts. This four-quadrant biplot was created with seed yield on the x-axis and WAASB values on the y-axis.

Results and discussion

ANOVA and mean performance

Pooled ANOVA showed significant differences among genotypes and indicated that studied genotypes are completely different for all the traits except for UPP (Table 1). It suggested that variation towards total variability (G+E+GEI) was the highest for BM (31.83%), closely followed by NB (30.49%), SUM (29.53%) and PH (27.42%), where genotypes had a maximum variation for PH (72.15%) followed by BM (64.57%) and NB (41.99%). These quality parameters exhibited a minimum total variation of 6.71%, 15.59%, and 16.38% for UMPP, DF, and TW, respectively. Umbel per plant (87.88 %), days to flowering (65.50%) and test weight (33.09%) showed maximum variation for environment towards total variation than other characters. Combined ANOVA indicates ample variability for traits under study, and the maximum portion of this variability was explained by environment (Table 1). In this study, cumin seed yield showed significant GEI, suggesting the importance of stability analysis for cumin genotypes across environments. Williams (2017) found similar results for green cob yield while evaluating sweet corn genotypes for adoption in processing. The mean seed yield was 485.99 kg/ha over the environment, with a range of 256.65 (E3) to 727.83kg/ha (E1) (Supplementary Table S1). The mean over environments of the other characters studied are given in Supplementary Table S2 and also displayed in Fig. 1. Abe and Adelegan (2019) also reported results for plant height, ear height, days to tasseling (55.2 days), days to silking (57.8 days) and cob length (15.7 cm) which are close to present study and suggested the presence of the significant amount of genetic variability among the traits under study.

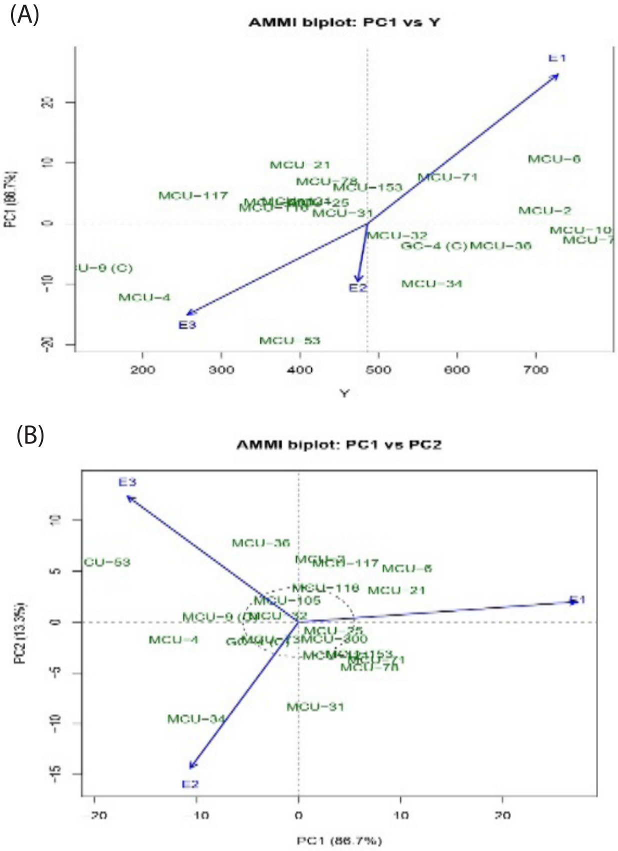


Fig. 2. (A) AMMI I biplot (seed yield vs IPCA I) of 21 cumin genotypes evaluated across three environments and (B) AMMI II biplot (IPCA I vs IPCA II) of 21 cumin genotypes evaluated across three environments

GEI analysis

The AMMI analysis for cumin seed yield reported that a significant additive portion of the total sum of squares contributed by the environmental effect (40.72%), followed by the genotypic effect (32.98%) and GEI effect (26.30%) (Table 1). Therefore, the results revealed that the performance of cumin seed yield is affected by the environment, genotype, and their interaction (GEI). AMMI divided the GEI effect into two interactive principal components (IPCA I and IPCA II) with 86.70 and 13.30% of GEI sum of squares (Supplementary Table S3). Yan et al. (2001) suggested that significant GEI effects reduce the gain for quantitative traits, such as yield in corn. Significant GEI effect and principal interactive component indicated the necessity to identify specific environments as well as genotypes.

AMMI biplot

Different biplots visualized the stability of genotypes, seed yield potential, and the association with test environments. The AMMI I biplot was developed by depicting mean seed yield on the abscissa, representing main effects, while IPCA I depicted the ordinate scores, indicating multiplicative or GEI effects (Ebdon and Gauch, 2002; Patel et al. 2023). AMMI I biplot (mean seed yield vs. IPCA I) revealed a relationship between genotype and environment (Fig. 2A). In the AMMI I biplot, E1 placed far from the origin with the longest vector represents strong interaction. On the other hand, E2 was closer to the origin, with the shortest vector indicating a poor interaction force. We can say that E2 is the least interactive and highly representative site for seed yield, while E1 is the most discriminative environment. E1 placed on the right-hand side of the grand mean line in the biplot, suggested that the year 2021-22 is favorable for cumin seed yield while the year 2020-21 (E2) and the year 2019-20 (E3) were declared as poor yielders as placed opposite to E1 (Fig. 2A). Shinde et al. (2002) and Mebratu et al. (2019) also explained similar results. Genotype- MCU-73, followed by MCU-105, MCU-6, MCU-2 and MCU-36, showed higher seed yield than overall mean performance (Fig. 2). Genotypes viz., MCU-32 followed by MCU-153 and MCU-31, placed near to origin are broadly adopted to all the environments with near to average mean seed yield production (Fig. 2) according to Ebdon and Gauch (2002). For the detailed exploration of the AMMI biplot, the AMMI II biplot was prepared using IPCA I and IPCA II (Supplementary Fig. SF2). In this plot, the polygon view of the line connected the vertex genotypes, which showed maximum seed yield in a specific environment. The perpendicular projection from the genotype to the environmental vector revealed the amount of interaction with the particular environment. Which won where, and what biplot depicts MCU-6 as the vertex genotype for E1, while MCU-73 and MCU-105 for E2 and E3 (Supplementary Fig. 2)? The present results show similarity with those of Elayaraja et al. (2022), who identified stable genotypes for sucrose percentage in sugarcane. According to AMMI stability value, genotypes MCU-105, MCU-32, MCU-31, MCU-2, MCU-116 and MCU-73 had low ASV values indicating higher stability, while MCU-53, MCU-4, MCU-6, MCU-36 and MCU-21 had higher ASV value indicating higher interaction with environments (Supplementary Table S4). YSI integrates green cob yield and stability across environments, and the lower YSI index represents higher stability and higher productivity of genotypes (Mohammadiet al. 2010). According to the YSI index, MCU-105, MCU-73, MCU-32, MCU-2 and GC-4 were detected as the best genotype for higher stability with greater yield, while genotypes MCU-4, MCU-53, MCU-9 (C), MCU-21 and MCU-117with poor production efficiency with lower stability (Supplementary Table S5). Similar results were reported by Wardofa et al. (2019) in wheat, demonstrating high performance and greater stability.

GGE Biplots

Which won where and what?

Which-won where pattern analysis facilitates the identification of the most appropriate genotype for a given environment. The outermost genotypes are joined to form a polygon in this biplot (Fig. 3). Polygon is also further divided into eleven different sectors using rays (dotted lines) that start from the origin of the plot and pass perpendicular to the sides of the polygon. This division helps to recommend genotypes for a particular sector (Gauch 2013). The biplot showed that environments E1 (year 2021-22), E2 (year 2020-21), and E3 (year 2019-20) fell under separate mega-environments. Biplot showed that MCU-6 is a high-yielding vertex genotype for E1 environment (Year 2021-22) while MCU-73 and MCU-105 for E2 (Year 2020-21) and E3 (Year 2019-20) (Fig. 3). Genotypes namely, MCU-21, MCU-117, MCU-9, MCU-4 and MCU-53 also were vertex genotypes but no environment falls in their sector indicating that they are low seed yielding genotypes at few or all years. Nzuve et al. (2013) analyzed genotype × environment interaction in maize hybrids and reported results concerning yield, finding three mega environments that contributed to a higher yield for four varieties.

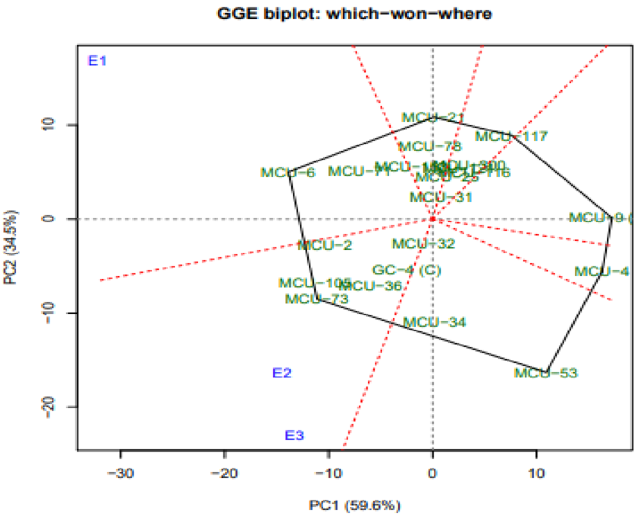


Fig. 3. Which-won-where view of 21 cumin genotypes evaluated across three environments for seed yield (kg/ha)

Table 2. Mean seed yield, PC1, PC2 score, AMMI stability value (ASV), rank of ASV (rASV), Yield stability Index (YSI) and rank of YSI of 21 cumin genotypes tested across three environments

Genotype	Mean	PC1	PC2	ASV	rASV	YSI	rYSI
GC-4 (C)	572.71	-3.84	-2.03	25.0	17	219	15
MCU-105	762.22	-1.11	2.11	7.5	3	95	3
MCU-116	366.52	2.65	3.35	17.5	23	163	22
MCU-117	263.98	4.62	5.76	30.5	31	282	29
MCU-121	395.74	3.68	-3.27	24.1	24	213	22
MCU-153	486.07	5.93	-3.16	38.7	23	311	22
MCU-2	711.57	2.11	6.19	15	8	243	13
MCU-21	400.56	9.64	3.10	62.7	31	542	31
MCU-25	423.52	3.41	-0.88	22.1	20	183	18
MCU-300	373.06	3.49	-1.66	22.7	25	184	23
MCU-31	454.89	1.70	-8.33	13.8	14	286	22
MCU-32	523.22	-2.01	0.62	13.1	11	107	11
MCU-34	568.00	-9.99	-9.55	65.6	26	590	26
MCU-36	655.37	-3.69	7.75	25.2	16	337	18
MCU-4	202.39	-12.21	-1.72	79.3	40	676	40
MCU-53	387.19	-19.38	5.91	126	37	1035	37
MCU-6	723.43	10.64	5.26	69.3	22	606	22
MCU-71	588.33	7.66	-3.74	49.9	22	403	21
MCU-73	773.33	-2.73	-1.68	17.8	7	157	4
MCU-78	434.17	6.95	-4.47	45.3	26	361	26
MCU-9 (C)	139.48	-7.51	0.41	48.8	36	409	37
E1	727.83	27.38	2.22	-	-	-	-
E2	473.48	-10.62	-15.96	-	-	-	-
E3	256.65	-16.76	13.74	-	-	-	-

Mean seed yield vs stability

The 2-D visualization of seed yield vs stability based on PCA I and PCA II scores were constructed according to reports of Yan et al. (2001). This plot is best suited for genotype evaluation, as it was developed using the row metric preserving method (Fig. 2B). An average environment coordination view was plotted to show the stability of the genotypes. A small perpendicular line represents highly stable genotypes to the AEC axis. Higher seed yield across the environment, as depicted by the AEC abscissa. Genotypes MCU-73, MCU-105, MCU-106, and MCU-2 were found to be highly stable with good yielding ability. AS per the A-R Model-Genotype MCU-105, MCU-73 and MCU-2 were found high yielding and stable genotypes with $b_i = 1$ and non-significant S^2di (Supplementary Fig. 1).

Discriminativeness vs representativeness

The cosine angle between environmental vectors explains the relationship between two environments (Yan 2002). A perfect 90° angle between two environments represents no correlation, an acute angle depicts a positive correlation and an obtuse angle indicates a negative correlation. A positive correlation was observed across all environments. In contrast, the longest vector of E1 (Year 2021-22) indicates that it is most discriminative environment. On the biplot, the length of the environment's vector is proportional to the standard deviation within that same environment and gives information regarding the environment's discriminating ability (Sserumaga et al. 2016; Samyuktha et al. 2020). The average environment axis is required to assess the representativeness of the environment. The discrimination and representativeness view of the GGE biplot has been studied in several crops (Reddy et al. 2022; Kottawa-Arachchi et al. 2022) to show the discriminating ability and representativeness of the test environments. A higher angle between AEA and the environmental vector indicates lower representativeness and vice versa. In the view of representativeness, E2 is highly representative

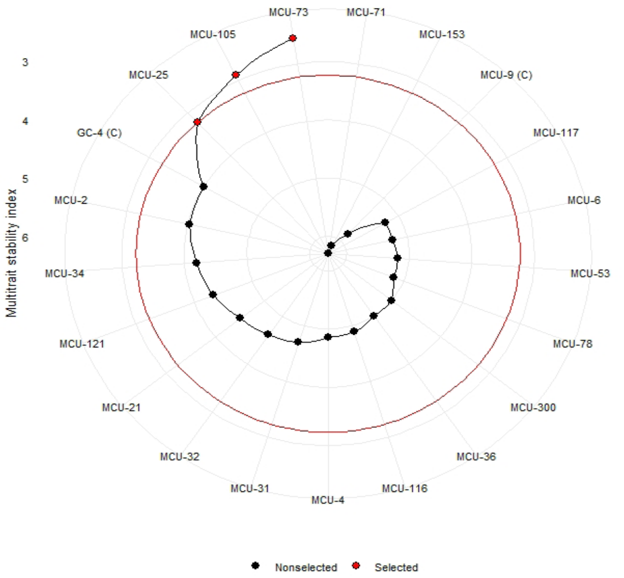


Fig. 4. Genotype ranking and selected genotypes among 21 cumin genotypes for multi-stability index (MTSI) considering 14 % selection intensity

environment. The present results indicated that widely adopted genotypes were selected from E2 (Year 2020-21), i.e., MCU-73, MCU-105, and MCU-2, while specifically adapted genotypes were MCU-6. were selected from the E1 (Year 2021-22) environment.

Multi-trait stability index (MTSI)

The primary purpose of any breeding strategy is to select high-performing genotypes with desired features. The majority of plant breeders used traditional stability indices based on first-degree statistics. The choice of a stable genotype based on mean, regression, and departure from regression parameters may not be sufficient to provide a straightforward interpretation of mean performance and trait stability. As a result, the MTSI approach is a sophisticated quantitative genetic tool for the exploitation of appropriate variations in all crop species (Olivoto et al. 2019b). It utilized the mean performance and stability of the genotype for multiple traits. Multi-Trait Stability Index, which is calculated based on the genotype-ideotype distance, considering multiple interacting variables. MTSI included all traits except DF because their p-value for likelihood ratio also found non-significant. The WAASBY values generated using a Pearson's correlation matrix and the retrieved high magnitude relationships were combined as a common factor. Exploratory factor analysis using 10 characters resulting from four PCs cumulatively explained 77.9 % of the variation (Supplementary Table S6). Communality, an indication of shared variance among traits, ranged from 0.561 (DM) to 0.939 (PH), with a mean of 0.77 after varimax rotation. Ten traits were grouped in the four factors by extracting WAASBY value from each character given in Supplementary Table S7. DF, DM, UMPP, UMUM and SUM were grouped in the FA1. NB, BM and YLD were in FA2. FA3 and FA4 had only one trait each i.e., PH and TW, respectively (Supplementary Table S7). The selection performed in Figure 4 was used to calculate the mean of the selected genotypes (XS), which was higher than the mean of the original population for mean performance. The selection differential for mean performance was with a range of -0.2 (DF) to 30.7 (YLD), while the selection differential for the WAASBY index was positive for all the traits. DF showed a negative value for the selection differential, so this trait was rejected for simultaneous selection for yield and stability. A similar approach was adopted to evaluate the relative effects of drought and saline stress on seed germination in sweet sorghum (Patanè et al. 2013) and cowpea (Murillo-Amador et al. 2002). The selection of stable genotypes with higher mean performance across various traits is crucial in stability analysis (Yue et al. 2021). It was performed using genotype-ideotype Euclidian distance-based scores. Scores for 21 genotypes, along with ideotype estimated in first four factors, were obtained through exploratory factor analysis (Supplementary Table S6).MTSI helps to select genotypes with higher stability, having a higher mean performance across all measured traits. Lower MTSI-valued genotypes were selected with 14% selection intensity. According to Fig. 4, MCU-73 (MTSI=2.56), MCU-105 (MTSI=2.90) and MCU-25 (MTSI=3.23) were selected with maximum stability and high mean performance of analysed traits. The red circle in Figure 4 indicates the cutoff point with an MTSI value of 3.23 of MCU-25. Genotype MCU-71 had a higher MTSI value (MTSI = 6.30), followed by MCU-153 (MTSI = 6.16) and MCU-9 (MTSI = 5.84). These genotypes were recognized as unstable, with poor performance for the traits under study.

These findings were comparable to that of Koundinya et al. (2021), who used MTSI to evaluate genotype-environment interactions, including leaf area index, yield per plant, harvest index, dry matter and starch yield per plant in 25 cassava genotypes. In the mean vs stability' biplot, the majority of genotypes identified by MTSI were shown to be closer to the AEC. Among these selected genotypes, MCU-73 (MTSI=2.56), MCU-105 (MTSI=2.90) had the lowest MTSI value and fell near to origin in which-won-where biplot and also found near to origin in AMMI II biplot. These results support the use of MCU-73 and MCU-105 as a genitor for future breeding and pre-breeding programs to develop new cultivars. Furthermore, MTSI also helps to focus on the selected trait to attain stability with great performance through factor analysis, as suggested by Koundinya et al. (2021) in cassava, Sellami et al. (2021) in lentil, and Memon et al. (2023) in castor.

Supplementary material

Supplementary Tasbles S1-S6 and Supplementary Fig. 1-2 are provided, which can be accessed at www.isgpb.org

Authors' contribution

Conceptualization of research (R, MK, MM); Designing of the experiments (R, MK, MM); Contribution of experimental materials (R, MK, MM); Execution of field/lab experiments and data collection (R, MK, RC); Analysis of data and interpretation (R, MN, N); Preparation of manuscript (N).

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Supplementary Table S1. Mean over environments of 21 cumin genotypes for different characters over environment

Genotype	DF	DM	PH	NB	UMPP	SUM	TW	BM	YLD
GC-4 (C)	66.56	130.06	32.18	8.03	61.70	33.05	5.15	1650.14	572.71
MCU-105	68.00	131.33	40.47	10.80	74.93	38.70	5.87	1659.50	762.22
MCU-116	65.56	120.56	35.76	7.00	55.37	30.12	5.48	1671.94	366.52
MCU-117	70.56	131.44	34.36	6.96	61.32	33.77	4.96	1086.28	263.98
MCU-121	68.28	128.67	31.29	8.36	67.11	33.32	5.41	1386.42	395.74
MCU-153	62.78	121.56	33.87	6.80	53.51	28.16	5.54	1687.78	486.07
MCU-2	66.11	129.00	32.13	8.64	60.80	32.68	4.59	1730.83	711.57
MCU-21	66.89	124.78	35.24	6.73	62.50	28.69	4.47	1307.72	400.56
MCU-25	66.00	123.44	41.24	7.36	56.46	32.76	5.50	1804.44	423.52
MCU-300	62.67	118.78	36.51	6.96	60.68	29.72	5.90	1532.22	373.06
MCU-31	64.44	123.33	35.38	6.96	68.86	31.66	5.47	1944.56	454.89
MCU-32	61.78	124.56	40.80	8.31	66.93	29.78	4.08	1484.56	523.22
MCU-34	62.89	120.89	38.38	6.82	66.10	30.90	4.89	1744.72	568.00
MCU-36	63.11	122.67	31.91	7.04	60.53	30.70	5.27	1532.22	655.37
MCU-4	66.00	126.44	38.33	6.67	56.38	31.20	4.61	1407.50	202.39
MCU-53	66.78	126.67	33.82	6.40	52.03	29.55	5.46	1166.94	387.19
MCU-6	66.67	125.78	35.16	7.36	68.11	29.49	4.66	2109.17	723.43
MCU-71	69.00	130.44	34.33	6.51	52.70	27.64	4.52	1941.39	588.33
MCU-73	63.11	125.78	41.87	9.20	63.40	37.42	5.39	1860.67	773.33
MCU-78	64.22	120.89	35.16	7.00	70.49	28.12	5.98	1539.28	434.17
MCU-9 (C)	65.33	126.56	38.56	6.24	47.35	28.66	5.30	948.89	139.48
Mean	65.56	125.41	36.03	7.44	61.30	31.24	5.17	1580.82	485.99
Min	61.78	118.78	31.29	6.24	47.35	27.64	4.08	948.89	139.48
Max	70.56	131.44	41.87	10.80	74.93	38.70	5.98	2109.17	773.33

Supplementary Table S2. Mean of quantitative traits of cumin genotypes in different environmets

Traits	E1: Year 2021-22	E2: Year 2020-21	E3: Year 2019-20	Mean over environments
DF	68.6	68.5	59.6	65.6
DM	120.8	125.9	129.6	125.4
PH	35.7	36.2	36.2	36.0
NB	7.13	8.62	6.55	7.44
UMPP	62.8	94.1	27.1	61.3
SUM	26.8	32.7	34.2	31.2
TW	4.46	5.91	5.13	5.17
BM	1666.4	1575.2	1500.8	1580.8
YLD	727.8	473.5	256.7	486.0

Supplementary Table S3. Analysis of variance based on AMMI model of seed yield per ha for 21 cumin genotypes across three environments

Source	Df	Sum Sq	Mean Sq	GEI Contributed (%)
Environment (E)	2	7008085	3504042.5	40.7
Replication/E	6	21646.788	3607.7979	
Genotype (G)	20	5674555.7	283727.78	33.0
GxE	40	4525729.5	113143.24	26.3
PC1	21	3921834.4	186754.02	86.7
PC2	19	603895.05	31783.95	13.3
Residuals	120	562344.51	4686.2043	

Supplementary Table S4. Eigenvalues, explained variance, factorial loadings after varimax rotation, and communalities and uniqueness obtained in the factor analysis of the 10 variables studied in 21 cumin genotypes across three environments

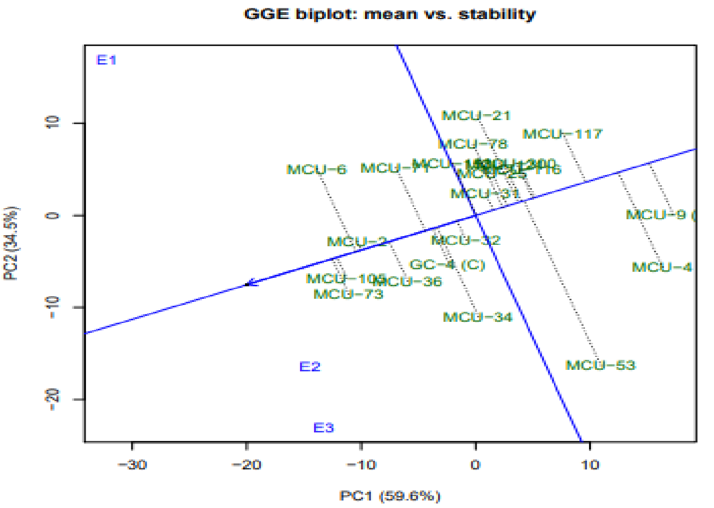
VAR	FA1	FA2	FA3	FA4	Communality	Uniqueness
DF	-0.787	0.223	0.0859	-0.0991	0.686	0.314
DM	-0.654	-0.182	-0.225	0.224	0.561	0.439
PH	0.0684	-0.0750	0.963	-0.0459	0.939	0.0609
NB	-0.410	-0.566	0.277	-0.488	0.803	0.197
UMPP	-0.653	-0.405	-0.236	-0.180	0.679	0.321
UMUM	-0.786	-0.236	-0.0998	-0.0357	0.684	0.316
SUM	-0.801	0.0777	0.441	-0.0381	0.843	0.157
TW	0.0274	0.0260	0.0149	-0.937	0.879	0.121
BM	0.0774	-0.876	0.0730	0.915	0.817	0.183
YLD	-0.155	-0.924	-0.0446	-0.142	0.899	0.101
Eigen value	3.39	1.88	1.45	1.07	-	-
Variance (%)	33.9	18.8	14.5	10.7	-	-
Accumulated (%)	33.9	52.7	67.3	77.9	-	-

Supplementary Table S5. Genotype -ideotype (ID) scores MTSI values for 21 cumin genotypes for the first four factors along with relative contribution of each factor towards the MTSI

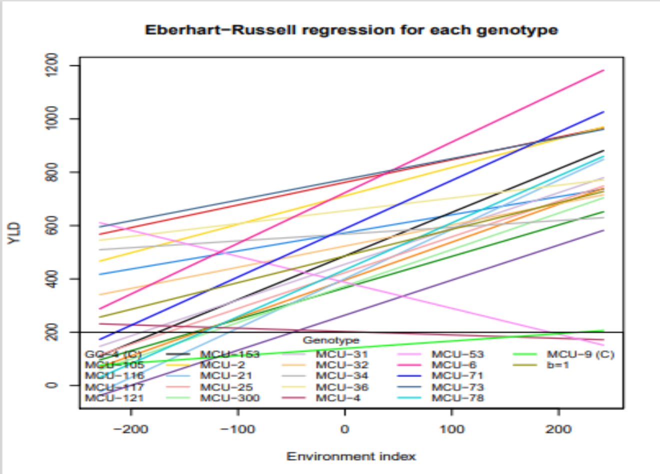
S. No.	Genotype	FA1	RC%	FA2	RC%	FA3	RC%	FA4	RC%	MTSI
1	GC-4 (C)	-3.82	29.1	-1.74	20.6	0.17	40.5	-2.92	9.9	4.00
2	MCU-105	-3.24	59.5	-2.80	9.9	2.34	17.2	-4.25	13.4	2.90
3	MCU-116	-2.04	43.7	-1.32	21.6	1.25	21.0	-2.43	13.6	4.89
4	MCU-117	-3.75	21.0	-0.32	28.1	0.67	23.6	-0.79	27.4	5.25
5	MCU-121	-4.43	19.2	-1.05	27.9	-0.20	42.2	-2.81	10.6	4.34
6	MCU-153	-0.75	48.6	-1.78	13.7	0.48	24.7	-2.27	12.9	6.16
7	MCU-2	-4.08	25.7	-2.46	10.8	-0.07	44.0	-2.24	19.4	4.03
8	MCU-21	-3.96	22.2	-0.52	30.5	0.84	25.6	-1.70	21.8	4.51
9	MCU-25	-3.64	37.9	-1.63	26.6	2.42	11.6	-2.20	23.9	3.23
10	MCU-300	-2.24	39.2	-1.53	18.1	0.69	25.8	-2.05	16.9	5.01
11	MCU-31	-3.18	30.5	-2.04	13.3	0.81	25.6	-0.88	30.6	4.70
12	MCU-32	-2.38	43.4	-1.96	15.7	2.26	10.6	-1.16	30.4	4.61
13	MCU-34	-2.91	38.0	-1.72	19.2	1.74	17.4	-1.61	25.5	4.19
14	MCU-36	-3.00	33.1	-1.95	14.6	-0.59	41.9	-2.72	10.5	4.99
15	MCU-4	-3.02	32.7	-0.17	34.5	2.46	7.4	-1.37	25.5	4.86
16	MCU-53	-2.93	29.8	-0.58	26.5	0.21	28.9	-2.16	14.8	5.18
17	MCU-6	-3.49	27.8	-3.07	1.9	1.10	23.0	0.51	47.3	5.23
18	MCU-71	-0.86	46.6	-2.57	6.2	0.29	26.0	-1.34	21.2	6.30
19	MCU-73	-3.59	61.1	-2.95	7.6	2.86	6.9	-2.71	24.3	2.56
20	MCU-78	-1.79	46.2	-1.45	20.0	0.70	27.0	-3.03	6.9	5.16
21	MCU-9 (C)	-2.16	36.7	0.87	40.1	1.97	11.2	-2.42	12.0	5.84

Supplementary Table S6. Selection differential for mean of the traits and WAASBY index for 9 traits of 21 cumin genotypes across three environments

		Mean performance				WAASBY			
Trait	Factor	Xo	Xs	SD	SD (%)	Xo	Xs	SD	SD (%)
DF	FA1	65.6	65.4	-0.1	-0.2	53.3	70.2	16.9	31.7
DM	FA1	125.0	127.0	1.3	1.1	57	63.2	6.2	10.9
UMPP	FA1	61.3	63.9	2.6	4.2	54.2	63.2	8.93	16.5
UMUM	FA1	5.3	5.5	0.2	3.3	50.7	63.5	12.9	25.4
SUM	FA1	31.2	34.3	3.0	9.6	46.8	55.7	8.87	18.9
NB	FA2	7.4	8.5	1.0	14.0	26.1	49	22.8	87.4
BM	FA2	1581	1742.0	161.0	10.2	54.5	68.3	13.9	25.5
YLD	FA2	486	635.0	149.0	30.7	54.7	78.2	23.5	43.1
PH	FA3	36	37.7	1.7	4.7	44.9	60.7	15.8	35.3
TW	FA4	5.2	0.1	1.3	0.8	62.8	75.1	12.3	19.5



Supplementary Fig. 1. Average environment coordination (AEC) view of the GGE- biplot based on environment focused scaling for mean performance and stability of 21 cumin genotypes evaluated across three environments



Supplementary Fig. 2. Eberhart-Russell regression graph of 21 cumin genotypes evaluated across three environments for seed yield (kg/ha)