

# Genetic Evaluation for Stability of Grain Yield and Yield Components in Foxtail Millet using GGE Biplot in Foothills of Nagaland

## ABSTRACT

**Aims:** Foxtail millet cultivation in India's North Eastern Hill region holds promise due to its adaptation to diverse environments and high-quality grain. Studying G x E interaction in this region will guide breeding programs to develop foxtail millet varieties adapted to local conditions. The objective of this study was to find out foxtail millet genotypes that produce high yield in diverse environments and to identify ideal mega-environments using GGE Biplot stability model analysis.

**Methods:** The investigation was carried out during July 2022 to May 2023 for four different dates of sowing with twenty-five days interval. Two environments maintained under rained condition and the remaining two environments are maintained under irrigated condition. The experiment was conducted in randomized complete block design with three replications in all environments.

**Results:** Analysis of variance revealed statistically significant differences (at 5%) among the 30 genotypes for all yield variables under evaluated. Genotype 'G1' exhibited superior performance for both yield and yield-related traits. In this study, four GGE biplots of GY, one is Discriminateness and representativeness in GGE biplots revealed E4 is identified as the most representative environment. At the same time, E3 also stands out for its strong discriminative capacity. Another one is Which Own Where" biplots revealed that G19 and G27 displayed superior and stable performance in E1. Similarly, G25 and G1 excelled in E2, E3, and E4. while mean vs stability biplots revealed that G1 is stable and performs well.

**Conclusion:** Genotypes, namely G1, G22, G25, and G21, exhibited stable and reliable performance across different conditions.

**Keywords:** Foxtail millet, genetic variability, GGE Biplot, PCA

## 1. INTRODUCTION

Foxtail millet (*Setaria italica* (L.) P. Beauv.) is a self-pollinating, C4 cereal crop with a rich history of cultivation dating back to 5000-6000 BC along the Yellow River in China [1]. The Food and Agriculture Organization of the United Nations/International Crops Research Institute for the Semi-Arid Tropics projected that the global foxtail millet production amounted about 6 million ton

in the year 2023, India alone contributed more than 50% of the total production. It is cultivated in an area of 2.15 million acres, amounting approximately 0.66 lakh tones with productivity of 762 kg/ha during 2015 – 2016 [2]. The International Year of Millets 2023, a United Nations initiative, aims to raise awareness about the significance of millets as a nutritious and sustainable food source, while promoting their cultivation, consumption, and trade.

GEI, which stands for Genotype by Environment Interaction, means that different plant types respond differently to a wide range of environments. This is well-known in crop breeding and can make it tricky for researchers to assess and choose the best plant types. It's especially important for breeders who want to develop and release new high-yielding plant varieties. Quantitative trait like yield, which have a big impact economically and in farming, can be significantly influenced by GEI. Because of this, breeders have to be really careful when picking and releasing plant types, ensuring they perform well in the target environment. However, GEI can also be a positive thing. That help breeders find plant types that perform well in a specific location (specific adaptation) or in most places (general adaptation). To do this, breeders grow different plant types in various environments to find out the performance of those plant types in response to the various environment provided and select the best plant type that performs well and is stable across different conditions [3].

There are two main groups of methods for analysing information from METs: univariate and multivariate methods. One important multivariate method is the AMMI model, which combines analysis of variance and principal components (PCs) analysis [3]. The GGE (Genotype and Genotype  $\times$  Environment interaction) biplot is a graphical tool used in the field of plant breeding and agricultural research to analyse and visualize complex genotype by environment interaction (G  $\times$  E) patterns [4].

In this study, 30 genotypes of foxtail millet were collected from Indian Institute of Millets Research-Hyderabad, Situated at 25.1944° N latitude and 71.7164° E longitude to evaluated their performance in different environmental conditions to find out the best performing genotypes in term of yield under foothill of Nagaland.

## **2. Material and Methods**

### **2.1 Experiment location:**

The investigation was carried out during July 2022 to May 2023 for four different dates of sowing with twenty-five days interval (Table 1.). Each sowing date was chosen to create varying environmental conditions, including different temperatures and moisture levels throughout the crop growth stages. Two environments maintained under rained condition and the remaining two environments are maintained under irrigated condition with seven days interval. The experiment was conducted at the Research Farm of the Department of Genetics and Plant Breeding SAS NU, located in Medziphema, India.

### **2.2 Plant materials**

Thirty genotypes of Foxtail millet, which include four check varieties were collected from Indian Institute of Millets Research (IIMR), Hyderabad. These 30 selected genotypes included one check variety were used to assess genetic variability, diversity, and stability across different environments. List of 30 genotypes represented in Table 2.

### **2.3 Experimental design and intercultural practice:**

The experiment used a randomized complete block design (RCBD) with three replications across different environments due to varying site fertility. Each of the three replications had 30 plots (1m x 1m) spaced 10cm apart, with plants and rows 10cm and 22.5cm apart, respectively. The total plot size was 30m x 5m, accommodating 90 beds. Recommended agricultural practices were followed throughout.

### **2.4 Data collection:**

To collect data, a total of Fourteen quantitative characteristics of foxtail millet were considered. These characteristics were chosen based on descriptions and guidelines provided by PPV&FR in 2001 (DUS). For each characteristic, data were gathered from five randomly selected plants within each genotype and replication. the quantitative data encompassed various traits, including days to 50% flowering (DF), days to maturity (DM), plant height (PH), panicle length (PL), flag leaf length (FL), flag leaf width (FW), peduncle length (PDL), total tiller numbers per plant (NT), panicle width (PW), biological yield (BY), harvest index (HI), test weight (TW), fodder yield per plant (FY), and grain yield per plant (GY).

### **2.5 Statistical analysis**

The analysis of variance was conducted using the OPSTAT open-source software to assess the pooled data. The factors considered for variance testing were genotype (G), environment (E), and the interaction between genotype and environment (G×E). Various statistical measures such as mean, range, coefficient of variation (CV), and standard deviation were calculated for each attribute. The visualization of multivariate stability analysis, GGE biplot was employed through the 'Metan' package in R-studio, a tool developed by the R Core Team [5].

**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 (KE)	25 <sup>0</sup> 45' 15.95" N	93 <sup>0</sup> 51' 44.71 E	310 MSL	31.66	22.30	91.75	69.64	51.92	2022
Env-2	26-07-2022	Kharif(Late)(KL)	25 <sup>0</sup> 45' 15.95" N	93 <sup>0</sup> 51' 44.71 E	311 MSL	32.09	22.84	92.10	69.99	55.19	2022
Env-3	01-01-2023	Summer (SE)	25 <sup>0</sup> 45' 15.95" N	93 <sup>0</sup> 51' 44.71 E	312 MSL	29.11	17.40	94.48	61.84	15.58	2023
Env-4	26-01-2023	Summer(Late) (SL)	25 <sup>0</sup> 45' 15.95" N	93 <sup>0</sup> 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

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

<b>ACC. No</b>	<b>IC. No</b>	<b>Source</b>	<b>Code</b>
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

### 3. RESULTS AND DISCUSSION

#### 3.1 Analysis of variance

The pooled analysis of variance (ANOVA) was used to examine the interactions between different genotypes and environments. Table 3 presents the results of the pooled ANOVA for all genotypes across various environments, focusing on yield and its components. There were significant variations observed among the different environments (E), genotypes (G), and the interaction between genotypes and environments (G×E). In fact, all the variables studied showed highly significant differences ( $P<0.05$ ) in terms of the environment, genotype, and genotype-environment interaction. These significant differences suggest that there is a substantial amount of genetic variation among the evaluated genotypes. Comparable findings are presented in studies conducted by [6] on foxtail millet.

**Table 3. Combined Analysis of variance for pooled data**

Source of Variation	Mean Squares				
	Seasons (DF=3)	Rep within Season (DF=8)	Genotypes (DF=29)	Year X Season (DF=87)	Pooled Error (DF=232)
Day to 50% flowering	63,745.27*	2.61	111.69*	34.26*	1
Day to maturity	2,39,669.82*	5.16	129.99*	37.73*	1
Plant height (cm)	38,415.20*	2.52	125.17*	43.80*	1
Panicle length (cm)	262.10*	0.52	36.42*	6.41*	1
Flag leaf length (cm)	60.75*	4.87	45.19*	10.65*	2.8
Flag leaf width (cm)	1.07*	0.27	1.31*	0.31*	0.06
Peduncle length (cm)	989.87*	0.84	23.51*	5.25*	1
No. of basal tillers	93.98*	3.98	5.40*	1.79*	1
Panicle width (cm)	188.85*	2.43	16.90*	3.11*	1
Biological yield (g)	1,236.78*	1.01	34.30*	5.04*	1
Harvest index (%)	2,636.12*	1.71	6.42*	2.97*	1
Fodder yield per plant(g)	423.90*	0.91	36.07*	4.50*	1
Test weight (g)	1.05*	0	0.36*	0.01*	0
Grain yield per plant(g)	490.15*	4.43	60.49*	13.12*	3.2

#### 3.2 GGE biplot graphical analysis

Various trials are carried out in all regions for major crops every year. Plant breeders and agronomists conduct these trials to find better genotypes and recommend superior cultivars to growers. Despite budget constraints, these trials continue annually, underscoring their vital role in agriculture and the economy. They are likely the well-funded applied research in agriculture. Variety trial data typically cover multiple traits, but most publications focus on a single trait, often crop yield. These traits can be grouped into three categories: target traits (economically valuable, like crop yield), explanatory traits (related to target traits), and marker traits (easily measured and less influenced by the environment). In multiyear variety data analysis, the key method is GGE biplot analysis. The challenge needs to be more balanced and complete data due to changing genotypes over the years. Two strategies are

used: 1) Analyzing yearly and summarizing results; 2) Evaluating consistency of patterns in grouping test locations and genotypes across years [7].

The GGE biplot results showed that the initial and second principal components accounted for DF: PC1 (54.5%), PC2 (28.7%) and total (83.2%), DM: PC1 (60.27%), PC2 (20.14%) and total (80.41%), PH: PC1(65.72%), PC2 (16.38%) and total (82.10%), PL: PC1 (61.46%), PC2 (24.02%) and total (81.60%), FL: PC1 (60.4%), PC2 (18.93%) and total (79.33%), FW: PC1 (61.46%), PC2 (24.02%) and total (81.60%), PDL: PC1 (64.83%), PC2 (14.58%) and total (79.38%), NBT: PC1 (52.35%), PC2 (29.72%) and total (82.07%), PW: PC1 (61.45%), PC2 (25.93%) and total (87.38%), BY: PC1 (73.11%), PC2 (12.79%) and total (85.90%), HI: PC1 (43.85%), PC2 (30.36%) and total (74.21%),FY: PC1 (75.14%), PC2 (12.96%) and total (88.10%), TW: PC1 (92.37%), PC2 (6.71%) and total (99.08%) and GY: PC1 (65.06%), PC2(17.51%) and total (82.57%)of the total variation of each trait respectively. This indicates strong support for the biplot's credibility in elucidating genotype and genotype by environment interaction (GEI) variations, as the first two principal components capture a significant portion of the variance. When these two components fall short of explaining most of the data variability, it suggests the complicated nature of GEI [8], but it does not condense the biplot invalid [8]. As [4] noted, when a biplot can account for at least 60% of the data's variance, it becomes a valuable tool for identifying meaningful patterns in genotype-environment interactions (MEs).

### **3.2.1 The mean v<sub>s</sub> stability biplots**

The mean vs stability biplots aid in understanding the average genotype performance across various environments. In GGE biplot methodology, the estimation of yield and stability of genotypes. The average environment axis (AEA) is a line with a single arrow in the biplot. It starts from the biplot origin and goes towards the average environment in GGE Biplot. This arrow indicates higher genotypic values for the genotypes it points to [8]. The average environment coordination (AEC) is a coordinate system with the AEA as the horizontal axis. It has a double-arrowed line that goes through the biplot origin and is perpendicular to the AEA. The two arrows on the AEC point outward from the origin and indicate higher instability for the genotypes, regardless of the direction [8]. The AEC ordinate distinguishes between genotypes with below-average means and those with above-average means. Additionally, the average yield of genotypes can be estimated by projecting their markers onto the AEC abscissa [9].

In this study, all locations are on the same side of the AEC in DF (Figure 1.1), DM (Figure 2.1), PH (Figure 3.1), PL (Figure 4.1), FL (Figure 5.1), FW (Figure 6.1), PDL (Figure 7.1), NBT (Figure 8.1), PW (Figure 9.1), BY (Figure 10.1), HI (Figure 11.1), FY (Figure 12.1), TW (Figure 13.1) and GY (Figure 14.1) indicating that the G/GE in this dataset is sizable and that the AEA is meaningful for genotype evaluation. If the locations are placed on both sides of the AEC ordinate, then the G/GE in the dataset would be too small for the AEC to be reliably used for genotype evaluation.

In this study genotypes of all traits exhibits DF: (G21-G3), DM (G5-G1), PH (G21-G1), PL (G10-G25), FL (G23-G5), FW (G28-G26), PDL (G6-G8), NBT (G17-G29), PW (G29-G30), BY (G17-G1), HI (G16-G20), FY (G13-G1), TW (G13-G2) and GY (G3-G1) were shows above average mean yields and

remain genotypes (from G30-G17) DF, (from G13-G8) DM, (from G8-G16) PH, (from G16-G11) PL, (from G7-G30) FL, (from G14-G3) FW, (from G13-G4) PDL, (from G9-G24) NBT, (from G2-G24) BY, (from G12-G3) HI, (from G11-G24) FY, (from G3-G23) TW and (from G20-G24) GY exhibits below average mean yield.

The length of the average environment vector, in relation to the biplot size, indicates how much the genotype's main effect matters compared to genotype-environment interaction (GEI). A longer vector signifies a greater importance of the genotype's main effect, making selection based on mean performance more meaningful [8]. In this study, the average environment vector's length was enough to choose genotypes based on their average yield performance. Genotypes in DF: (G4, G18, G1, G3), DM (G16, G18, G3, G1), PH (G24, G17, G28, G2, G30, G1), PL (G23, G9, G28, G30, G21, G22, G8, G25), FL (G16, G2, G28, G5), FW (G15, G8, G18, G17, G26), PDL (G28, G2, G29, G5, G1, G8), NBT (G29), PW (G19, G9, G18, G30), BY (G18, G19, G21, G8, G9, G3, G5, G22, G25, G1), HI (G20), FY (G15, G8, G18, G17, G26), TW (G1-G2), GY (G5, G21, G22, G25, G1) which had above-average yields, were selected, while the others were discarded respective traits. A longer projection on the AEC ordinate, in any direction, indicates that a genotype has a stronger genotype-environment interaction (GEI). This means it is less consistent and more variable across different environments, or the opposite [8]. Each genotype is connected to the AEA through a line, helping to display the average performance and stability of the genotypes. The length of the line for a genotype represents its position on the AEC ordinate, indicating the genotype's instability or its impact on genotype-environment interactions (GE). The ideal genotype is a virtual genotype that is defined to achieve the highest yield in trials (with the longest vector among all genotypes) and complete stability, placing it precisely on the AEA [8]. The desirability of the genotypes is judged by their closeness to this "ideal" genotype. Thus, (G1 and G4) in DF, (G16 and G18) in DM, (G1, G2, G28 and G17) in PH, (G9, G30, G8) in PL, (G28 and G5) in FL, (G18 and G17) in FW, (G28 and G1) in PDL, (G29) in NBT, (19 and G9) in PW, (G1, G25, G22 and G5) in BY, (G20) in HI, (G18 and G17) in FY, and (G21 and G22) in GY are the most desirable genotypes at respective traits.

### **3.2.2 Ranking genotypes**

An ideal genotype should ideally have the highest mean performance and absolute stability, meaning it performs exceptionally well in all environments. This ideal genotype is represented by a long arrow pointing to it in GGE biplot. While such an ideal genotype may not exist in reality, it serves as a reference for evaluating other genotypes. The closer a genotype is to this ideal, the more desirable it is. To visualize this, concentric circles were drawn around the ideal genotype as the center to show the distance between each genotype and the ideal one. In this evaluation, both PC1 and PC2 units for the genotypes are in the original yield units. Therefore, the units of the AEC abscissa (mean yield) and ordinate (stability) are also in the original yield units. The distance between genotypes and the ideal genotype is also measured in the original yield units. This ranking method assumes that stability and mean yield are equally important, as proposed by (Yan 2002). Figure 1.2- Figure 14.2, shows that G3 in DF, G1 and G18 in DM, G1 in PH, G8 and G25 in PL, G5 in FL, G17 in FW, G8 in PDL, G29 in NBT, G30 in PW, G1 in BY, G20 in HI, G1 in FY, G2 and G4 in TW and G1 and G25 in GY are positioned at

the center of the concentric circles, is an ideal genotype due to its higher yield and stability compared to the other genotypes.

### **3.2.3 Which Own Where biplot**

"Which Own Where" biplots serve to visually represent mega-environments and facilitate the identification of superior genotypes, made-to-order to specific environments. These biplots plot genotypic means against the IPCA-1, where each genotype is represented as a line with the IPCA serving as the slope. Such biplots are referred to as "which own where" biplots [8]. polygonal biplot is aide to identify MEs and superior genotypes in different environments. In this biplot, a polygon is drawn from the connection of the genotypes that have the maximum distance from the coordinate origin. The rays' lines in biplot that is perpendicular to the sides of the polygon or their extensions. In the GGE biplot DF:(Figure 1.3) genotypes G3, G18, G9, G21, G22, G6, G8, G17, G29, and G5, DM: (Figure 2.3) G12, G8, G7, G1, G3 and G10, PH: (Figure 3.3) G1, G30, G3, G5, G16, G15, and G6, PL: (Figure 4.3) G25, G23, G26, G8, G4, G11, and G12, FL: (Figure 5.3) G8, G26, G17, G22, G23, G3 and G28, FW: (Figure 6.3) G3, G23, G22, G17, G26, G8 and G28, PDL (Figure 7.3) G29, G27, G22, G28, and G24, NBT: (Figure 8.3) G29, G27, G22, G28, and G24, PW; (Figure 9.3) G15, G30, G18, G3, G26, G20 and G4, BY (Figure 10.3) G1, G3, G7, G24, G19, G4, and G27 , HI: (Figure 11.3) G20, G14, G23, G7, G10, G11, G6 and G3, FY (Figure 12.3) G1, G3, G24, G27 and G4, TW: (Figure 13.3) G2, G1, G6, G11, G16, G23, G30, G18 and G9 and GY: (Figure 14.3) G25, G1, G27, G19, G24, G29, and G11 were located at the farthest distance and formed a polygon.

The division of the plot into sectors and the allocation of environments within them vary based on the number of vertexes and equality lines. In the DF GGE Biplot, the biplot is divided into 8 sectors through 7 vertexes and one equality line, and the environments fall into 2 of these sectors. In contrast, the DM Biplot has 5 vertexes and no equality lines, resulting in the biplot being divided into 5 sectors, with the environments allocated into 2 of them. The PH Biplot involves 6 vertexes and one equality line, dividing the biplot into 7 sectors, with 2 sectors accommodating the environments. Similarly, the PL Biplot and FL Biplot, both having 7 vertexes, divide the biplot into 7 sectors with 2 sectors housing the environments, but without equality lines. The FW Biplot utilizes 5 vertexes and 2 equality lines, dividing the biplot into 7 sectors, and 2 sectors include the environments. In the PDL Biplot, 5 vertexes and 1 equality line create 6 sectors, with the environments falling into 2 of them. The NBT Biplot and PW Biplot both employ 5 vertexes but with different arrangements of equality lines, resulting in the biplot being divided into 5 sectors and environments falling into 2 of them. The BY Biplot, with 7 vertexes and no equality lines, divides the biplot into 7 sectors, and 1 of these sectors houses the environments. The HI Biplot, with 5 vertexes and 1 equality line, divides the biplot into 6 sectors, and 2 sectors accommodate the environments. Similarly, the FY Biplot with 5 vertexes but no equality lines divide the biplot into 5 sectors, and 1 sector includes the environments. In contrast, the TW Biplot utilizes 8 vertexes and no equality lines, resulting in the biplot being divided into 8 sectors, with 2 sectors accommodating the environments. Lastly, the GY Biplot, utilizing 7 vertexes and no equality lines, divides the biplot into 7 sectors, with the environments falling into 2 of them.

In the DF biplot, two environments, E1 and E2, were grouped into a similar sector, where the vertex genotypes G18, G9, and G21 indicated their ideal performance in those particular environments. Likewise, in the DM biplot, three environments (E2, E3, and E4) fell into a common sector, featuring vertex genotypes G3 and G1, highlighting the higher-yielding genotype for these environments. Moving to the PH biplot, environments E1 and E4 were clustered in a sector represented by the vertex genotype G1, indicating ideal performance. Conversely, E3 and E2 were in another sector with vertex genotype G30, signifying the higher-yielding genotype for these two environments. In the PL biplot, seven vertexes without equality lines divided the plot into seven sectors, with environments E1 and E2 falling into a similar sector characterized by vertex genotypes G25 and G23, suggesting their ideal performance. Additionally, environments E4 and E3 were grouped in another sector with vertex genotype G26, representing the higher-yielding genotype. The FL biplot demonstrated three environments (E1, E2, and E4) sharing a sector, with the vertex genotype G5 indicates ideal performance. On the other hand, environment E3 formed a separate sector, featuring vertex genotype G2, suggesting the higher-yielding genotype. In the FW biplot, three environments (E1, E2, and E4) clustered into a sector, embodying vertex genotypes G8, G26, and G17, symbolizing ideal performance in those environments. Conversely, environment E3 had a unique sector with vertex genotypes G22 and G23, representing the higher-yielding genotypes. Shifting to the PDL biplot, three environments (E1, E2, and E4) shared a sector characterized by vertex genotypes G8, G5, and G29, signifying ideal performance in those respective environments. On the other hand, environment E3 formed a separate sector, featuring vertex genotype G22, suggesting the higher-yielding genotype. In the NBT biplot, three environments (E1, E2, and E3) fell into a similar sector, showcasing vertex genotypes G22 and G29, denoting ideal performance in those environments. Conversely, environment E4 had a unique sector with vertex genotype G27, representing the higher-yielding genotype. In the PW biplot, three environments (E4, E2, and E3) grouped into a sector, characterized by vertex genotypes G15, G30, and G18, indicating ideal performance in those respective environments. On the contrary, environment E1 had a separate sector with vertex genotypes G3 and G26, suggesting the higher-yielding genotypes. Moving to the BY biplot, four environments (E4, E2, E1, and E3) shared a sector featuring vertex genotypes G3, G1, and G19, indicating ideal performance in those environments. In the HI biplot, three environments (E1, E2, and E3) fell into a similar sector with vertex genotypes G20, G14, and G23, signifying ideal performance. Conversely, environment E4 formed a separate sector with vertex genotype G7, representing the higher-yielding genotype. Lastly, in the FY biplot, four environments (E4, E2, E1, and E3) were grouped into a similar sector with the vertex genotype G1, indicating ideal performance in those specific environments. In the TW biplot, eight vertexes without equality lines divided the plot into eight sectors, and environments fell into two of them. Three environments (E4, E2, and E3) shared a sector featuring vertex genotypes G2, G1, and G6, suggesting their ideal performance. Conversely, environment E4 formed a separate sector, but no specific vertex genotypes were mentioned. In GY biplot, three environments—E4, E2, and E3—fell into a similar section, and the genotypes at the corners of this section were G25 and G1. This suggests that these genotypes performed exceptionally well in those specific environments. On the other hand, one environment, E1, fell into its single section, and the

genotypes at the corner of this section were G27 and G19. This indicates that these genotypes were the highest-yielding ones for this particular environment. Conversely, genotypes located in sections without associated environments are not as suitable for cultivation across the studied conditions. Among these, Genotypes G24, G29, and G11 were positioned in such sections, suggesting they may not perform well in the tested conditions in grain yield.

### **3.2.4 Discriminateness and Representativeness GGE Biplot**

A test location that can't effectively distinguish between cultivars doesn't give us any useful information. Another important aspect of a test location is how well it represents the environment we're interested in [8]. If a test location doesn't accurately represent the target environment, it's not only unhelpful but can also lead to misleading results because it only provides partial information about the tested cultivars [7]. An "ideal test location" is like a theoretical spot that's defined to have the longest vector among all locations, and it's perfectly representative, meaning it doesn't contribute to genotype-environment interactions (GE) and sits right on the AEA. The closer a real location is to this ideal one, the better it is as a core test location [7]. The concepts of discriminateness and representativeness in GGE biplots are crucial for identifying ideal environments that can effectively distinguish between genotypes. The use of AEC and test environments helps us visualize Environments-I, II, III, and IV more effectively and representation at Biplots (Figure. 1.4-14.4).

The length of the environment vector roughly corresponds to the standard deviation within each environment, indicating how distinct that environment is. Environments with longer vector lengths have higher standard deviations, indicating a stronger ability to distinguish between genotypes. E4 and E1 in DF, E1 in DM, E4 in PH and PL, E2 in FL and PDL, E2 and E4 in FW, E1 and E2 in NBT and BY, E3 and E4 in PW, E1, E2 and E3 in HI, E3 and E1 in TW and E2 in GY are characterized by short vectors, suggesting it has average discriminative power, representing the average performance of genotypes. E3 and E2 in DF, E1, E3, and E4 in DM and FL, E1, E2, and E3 in PH, HI and PL, E1 and E3 in FW, E1, E3, E4 in PDL, E4 and E3 in NBT and BY, E2 and E1 in PW, E4 and E2 in TW, E2 and E3 in FY and E3 in GY are long vector, signifying significant discriminative power and high-genotype performance. Notably, E1 in FW, E2 in PL and PW, E3 in DF, PH, FY, BY, and PDL, E4 in DM, FL, HI, TW and GY are exhibits narrower angle with the AEA, making it more representative compared to other environments.

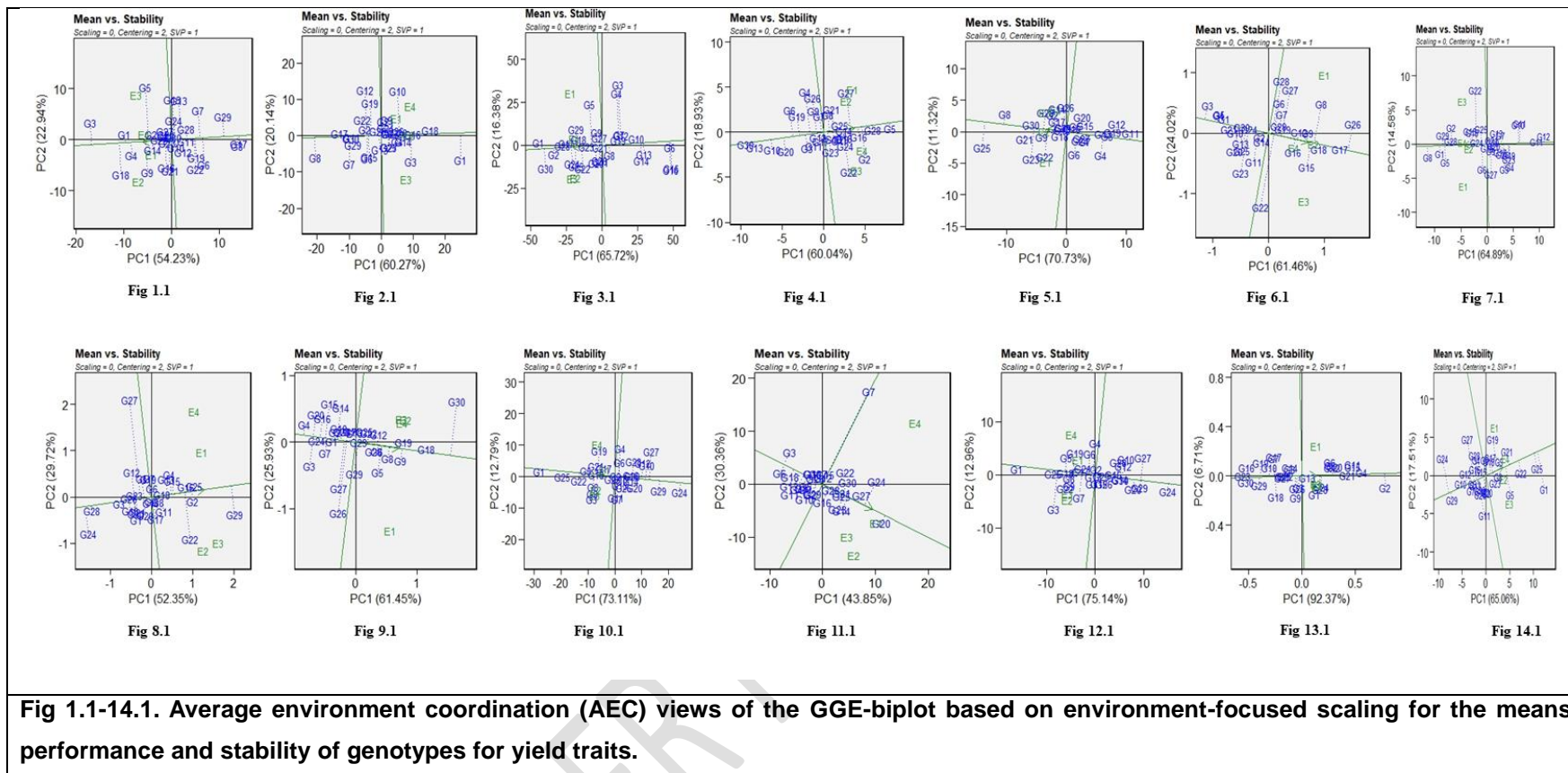
A previously similar study was conducted, and significant results are reported by [10] in barley, [11] in soybean, [12] in melon and [13] in melon.

## **4. Conclusion**

Environment E1, representing the as the ideal environment for foxtail millet cultivation in Nagaland. This means that planting during this season is most favourable for good yields. These genotypes, namely G1, G22, G25, and G21, exhibited stable and reliable performance across different conditions. Therefore, we recommend these genotypes for general cultivation in Nagaland, as they are likely to yield positive results in various agricultural settings. This conclusion is based on a rigorous analysis of

multi-environmental data, which provides practical guidance for farmers and cultivators in Nagaland looking to optimize their foxtail millet production.

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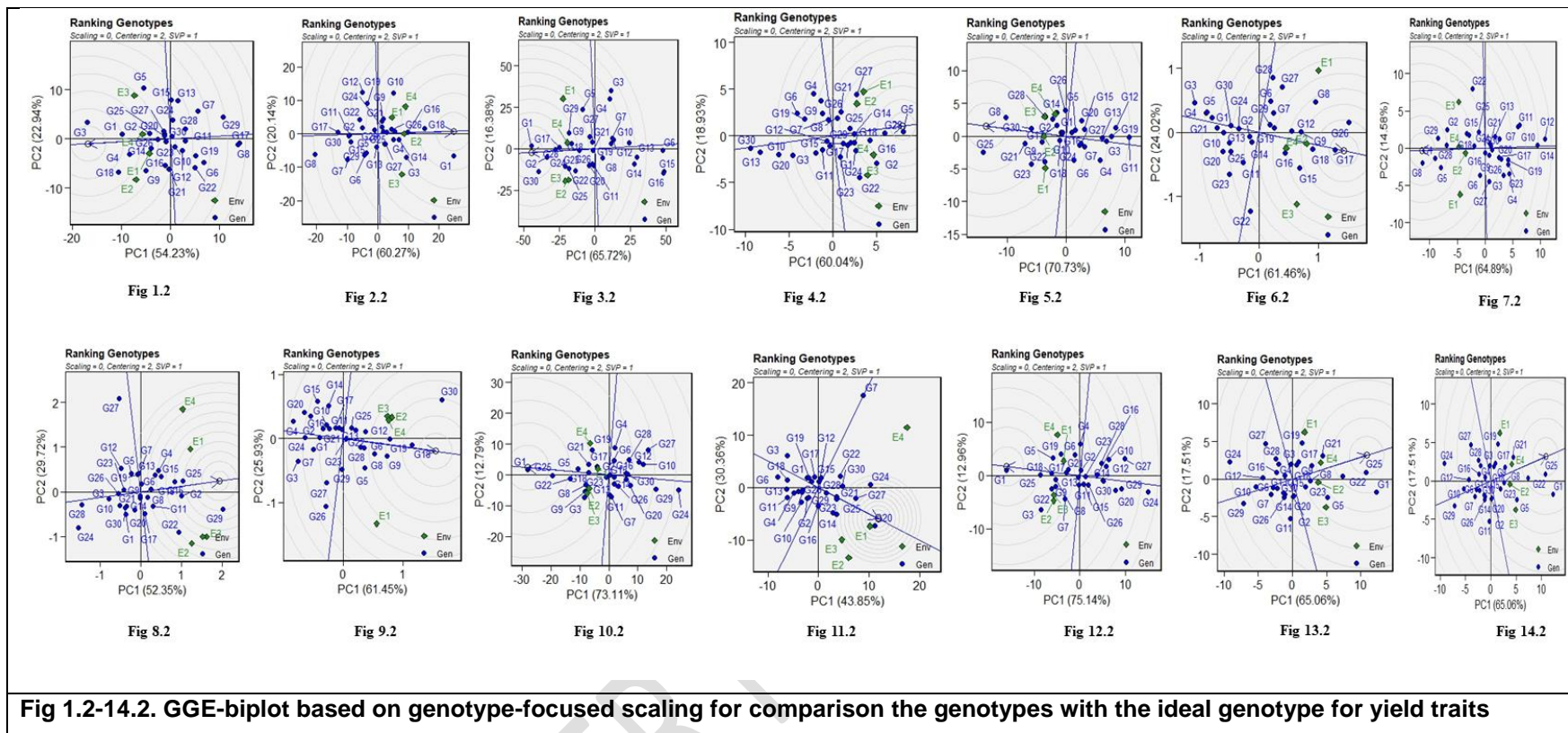


Fig 1.2-14.2. GGE-biplot based on genotype-focused scaling for comparison the genotypes with the ideal genotype for yield traits

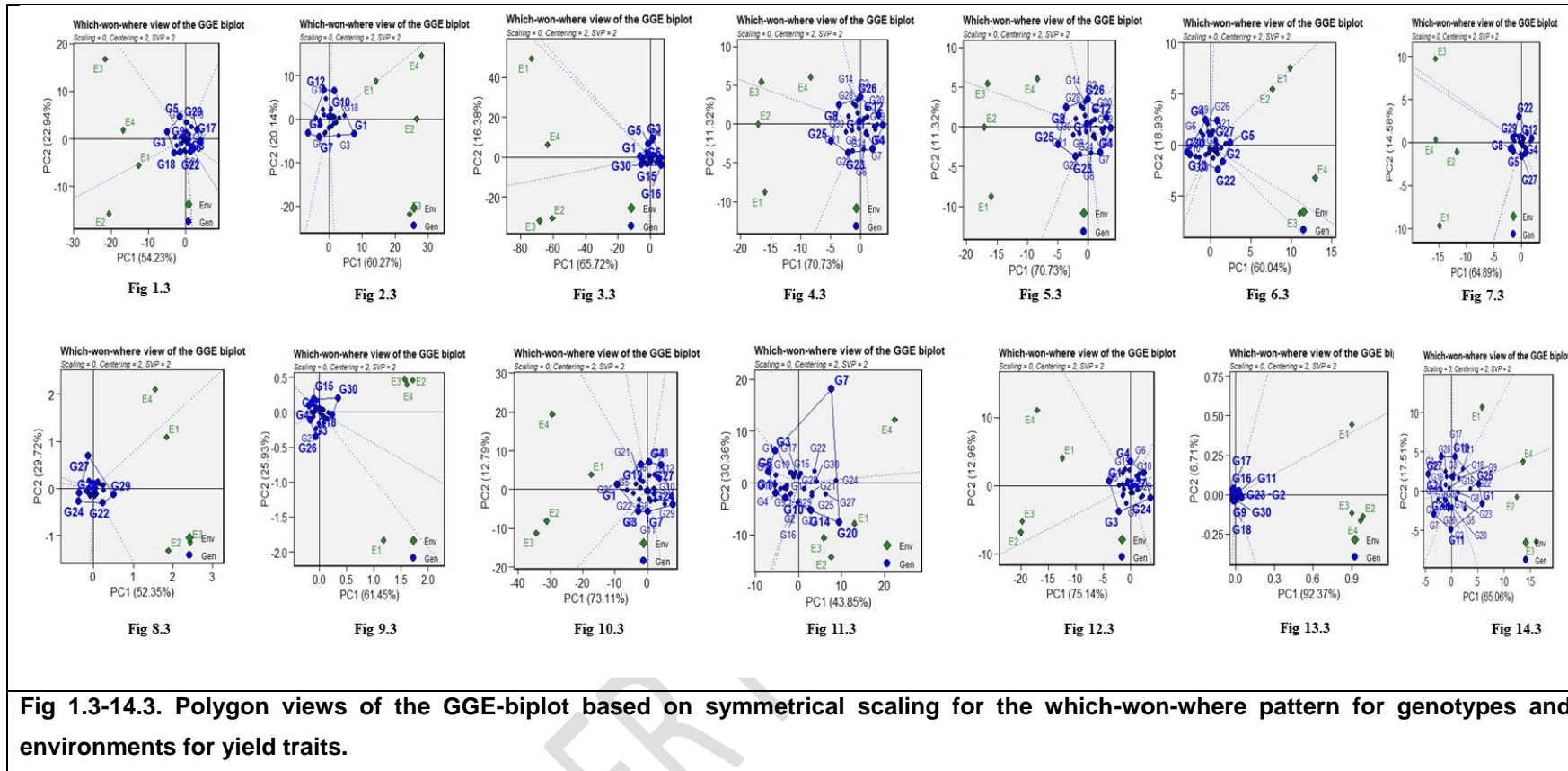
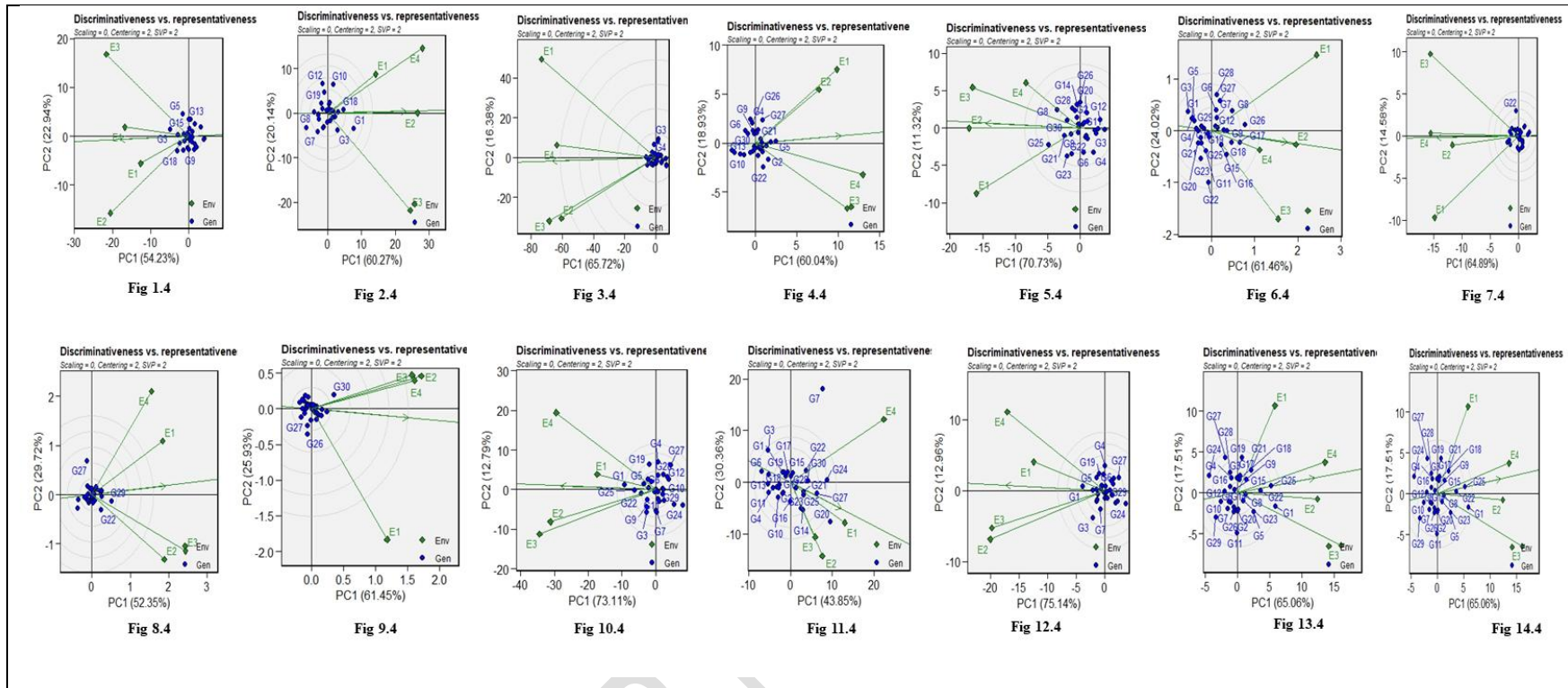


Fig 1.3-14.3. Polygon views of the GGE-biplot based on symmetrical scaling for the which-won-where pattern for genotypes and environments for yield traits.



**Fig 1.4-14.4. The GGE biplot 'Discriminativens vs. Representativens' pattern for genotype comparison with ideal genotype showing G+GxE interaction effect of 30 foxtail millet genotypes under four environments for yield traits.**

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