Yield Performance and Stability of White Cumin (*Trachyspermum ammi* L.) Genotypes under Multi Environmental Condition

**Abstract**

*The study was conducted to estimate the effects of genotype, environment, and their interaction on yield and to assess the stability of white cumin genotypes for yield across different testing environments. Nine white cumin genotypes were evaluated using RCBD with three replications at four locations in Ethiopia. The result of combined analysis of variance showed highly significant (p<0.01) differences among genotypes for all traits, the genotype × environment interaction showed highly significant differences for all traits except the number of umbels plant-1. The variances accounted for by the environment, genotypes, and interaction were 87.57%, 1.74%, and 10.66%, respectively. Kulumsa-2020 was the highest yielding (1617.98 kg ha-1), environment; Robe Arsi-2021 was the lowest yielding (165.63 kg ha-1), environment. The higher mean seed yield was recorded from G1 (2,160.4 kg ha-1) at environment 1 (E1), while the smallest mean seed yield was obtained from G8 (80.2 kg ha-1) at environment 2 (E2). The GGE biplot analysis explained 74.39% (IPC1=51.91and IPC2 =22.48%) of G+GEI and divided the eleven environments into three major groups: Group 1 includes E3, E7, E9 and E11;Group 2 were E1,E2,E5 and E10 ; while E4,E6 and E8, were in Group 3. The 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. Environments within the same group gave redundant information about the genotypes and were more correlated. The vertex genotypes G1, G3, G5, G8, and G9 are displayed in the corner of the polygon. G5, G1, and G8 are the most unstable genotypes, whereas G3, G4, and G6 are the most desired and closest to the center of the best genotypes. Environment (E5) was identified as an ideal environment and powerful to discriminate genotypes while environment E8 and E11 was the list discriminating environment. The result gives more information on the stability and genotype × environment interactions; therefore, special considerations should be given for those selected genotypes to future breeding programs in order to develop wide adaptive and yielding genotypes.*

**Key words:** AMMI, Discriminating, G*×E* interaction, Ideal genotypes, Stability

1. **Introduction**

“Ethiopian caraway (*Trachyspermum ammi* L. Sprague ex Turrill) is an annual medicinal plant belonging to Apiaceae family. It is cultivated in India, Iran, Pakistan, Egypt, and Ethiopia” (Dawit *et al.*, 2003; Tomar and Malik, 2014). “It is erect and branched cross-pollinated plant. Ethiopian caraway, also named as Bishop's weed (English) and Ajowan (Hindi), has white flowers and small gray brownish seeds” (Tomar and Malik, 2014). “Its seeds are widely used for medicinal and food flavoring purposes” (Dwivedi *et al*., 2012). “The seed revealed to have stimulant, carminative, diuretic, antimicrobial, nematodicidal, antihypertensive, antitussive, broncho dilatory, antioxidant, flavouring as preservatives, and most extensively in folk medicines, especially for remedies of stomach disorders and hypolipidemic effects” (Bairwa *et al*., 2012; Zarshenas *et al.*, 2014 and Asangi *et al*., 2023).

“White cumin is one of the most dominantly cultivated seed spices in Ethiopia for consumption and commercial purposes from mid-to-high attitudes from 1750 to 2200 m.a.s.l.” (Girma et al., 2022). “In Ethiopia, 5,887 tons of Ethiopian caraway and black cumin were harvested from 9,204 ha of land and both cumin are the export spice commodities ranked second next to ginger in spice export earnings accounting for 13.7% and 62% respectively, in 2006-2010” (MoARD, 2003, 2010). It is named differently in diverse languages: *nech azmud* (Amharic) and *abeshuda adi* (Afan Oromo) (Goettsch, 2009; Alemnew, 2021). “Several improved technologies including improved varieties and suitable agronomic practices had been generated and distributed to different agro ecologies to enhance the productivity of lowland and highland spices in Ethiopia. Despite its economic importance, Ethiopian caraway received less attention to improve its production and productivity and remained an underutilized spice crop in Ethiopia. Research work that has been carried out so far is limited to the collection and maintenance of germplasms and no significant effort applied to genetic improvement and agronomic practices. Until the present, no improved Ethiopian caraway variety has been nationally released in the country” (Hailemichael et al., 2016)..

“Plant breeders conduct multi-environment trials to identify favorable genotypes based on both average yield and performance stability. They also assess whether a test environment is homogeneous or should be divided into different mega-environments” (Gauch, 2006; Yan and Kang, 2003). To describe genotype-by-environment interaction (GEI) more effectively and facilitate genotype recommendations in multi-environment trials (MET), a distinct statistical model is applied. Yan et al. (2000) proposed a methodology called the GGE biplot for graphically displaying the patterns of genotype-environment interaction (GEI) in multi-environment trial (MET) data, which offers several advantages. GGE biplot analysis takes into account both genotype and GEI effects, presenting GEI visually in a two-way table (Yan et al., 2001). GGE biplot analysis (Genotype + Genotype × Environment interaction) is a robust statistical tool used in agricultural research to evaluate the performance and stability of genotypes across multiple environments. It facilitates the visual examination of relationships among test environments, genotypes, and the GEI. When applied to white cumin (*Trachyspermum ammi L.*), this analysis provides insights into genotype yield performance and environmental adaptability. “Most crop improvement programs aim at selecting genotypes for maximum yield. In parallel with improving the yield, a new improved variety should have consistent yield performance across a range of environments, which is considered stable or widely adaptable. Genotypes are commonly evaluated in multi-environments to select high-yielder and stable cultivars across diverse environments. In evaluating genotypes in multi-environment trials, the effects of genotype and genotype by environment interaction are the most relevant” (Yan and Kang, 2003). Thus, the study aimed to estimate the effects of genotype, environment, and their interaction on yield and yield-related traits and to assess the stability of white cumin genotypes for yield across different testing environments.

1. **Materials and Methods**
	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 below.

Table 1: Summary of experimental locations

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| **Environment** | **Year**  | **Location** | **Geographical position** | **Altitude** | **Temperature** | **Rainfall****(mm)** |
| **Latitude** | **Longitude** | **Minimum** | **Maximum** |
| E1 | 2020 | Kulumsa | 08001’10’’N | 39009’11’’E | 2200 | 10.5 | 22.8 | 820 |
| E2 | 2020 | Arsi-robe | 07053’02’’N | 39037’40’’E | 2340 | 8.13 | 22.51 | 1020 |
| E3 | 2021 | Kulumsa | 08001’10’’N | 39009’11’’E | 2200 | 10.5 | 22.8 | 820 |
| E4 | 2021 | Arsi-robe | 07053’02’’N | 39037’40’’E | 2340 | 8.8 | 23.6 | 1020 |
| E5 | 2022 | Kulumsa | 08001’10’’N | 39009’11’’E | 2200 | 10.5 | 22.8 | 820 |
| E6 | 2022 | Arsi-robe | 07053’02’’N | 39037’40’’E | 2340 | 5.8 | 22.6 | 1015 |
| E7 | 2022 | Ambo | 08058’10’’N | 37051’28’’E | 2164 | 12.07 | 26.13 | 1068 |
| E8 | 2022 | Sinana | 07006’12’’N | 4005 12’40’’E | 2400 | 9.5 | 21.5 | 1174 |
| E9 | 2023 | Kulumsa | 08001’10’’N | 39009’11’’E | 2200 | 10.5 | 22.8 | 820 |
| E10 | 2023 | Ambo | 08058’10’’N | 37051’28’’E | 2164 | 12.07 | 26.13 | 1068 |
| E11 | 2023 | Sinana | 07006’12’’N | 4005 12’40’’E | 2400 | 9.5 | 21.5 | 1174 |

* 1. **Experimental materials and designs**

The Ethiopian caraway landraces were originally collected from different Ethiopian caraway 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 caraway/white cumin genotypes were tested in eleven environments (year and location combinations) in Ethiopia under rain fed conditions. The experiment was carried out in randomized complete block design (RCBD) with three replications. Each genotype was planted on a plot size of 3.6 m2, with 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. The testing genotypes are listed below in Table 2.

Table 2: List of genotypes used for the experiments

|  |  |  |  |
| --- | --- | --- | --- |
| No- | Genotypes code | Genotype name | Source |
| 1. | G1 | Akiya-2007 | Collection |
| 2. | G2 | Shirka 001/2007  | Collection |
| 3. | G3 | Bale -2007 | Collection |
| 4. | G4 | Silingo-2007 | Collection |
| 5. | G5 | Sole-007  | Collection |
| 6. | G6 | Gedgeda-026  | Collection |
| 7. | G7 | Sagure-2007  | Collection |
| 8. | G8 | Takusa-01(St.check 1)  | Released variety |
| 9. | G9 | Dembia-01(St.check 2)  | Released variety |

* 1. **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 are expressed below.

**Phenological data**

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

**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.

**Agronomic, yield and yield related traits**

**Plant height:** anaverage 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 m2 (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.

* 1. **Statistical analysis**

Data were subjected to analysis of variance (ANOVA) for each environment separately; and also combined analysis of variance was conducted to determine the effect of environment (E), genotype (G) and GE interaction on the expression of traits. R-software packages were 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 randomized completed block design. The data were graphically presented for interpreting GE interaction using the GGE biplot software (Yan, 2001).

**2.5 Stability analysis**

The stability analysis among genotypes over environments was done using GGE biplot multivariate analysis methods. The GGE Biplot model utilizes biplots, an effective tool for visualizing two-way data commonly conducted in MET data analysis. The first component of the GGE biplot, when closely associated with the genotype main effect (G), indicates the proportion of production exclusively attributed to the genotype, while the second component represents the proportion explained by genotype-environment interaction (GEI). The GGE biplot was built according to the formula given by Yan *et al.* (2000):

$$Yij=μ+ βj+λ1ξi1ηj1+2ηj2+ εij$$

*where, Yij is the trait mean for genotype i in environment j, μ is the grand mean, βj is the main effect of environment j, μ + βj is the mean yield across all genotypes in environment j, λ1, and λ2 are the singular values (SV) for the first and second principal components (PC1 and PC2), respectively, ξi1 and ξi2 are eigenvectors of genotype i for PC1 and PC2, respectively, η j1 and ηj2 are eigenvectors of environment j for PC1 and PC2, respectively, εij is the residual associated with genotype i in environment j. In GGE biplot analysis, scores of PC1 were plotted against PC2.*

1. **Result and Discussion**

**Result**

* 1. **Combined analysis of variance**

The data recorded in each of the eleven environments were subjected to statistical analysis which indicated that genotypes were significant in each of the environment. The combined ANOVA given in Table 3 shows that the environment, genotype and GEI were highly significant (*p*<0.001) for all traits across environments in terms of seed yield, days to heading, days to maturity and plant height. The ANOVA results of agronomic and yield component traits showed that there was a significant and considerable variation among environments, suggesting that the environment had a major impact on the performances of genotypes under testing locations. Significant (p<0.05) and highly significant (p<0.01) genotype × environment interaction results were observed for all traits except number of umbels plant−1, this indicated that each genotype responded differently at each testing environments. The same genotype × environment interaction result was reported by Mesfin *et al,* (2020), Abera *et al.,* (2019) and Temesgen et al., (2015) for days to flowering, pods per plant and grain yield on faba bean genotypes. “In multi environment trials, variance of environment is known to be largest (80%) while G x E interaction and genotype are usually small” (Yan and Kang, 2003). “The largest environmental variance might be resulted from the agro-ecological variation among test locations” (Endalkachew *et al*., 2020). “However, the most relevant for genotype evaluation are the genotypic and G x E interaction effects and environment effect is usually ignored. In this study, the G x E effect exceeded the genotype effect 8 times, showing significant G x E interaction effect suggesting the possible presence of different mega environments with different top-yielding genotypes and the genotypes performed variably across environments” (Yan and Kang, 2003). Magari and Kang (1993) and Kang (1990) demonstrated that “significant interaction of genotype by environment creates trouble in selecting stable cultivars. Hence, selecting superior genotypes depending on stability and yield performance would be appropriate”.

Table 3: Mean squares from combined analysis for six traits of 9 white cumin genotypes

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| Response | Geno | Env | Env:Rep | Geno:Env | Residuals |
| 8 | 10 | 22 | 80 | 176 |
| DTF | 867.21\*\*\* | 1989.13\*\*\* | 35.86 | 61.57\*\*\* | 31.84 |
| DTM | 939.52\*\*\* | 587.32\*\*\* | 175.34\*\*\* | 118.46\*\*\* | 26.75 |
| PLH | 49.32\*\* | 2767.29\*\*\* | 26.77 | 25.92\* | 18.24 |
| NBPP | 2.914 | 245.189\*\*\* | 4.834\* | 4.703\*\* | 2.718 |
| NUPP | 234 | 127526\*\*\* | 1994\*\*\* | 380 | 321 |
| SYH | 261557\*\* | 8144537\*\*\* | 153436\* | 163224\*\*\* | 80461 |

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, Geno = genotype, Env = environment, Rep = replication

The total sum of squares was divided into components to estimate the magnitude of GEI for seed yield in white cumin genotypes. Data over four years indicated high seasonal variations at the same location, highlighting the need for multi-year testing. The environmental variance accounted for 87.57% of the total variance in seed yield, significantly higher than the genetic variance at 1.74% and interaction variance at 10.67%. This indicates that the seed yield of white cumin genotypes was primarily influenced by environmental changes, with notable variations among different environments affecting their performance. Similar findings on various crops show that environmental and interaction effects are more significant than genotype effects (Asrat et al., 2009; Yasin et al., 2014; Abebe et al., 2023). The significant environmental effect and its high variance are due to differences in altitude, daily temperature, and rainfall distribution at the test locations. The variance from GEI (10.67%) surpassed that of the genotype main effect (1.74%) (Table 4). For other crops, like bread wheat, the multi-environment data showed a significant GEI effect, highlighting notable differences in genotypic responses across test environments, consistent with Somayeh et al. (2019) and Assefa et al. (2020).This significant G×E interaction indicated variable performance of white cumin genotypes across different locations, complicating the genotype selection and recommendation. Thus, a selected white cumin genotype may not consistently perform well under varying environmental conditions.

Table 4. The contributions of the source of variation for seed yield of white cumin

|  |  |  |
| --- | --- | --- |
| Source of variation | Contribution  | Total Contribution |
| Environments | 87.57 | 87.57 |
| Genotype | 1.74 | 89.32 |
| Environment\*Genotype | 10.68 | 100.00 |

**3.2. Mean Performance of White Cumin Genotypes**

Evaluating the mean performance of white cumin genotypes involves comparing their average yield and other agronomic traits across multiple environments. The mean seed yield performance of the genotypes at each location and the combined mean performances of agronomic traits are presented in Table 4 and 5 below. This analysis is essential for identifying high-yielding and stable genotypes for wider cultivation. Genotypes showed varying average seed yields across environments, from 779.46 kg ha-1 for G5 to 1031.32 kg ha-1 for G3. Different locations ranked genotypes differently, indicating notable crossover interactions in performance (Kaya et al., 2006). Yan and Hunt (2001) noted that varying yield rankings across environments highlight the crossover nature of genotype-environment interactions.

The mean performance of seed yield showed that a higher mean seed yield was recorded from G8 (2,160.4 kg ha-1) at environment 1 (E1) followed by G3 (2,025.6 kg ha-1) and G6 (1,896.3 kg ha-1) at environment 5 (E5), while the smallest mean seed yield was obtained from G8 (80.2 kg ha-1) followed by G9 both from environment 2 (E2) (Table 5). This result showed that white cumin genotypes have diverse yield performance on seed yield among testing genotypes. The genotypes required 79 – 96 days for days to flowering which indicated that they require different days for flowering and 172 – 179 days to maturity. Plant height also ranged from 57 – 61 cm it shows the similarity in plant height with a minimum difference of 4 cm (Table 6). The genotypic yield performance across testing environments ranged from 80.2 at E2 to 2,160.4 kg ha-1 at E1. The combined seed yield performance ranged from 779.5 kg ha-1 from genotype G5 to 1,031.3 kg ha-1 from genotype G3. From individual environment seed yield performance, we observed that environments E4 and E6 were recorded as poor performance for white cumin production, while the highest mean seed yield performance was observed from environments E1, E5, E10, and E11 (Table 5).

Kulumsa-2012 had the highest mean yield at 1617.98 kg ha-1, followed by Ambo-2015 (1540.41 kg ha-1), Sinana-2015 (1516.44 kg ha-1), and Kulumsa-2014 (1475.38 kg ha-1). In contrast, Robe Arsi-2013 recorded the lowest yield at 165.63 kg ha-1, with Robe Arsi-2014 and Robe Arsi-2012 at 230.69 kg ha-1 and 358.12 kg ha-1, respectively. This variation highlights significant differences in wheat productivity across diverse climates in the country’s highlands. While Kulumsa offers ample rainfall, Robe Arsi has limited moisture. Five locations surpassed the average yield of 918.22 kg ha-1, while others fell below this average.

Table 5: Seed yield mean performance of 9 white cumin advanced genotypes at each testing location

|  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| G | **E1** | **E2** | **E3** | **E4** | **E5** | **E6** | **E7** | **E8** | **E9** | **E10** | **E11** | **Mean**  |
| **G1** | 1636.1 | 462.6 | 584.6 | 129.4 | 708.8 | 282.4 | 1040.7 | 1189.3 | 260.2 | 1361.3 | 1437.0 | 826.58 |
| **G2** | 1450.0 | 140.6 | 1001.8 | 253.8 | 1696.5 | 56.4 | 745.4 | 832.4 | 518.5 | 1135.7 | 1299.1 | 830.02 |
| **G3** | 1570.1 | 669.5 | 819.8 | 249.7 | 2025.6 | 255.0 | 844.4 | 735.6 | 555.0 | 1766.1 | 1853.7 | 1031.32 |
| **G4** | 1379.9 | 417.2 | 948.9 | 150.2 | 1748.5 | 291.4 | 730.6 | 1036.6 | 881.0 | 1519.6 | 1431.5 | 957.76 |
| **G5** | 1391.0 | 341.0 | 875.4 | 201.8 | 527.1 | 224.0 | 531.5 | 1084.3 | 215.3 | 1683.6 | 1499.1 | 779.46 |
| **G6** | 1338.9 | 510.4 | 882.8 | 130.3 | 1896.3 | 198.3 | 591.7 | 951.4 | 718.2 | 1796.9 | 1700.9 | 974.19 |
| **G7** | 1803.5 | 507.5 | 853.9 | 155.6 | 1637.5 | 313.6 | 640.7 | 1198.6 | 668.3 | 1731.1 | 1612.9 | 1011.20 |
| **G8** | 2160.4 | 80.2 | 771.8 | 123.1 | 1327.9 | 188.7 | 676.8 | 667.6 | 966.5 | 1472.9 | 1437.9 | 897.62 |
| **G9** | 1831.9 | 94.1 | 999.0 | 96.8 | 1710.2 | 266.4 | 885.2 | 963.4 | 895.0 | 1396.5 | 1375.9 | 955.85 |
| **Mean**  | 1617.98 | 358.12 | 859.78 | 165.63 | 1475.38 | 230.69 | 743.00 | 962.13 | 630.89 | 1540.41 | 1516.44 | 918.22 |

G = genotypes, E = environments

Table 6: Combined mean performance of six traits of 9 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, SYH = seed yield kg per hectare,

**GGE biplot analysis**

“Genotype main effect plus genotype by-environment interaction (GGE) biplot produces a graphical display of results that facilitates a better understanding of complex genotype by-environment interaction in Mult environment trials of breeding. The GGE Biplot facilitates a visual examination of the GE interaction patterns in multi-environment trial data” (Sawargaonkar et al., 2011).

**Which Won Where Pattern**

The "Which-Won-Where" analysis in crop breeding identifies the best genotypes for specific environments. It helps breeders select adaptable genotypes, understand G × E interactions, optimize breeding programs focusing on key environments, and provide tailored recommendations for farmers based on local conditions. According to Yan and Tinker (2006) and Hagos and Abay (2013), “the vertex genotypes were the most responsive as they had the longest distance from the origin in their direction. The vertex genotypes could be either the best performing or poorest at one or many environments” (Yan et al., 2007). If a genotype at an angular vertex of the polygon lies within a sector defined by environmental indicators, it indicates optimal yield capacity in that environment. The biplot highlights environmental groupings, suggesting different mega-environments. This approach enhances the precision of breeding programs, resulting in high-performing and adaptable crop varieties for specific or broad cultivation. As shown in Figure 1, 11 environments and genotypes were categorized into 3 mega-environment sectors. From the polygon views of Which-Won-Where/What as shown in Figure 1 below, five genotypes namely G1, G3, G5, G8, and G9 are vertex genotypes that are presented at the polygon’s corner by its longest distance from the center of origin. This indicated the highest-yielding genotypes for traits with respective environments. All environments are relatively distributed in all quadrants of the axis, hence each environment had best-adapted genotypes to their respective environments. Therefore, G8 performed well in one environment (E11), and genotypes G1 and G5 were well performed at E8. On the other hand, genotypes G3, and G6 perform relatively well in environments (E1, E2, and E10). Genotypes G2, G4, and G7 are located near the center of the axis and they are the lowest-yielding genotypes.



Figure 1: Which-won-where pattern of GGE biplot

* 1. **Mean performance and stability of genotypes using GGE biplot**

The mean performance of white cumin genotypes is essential for identifying superior varieties. When assessed alongside stability analysis and environmental adaptability, it provides insights for developing high-yielding and sustainable options. In the biplot, mean yield is on the X-axis and stability (G × E interaction) is on the Y-axis. Genotypes close to the origin (AEC) are ideal, combining high yield with stability. Stable genotypes show minimal yield fluctuation, while high-yielding genotypes are further from the AEC. The AEC ordinate distinguishes between below-average and above-average yields, indicating that moving away from the origin results in increased GEI effects and lower stability. The biplot illustrates the variability of genotypes, environments, and their interactions. Accordingly, G3, G6, G7, G2 and G9 were high yielding genotypes, while G1, and G5 were lower yielding genotypes. AEC coordinates are used to separate genotypes with better seed yield from those below-average seed yield genotypes. Hence G3, G6, G7, G2, and G9 exhibited above-average mean seed yield, while G1 and G5 genotypes had below-average mean seed yield. G9 is the highest-yielding and most unstable genotype, whereas G1, are low-yielding and relatively stable genotype. On the other hand, G8 was recorded as a low yielder and the most unstable genotype. Genotypes that have high mean seed yield and good stability are the primary considerations in the selection of the best genotypes. Thus, the highest mean seed yield and widely adapted genotypes are identified for future breeding programs. Hence, G3, G6, and G7 were relatively high-yielding and stable white cumin genotypes (Figure 2). Therefore, you should give special consideration to those genotypes in future breeding programs to develop wide adaptive and high seed yield genotypes.



Figure 2. *Mean performance and stability of genotypes using GGE biplot*

* 1. **Evaluation of White Cumin Genotypes Relative to Ideal Genotypes**

“Evaluating white cumin (Trachyspermum ammi L.) genotypes relative to an "ideal genotype" is crucial for identifying those with the best combination of high yield, stability, and adaptability across multiple environments. An ideal genotype has the highest mean grain yield and is stable across environments” (Yan and Kang, 2003; Farshadfar *et al.*, 2012). The ideal genotype serves as a benchmark for selecting high-performing genotypes, focusing on high yield and stability while minimizing genotype × environment (G × E) interactions. GGE biplot analysis helps breeders and farmers make informed selection decisions, leading to resilient, high-yielding white cumin varieties. Genotypes can be ranked by their closeness to the ideal genotype in the GGE biplot, with top performers prioritized for testing and breeding. Some genotypes may excel in specific environments, while high-yielding but less stable ones may risk yield losses in unfavorable conditions. A genotype is more desirable if it is closer to the ‘ideal’ genotype (Kaya *et al.*, 2006). The ideal genotype is located in the first concentric circle in the biplot (Figure 3). Therefore, G3, G4, and G6 are the genotypes that are closest to the center of the best genotypes and they are the most desirable genotypes (Figure 3). On the other hand, the high-yielding genotypes G9 are undesirable because they are unstable while the lowest-yielding genotypes G1, G5, and G8 are the most unstable and undesirable because of the distance from the center of the ideal genotypes. Our results confirm those of Sharma *et al.* (2010), who found outstanding genotypes near to the ideal genotype in wheat for five consecutive years, and those of Akter *et al.* (2015) who reported an ideal genotype of rice in the first concentric circle.

**Discriminating ability of testing environments**

In Genotype and genotype-environment interaction (GEI) (GGE) Biplot analysis, the discriminating ability of testing environments refers to the capacity of an environment (or group of environments) to distinguish or differentiate between the performance of different genotypes (Yan, 2002 GGE biplot analysis identifies the most discriminative locations for genotype evaluation. Longer vectors in the biplot indicate higher discrimination among genotypes. Environments with high discrimination show significant differences in performance, while those closer to the origin suggest similarities, complicating ranking. Ideal environments for distinguishing genotypes have long vectors and are far from the average (Yan and Tinke, 2006). Understanding the discriminating ability of testing environments is vital for efficient and effective genotype evaluation in crop breeding programs, aiding in the selection of high-performing and stable varieties. Accordingly, to this assumption from the eleven testing environments E5 has longer vectors as compared to other locations, and the most discriminating environments and gave more information about white cumin genotype performance, while E1, E2, E8, E9, E10, and E11 were moderately discriminating environments. On the other hand, environments (E1, E2, E8, E9, and E11) those are located near or close to the center of origin give little information about genotypes by means of its closest to the center of the biplots. E5 displays long vector and has relatively small angles with the AEC abscissa as compared to other genotypes. This indicates that environment (E5) is a more effective environment for discriminating white cumin genotypes and is the most representative and effective environment for genotype selection (Figure 3).



 Figure 3: Discriminating Ability of Testing Environments in GGE Biplot

**Evaluation of environments relative to the ideal environments**

Evaluating white cumin (Cuminum cyminum L.) genotypes relative to ideal environments involves assessing how different genotypes perform under varying environmental conditions to identify those best suited for specific regions or purposes. This process uses agro-climatic, genetic, and statistical tools to ensure accurate characterization and selection. The ideal test environment is an environment that has more power to discriminate genotypes in terms of the genotypic main effect as well as able to represent the overall environments. In such conditions, environments that fall near a small circle located in the center of concentric circles and an arrow pointing to it (ideal environment) are identified as the best desirable testing environments (Yan and Rajcan, 2002). Among the testing environments used in this study environment (E5) was identified as an ideal environment in terms of being the most representative of the overall environments and powerful in discriminating genotypes (Fig. 4). While environments E8 and E11 were the list discriminating environment for white cumin genotypes.

 Figure 4: Ranking environment

 **4. AMMI ANALYSIS**

The findings of the AMMI model regarding seed yield are detailed in Table 7. The AMMI multiplicative component has further divided the genotype-environment interaction into eight interaction principal component axes (IPCAs).The significant genotype × environment 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 6). 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 and Zobel, 1997; Purchase, 1997). Thus, genotypes with IPCA scores closer to zero are considered more stable across all testing environments (Purchase, 1997).

Table 7: 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.

**5. Conclusions**

Effectively evaluates white cumin genotypes' yield performance and stability under multi-environmental conditions very crucial. It identifies high-yielding, stable genotypes and optimal cultivation environments, supporting the development of sustainable production strategies for white cumin. The experiment was conducted assessing effects of genotype, environment, and their interaction on seed yield and yield-related traits on white cumin genotypes. The combined analysis of variance showed that a highly significant difference (*p*<0.01) was observed among genotypes for all traits except a number of primary branch plant−1 and a number of umbels plant−1. This indicated the presence of wide genetic variability among evaluated genotypes. The genotype × environment interaction effect exhibits a remarkably significant impact on the performance of genotypes for all traits, implies that the differential performances of white cumin genotypes across testing locations or the importance of evaluating genotypes across different environments to identify better-performing genotypes. GGE biplot analysis for the first IPCA1 explained about 51.91% and the second IPCA2 explained about 22.48% of the total sum square of genotype × environment interaction. The GGE biplot revealed that G3, G4, and G6 are genotypes that are closest to the center of the best genotypes and they are the most desirable genotypes, however, G5, G1, and G8 are the most unstable and undesirable genotypes. From the testing environments, E5 have more discriminating power than other testing environments. 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. The result indicated as great promise on the development and release of high yielding and stable white cumin varieties in the future breeding program.

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3.

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