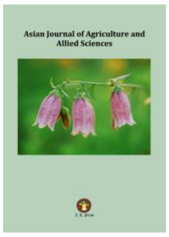

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AMMI Analysis for Genotype × Environment Interaction of White Cumin (*Trachyspermu mammi* L.) Genotypes in Potential Growing Areas of Ethiopia

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Authors' contributions

This work was carried out in collaboration among all authors. All authors read and approved the final manuscript.

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ABSTRACT

The experiment was conducted to select the best yielder and widely adaptable white cumin genotypes across different testing environments during the 2012, 2013, 2014, and 2015 main cropping seasons. Nine white cumin genotypes were evaluated in RCBD design using three replications at eleven environments. The combined mean performance recorded a higher mean seed yield from genotype G3 (1,031.3 kg ha^{-1}) followed by genotype G7 (1,011.2 kg ha^{-1}). The

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AMMI analysis of variance for seed yield showed a highly significant ($p<0.01$) difference among genotypes, environments, and genotype × environment. The environmental effect accounted for 64.03% of the total variation, whereas the genotype × environment and genotype effect accounted for about 1.65% and 10.27% of total sum squares respectively. The first IPCA captured about 50.4% of genotype × environmental interaction sum square, while the second IPCA explained about 25.2%. The two IPCs cumulatively explained 75.6% of genotype × environmental interaction sum square. Based on ASV scores G7 and G4 have the lowest ASV and they are the most widely stable genotypes across environments. In contrast, genotypes G5 and G1 score relatively the highest ASV and are considered unstable genotypes. E3 scored the least negative IPCA1 values, while environments E5, E8, and E9 scored maximum positive and negative IPCA1 values.

Keywords: AMMI; ASV; interaction; IPCA; stability; unstable.

1. INTRODUCTION

"White cumin (*Trachyspermum ammi* L.) is an annual cross-pollinated plant with a chromosome number of 2n=18 and it belongs to the Apiaceae (Umbelliferae) family" (Endalkachew, et al., 2020). "*Trachyspermum ammi* L is an herbaceous plant with white flowers and small brownish fruit growing in the east of India, Iran, Pakistan, Egypt, around the Mediterranean Sea, and Ethiopia" (Girma, et al., 2016, Habetewold, et al., 2017). The crop is dominantly cultivated in Ethiopia for consumption and commercial purposes from 1750 to 2200 m.a.s.l. (Habetewold, et al., 2017, Tesfa, et al., 2017, Girma, et al., 2022). "In Ethiopia, it is named differently in diverse languages: nech azmud (Amharic) and abesuda adi (Afan Oromo)" (Balakrishnan et al., 2016, Alemnew, 2021, Gizaw, et al., 2024). The Ethiopian variety of white cumin accumulates up to 9% essential oil, of which 55% is the volatile component thymol (Amare & Mekuria, 2013), making it valuable for use in personal hygiene, cooking, and medicine (Ravindran & Balachandran, 2004). Two registered varieties of white cumin, Takusa-01, and Dembia-01, had essential oil contents of 6.42% and 6.5%, which are responsible for the characteristic aroma, and oleoresin contents of 28.3% and 26.55%, respectively. It is useful for medicinal and culinary purposes (Aklilu, et al., 2020). In Ethiopia, the studies on Ethiopian white cumin focused mainly on its essential oil, medicinal properties, agronomic practices, genetic variability assessment, and multi-environment stability analysis (Amare & Mekuria, 2013, Seid, et al., 2013, Tesfaye, 2017, Endalkachew, et al., 2020). Seed yield is an intricate quantitative trait and considerable variations in seed yield are attributed to genetic character and the response of accessions to agro-climatic conditions (Gizaw, et al., 2024, Baraki, et al., 2024).

One of the multivariate techniques is the AMMI model. The AMMI model combines the analysis of variance for the genotype and environment main effects with principal components analysis of the G ×E interaction. The additive main effect and multiplicative interaction (AMMI) method proposed by Gauch (1992) was a significant advance in the analysis and interpretation of G×E interaction. "AMMI biplot analysis is considered to be an effective tool for diagnosing GEI patterns graphically. The model separates the additive variance from the multiplicative variance and then applies principal component analysis to the interaction portion to a new set of coordinate axes that explains in more detail the interaction pattern and the estimation accomplished using the least squares principle" (Thillanathan, et al., 2001). Purchase (1997) developed the AMMI Stability Value based on the AMMI model's principal components axis 1 and 2 respectively scores for each cultivar. Limited efforts have been made to understand the genetic differences and evaluation of accessions, genetic improvement, heritability, and the 5% selection intensity of target traits. In white cumin, conventional methods based on the selection of desirable genotypes have responded well to yield enhancement and quality traits; the evolution of the collected genotypes from different parts of the country is necessary for performing selection cycles in a population. So far, only Takusa-01 and Dembia-01 cultivars of white cumin have been registered in Ethiopia (Anonymous, 2022), it is one of the neglected areas of the research system where intensive research activities have not been conducted. Even though the initial evaluation of the germplasm has shown that the variability is enormous in this crop, the generation of information on those genotypes could help to advance to the next breeding stage of the crop and variety registration. Further studies are mandatory to fill the existing gaps and to develop high-yielding varieties with considerable quality traits. Thus, the study aimed to select the best yielder and widely adaptable white cumin genotypes across different testing environments.

2. MATERIALS AND METHODS

2.1 Description of Experimental Locations

The experiment was conducted in the main cropping season from 2020 to 2023 for four consecutive growing seasons at four locations, namely Arsi-Robe, Sinana, Ambo, and Kulumsa experimental station. Details of experimental sites were described in Table 1.

2.2 Experimental Materials and Designs

The Ethiopian white cumin landraces were originally collected from different Ethiopian white cumin growing areas of the Oromia region and then morphologically characterized. Then thirteen genotypes were selected from previous preliminary yield trials that had been conducted in consecutive years. A total of nine Ethiopian white cumin genotypes were tested in eleven environments (year and location combinations) in Ethiopia under rain-fed conditions. The testing genotypes were listed below in Table 2. The experiment was carried out in a randomized complete block design (RCBD) with three replications. Each genotype was planted on a plot size of 3.6 m^2, with a 2m length and 30cm spacing between rows. Each plot has 6 rows at all the testing sites. Recommended rate of NPS fertilizer was applied at the time of sowing to each testing locations.

2.3 Data Collected

Data were collected on a plot-by-plant basis. So the variables were gathered from ten randomly selected plants from the middle four rows of each plot. These traits were expressed below.

2.4 Phenological Data

Days to 50% emergency: number of days from the date of sowing to when 50% of the seedlings appeared above ground level.

Table 1. Summary of experimental locations

E	**Year**	**Location**	**Geographical position**		**Altitude**	**Temperature**		**Rainfall (mm)**
			Latitude	Longitude		Minimum	Maximum	
E_1	2020	Kulumsa	08001’10’’N	39009’11’’E	2200	10.5	22.8	820
E_2	2020	Arsi-robe	07^{0}53’02’’N	39^{0}37’40’’E	2340	8.13	22.51	1020
E_3	2021	Kulumsa	08001’10’’N	39009’11’’E	2200	10.5	22.8	820
E_4	2021	Arsi-robe	07^{0}53’02’’N	39^{0}37’40’’E	2340	8.8	23.6	1020
E_5	2022	Kulumsa	08001’10’’N	39009’11’’E	2200	10.5	22.8	820
E_6	2022	Arsi-robe	07^{0}53’02’’N	39^{0}37’40’’E	2340	5.8	22.6	1015
E_7	2022	Ambo	08^{0}58’10’’N	37^{0}51’28’’E	2164	12.07	26.13	1068
E_8	2022	Sinana	07^{0}06’12’’N	40^{0}5 12’40’’E	2400	9.5	21.5	1174
E_9	2023	Kulumsa	08001’10’’N	39009’11’’E	2200	10.5	22.8	820
E_{10}	2023	Ambo	08^{0}58’10’’N	37^{0}51’28’’E	2164	12.07	26.13	1068
E_{11}	2023	Sinana	07^{0}06’12’’N	40^{0}5 12’40’’E	2400	9.5	21.5	1174

E = environment, mm = milli meter

Table 2. List of genotypes used for the experiments

No.	**Genotypes code**	**Genotype name**	**Source**
1.	G_1	Akiya-2007	Collection
2.	G_2	Shirka 001/2007	Collection
3.	G_3	Bale -2007	Collection
4.	G_4	Silingo-2007	Collection
5.	G_5	Sole-007	Collection
6.	G_6	Gedgeda-026	Collection
7.	G_7	Sagure-2007	Collection
8.	G_8	Takusa-01(St.check 1)	Released variety
9.	G_9	Dembia-01(St.check 2)	Released variety

Days to 50% flowering: the days from sowing to 50% of the plants in a plot get bloomed.

Days to 90% physiological maturity: the number of days from the date of sowing to when the plant changed from a dark green to a brown color, 90% of the umbellets changed to brownish, and the fruits started to wither.

2.5 Agronomic, Yield and Yield Related Traits

Plant height: an average plant height (cm) was measured from 10 randomly selected plants from ground level to the tip of the umbels.

Number of primary branches plant^{-1}: the number of primary branches was recorded by counting branches from 10 plant parts raised from the main stem as primary branches.

Number of umbels plant^{-1}: the average number of effective umbels from the ten randomly selected plants was counted.

Number of umbellets umbel^{-1}: the average number of umbellets was counted from 10 randomly selected plants of effective 5 umbels from each plant.

Seed yield plant^{-1} (g): the average seed weight of 10 randomly selected and tagged plants was taken from the middle four rows excluding the border rows to avoid the border effect.

Seed yield ha^{-1} (kg): seed yield was determined by harvesting plants from the four middle rows from a net area of 2.4 m^2 (2 m × 1.2 m) to avoid border effects. Seeds, which were obtained from the corresponding net plot, were cleaned manually. After sun-dried and adjusted to 9.5% moisture content, it was weighed in grams by using a sensitive balance and recorded values of seed yield were converted to kg ha^{-1}.

2.6 Statistical Analysis

An R-software package was used for analysis of variance of the combined data over locations. The analysis of variance for grain yield and yield-related traits for combined analysis was analyzed by using a randomized completed block design. The combined analysis of variance across the environment was done to determine the differences between genotypes across environments, among environments, and their interaction using the following statistical models,

$$Yij = \mu + Ej + R\ (E) + Gi + GEij + eij$$

Where; Yij is the observed mean of the ith genotype (Gi) at the jth environments (Ej), μ is the general mean, Gi, Ej, and GEij represent the effects of the genotype, environment, and genotype by environment interaction respectively, R (E) is the effect of replications within environments, and eij is the average random error associated with the ith plot that receives the ith genotype in the jth environment.

2.6.1 AMMI model analysis

The Additive main effects and multiplicative interaction (AMMI) model was performed for grain yield of 9 white cumin genotypes using *performs. ammi* () function in *metan* packages of R software R 4.4.0 version. Therefore, the estimate of the response variable for the ith genotype in the jth environment (y_{ij}) using the AMMI model, is given as follows (Gauch, 1992).

$$Y_{ij} + \mu + G_i + E_j + (\sum_{k=1}^{n} \lambda_k \alpha_{ik} \gamma_{jk}) + \varepsilon_{ij}$$

where Y_{ij} = is the yield of the ith genotype in the jth environment; μ = is the grand mean; G_i and E_j are the genotype and environment deviations from the grand mean, respectively; λ_k = is the eigenvalue of the PCA analysis axis k; α_{ik} and $\boldsymbol{\gamma}_{jk}$ = are the genotype and environment principal component scores for axis k; n is the number of principal components retained in the model, and e_{ij} is the error term.

AMMI Stability Value (ASV) which is the distance from the coordinate point to the origin in a two-dimensional of IPCA1 score against IPCA2 scores in the AMMI model was calculated using the formula developed by (Purchase, et al., 2000).

$$ASV = \sqrt{[\frac{IPCA1\ sum\ squares}{IPCA2\ \ sum\ squares}(IPCA1score)]^{\mathbf{2}} + [\,IPCA2score]^2}$$

Where: IPCA1 = interaction principal component axis 1, IPCA2 = interaction principal component axis 2.

3. RESULTS AND DISCUSSION

A combined ANOVA analysis (Table 3) conducted on the seed yield of nine Ethiopian white cumin genotypes across eleven distinct environments revealed significant differences (P<0.01) attributable to genotype (G), environment (E), and the interaction between genotype and environment (G x E). Notably, the environment accounted for most of the total variance at 84.32%, underscoring its predominant influence on seed yield compared to the genotype's contribution of 2.17% and the G x E interaction's 13.52% (Table 3). In multi-environment trials, it is well-documented that environmental variance typically dominates at around 80%, while the contributions from G x E interaction and genotype remain relatively minor (Tena et al., 2019). The substantial environmental sum of squares indicates pronounced disparities among testing locations, leading to varied performances of different genotypes across these environments. This high environmental percentage suggests that the primary determinant of seed yield performance for white cumin genotypes in Ethiopia is indeed the environment. The significant environmental variance likely stems from the agro-ecological diversity present among the test locations (Table 1). Nevertheless, for genotype evaluation, the effects of genotype and G x E interaction are of paramount importance, often relegating the environmental effect to a secondary consideration (Tena et al., 2019).

The presence of strong genotype × environment interaction indicated higher differences or unstable performance of white cumin genotypes across different testing environments. The findings suggest that nine white cumin genotypes may not demonstrate uniform phenotypic performance across varying environmental conditions, or that different genotypes may react differently to a particular environment. Consequently, identifying consistently superior genotypes across diverse environments becomes challenging when the interaction between genotype and environment is highly significant. The analysis result indicated that there is different performance of genotypes over the testing environments. This suggests that a genetic variation existed among the genotypes concerning this trait.

3.1 Mean Performance of Genotypes

The combined mean performance of seed yield across environments showed that seed yield was ranged from 779.5 kg ha^{-1} to 1,031.3 kg ha^{-1}. Higher mean seed yield was recorded from genotype G3 (1,031.3 kg ha^{-1}) followed by genotype G7 (1,011.2 kg ha^{-1}) and genotype G6 (974.2 kg ha^{-1}), while the smallest mean seed yield was obtained from genotype G5 (779.5 kg ha^{-1}). This result showed the existence of great yield variation among the evaluated genotypes. The genotypes required 80 – 96 days for days to flowering and 172 – 189 days for days to maturity. Plant height also ranged from 57 – 61 cm showing the similarity in plant height with a minimum difference of 4 cm (Table 4).

3.2 AMMI Analysis

The findings of the AMMI model regarding seed yield are detailed in Table 3. The AMMI multiplicative component has further divided the genotype-environment interaction into eight interaction principal component axes (IPCAs). The significant genotype × environment

Table 3. AMMI analysis results

No.	Source	Df	Sum Square	Mean Square	Proportion	Accumulated
1	ENV	10	81445370	8144537***	84.31570379	84.31570379
2	GEN	8	2092458.5	261557.31**	2.166201849	86.48190564
3	GEN:ENV	80	13057902	163223.77**	13.51809436	100
4	PC1	17	6587165.7	387480.34**	50.4	50.4
5	PC2	15	3287387.6	219159.17**	25.2	75.6
6	PC3	13	1390515.1	106962.7*	10.6	86.3
7	PC4	11	954743.5	86794.864ns	7.3	93.6
8	PC5	9	511356.07	56817.341ns	3.9	97.5
9	PC6	7	233414.8	33344.972ns	1.8	99.3
10	PC7	5	78370.04	15674.008ns	0.6	99.9
11	PC8	3	14948.77	4982.922ns	0.1	100
12	Residuals	176	14161213	80461.44		
13	Total	376	127190438	338272.44		

*Df = Degree of freedom, ENV= environment, REP replication, GEN = genotypes, PC = principal components, ** and * significant difference at 1% and 5% respectively*

Table 4. Combined mean performance of six traits of nine white cumin genotypes

Genotype	SYH	DTF	DTM	PLH	NBPP	NUPP
G3	1031.3a	96.2a	189.2a	60.9a	9.2a	51.4a
G7	1011.2a	96ab	188a	60.7a	9ab	51.2ab
G6	974.2a	95.9ab	187.5ab	60.6a	8.9ab	48.5ab
G4	957.7ab	94.6abc	187.1ab	60.5a	8.7ab	48.2ab
G9	955.9ab	94.4abc	185.3b	60.4a	8.7ab	47.6ab
G8	897.6abc	93.8abc	185.3b	59.8a	8.6ab	47.5ab
G2	830bc	93.3bc	182c	59.6a	8.6ab	47ab
G1	826.6bc	92.1c	179.7c	59.6a	8.4b	46ab
G5	779.5c	79.7d	172.3d	56.9b	8.2b	42.5b
LSD	137.8	2.74	2.51	2.07	0.8	8.7

DTF = days to flowering, DTM= Days to maturity, PLH= Plant height, NBPP= number of primary branch plant^{-1}, NUPP = number of umbels plant^{-1}, GYH = seed yield per hectare, LSD = least significant difference

interaction was decomposed into the interaction principal component analysis (Gollob, 1968). The first principal component analysis explained about 50.4%, while the second and third interaction principal components additionally explained about 25.2% and 10.6% respectively (Table 4). The three principal component analyses explained about 86.2% of genotype × environment interactions. Tekalign, et al., (2015) reported 80.45% of the first two IPCA of the genotype by environment interaction of faba bean genotypes.

The AMMI biplot, which captured 75.6% of the genotype-environment interaction (GxE), presents the interaction principal component scores for the first and second interaction principal component axes (IPCA), with 32 degrees of freedom. The first principal component axis (PC1) accounted for 50.4% of the variation in GxE interaction, while the second axis contributed 25.2% to the overall variability. Numerous studies have indicated that the most accurate predictions from the AMMI model can be derived from the first two IPCAs (Yan, et al., 2000). In the context of AMMI analysis, the IPCA scores for a genotype serve as a measure of its stability across different environments (Gauch & Zobel, 1997, Purchase, 1997). Thus, genotypes with IPCA scores closer to zero are considered more stable across all testing environments (Purchase, 1997).

3.3 AMMI1 Biplot

The AMMI model was employed to examine the Biplot graph (Fig. 1), which illustrates the performance of white cumin genotypes across various environments in terms of mean grain yield. The X-axis represents the mean grain yield, whereas the Y-axis displays the scores for IPCA 1. As shown in Fig. 1, the main effects of each environment and variety are plotted on the x-axis against their respective IPCA1 scores on the y-axis. The black vertical line that runs through the center of the biplot represents the overall mean grain yield obtained from all varieties and environments, while the black horizontal line indicates the point at which the IPCA1 score is equal to zero. Those genotypes and environments that fall on the right side of the grand mean value of grain yield are rated as high-yielding genotypes and potential growing environments, and the remaining ones that fall on the left side of the grand mean are low-yielding genotypes and low-potential environments for white cumin production. Genotypes and environments located on the same side of the IPCA axis interact positively and produce desirable effects. From the AMMI1 biplot figure, four genotypes namely G7, G4, G3, and G6 were recorded as relatively higher grain yield than the other white cumin genotypes which are located on the right side of the grand mean (Fig. 1). The other remaining genotypes, G2, G9, G8, G1, and G5 were located on the left side of the grand mean, and the lowest mean grain yield was observed. For environment located on the right side of the grand mean was considered as favorable environment. The testing environment showed a great variation in the performance of white cumin genotypes, thus E6, E4, E2, E9, and E7 were categorized as unfavorable environmental conditions for white cumin production, while E1, E11, E10, E5, and E11 were categorized as the high potential growing environment for white cumin production.

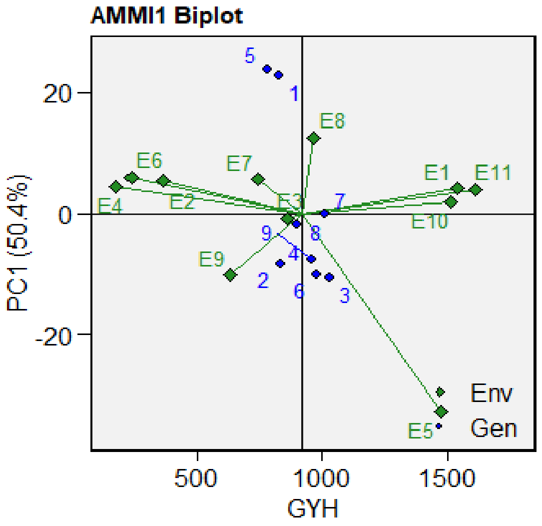

Fig. 1. Mean seed yield of white cumin genotypes plotted against with IPCA1 score across eleven environments

3.4 AMMI 2 Biplot

The AMMI2 biplot analysis, utilizing IPCA1 and IPCA2, is presented in Fig. 2. The AMMI2 biplot offers greater accuracy compared to the AMMI1 biplot, as it incorporates data from both IPCA1 and IPCA2. In the context of the AMMI2 model, genotypes situated closer to a particular environment are expected to exhibit superior performance in that environment compared to those that are more distantly located. Additionally, AMMI2 provides a measure of stability through the AMMI stability value (ASV). The AMMI analysis for the first IPCA1 explained about 50.4% and the second IPCA2 explained about 25.2% of the total sum square of genotype by environment interaction and the two IPCAs cumulatively taken about 75.6% of white cumin genotypes environmental interaction. In the IPCA1 and IPCA2 interactions, the closer the genotypes score to the center of the biplot, the more stable the genotype and the reverse is true (Purchase, 1997). Genotype environment projection on the polygon reflects the identification of the best genotypes with respect to the environments. According to these assumptions, G1 and G5 were identified as the highest yielding genotypes, while G8, G9, G3, and G6 were identified as the lowest yielding genotypes. G9 was the highest mean seed yield genotype at environment E9, and G8 at environment E11. Similarly, G5 and G1 also best performed and high yielding genotypes at environment E8. Genotypes within the polygon and nearest to the origin of the axes have wider adaptation to the environment and less response to environmental variation (Yan & Tinker, 2006, Gauch, et al. 2008, Voltas, et al., 2002). Accordingly, G7, G4, and G2 located near the center of the axis hence, they were demonstrated low interactions or stability over the environments. This indicated that these genotypes demonstrated lower environmental response to the change in the growing environments. G3, G6, G5, G1, G8, and G9 were unstable genotypes because of their long distances located far apart from the origin of the biplot as compared to the other genotypes. Environment E2, E1, E11, E5, and E9 were the most discriminating environments by its long distance from the origin of the axis, while E4, E6, E3, E7 have shortest distance from the center or located near to the center of the origin hence they considered as low discriminating environments for evaluated genotypes.

3.5 AMMI Stability Value (ASV)

The variation in stability measurement between the two primary components can be balanced by a corresponding proportional difference in the IPCAs (1:2), which is subsequently calculated using the Pythagorean theorem in relation to the AMMI stability value. AMMI stability value statistics (ASV) is developed to quantify and rank the genotypes based on their yield stability. Lower ASV value indicates the more stable genotypes whereas genotypes with high ASV value are more unstable (Purchase, et al., 2000). Therefore, based on ASV scores the genotypes G7, and G4 have the lowest ASV score, thus which are the most widely stable genotypes

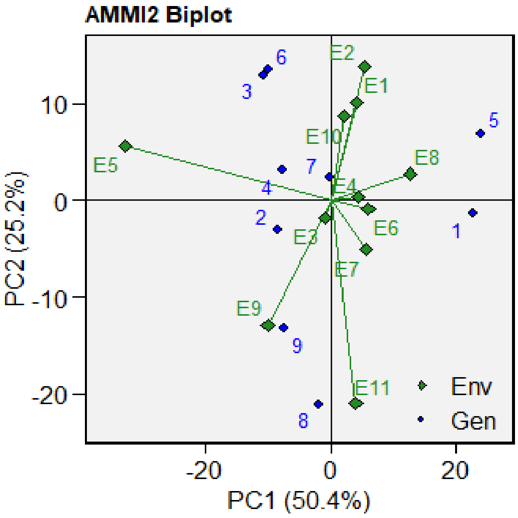

Fig. 2. AMMI2 biplots of PC1 vs PC2

Table 5. Seed yield, ranks by seed yield, AMMI stability index (ASI), AMMI Stability Value (ASV), ranks by ASV and IPCA1 scores of nine white cumin genotypes

GEN	Y	Y_R	PC1	ASI	ASI_R	ASV	ASV_R
1	826.6	8	22.60	11.4	8	45.3	8
2	830.0	7	-8.39	4.3	3	17.1	3
3	1031.3	1	-10.73	6.3	7	25.1	7
4	957.7	4	-7.61	3.9	2	15.6	2
5	779.5	9	23.79	12.1	9	48.2	9
6	974.2	3	-10.04	6.1	6	24.2	6
7	1011.2	2	-0.23	0.6	1	2.4	1
8	897.6	6	-1.84	5.4	5	21.4	5
9	955.9	5	-7.55	5.1	4	20.2	4

GEN = genotype, Y = yield, R = rank, PC1 = principal component 1, ASI = AMMI stability index, ASV = AMMI stability value

Table 6. Environment mean grain yield, IPCAe1, IPCAe2 and IPCAe3 scores

ENV	Code	Y	PC1	PC2	PC3
ENV	E1	1540.4111	4.0880886	10.200398	-13.771823
ENV	E10	1516.4481	1.9897492	8.6728021	-8.14409
ENV	E11	1617.9778	3.9574554	-21.002185	-10.434672
ENV	E2	358.1222	5.3373188	13.82614	-1.820328
ENV	E3	859.7889	-0.9652437	-1.7454997	8.455271
ENV	E4	165.6185	4.3537927	0.4238085	4.761272
ENV	E5	1475.3741	-32.741578	5.6365973	3.142683
ENV	E6	230.6963	5.965769	-0.8054858	1.045285
ENV	E7	742.9963	5.5688691	-5.0996741	10.425989
ENV	E8	962.137	12.525215	2.7745552	9.442952
ENV	E9	630.8852	-10.079436	-12.881456	-3.102541

ENV = environment, Y = mean seed yield, PC = principal component

across environments. However, genotypes G5 and G1 which score relatively high ASV values considered unstable genotypes across environments (Table 5). By considering IPCA1 scores alone and regardless of the positive or negative signs, genotypes with large scores have high interactions (unstable), whereas varieties with small IPCA1 scores close to zero have small interactions and are stable (Zobel, et al., 1988). Accordingly, G7 and G8 scored the lowest positive and negative IPCA1 values as compared to the other genotypes, which implies that the more stable genotypes across the testing environments, while G5 and G1 have large positive IPCA scores and considered the most unstable genotypes across the environments.

Environment E3 scored the least negative IPCA1 values, indicating that their minimum contribution to the genotype by environment interactions. While environment E5, E8, and E9 scored maximum positive and negative IPCA1 values. Four environments namely E1, E10, E11, and E8 recorded greater mean grain yield than the average mean grain yield of overall eleven environments (918.2 kg ha^{-1}), it indicates that these environments are the best potential white cumin growing seasons and environments as compared to the rest environments.

4. CONCLUSION

The study was carried out to assess and identify the most adaptable white cumin genotypes. The interaction between genotype and environment presents a significant challenge for researchers aiming to develop high-yielding and stable genotypes across various seasons and conditions. The ANOVA results revealed a highly significant genotype × environment interaction, indicating the inconsistent performance of white cumin genotypes in different growing conditions. The highest mean seed yield was observed in genotype G3 (1,031.3 kg ha^{-1}), followed closely by genotype G7 (1,011.2 kg ha^{-1}). Most of the evaluated genotypes exhibited minimal positive and negative IPCA1 values, suggesting their stability and adaptability across environments. The first IPCA accounted for approximately 50.4% of the genotype × environment sum of squares, while the second IPCA contributed about 25.2% to the total sum of squares for genotype × environment interaction. Together, these two IPCAs captured around 75.6% of the environmental interaction of white cumin genotypes. Overall, the experiment highlighted several promising white cumin genotypes with broad adaptability across different environments, indicating the need for further examination of these genotypes in varied conditions.

DISCLAIMER (ARTIFICIAL INTELLIGENCE)

Author(s) hereby declare that NO generative AI technologies such as Large Language Models (ChatGPT, COPILOT, etc) and text-to-image generators have been used during writing or editing of this manuscript.

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COMPETING INTERESTS

Authors have declared that no competing interests exist.

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