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RESEARCH ARTICLE

# Assessing foxtail millet (*Setaria italica* (L.) P. Beauv.) adaptability for fodder yield in the foothills of Nagaland using GGE biplot analysis

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## Abstract
Foxtail millet is a major millet crop cultivated in the foothills of Nagaland for both fodder and grain production. Hybrid development in foxtail millet is extremely challenging due to its minute flowers and highly self-pollinating nature. Therefore, identifying high-yielding pure lines for both specific and general adaptation is a priority in foxtail millet breeding programs. The present study evaluated 30 foxtail millet genotypes under different sowing dates in the foothills of Nagaland. Pooled analysis revealed significant effects of genotype, environment, and genotype-by-environment interactions on fodder yield. GGE biplot analysis showed that the first two principal components accounted for 75.14 and 12.96% of the total variation, respectively. Discriminativeness and representativeness analyses in GGE biplots identified *early kharif* as the most representative environment, while *late kharif* demonstrated the highest discriminative ability. The "Which Won Where" biplot indicated that Genotype G1 was stable across environments, a finding further confirmed by the mean vs. stability biplot.
**Keywords:** Foxtail millet, Fodder yield and GGE biplots.

## Introduction
Foxtail millet (*Setaria italica* (L.) P. Beauv.) is an ancient cereal crop cultivated for over 5000 years, primarily in Asia, Africa, and Europe. Its $C_4$ photosynthetic pathway allows it to thrive in harsh conditions like drought and poor soil, making it crucial for food security in semi-arid regions (Zhang *et al*., 2013). Widely grown in India, especially in the North Eastern Hill region, it is important for both grain and fodder production. Rich in proteins, dietary fiber, and minerals, foxtail millet contributes to a healthy diet and supports sustainable livestock farming, making it vital for climate-resilient agricultural systems (Madhavilatha *et al*., 20022). Foxtail millet is vital for fodder production in Nagaland's foothills, supporting livestock farming, especially during dry seasons when fodder is scarce. To ensure sustainable fodder production, it's essential to select high-yielding foxtail millet varieties suited to the region's diverse conditions (Rao and Chaturvedi, 2024). This approach not only enhances fodder security but also promotes soil health and nutrient cycling through crop rotations with other cereals and legumes, contributing to long-term agricultural sustainability.

Pooled analysis of variance (ANOVA) is a statistical method used to evaluate the effects of genotypes, environmental factors, and their interactions on crop yield (Rao and Chaturvedi, 2024). This study conducted a pooled ANOVA across multiple environments to assess dry fodder yield variability in foxtail millet genotypes (Wang *et al*., 2023). The results showed significant differences among genotypes, environments, and their interactions, highlighting the impact of environmental factors on genotype performance. These findings emphasize the importance of multi-environment testing to identify stable, high-yielding genotypes for large-scale cultivation and resilient breeding programs (Das *et al*., 2016).

GGE biplot analysis is a valuable tool for visualizing genotype performance across different environments and

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**Table 1:** Environmental description of the experimental site

| *Code* | *Sowing date* | *Season* | *Latitude* | *Longitude* | *Altitude* | *Av. Temp* | | *Av. Hum(%)* | | *Rainfall (mm)* | *Year* |
|---|---|---|---|---|---|---|---|---|---|---|---|
| | | | | | | *min* | *Max* | *min* | *Max* | | |
| Env-1 | 01-07-2022 | Kharif | 250 45’ 15.95» N | 930 51’ 44.71 E | 310 MSL | 31.66 | 22.30 | 91.75 | 69.64 | 51.92 | 2022 |
| Env-2 | 26-08-2022 | Kharif(Late) | 250 45’ 15.95» N | 930 51’ 44.71 E | 311 MSL | 32.09 | 22.84 | 92.10 | 69.99 | 55.19 | 2022 |
| Env-3 | 01-01-2023 | Summer (SE) | 250 45’ 15.95” N | 930 51’ 44.71 E | 312 MSL | 29.11 | 17.40 | 94.48 | 61.84 | 15.58 | 2023 |
| Env-4 | 26-02-2023 | Summer(Late) | 250 45’ 15.95» N | 930 51’ 44.71 E | 313 MSL | 28.28 | 15.97 | 95.29 | 60.11 | 8.46 | 2023 |

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

assessing genotype-environment interactions (Azam *et al*., 2020). This method combines principal component analysis (PCA) with graphical representation to evaluate the stability and adaptability of genotypes in breeding programs (Das *et al*., 2024). In this study, the first two principal components explained a significant proportion of variation in dry fodder yield. The “Which Won Where” biplot identified top-performing genotypes for specific environments, while the mean vs. stability biplot showcased the most stable and high-yielding genotypes (Wolde *et al*., 2018). Additionally, the analysis pinpointed the most informative environments for future breeding trials. The insights from the GGE biplot are crucial for foxtail millet improvement programs, guiding the selection of genotypes that are adaptable and suitable for various local conditions, thus enhancing yield stability and sustainability (Nagaraja *et al*., 2023).

Foxtail millet cultivation in Nagaland’s foothills faces challenges due to varying climatic and soil conditions. The demand for sustainable fodder calls for high-yielding genotypes suited to the region. This study aimed to: 1. Evaluate 30 foxtail millet genotypes across different sowing dates. 2. Analyze the effects of genotype, environment, and their interactions on dry fodder yield. 3. Identify stable, high-yielding genotypes using GGE biplot analysis. 4. Determine representative environments for breeding trials. 5. Provide insights for developing climate-resilient varieties for sustainable fodder production. These objectives will enhance fodder availability and food security in the region.

## Materials and Methods

### *Experiment location*

The investigation was conducted from July 2022 to May 2023 at the Research Farm of the Department of Genetics and Plant Breeding, School of Agricultural Sciences, Nagaland University, located in Medziphema, India. The experiment included four different sowing dates, each representing a distinct growing environment (Table 1). Among these, two seasons were rainfed, while the remaining two were under irrigated conditions with a seven-day irrigation interval. This experimental setup allowed for a comprehensive evaluation of foxtail millet genotypes under varying environmental conditions, providing valuable insights into their adaptability and performance.

### *Plant materials*

A total of 100 foxtail millet genotypes were procured from the Indian Institute of Millets Research (IIMR), Hyderabad, and evaluated during the Zaid season of 2022 under the same environmental conditions. Based on the mean fodder yield of each genotype, thirty superior genotypes were identified for further stability analysis. These selected genotypes, which demonstrated promising yield potential, were used for in-depth evaluation under different environmental conditions to assess their adaptability and stability. The details of these genotypes are presented in Table 2.

### *Experimental design:*

This experiment was conducted using a randomized complete block design (RCBD) with three replications across all environments to ensure reliable and unbiased results. Every replicate block consisted of 30 plots, with each plot measuring 1 × 1 meter. A spacing of 0.5 m was maintained between plots, while the replications were separated by a distance of 0.5 m. This design helped minimize experimental errors and allowed for an accurate assessment of genotype performance across different environmental conditions. Throughout the experiment, recommended agricultural practices were followed.

### *Data collection*

For data collection, five plants were randomly selected from each plot. After harvesting, the fodder was weighed for each individual plant, excluding the panicles. The average fodder yield was then calculated from these five plants to represent each genotype’s replication. This method ensured precise estimation of the fodder yield while accounting for variability within the plots.

### *Statistical analysis*

For the pooled analysis of variance and mean performances, the OPSTAT open-source software was utilized to assess the significance of genotypic, environmental, and genotype × environment interaction effects. To further analyze genotype stability and performance across different

**Table 2:** List of selected genotypes based on the mean yield

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

environments, GGE biplots were constructed using the 'Metan' package in R-Studio, a statistical tool developed by the R Core Team (Team, R. 2015)

## Results and Discussion

### *Analysis of variance*

The ANOVA model revealed that a substantial portion of the variability in fodder yield data was explained within each environment. Specifically, 86.96% of the variability in Environment-1, 86.21% in Environment-2, 83.80% in Environment-3, and 85.32% in Environment-4 was accounted for, with significant genotypic effects observed in all cases (Table 3). However, the effect of replication was found to be non-significant across all individual environments. In contrast, the pooled analysis across all environments explained 35.41% of the total variability (Table 4), where genotypic effects remained significant, but the effect of replication became significant. Additionally, a significant genotype × environment interaction was detected, highlighting differential genotype performance across the tested environments. Similar findings were reported by Gupta *et al*. (2016), who observed significant genotypic effects and non-significant replicate effects in their study on nine mustard genotypes evaluated across six different environments. Their results align with the present study, where genotypic effects were found to be significant in all individual environments, while the effect of replication remained non-significant. This further reinforces the reliability of genotypic variation in influencing fodder yield performance, emphasizing the importance of genotype selection under varying environmental conditions.

### *Mean Performance*

In a comprehensive analysis of dry fodder yield per plant across four distinct environments (E1, E2, E3, and E4), the performance of various genotypes was evaluated, in Environment E1, G9, G1, and G5 emerged as the top three genotypes, boasting impressive dry fodder yields of 24.37 ($g^{-1}$), 23.97 ($g^{-1}$), and 23.83 ($g^{-1}$), respectively. Conversely, G20, G14, and G30 found themselves among the lowest performing genotypes in this environment, with yields of 11.40 ($g^{-1}$), 13.57 ($g^{-1}$), and 14.80 ($g^{-1}$), respectively. In Environment E2, G3, G1, and G25 took the lead with yields of 26.81 ($g^{-1}$), 26.80 ($g^{-1}$), and 22.70 ($g^{-1}$), showcasing their adaptability to this specific condition. On the flip side, G24, G27, and G10 were among the least productive genotypes with yields as low as 10.13 ($g^{-1}$), 10.33 ($g^{-1}$), and 12.40 ($g^{-1}$). A similar pattern unfolded in Environment E3, where G1, G3, and G5 maintained their strong performance. However, G24, G12, and G27 continued to struggle, with the lowest yields of 9.53 ($g^{-1}$), 11.87($g^{-1}$), and 11.00 ($g^{-1}$), respectively. Lastly, in Environment (E4), G1, G19, and G4 displayed their dominance with yields of 27.07 ($g^{-1}$), 22.90 ($g^{-1}$), and 22.43 ($g^{-1}$), respectively. Unfortunately, G24, G29, and G10 faced challenges in this environment, yielding 5.67 ($g^{-1}$), 11.67 ($g^{-1}$), and 17.50 ($g^{-1}$), making them the lowest performers. This comprehensive data underscores the importance of selecting genotypes tailored to specific environmental conditions to optimize crop yields and ensure sustainable agricultural practices. Mean performance of dry fodder yield per plant across four environments is represented in Table 5.

### **GGE biplot graphical analysis.**

The GGE biplot is a powerful strategic tool used in MLT trials to display genotype performance across multiple environments. It helps in identifying stable and high-yielding genotypes by analyzing both genotypic main effects (G) and genotype-by-environment interactions

**Table 3:** Analysis of Variance of grain yield per plant and dry fodder yield per plant for different Seasons

| *Years* | *Source of Variation* | *DF* | *Sum of Squares* | *Mean Squares* | *F-Calculated* | *Significance* |
|---|---|---|---|---|---|---|
| | Replication | 2 | 6.454 | 3.227 | 1.555 | 0.21993 |
| FY E1 | Treatment | 29 | 849.971 | 29.309 | 14.12 | 0 |
| | Error | 58 | 120.392 | 2.076 | | |
| | Replication | 2 | 10.596 | 5.298 | 1.415 | 0.2513 |
| FY E2 | Treatment | 29 | 1,426.31 | 49.183 | 13.132 | 0 |
| | Error | 58 | 217.23 | 3.745 | | |
| | Replication | 2 | 0.137 | 0.069 | 0.015 | 0.98486 |
| FY E3 | Treatment | 29 | 1,356.87 | 46.789 | 10.391 | 0 |
| | Error | 58 | 261.156 | 4.503 | | |
| | Replication | 2 | 4.621 | 2.311 | 0.598 | 0.55334 |
| FY E4 | Treatment | 29 | 1,326.03 | 45.725 | 11.831 | 0 |
| | Error | 58 | 224.17 | 3.865 | | |

**Table 4:** Combined analysis of variance for pooled data of 4 environments on grain yield per plant

| | *Source of Variation* | *DF* | *Sum of Squares* | *Mean Squares* | *F-Calculated* | *Significance* |
|---|---|---|---|---|---|---|
| | Seasons | 3 | 1,274.63 | 424.88 | 474.01 | 0 |
| | Rep within Season | 8 | 7.17 | 0.90 | | |
| *FY* | Treatment | 29 | 1,044.13 | 36.01 | 36.01 | 0 |
| | Year X Season | 87 | 390.61 | 4.49 | 4.49 | 0 |
| | Pooled Error | 232 | 231.99 | 1.00 | | |
| | Total | 359 | 2,948.55 | | | |

(GE). The GGE biplot simplifies complex multi-environment trial data, allowing researchers to determine the best-performing genotypes, mega-environments, and the most representative test environments (Yan, 2014).

Phenotypic evaluations of 30 foxtail millet genotypes were illustrated in Fig. 1. The GGE biplot analysis revealed that the first two principal components (PCs) together explained 88.10% of the total variability for fodder yield, with PC1 accounting for 75.14% and PC2 accounting for 12.96%. According to Yan *et al*. (2009), a biplot explaining more than 60% of the variability in a dataset is considered valid for genotype-by-environment interaction (GEI) studies. Therefore, the high explanatory power of our biplots confirms their suitability for assessing GEI, providing valuable insights into genotype stability and adaptability across different environments. Among the 30 genotypes, G1–G4 (Fig. 1) were positioned on the left side of the biplot and exhibited higher mean fodder yield than the grand mean, whereas G5–G24, also located on the left side, showed lower yields than the grand mean. Notably, G1 and G25 were positioned closer to the x-axis, indicating minimal interaction with the environment. This suggests that these genotypes are stable yielders, as their performance remains consistent across different growing conditions. Their proximity to the x-axis further reinforces their adaptability and reliability for fodder yield stability.

The Mean vs. Stability biplot is a graphical tool used in GGE biplot analysis to assess both the mean performance and stability of genotypes across multiple environments. In this biplot, the average environment coordinate (AEC) abscissa represents the mean performance, while the AEC ordinate measures the stability of genotypes. A genotype with a longer projection on the AEC ordinate, in any direction, indicates a stronger genotype-environment interaction (GEI), making it less stable across environments (Yan, 2014). Based on the analysis, genotypes G1-G2 exhibited above-average yields (Fig. 1.1), while others were discarded. Among them, G1 and G5 were identified as the most desirable for dry fodder yield due to their proximity to the "ideal" genotype, indicating both high yield and stability across environments.

The ideal genotype ranking biplot is an effective tool for evaluating and visualizing genotype performance in terms of both mean yield and stability. In this biplot, the ideal genotype is located at the center of concentric circles, representing the most desirable combination of high yield

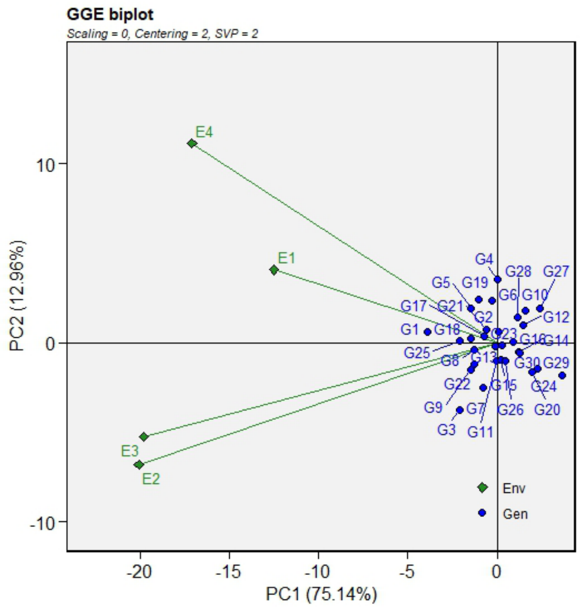


**Fig 1:** Mean performance and stability of 30 genotypes over four crop cycles based on GGE biplot analysis for fodder yield

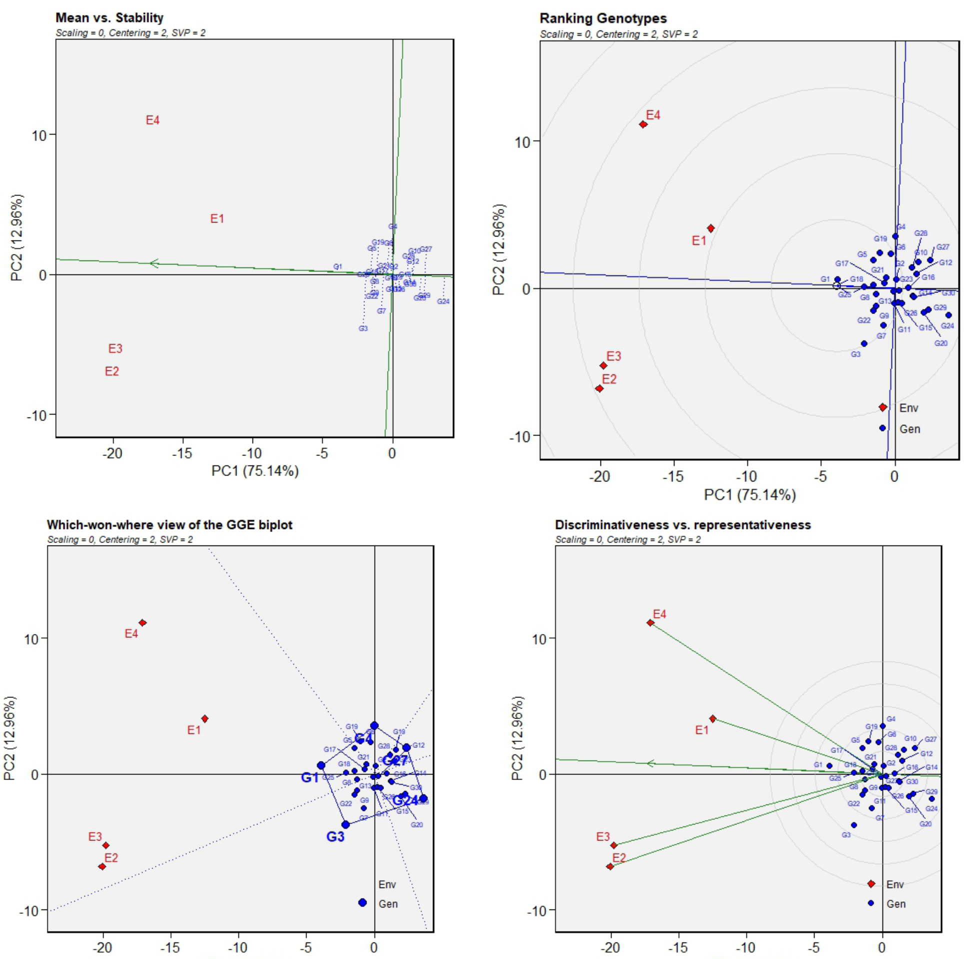


**Fig 1A-D:** Means performance and stability, ideal genotype, which-won-where and Discriminativeness vs. Representativeness GGE Biplots of dry fodder yield per plant.

**Table 5:** Environmental Wise Treatment Means of dry fodder yield per plant

| *S. No* | *Genotype* | *E1* | *E2* | *E3* | *E4* | *MEAN* |
|---|---|---|---|---|---|---|
| 1 | G1 | 23.97 | 26.80 | 25.77 | 27.07 | 25.90 |
| 2 | G2 | 18.40 | 16.36 | 17.80 | 18.93 | 17.87 |
| 3 | G3 | 20.20 | 26.81 | 23.03 | 17.37 | 21.85 |
| 4 | G4 | 21.00 | 16.36 | 13.50 | 22.43 | 18.32 |
| 5 | G5 | 23.83 | 16.61 | 22.37 | 22.20 | 21.25 |
| 6 | G6 | 21.13 | 15.62 | 17.47 | 21.17 | 18.85 |
| 7 | G7 | 19.57 | 21.14 | 21.00 | 15.93 | 19.41 |
| 8 | G8 | 22.17 | 19.76 | 21.63 | 19.17 | 20.68 |
| 9 | G9 | 24.37 | 21.34 | 20.67 | 17.07 | 20.86 |
| 10 | G10 | 16.87 | 12.40 | 13.33 | 17.50 | 15.02 |
| 11 | G11 | 18.73 | 16.95 | 19.97 | 16.57 | 18.05 |
| 12 | G12 | 17.37 | 15.18 | 11.87 | 16.60 | 15.25 |
| 13 | G13 | 20.47 | 17.03 | 18.63 | 17.13 | 18.32 |
| 14 | G14 | 13.57 | 14.92 | 16.03 | 16.47 | 15.25 |
| 15 | G15 | 17.10 | 17.81 | 18.03 | 16.90 | 17.46 |
| 16 | G16 | 16.30 | 16.56 | 14.47 | 17.03 | 16.09 |
| 17 | G17 | 18.60 | 17.51 | 20.97 | 20.47 | 19.39 |
| 18 | G18 | 21.40 | 21.82 | 19.83 | 21.30 | 21.09 |
| 19 | G19 | 22.10 | 18.52 | 17.73 | 22.90 | 20.31 |
| 20 | G20 | 11.40 | 14.48 | 14.97 | 14.00 | 13.71 |
| 21 | G21 | 19.97 | 19.10 | 17.80 | 20.27 | 19.28 |
| 22 | G22 | 18.53 | 22.41 | 22.17 | 19.97 | 20.77 |
| 23 | G23 | 15.77 | 17.17 | 17.40 | 18.53 | 17.22 |
| 24 | G24 | 18.53 | 10.13 | 9.53 | 5.67 | 10.97 |
| 25 | G25 | 22.57 | 22.70 | 21.97 | 22.10 | 22.33 |
| 26 | G26 | 18.73 | 16.59 | 17.77 | 15.33 | 17.11 |
| 27 | G27 | 17.10 | 10.33 | 11.00 | 15.33 | 13.44 |
| 28 | G28 | 17.47 | 13.93 | 14.07 | 17.73 | 15.80 |
| 29 | G29 | 15.17 | 13.80 | 12.97 | 11.67 | 13.40 |
| 30 | G30 | 14.80 | 14.80 | 15.80 | 15.63 | 15.26 |
| Mean | | 18.91 | 17.50 | 17.65 | 18.01 | 18.02 |

and stability (Yan and Wu, 2008). In our study, genotype G1 was positioned at the center (Fig 1.2), indicating its superiority in both yield and stability. Genotypes G25, G18, and G5, located on the next concentric circle, also exhibited desirable characteristics but with slightly lower stability or yield than G1. The remaining genotypes, positioned farther from the center, were less stable and, therefore, less desirable for selection.

The "Which Won Where" biplot is a powerful tool in GGE biplot analysis used to visually identify the best-performing genotype in specific environments. This biplot is constructed by drawing a polygon connecting the most extreme genotypes, with rays drawn perpendicular to the sides of the polygon or their extensions (Yan and Wu, 2008). These rays divide the biplot into different sectors, each representing a group of environments where a specific genotype performs best. In our study, five rays were drawn: ray one perpendicular to the side connecting genotype G27, ray 2 to G24, ray 3 to G3, ray 4 to G1, and ray 5 to G4 (Fig. 1.3). These rays divided the biplot into five distinct sectors, with the environments distributed across one of them. The vertex genotype, G1, is the most responsive in its respective sector, indicating that it performed best in the environments grouped within that sector.

The discriminativeness vs. representativeness GGE biplot is a valuable tool for identifying the most informative environments for genotype evaluation (Yan and Kang, 2002). In this biplot, the length of an environment's vector reflects its discriminative ability, while the angle with the Average Environment Axis (AEA) indicates its representativeness (Yang and Tinker, 2006). In our study, Environment 1 (E1) had short vectors (Fig. 1.4), suggesting moderate discriminative ability and representing the average genotype performance. In contrast, Environment 2 (E2) had a longer vector, indicating a high capacity to differentiate genotypes. Additionally, E1 formed a narrower angle with the AEA, making it the most representative environment, while E2 was the most discriminative.

## Conclusion

This study comprehensively evaluated the dry fodder yield of 30 foxtail millet genotypes across four diverse environments using GGE biplot analysis. The results highlighted significant genotype-by-environment interactions (GEI), emphasizing the importance of selecting stable and high-yielding genotypes. Among the genotypes, G1 consistently demonstrated superior performance across all environments, ranking as the most stable and high-yielding genotype. Other promising genotypes, such as G5, G18, and G25, also exhibited desirable traits but which are slightly lower stability. The Mean vs. Stability biplot confirmed the superiority of G1 and G5, while the ideal genotype ranking biplot further reinforced G1's reliability due to its central position in the concentric circles. The "Which Won Where" biplot identified five distinct sectors, with G1 emerging as the best performer in its respective environments. Additionally, the Discriminativeness vs. Representativeness biplot revealed that E1 was the most representative environment, making it ideal for genotype selection, while E2 displayed high discriminative power. These findings underscore the importance of selecting stable and high-yielding genotypes to enhance productivity and ensure sustainable millet cultivation under diverse environmental conditions.

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