Stability and Genetic Diversity Analyses in Foxtail Millet [*Setaria italica* (L.) P. Beauv.] Genotypes

Thesis

Submitted to

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In partial fulfilment of requirements for the degree

of

DOCTOR OF PHILOSOPHY

in

Genetics and Plant Breeding

by

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DECLARATION

I, Mr. **DATTI PURUSHOTAMA RAO** hereby declare that the subject matter of this thesis is the record of work done by me, that the contents of this thesis did not form the basis of the award of any previous degree to me or to the best of my knowledge to anybody else, and that the thesis has not been submitted by me for any research degree to any other university/institute.

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CERTIFICATE – I

This is to certify that the Thesis entitled "**Stability and Genetic Diversity Analyses in Foxtail Millet [*Setaria italica* (L.) P. Beauv.] Genotypes**" submitted to Nagaland University in partial fulfilment of the requirements for the degree of Doctor of philosophy in the discipline of Genetics and Plant Breeding is a record of research work carried out by Mr. Datti Purushotama Rao, Registration No. PhD/GPB/00459 under my personal supervision and guidance.

The results of the investigation reported in the thesis have not been submitted for any other degree or diploma. The assistance of all kinds received by the student has been duly acknowledged.

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This is to certify that the thesis entitled "**Stability and Genetic Diversity Analyses in Foxtail Millet [*Setaria italica* (L.) P. Beauv.] Genotypes**" submitted by Mr. Datti Purushotama Rao, Admission No. Ph-319/20, Registration No. PhD/GPB/00459 to the NAGALAND UNIVERSITY in partial fulfilment of the requirements for the award of degree of Doctor of Philosophy in Genetics and Plant Breeding has been examined by the Advisory Board and External examiner on …….....

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Place: Medziphema

Date: *(Datti Purushotama Rao)*

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LIST OF ABBREVIATIONS

%	: Percent
&	: And
/	: Per
@	: At the rate of
α	: Alpha
a.m.s.l.	: Above mean sea level
oC	: Degree celsius
oE	: Degree east
oN	: Degree north
AEA	: Average Environment Axis
AMMI	: Additive Main Effect and Multiplicative Interaction
ANNOVA	: Analysis of Variance
CD	: Critical Difference
cm	: Centimetre
CV	: Coefficient of variation
GGE	: Genotype and Genotype by Environment interaction
GE	: Genotype × Environment interaction
G × E	: Genotype × Environment Interaction
GEI	: Genotype × Environment Interaction
et al.	: Et alii (and others)
etc.	: Et cetera
Fig.	: Figure(s)
g	: Gram
ha	: Hectare
i.e.	: Id est (that is)

kg	: Kilo gram
L.	: Linnaeus
m	: Meter(s)
MET	: Multi Environment Trial
mm	: Millimetre
MS	: Mean Sum of Square
p	: Page(s)
IPCA	: Interaction Principal Component Axis
PC	: Principal Component
PCA	: Principal Component Analysis
SVD	: Singular Value Decomposition
SREG	: Site Regression
q	: Quintal
t	: Tonnes
viz.	: Namely

ABSTRACT

Foxtail millet cultivation in India's NEH 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 multivariate stability model analysis. In this study, 30 genotypes were evaluated at the Research Farm of the SAS, Nagaland University, Medziphema, India. The experiment was conducted during July 2022 to May 2023 involving four different environments. Two environments were rainfed and two were irrigated with weekly intervals. The experiment was conducted in randomized complete block design (RCBD) with three replications in all environments.

Analysis of variance (ANOVA) indicated statistically significant differences (at 5%) among the 30 genotypes for all yield variables evaluated. Genotype G1 exhibited superior performance for both yield and yield-related traits. The present study revealed substantial genetic variation for yield and yield-related traits, with high heritability for all traits except harvest index. Heritability estimates indicated high genetic potential for traits such as FY, PL, BY, FW, PDL, PW, and GY. A strong correlation was observed between grain yield per plant and several traits, including days to 50% flowering, days to maturity, plant height, panicle length, flag leaf length, peduncle length, biological yield, and fodder yield per plant. This correlation was consistent at both the genotypic and phenotypic levels. Biological yield exhibited the strongest direct influence on grain yield per plant, followed by harvest index, flag leaf width, and number of base tillers on genotypic and phenotypic levels.

D^2 analysis confirmed high genetic diversity among the genotypes. They were grouped into five clusters in the pooled environmental combination. All environments were considered together, Cluster-I remained the largest with 26 genotypes. The foxtail

millet genotypes exhibited a wide range of intra-cluster distances in each environment. In the pooled environmental analysis, Cluster-I had the highest intra-cluster distance (8.13) with 26 genotypes. Pooled environmental analysis showed clusters III and V with the highest inter-cluster distance. Mahalanobis' D^2 Statistics revealed the percentage contribution to genetic diversity in different environments. Test weight dominated in the pooled environmental analysis (22.30%). These findings highlight the genetic diversity and variability of foxtail millet genotypes across environments, offering valuable information for future breeding and improvement programs.

The AMMI analysis yielded highly significant results ($P<0.05$) for genotypes, environments, and their interactions, indicating that genotypes respond differently across various environments. In the AMMI biplot-1, specific genotypes were highlighted for different traits. For instance, genotypes G14, G23, G16, and G9 were notable for DF, while G23 and G28 stood out for PH. Similarly, G18 and G30 displayed significance for PL, and G18, G16, and G25 were significant for NT. Additionally, genotypes G13, G17, and G18 were prominent for FY, while G8, G9, G21, and G22 were notable for GY. Importantly, these genotypes exhibited nearly zero scores on the first PCA1 axis, suggesting minimal environmental influence and performance above average mean values. The first two principal components of the AMMI 2 biplot model explained a significant portion of the variation in G+G×E interaction for DF (83.7%), PH (81.1%), PL (77.7%), NT (89.1%), FY (86.9%), and GY (83.2%). In the AMMI Biplot-2, all environments (E1, E2, E3, and E4) are linked to the origin. Among these environments, for DF, PL, FY, and GY (E2 and E3), PH (E4 and E2), and NT (E3 and E2), we saw short lines indicating weaker interactions. In contrast, for DF, PL, FY, and GY (E1 and E4), PH (E1 and E3), and NT (E4 and E1), we observed long lines, indicating stronger interactions.

In this study among four GGE biplots of GY, Discriminativeness and representativeness revealed E4 as the most representative environment. At the same time, E3 also stand 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 performed well.

Present study, mean yield against the weighted average of absolute scores (WAAS) analysis was used to identify stably high-performing genotypes for several important yield traits. The study revealed that the following genotypes were stably high-performing for DF; G1 and G4, for PH; G1 and G28, for PL; G8, G21, and G30, for FL; G5 and G14, for FY; G25 and G18, and for GY; G25, G22, and G21. The likelihood ratio test revealed significant genotypic and genotype-by-environment interaction (GEI) effects for all traits under study. Based on BLUPs, G1 and G25 were identified as suitable genotypes for FY and GY due to their high mean values. However, in terms of DF; G3 and G18, PH; G1 and G30, PL; G25 and G28, FL; G5 and G28 obtained high mean values of the BLUP. Based on the multi-trait stability index, G30, G17, G21, and G8 were the most ideal genotypes. Ward's minimum variance technique revealed the categorization of 30 genotypes into four distinct responsive clusters.

Key words: Foxtail millet, genetic variability, heritability, correlation, path coefficient analysis, Genetic diversity, D^2 analysis, Tocher method, Cluster analysis, AMMI, BLUP’s, GGE Biplots, MTSI, MGIDI, IPCA, WAAS biplot and Ward's minimum variance technique.

CHAPTER-I

INTRODUCTION

INTRODUCTION

Millets have gained significant attention in recent years as a crucial field of study, captivating researchers and scientists worldwide (Delmer, 2005). Despite their unassuming appearance, these powerful nutri-cereals offer numerous compelling reasons that make them worthy of investigation. What distinguishes millets is their remarkable resilience, thriving in challenging conditions, especially in arid and semi-arid regions of Asia and Africa (Singh and Sood, 2020). Endowed with the ability to withstand scorching heat and flourish in problematic soils, millets exemplify nature's enduring spirit and the incredible adaptability of the human spirit.

Some of the popular types of millets include sorghum (*Sorghum bicolor*), pearl millet (*Pennisetum glaucum*), finger millet (*Elucine coracana*), proso millet (*Panicum miliaceum*), kodo millet (*Paspalum scorbiculatum*), barnyard millet (*Echinochloa esculenta*), foxtail millet (*Setaria italica*) and other millets (Dwivedi *et al*. 2012). Millets are not just ordinary crops; they are a farmer's dream come true. These versatile grains offer multiple income streams to farmers, as they can be used for a myriad of purposes such as food, fodder, biofuels, and even sugar production (Upadhyaya *et al.* 2016). With their unique ability to thrive without irrigation, millets are a symbol of hope for farmers in drought-prone regions (Vetriventhan *et al.* 2016). And if that wasn't impressive enough, these tiny grains are also incredibly adaptable to high-temperature climates and problematic soils, making them an ideal solution for sustainable agriculture. Millets, with their remarkable qualities, have emerged as a crucial player in climate-resilient solutions and a key contributor to the sustainable food supply chain (Serna-Saldivar, 2016). Truly, millets are a treasure trove of possibilities, waiting to be discovered and harnessed for the greater good of all. Exploring their genetic diversity,

agronomic practices, nutritional profiles, and potential applications can unlock a treasure trove of possibilities. By delving deeper into millet research, we can uncover innovative strategies for sustainable farming, climate adaptation, and enhancing the nutritional well-being of communities worldwide.

By 2030, according to CGIAR, the world's population is projected to reach a staggering 8.5 billion, and this number is expected to soar to 9.7 billion by 2050. In the face of this imminent challenge, exacerbated by climate change and escalating environmental stress, the need for a solution to feed the ever-growing population has become dire (Mrabet, 2023). However, the answer lies in crop diversification, and millets emerge as a promising remedy. These resilient grains hold the key to sustainable agriculture, offering a pathway to break free from the cycle of monocropping while reducing our dependence on petrochemical fertilizers and pesticides. Embracing millets paves the way for a greener and healthier future, not just for us but also for the generations yet to come (Mrabet, 2023).

Foxtail millet, a wonder crop with a rich history, has been a staple food in various parts of the world for centuries (Chandra *et al.* 2021). However, its versatility extends far beyond that. Across South and North America, China, India, and Japan, it is widely cultivated not only for its nutritional value but also for silage and hay purposes, making it a highly esteemed and widely grown crop (Lata *et al*. 2013). In fact, foxtail millet holds the distinction of being the second most cultivated crop globally after pearl millet (Ceasar *et al*. 2014). What adds to its remarkable legacy is the fact that foxtail millet is one of the oldest crops known to mankind. Its origins can be traced back around 7,400 to 7,900 years ago in the Yellow River Valley of northern China (Barton, 2009). This discovery is substantiated by the earliest archaeo-botanical macro remnants found in the region, shedding light on the significant role this humble grain has played in shaping our history. Even today, foxtail

millet continues to be a vital source of nourishment for people across the globe. Its enduring presence and nutritional value make it a crop of immense importance, demonstrating its continued significance in our lives (Hazareesingh, 2021). It is truly fascinating to contemplate the enduring impact of this unassuming grain and its ability to sustain and nourish diverse cultures throughout time.

The captivating realm of foxtail millet unfolds with its classification within the *Poaceae* family, subfamily *Panicoideae*, and the genus *Setaria*. Within this genus, *Setaria* 125 species are found, dispersed across the globe (Dyer, 2022). Among them, two species stand out as the most extensively cultivated, *S. italica* and *S. viridis*, commonly known as green foxtail. Green foxtail bears an AA genome, characterized by 2n = 2x = 18 chromosomes (Willweber-Kishimoto, 1962). Intriguingly, there are also weedy species, *Setaria faberii* and *Setaria verticillata*, which possess an AABB genome resulting from a natural cross between *S. viridis* and *Setaria adhaerans*. Another diploid species, *Setaria grisebachii*, harboring a CC genome, originates from Mexico (Muthamilarasan and Prasad, 2015). It is noteworthy to mention the distinctive autotetraploid (AAAA) species, *Setaria queenslandica*, which stands as the sole representative within the *Setaria* genus. However, it is important to acknowledge that other polyploid species, such as *Setaria pumila* and *Setaria pallide-fusca*, do not possess the AA genome. The remarkable diversity present within the *Setaria* genus serves as a testament to the remarkable evolutionary journey of plants throughout history (Prasad *et al*. 2017).

Introducing the hardy and resilient foxtail millet, a crop capable of thriving in challenging and arid environments characterized by low rainfall and poor soil conditions. This remarkable crop boasts a relatively short growing season, maturing within just 90-100 days from the time of planting. The

mature foxtail millet plant stands tall, reaching heights of 120-200 cm. Its slender and upright stems, adorned with soft and hairless leaves, contribute to its elegance and resilience (Vetriventhan *et al*. 2020). At the pinnacle of the plant, a spike-like panicle emerges, showcasing its unique beauty. This inflorescence carries 6-12 two-flowered sub-sessile spikelets, each delicately subtended by 1-3 bristles. Within the tightly enclosed ovary, two long styles culminate in a plumose stigma, cradling the precious fruit *caryopsis*. This fruit is encompassed by lemma and palea, completing the intricate structure (Prasad *et al*. 2017).

The foxtail millet stands as a truly remarkable crop, endowed with a unique set of traits that render it an ideal crop for cultivation in challenging environments. Notably, its possession of the C4 photosynthetic pathway sets it apart, enabling efficient utilization of water and nitrogen resources (Muthamilarasan *et al.* 2014). Moreover, the crop's deep root system, small leaf area, and thickened cell walls contribute to its exceptional tolerance to abiotic stressors, including drought and extreme temperatures. However, the extraordinary attributes of foxtail millet do not end there. Its impressive water efficiency further distinguishes it from other cereals such as rice, wheat, and maize (Prasad *et al*. 2017). This remarkable efficiency extends to biomass production as well, with a mere 257 g of water needed to produce 1 g of dry biomass. In comparison, wheat and maize demand 470 g and 510 g of water, respectively, for the same purpose. These remarkable water-saving capabilities make foxtail millet an increasingly compelling choice as a climate-resilient crop, deserving attention for future breeding efforts (Prasad *et al*. 2017).

Foxtail millet is a nutrient-dense cereal crop, rich in essential vitamins (Vit A: 32 mg/100g, Vit E: 31 mg/100g), minerals, and antioxidants. With 8-10% protein, high fiber content, and abundant B vitamins like niacin (0.85mg/100g), thiamin (0.59 mg/100g), and vitamin B6 (0.76 mg/100g), it

offers a wholesome nutritional profile (Sharma and Niranjan 2018 and Hariprasanna, 2023). Additionally, it contains minerals such as iron (2.8 mg/100g), magnesium (81 mg/100g), Zink (2.4 mg/100g), and manganese (0.6 mg/100g) while being low in fat (4-5%). Including foxtail millet as part of a balanced diet can provide numerous health benefits, thanks to its nutritional composition and the presence of beneficial phytochemicals (Amadou *et al.* 2013 and Hariprasanna, 2023).

Foxtail millet is an important crop grown in several parts of the world. According to the Food and Agriculture Organization (FAO) of the United Nations, the global production of foxtail millet was estimated to be around 10.4 million tons in 2020, with India being the largest producer, accounting for more than 50% of the total production (Chand and Thapak, 2023). Apart from India, foxtail millet is also grown in several other countries including China, Nepal, Nigeria, Sudan, and the United States. In China, foxtail millet is one of the most important cereal crops, grown in several provinces including Hebei, Henan, Shanxi, Shaanxi, and Inner Mongolia. In the United States, foxtail millet is mainly grown for forage and birdseed, with production concentrated in the Great Plains region (Chand and Thapak, 2023).

The productivity of foxtail millet varies widely among different countries and regions. In India, the average yield of foxtail millet is around 1.2 tons per hectare, which is lower than the average yield of other major cereals such as rice and wheat (Laxmi *et al.* 2015). In China, the average yield of foxtail millet is around 3.3 tons per hectare, while in the United States, the yield is around 2.2 tons per hectare (Zhang *et al*. 2018). In some African countries such as Nigeria and Sudan, the productivity of foxtail millet is still low, mainly due to the lack of modern agricultural practices and infrastructure (Das *et al*. 2016). Overall, foxtail millet is an important crop with significant potential to contribute to global food security, particularly in regions with

marginal soils and low rainfall. However, there is still a need to improve its productivity and make it more resilient to climate change and other challenges.

The International Year of Millets 2023 is a United Nations initiative to raise awareness about the importance of millets as a nutritious and sustainable food source, and to promote their cultivation, consumption and trade (Nesari,2023). The year 2023 has been declared as the International Year of Millets to highlight the role of millets in food and nutritional security, and to contribute to the achievement of the Sustainable Development Goals (Kennedy *et al*. 2022). The goals of the International Year of Millets 2023 are to promote the cultivation and consumption of millets, to improve their value chain, and to enhance the livelihoods of smallholder farmers who grow them. The year 2023 will be a platform to share knowledge, best practices, and innovations in millet farming, processing, marketing, and consumption (Sahoo and Mahapatra 2023).

Foxtail millet is a popular and ancient cereal crop that has been cultivated in India for thousands of years. It is known by several different names in different regions of India, reflecting its cultural significance and diverse culinary uses. In the southern Indian states of Tamil Nadu, Andhra Pradesh, and Karnataka, foxtail millet is commonly called "thinai" or "navane". In the northern state of Haryana, it is known as "kangni" or "rala", while in the western state of Maharashtra, it is called "kang" or "rala". Other regional names for foxtail millet in India include "kakum" in Gujarat, "kora" in Odisha, and "chama" in Kerala. Regardless of its name, foxtail millet is a versatile and nutritious grain that has played an important role in Indian cuisine for generations (Morrison, 2016).

According to the data from the Ministry of Agriculture and Farmers' Welfare, the production of foxtail millet in India has been steadily increasing over the years. In 2019-20, the country produced 1.84 million metric tons of

foxtail millet, which is a significant increase from the 1.43 million metric tons produced in 2015-16 (Hariprasanna, 2023). The productivity of foxtail millet in India isalso improving, with the average yield increasing from 640 kg per hectare in 2015-16 to 844 kg per hectare in 2019-20 (Hariprasanna, 2023). The government of India has also been promoting the cultivation of foxtail millet through various initiatives, such as the National Food Security Mission and the Rashtriya Krishi Vikas Yojana. These initiatives provide farmers with financial support and technical assistance to improve the productivity and quality of their crops. In addition, several research institutions and universities are working on developing improved varieties of foxtail millet that are more resistant to pests and diseases, have higher yields, and better nutritional value.

Nestled in the scenic hills of Nagaland, the Chakhesang Naga community has long celebrating the cultural significance of millets, honoring the crop with a vibrant week-long festival each year. However, it was in the sparsely populated district of Phek, where the village of Chizami was chosen as a hub for millet cultivation experimentation in 2009. This decision was made by a group of trailblazing women from the North East Network, who were attending the Convention of Biological Diversity in the city. Since then, the village has become a thriving hotspot for millet cultivation, with its innovative farming techniques and community-driven approach paving the way for a sustainable and prosperous future.

Genetic variability is a term used to describe the natural or human-induced differences in the genetic makeup of individuals within a given population (Kilpinen *et al*. 2017). This concept plays an important role in the field of agriculture, as it offers an opportunity to develop new and improved crop varieties that are more resilient and adaptable to different environmental conditions, pest pressures, and consumer preferences (Borron, 2006). Genetic variability can occur through natural processes such as mutation,

recombination, and genetic drift, or through human intervention, such as selective breeding programs (Eriksson *et al*. 1993). By carefully selecting and crossing individuals with desirable traits, breeders can create new crop varieties with improved agronomic characteristics, such as increased yield, improved resistance to pests and diseases, and enhanced tolerance to environmental stress. This helps to ensure a sustainable supply of high-quality crops to meet the growing demand for food in an ever-changing world.

Estimating and understanding genetic parameters, such as phenotypic variance, genotypic variance, heritability, and genetic advance as a percentage of mean, plays a vital role in foxtail millet breeding across diverse environments, with a focus on yield and yield components. Phenotypic variance allows breeders to assess the overall variability observed in traits related to yield and yield components, providing valuable insights into the trait's response to environmental factors (Hammer *et al.* 2005). Genotypic variance, on the other hand, quantifies the genetic contribution to trait variability, helping breeders identify the extent of genetic control over these traits (Caballero, 2020). Heritability estimation provides an understanding of the proportion of phenotypic variance that can be attributed to genetic factors. High heritability suggests that genetic factors play a significant role in determining the trait, enabling breeders to make more accurate predictions of trait performance in future generations (Schmidt *et al.* 2019). These genetic parameters aid breeders in identifying the most promising individuals with desirable traits for further breeding and selection, facilitating the development of high-yielding and adaptable foxtail millet varieties across various environments.

The role of genotypic and phenotypic correlations in foxtail millet breeding, particularly in multi-environment trials focusing on yield and yield components, is crucial. In multi-environment trials, considering genotypic and

phenotypic correlations aids breeders in identifying stable and adaptable genotypes across different environments (Crossa and Romagosa, 1997). Genotypic correlation measures the strength and direction of the relationship between different traits at the genetic level. It helps breeders understand how traits are genetically linked and how changes in one trait can affect another (Farheen *et al.* 2023). Phenotypic correlation, on the other hand, assesses the relationship between traits based on their observed phenotypic expression. It takes into account both genetic and environmental factors (Salini *et al.* 2010). By studying genotypic and phenotypic correlations, breeders can strategically select and prioritize traits during the breeding process. Positive correlations between yield and yield components help identify traits that can be indirectly improved by selecting for a correlated trait. Conversely, negative correlations can guide breeders to balance trade-offs between traits.

Genotypic and phenotypic path analyses are powerful tools in foxtail millet breeding for multi-environment trials focusing on yield and its components. Genotypic path analysis reveals the direct and indirect genetic effects of traits on yield, guiding trait selection for enhanced productivity (Nithya *et al.* 2020). Phenotypic path analysis assesses the overall effects of traits, considering both genetic and environmental factors, providing a comprehensive understanding of trait relationships. By employing these analyses, breeders can strategically improve yield by targeting traits with significant direct and indirect effects, optimizing genetic gains across diverse environments (Hampannavar *et al.* 2018). These insights facilitate the development of high-yielding foxtail millet varieties adapted to multi-environment conditions, contributing to sustainable agriculture and food production.

Genetic diversity is a crucial aspect of sustainable agriculture, as it encompasses the range of genetic variation within a species, including

differences in individual genes and the frequency of specific genes within a population. In agriculture, genetic diversity plays a significant role in the development of crops that are better suited to various growing conditions, pests, and diseases. By increasing the range of genetic variation in a crop species, breeders can select for specific traits that make the plants more resistant to challenges, leading to increased productivity and stability. Ultimately, genetic diversity is an essential element of sustainable agriculture as it supports farmers and breeders in producing crops that are adapted to local growing conditions, ensuring the long-term health and stability of our food systems.

Stability analysis is a powerful tool in the field of agriculture that helps farmers and researchers to evaluate the performance of crops or varieties across different environments (Osei *et al.* 2018). The main aim of stability analysis is to identify crops or varieties that perform consistently well under varying environmental conditions, and to understand the environmental factors that influence their performance (Chenu, 2015). This allows researchers to make informed decisions about which crops or varieties to use in different locations or under different growing conditions (Taleghani *et al.* 2023). For instance, a stability analysis might be used to determine which varieties of a crop perform best under varying soil types, temperatures, or rainfall conditions. Statistical techniques such as regression analysis, ANOVA, and mixed model analysis are often used in stability analysis to identify the important environmental factors that affect crop performance and quantify their effects (Olivoto *et al.* 2019). Overall, stability analysis is an invaluable tool for improving crop performance and adaptability, and for helping farmers and researchers to make well-informed decisions about crop management and selection.

The AMMI (Additive Main effects and Multiplicative Interaction) model is a statistical method used in crop varietal trials to analyze and interpret the results obtained from multi-environment trials (METs). METs are conducted to evaluate the performance of different crop varieties across multiple environments, such as different locations or growing seasons (Khan *et al*. 2021). The AMMI model combines both the main effects (varietal performance) and the interaction effects (variety-environment interactions) to better understand the variations in crop performance across different environments. It helps to identify which varieties are more stable in their performance across various conditions and which ones are specifically well-suited for particular environments (Ndhlela *et al*. 2014).

The main components of the AMMI model are:

1. Additive Effects: These represent the main effects of crop varieties and environmental factors, indicating how each variety performs on average and how different environments affect crop growth.

2. Multiplicative Interaction Effects: These capture the interactions between the crop varieties and the environments. They help to identify which crop varieties are best suited to specific environmental conditions and which ones are more stable across different environments.

The significance in crop varietal trials lies in understanding the interactions between crop varieties and environments (Mohamed *et al.* 2013). This information is crucial for making informed decisions about which varieties to recommend to farmers based on their specific locations and conditions. By identifying which varieties perform well across a range of environments and which ones are more sensitive to specific conditions, agricultural researchers can recommend the most suitable and stable crop varieties to maximize yield and reduce risks for farmers (Haider *et al.* 2017).

The AMMI model also provides valuable insights into genotype-by-environment interactions, helping plant breeders and agronomists to develop more resilient and adaptable crop varieties that can withstand varying environmental conditions and contribute to food security and sustainable agriculture (Hagos and Abay, 2013).

The GGE biplot model, also known as the Genotype plus Genotype-by-Environment Interaction biplot model, is a statistical tool used in crop variety trials and agricultural research. It is similar to the AMMI model but offers some additional advantages in visualizing genotype-by-environment interactions (Kendal *et al.* 2019). In crop varietal trials, researchers evaluate the performance of different crop varieties across multiple environments to understand how they respond to various conditions. The GGE biplot model helps to analyze and interpret the complex genotype-by-environment interactions in a graphical format.

The significance of the GGE biplot model in crop varietal trials lies in its ability to provide valuable insights and aid in decision-making for crop breeding and selection. Here are some of its key advantages:

1. Visualization of Complex Data: The GGE biplot provides a clear graphical representation of complex data, making it easier to interpret the genotype-by-environment interactions and identify patterns of performance.

2. Selection of Superior Varieties: By considering both average performance and stability across environments, the GGE biplot helps researchers select the most promising and widely adaptable crop varieties.

3. Targeted Breeding Strategies: Understanding the genotype-by-environment interactions allows breeders to target specific

environments with suitable varieties and develop more tailored breeding strategies.

4. Increased Crop Yield and Stability: Selecting stable and high-performing varieties based on GGE biplot analysis can lead to improved crop yield and stability, reducing the risk for farmers and contributing to food security.

Overall, the GGE biplot model is a valuable tool in agricultural research, helping to optimize crop variety selection, enhance breeding efforts, and ultimately improve agricultural productivity and sustainability.

The BLUP (Best Linear Unbiased Prediction) model is a statistical method used in crop varietal trials and agricultural research. It is a type of mixed-effects model that aims to estimate the genetic performance of crop varieties, taking into account both the observed data from the trials and the genetic relationships between the varieties (Harville, 1990).In crop varietal trials, researchers evaluate the performance of different crop varieties across various locations or environments. The BLUP model takes into account both the phenotypic data (actual performance of varieties) and the genetic relatedness among the varieties to estimate their genetic values. It is called "Best Linear Unbiased Prediction" because it provides the best linear unbiased estimates of the genetic values (Piepho, 1994).

The resurgence of millets is like a rising phoenix, not just a revival of a forgotten and underutilized crop, but also a step towards achieving the sustainable development goals (SDGs). By embracing millets, we can make strides towards SDG 2 (zero hunger), SDG 3 (good health and well-being), SDG 12 (sustainable consumption and production), and SDG 13 (climate action). It's like a domino effect, where one small step can create a ripple of positive impact on multiple fronts.

To ensure that this positive change is sustainable, it's crucial to invest in research and development, and provide opportunities for farmers to secure better connectivity with efficient value chains and markets. This is like laying a strong foundation for the growth of the millet movement, ensuring that it can flourish and continue to benefit communities for years to come. By working together towards these goals, we can create a brighter, more sustainable future for all.

The existing research on stability and genetic diversity analyses in foxtail millet genotypes (*Setaria italica*) has laid a foundation, but there are specific research gaps that need to be addressed in the context of the Nagaland region. Firstly, there is a lack of comprehensive studies focusing on the genetic variation specifically among foxtail millet genotypes from Nagaland. Conducting a preliminary screening to assess genetic variation would provide crucial insights into the extent of diversity present in the germplasm, benefiting crop improvement programs and conservation efforts. Furthermore, there is a need for more information on the genetic diversity among selected foxtail millet genotypes in Nagaland. Understanding the genetic diversity within these genotypes is vital for their effective utilization and management. Another research gap is the limited exploration of the genotype × environment interaction. This interaction significantly influences the stability and adaptability of foxtail millet genotypes across diverse agro-climatic conditions. By employing advanced statistical techniques such as AMMI and GGE biplot analysis, researchers can assess stability and identify genotypes that consistently perform well in different environments in Nagaland.

Additionally, there is a lack of studies estimating Best Linear Unbiased Predictors (BLUPs) for foxtail millet genotypes. Estimating BLUPs can help identify superior genotypes that exhibit improved performance across multiple environments, taking into account the genotype × environment interaction.

Selecting stable and high-performing genotypes through BLUP estimation would support the cultivation of suitable varieties in the Nagaland region. Addressing these research gaps by conducting studies on "Stability and Genetic Diversity Analyses in Foxtail Millet [*Setaria italica* (L.) P. Beauv.] Genotypes"will provide valuable insights. These findings will contribute to crop improvement strategies, germplasm conservation, and the adoption of sustainable agriculture practices tailored to the local agro-ecological conditions in Nagaland.

Objectives

1. Preliminary screening of genotypes for genetic variation.
2. To estimate genetic variation and genetic diversity among selected genotypes.
3. To evaluate the genotype × environment interaction using AMMI and GGE biplot for stability of foxtail millet genotypes.
4. To estimate BLUPs for identification of superior genotypes.

CHAPTER-II
REVIEW OF LITERATURE

REVIEW OF LITERATURE

The review of earlier works carried out by various aspects in India and abroad, pertaining to the present investigating is prompted under the following heads.

2.1 Variability, Heritability and Genetic advance

2.2 Correlation coefficient

2.3 Path coefficient analysis

2.4 Genetic divergence

2.5 Stability (AMMI, GGE biplot and BLUPs)

2.1 Variability, Heritability and Genetic advance

Breeding programs require knowledge of genotypic and phenotypic variability in crop species. Phenotypic expression results from genotype-environment interaction, and variation must be partitioned into heritable and non-heritable components to assess true breeding behavior. The efficiency of selection in plant breeding largely depends on the amount of heritable variation. Variability is the most important characteristic of any population, providing greater opportunities for improvement. A plant population with higher variability offers more chances for improvement. Therefore, it is essential to study and utilize existing variability in the population. Johansen (1903) introduced the concept of variability and pure line. Vavilov (1957) confirmed that greater variability increases the chances of obtaining desirable types, proving it to be a fundamental aspect for improving crop plants through selection.

Improvement in any crop species depends upon the amount of variation present in a given population. The variability expressed by a genotype can be partitioned into genotypic and phenotypic components. The genotypic

component being the heritable part of the total variability, its magnitude for yield and its component characters influences the selection strategies to be adopted by the breeders. The efficiency of selection in improving a plant character depends largely on the extent of transmissibility of the character. The presence of high magnitude of variability in the germplasm or breeding materials only indicates the greater possibility of improvement through selection but the existence of high transmissibility is an important pre-requisite for realization of such possibility. The direct selection parameters like heritability in broad sense (Burton and Devane, 1953), genetic advance in percent of mean (Johnson *et al.* 1955) are helpful in assessment of transmissibility of characters and role of environment.

Fisher (1918) portioned the total phenotypic variance into genotypic variance and environmental variance. He further divided the genotypic variance into additive, dominance and epistatic effects. However, it is only the genetic variation, which is heritable. Selection is effective when genetic variation is significant among the individual population. Hence genetic variability is of paramount importance of plant breeder for starting a breeding programme in any crop.

Burton and Devane (1953) suggested that genotypic coefficient of variation together with heritability estimates would give best picture about the extent of advance to be expected by selection. High heritability along with high genetic advance arises due to action of additive gene.

Prasanna *et al.* (2013a) The study assessed genetic variation in 34 Italian millet genotypes during Autumn 2008 and Spring 2009. Grain yield per plant, ear weight, calcium content, and carotene exhibited high phenotypic and genotypic coefficients of variation in both seasons. In Autumn, 1000 grain weight had high PCV and GCV, while the number of productive tillers per plant and straw weight did so in Spring. Straw weight also showed high GCV in Autumn,

indicating broad variability in these traits. Most traits had high heritability and genetic advance, suggesting potential for improvement through simple selection, except for days to 50% flowering, days to maturity, and plant height.

Brunda *et al.* (2014) investigated genetic variability in foxtail millet germplasm during rainy and post-rainy seasons. Significant diversity was found in all studied traits, indicating a diverse genetic pool. Genotypes varied notably in yield-related traits, with tillers per plant showing the highest phenotypic and genotypic coefficients of variation. Other traits like flowering time and panicle length showed moderate variation, while days to maturity and plant height exhibited low variability. Notably, grain yield and its components showed substantial genetic advance and heritability, suggesting potential for improvement through selective breeding.

Selvi *et al.* (2014) In a study of 109 little millet genotypes, high genotypic and phenotypic coefficients of variation were found for several traits, including panicle exertion, single plant dry matter yield, culm branches per plant, flag leaf width, single plant grain yield, and basal tillers per plant. Most traits displayed moderate to high heritability, suggesting genetic control. Traits like panicle exertion, grain yield, dry matter yield, 1000 grain weight, flag leaf width, culm branches, basal tillers, and plant height had high heritability and genetic advance, indicating additive gene action. Selection based on phenotype would be effective for these traits. Flag leaf length and days to flowering showed high heritability but moderate genetic advance.

Kumar *et al.* (2015) carried out field investigation to estimate the genetic variability, heritability and genetic advance in the pearl millet hybrids. The phenotypic coefficient of variation (PCV) was higher than the genotypic coefficient of variation (GCV) in all the characters. The highest GCV associated with high heritability of with good genetic advance was observed for biological yield per plant followed by harvest index. The lowest variability

associated with low heritability and low genetic advance as per cent of mean was observed for plant height. High heritability in association with high genetic advance observed for biological yield per plant and moderate heritability coupled with high genetic advance observed for harvest index. It indicates that most likely the heritable is due to the preponderance of additive gene effects and the potential of selection for these characters to improve yield.

Johar (2015) studied in 34 exotic foxtail millet genotypes and estimated that high heritability and genetic advance, an indicator of additive gene action was noted in all the characters except for days to 50% flowering, days to maturity and plant height reveals the operation of additive gene action in the inheritance of these traits and improvement in these characters is possible through simple selection.

Jyothsna *et al.* (2016) carried out an experiment to estimate the genetic parameters like variability, heritability and genetic advance for eight quantitative characters in 25 genotypes of Finger Millet (*Eluesine Coracana* L. Gaertn). The genotypic coefficients of variation for all the characters studied were lesser than the phenotypic coefficients of variation indicating the interaction of genotypes with environment. High heritability coupled with high genetic advance was observed for grain yield per plot and straw yield per plot indicating the importance of additive gene action in governing the inheritance of these traits. Hence, simple selection is effective to improve the respected trait.

Kavya *et al.* (2017) assessed 40 genotypes of foxtail millet and revealed that high heritability coupled with high genetic advance as percent of mean was observed for number of basal tillers, number of culm branches, panicle exertion, ear length, ear width, 1000 seed weight, seed yield / plant, straw yield / plant and protein content indicating that these traits were predominantly

under the control of additive gene action and hence these characters can be improved by selection.

Amarnath *et al.* (2018) studied on 50 Indian foxtail millet genetic resources to estimate the extent of heritability (broad sense) and genetic advance as per cent of mean for 12 metric traits. High heritability (>60%) coupled with high genetic advance as per cent of mean was registered for culm branches, number of productive tillers / plant and grain yield / plant indicating that these characters were governed by additive gene effects and may be chosen as selection criteria for formulating breeding strategies in foxtail millet.

Ayesha *et al.* (2019) investigated heritability and genetic advance for 13 grain yield and quality components in 50 genotypes of foxtail millet germplasm collections. The traits viz. days to 50% flowering, plant height, panicle length, protein, fat, iron, phosphorus and calcium exhibited high genetic advance as per cent of mean coupled with high estimates of heritability indicating preponderance of additive gene action in governing the inheritance of these traits and hence, direct phenotypic selection may be deployed for improvement of these traits.

Srilatha *et al*. (2020) studied 76 foxtail millet genotypes in 2019-2020 which showed significant genetic variability for yield and quality traits. Genotypes exhibited diversity for most traits. Environmental influence was evident, with higher phenotypic coefficients of variation compared to genotypic coefficients. Traits like plant height, panicle length, productive tillers, SCMR at grain filling, mineral content, protein, and antioxidant activity had moderate PCV and GCV. These traits also displayed high heritability and genetic advance, indicating additive gene action. Direct phenotypic selection is recommended for further foxtail millet breeding.

Karvar *et al*. (2021) studied 52 foxtail millet genotypes in Akola during 2018-19 and 2019-20 which revealed significant genetic variability for yield and quality traits. Genotypes were diverse for most traits, influenced by the environment. High variability was observed in iron (Fe) and zinc (Zn) content, productive tillers, fodder yield, and grain yield. Traits like panicle girth, Fe content, Zn content, fodder yield, and grain yield showed high heritability and genetic advance, indicating an additive gene nature, making them responsive to selection.

Singh *et al*. (2022) characterized 50 genotypes initially and 10 genotypes later, revealing significant variation in both qualitative and quantitative traits. High genetic variation was observed for grain yields, panicle lengths, and organic outcomes. Plant height and leaf length had high phenotypic variation, while leaf length and days to 50% flowering had low variation. Panicle weight, test weight, and straw weight showed a strong positive correlation with grain yield per plant in both seasons, facilitating indirect selection. The variability in foxtail millet germplasm enables effective genetic improvement through selective breeding.

Toppo *et al.* (2023) studied 20 foxtail millet genotypes to assess variability and identify diverse parents for various traits during the 2021 *kharif* season. Twelve quantitative traits were examined, with high genetic and phenotypic coefficients of variation observed for test weight, flag leaf length, tillers per plant, grain yield per plant, productive tillers per plant, flag leaf width, and peduncle length. Traits like test weight, tillers per plant, flag leaf length, grain yield per plant, and others displayed high heritability and genetic advance, indicating potential for improvement through selection.

Sintia *et al*. (2023) studied F2 foxtail millet population derived from ICERI-5 and Botok-10 cross to assess genetic variability and predict selection response. The F2 population displayed shorter plant height and earlier flowering

compared to Botok-10 and higher grain weight per plant compared to ICERI-5. Plant height, flowering time, and grain weight per plant showed moderate to high genetic variation and broad-sense heritability. Using a weighted selection index for three target traits, ten F2 individuals were identified with higher selection indices compared to both parents, with I5B10-4-96 having the highest selection index. This suggests an expected decrease in flowering time and an increase in grain weight per plant in the next generation.

2.2 Correlation coefficient

Correlation coefficient is a statistical measure which is used to find out the degree (strength) and direction of relationship between two or more variables. The study of association between different characters may help the plant breeder to know how the improvement of one character will bring simultaneous changes in other characters. Character association studies indicate the magnitude of association between pairs of characters and are useful for selecting genotypes with desirable combination of characters thereby aiding in the improvement of the concerned trait. Yield is complex characters govern by polygenes and depend upon number of yield components. Knowledge about association of yield with each other component will be useful in its improvement. If the number of characters is more, it is essential to measure their contribution with the observed character. Correlation studies form the basis for determining selection index there by helping the plant breeder for crop improvement. Literature reviewed on the scientific studies made by several workers on correlation in foxtail millet is summarized below.

Prasanna *et al*. (2013a) analyzed 13 characters in 18 Indian genotypes of Italian millet through correlation analysis. The study revealed that positive significant correlation of days to 50% flowering, plant height, number of productive tillers per plant, flag leaf area, ear length, ear weight, straw weight

and protein content with grain yield per plant and improvement of seed yield may be possible if the above traits are considered in the selection programme.

Prasanna *et al.* (2013b) analyzed 13 characters in 34 exotic genotypes of Italian millet through correlation analysis. The analysis revealed that positive significant correlation of days to 50% flowering, plant height, days to maturity, number of productive tillers per plant, ear length, ear weight and straw weight with yield per plant where as during rabi besides these characters flag leaf area and 1000 grain weight were also observed to influence yield.

Shinde *et al.* (2014) carried out correlation analysis in 41 finger millet genotypes for 12 characters and observed that grain yield per plant was positively and significantly correlated with productive tillers per plant, plant height, finger length and number of fingers/main ear head both at genotypic and phenotypic levels. These traits could be considered for grain yield selection.

Ulaganathan and Nirmalakumari (2014) studied on correlation analysis in 305 finger millet genotypes for 13 quantitative traits and noticed that phenotypic correlation between grain yield per plant was highly significant and positively associated with days to flowering, productive tillers per plant, plant height, 1000-grain weight, flag leaf sheath length, days to maturity, flag leaf blade length and finger width. These traits could be considered for grain yield selection.

Bastola *et al.* (2015) analyzed 50 finger millet landraces by correlation analysis. It was noted that grain yield per plant was positive and highly significant correlated with grain yield per ear followed by plant height, productive tillers number, days to maturity, days to heading, days to flowering, straw yield per plant, finger number per ear, thousand kernel weight, flag leaf

sheath width and finger length. These traits could be considered for grain yield selection.

Brunda *et al*. (2015a) studied correlation analysis in 78 foxtail millet genotypes for 10 characters during rainy season and summer season in 2013 and 2014. The study indicated that direct selection based on the traits, days to maturity, plant height, number of tillers, panicle length, panicle weight, test weight and straw weight during rainy season where as in post-rainy season days to maturity, panicle length, panicle breadth, panicle weight and straw weight are effective as the association and direct effects were positive for these traits with grain yield.

Jadhav *et al*. (2015) performed correlation analysis in 40 finger millet genotypes for 11 quantitative characters and noted that the 1000-seed weight, number of fingers per ear, ear weight per plant, finger length, days to maturity, productive tillers per plant, days to 50% flowering and plant height possessed significant positive association with seed yield plant both at genotypic and phenotypic levels. These characters could be considered for grain yield selection.

Ashok *et al*. (2016) analyzed five characters in 13 foxtail millet genotypes through correlation analysis. The analysis revealed that plant height and number of tillers per plant showed significant positive correlation grain yield per plot at both phenotypic and genotypic levels.

Jyothsna *et al.* (2016b) studied correlation in 24 barnyard millet genotypes for five quantitative characters and reported that the traits number of productive tillers per plant, days to 50% flowering, days to maturity were found to possess significant association in desirable direction with grain yield per plot at both genotypic and phenotypic levels. Hence, selecting these characters with high positive correlation would improve the grain yield.

Nandini *et al.* (2016) carried out correlation analysis for seven quantitative traits in 542 F3 progeny lines developed from cross JK 8 x Peddasame (Purple late) of little millet and noted that grain yield per plant possessed significant positive correlation with plant height, panicle length, number of productive tillers per plant and 1000 seed weight indicating that improvement in these characters will lead to improvement in yield.

Sapkota *et al*. (2016) performed correlation analysis in 10 foxtail millet accessions for 15 characters. The results revealed that grain yield was positively influenced by the traits like peduncle exertion, panicle length, peduncle length, flag leaf length, stay green period, five panicle weight and number of panicle per square meter. Hence, selecting these characters with high positive correlation would improve the grain yield.

Shingane *et al*. (2017) analyzed 44 foxtail millet genotypes through correlation analysis. The analysis revealed that grain yield plant was highly significant and positively correlated with number of productive tillers plant, panicle length, number of panicles plant, 1000-grain weight, straw yield plant and protein content. The selection in positive direction for these traits with grain yield plant can be practiced for genetic enhancement of grain yield.

Arya *et al*. (2017) performed correlation analysis in 35 diverse barnyard millet genotypes including three checks for 13 quantitative traits and found that biological yield per plant, number of fingers per ear, number of leaves on main tiller and 1000 seed weight exerted a very strong positive association towards grain yield per plant at phenotypic and genotypic levels. This suggests selecting for the characters with high positive correlation would improve the grain yield.

Kumari *et al*. (2017) conducted character association studies in 139 finger millet accessions for 14 quantitative characters and reported that the grain

yield was positive and significantly correlated with number of productive tillers, weight of 20 mature ears, threshing ratio and panicle exertion. Hence, selecting these characters with high positive correlation would improve the grain yield.

Amarnath *et al.* (2018b) studied character association in 50 foxtail millet genetic resources for 12 quantitative characters. The study revealed positively significant association of grain yield / plant with majority of traits viz. plant height, peduncle length, panicle length, flag leaf blade length, flag leaf blade width and 1000 grain weight at both phenotypic and genotypic levels implying that these traits are predominantly governed by additive gene action and hence direct selection for these traits will lead to simultaneous improvement in grain yield.

Anuradha *et al.* (2018) analyzed 13 characters in 130 pearl millet lines through correlation analysis. The analysis indicates that grain yield showed significant positive correlation (phenotypic) with Fe, Zn, Cu and Mn content but, genotypically the grain yield was correlated with Fe content only indicating the role of environment for association of Zn, Cu and Mn content with grain yield.

Sapkal *et al*. (2019) performed correlation Analysis for 11 characters in 40 finger millet germplasm and reported that grain yield per plant was positively and significantly correlated with number of tillers per plant, number of productive tillers per plant, main earhead length, number of fingers per plant. Therefore, direct selection for these traits will lead to simultaneous improvement in grain yield.

Nagar *et al*. (2020) studied character association and Path coefficient analysis for grain yield and its influencing traits in little millet (*Panicum sumatrense*) to estimate genetic variability, character association, path analysis and genetic divergence. Grain yield/plant showed highly significant and positive

phenotypic correlation with harvest index, length of inflorescence, biological yield/plant and peduncle length. Path coefficient analysis indicated that the maximum positive direct effect on grain yield/plant followed by biological yield/plant, days to 50% flowering, length of inflorescence, peduncle length, tillers/plant and 1000 grain weight.

Patil *et al*. (2021) studied correlation coefficients among grain yield and yield contributing characters in 14 parental lines (4 lines and 10 testers) and their 40 hybrids of pearl millet. Positive and significant correlations were observed for 1000 seed weight followed by fodder yield per plant, harvest index, earhead girth, number of effective tillers per plant, earhead length and plant height while, negative association with days to 50% flowering at both genotypic and phenotypic level with grain yield per plant. Based on correlations analysis, it is concluded that the selection for these characters would help improve the yield potential of pearl millet.

Rani *et al.* (2022) studied genetic variability for dry fodder yield and its attributing traits using 30 inbred lines in pearl millet at ICAR-AICRP on Pearl Millet, Project Coordinating Unit, Mandor-Jodhpur. Correlation study revealed a positive and significant association of dry fodder yield with green fodder yield per plant, grain yield per plant, days to 50% flowering, days to maturity, plant height and stem girth at both phenotypic and genotypic level, while leaf area at genotypic level. Hence, these traits are more helpful in boosting the dry fodder yield performance of inbred lines.

Dalsaniya *et al.* (2023) studied 49 kodo millet genotypes during the 2021 *kharif* season for 19 quantitative traits. Genotypic (rg) and phenotypic (rp) correlation coefficients were calculated, followed by path coefficient analysis. The results suggest that direct selection based on harvest index and fodder yield per plant could significantly enhance grain yield, as these traits displayed the strongest positive association and maximum direct effect on grain yield per

plant. Crude protein content (%) and plant height were identified as vital characters for indirect selection.

2.3 Path coefficient analysis

Path coefficient analysis is an important tool for partitioning the correlation coefficient in to direct and indirect effects of an independent variable and dependent variable. Though correlation gives information about the component traits associated with the characters, they could not provide an exact picture of relative importance of the direct and indirect contribution of the component character. Thus, correlation in combination with path analysis would give a better insight in to the cause-and-effect relationship between different pairs of characters. Path coefficient analysis is a standardized partial regression coefficient, which splits the correlation coefficient into measure of direct and indirect effect and also measures the direct and indirect contribution of various independent variables on the dependent variable. The direct and indirect effects of various yield components on single plant yield were presented here under.

Prasanna *et al.* (2013a) analyzed 13 characters in 18 Indian genotypes of Italian millet through path analysis. The path analysis study in Indian genotypes indicated that direct selection based on the characters, number of productive tillers per plant and ear weight during kharif where as in rabi days to maturity and ear weight are effective as their association and direct effects were positive.

Prasanna *et al.* (2013b) analyzed 13 characters in 34 exotic genotypes of Italian millet through path analysis. The study of exotic genotypes indicated that direct selection based on the characters, number productive tillers per plant during kharif where as in rabi ear weight and straw weight are effective as the association and direct effects were positive for these traits.

Brunda *et al*. (2015a) studied path analysis in 78 foxtail genotypes for 10 characters during rainy season and summer season in 2013 and 2014. The analysis revealed that direct selection based on the characters, panicle weight, test weight and straw weight showed high and positive effect on grain yield per plant in both rainy and summer season indicating the true relationship between these characters with grain yield per plant, which helps in direct selection for these traits thus in improving the grain yield per plant.

Jadhav *et al.* (2015) performed path analysis in 40 finger millet genotypes for 11 quantitative characters and showed that 1000-seed weight, number of fingers per ear, days to maturity, ear weight per plant, finger length and days to 50% flowering exhibited true relationship with seed yield per plant through positive and high direct effect.

Ashok *et al*. (2016) analyzed five characters in 13 foxtail millet genotypes through path analysis. The studies revealed that plant height, number of tillers per plant and days to 50% flowering showed true relationship by establishing positive association and positive direct effect on grain yield per plant both at genotypic and phenotypic levels.

Jyothsna *et al.* (2016a) carried out path analysis in 25 finger millet genotypes for eight quantitative characters. The results revealed that plant height and main ear length showed true relationship by establishing positive association and direct effect on grain yield per plant both at genotypic and phenotypic levels and number of productive tillers per plant, days to 50% flowering and number of fingers per ear at genotypic level and days to maturity at phenotypic level.

Eric *et al.* (2016) conducted path co-efficient analysis for 19 quantitative traits in 340 finger millet landraces collected from various places and 80 global minicore accessions from ICRISAT Gene bank in India. The results inferred

that productive tiller per plant, 1000 grain mass, grains per spikelet and threshing per cent had positive, direct effects on grain yield. Hence, these traits could be used as a suitable selection criterion for evolving high yielding genotypes.

Nandini *et al*. (2016) performed path analysis for nine characters in 542 F3 progeny lines developed from cross JK 8 x Peddasame (purple late) of little millet. The findings showed that number of productive tillers per plant imparted direct effect on grain yield followed by panicle length, 1000 seed weight and plant height. Hence, these characters used as a suitable selection criterion for evolving high yielding genotypes.

Shingane *et al.* (2017) analyzed 44 foxtail millet genotypes through path analysis. The analysis revealed that 1000-grain weight had the highest positive direct effects on grain yield plant. The indirect effect of number of panicles, panicle length, number of productive tillers and straw yield through 1000-grain weight was positive and moderate to high indicating the direct selection for 1000-grain weight in foxtail millet will lead to simultaneous indirect selection of these traits for increased grain yield plant.

Arya *et al.* (2017) carried out path analysis in 35 diverse genotypes of barnyard millet for 14 quantitative traits. The results revealed that maximum positive direct effect on grain yield per plant was imposed by biological yield per plant and harvest index at genotypic and phenotypic level. Hence, direct selection of these traits would be effective in enhancing the grain yield.

Kavya *et al*. (2017c) evaluated 40 genotypes of foxtail millet for 15 characters to measure path coefficients. The path analysis revealed that number of basal tillers, number of culm branches, ear length, ear width and straw yield/plant are the most important characters which could be used as selection criteria for effective improvement of grain yield. these characters can be used as most

important traits which should be used as selection criteria to develop high yielding cultivars in Italian millet.

Amarnath *et al.* (2018b) performed path coefficient analysis in 50 foxtail millet genetic resources for 12 quantitative characters. The results showed that the traits, plant height and flag leaf blade length exhibited high positive direct effect on grain yield / plant suggesting the importance of direct selection for these traits in attaining higher grain yields.

Vishnuprabha and Vanniarajan (2018) carried out path analysis in 25 genotypes comprising of five parents and their 20 F1 crosses of barnyard millet for five characters. Total phenols and iron content recorded moderate positive direct effects on single plant yield while total anti-oxidant and zinc content showed negative direct effects on single plant yield. Hence, improvement of yield will simultaneously bring improvement on total phenols and iron content directly and on total anti-oxidant activity and zinc content indirectly.

Ayesha *et al*. (2019c) analyzed path analysis in 50 genotypes of foxtail millet for 13 characters. The analysis studies revealed that panicle length, number of productive tillers per plant, test weight and carbohydrate had true relationship with grain yield per plant by establishing significant positive association and positive direct effect at phenotypic level.

Chavan *et al*. (2020) studied correlation and path analysis in finger millet during *Kharif*-2017 on 13 genotypes and 2 checks. Harvest index (%) was found to be the major contributor to grain yield per plant (g), followed by straw yield per plant (g), number of fingers per ear, number of tillers per plant, and plant height. These traits had the highest direct effects on grain yield per plant at both genotypic and phenotypic levels.

Madhavilatha *et al*. (2020) studied genetic parameters, character association, and path analysis in fifty little millet elite germplasm lines for nine quantitative traits. Path analysis indicated that plant height, number of effective tillers per plant, and length of inflorescence positively correlated with and had a direct effect on grain yield per plant at both phenotypic and genotypic levels.

Madhavilatha *et al*. (2021) evaluated 26 finger millet varieties for path analysis and found that the number of fingers per ear had the most significant direct contribution to grain yield, followed by the number of productive tillers per plant, fodder yield, plant height, and SCMR (stay green phenotype) on grain yield.

Arvinth *et al*. (2021) studied 22 sorghum genotypes during kharif-2020 for genetic variability, character association, and path analysis were assessed. Genotypic path analysis revealed that dry fodder yield per plant had a high positive direct effect on green fodder yield per plant, followed by days to 50 per cent flowering, leaf length of blade, number of leaves per plant, and leaf width of blade.

Kawadiwale *et al*. (2022) evaluated 32 pearl millet restorer lines for direct and indirect effect of different characters on yield through path analysis. It showed dry fodder yield per plant had the highest positive direct effect on grain yield per plant. Additionally, the number of effective tillers, ear head girth, and ear head weight had low but positive indirect effects on grain yield per plant through dry fodder yield per plant. These traits can be used as selection criteria for improving pearl millet yield.

Patel *et al*. (2023) In a study of 50 little millet genotypes during *kharif*-2021, the assessment of interrelationships among 16 quantitative traits identified important yield component traits. Direct selection based on fodder yield per

plant, plant height, and 1000 seed weight can enhance grain yield. Harvest index was highlighted as the most crucial character for indirect selection.

Rajpoot *et al.* (2023) In the study of 75 pearl millet germplasm lines during Kharif 2021, correlation and path analysis suggested that harvest index, biological yield, and the number of productive tillers per plant could serve as effective selection criteria for improving yield in pearl millet.

2.4 Genetic divergence

Genetic diversity is the variation of heritable characteristics in a population. It results from one or more of the following; evolution, mutation, migration, domestication, plant breeding and selection. Knowledge about genetic diversity and relationships among plants may be an invaluable aid in plant breeding and classification. The plant breeder's choice of source germplasm determines the potential improvement for traits under selection in a breeding programme as it will provide greater chances of obtaining the desirable gene combinations. The success of any breeding method depends on the availability of genetic diversity in the base population. Utilisation of diverse parents in hybridisation programmes has been observed to yield better hybrids. Three important points are to be considered while selecting genotypes for hybridization purpose. 1. Choice of the particular cluster from which genotypes are to be used as parents. 2. Selection of particular genotypes from selected cluster. 3. Relative contribution of characters towards total divergence. To identify the parents that nick better, several methods of divergence analysis based on quantitative characters have been proposed to suit various objectives.

Karad and Patil (2013) analysed 65 finger millet accessions for 12 morphological characteristics using Mahalanobis D^2 statistics and grouped them into five clusters. Genotypes falling between cluster III and IV exhibited

maximum inter-cluster distances followed by cluster I and cluster IV and cluster III and cluster V suggesting wider diversity between genotypes based on clustering pattern. The minimum inter cluster distance was found in cluster III, followed by cluster I. The maximum intra cluster distance was observed for the genotype falling in cluster II. This implies that these clusters have the genotypes with varied genetic architecture. The clusters IV and cluster V showed zero intra cluster distance due to mono genotypic nature.

Shinde *et al*. (2013) estimated genetic distance using D^2 statistics in 41 finger millet genotypes for 12 characters and grouped the genotypes into seven clusters. The highest inter-cluster distance was observed between clusters II and VII followed by IV and VII suggesting the use of genotypes from these clusters to serve as potential parents for hybridization programme. The characters iron content contributed maximum towards divergence followed by plant height, days to physiological maturity and days to 50% flowering.

Anuradha *et al*. (2014) assessed 21 barnyard millet germplasm lines for genetic divergence through Mahalanobis D^2 statistics and grouped them into four clusters. The inter cluster D^2 values were maximum between cluster I and IV followed by cluster IV and III while for intra cluster D^2 values, cluster II registered maximum followed by cluster I. The widest inter cluster distance between cluster I and IV gives scope for hybridization programme with improvement of genotypes.

Suryanarayana *et al.* (2014) reported six clusters for 35 finger millet genotypes through MahalanobisD^2 statistics. The maximum D^2 values registered for inter-cluster was between cluster II and V while it was in cluster III for intra cluster. The trait plant height contributed maximum towards total diversity followed by seed yield per plant, main ear length, number of fingers per ear, productive tillers per plant and days to 50% flowering.

Kumari and Singh (2015) grouped 35 finger millet genotypes into six clusters using Tocher's method. The highest intra-cluster distance was observed in cluster IV followed by cluster II and cluster I indicating differences in genotypes within cluster. The genotypes in cluster IV and cluster VI due to maximum inter-cluster distance between them, exhibited high degree of genetic diversity and thus may be utilized under inter-varietal hybridization programme for getting high yield recombinants. The maximum contribution in the manifestation of genetic divergence was exhibited by days to 50% flowering followed by days to maturity and grain yield per plant suggesting scope for improvement in these characters.

Yogeesh *et al*. (2015) grouped 52 germplasm accessions of foxtail millet into three clusters based on Ward's analysis. Cluster III was the largest one comprising of 20 genotypes followed by cluster I with 17 genotypes and cluster II with 15 genotypes. Among the five characters studied, the seed yield showed greater diversity as compared to days to 50% flowering, plant height and length of inflorescence.

Gangurde *et al*. (2016) conducted divergence studies in 66 foxtail millet genotypes through D^2 statistics and grouped them into five distinct non-overlapping clusters. Inter- cluster distance was observed to be maximum between cluster III and IV followed by cluster IV and V. The highest intra-cluster distance was found in cluster II followed by clusters II and I. The traits grain iron content (ppm) followed by flag leaf length (cm), grain zinc content (ppm), straw weight, flag leaf area, plant height(cm), flag leaf width, panicle weight (g) and grain yield contributed highest in the manifestation of genetic divergence.

Sao *et al*. (2016) carried out genetic divergence analysis through Mahalonobis D^2 statistics in 27 kodo millet advanced breeding lines and grouped them into four clusters. The inter cluster distance was maximum between cluster II and

IV while for intra cluster distance, cluster II recorded the highest. The traits days to maturity followed by days to 50% flowering showed maximum contribution towards genetic divergence.

Singh *et al*. (2016) evaluated 34 foxtail millet genotypes to assess morphological diversity for 12 quantitative traits using Mahalonobis D^2 statistics and grouped the genotypes into six clusters. The genotypes in cluster IV and cluster VI due to maximum inter cluster distance between them, exhibited high degree of genetic diversity and thus may be utilized under inter varietal hybridization programme. The maximum contribution in the manifestation of genetic divergence was exhibited by inflorescence length followed by flag leaf blade length, basal tillers number and panicle exertion suggesting scope for improvement in these characters.

Bheemesh (2017) studied the genetic divergence of 60 foxtail millet genotypes for 19 characters. Based on the genetic distance (D^2 value), the 60 accessions were grouped into 13 clusters. Of them, cluster I with 36 genotypes forms the largest followed by cluster IV and II with eight and five in each. The character relative injury at 30 DAS contributed the maximum to the divergence. Based on the average inter-cluster distance (D), the clusters XII and XII followed by clusters VIII and XIII were found to be highly divergent from the other clusters. Selection of parents from these clusters and using them in a breeding programme is advocated to develop divergence lines.

Devaliya *et al.* (2017) studied genetic divergence in 68 finger millet genotypes for 13 quantitative traits using Mahalanobis D^2 statistics and classified them into eight clusters. The maximum inter-cluster distance was observed between cluster VIII and cluster III followed by cluster VII and IV indicating that the genotypes belonging to the distinct cluster (VIII and III) could be used in hybridization programme for obtaining a wide spectrum of variation among the segregants. At the intra cluster level cluster VIII had the highest value. The

character iron content contributed maximum towards genetic divergence followed by main earhead length, harvest index, test weight and number of productive tillers per plant while calcium content, days to maturity, grain yield per plant and straw yield per plant contributed very low towards divergence.

Suryanarayana and Sekhar (2018) carried out Mahalanobis D^2 statistics to estimate the genetic divergence of 23 little millet genotypes for five quantitative traits. All the genotypes were grouped into six clusters. Maximum number of genotypes (8) were included in cluster VI followed by cluster-I (7), cluster-II, III, IV and V with two genotypes in each cluster. Considering the inter cluster distances, it was highest between cluster IV and V (163.09) followed by V and VI (145.69). Among the five characters studied, grain yield (q/ha), days to 50% flowering and plant height (cm) contributed maximum towards the total divergence and were found to be responsible for primary differentiation.

Thippeswamy *et al.* (2018) analysed the genetic diversity for yield and its components in 149 germplasm accessions of foxtail millet for 19 characters. Based on D^2 values, the genotypes were grouped into 15 clusters. Maximum intra cluster distance among the genotypes was recorded by cluster I having 134 genotypes followed by cluster VIII with two genotypes. The maximum inter cluster distance was found between clusters IX and XIV followed by cluster VI and XIV. The maximum contribution towards divergence was recorded by number of tillers per meter row length and 1000 seed weight.

Amarnath *et al.* (2019) grouped 50 accession of foxtail millet into 9 distinct non-overlapping clusters. Among the 9 clusters, Cluster I contains 36 accessions followed by cluster II with 7 accessions and the remaining clusters III, IV, V, VI, VII, VIII and IX containing only one accession each indicating high degree of divergence among the genotypes. Among all the characters

studied, culm branches have maximum contribution towards genetic divergence followed by 1000 grain weight.

Ayesha *et al.* (2019) grouped the 50 foxtail millet genotypes into eight clusters. Of the 8 clusters, cluster III was the largest one containing 13 genotypes followed by Cluster II and IV are the second largest clusters with 10 genotypes each. Third largest cluster was Cluster I having nine genotypes followed by cluster VI with five genotypes each. Clusters V, VII and VIII where solitary clusters contain one genotype each. Among the 13 characters studied plant height recorded maximum contribution towards genetic divergence followed by iron, grain yield per plant, calcium, days to maturity, carbohydrate, days to 50% flowering, protein and fat while panicle length, number of productive tillers per plant, test weight and phosphorus contributed least towards the genetic divergence.

Dhanalakshami *et al*. (2019) grouped 99 barnyard millet genotypes into 13 clusters, Cluster I was the largest, consisting of 39 genotypes followed by cluster XIII with 35 genotypes. Cluster XII and XI had four and three genotypes, respectively. The remaining nine clusters II, III, IV, V, VI, VII, VIII, IX and X included only two genotypes per cluster. Highest 17 intra-cluster distance was recorded for Cluster XI followed by cluster XIII. Clusters I and XI recorded maximum inter-cluster distance followed by clusters VIII and XI. Among the all traits, grain yield per plant and plant height contributed maximum to the genetic diversity.

Swamynatham *et al*. (2020) study of fifty pearl millet germplasms, significant diversity was observed in fourteen traits. Clustering analysis grouped them into sixteen clusters, with the highest inter-cluster distance between clusters XV and XVI. Genotypes PPBI-04, PPBI-34, PPBI-38, and PPBI-39 were selected for their superior performance in yield-related traits. Despite lower inter-cluster distances, PPBI-31 and PPBI-44 from cluster I were chosen for their

high grain yield and important yield traits. Hybridizing these genotypes can create heterotic combinations for improving grain yield. Additionally, including PPBI-34 and PPBI-44 in the crossing program may yield drought-tolerant varieties based on their performance in SPAD chlorophyll meter readings at 45 DAS.

Rasitha *et al*. (2020) assessed genetic diversity among pearl millet seed parents and restorers for effective selection of potential parents. A total of 59 parental lines were characterized based on quantitative traits, showing significant variation. Genetic divergence analysis grouped the lines into five clusters, with cluster V performing well in yield-related traits and cluster IV excelling in tillering and plant height.

Sharma *et al*. (2020) assessed genetic diversity in 60 pearl millet inbred restorers for 10 agro-morphological and six seed quality traits. High range of variation was observed and trait contribution to genetic diversity depicted that panicle length contributed the maximum (19.04 %) followed by panicle girth (18.76 %). Based on the clustering pattern, a total of 09 clusters were obtained of which Cluster II was the largest and comprised of 39 inbreds followed by cluster III with 10. Cluster mean depicted that cluster I, III and IX comprised of potential lines having a desirable mean performance for the traits studied. Cluster distance was also high among these aforesaid clusters thus suggesting their use in hybrid development as well as in recombination breeding for generating better inbreds in pearl millet.

Saikumar *et al*. (2021) studied genetic diversity in 37 parental lines of pearl millet includes 10 maintainer and 27 restorer lines for grain yield and its attributes through Mahalanobis D^2 statistics. All the 37 genotypes were assigned into eight different clusters. Cluster II was the largest one composed of 12 genotypes subsequently cluster V with eight genotypes, cluster VII contains seven genotypes and cluster I had five genotypes. Whereas, clusters

III, IV and VIII were solitary. High order of genetic divergence was noticed between cluster VI and VII (109.29), followed by cluster VII and VIII (72.27), cluster III and VII (66.65). Hybridization between genotypes from divergent clusters and with the best mean performance for productivity traits could be beneficial for developing promising hybrids.

Gopi *et al*. (2021) evaluated a total of 80 foxtail millet genotypes for ten quantitative characters at MARS (Main Agricultural Research Station), UAS (University of Agricultural Sciences), Raichur during kharif 2018 to assess the genetic diversity using Mahalanobis D^2 statistics. The eighty genotypes were grouped into twelve clusters. The highest inter-cluster distance (6623.62) was observed between cluster-VIII and cluster-XII. The highest intra-cluster distance was observed in cluster VII (529.01). A high mean grain yield was observed in cluster-XI (59.72g). Plant height (46.96%) and grain yield (46.39%) have the highest contribution to the total divergence.

Barathi and Reddy (2022) studied thirty pearl millet landraces along with two male sterile lines to estimate the genetic distances and to identify the desired cross combinations for the development of high yielding hybrids. Based on the Mahalanobis' D^2 analysis, the 32 germplasm lines were grouped under eight clusters. A high range of variation for trait contribution to the total diversity was observed and grain yield (19.14%) contributed the maximum, followed by dry fodder yield (11.69%). Cluster I was the largest with 25 genotypes and the remaining seven were solitary clusters. Clusters VI had a maximum mean performance for most of the traits, followed by clusters III and VIII. The cluster distances among these were also high, hence, the genotypes from these clusters can be used in hybrid development as well as in the development of new inbred lines.

Selvaraj *et al*. (2023) study of seventeen little millet landraces and varieties, they were characterized for eleven quantitative and six qualitative traits. The

diversity of the accessions for quantitative traits with major contributors as 1000 seed weight and plant height grouped the genotypes into five clusters. Five genotypes each were grouped under cluster III and cluster V. The maximum inter cluster distance was found between cluster I and cluster II. Subsequently, cluster I had higher desirable mean for plant height, number of basal tillers, panicle length, number of branches per panicle and grain yield per plant while cluster III had early flowering. The qualitative traits viz., grain colour, panicle compactness and pigmentation of leaf sheath were also highly variable in the present material and were grouped into six clusters based on these traits. Hence, these highly variable qualitative traits could be employed as major indicators in the identification of these landraces.

2.5 Stability (AMMI, GGE biplot and BLUPs)

In the realm of agricultural research and statistical analysis, three powerful tools have emerged to address the complex interactions between genotypes and environmental factors, aiding in the advancement of crop improvement and yield optimization. These tools are AMMI (Additive Main effects and Multiplicative Interaction), GGE Biplot (Genotype Main Effects plus Genotype-by-Environment Interaction Biplot), and BLUP (Best Linear Unbiased Prediction).

AMMI is a statistical technique used to analyze genotype-by-environment interaction (GEI) in multi-environment trials. It combines both additive and multiplicative effects of genotypes and environments, providing insights into the performance of genotypes across various environments. AMMI helps researchers identify stable genotypes and understand their adaptability to different environmental conditions.

GGE Biplot is a graphical tool widely used in the analysis of genotype-by-environment interactions. It assists in visualizing and interpreting complex

interactions between genotypes and environments in multi-environment trials. GGE Biplot provides a clear representation of the performance and stability of genotypes, helping researchers make informed decisions in plant breeding and selection.

BLUP is a statistical estimation method used to predict the genetic worth of genotypes, taking into account various sources of information, including phenotypic data and genetic relatedness. It offers a robust and efficient approach to estimate genetic values, enabling accurate selection of superior genotypes for traits of interest in breeding programs. BLUP is widely utilized in modern plant breeding to optimize breeding strategies and enhance crop productivity.

Negash *et al.* (2013) assessed wheat genotypes in six diverse environments to understand G×E interactions and stability. Additive Main Effects and Multiplicative Interactions (AMMI) analysis for grain yield exhibited significant variation due to environments, genotypes, and G×E ($p < 0.01$). Stability assessment for grain yield was conducted using Genotype plus Genotype by Environment Interaction (GGE) biplot analysis, offering insights into genotype adaptability across locations and years. The resulting GGE biplot illustrated a 'which-won-where' pattern based on genotype performance in multiple locations. However, the repeatability of this pattern across years remains uncertain, emphasizing the need for stable and predictable performance for effective mega-environment delineation and genotype recommendation.

Lule *et al*. (2014) conducted experiment in 2012 & 2013 and assessed 30 advanced finger millet genotypes alongside two standard checks (Gute and Taddese) at four locations (Arsi Negele, Assosa, Bako, and Gute). Additive Main effect and Multiplicative Interaction (AMMI), Genotype and Genotype by Environment interaction (GGE) biplot analysis and, Eberhart and Russell

model revealed that Acc. 203544 is stable high yielding (3.16-ton ha^{-1}) with a yield advantage of 13.7% over the best standard check, Gute (2.78-ton ha-^{1}), and thus should be recommended for possible release with wider environmental adaptability. Acc. 242111 (3.08-ton ha^{-1}), Acc. BKFM0051 (3.07-ton ha^{-1}) and Acc.229738 (2.99-ton ha^{-1}) were also high yielding, but showed narrow stability and thus should be recommended for verification and possible release for specific environments.

Rono *et al.* (2016) reported the genotype and environment interaction influences the selection criteria of sorghum (*Sorghum bicolor*) genotypes. Eight sweet sorghum genotypes were evaluated at five different locations in two growing seasons of 2014. The combined analysis of variance of cane and juice yield of sorghum genotypes showed that sweet sorghum genotypes were significantly () affected by environments (E), genotypes (G) and genotype by environment interaction (GEI). GGE biplot showed high yielding genotypes EUSS10, ACFC003/12, SS14, and EUSS11 for cane yield; EUSS10, EUSS11, and SS14 for juice yield; and EUSS10, SS04, SS14, and ACFC003/12 for ethanol yield. Genotype SS14 showed high general adaptability for cane, juice, and ethanol yield.

Zhang *et al*. (2016) experiments were conducted for three consecutive years across 14 locations using 9 non-waxy proso millet genotypes and 16 locations using 7 waxy proso millet genotypes in China. The objectives of this study were to analyze yield stability and adaptability of proso millets and to evaluate the discrimination and representativeness of locations by analysis of variance (ANOVA) and genotype and genotype by environment interaction (GGE) biplot methods. Grain yields of proso millet genotypes were significantly influenced by environment (E), genotype (G) and their interaction (G×E) ($P<0.1\%$). G×E interaction effect was six times higher than G effect in non-waxy group and seven times in waxy group. N04-339 in non-waxy and Neimi

6 (NM6) in waxy showed higher grain yields and stability compared with other genotypes. Also, Neimi 9 (NM9, a non-waxy cultivar) and 90322-2-33 (a waxy cultivar) showed higher adaptability in 7 and in 11 locations, respectively. For non-waxy, Dalat, Inner Mongolia (E2) and Wuzhai, Shanxi (E5) were the best sites among all the locations for maximizing the variance among candidate cultivars, and Yanchi, Ningxia (E10) had the best representativeness. Wuzhai, Shanxi (e9) and Yanchi, Ningxia (e14) were the best representative locations, and Baicheng, Jilin (e2) was better discriminating location than others for waxy genotypes.

Anuradha *et al.* (2017) conducted experiment at three different agro climatic zones during the year 2014 for grain iron (Fe) and zinc (Zn) contents using Atomic Absorption Spectrometry. The genotypes contributed 58.3% and 52.8% of the total variation for grain Fe and Zn content, respectively. The magnitude of variation contributed by interaction component was also relatively high (39.7% and 32.5% for grain Fe and Zn). Both AMMI and GGE biplot analysis identified desirable genotypes; PPMI 708 (G40), PPMI 1102 (G25) and PPMI 683 (G39) for grain Fe content, whereas PPMI 708 (G40), PPMI 1116 (G24) and PPMI 683 (G39) for grain Zn content. The Pearson correlation coefficient for grain Fe and Zn content showed that both traits are highly associated (r = 0.8, p less than 0.01) and these traits did not associate significantly with grain yield. Hence, there is possibility for simultaneous improvement of both grain Fe and Zn content without compromising for grain yield.

Chaithra *et al*. (2017) reported that stability in performance is one of the most desirable properties of a genotype to be released as a variety for varied regions. Genotype x environmental interactions and stability were investigated on grain yield with 16 finger millet genotypes in 33 environments. The ANOVA for grain yield revealed highly significant difference ($p< 0.01$) and cumulatively

contributed 60.28 per cent of the total G x E interaction. The biplot technique used to identify appropriate genotypes across environments showed that the genotypes KOPN 933, VL 149, VR 708 and GPU 78 had moderate grain yield with low interaction and hence considered as stable genotypes.

Sood *et al*. (2017) conducted a study in five national finger millet cultivars at ICAR-Vivekananda Institute of Hill Agriculture for six consecutive years to evaluate the grain yield stability. The combined ANOVA showed that finger millet grain yield was significantly affected by environment, which explained 54.67% of the total treatment (G+E+GE) variation, whereas the G and GEI accounted for 10.38% and 34.96%, respectively. The partitioning of GEI sum of squares using AMMI analysis indicated that the first two PCAs were highly significant. The first IPCA axis (IPCA1) accounted for 50.3% of the G×E interaction sum of squares. The second IPCA axis accounted for 38.2% of the interaction sum of squares. Both represented a total of 88.5% variation. AMMI 1 biplot indicated the general adaptation of genotype HR 374 across the environments, whereas the other genotypes showed specific adaptation to one or other environments. GGE-biplot graphical analysis further confirmed the results and revealed that HR 374 as an ideal genotype in terms of high yield and stability followed by RAU 8 as desirable genotype.

Mamo *et al*. (2018) conducted an experiment to study the adaptability and genotype × environment interaction of finger millet varieties in the north eastern part of Ethiopia. Eight finger millet varieties and a local check were tested at Sirinka, Kobo, and Jari in 2013 and 2014 cropping season. The Additive Main-effect and Multiplicative Interaction (AMMI) analysis showed that the best fit model was AMMI1 and it explained 68.54% of the genotype × environment interaction. Genotypes Bareda, the local check and Gute had higher grain yield in that order. Similarly, environments SR13, JR13 and KB13 had above average grain yield. Varieties Tadesse and Padet had small

interaction effect; however, Bareda and Gute exerted relatively higher interaction effect. Similarly, environment SR13 contributed minimum interaction effect; whereas KB13 and JR13 contributed higher interaction effect. Genotype and genotype × environment (GGE) biplot identified the local check, Bareda and Gute as more desirable varieties.

Simon and Getachew (2018) conducted experiment at multi-locations namely Jinka, Kako and Alaba in two consecutive years (2011 and 2012 Gc) to identify high yielding, disease resistant/tolerant and stable performing finger millet genotype for potential areas of Southern region. Additive Main effect and Multiplicative Interaction (AMMI), Genotype and Genotype by Environment interaction (GGE) biplot analysis model revealed that environment effects and genotype effects were highly significant implies environments are diverse and genotype were performing differently. According genotype LR004 &LR005 showed stable and above mean performance across testing location and season. So, this varieties should take for verification trial with standard checks (recently released varieties) under locations where regional variety trials were conducted.

Mamata and Hooda (2019) studied G×E interaction in pearl millet genotypes from zone-A of India using AMMI and GGE biplot analyses. A new Weighted Stability Index (WSI) has been proposed for determining the high yielding and stable genotypes based on the normalized indices for grain yield and ASV indices. The three interaction principal component axes (IPCA1, IPCA2 and IPCA3) have been found to be significant for this zone. AMMI Stability Value (ASV) and Stability Index have been used to find the most stable genotypes while indices YSI and WSI have been used to find both the most stable and high yielding genotypes. On the basis of ASV, genotypes MH 2120, MH 2109 and MH 2116 have been found to be the most stable for this Zone.

Kebede *et al.* (2019) conducted field experiment using twelve black seeded finger millet (*Eleusine coracana subsp. coracana*) genotypes, including local and standard checks (Degu) at two locations (Bako and Gute) in Ethiopia for three years (2014 - 2016). The additive main effect and multiplicative interaction (AMMI) model analysis of variance revealed highly significant ($P<0.01$) differences between environments, genotype, and Interaction Principal Component Analysis (IPCA-I), but significant variations ($P<0.05$) for G x E interactions. This indicates that the genotypes performed differently over environments and that the test environments are highly variable. Only the first IPCA-I showed high significance ($P<0.01$) and contributed 48.39% of the total genotype by environment interaction (G x E). Genotypes BKFM0020, BKFM0006 and BKFM0010, which had high grain yield, but with IPCA value close to zero, indicated the wide adaptability/stability.

Ataei and Shiri (2020) studied five advanced lines and one commercial check (Bastan) by testing across12 (six locations and two years) environments. Combined analysis of variance for forage yield showed that the genotypes, environments, and the interaction effects were highly significant ($P \leq 0.01$). The environment, genotype and interaction effects accounted for 76.38%, 6.97% and 8.92% of the total forage yield variation, respectively. GGE biplot analysis showed that G5 has both high forage yield and stability across the studied environments and E3 and E4 were high-yielding environments in this study. Which-won-where study partitioned the testing locations into two mega-environments with G5 and G3 as winning genotypes in the first and second mega-environment, respectively. According to discriminate ability and representativeness, the E4 and E12 environments were perfect environments.

Al-Naggar *et al.* (2020) conducted experiments in six environments with 25 sorghum B-lines were conducted at two locations in Egypt (Giza and Shandaweel) in two years and two planting dates in one location (Giza). The

AMMI analysis of variance indicated that the genotype (G), environment (E) and GE interaction had significant influence ($p \leq 0.01$) on sorghum grain yield. Based on AMMI model, BTX TSC-20 followed by ICSB-1808 showed both high yielding and stability across the test environments. However, ICSB-8001 (G11) and BTX-407 (G21), showed maximum stability, but with moderate grain yield. Based on GGE-biplot method, BTX TSC-20 (G25) was the winning genotype for the mega-environment which consists of E1 and E3, ICSB-14 (G3) for the mega-environment (E2 and E4), while BTX 2-1 (G20) for E5 mega-environment, ICSB-88003 (G12) and ICSB-70 (G6) for the mega-environment E6. These genotypes are the most adapted to the respective environments.

Raihan *et al*. (2021) studied seven proso millet advanced lines including one check variety, BARI Cheena-1 (BC-1) across 3 locations (Gazipur, Jamalpur and Rangpur) of Bangladesh during 2019-20. The results of the AMMI analysis indicated that the main effects due to genotype (G), environment (E) and GE interaction were significant, representing differential responses of the lines to the varied environments. Based on the AMMI stability parameter BD-1447, BD-1411 and BD-777 were the most stable lines across the environments, of which BD-777 was most stable. Biplot showed that the environment of Rangpur was poor; but that of Gazipur and Jamalpur were better for proso millet cultivation. Results also suggested that BD-1447, BD-1411 and BD-777 could be included in breeding programs due to their higher grain yield.

Sanjana Reddy *et al.* (2021) at All India Coordinated Research Project on Pearl Millet (AICRP-PM) evaluates and releases pearl millet cultivars, hybrids, and OPVs (open pollinated varieties) in three categorized zones (A1, A, and B) based on rainfall patterns. Hybrid varieties dominate due to hybrid vigor and private sector involvement, although OPVs remain significant due to wide

adaptability, cost-effectiveness, and timely seed availability. Across 20 locations in A1, A, and B zones, six pearl millet varieties were evaluated during the 2019 rainy season. Genotype main effects and genotype × environment interaction biplot method were employed for data analysis. Genotype × environment (G × E) interaction proved highly significant for grain yield, agronomic traits, and micronutrients (iron and zinc). Interestingly, genotypic effect (G) was significantly higher than G × E interaction effect, showcasing OPVs' adaptability. Ananthapuramu emerged as the ideal test site for selecting adaptable pearl millet cultivars across India. OPVs MP 599 and MP 600 displayed higher grain and fodder yields and stability, making them ideal genotypes. Furthermore, iron and zinc concentration displayed a significant positive correlation, suggesting effective simultaneous selection for both traits.

Anuradha *et al.* (2022) sixty finger millet varieties were evaluated over six consecutive rainy seasons (2011-2016) at the Agricultural Research Station, Vizianagaram. Genotype × environment interaction (GEI) was significant, contributing to 89% of total variation in Additive Main effects and Multiplicative Interaction (AMMI) analysis. Eleven stability parameters indicated strong positive associations among genotypes. Non-parametric and Parametric Simultaneous Selection indices (NP-SSI and P-SSI) were calculated using AMMI-based stability parameters for identifying stable high-yielders. C-SSI method, introducing initial culling, identified top ten genotypes as above-average yielders. BLUP-based simultaneous selections (HMGV, RPGV and HMRPGV) confirmed that none of the top ten entries had below-average yield. The study demonstrated that C-SSI and BLUP-based methods were equally effective in selecting high-yielding genotypes with stable performance. Indaf-9, Sri Chaitanya, PR-202, and A-404; and VL324 and VL146 were identified as the most stable high-yielding genotypes in medium-to-late and early maturity groups.

Madhavilatha *et al*. (2022) reported genotype and environment interaction were significant though comparatively less than location and genotype effects. The study has spotted the best varieties suitable for cultivation across five zones of finger millet growing areas of Andhra Pradesh. The cultivar PPR-1152 is recognized as the perfect genotype as it showed higher grain yield and stability compared with other cultivars in all places. Among locations Vizianagaram was the best discriminative and better representative location than other locations and perfect testing site for choosing finger millet cultivars effectively for adaptation in Andhra Pradesh.

Gangashetty *et al*. (2023) studied 20 top-performing pearl millet hybrids, identified based on starch data, in a randomised block design with three replications at five locations in West Africa, viz. Sadore and Konni (Niger), Bambey (Senegal), Kano (Nigeria), and Bawku (Ghana). Phenotypic variability was assessed for agronomic traits and mineral traits (Fe and Zn). Analysis of variance demonstrated significant genotypic, environmental, and GEI effects among five testing environments for agronomic traits (days to 50% flowering, panicle length, and grain yield), starch traits (rapidly digestible starch, slowly digestible starch, resistant starch, and total starch), and mineral trait (iron and zinc). Starch traits, such as rapidly digestible starch (RDS) and slowly digestible starch (SDS), showed nonsignificant genotypic and environmental interactions but high heritability, indicating the lower environmental influence on these traits in the genotype × testing environments. Genotype stability and mean performance across all the traits were estimated by calculating the multi-trait stability index (MTSI), which showed that genotypes G3 (ICMX207070), G8 (ICMX207160), and G13 (ICMX207184) were the best performing and most stable among the five test environments.

Memon *et al.* (2023) conducted an experiment using 90 genotypes, the genotype × environment interaction was found to be significant for seed yield

per plant as well as for plant height up to primary raceme, total length of primary raceme, effective length of primary raceme, capsules on main raceme and effective number of racemes per plant. E1 is the least interactive and highly representative site for seed yield. Which won where and what biplot decipher ANDCI 10-01 as vertex genotype for E3 while ANDCI 10-03 and P3141 for E1 and E2. Average Environment co-ordinate identify ANDCI 10-01, P3141, P3161, JI 357 and JI 418 as tremendously stable and high seed yielding genotypes. The study outlined the pertinency of Multi Trait Stability Index that calculated based on the genotype-ideotype distance as the multiple interacting variables. MTSI evaluated all genotypes and sort ANDCI 12-01, JI 413, JI 434, JI 380, P3141, ANDCI 10-03, SKI 215, ANDCI 09, SI 04, JI 437, JI 440, RG 3570, JI 417 and GAC 11 with maximum stability and high mean performance of analyzed interacting traits.

Narasimhulu *et al*. (2023) This study evaluated 12 pearl millet varieties and hybrids across rainy seasons in 2018, 2019, and 2020. The environment and genotype effects were highly significant in the Additive Main Effect and Multiplicative Interaction (AMMI) model, implying that environments are varied and genotypes performed differently in each environment offering a great scope for selecting better adaptive genotypes. Apart from moisture stress, the amount of rainfall received during both the anthesis and grain maturation stages were influenced grain yield through plant height, 1000- grain weight and dry fodder yield. Environment 3 was the best discriminating environment and the hybrids Pratap, 86M86 and NBH 5767 had outperformed the popular open pollinated varieties in ideal conditions.

Zhang *et al.* (2023) Studied 12 genotypes in eight environments of early-maturing growing areas. AMMI analysis of variance (ANOVA) indicated that genotype (G), environment (E), and GEI effects were highly significant ($p < 0.01$), with contributions to total observed variation of 19.5%, 43.4%, and

28.6%. Six stability parameters based on AMMI were used to analyze yielding stability. YG35, FH9, DT29, and ZZG21 were more stable. GGE biplot analysis revealed the same cultivars (YG35, ZZG21, and DT29) as the best performers for being closest to the ideal cultivar. The test sites were classified into two mega-environments using GGE biplot analysis for genotype assessment and seed production. Chifeng (CF) and Wulumuqi (XJ) were identified as the closest to the ideal test site, with relatively strong discriminatory ability and representativeness. Therefore, the findings of this study provide insights for the regional planting and breeding of foxtail millet in the future.

CHAPTER-III
MATERIAL AND METHODS

MATERIALS AND METHODS

The present investigation entitled “Stability and Genetic Diversity Analyses in Foxtail Millet [*Setari aitalica* (L.) P. Beauv.] Genotypes” was carried out to know the genetic diversity and stability of foxtail millet genotypes based on various morphological characters. This chapter includes all the materials used and methods employed during the course of investigation. All the techniques used are detailed under respective headings and their original references quoted.

The research took place between July 2022 and May 2023 in four different environments, and it was carried out on four different dates of sowing (Table 3.1), with a gap of 25 days between each sowing. 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 remain two environments were maintained under irrigated condition with irrigation intervals are once in week. The experiment was conducted at the Research Farm of the Department of Genetics and Plant Breeding, School of Agricultural Sciences (SAS), Medziphema Campus, Nagaland University, India. The precise coordinates of the research farm are “$25^0 45^0 35^0$ N and $95^0 25^0 45^0$ E” with altitude of 310 m above mean sea level.

The experimental locations fall under subtropical climate with high humidity, moderate temperatures, and moderate to high rainfall. It is neither a hill nor a valley and it gently slopes down towards the southern region from the north-eastern side of the town. This town actually represents an interface of the hilly Nagaland and the valleys as the actual hill region. we can observe distinct seasonal variations in temperature, humidity, and rainfall for the years

2022 and 2023 in different environmental conditions. During the Kharif season in 2022, Env-1 and Env-2 experienced average temperatures of 31.66°C and 32.09°C, respectively, with relatively high humidity levels averaging around 91.75% to 92.10%. Rainfall in these environments differed significantly, with Env-1 receiving 51.92mm and Env-2 receiving 55.19mm. In contrast, the Rabi season of 2023 in Env-3 and Env-4 witnessed slightly cooler temperatures, averaging around 28.28°C and 29.11°C, along with humidity levels ranging from 94.48% to 95.29%. However, rainfall during this period showed considerable variation, with Env-3 receiving 15.58mm and Env-4 receiving only 8.46mm. These variations in climatic parameters highlight the importance of understanding local environmental conditions for various agricultural and ecological purposes. The meteorological data during the experiment period regarding distribution of rainfall maximum and minimum temperature and relative humidity was obtained from ICAR regional centre Jharnapani. Which was shown in table 3.1.

Soil sampling and analysis: The top layer of soil, up to a depth of 0-15 cm, was randomly collected from the field from all the four environments. To gather the soil samples, a combination of a sharp tool called a cutlass and a small hand trowel was used. Once the samples were collected, they were combined and organized based on their location to create a composite sample after the experiment was completed. This composite sample was then taken to the university laboratory for analysis. To ensure consistency in the distribution of nutrients and to accurately represent the plots, the samples were dried in a shaded area and grounded using a glass mortar and pestle. After this process, the sample was sifted, and various tests were conducted to analyze its chemical properties and particle size distribution. These tests included examining the levels of sand, clay, silt, pH, organic carbon (OC), available nitrogen (N), available potassium (K) and available phosphorus (P). which are represented in Table 3.2.

Table 3.1. 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*	25^0 45' 15.95" N	93^0 51' 44.71 E	310 MSL	31.66	22.30	91.75	69.64	51.92	2022
Env-2	26-07-2022	*Kharif* (Late)	25^0 45' 15.95" N	93^0 51' 44.71 E	311 MSL	32.09	22.84	92.10	69.99	55.19	2022
Env-3	01-01-2023	*Rabi*	25^0 45' 15.95" N	93^0 51' 44.71 E	312 MSL	29.11	17.40	94.48	61.84	15.58	2023
Env-4	26-01-2023	*Rabi* (Late)	25^0 45' 15.95" N	93^0 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, Min= minimum and Max= maximum

Table 3.2. Characterization of soil properties of the experimental region

Determination	Field-1	Field-2	Field-3	Field-4
Physical analysis	Value			
Sand (%)	42.8	43.4	42.9	45.1
Silt (%)	24.9	26.7	35.1	34.5
Clay (%)	32.2	29.8	21.9	14.2
Textural classes (USDA)	Clay loam	Clay loam	Loam	Sandy Loam
Chemical analysis	Value			
pH	4.68	5.49	6.48	5.74
Organic matter (%)	0.89	0.98	0.94	1.03
Available nitrogen (Kg ha^{-1})	193.56	197.94	195.75	207.20
Available phosphorus (Kg ha^{-1})	17.08	17.56	16.05	16.85
Available potassium (Kg ha^{-1})	124.54	128.36	121.87	120.89

3.1. Experimental details:

3.1.1 Source of materials

We obtained a collection of one hundred foxtail millet germplasm's including four standard checks, which included reference varieties, from the Indian Institute of Millets Research (IIMR)-Hyderabad. These samples were evaluated during the *Zaid* season of 2022 at same environment. Based on the results of this evaluation, we identified the top 30 (29+1 check) genotypes that showed the highest grain yield specifically in this Nagaland region. These 30 selected genotypes were used in our study to assess genetic variability, diversity, and stability across different environments. List of 100 and 30 genotypes are represented in Table 3.3, Fig 3.1 and Table 3.4, Fig 3.2.

Table 3.3: Details of the foxtail millet genotypes and their place of collection

S.No	ACC. No	IC. No	Source
1	ERP 14	IC0622062	Tamil Nadu
2	ERP 26	IC0622071	Tamil Nadu
3	ERP 57	IC 0622094	Tamil Nadu
4	ERP 76	IC 0622109	Tamil Nadu
5	ERP 82	IC 0622113	Tamil Nadu
6	ERP 90	IC 0622117	Tamil Nadu
7	ERP 95	IC 0622121	Tamil Nadu
8	ERP 104	IC 0622127	Tamil Nadu
9	ERP 111	IC 0622133	Tamil Nadu
10	ESD 3	IC 0618597	Maharashtra
11	ESD 41	IC 0618629	Maharashtra
12	ESD 42	IC 0618630	Maharashtra
13	ESD 46	IC 0618634	Maharashtra
14	ESD 49	IC 0618636	Maharashtra
15	ESD 53	IC 0618638	Maharashtra
16	ESD 56	IC 0618641	Maharashtra

17	ESD 67	IC 0618650	Maharashtra
18	ESD 71	IC 0618654	Maharashtra
19	ESD 75	IC 0618657	Maharashtra
20	ESD 79	IC 0618660	Maharashtra
21	ESD 87	-	Maharashtra
22	ESD 90	IC 0618671	Maharashtra
23	ESD 91	IC 0618672	Maharashtra
24	ESD 95	IC 0618676	Maharashtra
25	ELS 2	IC 0621985	Andhra Pradesh
26	ELS 8	IC 0621987	Andhra Pradesh
27	ELS 20	IC 0621991	Andhra Pradesh
28	ELS 34	IC 0621998	Andhra Pradesh
29	ELS 36	IC 0621999	Andhra Pradesh
30	ELS 40	IC 0622003	Andhra Pradesh
31	ELS 43	IC 0622006	Andhra Pradesh
32	ELS 68	IC 0622015	Andhra Pradesh
33	ELS 87	IC 0622024	Odisha
34	ELS 108	IC 0622038	Andhra Pradesh
35	ELS 115	IC 0622043	Andhra Pradesh
36	ELS 119	IC0622044	Andhra Pradesh
37	ELS 125	IC 0622050	Andhra Pradesh
38	FOX 4435	IC0046673	Andhra Pradesh
39	FOX 4436	IC0077664	Andhra Pradesh
40	FOX 4437	IC 0077683	Andhra Pradesh
41	FOX 4438	IC 0077702	West Bengal
42	FOX 4440	IC 0077761	Gujarat
43	FOX 4441	IC 0077784	Jammu
44	FOX 4464	IC0481272	Maharashtra
45	FOX 4465	IC0481448	Bihar
46	FOX 4466	IC 0614786	Andhra Pradesh
47	FOX 4467	IC 0614787	Andhra Pradesh

48	FOX 4469	IC 0614789	Tripura
49	FOX 4475	IC0077964	Karnataka
50	FOX 4477	IC 0078004	Uttar Pradesh
51	FOX 4478	IC 0078006	Uttar Pradesh
52	FOX 4489	IC 0078200	Tamil Nadu
53	FOX 4311	IC 0337311	Uttarakhand
54	FOX 4312	IC 0337318	Uttarakhand
55	FOX 4318	IC 0355800	Uttarakhand
56	FOX 4320	IC 0383565	Uttarakhand
57	FOX 4329	IC 0596777	Arunachal Pradesh
58	FOX 4330	IC 0596783	Arunachal Pradesh
59	FOX 4336	IC 0597710	Andhra Pradesh
60	FOX 4339	IC 0597715	Andhra Pradesh
61	FOX 4341	IC 0597722	Andhra Pradesh
62	FOX 4347	IC 0597757	Arunachal Pradesh
63	FOX 4348	IC 0597758	Arunachal Pradesh
64	FOX 4384	IC 0610531	Andhra Pradesh
65	FOX 4386	IC 0610533	Andhra Pradesh
66	FOX 4385	IC 0610532	Andhra Pradesh
67	FOX 4389	IC 0610536	Andhra Pradesh
68	FOX 4390	IC 0610537	Andhra Pradesh
69	FOX 4392	IC 0610539	Andhra Pradesh
70	FOX 4394	IC0610541	Andhra Pradesh
71	FOX 4396	IC 0610543	Andhra Pradesh
72	FOX 4403	IC 0610550	Andhra Pradesh
73	FOX 4402	IC 0610549	Andhra Pradesh
74	FOX 4428	IC 0850064	Unknown
75	FOX 4419	IC 0613572	Karnataka
76	FOX 4420	IC 0613573	Andhra Pradesh
77	FOX 4418	IC0613525	Tamil Naidu
78	FOX 1974	IC0479270	Unknown

79	FOX 1975	IC 0479315	Unknown
80	FOX 1976	IC 0479317	Unknown
81	FOX 1977	IC 0479341	Unknown
82	FOX 1978	IC 0479350	Unknown
83	FOX 1979	IC 0479403	Unknown
84	FOX 1980	IC 0479411	Unknown
85	FOX 1981	IC 0479424	Unknown
86	FOX 1982	IC 0479445	Unknown
87	FOX 1983	IC 0479498	Unknown
88	FOX 1984	IC 0479506	Unknown
89	FOX 1985	IC 0479544	Unknown
90	FOX 1986	IC 0479569	Unknown
91	FOX 1987	IC 0479570	Unknown
92	FOX 1988	IC 0479573	Unknown
93	FOX 1989	IC 0479576	Unknown
94	FOX 1900	IC 0479582	Unknown
95	FOX 1991	IC0479598	Unknown
96	FOX 1992	IC 0479606	Unknown
Checks			
1	Prasad	Selection from Dronachalam village, Andhra Pradesh	
2	Suryanandi	Pureline selection from SiA 1244, Andhra Pradesh	
3	SiA 3156	Pureline selection from SiA 2871, Andhra Pradesh	
4	SiA 3085	Selection from SiA 2644 from farmers field A.P	

Table 3.4 List of selected genotypes based on the mean yield

ACC. No	IC. No	Source	Code	GY (g)
ELS 20	IC 0621991	Andhra Pradesh	G1	26.40
FOX 4438	IC 0077702	West Bengal	G2	23.00
FOX 4394	IC0610541	Andhra Pradesh	G3	22.20
FOX 4339	IC 0597715	Andhra Pradesh	G4	21.40
ERP 82	IC 0622113	Tamil Nadu	G5	21.20
FOX 4384	IC 0610531	Andhra Pradesh	G6	20.80
FOX 4396	IC 0610543	Andhra Pradesh	G7	20.20
FOX 4403	IC 0610550	Andhra Pradesh	G8	20.20
FOX 4428	IC 0850064	Unknown	G9	19.80
ESD 79	IC 0618660	Maharashtra	G10	19.80
FOX 4336	IC 0597710	Andhra Pradesh	G11	19.60
FOX 4386	IC 0610533	Andhra Pradesh	G12	19.20
ERP 26	IC0622071	Tamil Nadu	G13	18.40
ESD 3	IC 0618597	Maharashtra	G14	18.20
ELS 40	IC 0622003	Andhra Pradesh	G15	18.00
ERP 90	IC 0622117	Tamil Nadu	G16	18.00
FOX 4478	IC 0078006	Uttar Pradesh	G17	17.80
FOX 4489	IC 0078200	Tamil Nadu	G18	17.80
FOX 4392	IC 0610539	Andhra Pradesh	G19	17.20
FOX 4390	IC 0610537	Andhra Pradesh	G20	16.60
FOX 4330	IC 0596783	Arunachal Pradesh	G21	16.60
ESD 75	IC 0618657	Maharashtra	G22	16.60
ESD 46	IC 0618634	Maharashtra	G23	16.60
ERP 57	IC 0622094	Tamil Nadu	G24	16.00
FOX 4341	IC 0597722	Andhra Pradesh	G25	16.00
FOX 4440	IC 0077761	Gujarat	G26	15.80
FOX 4420	IC 0613573	Andhra Pradesh	G27	15.20
ELS 36	IC 0621999	Andhra Pradesh	G28	15.00
ELS 34	IC 0621998	Andhra Pradesh	G29	14.60
Surya Nandi	Check	Andhra Pradesh	G30	14.65

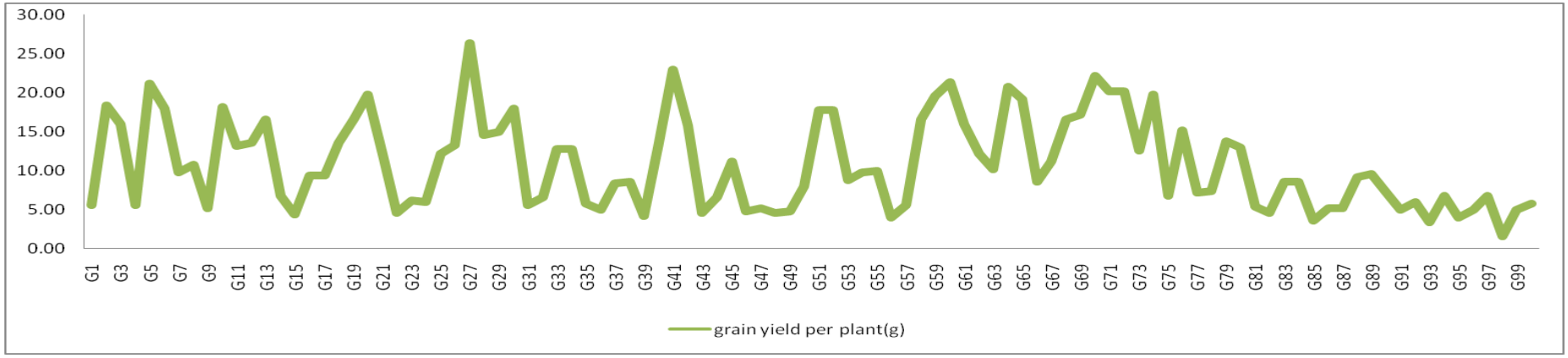


Fig 3.1 Mean yield performance of the 100 foxtail millet genotypes during *Zaid* -2022.

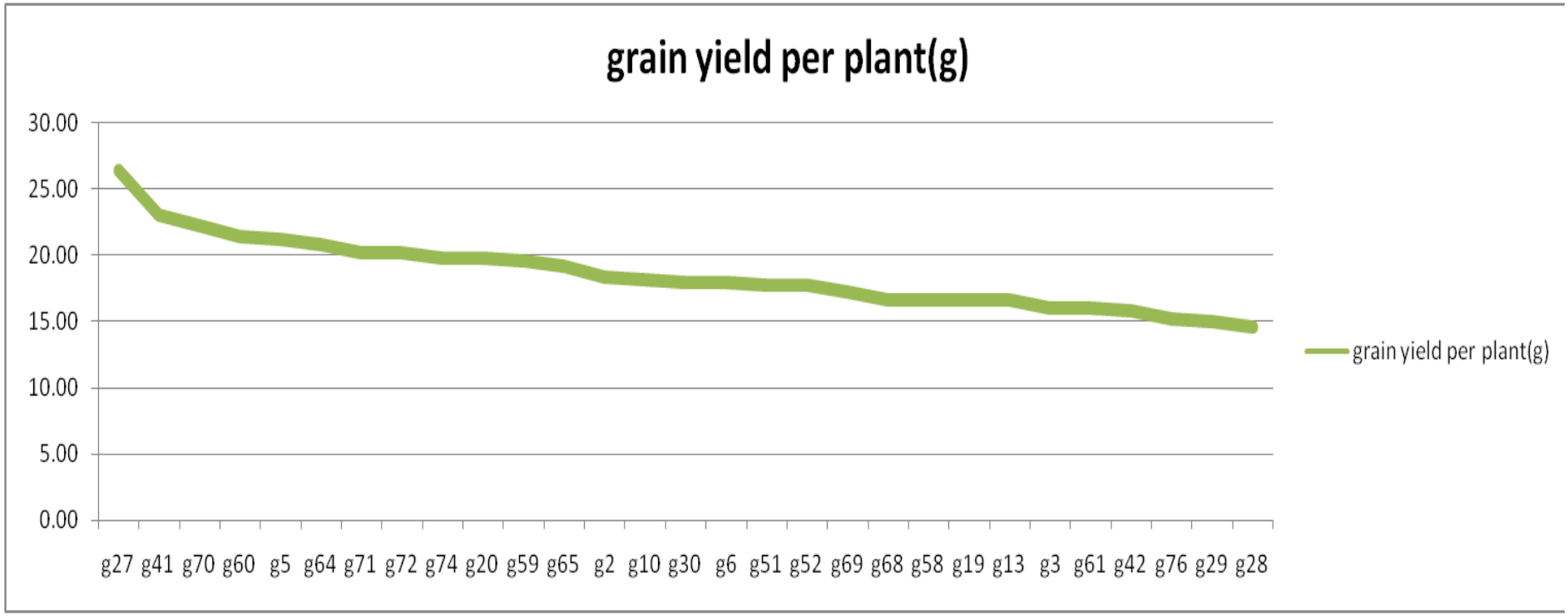


Fig 3.2 Mean yield performance of the selected 30 foxtail millet genotypes during *Zaid* -2022.

3.1.2 Design of Experiment and Layout Description

3.1.2.1 Experiment-I (For characterization of germplasm) (Fig 3.3)

Location	Department of Genetics and Plant Breeding, farm at SAS NU, Medziphema
Season	*Zaid*-2022
Design	Augmented Randomized Complete Block Design (ARCBD)
Entries	100 (96+4 Checks)
Spacing	22.5 cm × 10 cm
Number of rows	1 row / genotype
Row length	3m
Plot size	3.5 X 3 m per each block
Fertilizers	40:30:10 N:P: K

3.1.2.2Experiments II-V (For genetic diversity and stability analyses)

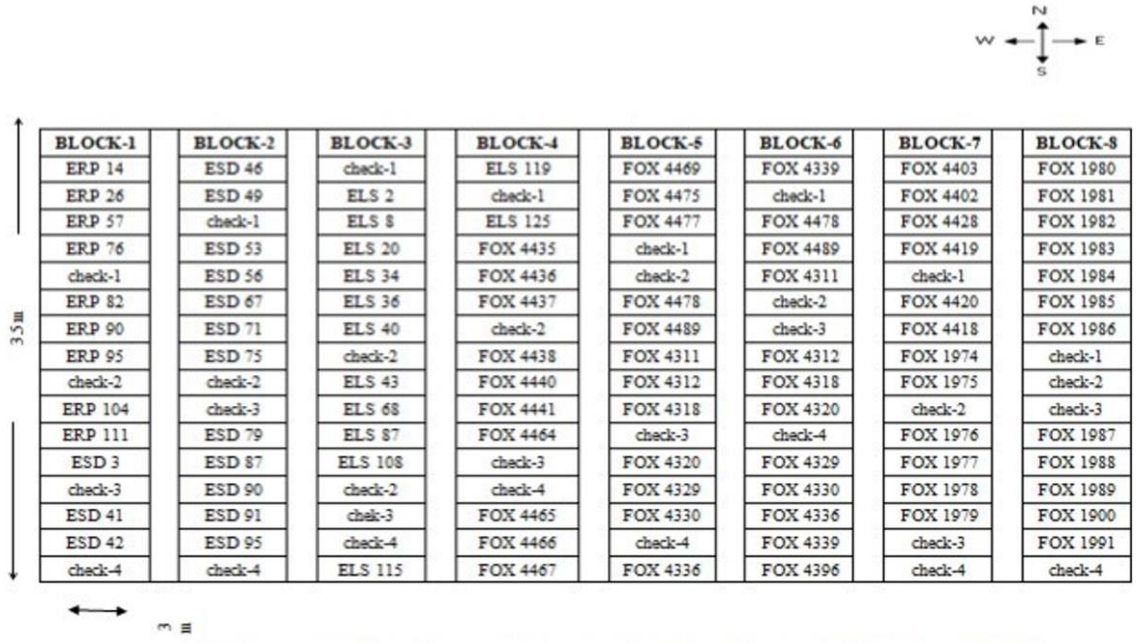
Based on mean performance of grain yield in experiment-I 30 (29 + 1 checks) superior genotypes were selected for genetic diversity and stability analyses.

Experiments No.	**Date of sowing**	**Location**
II	5-07-2022	NU SAS, Medziphema
III	25-07-2022	NU SAS, Medziphema
IV	10-01-2023	NU SAS, Medziphema
V	30-01-2023	NU SAS, Medziphema

Field Layout

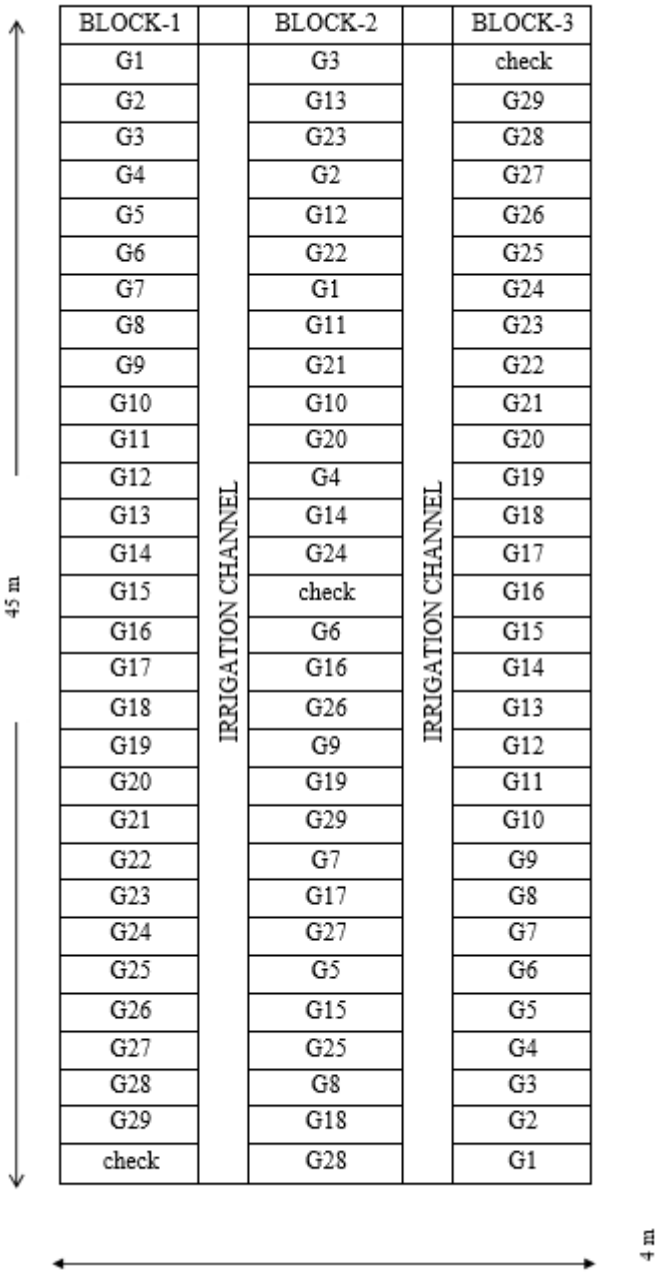
Design	Randomized Complete Block Design (RBD), The layout of the experiment is presented in the Fig: 3.4
Entries	30 (29+1Check)
Spacing	22.5 cm × 10 cm
Number of rows	4 rows / block
Row length	1m

Plot size	1 X 1 m per each block
Fertilizers	40:30:10 N:P: K
Distance between the genotypes	0.5 m
Distance between the replications	0.5 m



BLOCK-1	BLOCK-2	BLOCK-3	BLOCK-4	BLOCK-5	BLOCK-6	BLOCK-7	BLOCK-8
ERP 14	ESD 46	check-1	ELS 119	FOX 4469	FOX 4339	FOX 4403	FOX 1980
ERP 26	ESD 49	ELS 2	check-1	FOX 4475	check-1	FOX 4402	FOX 1981
ERP 57	check-1	ELS 8	ELS 125	FOX 4477	FOX 4478	FOX 4428	FOX 1982
ERP 76	ESD 53	ELS 20	FOX 4435	check-1	FOX 4489	FOX 4419	FOX 1983
check-1	ESD 56	ELS 34	FOX 4436	check-2	FOX 4311	check-1	FOX 1984
ERP 82	ESD 67	ELS 36	FOX 4437	FOX 4478	check-2	FOX 4420	FOX 1985
ERP 90	ESD 71	ELS 40	check-2	FOX 4489	check-3	FOX 4418	FOX 1986
ERP 95	ESD 75	check-2	FOX 4438	FOX 4311	FOX 4312	FOX 1974	check-1
check-2	check-2	ELS 43	FOX 4440	FOX 4312	FOX 4318	FOX 1975	check-2
ERP 104	check-3	ELS 68	FOX 4441	FOX 4318	FOX 4320	check-2	check-3
ERP 111	ESD 79	ELS 87	FOX 4464	check-3	check-4	FOX 1976	FOX 1987
ESD 3	ESD 87	ELS 108	check-3	FOX 4320	FOX 4329	FOX 1977	FOX 1988
check-3	ESD 90	check-2	check-4	FOX 4329	FOX 4330	FOX 1978	FOX 1989
ESD 41	ESD 91	chek-3	FOX 4465	FOX 4330	FOX 4336	FOX 1979	FOX 1900
ESD 42	ESD 95	check-4	FOX 4466	check-4	FOX 4339	check-3	FOX 1991
check-4	check-4	ELS 115	FOX 4467	FOX 4336	FOX 4396	check-4	check-4

Fig 3.3 Experimental field layout in Augmented Randomized Complete Block design (ARCBD)



BLOCK-1	BLOCK-2	BLOCK-3
G1	G3	check
G2	G13	G29
G3	G23	G28
G4	G2	G27
G5	G12	G26
G6	G22	G25
G7	G1	G24
G8	G11	G23
G9	G21	G22
G10	G10	G21
G11	G20	G20
G12	G4	G19
G13	G14	G18
G14	G24	G17
G15	check	G16
G16	G6	G15
G17	G16	G14
G18	G26	G13
G19	G9	G12
G20	G19	G11
G21	G29	G10
G22	G7	G9
G23	G17	G8
G24	G27	G7
G25	G5	G6
G26	G15	G5
G27	G25	G4
G28	G8	G3
G29	G18	G2
check	G28	G1

Fig 3.4 Experimental field layout in Randomized Complete Block Design (RBD)

3.2 Observations recorded:

The observations were recorded on 5 randomly sampled plants from each replicate. These carefully chosen traits were selected based on the comprehensive descriptions and guidelines provided by the Plant Protection Variety and Farmers' Rights Authority (PPV&FR) in 2001, ensuring a robust and standardized framework for analysis.

3.2.1 Qualitative traits

1	Leaf colour	1=green; 3=pigmented
2	Blade pubescence	1=essentially glabrus; 5=medium pubescent; 9=strongly pubescent
3	Sheath pubescence	1=essentially glabrus; 5=medium pubescent; 9=strongly pubescent
4	Degree of lodging at maturity	1=very slight; 5=medium; 9=extensive
5	Senescence	Degree to which the plant is still green at time the primary inflorescence on each culm (tiller) reaches maturity: 1=actively growing; 9=dead
6	Inflorescence lobes	0=absent; 3=short; 7=long; 9=large and thick
7	Inflorescence bristles	1=very short; 3=short but obvious; 5=medium; 7=long; 9=carrying a spikelet
8	Inflorescence Compactness	3=loose; 5=medium; 7=compact; 9=sponge
9	Lobe compactness	3=loose; 5=medium; 7=compact; 9=sponge
10	Inflorescence shape	1=oblong; 3=ovate; 5=elliptic; 7= obviate
11	Seed colour	1=red; 2=black; 3=white; 4=yellow
12	Grain shape	1=oval; 2=elliptical
13	Plant pigmentation	1= Absent, 9= Present
14	Plant: Growth habit	1=Erect, 5=Decumbent, 7=Prostrate
15	Plant: Pigmentation at auricle	1= Absent, 9= Present
16	Leaf: Attitude	3= Erect, 7= Droopy
17	Leaf sheath: Intensity of Pubescence	3= Low, 5= Medium, 7= High

18	Inflorescence: Apical sterility	1= Absent, 9= Present

3.2.2 Quantitative traits

1	Days to 50% flowering	The number of days taken by each genotype, from sowing to the day when 50 % of the plants were seen flowering in the population.
2	Days to maturity	The number of days taken by each genotype, from sowing to the day when it reaches physiological maturity
3	Plant height (cm)	It is the height of the main tiller from ground level to the tip of the panicle and is measured at the time of maturity.
4	Panicle length (cm)	It is measurement of the length from base to tip of the ear, at the time of maturity.
5	Flag leaf length (cm)	Measured from ligule to tip
6	Flag leaf width (cm)	Measured at widest point (center of the flag leaf)
7	Peduncle length (cm)	Measured from the top most node to base of the inflorescence
8	Number of productive tillers/plants	It refers to counting of basal ear bearing tillers at harvest stage
9	panicle width (cm)	It is measurement of the width from panicle
10	Biological yield (g)	The crop was harvested and sun drying to 5 - 8 days and weight of biomass each plant except root was recorded in grams
11	Harvest index (%)	The ratio of economic yield to biological yield
12	1000 grain weight (g)	Weight of random sample of 1000 seeds from the total harvest of an accession
13	Fodder yield per plant (g)	Fodder yield was recorded after threshing and reported in t/ha.
14	Grain yield/plant (g)	Weight of the total grain yield of tagged plants was recorded and the mean yield per plant was calculated after harvest

3.2.3 Estimation of Nutritional parameters		
1	Protein analysis	Protein content was estimated by Micro – Kjeldhal method by the AOAC (1984) procedure.
2	Calcium, Magnesium, Iron and Zinc	Estimation of mineral nutrients (Calcium, Magnesium, Iron and Zinc) in mg/100) by Di-acid mixture method

3.3 Statistical analysis:

The experimental data collected on fourteen characters were compiled by taking the mean values over selected plants for each replication. It was then analyzed for various statistical parameters as follows:

3.3.1 Analysis of variance

The genotypic differences between the entries were examined before moving on to the biometrical genetic analysis of the data. Further analysis was done, only when the mean squares attributable to genotypes were significant. As a result, the data for distinct characters were statistically examined for significance using pooled analysis of variance and coefficients of variance computed according to formulae given by Chaudhary and Prasad (1968). The chosen design was a three-fold replication of the Randomized Block Design (RBD). Analysis of variance was done under the fixed effective model given below:

To test the hypothesis

H_0 : $t_1 = t_2 \ldots\ldots\ldots\ldots = t_{20}$, the fixed effect model for the analysis of variance in RBD is as follows:

$$\mathbf{Y_{ij} = \mu + g_i + r_j + e_{ij}}$$

Where,

Y_{ij} = phenotypic observation in the i^{th} treatment and j^{th} replication

μ = Overall mean

g_i= effect of i^{th} treatment

r_j = effect of j^{th} replication

e_{ij} = Random error associated with i^{th} treatment and j^{t}h replication

i = No. of treatments

j = No. of replications

Table 3.5: Pooled analysis of variance (ANOVA) for RBD

Sources of variation	Degree of freedom (d.f)	Sum of Square (SS)	Mean square (MS)	Variance ratio
Year (Y)	(Y-1)	Y SS	Y MS	Y MS/EMS
Replication within year	Y (R-1)	R SS	R MS	R MS/EMS
Treatment (T)	(T-1)	T SS	T MS	T MS/EMS
Year x genotype	(Y-1)(T-1)	Y SS x T SS	Y x T MS	Y x T MS /EMS
Pooled error	Y(R-1)(R-1)	E SS	EMS	
Total	(YRT-1)			

Where,

Y = No. of years (season)

R = No. of replications

T = No. of treatments

Y SS = sum of square due to year

R SS = sum of squares due to replications within year

T SS = sum of squares due to genotypes

E SS = sum of squares due to pooled error

TSS = Treatment sum of squares

Y MS = Mean sum of square due to year

R MS = Mean sum of square due to replication within year

T MS = Mean sum of squares due to treatments

EMS = Error mean sum of squares

Critical difference

Critical difference was calculated by following formula:

$$\textbf{CD} = \sqrt{\frac{2EMS}{r}} \times t - value$$

t-value = table value of error d.f at 5% level of significance

Where,

r = number of replications

EMS = error mean sum of squares

Significant "F" value indicates that, there is significant difference among the treatments. But, to compare the difference between any two particular treatments, it is tested against CD value.

3.3.2 Variability parameters

(i) Genotypic variance

The genotypic variance (σ_g^2) is the variance due to the genotypes present in the population. The formula used for calculation of genotypic variance was as follows:

$$\textbf{Genotypic variance } \left(\boldsymbol{\sigma_g^2}\right) = \frac{\mathbf{MS_g - EMS}}{\mathbf{r}}$$

(ii) Environmental or Error variance

Environmental variance (σ_e^2) is the variance due to environmental deviation.

$$\boldsymbol{\sigma_e^2 = EMS}$$

(iii) Phenotypic variance

Phenotypic variance (σ_p^2) denotes the total variance present in a Population for particular character and is calculated by following formula:

$$\boldsymbol{\sigma_p^2 = \sigma_g^2 + \sigma_e^2}$$

Where,

$\boldsymbol{\sigma_g^2}$= Genotypic variance

$\boldsymbol{\sigma_e^2}$= Error variance

3.3.3 Coefficient of variation

It is the measure of variability observed. Coefficient of variation is the ratio of standard deviation of a sample to its mean and expressed in percentage.

$$\mathbf{CV}\ (\%) = \frac{\mathbf{Standard\ deviation}}{\mathbf{Mean}}\ \mathbf{X\ 100}$$

In the present investigation, three types of coefficients of variation were estimated *viz*., phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV) and error/environmental coefficient of variation (ECV). The formulae used to calculate PCV, GCV and ECV were given by Burton and Devane (1953):

Phenotypic coefficient of variation (P.C.V):

$$\mathbf{PCV} = \frac{\sqrt{\boldsymbol{\sigma}_{\mathbf{p}}^{2}}}{\bar{\mathbf{X}}}\ \mathbf{X\ 100}$$

Genotypic coefficient of variation (G.C.V):

$$\mathbf{GCV} = \frac{\sqrt{\boldsymbol{\sigma}_{\mathbf{g}}^{2}}}{\bar{\mathbf{X}}}\ \mathbf{X\ 100}$$

Environmental coefficient of variation (E.C.V):

$$\mathbf{ECV} = \frac{\sqrt{\boldsymbol{\sigma}_{\mathbf{e}}^{2}}}{\bar{\mathbf{X}}}\ \mathbf{X\ 100}$$

Where,

$\sqrt{\sigma_p^2}$ = Phenotypic standard deviation

$\sqrt{\sigma_g^2}$ = Genotypic standard deviation

$\sqrt{\sigma_e^2}$ = Error standard deviation

$\overline{X}$ = General mean of the character

σ_p^2 = Phenotypic variance

σ_g^2 = Genotypic variance

σ_e^2 = Environmental variance

GCV and PCV values were categorized as low, moderate and high as indicated by Siva subrananian and Menon (1973). It is as follows:

0-10% = Low

10-20% = Moderate

>20% = High

3.3.4 Heritability

Heritability is the ratio of genotypic variance to the total phenotypic variance. Broadly, it was estimated according to the formula given by Allard (1960).

$$\mathbf{h^2\ (broad\ sense) = \frac{\sigma_g^2}{\sigma_p^2}\ X\ 100}$$

Where,

h^2 = Heritability in broad sense

σ_g^2 = Genotypic variance

σ_p^2 = Phenotypic variance

Heritability values are ranked as low, moderate and high according to Robinson *et al*. (1949)

0-30% = Low

30-60% = Moderate

>60% = High

3.3.5 Genetic advance

Genetic advance is defined as an increase in the mean genotypic value of selected plants over the parental population. The estimates of genetic advance were obtained by the formula given by Lush (1949), Johnson *et al.* (1955) and Allard (1960):

$$\mathbf{GA = k.\sigma_p.h^2}$$

Where,

GA = Expected genetic advance

k = Constant (Standard selection differential) having the value of 2.06 at 5% level of selection intensity

σ_p = Phenotypic standard deviation

h^2 = Heritability in broad sense

In order to visualize the relative utility of genetic advance among the characters, genetic advance as percent of mean was computed as follows:

$$\textbf{Genetic advance as percent of mean} = \frac{\textbf{Genetic advance}}{\textbf{Grand mean}} \textbf{ X 100}$$

The range of genetic advance is classified as suggested by Johonson *et al.* (1955):

< 10 % = low

10-20 % = moderate

> 20 % = high

3.3.6 Correlation coefficient

Correlation coefficient is the mutual association between variables without implying any cause-and-effect relationship. Simple correlation coefficients were computed at genotypic and phenotypic levels between pair of characters adopting

following formula given by Al-Jibouri *et al.* (1958) as well as Panse and Sukhatme (1967).

Phenotypic correlation coefficients

Phenotypic correlation coefficient between character x and y

$$\mathbf{r_{xy}(p)} = \frac{\boldsymbol{\sigma^2_p\,(xy)}}{\sqrt{\boldsymbol{\sigma^2_p\,(x)\ .\ \sigma^2_p\,(y)}}}$$

Where,

rxy (p) = Phenotypic correlation between x and y

σ^2_p(xy) = Phenotypic covariance between traits x and y

σ^2_p (x) = Phenotypic variance for x

σ^2_p (y) = Phenotypic variance for y

Genotypic correlation coefficients

Genotypic correlation coefficient between character x and y

$$\mathbf{r_{xy}(g)} = \frac{\boldsymbol{\sigma^2_g(xy)}}{\sqrt{\boldsymbol{\sigma^2_g(x)\ X\ \sigma^2_g\,(y)}}}$$

Where,

r_{xy} (g) = Genotypic correlation between x and y

σ^2_g (x y) = Genotypic covariance between traits x and y

σ^2_g (x) = Genotypic variance for x

σ^2_g (y) = Genotypic variance for y

Test of significance

The calculated values were compared with the table value of the correlation coefficient recommended by Fisher and Yates (1938), at (n-2) treatment degree of freedom at 5% and 1% level of significance in order to determine the significance of

the correlation coefficient. It is considered to be significant if the calculated value of correlation coefficient is higher than the tabular value.

3.3.7 Path coefficient analysis

The use of path coefficient analysis explains cause and effect of relationship among the variables. It is a standardized partial regression coefficient and as such measures the direct influence of one variable upon another and permits the separation of the correlation coefficients into components of direct and indirect effects (Dewey and Lu 1959). This method permits breeder to identify relatively important components of a variable, on the basis of their direct and indirect influences.

The direct and indirect effects both at genotypic and phenotypic level were estimated with grain yield per plant as dependent variable using path coefficient analysis suggested by Wright (1921) and Dewey and Lu (1959). The following set of simultaneous equations were formed and solved for estimating various direct and indirect effects.

$$r_{1y} = P_{1y} r_{11} + P_{2y} r_{12} + P_{3y} r_{13} \ldots\ldots\ldots\ldots + P_{ny} r_{1n}$$

$$r_{2y} = P_{1y} r_{21} + P_{2y} r_{22} + P_{3y} r_{23} \ldots\ldots\ldots\ldots + P_{ny} r_{2n}$$

$$\begin{array}{ccccc} . & . & . & . & . \\ . & . & . & . & . \\ . & . & . & . & . \end{array}$$

$$r_{ny} = P_{1y} r_{n1} + P_{2y} r_{n2} + P_{3y} r_{n3} \ldots\ldots\ldots\ldots + P_{ny} r_{nn}$$

Where,

1, 2 . . . . . n = Independent variable

y = Dependent variable (yield per plant)

r1y r2y . . . rny = Coefficient of correlation between causal factors‘1’ to ‘n’ on dependent character 1

P1y P2y . . . .Pny = Direct effect of characters ‘1’ to ‘n’ on character Y

The above equations can be written in matrix form as:

A C B

$$\begin{pmatrix} r_{1y} \\ r_{2y} \\ : \\ : \\ r_{ny} \end{pmatrix} \begin{pmatrix} 1 & r_{12} & r_{13} & \dots\dots r_{1n} \\ r_{21} & 1 & r_{23} & \dots\dots . r_{2n} \\ : & : & : & : \\ : & : & : & : \\ r_{n1} & r_{n2} & r_{n3} & \dots\dots 1 \end{pmatrix} \begin{pmatrix} \mathrm{P}_{1y} \\ \mathrm{P}_{24} \\ : \\ : \\ P_{ny} \end{pmatrix}$$

A and B vector values are known. Hence, to calculate C vector

$B = [C]^{-1} A$

Where,

$$C^{-1} = \begin{pmatrix} \mathrm{C}_{11} & \mathrm{C}_{12} & \mathrm{C}_{13} & \dots\dots \mathrm{C}_{1n} \\ \mathrm{C}_{21} & \mathrm{C}_{22} & \mathrm{C}_{23} & \dots\dots \mathrm{C}_{2n} \\ : & : & : & : \\ : & :: & : & : \\ \mathrm{C}_{n1} & \mathrm{C}_{n2} & \mathrm{C}_{n3} & \dots\dots \mathrm{C}_{nn} \end{pmatrix}$$

Direct effects were as follows:

$P_{1y} = \sum_{i=1}^{k} \mathrm{C}_{1i}\mathrm{r}_{iy}$

$P_{2y} = \sum_{i=1}^{k} \mathrm{C}_{2i}\mathrm{r}_{iy}$

$P_{ny} = \sum_{i=1}^{k} \mathrm{C}_{ni}\mathrm{r}_{iy}$

Residual Effect

In plant breeding, it is very difficult to have complete knowledge of all component traits of yield. The residual effect permits precise explanation about the pattern of interaction of other possible components of yield. In other words, residual effects measure the role of other possible independent variables which were not included in the study on the dependent variable. The residual effect is estimated with the help of direct effects and simple correlation coefficients. It was calculated by using following formulae.

$$\mathbf{Pry} = \sqrt{\mathbf{1} - (\mathbf{p_{1y}r_{iy}} + \mathbf{p_{2y}r_{iy}} + \cdots + \mathbf{p_{ny}r_{ny}})}$$

Where,

p_{ny} = direct effect of X_n on Y

r_{iy} = correlation coefficient of X_n on Y

The direct and indirect effects are rated as follows by Lenka and Mishra (1973).

0.00-0.09 – Negligible

0.10-0.19 – Low

0.20-0.29 – Moderate

0.30-0.99 – High

>1.00 –Very high significant and vice-versa

3.3.8 Estimation of Genetic Divergence

Usually to assess the diversity in population of diverse origin, important method *i.e*. Mahalanobis D^2 Statistics is employed.

Mahalanobis' D^2 analysis

The data collected on different characters were analysed through Mahalanobis' D^2 analysis to determine the genetic divergence among the genotypes. D^2 value between i^{th} and j^{th} genotypes for 'P' characters was calculated as:

$$\mathbf{D_{ij}^2} = \sum_{\mathbf{t=1}}^{\mathbf{P}} \left(\mathbf{Y_i^t - Y_j^t}\right)^2$$

Where,

Y_i^t = Uncorrelated mean value of i^{th} genotype for 't' characters

Y_j^t = Uncorrelated mean value of j^{th} genotype for 't' characters

D^2_{ij} = D^2 value between i^{th} and j^{th} genotypes.

The various steps involved in estimation of D^2 values are given below:

i) Test of significance

Variances were calculated for all the characters investigated and test of significance was done. Analysis of covariance for the character pairs was estimated on the basis of mean values (Panse and Sukhatme 1967). After testing difference between genotypes for each of the characters, a simultaneous test of significance for the differences in the mean values of a number of correlated variables with regard to the pooled effect of characters was carried out using V statistic, which in turn utilizes Wilk's criterion. The sum of squares and sum of products of error and error + variety, variance and covariance matrix were used for this purpose. The estimation of Wilk's criterion was done using following relationship.

$$\text{‹}\Lambda\text{›} = \frac{|E|}{|E+V|}$$

Where,

Λ = Wilk's criterion

$|E|$ = Determinant of error matrix and

$|E + V|$ = Determinant of error + variety matrix

The significance of '^' was tested by:

$$\mathbf{V\ (Stat) = -m \log e\ \Lambda = -\ [n - (P + Q + 1) / 2] \log e\ '\Lambda'}$$

Where, m = n-(P + Q +1) / 2

P = Number of variables or characters i.e.14

Q = Number of varieties -1 (or d.f. for populations) i.e., 20-1 = 19

n = degree of freedom for error + varieties

$$\text{Log e '}\Lambda\text{'} = 2.3026 \log 10\ '\Lambda'$$

V (Stat) is distributed as χ^2 with PQ degrees of freedom i.e., (14 x 19) = 266 in the present study.

ii) Transformation of correlated variables

In the present model, computation of D^2 values were reduced to simple summation of the differences in mean values of various characters of the two genotypes *i.e.* Σd^2_i. Therefore, transformation of correlated variables into uncorrelated ones was done before working out the D^2 values. Transformation was done using pivotal condensation method.

iii) Computation of D^2 values

For the given combination of i and j genotype, the mean deviation *i.e.* Yit – Yjt, where t = 1, 2…p variables are computed and the D^2 values were calculated.

iv) Testing the significance of D^2 values

The D^2 value obtained for a pair of population is taken as calculated value of χ^2 and is tested against the tabulated value of χ^2 for P degree of freedom where P is the number of characters considered. In the present study P is 14.

v) Contribution of individual characters towards divergence

In all combinations each character was ranked based on their contribution towards divergence between two entries ($d_i = Y_i^t - Y_j^t$). Rank 1 is given to the highest mean difference and rank P to the lowest difference, where, P is the total number of characters. Percentage contribution towards genetic divergence was calculated using the following formula.

$$\textbf{Percentage contribution of a character X} = \frac{N}{M} \times 100$$

Where,

X = Percent contribution of character

N = Number of genotype combinations where the character was ranked first.

M = All possible combinations of number of genotypes considered in the present study.

vi) Grouping of genotypes into various clusters

The grouping of genotypes into different clusters was done using the Tocher's method as described by Rao (1952). The criterion was that the two varieties belonging to the same cluster should at least on an average show a smaller

D^2 value than those belonging to different clusters. For this purpose D^2 values of all combinations of each genotype were arranged in ascending order of magnitude in tabular form as described by Singh and Chaudhary (1977). To start with, two populations having the smallest D^2 value from the first two populations was added. Similarly, the next nearest fourth population was considered and this procedure was continued. At certain stage when it was felt that after adding a particular population there was an increase in the average D^2, that population was not considered for including in that cluster. The genotypes of the first cluster were then eliminated and the rest were treated in a similar way. This procedure was continued until all the genotypes were included into one or other clusters.

vii) Average intra-cluster distance

The average intra cluster distances were calculated by formula given by Singh and Chaudhary (1977).

$$\textbf{Square of the intra cluster distances} = \frac{\sum D_i^2}{n}$$

Where,

$\Sigma D_i^{2=}$ sum of distances between all possible combinations (n) of the populations included in a cluster.

n = number of possible combinations

viii) Average inter-cluster distance

Clusters were taken one by one and the distances from other clusters were calculated. The distance between two clusters was the sum of D^2 values between the genotypes of one cluster to each of the genotypes of the other cluster divided by the product of number of genotypes in both the clusters under consideration. The square root of the average D^2 value gave the genetic distance between the clusters. Based on D^2 values (inter cluster distance) the scale given by Rao (1952) for rating of the disease was adopted and the cluster diagram was prepared.

$$\textbf{Average-inter cluster distance} = \frac{\sum D_i^2}{(n_1 \, X \, n_2)}$$

Where,

D^2i = Sum distances between all possible combinations (n1, n2) of the entries included in the cluster study.

n_1 and n_2 = number of genotypes of two clusters.

Category 'D' Value

Closely related	: Below 22
Moderately divergent	: Between 22 and 30
Highly divergent	: Above 30

ix) Cluster Diagram

The clusters and their mutual relationship were presented diagrammatically. The square root of average D^2, which is an approximate measure of divergence between groups, had been used to denote the distance.

3.3.9 The Additive Main effects and Multiplicative Interaction (AMMI)

The Additive Main effects and Multiplicative Interaction (AMMI) model is a statistical model used in the analysis of multi-environment trial data, often in agricultural research. It's used to partition the variability in a dataset into additive effects and multiplicative interactions between factors Patterson and Williams (1976). The AMMI model can be expressed as follows:

$$Y_{ij} = \mu + g_i + e_j + \sum_{n=1}^{N} \tau_n \gamma_{in} \delta_{jn} + \varepsilon_{ij}$$

Where,

Y_{ij}	Observed mean yield of the i^{th} genotype (i=1,….,I) in the j^{th} environment (j=1,..,J)
μ	The grand mean

gi	the genotype deviations from the grand mean
ej	environment deviations from the grand mean
τn	The eigenvalue of the PC analysis for axis *n*
γin	The i^{th} genotype principal components cores for axis *n*
δjn	the j^{th} environment principal component scores for axis *n*
N	the number of principal components retained in the model
Eij	The error term

Table 3.6: Pooled analysis of variance as per AMMI model

Sourceof variation	d. f.	Meansquare	ExpectedMS
Total	(ger-1)		
Treatment	(ge-1)		
Genotypes	(g-1)	MS1	MS1/Ms3
Environment	(e-1)	MS2	MS2/Ms3
G X E	(g-1) (e-1)	MS3	MS3/Mse
IPCAI	(g+e-1-2n)	MS4	MS4/Mse
IPCAII	(g+e-1-2n)		
IPCAIII	(g+e-1-2n)		
Residual	(g+e-1-2n)	MSe	

Interpretation of AMMI biplots

The abscissa of the biplot represents the main effects, while its ordinates represent the IPC1 scores showing GE of the genotypes and environments. Displacements from the X-axis indicate differences in main (additive) effects, whereas displacement from the Y-axis

indicates differences in interaction effects. An important interpretation of the biplot is that the main effect for genotypes reflects breeding advances, while the main effect for environments reflects the overall comparison of environments. From the biplot the genotypes are classified in four distinct classes *viz.*, genotypes with high mean and positive IPCAI; genotypes with high mean and negative IPCAI; genotypes with low mean and negative IPCAI and genotypes with low mean and positive IPCAI.

Genotypes with high mean performance and stability must fulfill two criteria *viz.*, least deviation from the horizontal line (IPCAI score = 0) and high mean performance (right- hand side from the vertical line) while the genotypes having most deviating IPCA scores are regarded as least stable genotypes.

In AMMI 2 interaction biplot between IPCAI and IPCAII, the environmental scores are joined to the origin by side-lines. Sites with short spokes do not exert strong interactive forces. Those with long spokes exert strong interaction. The genotypes occurring close together on the plot will tend to have similar yields in all environments, while genotypes far apart may either differ in mean yield or show a different pattern of response over the environments. Hence, the genotypes near the origin are not sensitive to environmental interaction and those distant from the origins are sensitive and have large interaction. Genotypes and environments that fall in the same sectors interact positively; if they fall in opposite sectors interact negatively and if they fall into adjacent sectors, interaction is somewhat more complex.

AMMI-based stability indexes

First, let's define some symbols: *N'*is the number of significant interation principal component axis (IPCs) that were retained in the AMMI model via F tests); λ_n is the singular value for the IPC and correspondingly λ^2_n its eigen value; γ_{in} is the eigenvector value for i^{th} genotype; δ_{jn} is the eigenvector value for the t^h environment. PC1, PC2, and PCn.. are the scores of 1st, 2nd, and nth IPC; respectively; *θ1, θ2*, and *θn* are percentage sum of squares explained by the 1st, 2nd, and nth IPC, respectively.

AMMI Based Stability Parameter (ASTAB) (Rao and Prabhakaran 2005).

$$ASTAB = \sum_{n=1}^{N'} \lambda_n \gamma_{in}^2$$

AMMI Stability Index (ASI) (Jambhulkar *et al*. 2017)

$$ASI = \sqrt{\left[PC_1^2 \times \theta_1^2\right] + \left[PC_2^2 \times \theta_2^2\right]}$$

AMMI-stability value (ASV) (Purchase *et al*. 2000).

$$ASV_i = \sqrt{\frac{SS_{IPCA1}}{SS_{IPCA2}}(\text{IPCA1})^2 + (\text{IPCA2})^2}$$

Weighted average of absolute scores (WAAS) (Olivoto *et al*. 2019)

$$WAAS_i = \sum_{k=1}^{p} |IPCA_{ik} \times \theta_k / \sum_{k=1}^{p} \theta_k$$

3.3.10 Weighted Average of Absolute Scores

Compute the Weighted Average of Absolute Scores (Olivoto *et al*. 2019) for quantifying the stability of *g* genotypes conducted in *e* environments using linear mixed-effect models. The weighted average of absolute scores is computed considering all Interaction Principal Component Axis (IPCA) from the Singular Value Decomposition (SVD) of the matrix of genotype-environment interaction (GEI) effects generated by a linear mixed-effect model, as follows:

$$WAASB_i = \sum_{k=1}^{p} |IPCA_{ik} \times EP_k| / \sum_{k=1}^{p} EP_k$$

where $WAASB_i$ is the weighted average of absolute scores of the *i*th genotype; $IPCA_{ik}$ is the score of the *i*th genotype in the *k*th Interaction Principal Component Axis (IPCA); and EP_k is the explained variance of the *k*th IPCA for *k* = 1,2,..,*p*, considering $p = min(g - 1; e - 1)$.

3.3.11 Analysis as per GGE biplot model

GGE (Genotype main effect plus GE Interaction) is a linear-bilinear model that removes the effect of environment and expresses the function of genotypes and the genotype × environment interaction effects. This model is used when the environments are the main source of variation in relation to the contributions of the genotypes and the genotype × environment interaction with respect to the total variability. A Microsoft Windows application, GEA-R, was used to construct the GGE biplots and the results were further confirmed by a software named PB tools. The GGE biplot were constructed using the first two principal components PC1 and PC2 that were derived from subjecting environment centered data for each trait. The data were not transformed ("Transform= 0"), un-scaled ("scaling = 0") and were environment-centered ("Cantering = 2"). This provided informationon the cultivars that were suitable for the different environments, investigation of stability of cultivars.

$$Y_{ij} = \mu + e_j + \sum_{n=1}^{N} \tau_n \gamma_{in} \delta_{jn} + \varepsilon ij$$

The linear model for GGE biplot,

Where,

Yij	=	the yield of the ith genotype(*i=1,..,i*) in the jth environment (*j=1,..,j*)
μ	=	The grand mean
ej	=	The environment deviations from the grand mean
τn	=	The eigen value of the PC analysis axis *n*
γin	=	The genotype and environment principal components score for axis *n*
δjn	=	The genotype and environment principal components score for axis *n*
N	=	The number of principal components retained in the model
εij	=	The error term

Interpretation of GGE biplots

The inner product property of the biplot is the value of each element is visualized by product of length of genotype vector, environment vector and cosine value of the angle between them in the biplot which is the basis of genotype and test environment evaluation. The biplot shows specific interactions between a genotype and an environment. Biplot can be interpreted as: if the angle between environmental and genotypic vector is less than 90° (acute) than the performance of a genotype in an environment is better than average; it is lower than average if the angle is more than 90° (obtuse); and it is near average if the angle is about 90°. These interpretation of "inner product" principle are valid regardless of the single value partitioning method. Ranking the genotypes based on performance in any environment and for ranking the environments on the basis of relative performance of any genotype can be concluded by this graph.

The "which won where" function of a GGE biplot is an extended form of the "pair- wise comparison" of genotypes in which an irregular polygon is depicted on the genotypes that are furthest from the biplot origin and a set of straight line that radiate from the biplot origin which intersects with the polygon sides at right angle. Each section points out that genotypes presented in that section performed equally well in those environments which were also present in concerned section. While genotypes located on the opposite section are having the cross-over G × E interactions.

The purpose of test environment evaluation is to identify the superior genotypes for mega-environment. It is done by elucidating the "discriminativeness vs. representativeness" view of GGE biplot where an ideal test environment should be discriminating the genotypes as well as representing the mega-environment. The GGE biplot based on un-scaled, non-transformed and environment focused data, the environment vectors shows

mean standard deviation of varietal means. This can be used for identifying the representative environment which can evaluate/ discriminate the genotypes. The environment with longest vector and smallest angle with average environmental axis (AEA) are interpreted as most discriminating environment, while the longer environmental vector with larger angle can be useful to identify the unstable genotypes during selection in that environment.

The “mean vs. stability” view of GGE biplot based on un-scaled, non-transformed and genotype focused SVP of the data is an effective tool to identify the genotypes with higher mean performance and higher stability across a mega-environment. In biplot, the small circle points out the average environment (the average coordinates of all test environments) and a single line with arrow passes through biplot origin and average environment is called as average environment axes (AEA). The arrow points towards high performance for that character. The line perpendicular to the AEA shows the variability in particular genotype for concerning trait. The stable genotype should have higher than the mean performance and least deviation from the average environment axis (AEA).

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).

CHAPTER-IV
RESULTS AND DISCUSSION

RESULTS AND DISCUSSION

The primary objective of this study was to enhance our comprehension of the variations, diversities, and interrelationships among qualitative, quantitative, and biochemical characteristics of Foxtail millet. The research project titled "Stability and Genetic Diversity Analyses in Foxtail Millet [*Setaria italica* (L.) P. Beauv.] Genotypes" was conducted at the School of Agricultural Sciences (SAS), Medziphema Campus, Nagaland. The experimentation took place at the experimental farm specializing in Genetics and Plant Breeding, spanning the *kharif* season of 2022 and the *Rabi* season of 2023. The study encompassed four distinct environments featuring varied sowing dates.

The data was recorded on 18 qualitative, 14 quantitative and five micronutrient parameters characters and analysed by using statistical methods and results are discussed under following headings.

4.1. QUALITATIVE TRAITS

4.1.1 Frequency Distribution

The frequency distributions of different phenotypic classes of the 14 qualitative traits revealed large variation for each trait. The results for each trait are described below briefly and presented in Table 4.1.

4.1.1.1 Plant: Growth habit

Growth habit of the 3 classes (erect, decumbent, and prostrate) revealed intriguing insights within a dataset of 30 foxtail millet genotypes. Among these genotypes, 70 per cent displayed an erect growth habit, comprising 21 genotypes. Conversely, the decumbent growth habit was observed in 20 per cent of the genotypes, accounting for six genotypes. The remaining 10 per cent exhibited a prostrate growth habit, totalling three genotypes.

4.1.1.2 Leaf: Colour

The observed leaf colors range from light green to dark green, with a small representation of purple; no genotypes displayed yellow or deep purple leaf colors in this dataset. This study delves into the leaf color characteristics of a diverse set of genotypes encompassing 30 foxtail millet variants. The results highlight a spectrum of leaf colors within the population. Notably, the most prevalent leaf color was light green, accounting for 46.67 per cent of the genotypes, with 14 instances observed. Green leaves were also common, constituting 26.67 per cent of the genotypes, with eight occurrences. Meanwhile, dark green leaves were observed in 20 per cent of the genotypes, totalling six instances. Remarkably, there were no genotypes exhibiting yellow or deep purple leaf colors, while a modest 6.67 per cent of the genotypes exhibited a striking purple hue, represented by two genotypes.

4.1.1.3 Plant: Pigmentation at auricle

This study delves into the intriguing aspect of pigmentation at the auricle of 30 different foxtail millet genotypes. The results illuminate a distinct divide within the population regarding this trait. A significant majority, constituting 83.33 per cent of the genotypes, displayed an absence of pigmentation at the auricle, encompassing 25 genotypes. In contrast, a smaller proportion, representing 16.67 per cent of the genotypes, exhibited the presence of pigmentation at the auricle, accounting for five genotypes. This classification of the presence or absence of pigmentation at the auricle serves as a valuable marker for distinguishing foxtail millet genotypes, providing insights into the genetic diversity underlying this particular trait.

4.1.1.4 Leaf: Attitude

This study revealed leaf attitude characteristics among 30 different foxtail millet genotypes. The findings reveal a clear divergence in this trait within the

population. Notably, 73.33 per cent of the genotypes displayed a droopy leaf attitude, representing the majority with 22 instances. In contrast, a smaller proportion, constituting 26.67 per cent of the genotypes, exhibited an erect leaf attitude, accounting for eight genotypes. This classification, distinguishing between erect and droopy leaf attitudes, provides valuable insights into the variation present among foxtail millet genotypes, shedding light on an essential aspect of their growth and development.

4.1.1.5 Leaf Sheath: Pubescence

This study investigated into the intriguing trait of leaf sheath pubescence among 30 diverse foxtail millet genotypes. The results illuminate a distinct division within the population in relation to this characteristic. A substantial majority, comprising 70 per cent of the genotypes, exhibited an absence of leaf sheath pubescence, totalling 21 genotypes. In contrast, a smaller yet significant proportion, accounting for 30 per cent of the genotypes, displayed the presence of leaf sheath pubescence, encompassing nine genotypes. This classification, differentiating between the absence and presence of leaf sheath pubescence, offers valuable insights into the genetic diversity within foxtail millet genotypes.

4.1.1.6 Leaf sheath: Intensity of Pubescence

This study investigated the intriguing trait of leaf sheath pubescence intensity across 30 diverse foxtail millet genotypes. The findings illuminate a nuanced picture within the population regarding this particular characteristic. A significant majority, comprising 73.33 per cent of the genotypes, exhibited low intensity of leaf sheath pubescence, represented by 22 instances. In contrast, only 3.33 per cent of the genotypes displayed a medium intensity of pubescence, accounting for a single genotype. Moreover, 23.33 per cent of the genotypes showcased a high intensity of leaf sheath pubescence, constituting 7

genotypes. This classification, differentiating between low, medium, and high levels of pubescence intensity, provides valuable insights into the range of diversity within foxtail millet genotypes.

4.1.1.7 Leaf Blade: Pubescence

This study delves into the fascinating characteristic of leaf blade pubescence among 30 diverse foxtail millet genotypes. The results unveil a clear divide within the population in relation to this trait. The majority, representing 86.66 per cent of the genotypes, exhibited an absence of leaf blade pubescence, totalling 26 genotypes. In contrast, a smaller yet noteworthy proportion, accounting for 13.33 per cent of the genotypes, displayed the presence of leaf blade pubescence, encompassing four genotypes. This classification, distinguishing between the absence and presence of leaf blade pubescence, provides valuable insights into the genetic diversity within foxtail millet genotypes.

4.1.1.8 Inflorescence: Shape

This study explores the intriguing diversity in inflorescence shape among 30 distinct foxtail millet genotypes. The findings reveal a pronounced variance within the population with regard to this specific characteristic. A substantial majority, comprising 86.67 per cent of the genotypes, exhibited an oblong inflorescence shape, representing 26 genotypes. In contrast, a much smaller proportion, accounting for 6.67 per cent each, showcased a pyramidal or cylindrical inflorescence shape, with two genotypes in each category. This classification, differentiating among oblong, pyramidal, and cylindrical inflorescence shapes, offers valuable insights into the genetic diversity inherent to foxtail millet genotypes.

4.1.1.9 Inflorescence: Bristles

This study delves into the intriguing trait of inflorescence bristles among 30 diverse foxtail millet genotypes. The results emphasize a clear majority within the population concerning this characteristic. An overwhelming 93.33 per cent of the genotypes exhibited the presence of inflorescence bristles, constituting 28 genotypes. In contrast, a significantly smaller proportion, representing only 6.67 per cent of the genotypes, displayed the absence of inflorescence bristles, with just two genotypes falling into this category. This classification, distinguishing between the presence and absence of inflorescence bristles, underscores the prevalence of this trait within foxtail millet genotypes.

4.1.1.10 Inflorescence: Apical sterility

This study investigated into the intriguing characteristic of inflorescence apical sterility among 30 diverse foxtail millet genotypes. The findings reveal a noticeable division within the population with respect to this trait. A substantial majority, constituting 76.67 per cent of the genotypes, exhibited the absence of inflorescence apical sterility, comprising 23 genotypes. In contrast, a noteworthy proportion, accounting for 23.33 per cent of the genotypes, displayed the presence of apical sterility in their inflorescences, totalling seven genotypes. This classification, distinguishing between the absence and presence of inflorescence apical sterility, offers valuable insights into the genetic diversity within foxtail millet genotypes.

4.1.1.11 Inflorescence: Compactness

This study delves into the intriguing trait of inflorescence compactness among 30 diverse foxtail millet genotypes, shedding light on the varying characteristics within the population. Notably, the majority, constituting 60.00 per cent of the genotypes, exhibited a compact inflorescence structure, accounting for 18 genotypes. In contrast, 23.33 per cent of the genotypes

displayed a medium compactness level, with seven genotypes falling into this category. A smaller yet significant proportion, representing 16.67 per cent of the genotypes, showcased a lax inflorescence structure, totalling five genotypes. This classification, differentiating between lax, medium, and compact inflorescence compactness, provides valuable insights into the genetic diversity present among foxtail millet genotypes.

4.1.1.12 Inflorescence: Lobes

This study delves into the intriguing characteristic of inflorescence lobes among 30 diverse foxtail millet genotypes, providing insights into the variation within the population. A substantial majority, comprising 53.33 per cent of the genotypes, displayed the absence of inflorescence lobes, encompassing 16 genotypes. In contrast, 46.67 per cent of the genotypes exhibited the presence of lobes in their inflorescences, with 14 genotypes falling into this category. This classification, distinguishing between the absence and presence of inflorescence lobes, underscores the diversity within foxtail millet genotypes concerning this specific trait.

4.1.1.13 Seed: Colour

This study investigated the intriguing diversity in seed color among 30 distinct foxtail millet genotypes, shedding light on the variation within the population. Remarkably, the vast majority, accounting for 86.67 per cent of the genotypes, displayed brown-colored seeds, totaling 26 genotypes. Yellow-colored seeds were observed in 10.00 per cent of the genotypes, comprising three instances, while a single genotype, representing 3.33 per cent, exhibited orange-colored seeds. Strikingly, no genotypes exhibited whitish or black seed colors in this dataset. This classification, distinguishing between the different seed colors, offers valuable insights into the genetic diversity inherent in foxtail millet genotypes.

4.1.1.14 Seed: Shape

This study investigated into the intriguing characteristic of seed shape among 30 diverse foxtail millet genotypes, providing illuminating insights into the uniformity within the population. Remarkably, all of the genotypes, representing 100.00 per cent of the total, exhibited an oval seed shape, totalling 30 genotypes. Notably, none of the genotypes displayed an elliptical seed shape in this dataset. This classification, differentiating between oval and elliptical seed shapes, highlights the consistent nature of seed shape among foxtail millet genotypes and serves as a foundational element for further research aimed at understanding the implications of seed shape on crop development, yield, and adaptability, offering valuable information for agricultural practices and breeding programs.

4.1.1.15 Degree of lodging at maturity

The assessment focuses on the degree of lodging at maturity for foxtail millet. The lodging, or bending or breaking of the plant stems near the base, was categorized into three levels: very slight, medium, and extensive. Among the observed genotypes, an impressive 100 per cent—a total of 30 genotypes—demonstrated a very slight degree of lodging at maturity. Interestingly, there were no genotypes recorded with a medium or extensive degree of lodging.

4.1.1.16 Senescence

Senescence, the biological aging or deterioration of cells or tissues, was categorized into two statuses: actively growing and dead. Among the observed genotypes, all 30 genotypes—constituting 100 per cent of the observed genotypes—were found to be in the actively growing status, displaying no instances of being in a dead status. This data highlights a crucial aspect of the study, emphasizing the vitality and active growth within the genotypes under consideration.

4.1.1.17 Lobe compactness

Present study on foxtail millet, focusing on lobe compactness. The character was assessed in three categories: lax, medium, and compact. Out of the observed genotypes, 16.67 per cent (five genotypes) exhibited lax lobe compactness, indicating a less tightly packed structure. A higher percentage, constituting 23.33 per cent (seven genotypes), displayed a medium lobe compactness, suggesting a moderate level of compactness. However, the majority, accounting for 60.00 per cent (18 genotypes), showcased a compact lobe structure, reflecting a tightly packed arrangement.

4.1.1.18 Plant: Pigmentation

A characterization study concerning plant pigmentation in 30 foxtail millet genotypes, the character "Plant: Pigmentation" was categorized into two statuses: absent and present. Out of the observed genotypes, a significant majority of 83.33 per cent (25 genotypes) showed an absence of pigmentation, indicating a lack of coloration or pigmented elements. On the other hand, a smaller percentage, constituting 16.67 per cent (5 genotypes), exhibited the presence of pigmentation, signifying the existence of color or pigmented features within the plants.

All qualitative traits photographs represented in Appendices (Plate 4.1-4.9).

Table 4.1 Frequency distribution of 14 qualitative traits in the 30 foxtail millet genotypes.

S. No	Character	Status	Number of genotype	Percentage
1	Plant: Growth habit	Erect	21	70.00
		Decumbent	6	20.00
		Prostrate	3	10.00
2	Leaf: Colour	Light Green	14	46.67
		Green	8	26.67

		Dark green	6	20.00
		Yellow	0	0.00
		Purple	2	6.67
		Deep purple	0	0.00
3	Plant: Pigmentation at auricle	Absent	25	83.33
		Present	5	16.67
4	Leaf: Attitude	Erect	8	26.67
		Droopy	22	73.33
5	Leaf Sheath: Pubescence	Absent	21	70.00
		Present	9	30.00
6	Leaf sheath: Intensity of Pubescence	Low	22	73.33
		Medium	1	3.33
		High	7	23.33
7	Leaf Blade: Pubescence	Absent	26	86.66
		Present	4	13.33
8	Inflorescence: Shape	Oblong	26	86.67
		Pyramidal	2	6.67
		Cylindrical	2	6.67
9	Inflorescence: Bristles	Absent	2	6.67
		Present	28	93.33
10	Inflorescence: Apical sterility	Absent	23	76.67
		Present	7	23.33
11	Inflorescence: Compactness	Lax	5	16.67
		Medium	7	23.33
		Compact	18	60.00
12	Inflorescence: Lobes	Absent	16	53.33
		Present	14	46.67
13	Seed : Colour	Whitish	0	0.00
		Yellow	3	10.00
		Brown	26	86.67
		Orange	1	3.33
		Black	0	0.00
14	Seed: Shape	Elliptical	0	0.00
		Oval	30	100.00
15	Degree of lodging at maturity	very slight	30	100
		medium	0	0
		extensive	0	0
16	Senescence	actively growing	30	100
		dead	0	0
17	Lobe compactness	Lax	5	16.67

		Medium	7	23.33
		Compact	18	60.00
18	Plant: Pigmentation	Absent	25	83.33
		Present	5	16.67

A

Fig 4.1 (A, B, C) Frequency distribution of 14 qualitative traits in the 30 foxtail millet genotypes.

B

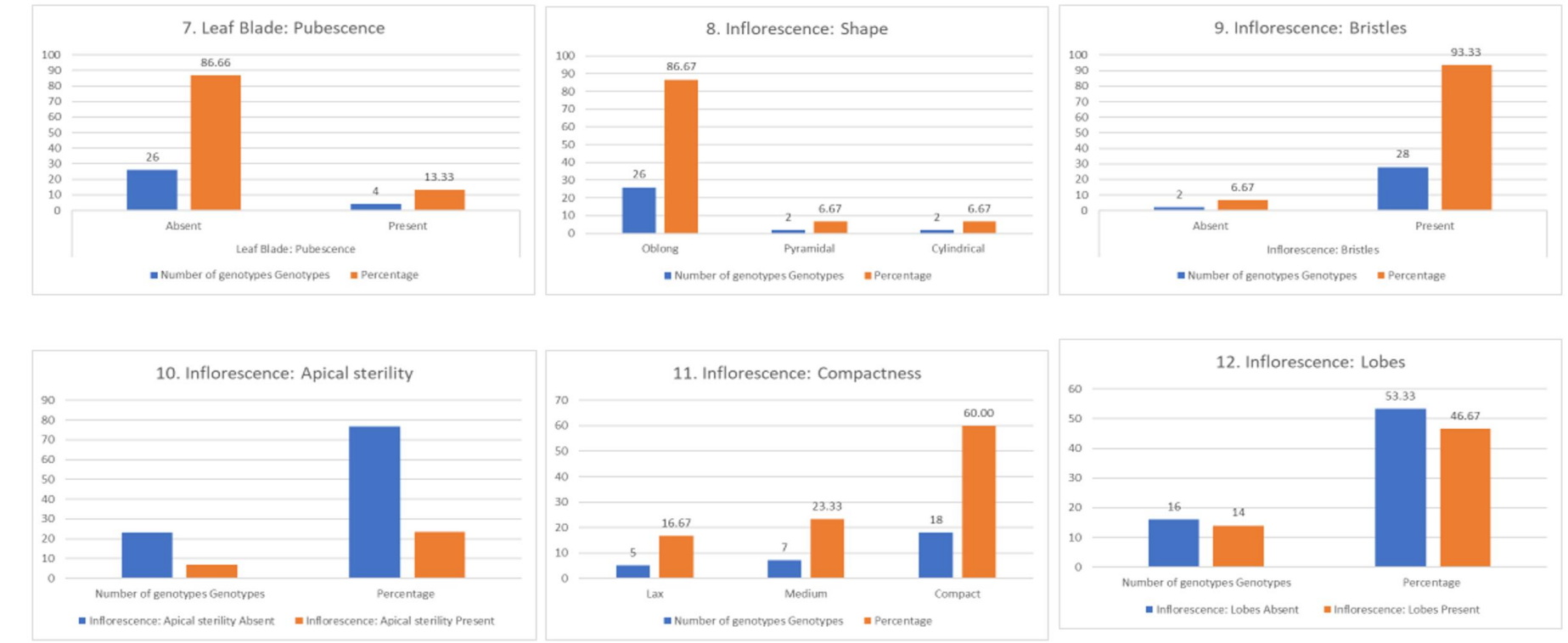


Fig 4.1(A, B, C) Frequency distribution of 14 qualitative traits in the 30 foxtail millet genotypes.

C

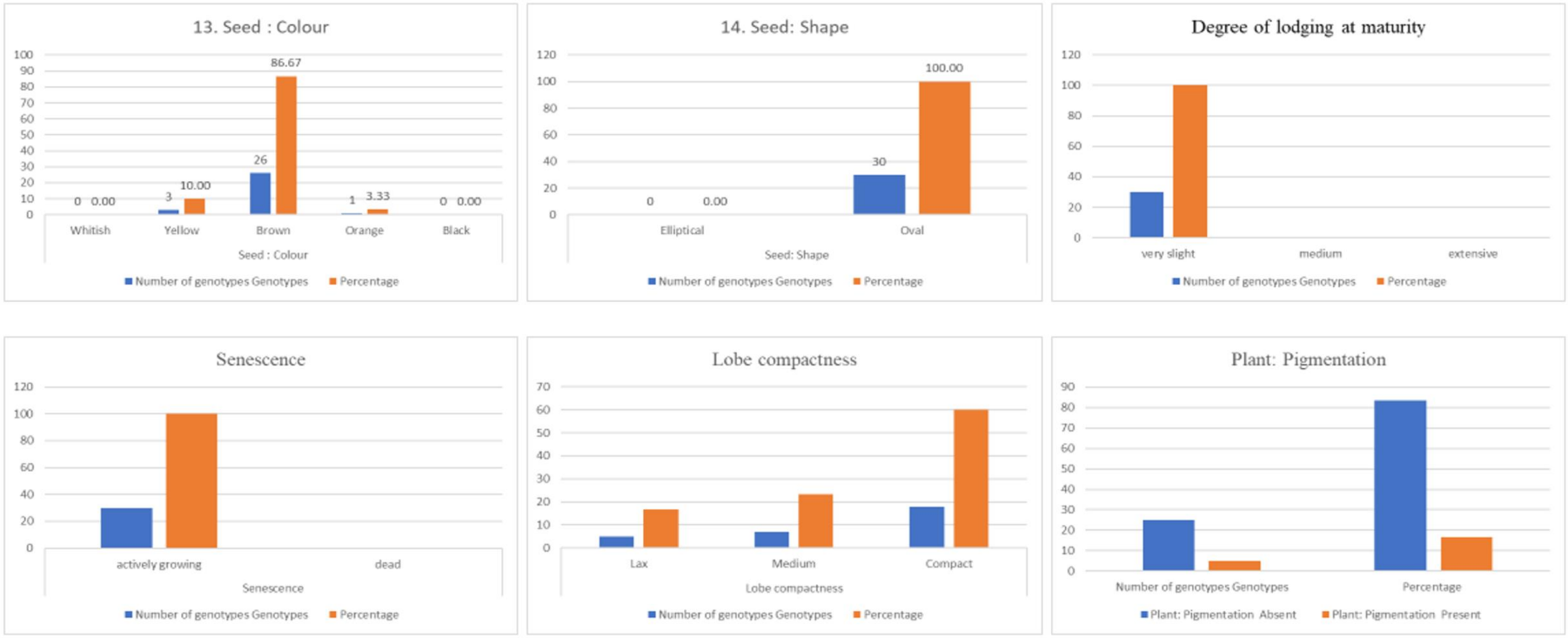


Fig 4.1 (A, B, C) Frequency distribution of 14 qualitative traits in the 30 foxtail millet genotypes.

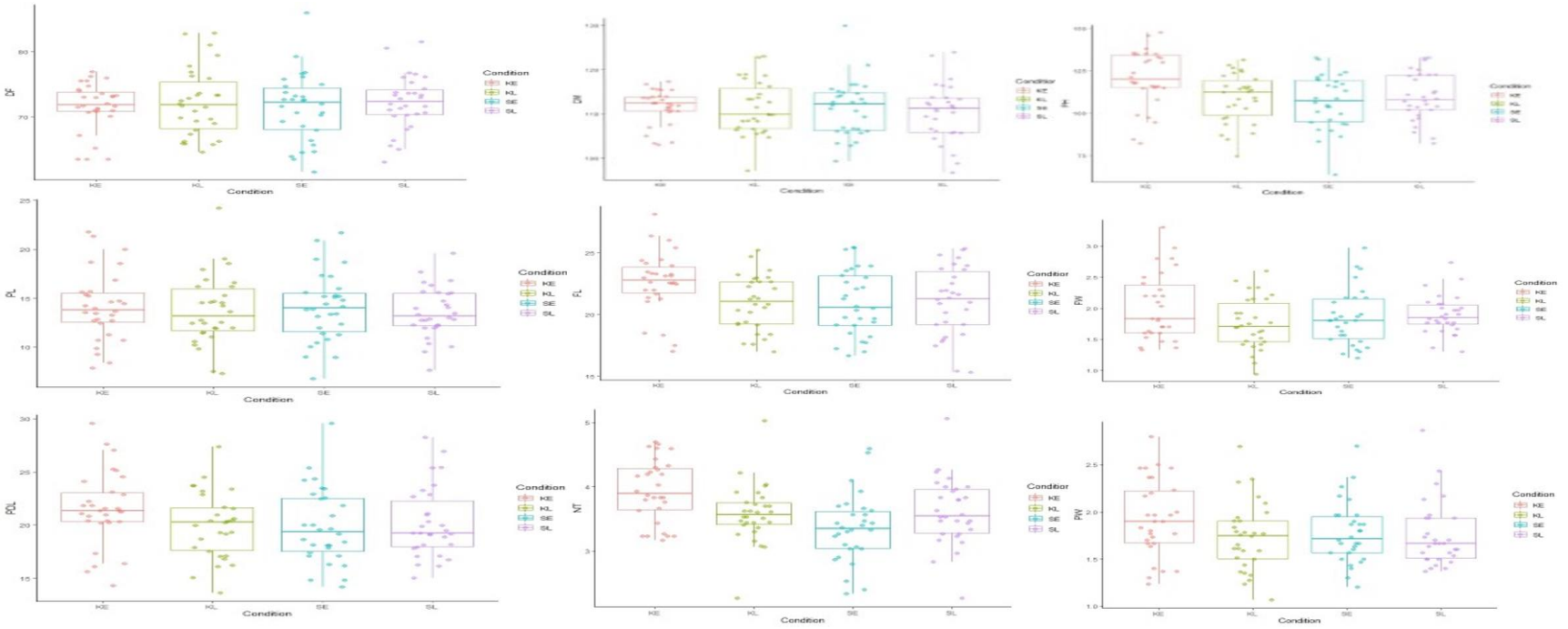
4.2 Analysis of variance

The pooled analysis of variance (ANOVA) was used to examine the interactions between different genotypes and environments. Table 4.2. Presents the results of the combined ANOVA for all genotypes across various environments, focusing on yield and its components. As indicated in Table 4.2, 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 ($p \leq 0.05$) 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.

Table 4.2. Combined Analysis of variance for pooled data

		Mean Squares							
S. No	**Source of Variation**	**Seasons (DF=3)**	**Rep within Season (DF=8)**	**Genotypes (DF=29)**	**Year X Season (DF=87)**	**Pooled Error (DF=232)**	**CD for Seasons**	**CD for Genotypes**	**CD for Season X Genotypes**
1	**Days to 50 per cent flowering**	63,745.27*	2.61	111.69*	34.26*	1.00	0.63	1.06	2.12
2	**Days to maturity**	2,39,669.82*	5.16	129.99*	37.73*	1.00	0.88	1.06	2.12
3	**Plant height (cm)**	38,415.20*	2.52	125.17*	43.80*	1.00	0.61	1.06	2.12
4	**Panicle length (cm)**	262.10*	0.52	36.42*	6.41*	1.00	0.28	1.06	2.12
5	**Flag leaf length (cm)**	60.75*	4.87	45.19*	10.65*	2.80	0.85	1.77	3.55
6	**Flag leaf width (cm)**	1.07*	0.27	1.31*	0.31*	0.06	0.2	0.27	0.53
7	**Peduncle length (cm)**	989.87*	0.84	23.51*	5.25*	1.00	0.36	1.06	2.12
8	**No. of tillers per plant**	93.98*	3.98	5.40*	1.79*	1.00	0.77	1.06	2.12
9	**Panicle width (cm)**	188.85*	2.43	16.90*	3.11*	1.00	0.6	1.06	2.12
10	**Biological yield (g)**	1,236.78*	1.01	34.30*	5.04*	1.00	0.39	1.06	2.12
11	**Harvest index (per cent)**	2,636.12*	1.71	6.42*	2.97*	1.00	0.51	1.06	2.12
12	**Fodder yield per plant(g)**	423.90*	0.91	36.07*	4.50*	1.00	0.37	1.06	2.12
13	**Test weight**	1.05*	0	0.36*	0.01*	0.00	0.01	0.06	0.11
14	**Grain yield per plant(g)**	490.15*	4.43	60.49*	13.12*	3.20	0.82	1.9	3.79

Significance at 5 per cent (*).



A

Fig 4.2. (A, B). Box Plots Illustrating Four Environmental Variances of yield and yield related traits

B

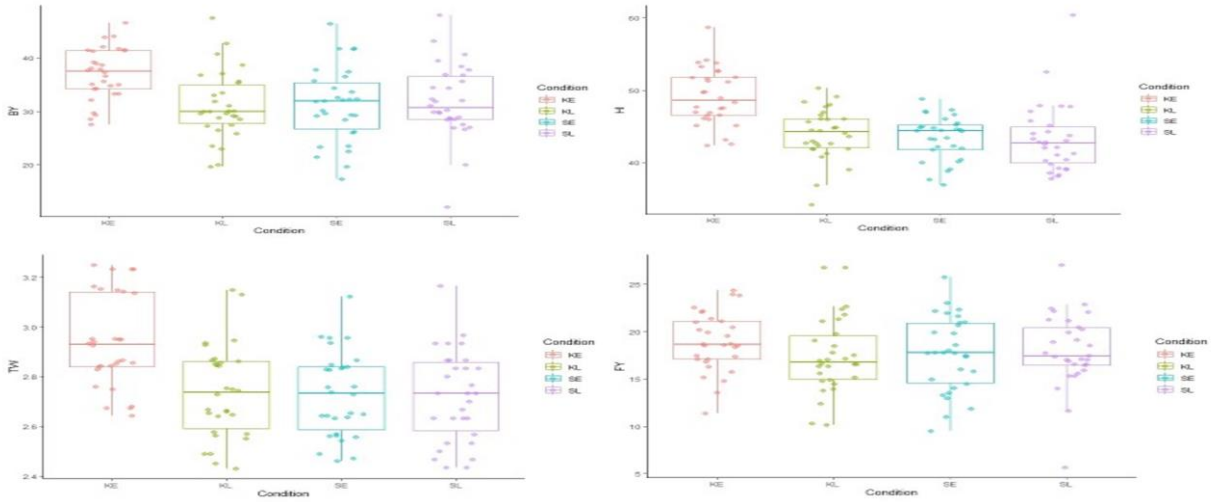


Fig 4.2 (A, B). Box Plots Illustrating Four Environmental Variances of yield and yield related traits

4.3 Mean performance and range

Table 4.3 presents the mean, range, and coefficient of variation pertaining to the diverse traits observed within the set of 30 foxtail millet genotypes of pooled environmental data. This table illustrates the collective performance averages and the extent of diversity across the 30 tested genotypes concerning fourteen distinct characteristics. The majority of traits exhibited a considerable span of variation across the genotypes, as indicated by their mean performances. Analysing the differences in mean values underscored noteworthy levels of variability within these traits among the genotypes. The subsequent description outlines the performance of each individual trait.

4.3.1 Days to 50 per cent flowering

The study revealed a significant range in the number of days required for 50 per cent flowering, spanning from a minimum of 64.53 days to a maximum of 79.58 days, with a mean of 71.88 ± 1.83 days. This substantial variability underscores the diverse flowering patterns within the genotypes under investigation. Notably, the top 5 genotypes with the lowest days to 50 per cent flowering are G8 (64.94 days), G17 (64.53 days), G7 (68.28 days), G6 (68.32 days), and G19 (69.91 days). These genotypes exhibit an expedited flowering process, potentially indicating favourable characteristics for a quicker developmental cycle. Conversely, the lowest 5genotypes with the highest days to 50 per cent flowering include G3 (79.58 days), G18 (77.24days), G1 (76.46 days), G4 (75.76 days), and G5 (74.56 days). These genotypes demonstrated delayed flowering pattern, suggesting a longer duration for reaching the 50 per cent flowering stage, which could be of interest for specific breeding or growth strategies.

4.3.2 Days to maturity

The days to maturity in the study varied from G1 (122.99) exhibits maximum, while G8 (101.00) exhibits lowest with grand mean was111.11 ± 2.15. Table4.3 presents data concerning the days to maturity across various genotypes of foxtail millet. Among these genotypes, G1 exhibits the lengthiest time to maturity with a score of 122.99, followed by G3 at 115.72, G16 at 115.53, and G18 at 118.67. Conversely, the genotypes with the shortest maturity period are G8 at 101, G17 at 104.23, G30 at 106.09, and G29 at 106.64. Notably, G8 demonstrates the most favourable trait of the shortest time to maturity.

4.3.3 Plant height (cm)

The study focused on the plant height variability within different genotypes. The range of plant heights was substantial, spanning from the tallest genotype G1, which reached a height of 133.6, to the shortest genotype G15, with a height of 87.53. The overall average height across all genotypes was 111.47 ± 5.18. The four genotypes with the greatest plant heights were G1 at 133.6, G2 at 128.44, G17 at 123.86, and G30 at 131.69. Conversely, the four genotypes with the lowest plant heights were G6 at 87.73, G15 at 87.53, G16 at 87.64, and G13 at 96.8. This data underscores the significant variation in plant heights among different genotypes, with G1 emerging as the tallest and G15 as the shortest among them.

4.3.4 Panicle length (cm)

The study investigated the diversity in panicle length among different genotypes. The range of panicle lengths was notable, ranging from the longest in genotype G25 at 20.13 cm to the shortest in genotype G11 at 8.29 cm. The average panicle length across all genotypes was 13.08 ± 1.09 cm. The top four genotypes with the longest panicle lengths were G25 at 20.13 cm, G8 at 19.29

cm, and G21 at 17.38 cm, and G30 at 16.96 cm. On the other hand, the four genotypes with the shortest panicle lengths were G11 at 8.29 cm, G19 at 9.88 cm, G12 at 9.87 cm, and G3 at 10.97 cm. This data emphasizes the considerable variability in panicle lengths among different genotypes, with G25 having the longest panicles and G11 having the shortest among the studied genotypes.

4.3.5 Flag leaf length (cm)

The study delved into the variation of flag leaf lengths among different genotypes. The range of flag leaf lengths was significant, with the maximum length observed in genotype G5 at 25.47 cm, and the minimum in genotype G30 at 16.73 cm. The overall average flag leaf length across all genotypes was 21.4 ± 0.94 cm. Among the top four genotypes with the longest flag leaf lengths were G5 at 25.47 cm, G28 at 24.25 cm, G2 at 23.75 cm, and G16at23.53 cm. On the contrary, the four genotypes with the shortest flag leaf lengths were G30 at 16.73 cm, G13 at 17.19 cm, G10 at 18.2 cm, and G19 at 19.83 cm. This data highlights substantial diversity in flag leaf lengths across different genotypes, with G5 exhibiting the longest flag leaf and G30 shows the shortest among the studied genotypes.

4.3.6 Flag leaf width (cm)

The study investigated the variation in flag leaf widths among different genotypes. The observed flag leaf widths showed a notable range, with the widest leaf observed in genotype G26 at 2.54 cm and the narrowest in genotype G3 at 1.30 cm. The average flag leaf width across all genotypes was 1.88 ± 0.16 cm. The top four genotypes with the widest flag leaf widths were G26 at 2.54 cm, G17 at 2.49 cm, G18 at 2.39 cm, and G8 at 2.3 cm. Conversely, the four genotypes with the narrowest flag leaf widths were G3 at 1.3 cm, G4 at 1.39 cm, G20at 1.53 cm, and G1 at 1.5 cm. This data

underscores the substantial variability in flag leaf widths among different genotypes, with G26 having the widest flag leaves and G3 having the narrowest flag leaves among the genotypes examined.

4.3.7 Peduncle length (cm)

The study explored the variability in peduncle lengths among different genotypes. The observed peduncle lengths displayed a significant range, with the longest observed in genotype G8 at 26.01 cm and the shortest in genotype G12 at 15.12 cm. The overall average peduncle length across all genotypes was 20.14 ± 1.16 cm. Among the top four genotypes with the longest peduncle lengths were G8 at 26.01 cm, G29 at 24.63 cm, G1 at 24.78 cm, and G2 at 23.82 cm. On the contrary, the four genotypes with the shortest peduncle lengths were G12 at 15.12 cm, G11 at 17.06 cm, G10 at 17.53 cm, and G4 at 18.38 cm. This data emphasizes the considerable variation in peduncle lengths among different genotypes, with G8 having the longest peduncles and G12 having the shortest peduncles among the genotypes studied.

4.3.8 No. of tillers per plant

The study examined the variation in the number of tillers per plant among different genotypes. The observed tiller counts demonstrated a significant range, with the highest number of tillers observed in genotype G29 at 4.62 and the lowest in genotype G24 at 2.84. The average number of tillers per plant across all genotypes was 3.63 ± 0.20. The top four genotypes with the highest number of tillers per plant were G29 at 4.62, G2 at 4.11, G25 at 4.15, and G16 at 4.05. In contrast, the four genotypes with the lowest number of tillers per plant were G24 at 2.84, G27 at 2.9, G10 at 3.35, and G21 at 3.43. This data highlights the considerable variation in the number of tillers per plant among different genotypes, with G29 displaying the highest tiller count and G24 showing the lowest among the genotypes studied.

4.3.9 Panicle width (cm)

The study examined the variation in panicle widths among different genotypes. The observed panicle widths displayed a significant range, with the widest panicle width observed in genotype G30 at 2.58 cm and the narrowest in genotype G4 at 1.38 cm. The overall average panicle width across all genotypes was 1.8 ± 0.13 cm. The top four genotypes with the widest panicle widths were G30 at 2.58 cm, G18 at 2.38 cm, G8 at 2.08 cm, and G9 at 2.18 cm. On the other hand, the four genotypes with the narrowest panicle widths were G4 at 1.38 cm, G15 at 1.55 cm, G23 at 1.49 cm, and G3 at 1.45 cm. This data underscores the substantial variation in panicle widths among different genotypes, with G30 having the widest panicles and G4 having the narrowest among the genotypes studied.

4.3.10 Biological yield (g)

The study explored the variation in biological yields among different genotypes. The observed biological yields exhibited a notable range, with the highest yield observed in genotype G1 at 46.04 g and the lowest in genotype G24 at 21.75 g. The overall average biological yield across all genotypes was 32.64 ± 1.99 g. The top four genotypes with the highest biological yields were G1 at 46.04 g, G25 at 42.3 g, G22 at 38.88 g, and G18 at36.21g. In contrast, the four genotypes with the lowest biological yields were G24 at 21.75 g, G10 at 26.84 g, G27 at 26.7 g, and G12 at 27.71 g. This data emphasizes the substantial variation in biological yields among different genotypes, with G1 having the highest yields and G24 having the lowest among the genotypes studied.

4.3.11 Harvest index (%)

The study examined the diversity in harvest indices across different genotypes. The observed harvest indices displayed a significant range, with the highest

index observed in genotype G20 at 51.39 per cent and the lowest in genotype G3 at 40.43 per cent. The average harvest index across all genotypes was 44.91 ± 1.72 per cent. The top four genotypes with the highest harvest indices were G20 at 51.39 per cent, G24 at 49.33 per cent, G14 at 47.5 per cent, and G23 at 47.15 per cent. Conversely, the four genotypes with the lowest harvest indices were G3 at 40.43 per cent, G6 at 40.93 per cent, G13 at42.19 per cent, and G11 at 42.93 per cent. This data highlights the considerable variation in harvest indices among different genotypes, with G20 exhibiting the highest indices and G3 demonstrating the lowest among the genotypes studied.

4.3.12 Fodder yield per plant (g)

The study investigated the variation in fodder yields per plant across different genotypes. The observed fodder yields exhibited a substantial range, with the highest yield recorded in genotype G1 at 25.91 g and the lowest in genotype G24 at 10.97 g. The average fodder yield per plant across all genotypes was 18.02 ± 1.13 g. The top four genotypes with the highest fodder yields were G1 at 25.91 g, G25 at 22.34 g, G3 at 21.86 g, and G22 at 20.78 g. Conversely, the four genotypes with the lowest fodder yields were G24 at 10.97 g, G20 at 13.72 g, G27 at 13.44 g, and G28 at 13.4 g. This data underscores the significant variability in fodder yields among different genotypes, with G1 having the highest yields and G24 having the lowest among the genotypes studied.

4.3.13 Test weight (g)

The study focused on variations in test weights among different genotypes. The observed test weights showed a notable range, with the highest weight recorded in genotype G2 at 3.17 g and the lowest in genotype G16 at 2.52 g. The average test weight across all genotypes was 2.79 ± 0.03 g. The top four genotypes with the highest test weights were G2 at 3.17 g, G15 and G11 at

3.03 g each, and G21 at 3.00 g. On the contrary, the four genotypes with the lowest test weights were G16 and G23 at 2.52 g each, G29 at 2.59 g, and G19 at 2.60 g. This data highlights significant variability in test weights among different genotypes, with G2 displaying the highest weights and G16 demonstrating the lowest among the genotypes studied.

4.3.14 Grain yield per plant (g)

The study focused on variations in grain yields per plant across different genotypes. The observed grain yields exhibited a significant range, with the highest yield recorded in genotype G1 at 20.14 g and the lowest in genotype G24 at 10.78 g. The average grain yield per plant across all genotypes was 14.65 ± 1.05 g. The top four genotypes with the highest grain yields per plant were G1 at 20.14 g, G25 at 19.98 g, G22 at 18.14 g, and G21 at 17.17 g. Conversely, the four genotypes with the lowest grain yields per plant were G24 at 10.78 g, G29 at 10.82 g, G12 at 12.46 g, and G10 at 11.84 g. This data underscores the considerable variability in grain yields among different genotypes, with G1 displaying the highest yields and G24 having the lowest among the genotypes studied.

Table 4.3. Mean performance of 30 foxtail millet genotypes across four environments

	DF	DM	PH	PL	FL	FW	PDL	NT	IW	BY	HI	TW	FY	GY
G1	76.46	122.99	133.60	14.50	22.16	1.50	24.78	3.42	1.61	46.04	43.75	25.91	2.83	20.14
G2	74.37	108.92	128.44	15.32	23.75	1.80	23.82	4.11	1.63	32.17	44.48	17.88	3.17	14.32
G3	79.58	115.72	104.73	10.97	20.19	1.30	18.74	3.22	1.45	36.87	40.43	21.86	2.77	15.02
G4	75.76	113.33	106.36	11.08	20.75	1.39	18.38	3.90	1.38	32.18	42.95	18.33	3.07	13.86
G5	74.56	111.73	114.36	13.25	25.47	1.43	24.49	3.53	2.01	37.94	44.02	21.26	2.92	16.68
G6	68.32	108.85	87.73	12.87	19.68	1.95	20.89	3.66	1.98	31.89	40.93	18.85	2.92	13.02
G7	68.28	105.80	105.32	12.41	21.35	1.99	19.31	3.63	1.58	31.77	44.99	19.42	2.67	13.01
G8	64.94	101.00	108.96	19.29	21.68	2.30	26.01	3.70	2.08	36.65	43.33	20.68	2.73	16.00
G9	74.53	112.25	112.85	15.65	20.97	2.21	20.11	3.60	2.18	37.38	43.63	20.86	2.76	16.53
G10	71.82	113.43	99.48	14.47	18.20	1.59	17.53	3.35	1.65	26.84	43.99	15.03	2.64	11.84
G11	70.63	107.48	111.59	8.29	20.84	1.78	17.06	3.75	1.76	31.94	42.93	18.06	3.03	13.88
G12	71.19	108.55	104.99	9.87	20.81	2.19	15.12	3.43	1.98	27.71	44.84	15.25	2.93	12.46
G13	71.03	111.00	96.80	10.77	17.19	1.64	19.48	3.83	1.79	31.81	42.19	18.31	2.80	13.50
G14	73.86	114.54	97.84	15.05	22.72	1.83	15.66	3.60	1.65	29.04	47.50	15.25	2.73	13.82
G15	71.77	109.48	87.53	12.30	21.89	2.29	21.97	3.90	1.55	31.62	44.55	17.46	3.03	14.17
G16	72.45	115.53	87.64	13.31	23.53	2.13	20.24	4.05	1.51	29.77	45.52	16.09	2.52	13.69
G17	64.53	104.23	123.86	14.83	21.25	2.49	19.19	3.63	1.73	34.68	43.83	19.39	2.65	15.32
G18	77.24	118.67	119.79	14.44	22.70	2.39	21.77	3.74	2.38	36.32	41.64	21.09	2.67	15.24
G19	69.91	109.82	105.86	9.88	19.83	2.00	18.24	3.61	2.19	36.21	43.43	20.33	2.60	15.88
G20	72.45	113.81	113.66	12.62	19.02	1.62	19.85	3.53	1.45	28.18	51.39	13.72	2.95	14.44
G21	72.18	111.71	112.10	17.38	22.01	1.53	20.02	3.43	1.68	36.45	46.85	19.29	3.00	17.17
G22	69.88	108.57	118.81	15.18	22.52	1.94	21.26	4.02	1.91	38.88	46.44	20.78	2.72	18.14
G23	72.25	112.53	116.77	16.87	21.73	1.69	18.21	3.44	1.83	32.64	47.15	17.22	2.52	15.42
G24	72.13	112.26	122.22	12.77	22.29	1.73	21.76	2.84	1.49	21.75	49.33	10.97	2.89	10.78
G25	72.38	112.17	121.09	20.13	22.36	1.68	20.97	4.15	1.86	42.30	47.21	22.34	2.70	19.98
G26	73.19	113.37	112.39	13.89	21.06	2.54	19.01	3.36	1.73	30.85	44.27	17.11	2.74	13.74

G27	72.33	112.18	111.97	12.55	22.70	2.00	19.98	3.49	1.71	26.70	48.46	13.44	2.69	13.26
G28	70.53	110.70	125.40	15.57	24.25	1.92	23.89	2.90	1.96	29.62	45.84	15.80	2.87	13.82
G29	66.24	106.64	120.38	13.92	22.51	1.95	24.63	4.62	1.82	24.23	44.46	13.40	2.59	10.82
G30	71.63	106.09	131.69	16.96	16.73	1.63	19.99	3.41	2.58	28.87	47.00	15.26	2.52	13.61
Mean	71.88	111.11	111.47	13.88	21.40	1.88	20.41	3.63	1.80	32.64	44.91	18.02	2.79	14.65
Max	79.58	122.99	133.60	20.13	25.47	2.54	26.01	4.62	2.58	46.04	51.39	25.91	3.17	20.14
Min	64.53	101.00	87.53	8.29	16.73	1.30	15.12	2.84	1.38	21.75	40.43	10.97	2.52	10.78
C.V.	5.08	3.88	9.30	15.69	8.80	17.21	11.33	11.11	14.57	12.18	7.66	12.52	2.23	14.28
F ratio	3.35	4.05	5.68	6.18	4.24	4.18	5.39	3.18	4.64	6.94	2.05	8.20	31.11	4.61
F Prob.	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00	0.00	0.00
S.E.	1.83	2.15	5.18	1.09	0.94	0.16	1.16	0.20	0.13	1.99	1.72	1.13	0.03	1.05
C.D. 5 per cent	5.13	6.05	14.57	3.06	2.65	0.45	3.25	0.57	0.37	5.59	4.83	3.17	0.09	2.94
C.D. 1 per cent	6.80	8.02	19.31	4.06	3.51	0.60	4.31	0.75	0.49	7.40	6.40	4.20	0.12	3.89

Days to 50 per cent flowering (DF), Days to maturity (DM), Plant height (PH), Panicle length (PL), Flag leaf length (FL), Flag leaf width (FW), Peduncle length (PDL), No. of basel tillers per plant (NT), Panicle width (PW), Biological yield (BY), Harvest index (HI), Fodder yield per plant (FY) and Grain yield per plant (GY).

4.4 Variance component analysis

Genetic variability within a gene pool is a crucial factor for any breeding program. This variability is assessed through measures like genotypic and phenotypic variances, genotypic coefficient of variance (GCV), phenotypic coefficient of variance (PCV), heritability in broad sense (h2), and genetic advance. The genotypic coefficient of variation specifically gauges the extent of genetic diversity within a crop, representing the heritable component of variability. Hence, it is considered more informative than the phenotypic coefficient of variation. Additionally, the disparity between phenotypic and genotypic coefficients of variation indicates the influence of environmental factors (Amarnath *et al*. 2019). Furthermore, heritability and genetic advance are deemed significant parameters for selection. In this study, we computed and discussed the estimates of pooled variability and genetic parameters, including genotypic and phenotypic variances, phenotypic (PCV) and genotypic (GCV) coefficients of variation, heritability in broad sense, genetic advance, and genetic advance as a percentage of the mean. The subsequent results from this analysis are outlined and discussed below.

4.4.1 Estimation of genotypic and phenotypic coefficient of variation:

Variance is critical in crop breeding for selection, driven by both genetic and environmental factors that shape overall population variation. Genetic variance is essential for successful plant breeding, representing the inheritable component of variation. Phenotypic variance encompasses both genetic and environmental variances, where the former is inheritable to offspring, unlike the latter (Anuradha *et al.* 2014). Studies on GCV and PCV highlight significant variation and the impact of the environment on trait expression. PCV was notably higher than GCV for all traits, suggesting a strong genotype-environment interaction. The traits examined in this study demonstrated low (less than 10 per cent), moderate (10-20 per cent), and high (more than 20 per

cent) phenotypic and genotypic coefficients of variation, as classified by Sivasubramanian and Madhava Menon (1973). Detailed GCV and PCV estimates from this study are provided in Table 4.4 and Figure 4.17.

In this experiment, some traits exhibited low variability (<10 per cent), indicating consistent and stable performance. These traits, such as "days to 50 per cent flowering" (GCV: 3.89, PCV: 4.65), "days to maturity" (GCV: 3.39, PCV: 3.90), "harvest index" (GCV: 3.93, PCV: 5.49), "flag leaf length"(GCV: 7.92, PCV: 9.06), "test weight" (GCV: 6.13, PCV: 6.23), and "No. of tillers per plant" (GCV: (GCV: 8.21, PCV: 9.91), consistently reached their respective developmental stages within a narrow range of time. On the other hand, several traits demonstrated moderate variability (10-20 per cent), indicating moderate fluctuations in their measurements. Traits such as "plant height"(GCV: 10.06, PCV: 11.09), "peduncle length" (GCV: 11.87, PCV: 13.16), "panicle width" (GCV: 13.90, PCV: 15.69), "grain yield per plant" (GCV: 13.56, PCV: 15.33), "biological yield" (GCV: 14.85, PCV: 16.05), "flag leaf width" (GCV: 15.35, PCV: 17.60), "fodder yield per plant" (GCV: 16.80, PCV: 17.93), and "panicle length" (GCV: 17.85, PCV: 19.50) may exhibit slight variations but generally remain within an acceptable range.

4.4.2 Heritability and Genetic Advance:

Heritability measures how much a trait's variation is influenced by genes. Many researchers rely on heritability as a reliable indicator to effectively enhance the desired trait through selection. Broad-sense heritability, as defined by Johnson *et al.* (1955), is the proportion of total genetic variation to overall phenotypic variation, expressed as a percentage. Understanding a trait's heritability is crucial as it revealed the potential and extent of improvement achievable through selection. It gauges the parent-progeny relationship, shedding light on how much a trait can be passed down from parent to offspring. Moreover, it helps determine the role of heritability versus the

environment in trait expression. Johnson *et al*. (1955) categorized heritability as low (0-30 per cent), moderate (30-60 per cent), and high (above 60 per cent). Traits with high heritability can be effectively used by breeders to choose superior genotypes based on observable features.

Heritability, expressed as a percentage, provides valuable information about the degree to which genetic factors contribute to the variation of a trait. In this present study, test weight (96.80 per cent) exhibits high heritability, meaning that genetics largely determine the weight of the grains. similarly, "fodder yield per plant" (87.80 per cent), “grain yield per plant” (78.30 per cent), and "biological yield" (85.60 per cent) also have high heritability, suggesting that genetic factors significantly contribute to the crop's yield potential. "Plant height" (82.40 per cent), "panicle length" (83.80 per cent), "flag leaf length" (76.40 per cent), "flag leaf width" (76.10 per cent), "peduncle length" (81.40 per cent), days to 50 per cent flowering (70.10 per cent), days to maturity (75.30 per cent), panicle width (78.50 per cent), and number of basal tillers (68.60 per cent) also demonstrate high heritability. On the other hand, traits with medium heritability are influenced more by environmental factors than genetic factors. "Harvest index" (51.30 per cent) has medium heritability, indicating that variations in this trait are primarily influenced by non-genetic factors such as management practices and environmental conditions.

The Genetic Advance of yield traits provides valuable information about the potential for improvement through breeding efforts. Traits with high Genetic Advance values indicate significant progress and potential for substantial improvement through targeted breeding programs. For example, traits like "Fodder yield per plant" (32.44) and "Panicle length"(33.67) showed high Genetic Advance, suggesting that these traits can be significantly enhanced through focused breeding strategies. Similarly, "Biological yield" (28.29) and "Flag leaf width" (27.58) also demonstrate high Genetic Advance, indicated

the potential for substantial genetic improvements in crop productivity and leaf characteristics. Traits such as "Peduncle length" (22.07), "Panicle width" (25.36), and "Grain yield per plant" (24.73) exhibit high Genetic Advance values, presenting opportunities for targeted selection and accelerated genetic improvement. Traits like "Plant height" (18.82), "Test weight" (12.43), "No. of tillers per plant" (14.00), and "Flag leaf length" (14.27) demonstrate moderate Genetic Advance values, indicating moderate progress and potential for further improvement. On the other hand, traits with low Genetic Advance values indicate slower progress and limited potential for significant improvement through genetic selection alone. Traits such as "Days to 50 per cent flowering" (6.71), "Days to maturity" (6.05), and "Harvest index" (5.80) exhibit low Genetic Advance, suggesting that improving these traits may require a more comprehensive approach that considers other factors such as management practices and environmental influences.

Traits such as fodder yield per plant, panicle length, biological yield, flag leaf width, peduncle length, panicle width, and grain yield per plant showed high heritability coupled with high genetic advance, indicating that they are strongly influenced by genetic factors and can be improved through traditional breeding methods. These traits predominantly exhibited additive gene action. Traits like plant height, test weight, number of basal tillers, and flag leaf length exhibit high heritability coupled with moderate genetic advance its implies both additive and non-additive gene actions. This suggests that genetic improvement can be achieved through traditional breeding methods, as well as by harnessing non-additive gene interactions. On the other hand, traits such as days to 50 per cent flowering and days to maturity have high heritability but low genetic advance. This suggests that their improvement through selection and breeding might be limited. This could be due to the involvement of non-additive gene actions, where gene interactions play a larger role than individual genes. The medium heritability and low genetic advance observed

in traits like harvest index indicated that their expression is strongly influenced by environmental factors and involves non-additive gene action. These complex traits require specialized breeding strategies and alternative approaches to achieve significant improvements.

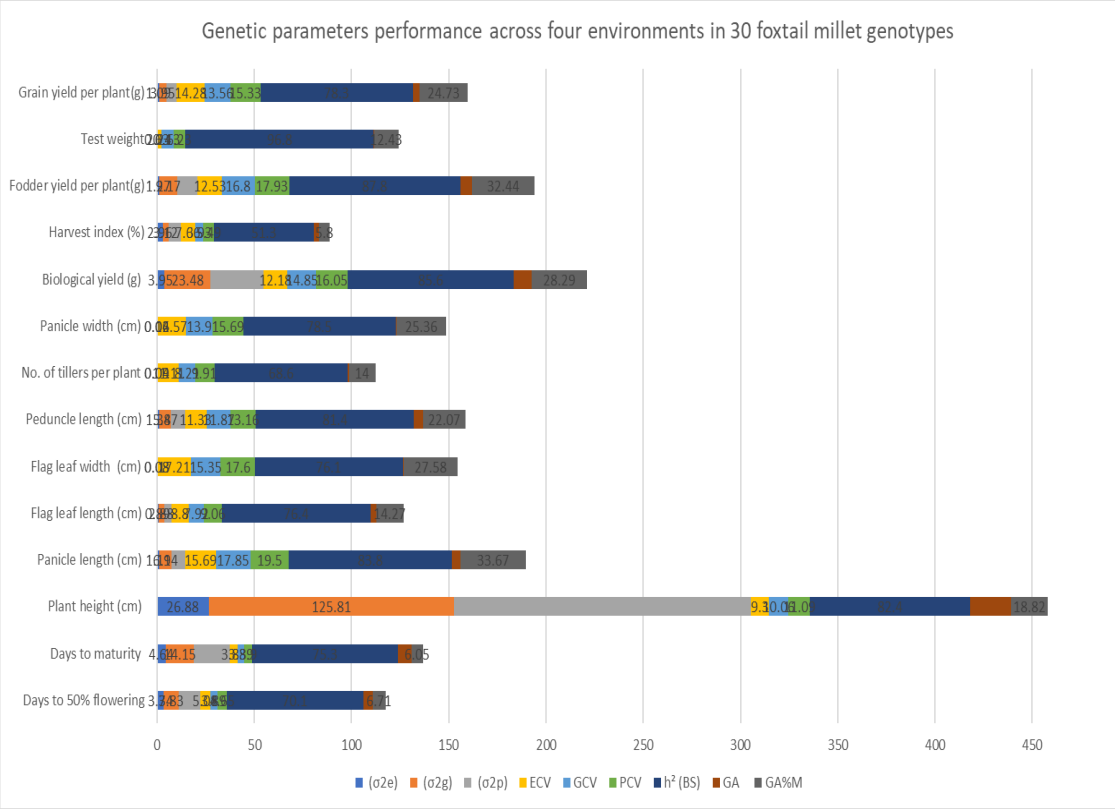


Table 4.3 Genetic parameters performance across four environments in 30 foxtail millet genotypes

Table 4.4. Genetic parameters performance across four environments in 30 foxtail millet genotypes

	(σ^2e)	(σ^2g)	(σ^2p)	ECV	GCV	PCV	h^2 (BS)	GA	GA per centM
Days to 50 per cent flowering	3.34	7.83	11.16	5.08	3.89	4.65	70.10	4.83	6.71
Days to maturity	4.64	14.15	18.79	3.88	3.39	3.90	75.30	6.73	6.05
Plant height (cm)	26.88	125.81	152.69	9.30	10.06	11.09	82.40	20.97	18.82
Panicle length (cm)	1.19	6.14	7.33	15.69	17.85	19.50	83.80	4.67	33.67
Flag leaf length (cm)	0.89	2.88	3.76	8.80	7.92	9.06	76.40	3.05	14.27
Flag leaf width (cm)	0.03	0.08	0.11	17.21	15.35	17.60	76.10	0.52	27.58
Peduncle length (cm)	1.34	5.87	7.21	11.33	11.87	13.16	81.40	4.51	22.07
No. of tillers per plant	0.04	0.09	0.13	11.11	8.21	9.91	68.60	0.51	14.00
Panicle width (cm)	0.02	0.06	0.08	14.57	13.90	15.69	78.50	0.46	25.36
Biological yield (g)	3.95	23.48	27.44	12.18	14.85	16.05	85.60	9.24	28.29
Harvest index (per cent)	2.96	3.12	6.07	7.66	3.93	5.49	51.30	2.60	5.80
Fodder yield per plant(g)	1.27	9.17	10.44	12.53	16.80	17.93	87.80	5.85	32.44
Test weight	0.00	0.03	0.03	2.24	6.13	6.23	96.80	0.35	12.43
Grain yield per plant(g)	1.09	3.95	5.04	14.28	13.56	15.33	78.30	3.62	24.73

σ^2e= Environment variance, σ^2g= Genotypic variance, σ^2p= Phenotypic variance, h^2= Broad sense heritability, GCV = Genotypic coefficient variation, PCV = Phenotypic coefficient variation, GA= Genetic advance, GA per centM= Genetic advance percent mean

4.5. Estimation of correlation coefficients

Correlation coefficient is a statistical measure which is used to find out the degree (strength) and direction of relationship between two or more variables. It is represented by *r*. A positive value of *r* shows that the changes of two variables are in the same directions, *i.e.,* high values of one variable are associated with high values of other and vice-versa. When *r* is negative, the movements are in opposite directions, *i.e.,* high values of one variable are associated with low values of other.

Correlation studies in the breeding material will help in developing a selection scheme, which would help in enhancing the genetic potential of a crop. It also provides reliable information in nature extent and the direction of the selection especially when the breeder needs to combine high yield potential with desirable traits and grain quality characters. In the present investigation the pooled genotypic and phenotypic correlation coefficient of different characters with grain yield per plant and their relationship among themselves are presented in tables 4.5 and this is discussed individually here as under following points.

4.5.1 Genotypic correlation coefficient

The heritable association between two variables is known as genotypic correlation. This type of correlation may be either due to pleiotropic actions of genes or due to linkage. The information of genotypic correlation is more stable and is of paramount importance for a plant breeder to bring about genetic improvement by selecting the characters of a pair that is genetically correlated.

4.5.1.1 Correlation between Grain yield per plant (g) and other characters

The correlation analysis revealed several significant associations among various agronomic traits in this study. Notably, grain yield per plant exhibited

a highly positive and significant correlation with biological yield (r = 0.924**) and fodder yield per plant (r = 0.868**), indicating a strong relationship between these traits. Additionally, grain yield per plant also positively correlated with panicle length (r = 0.513**), plant height (r = 0.331**), days to maturity (r = 0.276**), peduncle length (r = 0.278**), and days to 50 per cent flowering (r = 0.232*), suggesting that these traits might collectively contribute to higher grain yield. Conversely, flag leaf width exhibited a negative and significant correlation with grain yield per plant (r = -0.279**), as did harvest index (r = -0.247**), indicating that these traits might have an adverse effect on grain yield. In contrast, panicle width (r = 0.131), number of tillers per plant (r = 0.022), and test weight (r = 0.011) showed positive but non-significant associations with grain yield per plant. Notably, there were no negative non-significant associations observed among the traits under investigation. These correlation findings provide valuable insights into the interplay of these traits and can aid in designing more effective crop improvement strategies.

4.5.1.2. Character association among other characters:

4.5.1.3 Days to 50 per cent flowering

The study explored the correlations involving "Days to 50 per cent flowering" as a focal trait. Notable positive correlations were identified between "Days to 50 per cent flowering" and traits such as "Days to maturity" (0.850**), "Test weight" (0.283**), "Fodder yield per plant" (0.223*), "Grain yield per plant" (0.232*), and "Biological yield" (0.208*). Conversely, significant negative associations were established between "Days to 50 per cent flowering" and attributes including "Flag leaf width" (-0.596**), "No. of tillers per plant" (-0.257**), "Panicle width" (-0.206*), and "Panicle length" (-0.187*). Additionally, non-significant positive relationships emerged with traits like "Plant height" (0.08) and "Flag leaf length" (0.081). However, "Peduncle

length" exhibited a non-significant negative correlation (-0.09), and "Harvest index" displayed a non-significant negative association (-0.097). These findings provide insights into how "Days to 50 per cent flowering" interacts with various attributes, shedding light on potential genetic and environmental influences governing these connections.

4.5.1.4 Days to maturity

The study focused on investigating correlations cantered around the trait "Days to maturity." Noteworthy positive correlations were established between "Days to maturity" and traits including "Days to 50 per cent flowering" (0.850**), "Grain yield per plant" (0.276**), and "Biological yield" (0.191*). On the other hand, significant negative associations were observed between "Days to maturity" and attributes like "Flag leaf width" (-0.413**), "Panicle width" (-0.349**), and "No. of tillers per plant" (-0.290**). Among non-significant relationships, a positive trend emerged with "Fodder yield per plant" (0.174) and "Harvest index" (0.093), while negligible associations were identified with "Test weight" (0.033), "Plant height" (0.006), and "Flag leaf length" (0.119). Conversely, non-significant negative correlations were noted with "Panicle length" (-0.132) and "Peduncle length" (-0.03). These findings provide insights into the interplay between "Days to maturity" and various traits, elucidating potential genetic and environmental influences that underlie these connections.

4.5.1.5 Plant height (cm)

The study delved into correlations cantered on the trait "Plant height." Remarkable positive correlations were found between "Plant height" and traits including "Panicle length" (0.426**), "Peduncle length" (0.446**), "Grain yield per plant" (0.331**), "Harvest index" (0.376**), "Panicle width" (0.256**), and "Flag leaf length" (0.207*). Additionally, a positive association was noted with "Biological yield" (0.184*). Conversely, significant negative

correlations were evident with "Flag leaf width" (-0.230*) and "No. of tillers per plant" (-0.203*). Non-significant relationships showed a positive trend with "Fodder yield per plant" (0.106), while negligible associations were observed with "Days to 50 per cent flowering" (0.08) and "Days to maturity" (0.006). Conversely, a non-significant negative correlation was found with "Test weight" (-0.044). These findings offer insights into how "Plant height" interacts with various traits, providing implications for potential genetic and environmental factors influencing these relationships.

4.5.1.6 Panicle length (cm)

The study focused on investigating correlations cantered around the trait "Panicle length." Significant positive associations were established between "Panicle length" and various traits, including "Grain yield per plant" (0.513**), "Plant height" (0.426**), "Peduncle length"(0.467**), "Panicle width" (0.326**), "Biological yield" (0.318**), "Harvest index"(0.387**), and "Flag leaf length" (0.217*). Additionally, a positive relationship was noted with "Fodder yield per plant" (0.211*). Conversely, significant negative correlations were evident with "Test weight" (-0.319**) and "Days to 50 per cent flowering" (-0.187*). Non-significant relationships showed a positive trend with "Flag leaf width" (0.073) and "No. of tillers per plant" (0.07), while a non-significant negative correlation was identified with "Days to maturity" (-0.132). These findings offer insights into the interactions between "Panicle length" and various traits, suggesting potential genetic and environmental influences shaping these associations.

4.5.1.7 Flag leaf length (cm)

The study focused on examining correlations centred around the trait "Flag leaf length." Notable positive correlations were established between "Flag leaf length" and traits such as "Peduncle length" (0.500**), "Plant height" (0.207*),

"Panicle length" (0.217*), "Grain yield per plant" (0.190*), and "Test weight" (0.183*). Conversely, a significant negative association was observed with "Panicle width" (-0.281**). Non-significant relationships exhibited a positive trend with "Days to 50 per cent flowering" (0.081), "Days to maturity" (0.119), "Flag leaf width" (0.037), "No. of tillers per plant" (0.072), "Biological yield" (0.147), "Harvest index" (0.11), and "Fodder yield per plant" (0.106). Notably, there were no significant negative associations. These findings provide insights into the connections between "Flag leaf length" and various traits, indicating potential genetic and environmental factors that influence these relationships.

4.5.1.8 Flag leaf width (cm)

The study investigated correlations related to the trait "Flag leaf width." Significant positive associations were found between "Flag leaf width" and "Panicle width" (0.206*). Conversely, negative significant correlations were observed with "Days to 50 per cent flowering" (-0.596**),"Days to maturity" (-0.413**), "Plant height" (-0.230*), "Harvest index" (-0.259**), "Testweight" (-0.268**), "Grain yield per plant" (-0.279**), and "Biological yield" (-0.188*).Non-significant positive relationships were identified with "No. of tillers per plant" (0.122), "Panicle length" (0.073), and "Flag leaf length" (0.037). On the other hand, non-significant negative associations were noted with "Fodder yield per plant" (-0.134) and "Peduncle length" (-0.067). These findings provide insights into the relationships between "Flag leaf width" and various traits, offering implications for potential genetic and environmental influences shaping these associations.

4.5.1.9 Peduncle length (cm)

The study examined correlations associated with the trait "Peduncle length." Notable positive associations were established between "Peduncle length" and traits including "Flag leaf length" (0.500**), "Plant height" (0.446**), "Panicle

length" (0.467**), "Biological yield"(0.271**), "Fodder yield per plant" (0.276**), and "Grain yield per plant" (0.278**). No negative significant associations were observed. Non-significant positive relationships emerged with "No. of tillers per plant" (0.146), "Panicle width" (0.118), and "Test weight" (0.115). Conversely, non-significant negative associations were found with "Harvest index" (-0.132), "Days to 50 per cent flowering" (-0.09), "Days to maturity" (-0.03), and "Flag leaf width" (-0.067). These findings offer insights into the connections involving "Peduncle length" and various traits, providing implications for potential genetic and environmental factors influencing these relationships.

4.5.1.10 No. of tillers per plant

The study examined correlations related to the trait "No. of tillers per plant." No positive significant associations were observed. However, significant negative correlations were identified with "Harvest index" (-0.361**), "Days to 50 per cent flowering" (-0.257**), "Days to maturity" (-0.290**), and "Plant height" (-0.203*). Non-significant positive relationships were found with "Peduncle length" (0.146), "Flag leaf width" (0.122), "Panicle length" (0.07), "Flag leaf length" (0.072), "Fodder yield per plant" (0.115), "Grain yield per plant" (0.022), and "Biological yield" (0.073). Conversely, non-significant negative associations were noted with "Test weight" (-0.083) and "Panicle width" (-0.072). These findings provide insights into the interactions involving "No. of tillers per plant" and various traits, indicating potential genetic and environmental influences on these relationships.

4.5.1.11 Panicle width (cm)

The study explored correlations related to the trait "Panicle width." Positive significant associations were found between "Panicle width" and traits like "Panicle length" (0.326**), "Plant height" (0.256**), "Fodder yield per plant"

(0.193*), and "Flag leaf width" (0.206*). Conversely, negative significant correlations were evident with "Test weight" (-0.402**), "Harvest index" (-0.376**), "Days to maturity" (-0.349**), and "Flag leaf length" (-0.281**). A non-significant positive association was noted with "Grain yield per plant" (0.131), "Peduncle length" (0.118), and "Biological yield" (0.142). Additionally, a non-significant negative correlation was identified with "No. of tillers per plant" (-0.072). These findings provide insights into the interactions involving "Panicle width" and various traits, indicating potential genetic and environmental influences on these relationships.

4.5.1.12 Biological yield (g)

The study examined correlations related to the trait "Biological yield." Positive significant associations were identified between "Biological yield" and traits like "Fodder yield per plant" (0.997**), "Grain yield per plant" (0.924**), "Panicle length" (0.318**), "Peduncle length" (0.271**), "Days to 50 per cent flowering" (0.208*), "Days to maturity" (0.191*), and "Plant height" (0.184*). Conversely, significant negative correlations were observed with "Harvest index" (-0.625**) and "Flag leaf width" (-0.188*). Non-significant positive relationships emerged with "Flag leaf length" (0.147), "Panicle width" (0.142), and "No. of tillers per plant" (0.073). Conversely, non-significant correlations were noted with "Test weight" (0.012). These findings provide insights into the interactions involving "Biological yield" and various traits, suggesting potential genetic and environmental influences on these relationships.

4.5.1.13 Harvest index (%)

The study investigated correlations associated with the trait "Harvest index." Positive significant associations were established between "Harvest index" and "Plant height" (0.376**) as well as "Panicle length" (0.387**). Conversely, significant negative correlations were observed with "Fodder yield per plant"

(-0.698**), "Biological yield" (-0.625**), "No. of tillers per plant" (-0.361**), "Panicle width" (-0.376**), "Flag leaf width" (-0.259**), and "Grain yield per plant" (-0.247**). Non-significant positive relationships emerged with "Flag leaf length" (0.11) and "Days to maturity" (0.093). Conversely, non-significant negative associations were identified with "Peduncle length" (-0.132), "Test weight" (-0.106), and "Days to 50 per cent flowering" (-0.097). These findings provide insights into the interactions involving "Harvest index" and various traits, indicating potential genetic and environmental influences on these relationships.

4.5.1.14 Test weight (g)

The study examined correlations related to the trait "Test weight." Positive significant associations were identified between "Test weight" and "Days to 50 per cent flowering" (0.283**), as well as "Flag leaf length" (0.183*). Conversely, significant negative correlations were observed with "Panicle length" (-0.319**), "Panicle width" (-0.402**), and "Flag leaf width"(-0.268**). Non-significant positive relationships emerged with "Days to maturity" (0.033),"Peduncle length" (0.115), "Biological yield" (0.012), "Fodder yield per plant" (0.041), and "Grain yield per plant" (0.011). Conversely, non-significant negative associations were noted with "No. of tillers per plant" (-0.083), "Plant height" (-0.044), and "Harvest index" (-0.106). These findings offer insights into the interactions involving "Test weight" and various traits, suggesting potential genetic and environmental influences on these relationships.

4.5.1.15 Fodder yield per plant (g)

The study examined correlations related to the trait "Fodder yield per plant." Significant positive associations were identified between "Fodder yield per plant" and traits like "Biological yield" (0.997**), "Grain yield per plant"

(0.868**), "Days to 50 per cent flowering" (0.223*), "Panicle length" (0.211*), "Peduncle length" (0.276**), and "Panicle width" (0.193*). A significant negative correlation was observed with "Harvest index" (-0.698**). Non-significant positive relationships emerged with "Days to maturity" (0.174), "No. of tillers per plant" (0.115), "Plant height" (0.106), "Flag leaf length" (0.106), and "Test weight" (0.041). Conversely, a non-significant negative association was noted with "Flag leaf width" (-0.134). These findings provide insights into the interactions involving "Fodder yield per plant" and various traits, suggesting potential genetic and environmental influences on these relationships.

4.5.2. Phenotypic correlation coefficient

Phenotypic correlation determines the association between two variables which can be directly observed. It includes both genotypic and environmental effects and therefore differs under different environmental conditions.

4.5.2.1 Correlation between Grain yield per plant (g) and other characters

The correlation analysis revealed significant associations among various agronomic traits in this study. Notably, grain yield per plant exhibited highly positive and significant correlations with biological yield (r = 0.889**), indicating a strong relationship between these traits in contributing to overall grain yield. Additionally, panicle length (r = 0.356**), plant height (r = 0.312**), flag leaf length (r = 0.297**), days to 50 per cent flowering (r = 0.238**), days to maturity (r = 0.257**), peduncle length (r = 0.236**), and number of tillers per plant (r = 0.225*) showed positive and significant associations with grain yield per plant, suggesting their potential influence on grain production. Furthermore, panicle width (r = 0.218*) exhibited a positive but non-significant association with grain yield per plant. In contrast, flag leaf width (r = 0.052) and harvest index (r = 0.163) showed positive associations

with grain yield per plant, but these were not statistically significant. Interestingly, test weight (r = -0.011) and fodder yield per plant (r = -0.011) exhibited negative but non-significant associations with grain yield per plant. These correlation findings provide valuable insights into the interrelationships among these traits and can inform breeding strategies to enhance grain yield.

4.5.1.2. Character association among other characters:

4.5.2.3 Days to 50 per cent flowering

The study focused on investigating correlations related to the trait "Days to 50 per cent flowering." Positive significant associations were observed between "Days to 50 per cent flowering" and traits like "Days to maturity" (0.779**), "Fodder yield per plant" (0.248**), "Grain yield per plant" (0.238**), "Biological yield" (0.223*), and "Test weight" (0.182*). Conversely, negative significant correlations were identified with "Flag leaf width" (-0.245**) and "No. of tillers per plant" (-0.206*). Non-significant positive relationships emerged with "Flag leaf length" (0.137) and "Plant height" (0.041), while non-significant negative associations were noted with "Peduncle length" (-0.168), "Panicle width" (-0.118), "Panicle length" (-0.073), and "Harvest index" (-0.073). These findings provide insights into the interactions involving "Days to 50 per cent flowering" and various traits, suggesting potential genetic and environmental influences on these relationships.

4.5.2.4 Days to maturity

The study examined correlations related to the trait "Days to maturity." Positive significant associations were identified between "Days to maturity" and traits like "Days to 50 per cent flowering" (0.779**), "Fodder yield per plant" (0.241**), "Grain yield per plant" (0.257**), and "Biological yield" (0.224*). Conversely, a negative significant correlation was observed with "Flag leaf width" (-0.202*). Non-significant positive relationships emerged

with "Flag leaf length" (0.171) and "Plant height" (0.045), while non-significant negative associations were noted with "Test weight" (0.032), "Peduncle length" (-0.125), "No. of tillers per plant" (-0.141), "Panicle width" (-0.145), "Harvest index" (-0.045), and "Panicle length" (-0.035). These findings offer insights into the interactions involving "Days to maturity" and various traits, indicating potential genetic and environmental influences on these relationships.

4.5.2.5 Plant height (cm)

The study explored correlations related to the trait "Plant height." Positive significant associations were observed between "Plant height" and traits like "Panicle length" (0.362**), "Grain yield per plant" (0.312**), "Peduncle length" (0.313**), "Panicle width" (0.308**), "Biological yield" (0.225*), "Harvest index" (0.180*), and "Flag leaf length" (0.196*). Notably, no negative significant correlations were found. Non-significant positive relationships emerged with "Fodder yield per plant" (0.151), "Days to 50 per cent flowering" (0.041), "Days to maturity" (0.045), and "Flag leaf width" (0.035). Conversely, non-significant negative associations were identified with "No. of tillers per plant" (-0.053) and "Test weight" (-0.049). These findings provide insights into the interactions involving "Plant height" and various traits, suggesting potential genetic and environmental influences on these relationships.

4.5.2.6 Panicle length (cm)

The study investigated correlations centered around the trait "Panicle length." Positive significant associations were found between "Panicle length" and traits like "Plant height" (0.362**), "Grain yield per plant" (0.356**), "Peduncle length" (0.352**), "Biological yield" (0.243**), "Harvest index" (0.214*), "Flag leaf length" (0.227*), and "Panicle width" (0.212*).

Conversely, a negative significant correlation was identified with "Test weight" (-0.222*). Non-significant positive relationships emerged with "Fodder yield per plant" (0.143), "Flag leaf width" (0.055), and "No. of tillers per plant" (0.076). On the other hand, non-significant negative associations were observed with "Days to 50 per cent flowering" (-0.073) and "Days to maturity" (-0.035). These findings provide insights into the interactions involving "Panicle length" and various traits, suggesting potential genetic and environmental influences on these relationships.

4.5.2.7 Flag leaf length (cm)

The study examined correlations related to the trait "Flag leaf length." Positive significant associations were identified between "Flag leaf length" and traits such as “Peduncle length"(0.400**), "Flag leaf width" (0.302**), "Grain yield per plant" (0.297**), "Panicle length"(0.227*), "Plant height" (0.196*), "Biological yield" (0.211*), and "No. of tillers per plant" (0.186*). Notably, no negative significant correlations were found. Non-significant positive relationships emerged with "Harvest index" (0.153), "Test weight" (0.138), "Fodder yield per plant" (0.14), "Days to 50 per cent flowering" (0.137), "Days to maturity" (0.171), and "Panicle width" (0.048). These findings offer insights into the interactions involving "Flag leaf length" and various traits, suggesting potential genetic and environmental influences on these relationships.

4.5.2.8 Flag leaf width (cm)

The study investigated correlations centered around the trait "Flag leaf width." Positive significant associations were found between "Flag leaf width" and traits like "Panicle width" (0.410**), "Flag leaf length" (0.302**), and "No. of tillers per plant" (0.180*). Conversely, negative significant correlations were identified with "Days to 50 per cent flowering" (-0.245**), "Days to maturity" (-0.202*), and "Test weight" (-0.183*). Non-significant positive relationships

emerged with "Peduncle length" (0.156), "Biological yield" (0.053), "Fodder yield per plant" (0.034), "Plant height" (0.035), "Panicle length" (0.055), "Grain yield per plant" (0.052), and "Harvest index" (0.005). These findings provide insights into the interactions involving "Flag leaf width" and various traits, suggesting potential genetic and environmental influences on these relationships.

4.5.2.9 Peduncle length (cm)

The study focused on correlations associated with the trait "Peduncle length." Positive significant associations were identified between "Peduncle length" and traits such as "Flag leaf length" (0.400**), "Plant height" (0.313**), "Panicle length" (0.352**), "Grain yield per plant" (0.236**), "No. of tillers per plant" (0.241**), "Biological yield" (0.219*), and "Fodder yield per plant" (0.198*). Notably, no negative significant correlations were found. Non-significant positive relationships emerged with "Flag leaf width" (0.156), "Panicle width" (0.173), "Harvest index" (0.014), and "Test weight" (0.092). Conversely, non-significant negative associations were observed with "Days to 50 per cent flowering" (-0.168) and "Days to maturity" (-0.125). These findings provide insights into the interactions involving "Peduncle length" and various traits, suggesting potential genetic and environmental influences on these relationships.

4.5.2.10 No. of tillers per plant

The study examined correlations related to the trait "No. of tillers per plant." Positive significant associations were found between "No. of tillers per plant" and traits like "Fodder yield per plant" (0.226*), "Grain yield per plant" (0.225*), "Biological yield" (0.246**), "Peduncle length" (0.241**), "Flag leaf length" (0.186*), and "Flag leaf width" (0.180*). Conversely, a negative significant correlation was identified with "Days to 50 per cent flowering" (-

0.206*). Non-significant positive relationships emerged with "Panicle length" (0.076) and "Panicle width" (0.078). On the other hand, non-significant negative associations were observed with "Days to maturity" (-0.141), "Harvest index" (-0.039), "Test weight" (-0.036), and "Plant height" (-0.053). These findings provide insights into the interactions involving "No. of tillers per plant" and various traits, suggesting potential genetic and environmental influences on these relationships.

4.5.2.11 Panicle width (cm)

The study explored correlations associated with the trait "Panicle width." Positive significant associations were identified between "Panicle width" and traits like "Flag leaf width" (0.410**), "Plant height" (0.308**), "Panicle length" (0.212*), "Biological yield" (0.208*), "Grain yield per plant" (0.218*), and "Fodder yield per plant" (0.192*). Conversely, a negative significant correlation was observed with "Test weight" (-0.312**). Non-significant positive relationships emerged with "Peduncle length" (0.173) and "No. of tillers per plant" (0.078). On the other hand, non-significant negative associations were identified with "Days to 50 per cent flowering" (-0.118), "Days to maturity" (-0.145), and "Harvest index" (-0.025). These findings provide insights into the interactions involving "Panicle width" and various traits, suggesting potential genetic and environmental influences on these relationships.

4.5.2.12 Biological yield (g)

The study delved into correlations associated with the trait "Biological yield." Positive significant associations were identified between "Biological yield" and traits such as "Fodder yield per plant" (0.929**), "Grain yield per plant" (0.889**), "Days to 50 per cent flowering" (0.223*), "Days to maturity" (0.224*), "Plant height" (0.225*), "Panicle length" (0.243**), "Flag leaf

length" (0.211*), "Peduncle length" (0.219*), "No. of tillers per plant" (0.246**), and "Panicle width" (0.208*). Notably, no negative significant correlations were found. A non-significant positive relationship emerged with "Flag leaf width" (0.053), while non-significant negative associations were observed with "Harvest index" (-0.088) and "Test weight" (-0.021). These findings offer insights into the interactions involving "Biological yield" and various traits, suggesting potential genetic and environmental influences on these relationships.

4.5.2.13 Harvest index (%)

The study investigated correlations related to the trait "Harvest index." Positive significant associations were found between "Harvest index" and traits such as "Panicle length" (0.214*) and "Plant height" (0.180*). Conversely, a negative significant correlation was identified with "Fodder yield per plant" (-0.438**). Non-significant positive relationships emerged with "Flag leaf length" (0.153), "Flag leaf width" (0.005), "Peduncle length" (0.014), and "Grain yield per plant" (0.163). On the other hand, non-significant negative associations were observed with "Days to 50 per cent flowering" (-0.073), "Days to maturity" (-0.045), "No. of tillers per plant" (-0.039), "Panicle width" (-0.025), "Biological yield" (-0.088), and "Test weight" (-0.05). These findings provide insights into the interactions involving "Harvest index" and various traits, suggesting potential genetic and environmental influences on these relationships.

4.5.2.14 Fodder yield per plant (g)

The study investigated correlations associated with the trait "Fodder yield per plant." Positive significant associations were identified between "Fodder yield per plant" and traits like "Biological yield" (0.929**), "Grain yield per plant" (0.756**), "Days to 50 per cent flowering" (0.248**), "Days to maturity" (0.241**), "No. of tillers per plant" (0.226*), "Peduncle length" (0.198*), and

"Panicle width" (0.192*). Conversely, a negative significant correlation was observed with "Harvest index" (-0.438**). Non-significant positive relationships emerged with "Plant height" (0.151), "Panicle length" (0.143), "Flag leaf length" (0.14), "Flag leaf width" (0.034), and "Test weight" (0.012). These findings provide insights into the interactions involving "Fodder yield per plant" and various traits, suggesting potential genetic and environmental influences on these relationships.

4.5.2.15 Test weight (g)

The study explored correlations related to the trait "Test weight." Positive significant associations were identified between "Test weight" and "Days to 50 per cent flowering" (0.182*). Negative significant correlations were observed with "Panicle width" (-0.312**), "Flag leaf width" (-0.183*), and "Panicle length" (-0.222*). Non-significant positive relationships emerged with "Flag leaf length" (0.138), "Peduncle length" (0.092), "Days to maturity" (0.032), and "Fodder yield per plant" (0.012). Conversely, non-significant negative associations were identified with "Plant height" (-0.049), "No. of tillers per plant" (-0.036), "Biological yield" (-0.021), "Harvest index" (-0.05), and "Grain yield per plant" (-0.011). These findings provide insights into the interactions involving "Test weight" and various traits, suggesting potential genetic and environmental influences on these relationships.

Table 4.5. Genotypic (rg) and phenotypic (rp) correlation among yield and yield components of 30 foxtail millet genotypes

Genotypic Correlations Matrix / Phenotypic Correlations Matrix

	DF	DM	PH	PL	FL	FW	PDL	NT	IW	BY	HI	TW	FY	GY
DF	1	0.779**	0.041NS	-0.073NS	0.137NS	-0.245**	-0.168NS	-0.206*	-0.118NS	0.223*	-0.073NS	0.182*	0.248**	0.238**
DM	0.850**	1	0.045NS	-0.035NS	0.171NS	-0.202*	-0.125NS	-0.141NS	-0.145NS	0.224*	-0.045NS	0.032NS	0.241**	0.257**
PH	0.080NS	0.006NS	1	0.362**	0.196*	0.035NS	0.313**	-0.053NS	0.308**	0.225*	0.180*	-0.049NS	0.151NS	0.312**
PL	-0.187*	-0.132NS	0.426**	1	0.227*	0.055NS	0.352**	0.076NS	0.212*	0.243**	0.214*	-0.222*	0.143NS	0.356**
FL	0.081NS	0.119NS	0.207*	0.217*	1	0.302**	0.400**	0.186*	0.048NS	0.211*	0.153NS	0.138NS	0.140NS	0.297**
FW	-0.596**	-0.413**	-0.230*	0.073NS	0.037NS	1	0.156NS	0.180*	0.410**	0.053NS	0.005NS	-0.183*	0.034NS	0.052NS
PDL	-0.090NS	-0.030NS	0.446**	0.467**	0.500**	-0.067NS	1	0.241**	0.173NS	0.219*	0.014NS	0.092NS	0.198*	0.236**
NT	-0.257**	-0.290**	-0.203*	0.070NS	0.072NS	0.122NS	0.146NS	1	0.078NS	0.246**	-0.039NS	-0.036NS	0.226*	0.225*
IW	-0.206*	-0.349**	0.256**	0.326**	-0.281**	0.206*	0.118NS	-0.072NS	1	0.208*	-0.025NS	-0.312**	0.192*	0.218*
BY	0.208*	0.191*	0.184*	0.318**	0.147NS	-0.188*	0.271**	0.073NS	0.142NS	1	-0.088NS	-0.021NS	0.929**	0.889**
HI	-0.097NS	0.093NS	0.376**	0.387**	0.110NS	-0.259**	-0.132NS	-0.361**	-0.376**	-0.625**	1	-0.050NS	-0.438**	0.163NS
TW	0.283**	0.033NS	-0.044NS	-0.319**	0.183*	-0.268**	0.115NS	-0.083NS	-0.402**	0.012NS	-0.106NS	1	0.012NS	-0.011NS
FY	0.223*	0.174NS	0.106NS	0.211*	0.106NS	-0.134NS	0.276**	0.115NS	0.193*	0.997**	-0.698**	0.041NS	1	0.756**
GY	0.232*	0.276**	0.331**	0.513**	0.190*	-0.279**	0.278**	0.022NS	0.131NS	0.924**	-0.247**	0.011NS	0.868**	1

Days to 50 per cent flowering (DF), Days to maturity (DM), Plant height (PH), Panicle length (PL), Flag leaf length (FL), Flag leaf width (FW), Peduncle length (PDL), No. of tillers per plant (NT), Panicle width (PW), Biological yield (BY), Harvest index (HI), Fodder yield per plant (FY), Test weight (TW) and Grain yield per plant (GY).

4.6. Path Co-efficient analysis:

Simple correlation does not provide the true association of the characters with each other as these attributes are interrelated among them and considerably influenced by each character. Path coefficient analysis splits the correlation coefficient into the measure of direct and indirect effect i.e., direct and indirect contribution of various independent characters on a dependent character. The result obtained has been presented in Table 4.6.1 and 4.6.2.

4.6.1. Genotypic path coefficient analysis

An analysis of the results on path coefficient for yield and yield components genotypic to be of similar direction and magnitude in general. Further the genotypic path co-efficient were observed to be of higher magnitude, compared to phenotypic path coefficient indicating the masking effect of environment.

The genotypic path coefficient analysis provided insights into the direct effects of various traits on grain yield per plant. Days to 50 per cent flowering showed a positive direct effect of (0.0329), implying that a delay in flowering may lead to an increase in grain yield per plant. Similarly, flag leaf length had a direct positive effect of (0.0027), flag leaf width had an effect of (0.015), peduncle length had an effect of (0.0036), and the number of tillers per plant had an effect of (0.0056), all contributing positively to grain yield per plant. Notably, biological yield exhibited a substantial positive direct effect of (2.0936), suggesting its significant contribution to grain yield per plant. Harvest index also had a positive direct effect of (0.0915) on grain yield per plant. Conversely, days to maturity showed a negative direct effect of (-0.0383), as did plant height with an effect of (-0.0084), panicle length with an effect of (-0.0113), panicle width with an effect of (-0.0058), fodder yield per plant with an effect of (-1.1076), and test weight with an effect of (-0.0152), all indicating

a negative impact on grain yield per plant. These findings offer valuable insights for crop improvement strategies by highlighting the direct impacts of specific traits on grain yield per plant.

4.6.1.1 Days to 50 per cent flowering

The genotypic path analysis of grain yield per plant in relation to days to 50 per cent flowering revealed several significant direct and indirect effects. The direct effect of days to 50 per cent flowering on grain yield per plant is positive (0.0329), suggesting that a delay in flowering is associated with a higher grain yield. Additionally, days to maturity (0.0279), biological yield (0.0078), fodder yield per plant (0.0073), and test weight (0.0092) also exhibit positive indirect effects on grain yield. Conversely, certain traits show negative indirect effects, including panicle length (-0.0061), flag leaf length (0.0027), flag leaf width (-0.0197), peduncle length (-0.0029), number of basal tillers (-0.0085), inflorescence width (-0.0068), and harvest index (-0.0032). These findings provide insights into the complex interplay between these genotypic factors and their impact on grain yield in the studied plant population.

4.6.1.2 Days to maturity

The genotypic path analysis of grain yield per plant with respect to days to maturity revealed noteworthy direct and indirect effects. The direct effect of days to maturity on grain yield per plant is negative (-0.0383), indicating that a delayed maturity is associated with a reduction in grain yield. Among the positive indirect effects, panicle length (0.0051), flag leaf width (0.0159), peduncle length (0.0011), and number of basal tillers (0.0111) exhibit contributions to increased grain yield. Conversely, several traits demonstrate negative indirect effects, including days to 50 per cent flowering (-0.0326), plant height (-0.0002), flag leaf length (-0.0045), biological yield (-0.0087), harvest index (-0.0035), fodder yield per plant (-0.0067), and test weight (-

0.0011). These findings elucidate the intricate relationships between genotypic factors and their impact on grain yield within the context of days to maturity in the studied plant population.

4.6.1.3 Plant height (cm)

The genotypic path analysis of grain yield per plant concerning plant height revealed significant direct and indirect effects. The direct effect of plant height on grain yield per plant is negative (-0.0084), indicating that increased plant height is associated with a reduction in grain yield. Among the positive indirect effects, flag leaf width (0.0019), test weight (0.0003), and the number of basal tillers (0.0017) contribute to higher grain yield. Conversely, negative indirect effects are observed, including days to 50 per cent flowering (-0.0007), panicle length (-0.0036), flag leaf length (-0.0017), peduncle length (-0.0037), inflorescence width (-0.0021), biological yield (-0.0017), harvest index (-0.0032), and fodder yield per plant (-0.0009). These findings offer insights into the complex interactions between genotypic factors and their influence on grain yield within the context of plant height in the studied plant population.

4.6.1.4 Panicle length (cm)

The genotypic path analysis of grain yield per plant in relation to panicle length revealed significant direct and indirect effects. The direct effect of panicle length on grain yield per plant is negative (-0.0113), indicating that increased panicle length is associated with a decrease in grain yield. Among the positive indirect effects, days to 50 per cent flowering (0.0021), days to maturity (0.0015), and test weight (0.0036) contribute positively to grain yield. Conversely, negative indirect effects are observed, including plant height (-0.0048), flag leaf length (-0.0025), flag leaf width (-0.0008), peduncle length (-0.0053), number of basal tillers (-0.0008), inflorescence width (-0.0037),

biological yield (-0.0039), harvest index (-0.0044), and fodder yield per plant (-0.0024). These findings offer insights into the intricate relationships between genotypic factors and their impact on grain yield within the context of panicle length in the studied plant population.

4.6.1.5 Flag leaf length (cm)

The genotypic path analysis of grain yield per plant concerning flag leaf length highlights both direct and indirect effects. The direct effect of flag leaf length on grain yield per plant was positive (0.0027), indicating that an increase in flag leaf length is associated with higher grain yield. Among the positive indirect effects, days to 50 per cent flowering (0.0002), days to maturity (0.0003), plant height (0.0005), panicle length (0.0006), flag leaf width (0.0001), peduncle length (0.0013), number of tillers per plant (0.0002), biological yield (0.0004), harvest index (0.0003), fodder yield per plant (0.0003), and test weight (0.0005) contribute positively to grain yield. On the other hand, a single negative indirect effect is observed, involving panicle width (-0.0008). These findings provide insights into the complex relationships between genotypic factors and their impact on grain yield, specifically focusing on flag leaf length, in the studied plant population.

4.6.1.6 Flag leaf width (cm)

The genotypic path analysis of grain yield per plant with regard to flag leaf width revealed significant direct and indirect effects. The direct effect of flag leaf width on grain yield per plant is positive (0.015), suggesting that an increase in flag leaf width is associated with higher grain yield. Among the positive indirect effects, panicle length (0.0011), flag leaf length (0.0005), number of tillers per plant (0.0018), and panicle width (0.0031) contribute positively to grain yield. Conversely, negative indirect effects include days to 50 per cent flowering (-0.009), days to maturity (-0.0062), plant height (-

0.0035), peduncle length (-0.001), biological yield (-0.003), harvest index (-0.004), fodder yield per plant (-0.002), and test weight (-0.004). These findings illuminate the intricate relationships between genotypic factors and their influence on grain yield within the context of flag leaf width in the studied plant population.

4.6.1.7 Peduncle length (cm)

The genotypic path analysis of grain yield per plant in relation to peduncle length revealed significant direct and indirect effects. The direct effect of peduncle length on grain yield per plant is positive (0.0036), indicating that an increase in peduncle length is associated with higher grain yield. Among the positive indirect effects, plant height (0.0016), panicle length (0.0017), flag leaf length (0.0018), number of tillers per plant (0.0005), panicle width (0.0004), fodder yield per plant (0.001), biological yield (0.001), and test weight (0.0004) contribute positively to grain yield. Conversely, negative indirect effects involve days to 50 per cent flowering (-0.0003), days to maturity (-0.0001), flag leaf width (-0.0002), and harvest index (-0.0005). These findings shed light on the complex relationships between genotypic factors and their impact on grain yield within the context of peduncle length in the studied plant population.

4.6.1.8 Number of tillers per plant

The genotypic path analysis of grain yield per plant with respect to the number of tillers per plant revealed significant direct and indirect effects. The direct effect of the number of tillers per plant on grain yield per plant is positive (0.0056), indicating that a higher number of tillers is associated with increased grain yield. Among the positive indirect effects, panicle length (0.0004), flag leaf length (0.0004), flag leaf width (0.0007), peduncle length (0.0008), biological yield (0.0004), and fodder yield per plant (0.0006) contribute

positively to grain yield. Conversely, negative indirect effects involve days to 50 per cent flowering (-0.0014), days to maturity (-0.0016), plant height (-0.0011), panicle width (-0.0004), harvest index (-0.002), and test weight (-0.0004). These findings provided insights into the intricate relationships between genotypic factors and their impact on grain yield within the context of the number of tillers per plant in the studied plant population.

4.6.1.9 Panicle width (cm)

The genotypic path coefficient analysis provided valuable insights into the relationship between various traits and grain yield per plant. Specifically, panicle width was found to have a negative direct effect on grain yield per plant, with a magnitude of -0.0058, suggesting that an increase in panicle width may lead to a decrease in grain yield. On the other hand, there were positive indirect effects on grain yield per plant from days to 50 per cent flowering (0.0012), days to maturity (0.002), number of tillers per plant (0.0004), harvest index (0.0022), and test weight (0.0023). These indirect effects indicate that these traits indirectly influence grain yield per plant through other pathways. Conversely, there were negative indirect effects from plant height (-0.0015), panicle length (-0.0019), flag leaf length (0.0016), flag leaf width (-0.0012), peduncle length (-0.0007), biological yield (-0.001), and fodder yield per plant (-0.0011) on grain yield per plant. These findings provide crucial insights into the intricate relationships among traits and their impacts on grain yield, aiding in the development of targeted crop improvement strategies.

4.6.1.10 Biological yield (g)

The genotypic path analysis of grain yield per plant concerning biological yield uncovers significant direct and indirect effects. The direct effect of biological yield on grain yield per plant was notably positive (2.0936),

signifying a strong influence of biological yield on increasing grain yield. Among the positive indirect effects, fodder yield per plant (2.0442), test weight (0.0725), days to 50 per cent flowering (0.4988), days to maturity (0.4759), plant height (0.428), panicle length (0.7207), flag leaf length (0.2996), peduncle length (0.6033), and the number of tillers per plant (0.1629) contribute to elevated grain yield. Conversely, negative indirect effects involve flag leaf width (-0.4207) and harvest index (-1.0949), suggesting that wider flag leaves and lower harvest indices are associated with decreased grain yield. These findings illuminate the complex interactions between genotypic factors and their impact on grain yield within the context of biological yield in the studied plant population.

4.6.1.11 Harvest index (%)

The genotypic path analysis of grain yield per plant in relation to harvest index revealed significant direct and indirect effects. The direct effect of harvest index on grain yield per plant was positively noteworthy (0.0915), indicating that an increased harvest index was associated with higher grain yield. Among the positive indirect effects, days to maturity (0.0084), plant height (0.0345), panicle length (0.0353), and flag leaf length (0.0101) contribute to enhanced grain yield. Conversely, negative indirect effects involve flag leaf width (-0.0243), peduncle length (-0.012), the number of tillers per plant (-0.0325), panicle width (-0.0342), biological yield (-0.0478), days to 50 per cent flowering (-0.0088), fodder yield per plant (-0.0638), and test weight (-0.0081). These findings illuminate the intricate relationships between genotypic factors and their influence on grain yield within the context of harvest index in the studied plant population.

4.6.1.12 Fodder yield per plant (g)

The genotypic path analysis of grain yield per plant with regard to fodder yield per plant unveils significant direct and indirect effects. The direct effect of fodder yield per plant on grain yield per plant is negatively substantial (-1.1076), indicating that higher fodder yield is associated with reduced grain yield. Among the positive indirect effects, harvest index (0.7727) contributes positively to grain yield. Conversely, negative indirect effects involve days to 50 per cent flowering (-0.2468), days to maturity (-0.1936), plant height (-0.1176), panicle length (-0.234), flag leaf length (-0.1178), peduncle length (-0.3054), the number of tillers per plant (-0.1233), panicle width (-0.2096), biological yield (-1.0815), and test weight (-0.0447). These findings offer insights into the complex relationships between genotypic factors and their impact on grain yield within the context of fodder yield per plant in the studied plant population.

4.6.1.13 Test weight (g)

The genotypic path analysis of grain yield per plant concerning test weight revealed significant direct and indirect effects. The direct effect of test weight on grain yield per plant is negative (-0.0152), indicating that a decrease in test weight is associated with lower grain yield. Among the positive indirect effects, plant height (0.0006), panicle length (0.0049), flag leaf width (0.0041), the number of tillers per plant (0.001), panicle width (0.0061), and harvest index (0.0013) contribute positively to grain yield. Conversely, negative indirect effects involve days to 50 per cent flowering (-0.0042), days to maturity (-0.0005), flag leaf length (-0.0029), peduncle length (-0.0017), biological yield (-0.0005), and fodder yield per plant (-0.0006). These findings offer insights into the complex interactions between genotypic factors and their impact on grain yield within the context of test weight in the studied plant population.

Table 4.6.1. Genotypic (r_g) path co-efficient analysis among yield and yield components of 30 foxtail millet genotypes

	DF	DM	PH	PL	FL	FW	PDL	NT	PW	BY	HI	FY	TW
DF	**0.0329**	0.0279	0.0026	-0.0061	0.0027	-0.0197	-0.0029	-0.0085	-0.0068	0.0078	-0.0032	0.0073	0.0092
DM	-0.0326	**-0.0383**	-0.0002	0.0051	-0.0045	0.0159	0.0011	0.0111	0.0135	-0.0087	-0.0035	-0.0067	-0.0011
PH	-0.0007	0	**-0.0084**	-0.0036	-0.0017	0.0019	-0.0037	0.0017	-0.0021	-0.0017	-0.0032	-0.0009	0.0003
PL	0.0021	0.0015	-0.0048	**-0.0113**	-0.0025	-0.0008	-0.0053	-0.0008	-0.0037	-0.0039	-0.0044	-0.0024	0.0036
FL	0.0002	0.0003	0.0005	0.0006	**0.0027**	0.0001	0.0013	0.0002	-0.0008	0.0004	0.0003	0.0003	0.0005
FW	-0.009	-0.0062	-0.0035	0.0011	0.0005	**0.015**	-0.001	0.0018	0.0031	-0.003	-0.004	-0.002	-0.004
PDL	-0.0003	-0.0001	0.0016	0.0017	0.0018	-0.0002	**0.0036**	0.0005	0.0004	0.001	-0.0005	0.001	0.0004
NT	-0.0014	-0.0016	-0.0011	0.0004	0.0004	0.0007	0.0008	**0.0056**	-0.0004	0.0004	-0.002	0.0006	-0.0004
PW	0.0012	0.002	-0.0015	-0.0019	0.0016	-0.0012	-0.0007	0.0004	**-0.0058**	-0.001	0.0022	-0.0011	0.0023
BY	0.4988	0.4759	0.428	0.7207	0.2996	-0.4207	0.6033	0.1629	0.3682	**2.0936**	-1.0949	2.0442	0.0725
HI	-0.0088	0.0084	0.0345	0.0353	0.0101	-0.0243	-0.012	-0.0325	-0.0342	-0.0478	**0.0915**	-0.0638	-0.0081
FY	-0.2468	-0.1936	-0.1176	-0.234	-0.1178	0.1492	-0.3054	-0.1233	-0.2096	-1.0815	0.7727	**-1.1076**	-0.0447
TW	-0.0042	-0.0005	0.0006	0.0049	-0.0029	0.0041	-0.0017	0.001	0.0061	-0.0005	0.0013	-0.0006	0.0101
GY	0.2314	0.2758	0.3308	0.5128	0.1899	-0.2801	0.2775	0.0203	0.1278	0.9551	-0.2475	0.8683	0.0155
R^2	0.0076	-0.0106	-0.0028	-0.0058	0.0005	-0.0042	0.001	0.0001	-0.0007	1.9996	-0.0226	-0.9617	-0.0002

Residual effect= rg (0.0001), Days to 50 per cent flowering (DF), Days to maturity (DM), Plant height (PH), Panicle length (PL), Flag leaf length (FL), Flag leaf width (FW), Peduncle length (PDL), No. of tillers 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).

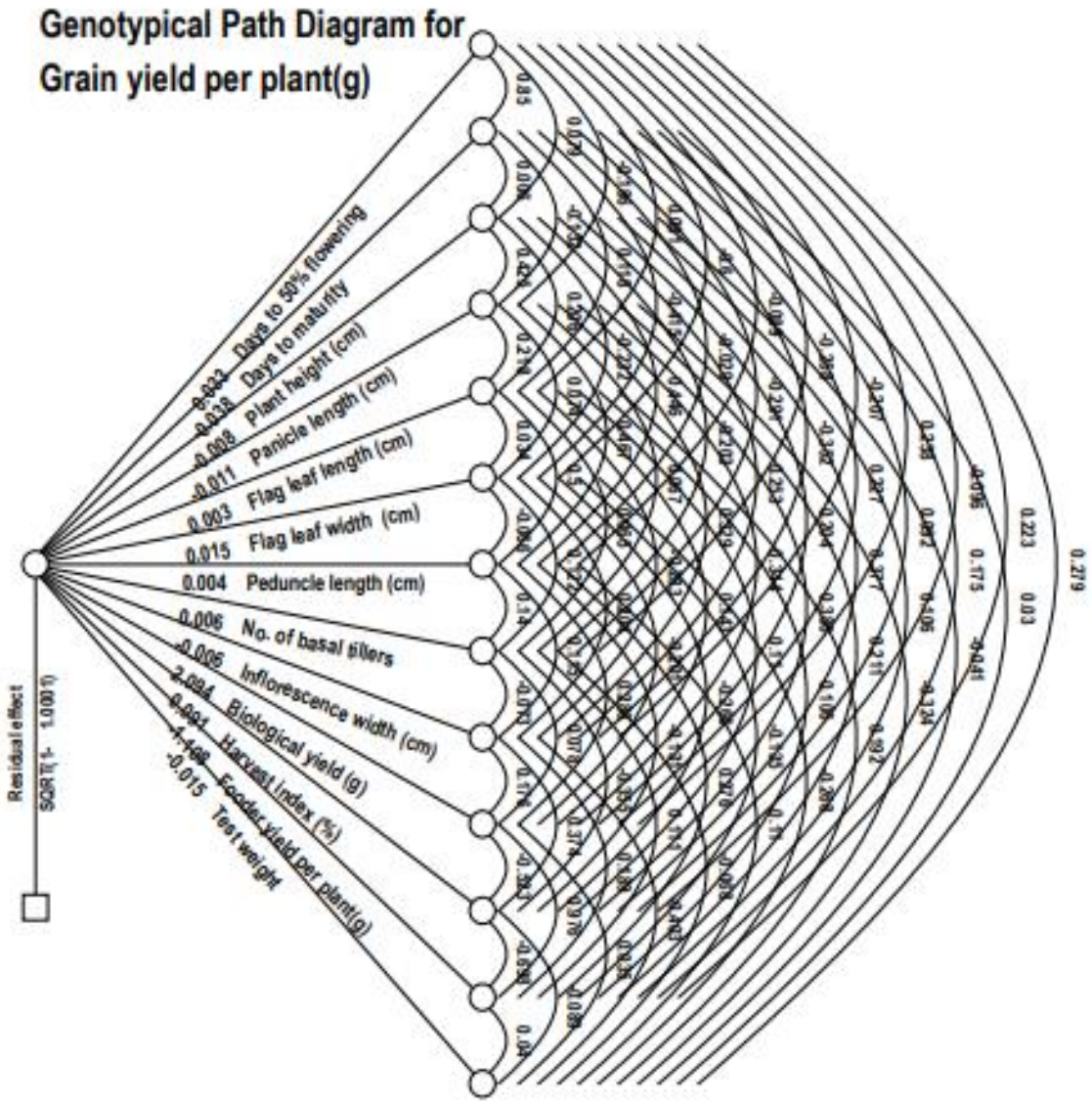


Fig 4.4.1. Genotypic (r_g) path co-efficient analysis among yield and yield components of 30 foxtail millet genotypes

4.6.2. Phenotypic Path Coefficient Analysis

Path coefficients which are worked out from phenotypic correlation coefficient are referred to as phenotypic path. It splits the phenotypic correlation coefficients into the measures of direct and indirect effects (Dewey and Lu, 1959).

The phenotypical path matrix of grain yield per plant revealed critical direct effects of various traits on this important parameter. Panicle length exhibited a positive direct effect of 0.0063 on grain yield per plant, indicating that an increase in panicle length could lead to higher grain yield. Similarly, flag leaf length (0.0066), flag leaf width (0.0013), number of tillers per plant (0.0053), biological yield (1.9569), and harvest index (0.0987) all demonstrated positive direct effects on grain yield per plant. Notably, biological yield had a substantial positive effect, suggesting its significant contribution to grain yield. Conversely, there were negative direct effects on grain yield per plant from days to 50 per cent flowering (-0.0020), days to maturity (-0.0061), plant height (-0.0008), peduncle length (-0.0103), panicle width (-0.0010), fodder yield per plant (-1.0134), and test weight (-0.0025). These direct effects provide crucial insights into how specific traits directly impact grain yield per plant, aiding in targeted crop improvement strategies.

4.6.2.1 Days to 50 per cent flowering

The Phenotypical path analysis of grain yield per plant in relation to days to 50 per cent flowering revealed notable direct and indirect effects. The direct effect of days to 50 per cent flowering on grain yield per plant is negatively modest (-0.002), suggesting that a delay in flowering is associated with a slight reduction in grain yield. Among the positive indirect effects, panicle length (0.0003), flag leaf width (0.0009), peduncle length (0.0003), the number of tillers per plant (0.0005), panicle width (0.0003), and harvest index (0.0002)

contribute positively to grain yield. Conversely, negative indirect effects involve days to maturity (-0.0017), plant height (-0.0001), flag leaf length (-0.0002), biological yield (-0.0005), fodder yield per plant (-0.0005), and test weight (-0.0005). These findings provide insights into the intricate interactions between Phenotypical factors and their influence on grain yield within the context of days to 50 per cent flowering in the studied plant population.

4.6.2.2 Days to maturity

The phenotypical path analysis of grain yield per plant with respect to days to maturity revealed significant direct and indirect effects. The direct effect of days to maturity on grain yield per plant is negatively notable (-0.0061), suggesting that a longer time to maturity was associated with decreased grain yield. Among the positive indirect effects, flag leaf width (0.002), peduncle length (0.0004), the number of tillers per plant (0.0013), panicle width (0.0016), and panicle length (0.0006) contribute positively to grain yield. Conversely, negative indirect effects involve days to 50 per cent flowering (-0.005), plant height (-0.0001), flag leaf length (-0.0009), biological yield (-0.0015), harvest index (-0.0001), fodder yield per plant (-0.0012), and test weight (-0.0002). These findings provide insights into the complex relationships between phenotypical factors and their impact on grain yield within the context of days to maturity in the studied plant population.

4.6.2.3 Plant height (cm)

The phenotypical path analysis of grain yield per plant concerning plant height unveils both direct and indirect effects. The direct effect of plant height on grain yield per plant was slightly negative (-0.0008), suggesting that increased plant height was associated with a minor reduction in grain yield. Among the positive indirect effects, days to maturity (0.0000), flag leaf width (0.0001), the number of tillers per plant (0.0001), and test weight (0.0000) contribute

slightly positively to grain yield. Conversely, negative indirect effects involve days to 50 per cent flowering (-0.0001), panicle length (-0.0003), flag leaf length (-0.0002), peduncle length (-0.0003), panicle width (-0.0002), biological yield (-0.0002), harvest index (-0.0002), and fodder yield per plant (-0.0001). These findings provide insights into the intricate relationships between phenotypical factors and their impact on grain yield within the context of plant height in the studied plant population.

4.6.2.4 Panicle length (cm)

The phenotypical path analysis of grain yield per plant in relation to panicle length revealed significant direct and indirect effects. The direct effect of panicle length on grain yield per plant was positive (0.0063), indicating that an increase in panicle length was associated with higher grain yield. Among the positive indirect effects, plant height (0.0025), flag leaf length (0.0014), flag leaf width (0.0004), peduncle length (0.0027), the number of basal tillers (0.0004), inflorescence width (0.0018), biological yield (0.002), harvest index (0.0019), and fodder yield per plant (0.0012) contribute positively to grain yield. Conversely, negative indirect effects involve days to 50 per cent flowering (-0.0009), days to maturity (-0.0006), and test weight (-0.0018). These findings provide insights into the complex relationships between phenotypical factors and their influence on grain yield within the context of panicle length in the studied plant population.

4.6.2.5 Flag leaf length (cm)

The phenotypical path analysis of grain yield per plant concerning flag leaf length revealed significant direct and indirect effects. The direct effect of flag leaf length on grain yield per plant was positive (0.0066), suggesting that an increase in flag leaf length was associated with higher grain yield. Among the positive indirect effects, days to 50 per cent flowering (0.0007), days to

maturity (0.0009), plant height (0.0013), panicle length (0.0015), flag leaf width (0.001), peduncle length (0.003), the number of tillers per plant (0.0008), biological yield (0.0012), harvest index (0.0009), fodder yield per plant (0.0008), and test weight (0.0011) contribute positively to grain yield. Conversely, a single negative indirect effect involves panicle width (-0.001). These findings provide insights into the intricate relationships between phenotypical factors and their impact on grain yield within the context of flag leaf length in the studied plant population.

4.6.2.6 Flag leaf width (cm)

The phenotypical path analysis of grain yield per plant with regard to flag leaf width revealed significant direct and indirect effects. The direct effect of flag leaf width on grain yield per plant was slightly positive (0.0013), indicating that an increase in flag leaf width was associated with a minor improvement in grain yield. Among the positive indirect effects, panicle length (0.0001), flag leaf length (0.0002), the number of tillers per plant (0.0002), and panicle width (0.0004) contribute slightly positively to grain yield. Conversely, negative indirect effects involve days to 50 per cent flowering (-0.0006), days to maturity (-0.0004), plant height (-0.0002), biological yield (-0.0001), harvest index (-0.0002), fodder yield per plant (-0.0001), and test weight (-0.0003). These findings provide insights into the complex interactions between phenotypical factors and their impact on grain yield within the context of flag leaf width in the studied plant population.

4.6.2.7 Peduncle length (cm)

The phenotypical path analysis of grain yield per plant concerning peduncle length unveils significant direct and indirect effects. The direct effect of peduncle length on grain yield per plant was negative (-0.0103), suggesting that longer peduncle lengths are associated with reduced grain yield. Among

the positive indirect effects, days to 50 per cent flowering (0.0013), days to maturity (0.0007), and harvest index (0.0006) contribute slightly positively to grain yield. Conversely, negative indirect effects involve plant height (-0.0041), panicle length (-0.0044), flag leaf length (-0.0047), flag leaf width (-0.0003), the number of tillers per plant (-0.0019), panicle width (-0.0014), biological yield (-0.0027), fodder yield per plant (-0.0025), and test weight (-0.0011). These findings provide insights into the complex relationships between phenotypical factors and their impact on grain yield within the context of peduncle length in the studied plant population.

4.6.2.8 Number of tillers per plant

The phenotypical path analysis of grain yield per plant with respect to the number of tillers per plant revealed significant direct and indirect effects. The direct effect of the number of tillers per plant on grain yield per plant was positive (0.0053), suggesting that an increased number of tillers was associated with higher grain yield. Among the positive indirect effects, panicle length (0.0004), flag leaf length (0.0006), flag leaf width (0.0008), peduncle length (0.0010), and biological yield (0.0008) contribute positively to grain yield. Conversely, negative indirect effects involve days to 50 per cent flowering (-0.0012), days to maturity (-0.0012), plant height (-0.0007), test weight (-0.0003), and harvest index (-0.0010). These findings provide insights into the intricate relationships between phenotypical factors and their impact on grain yield within the context of the number of tillers per plant in the studied plant population.

4.6.2.9 Panicle width (cm)

The phenotypical path analysis of grain yield per plant concerning panicle width revealed significant direct and indirect effects. The direct effect of panicle width on grain yield per plant was slightly negative (-0.0010),

suggesting that wider panicle widths are associated with a minor reduction in grain yield. Among the positive indirect effects, days to 50 per cent flowering (0.0002), days to maturity (0.0003), flag leaf length (0.0001), the number of tillers per plant (0.0000), harvest index (0.0002), and test weight (0.0004) contribute slightly positively to grain yield. Conversely, negative indirect effects involve plant height (-0.0003), panicle length (-0.0003), flag leaf width (-0.0003), peduncle length (-0.0001), biological yield (-0.0002), and fodder yield per plant (-0.0002). These findings provide insights into the complex relationships between phenotypical factors and their impact on grain yield within the context of panicle width in the studied plant population.

4.6.2.10 Biological yield (g)

The phenotypical path analysis of grain yield per plant in relation to biological yield revealed significant direct and indirect effects. The direct effect of biological yield on grain yield per plant was substantial and positive (1.9569), indicating that higher biological yields are strongly associated with increased grain yield. Among the positive indirect effects, days to 50 per cent flowering (0.4845), days to maturity (0.4763), plant height (0.4225), panicle length (0.6064), flag leaf length (0.3400), peduncle length (0.5202), the number of tillers per plant (0.2801), panicle width (0.3721), fodder yield per plant (1.8938), and test weight (0.0506) contribute positively to grain yield. Conversely, negative indirect effects involve flag leaf width (-0.2062) and harvest index (-0.6962). These findings offer valuable insights into the complex interactions between phenotypical factors and their impact on grain yield within the context of biological yield in the studied plant population.

4.6.2.11 Harvest index (%)

The phenotypical path analysis of grain yield per plant concerning harvest index unveils significant direct and indirect effects. The direct effect of harvest

index on grain yield per plant was positive (0.0987), suggesting that a higher harvest index was associated with an increase in grain yield. Among the positive indirect effects, days to maturity (0.0019), plant height (0.0267), panicle length (0.0288), and flag leaf length (0.0128) contribute positively to grain yield. Conversely, negative indirect effects involve days to 50 per cent flowering (-0.0081), flag leaf width (-0.0120), peduncle length (-0.0056), the number of tillers per plant (-0.0176), panicle width (-0.0186), biological yield (-0.0351), fodder yield per plant (-0.0545), and test weight (-0.0066). These findings provide insights into the intricate relationships between phenotypical factors and their impact on grain yield within the context of harvest index in the studied plant population.

4.6.2.12 Fodder yield per plant (g)

The phenotypical path analysis of grain yield per plant concerning fodder yield per plant revealed significant direct and indirect effects. The direct effect of fodder yield per plant on grain yield per plant was notably negative (-1.0134), indicating that a higher fodder yield was associated with a substantial reduction in grain yield. Among the positive indirect effects, flag leaf width (0.0712) and harvest index (0.5594) contribute positively to grain yield. Conversely, negative indirect effects involve days to 50 per cent flowering (-0.2342), days to maturity (-0.2024), plant height (-0.1237), panicle length (-0.1892), flag leaf length (-0.1206), peduncle length (-0.2502), the number of tillers per plant (-0.1580), panicle width (-0.1905), biological yield (-0.9807), and test weight (-0.0323). These findings provide insights into the complex interactions between phenotypical factors and their impact on grain yield within the context of fodder yield per plant in the studied plant population.

4.6.2.13 Test weight (g)

The phenotypical path analysis of grain yield per plant with regard to test weight revealed significant direct and indirect effects. The direct effect of test weight on grain yield per plant was negative (-0.0025), indicating that a higher test weight was associated with a decrease in grain yield. Among the positive indirect effects, plant height (0.0001), panicle length (0.0007), flag leaf width (0.0006), the number of tillers per plant (0.0001), panicle width (0.0009), and harvest index (0.0002) contribute slightly positively to grain yield. Conversely, negative indirect effects involve days to 50 per cent flowering (-0.0006), days to maturity (-0.0001), flag leaf length (-0.0004), peduncle length (-0.0003), biological yield (-0.0001), and fodder yield per plant (-0.0001). These findings provide insights into the complex relationships between phenotypical factors and their impact on grain yield within the context of test weight in the studied plant population.

Table 4.6.2. Phenotypic (rp) path co-efficient analysis among yield and yield components of 30 foxtail millet genotypes

	DF	DM	PH	PL	FL	FW	PDL	NT	PW	BY	HI	FY	TW
DF	**-0.0020**	-0.0017	-0.0001	0.0003	-0.0002	0.0009	0.0003	0.0005	0.0003	-0.0005	0.0002	-0.0005	-0.0005
DM	-0.0050	**-0.0061**	-0.0001	0.0006	-0.0009	0.0020	0.0004	0.0013	0.0016	-0.0015	-0.0001	-0.0012	-0.0002
PH	-0.0001	0.0000	**-0.0008**	-0.0003	-0.0002	0.0001	-0.0003	0.0001	-0.0002	-0.0002	-0.0002	-0.0001	0.0000
PL	-0.0009	-0.0006	0.0025	**0.0063**	0.0014	0.0004	0.0027	0.0004	0.0018	0.0020	0.0019	0.0012	-0.0018
FL	0.0007	0.0009	0.0013	0.0015	**0.0066**	0.0010	0.0030	0.0008	-0.0010	0.0012	0.0009	0.0008	0.0011
FW	-0.0006	-0.0004	-0.0002	0.0001	0.0002	**0.0013**	0.0000	0.0002	0.0004	-0.0001	-0.0002	-0.0001	-0.0003
PDL	0.0013	0.0007	-0.0041	-0.0044	-0.0047	-0.0003	**-0.0103**	-0.0019	-0.0014	-0.0027	0.0006	-0.0025	-0.0011
NT	-0.0012	-0.0012	-0.0007	0.0004	0.0006	0.0008	0.0010	**0.0053**	0.0000	0.0008	-0.0010	0.0008	-0.0003
PW	0.0002	0.0003	-0.0003	-0.0003	0.0001	-0.0003	-0.0001	0.0000	**-0.0010**	-0.0002	0.0002	-0.0002	0.0004
BY	0.4845	0.4763	0.4225	0.6064	0.3400	-0.2062	0.5202	0.2801	0.3721	**1.9569**	-0.6962	1.8938	0.0506
HI	-0.0081	0.0019	0.0267	0.0288	0.0128	-0.0120	-0.0056	-0.0176	-0.0186	-0.0351	**0.0987**	-0.0545	-0.0066
FY	-0.2342	-0.2024	-0.1237	-0.1892	-0.1206	0.0712	-0.2502	-0.1580	-0.1905	-0.9807	0.5594	**-1.0134**	-0.0323
TW	-0.0006	-0.0001	0.0001	0.0007	-0.0004	0.0006	-0.0003	0.0001	0.0009	-0.0001	0.0002	-0.0001	**-0.0025**
GY	0.2340	0.2677	0.3232	0.4509	0.2348	-0.1404	0.2608	0.1115	0.1645	0.9397	-0.0357	0.8241	0.0066
Partial R^2	-0.0005	-0.0016	-0.0003	0.0029	0.0016	-0.0002	-0.0027	0.0006	-0.0002	1.8388	-0.0035	-0.8351	0.0000

Residual effect= rp (0.0139), Days to 50 per cent flowering (DF), Days to maturity (DM), Plant height (PH), Panicle length (PL), Flag leaf length (FL), Flag leaf width (FW), Peduncle length (PDL), No. of tillers 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).

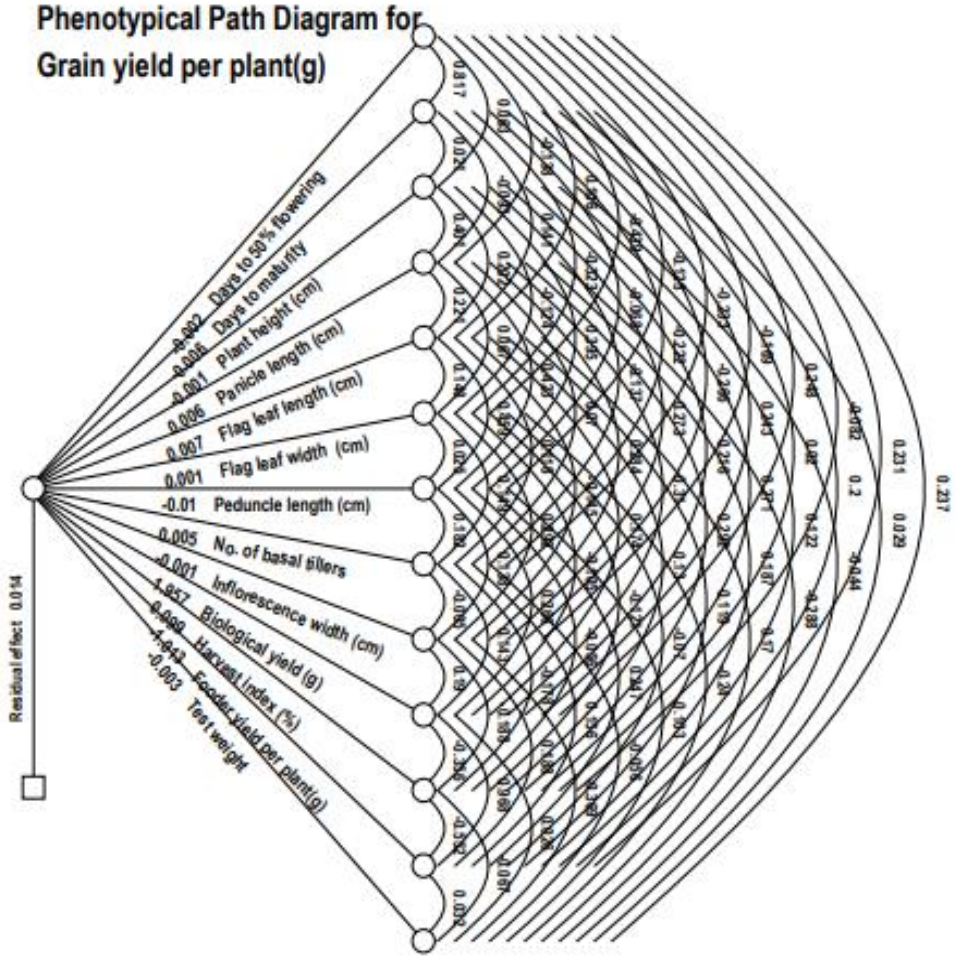


Fig 4.4.2. Phenotypic (r_g) path co-efficient analysis among yield and yield components of 30 foxtail millet genotypes

4.7 Genetic Diversity by Mahalanobis' D^2 Statistic

In the world of plant breeding, the genetic diversity of genotypes is often measured by Mahalanobis' D^2method. In this study, Mahalanobis' D^2 Statistic was used to group the genotypes into clusters based on their similarities and differences in various traits. These clusters help plant breeders understand the genetic diversity among the foxtail millet genotypes and how they perform under different environmental conditions. This study aimed to identify suitable parents for hybridization by analyzing the genetic diversity of 30 foxtail millet genotypes across four environments.

4.7.1 Clustering pattern

In the study, we observed 30 foxtail millet genotypes in four different environments. The results of the D^2 analysis confirmed the presence of high genetic diversity among the genotypes. It was found that there were many differences in the traits among these genotypes. In the first environment, 30 genotypes grouped into nine clusters (Fig 4.20 (A).) based on their similarities using by Tocher method, followed by six clusters in environment-2 (Fig 4.20. (B)), seven clusters in environment-3 (Fig 4.20. (C)), ten clusters in environmental-4 (Fig 3. (D)) and five clusters in the pooled environmental combination (Fig 4.20. (E)).

Under environmental-1 (Table 4.6.1.1.), there were four clusters (Cluster-I, IV, V, and VI) with a maximum of five genotypes each, followed by Cluster-III with four genotypes, Cluster-IX with three genotypes, and Cluster-II, VII, and VIII, each having only one genotype. In environmental-2 (Table 4.6.1.2.), Cluster-I was the largest, containing the highest number of genotypes (20), followed by Cluster-II with six genotypes, and Cluster-II, IV, V, and VI, each with only one genotype. In environmental-3 (Table 4.6.1.3.), Cluster-I was the largest, containing the maximum number of genotypes (24), followed by mono solitary clusters (Cluster-II, III, IV, V, VI, and VII). In environmental-4 (Table

4.6.1.4.), Cluster-I was the largest, containing the maximum number of genotypes (18), followed by Cluster-V with four genotypes, and mono solitary clusters (Cluster-II, III, IV, VI, VII, VIII, IX, and X). However, when considering pooled environments together (Table 4.6.1.5.), Cluster-I was the largest, containing the maximum number of genotypes (26), followed by mono solitary clusters (Cluster-II, III, IV, and V).

Table 4.7.1. Clustering by Tocher Method in Environmental-1

Cluster	No. of genotypes	List of genotypes
Cluster. 1	5	G9, G18, G3, G24, G28
Cluster. 2	1	G27
Cluster. 3	4	G2, G4, G11, G12
Cluster. 4	5	G21, G22, G25, G10, G23
Cluster. 5	5	G19, G26, G13, G14, G20
Cluster. 6	5	G7, G17, G29, G30, G8
Cluster. 7	1	G5
Cluster. 8	1	G1
Cluster. 9	3	G15, G16, G6

Table 4.7.2. Clustering by Tocher Method in Environmental-2

Cluster	No. of genotypes	List of genotypes
Cluster.1	20	G11, G12, G15, G13, G6, G5, G19, G10, G7, G17, G26, G22, G28, G29, G27, G23, G14, G25, G30
Cluster.2	1	G16
Cluster.3	6	G9, G21, G18, G1, G4, G3
Cluster.4	1	G2
Cluster.5	1	G8
Cluster.6	1	G24

Table 4.7.3. Clustering by Tocher Method in Environmental-3

Cluster	No. of genotypes	List of genotypes
Cluster.1	24	G10, G19, G7, G29, G23, G14, G27, G16, G 18, G30, G9, G26, G25, G8, G17, G24, G13, G28, G20, G 6, G22, G21, G12, G11
Cluster.2	1	G15
Cluster.3	1	G3
Cluster.4	1	G5
Cluster.5	1	G2
Cluster.6	1	G4
Cluster.7	1	G1

Table 4.7.4. Clustering by Tocher Method in Environmental-4

Cluster	No. of genotypes	List of genotypes
Cluster. 1	18	G9, G13, G14, G26, G12, G20, G28, G3, G21, G25, G10, G18, G22, G19, G23, G4, G15, G6
Cluster. 2	1	G11
Cluster. 3	1	G16
Cluster. 4	1	G27
Cluster. 5	4	G7, G29, G17, G8
Cluster. 6	1	G24
Cluster. 7	1	G2
Cluster. 8	1	G5
Cluster. 9	1	G30
Cluster. 10	1	G1

Table 4.7.5. Clustering by Tocher Method in pooled Environmental

Cluster	No. of genotypes	List of genotypes
Cluster. 1	26	G22, G23, G10, G14, G9, G19, G13, G18, G6, G7, G21, G3, G4, G11, G15, G12, G26, G27, G17, G20, G28, G2, G8, G5, G16, G25
Cluster. 2	1	G24
Cluster. 3	1	G1
Cluster. 4	1	G29
Cluster. 5	1	G30

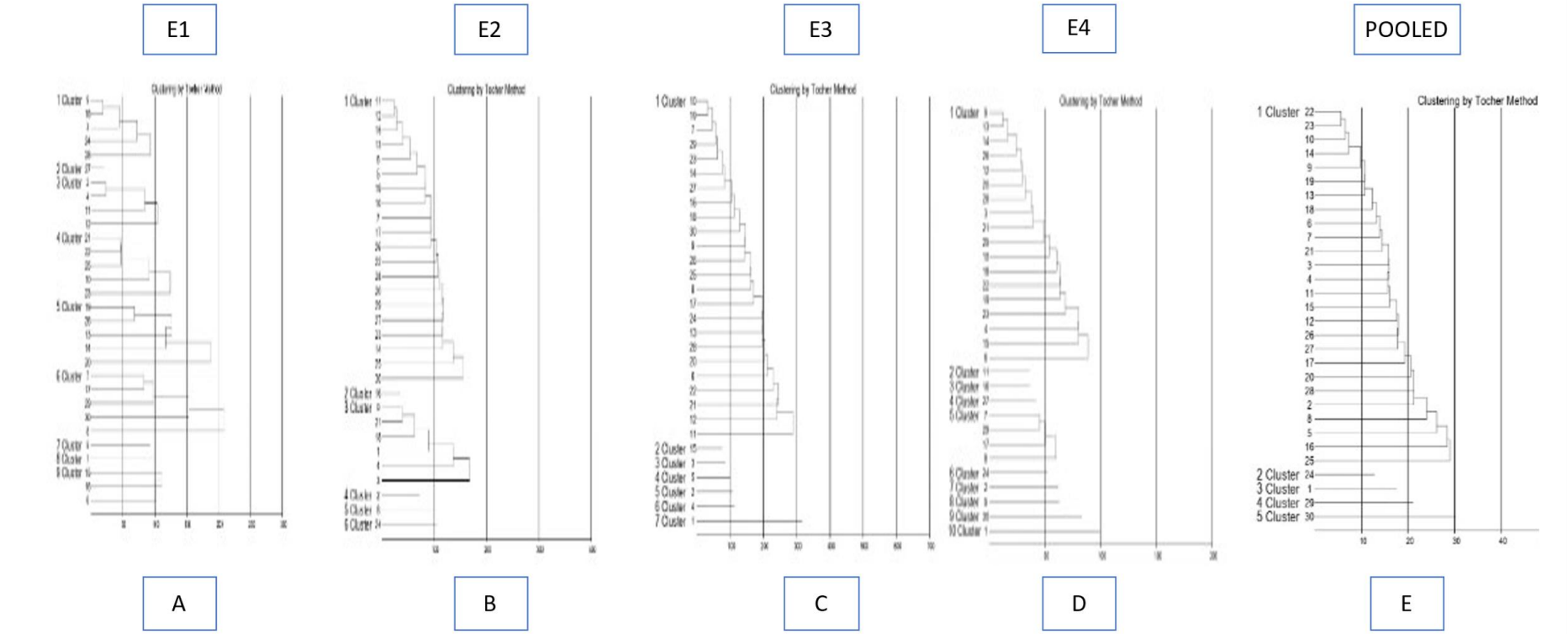


Fig 4.5. (A, B, C, D, E) Clustering by Tocher Method over five environments

4.7.2 Intra and inter-cluster distance

Mahalanobis' D2 Statistic is a powerful tool for clustering analysis in multidimensional datasets. It considers the data's covariance structure and correlations between variables, making it robust. By examining intra-cluster and inter-cluster distances, researchers gain insights into data patterns, revealing natural groupings and relationships among observations. In Environmental-1 (Table 4.7.1.), the foxtail millet genotypes exhibited a broad range of intra-cluster distances, spanning from 0.00 to 14.26. Cluster-VI displayed the highest intra-cluster distance (14.26), comprising five genotypes, followed by cluster-V (13.61) with five genotypes, cluster-IX (11.81) with three genotypes, cluster-IV (10.83) with five genotypes, cluster-III (10.76) with four genotypes, and cluster-I (9.54) with five genotypes. Additionally, three mono solitary clusters, namely cluster-II, VII, and VIII, showed an intra-cluster distance of 0.00, indicating that the genotypes within these clusters were highly similar and formed distinct, separate groups. In Environmental-2 (Table 4.7.2.), the intra-cluster distances ranged from 0.00 to 12.31. Cluster-III displayed the highest intra-cluster distance (12.31) among all clusters, consisting of six genotypes, followed by cluster-I (10.90) with 20 genotypes. Similar to Environmental-1, clusters II, IV, V, and VI were mono solitary with an intra-cluster distance of 0.00. In Environmental-3 (Table 4.7.3.), the intra-cluster distances varied from 0.00 to 14.25. Cluster-I exhibited the highest intra-cluster distance (14.25) among all clusters, comprising 24 genotypes. Similar to the previous environments, clusters II, III, IV, V, VI, and VII were mono solitary with an intra-cluster distance of 0.00. In Environmental-4 (Table 4.7.4), the intra-cluster distances ranged from 0.00 to 8.13. Cluster-I had the highest intra-cluster distance (8.13) and included 18 genotypes, while cluster-V was mono solitary with an intra-cluster distance of 0.00, consisting of four genotypes. While cluster-II, III, IV, VI, VII, VIII, IX and X are mono solitary clusters with intra-cluster distance of 0.00. Finally, in the pooled

environmental analysis (Table 4.7.5.), the inter-cluster distances ranged from 4.59 to 0.00. Cluster-I had the highest intra-cluster distance (8.13) and comprised 26 genotypes. In contrast, four mono solitary clusters (clusters II, III, IV, and V) displayed an intra-cluster distance of 0.00, indicating highly similar genotypes within each of this clusters.

In the analysis of different environments, using Mahalanobis' D^2 Statistic, inter-cluster distances were observed to vary among foxtail millet genotypes, providing insights into their genetic relationships. In Environmental-1 (Table 4.7.1.), the inter-cluster distances ranged from 35.09 to 11.25. Clusters VIII and IX showed the maximum inter-cluster distance (35.09), followed by clusters VII and IX (34.99), clusters I and IX (30.07), clusters VI and IX (27.53), clusters III and IX (26.87), clusters II and IX (26.5), clusters IV and IX (22.52), and clusters V and IX (18.97). Similarly, in Environmental-2 (Table 4.7.2.), the inter-cluster distances ranged from 22.94 to 11.71. Clusters III and IV exhibited the maximum inter-cluster distance (22.94), followed by clusters II and V (21.72), clusters V and VI (16.53), clusters IV and V (16.39), and clusters III and I (16.04). In Environmental-3 (table 4.7.3.), the inter-cluster distances ranged from 25.56 to 10.59. Cluster I and VII showed the maximum inter-cluster distance (25.56), followed by clusters VI and VII (25.00), clusters V and VII (24.36), clusters I and V (23.64), clusters III and V (20.22), clusters I and VI (19.94), clusters II and VII (19.94), clusters III and VII (19.85), and clusters IV and VII (19.61). In Environmental-4 (table 4.7.4.), the inter-cluster distances ranged from 21.35 to 6.46. Clusters II and X exhibited the maximum inter-cluster distance (21.35), followed by clusters V and X (20.61), clusters IV and X (19.4), clusters III and X (19.25), clusters III and VII (19.61), clusters V and VII (18.55), clusters V and VIII (18.12), clusters VII and IX (18.12), clusters VI and X (17.94), clusters IV and VII (16.99), clusters II and IX (16.88), clusters II and VIII (16.71), clusters IX and X (16.71), and clusters VIII and IX (16.71). Finally, in the pooled

environmental analysis (Table 4.7.5.), inter-cluster distances ranged from 8.75 to 6.01. Clusters III and V displayed the maximum inter-cluster distance (8.75), followed by clusters III and IV (8.01), clusters II and V (7.92), clusters I and V (7.02), and clusters IV and V (6.85).

Table 4.8.1. Cluster Distances in Environmental-1

	Cluster. 1	Cluster. 2	Cluster. 3	Cluster. 4	Cluster. 5	Cluster. 6	Cluster. 7	Cluster. 8	Cluster. 9
Cluster. 1	9.54	12.23	14.09	15.04	18.28	25.62	13.89	12.78	30.07
Cluster. 2		0.00	14.79	13.94	17.27	17.82	13.26	16.00	26.50
Cluster. 3			10.76	16.02	16.32	25.78	15.98	19.63	26.87
Cluster. 4				10.83	15.71	20.53	19.33	18.28	22.52
Cluster. 5					13.61	24.99	24.27	24.23	18.97
Cluster. 6						14.26	24.56	26.12	27.53
Cluster. 7							0.00	11.25	34.99
Cluster. 8								0.00	35.09
Cluster. 9									11.81

Table 4.8.2. Cluster Distances in Environmental-2

	Cluster. 1	Cluster. 2	Cluster. 3	Cluster. 4	Cluster. 5	Cluster. 6
Cluster.1	10.9	14.0	16.0	13.2	13.9	14.1
Cluster.2		0.0	12.9	19.1	21.7	20.2
Cluster.3			12.3	15.5	22.9	20.1
Cluster.4				0.0	16.4	11.7
Cluster.5					0.0	16.5
Cluster.6						0.0

Table 4.8.3. Cluster Distances in Environmental-3

	Cluster.1	Cluster.2	Cluster.3	Cluster.4	Cluster.5	Cluster.6	Cluster.7
Cluster.1	14.25	17.82	18.50	18.72	23.64	19.94	25.56
Cluster.2		0.00	13.48	11.74	13.54	10.61	19.94
Cluster.3			0.00	10.59	20.22	14.51	19.85
Cluster.4				0.00	12.27	16.63	19.61
Cluster.5					0.00	19.38	24.36
Cluster.6						0.00	25.00
Cluster.7							0.00

Table 4.8.4. Cluster Distances in Environmental-4

	Cluster. 1	Cluster.2	Cluster. 3	Cluster. 4	Cluster. 5	Cluster. 6	Cluster. 7	Cluster. 8	Cluster. 9	Cluster. 10
Cluster. 1	8.13	11.20	11.24	10.09	11.64	11.08	12.88	11.14	11.77	14.68
Cluster. 2		0.00	15.07	11.95	12.17	12.50	14.60	16.71	16.88	21.35
Cluster. 3			0.00	6.46	11.25	13.84	19.61	13.92	14.65	19.25
Cluster. 4				0.00	9.98	11.90	16.99	13.73	14.30	19.40
Cluster. 5					8.51	13.92	18.55	18.12	12.52	20.61
Cluster. 6						0.00	13.87	13.79	14.77	17.94
Cluster. 7							0.00	10.66	18.12	12.32
Cluster. 8								0.00	16.46	9.94
Cluster. 9									0.00	16.71
Cluster. 10										0.00

Table 4.8.5. Cluster Distances in Pooled Environmental					
	Cluster. 1	Cluster. 2	Cluster. 3	Cluster. 4	Cluster. 5
Cluster. 1	4.59	6.26	6.01	6.45	7.02
Cluster. 2		0.00	6.49	6.77	7.92
Cluster. 3			0.00	8.01	8.75
Cluster. 4				0.00	6.85
Cluster. 5					0.00

4.7.3 Cluster mean performance

Cluster mean, represents the average values of all the variables for the data points belonging to a particular cluster. In Environmental-1 (Table 4.8.1.), clusters II, VII, and VIII consisted of single genotypes viz. G27, G5, and G1, respectively. G27 exhibits long flag leaf area (FL: 28.13, FW: 2.8), high harvest index (54.17), and grain yield per plant (20.23). G5 and G1 both show higher peduncle length (27.60, 27.07) and biological yield (41.50, 42.10). Cluster I have 5 genotypes and this cluster means revealed these genotypes are higher days to flowering (74.79), days to maturity (114.99), and grain yield per plant (20.67). Cluster III has 4 genotypes (G2, G4, G11, and G12) and these genotypes are exhibits highest cluster mean of peduncle length (18.48), number of base tillers (4.13), low panicle width (1.69), low biological yield (35.17), lowest grain yield per plant (16.30), and highest test weight (3.22). Cluster V has 5 genotypes that are exhibited an average performance of all traits. Cluster VI had 5 genotypes (G7, G17, G29, G30, and G8) which are exhibits lowest days to flowering (65.37), days to maturity (104.36), flag leaf length (21.69), biological yield (34.87), test weight (2.83), and grain yield per plant (16.81). Cluster IX had 3 genotypes (G15, G16, G6) those are exhibits lowest days to flowering (69.62), lowest days to maturity (110.12), lowest plant height (87.04), lowest panicle width (1.61), and highest number of base tillers (4.43).

In Environmental-2 (Table 4.8.2.), clusters II, IV, V, and VI are solitary clusters those are containing G16, G2, G8, and G24 genotypes, respectively. G16 exhibited highest cluster mean flag leaf length (23.6) and remain traits are shows average cluster mean values. G2 exhibits highest cluster mean number of base tillers (4.03) and test weight (3.17). G8 exhibits highest cluster mean panicle length (17.97), flag leaf width (2.17), panicle width (2.10), and lowestdays to flowering (65.97), days to maturity (97.17). G24 exhibits lowest cluster mean ofpanicle length (11.47), flag leaf length (18.40), flag leaf width

(1.47), panicle width (1.37),and most of traits shows lowest mean values include grain yield per plant. Cluster III had 6 genotypes, which are exhibits highest cluster mean values of days to flowering (80.01), days to maturity (119.77), biological yield (38.19), harvest index (42.37), fodder yield (22.06), and grain yield per plant (16.14). Cluster I had 20 genotypes which are exhibits average cluster mean value of all traits.

In Environmental-3 (Table 4.8.3), clusters II, III, IV, and V is solitary. Those are containing G15, G3, G5, G2, G4, and G1, respectively. G15 exhibited highest cluster mean of flag leaf length (2.5) and remain traits are shows average cluster mean values. G3 exhibits highest cluster mean of days to flowering (85.93) and lowest cluster mean of flag leaf width (1.20), panicle width (1.20), and harvest index (36.87). G5 exhibits highest cluster mean of flag leaflength 25.43), number of tillers (3.03), panicle width (1.97), and grain yield per plant (19.50). G2 exhibits lowest days to maturity (106.83), highest panicle length (17.23), peduncle length (24.23), number of base tillers (4.10), and test weight (3.12). G4 exhibits lowest cluster mean of plant height (63.73), panicle length (6.8), flag leaf length (17.27), peduncle length (14.87), biological yield (23.3), fodder yield (13.5), and grain yield per plant (9.83). G1 exhibits highest cluster mean of all traits including grain yield per plant. Cluster-I have 24 genotypes those are exhibits average cluster mean of all traits.

In Environmental-4 (Table 4.8.4.), Cluster I have 18 genotypes those are exhibits the lowest cluster mean of peduncle length (18.76), and remain traits exhibit average cluster means. Cluster V has 4 genotypes, those are exhibiting the lowest days to flowering (65.62). Cluster II is mono solitary (G11) which is exhibits the lowest days to maturity (98.83), panicle length (7.67), and harvest index. Cluster-III, IV, VI, VII, VIII, IX, and X are mono solitary clusters and those are containing G16, G27, G7, G24, G2, G5, G30, and G1 respectively. G16 exhibits the lowest cluster mean of days to maturity (98.83), panicle

length (7.67), and harvest index (37.73). G27 exhibits the lowest cluster mean of plant height (82.27), flag leaf width (2.2), and test weight (2.43). G7 exhibits the highest cluster mean of number of base tillers (5.07) and lowest panicle width (1.37). G24 exhibits the highest cluster mean of flag leaf length (25.33) and the lowest number of base tillers (2.27), biological yield (12.07), fodder yield (5.67), and grain yield per plant (6.40). G2 and G5 both are exhibits average cluster mean values of all traits. G30 exhibits the highest cluster mean of plant height (132.67), panicle length (16.8), panicle width (2.87), and the lowest flag leaf length (15.43). G1 exhibits the highest cluster mean values of days to maturity (123.23), peduncle length (26.93), biological yield (48.07), and grain yield per plant (21.00).

In pooled environmental (Table 4.8.5.), cluster-II, III, IV and V are solitary, these are containingG24, G1, G29 and G30 respectively. G24 exhibits lowest cluster means of the most of traits. G1 exhibits highest cluster means of the most of traits. G29 and G30 both are exhibits lowest days to flowering, and days to maturity. Cluster-I have 26 genotypes which are exhibits average cluster mean values.

Table 4.9.1. Cluster Mean in Environmental-1

	DF	DM	PH	PL	FL	FW	PDL	NT	PW	BY	HI	FY	TW	GY
Cluster.1	74.79	114.99	133.42	14.47	23.77	2.23	22.47	3.70	2.15	41.07	50.49	20.39	2.83	20.67
Cluster.2	70.97	110.40	133.13	13.47	28.13	2.80	24.57	4.20	2.47	37.33	54.17	17.10	2.87	20.23
Cluster.3	74.72	112.71	124.47	11.12	22.21	1.79	18.48	4.13	1.69	35.17	46.34	18.88	3.22	16.30
Cluster.4	72.39	112.78	118.43	19.27	22.04	1.45	19.70	3.71	1.81	38.00	50.69	18.74	2.90	19.27
Cluster.5	73.08	113.63	108.30	10.67	21.24	2.05	20.31	3.85	1.90	34.73	50.97	17.25	2.94	17.49
Cluster.6	65.37	104.36	126.67	15.28	21.69	2.43	22.23	4.09	2.07	34.87	48.10	18.06	2.83	16.81
Cluster.7	71.17	110.60	147.67	13.30	26.00	1.70	27.60	4.23	2.50	41.50	42.53	23.83	3.13	17.67
Cluster.8	70.73	115.73	145.73	15.37	22.60	1.63	27.07	3.27	1.77	42.10	43.10	23.97	2.87	18.13
Cluster.9	69.62	110.12	87.04	13.00	23.26	2.18	23.33	4.43	1.61	35.50	48.93	18.18	3.06	17.32

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), No. of tillers per plant (NT), Panicle width (PW), Biological yield (BY), Harvest index (HI), Fodder yield per plant (FY), Test weight (TW), and Grain yield per plant (GY).

Table 4.9.2. Cluster Mean in Environmental-2

	DF	DM	PH	PL	FL	FW	PDL	NT	PW	BY	HI	FY	TW	GY
Cluster.1	70.30	109.47	107.21	13.68	20.66	1.77	19.33	3.57	1.76	29.40	44.01	16.50	2.70	12.90
Cluster.2	76.90	118.93	93.60	14.57	23.60	2.13	17.10	3.90	1.63	29.63	44.10	16.57	2.43	13.07
Cluster.3	80.01	119.77	110.73	13.76	21.77	1.63	20.25	3.52	1.73	38.19	42.37	22.06	2.86	16.14
Cluster.4	71.53	109.83	125.63	12.77	22.90	1.80	23.40	4.03	1.60	30.07	45.63	16.37	3.17	13.73
Cluster.5	65.97	97.17	113.70	17.97	20.40	2.17	23.70	3.70	2.10	35.60	44.37	19.73	2.67	15.83
Cluster.6	66.33	106.33	126.67	11.47	18.40	1.47	27.37	3.53	1.37	19.60	49.10	10.13	2.87	9.47

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), No. of tillers per plant (NT), Panicle width (PW), Biological yield (BY), Harvest index (HI), Fodder yield per plant (FY), Test weight (TW), and Grain yield per plant (GY).

Table 4.9.3. Cluster Mean in Environmental-3

	DF	DM	PH	PL	FL	FW	PDL	NT	PW	BY	HI	FY	TW	GY
Cluster.1	69.82	109.79	107.58	14.42	20.67	1.92	19.66	3.36	1.82	30.23	43.56	17.04	2.68	13.19
Cluster.2	75.77	115.13	86.23	13.17	22.07	2.50	22.93	3.33	1.70	30.17	40.40	18.03	2.96	12.20
Cluster.3	85.93	121.00	93.57	8.97	20.37	1.20	17.13	3.03	1.20	36.57	36.87	23.03	2.74	13.53
Cluster.4	79.27	114.17	121.23	14.17	25.43	1.33	22.57	3.03	1.97	41.87	46.63	22.37	2.84	19.50
Cluster.5	73.23	106.83	124.23	17.23	25.27	1.80	24.23	4.10	1.63	32.23	44.83	17.80	3.12	14.47
Cluster.6	76.13	113.87	63.73	6.80	17.27	1.27	14.87	3.07	1.40	23.30	42.27	13.50	2.96	9.83
Cluster.7	76.80	129.93	131.70	15.20	22.20	1.30	23.43	3.37	1.57	46.47	44.60	25.77	2.83	20.73

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), No. of tillers per plant (NT), Panicle width (PW), Biological yield (BY), Harvest index (HI), Fodder yield per plant (FY), Test weight (TW), and Grain yield per plant (GY).

Table 4.9.4. Cluster Mean in Environmental-4

	DF	DM	PH	PL	FL	FW	PDL	NT	PW	BY	HI	FY	TW	GY
Cluster. 1	72.81	111.75	107.71	13.24	20.54	1.89	18.76	3.61	1.79	32.22	42.24	18.60	2.74	13.63
Cluster. 2	66.40	98.83	98.70	7.67	17.83	1.77	20.33	3.27	1.50	26.63	37.73	16.57	2.93	10.03
Cluster. 3	73.37	116.40	82.27	12.77	23.63	2.20	20.97	3.93	1.50	28.63	40.40	17.03	2.43	11.63
Cluster. 4	70.33	110.33	91.63	12.27	24.10	1.90	21.10	5.07	1.37	29.87	47.83	15.33	2.63	14.53
Cluster. 5	65.62	101.88	113.67	15.00	20.78	2.02	23.00	3.63	1.66	28.37	45.99	16.81	2.55	11.80
Cluster. 6	73.33	113.33	119.63	12.77	25.33	2.00	19.27	2.27	1.47	12.07	52.53	5.67	2.87	6.40
Cluster. 7	76.77	106.60	131.40	16.63	24.83	1.77	25.43	3.97	1.60	32.07	41.00	18.93	3.17	13.13
Cluster. 8	81.47	116.63	104.00	13.97	25.23	1.57	23.27	3.63	1.63	38.40	42.10	22.20	2.83	16.17
Cluster. 9	72.00	106.07	132.67	16.80	15.43	1.63	18.90	3.47	2.87	29.87	47.73	15.63	2.47	14.27
Cluster. 10	80.50	123.23	132.43	15.47	22.53	1.87	26.93	3.33	1.77	48.07	43.70	27.07	2.80	21.00

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), No. of tillers per plant (NT), Panicle width (PW), Biological yield (BY), Harvest index (HI), Fodder yield per plant (FY), Test weight (TW), and Grain yield per plant (GY).

Table 4.9.5. Cluster Mean in Pooled Environmental

	DF	DM	PH	PL	FL	FW	PDL	NT	PW	BY	HI	FY	TW	GY
Cluster. 1	71.92	110.97	109.09	13.78	21.48	1.91	20.04	3.64	1.79	33.01	44.72	18.27	2.80	14.78
Cluster. 2	72.13	112.26	122.22	12.77	22.29	1.73	21.76	2.84	1.49	21.75	49.33	10.97	2.88	10.78
Cluster. 3	76.46	122.99	133.60	14.50	22.16	1.50	24.78	3.42	1.61	46.04	43.75	25.91	2.83	20.14
Cluster. 4	66.24	106.64	120.38	13.92	22.51	1.95	24.63	4.61	1.82	24.23	44.46	13.40	2.59	10.82
Cluster. 5	71.63	106.08	131.69	16.96	16.73	1.63	19.99	3.41	2.58	28.87	47.00	15.26	2.52	13.61

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), No. of tillers per plant (NT), Panicle width (PW), Biological yield (BY), Harvest index (HI), Fodder yield per plant (FY), Test weight (TW), and Grain yield per plant (GY).

4.7.4 Percentage contribution of characters towards total divergence

In Mahalanobis' D^2 Statistic, the percentage contribution to genetic diversity is represented by the eigenvalues associated with the principal components used in the analysis. The eigenvalues provide information about the amount of variance explained by each principal component. In Environmental-1 (Table 4.9.), plant height had the highest contribution to the total genetic divergence (48.74%), appearing 212 times in the first rank. It was followed by days to flowering (21.84%) with 95 times in the first rank, test weight (11.49%) with 50 times in the first rank, and panicle length (7.13%) with 31 times in the first rank. Together, these four traits accounted for 89.2% of the total diversity in Environmental-1. In Environmental-2 (Table 4.9), test weight played the most significant role in the total genetic divergence (31.03%), being ranked first 135 times. Days to flowering (20.69%) followed, ranked first 90 times, then days to maturity (17.24%) in first rank with 75 times, and biological yield (7.13%) in first rank with 31 times. These four traits together contributed to 76.09% of the total diversity in Environmental-2. In Environmental-3 (Table 4.9), test weight had the highest contribution to the total genetic divergence (53.56%), ranked first 233 times. Days to flowering (13.56%) ranked first 59 times, followed by days to maturity (14.94%) ranked first 65 times, and biological yield (5.74%) ranked first 25 times. These four traits collectively accounted for 87.81% of the total diversity in Environmental-3. In Environmental-4 (Table 4.9), test weight had the greatest contribution to the total genetic divergence (36.78%), ranked first 160 times. Days to flowering (18.85%) ranked first 82 times, biological yield (15.17%) ranked first 66 times, and plant height (5.52%) ranked first 24 times. Together, these four traits contributed to 76.32% of the total diversity in Environmental-4. In the pooled environmental analysis (Table 4.9), test weight showed the highest contribution to the total genetic divergence (22.30%), ranked first 97 times. Panicle width (17.24%) ranked first 75 times, followed by flag leaf width (10.57%) in first rank with 46 times,

and biological yield (9.43%) ranked first 41 times. These four traits collectively accounted for 59.54% of the total diversity in the pooled environmental analysis.

Fig 4.6. Cluster Mean in Pooled Environmental

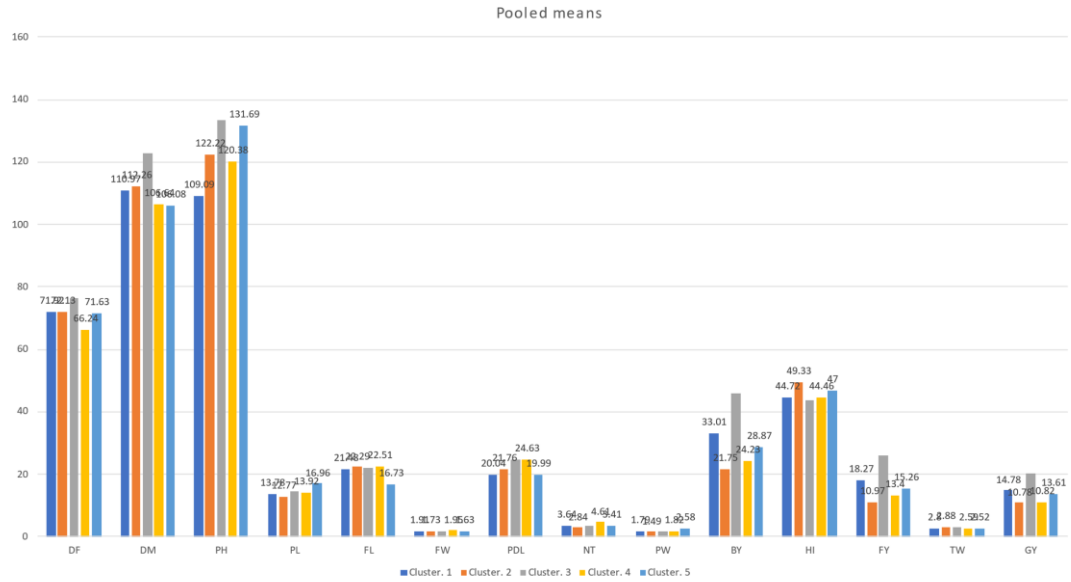


Table 4.10. Per cent contribution of different traits towards total divergence of different environments

	TR	CB	TR	CB	TR	CB	TR	CB	TR	CB
Source	E1		E2		E3		E4		POOLED	
1 Days to 50% flowering	95	21.84%	90	20.69%	59	13.56%	82	18.85%	9	2.07%
2 No. of Days to maturity	24	5.52%	75	17.24%	65	14.94%	19	4.37%	3	0.69%
3 Plant height (cm)	212	48.74%	19	4.37%	21	4.83%	24	5.52%	10	2.30%
4 Panicle length (cm)	31	7.13%	22	5.06%	3	0.69%	13	2.99%	38	8.74%
5 Flag leaf length (cm)	2	0.46%	2	0.46%	5	1.15%	8	1.84%	14	3.22%
6 Flag leaf width (cm)	4	0.92%	16	3.68%	5	1.15%	9	2.07%	46	10.57%
7 Peduncle length (cm)	1	0.23%	2	0.46%	8	1.84%	11	2.53%	29	6.67%
8 No. of basal tillers	0	0.00%	2	0.46%	1	0.23%	13	2.99%	34	7.82%
9 Inflorescence width (cm)	0	0.00%	20	4.60%	10	2.30%	13	2.99%	75	17.24%
10 Biological yield (g)	5	1.15%	31	7.13%	25	5.75%	66	15.17%	41	9.43%
11 Harvest index (%)	5	1.15%	9	2.07%	0	0.00%	2	0.46%	2	0.46%
12 fodder yield per plant(g)	6	1.38%	12	2.76%	0	0.00%	15	3.45%	21	4.83%
13 Test weight	50	11.49%	135	31.03%	233	53.56%	160	36.78%	97	22.30%
14 grain yield per plant(g)	0	0.00%	0	0.00%	0	0.00%	0	0.00%	16	3.68%
Tocher Cut-off Value	126.44		171.46		315.85		98.78		30.28	

TR=Times Ranked 1st, CB=Contribution %

4.8 Additive main effects and multiplicative interaction (AMMI)

AMMI stands for Additive Main Effects and Multiplicative Interaction, a statistical method used to analyses data from multi-environment trials (METs) or trials conducted in multiple locations or years. It helps in understanding genotype-by-environment interactions in crop variety trials. AMMI enhances understanding of foxtail millet's genotype-environment interactions, aiding in stable variety identification and adaptable cultivar selection. It optimizes resource allocation, guides hybridization, accelerates breeding and strategically improves traits to meet market demands.

4.8.1 Analysis of variance for the additive model

The AMMI analysis of variance was conducted to investigate the impact of environmental factors (ENV), replicated environments (REP (ENV)), genotypes (GEN), and the interaction between genotype and environment (GEN: ENV) on yield and yield attributes across multiple experimental conditions. The results revealed significant insights into the sources of variability in the dataset. All traits of AMMI ANOVA are represented in Table 4.10.1-4.10.14.

Environmental Factors (ENV): Environmental factors exhibited considerable significance at DF: $P < 0.05$ ($F = 6.12$, $p < 0.018$), DM: $P<0.05$ ($F = 3.79$, $p = 0.0585$), PH: $P <0.05$ ($F = 148.15$, $p < 0.001$), PL:P <0.05 ($F = 3.93$, $p = 0.0541$), FL: $P <0.05$($F = 12.45$, $p = 0.0022$), FW: $P<0.05$ ($F = 4.02$, $p = 0.05$), PDL: <0.005 ($F = 12.86$, $p = 0.002$), NT: $P<0.05$ ($F = 3.62$, $p = 0.05$), PW $P<0.05$ ($F = 5.50$, $p = 0.02$), HI: $P<0.05$ ($F = 26.21$, $p = 0.00$), BY: $P<0.05$ ($F = 74.25$, $p = 0.00$), FY: <0.005 ($F =74.25$, $p =0.01$), TW: <0.005 ($F =5572.70$, $p =0.00$) and GY: $P < 0.05$ ($F = 111.558$, $p < 0.001$). Environmental factors (ENV) exhibited an ample proportion of the variance in DF (41.8%), DM (0.44%), PH (8.29%), PL

(33.06%), FL (4.51%), FW (2.84%), PDL (2.47%), NT (7.01%), PW (2.57), HI (14.38%), BY (10.38%), FY (1.47%), TW (19.65%) and GY (23.42%) respectively.

Replicated Environments (REP (ENV)): In contrast, the impact of replicated environments (REP (ENV)) was not statistically significant at Conversely, the impact of replicated environments (REP (ENV)) was not statistically significant at DF: P <0.05(F = 1.7, p = 0.8), DM: (F = 1.66, p = 0.1097), PH: P <0.05(F = 0.81, p = 0.597), PL: P <0.05 (F = 0.61, p = 0.7685), FL: P <0.05 (F =1.74, p = 0.0895), FY: P <0.05 (F =0.78, p = 0.062), PW P<0.05 (F =1.87, p = 0.06), HI: P <0.05 (F =1.50, p = 0.16), BY: P <0.05 (F =0.39, p = 0.39), TW: P <0.05 (F =0.28, p = 0.97), NT: significant at P<0.05 (F = 4.92, p = 0.001), FW: P<0.05 (F = 4.23, p < 0.001), PDL: P <0.05 (F = 0.93, p = 0.495), and GY not statistically significant at P <0.05(F = 1.382, p = 0.2),contributing minimally to the variability in DF (18.21%), DM (0.31), PH (0.15%), PL (22.82%), FL (0.97%), FW (1.89%), PDL (0.51%), NT (5.16%), PW (1.25%), BY: (0.37%), HI (1.46%), FY (0.31%), TW (0.97%) and GY (0.56%) respectively. The outcome suggests a consistent and stable performance exhibited by the genotypes across different environments.

Genotypes (GEN): Genotypes demonstrated high significance at Genotypes are (GEN) demonstrated high significance at DF: P<0.05(F = 93.57, p < 0.001), DM: P<0.05 (F = 55.69, p < 0.001), PH: P <0.05(F = 62.58, p = 0.001), PL: P<0.05(F = 33.18, p < 0.001), FL: P<0.05(F = 16.16, p = 0.001), FW P<0.05 (F = 20.87, p < 0.001), PDL: P<0.05 (F = 3.55, p =0.001), NT: <0.05 (F = 5.23, p =0.001), PW: P<0.05 (F=27.80, p =0.00), BY: P<0.05 (F = 33.65, p =0.00), HI: (F = 4.01, p =0.00), FY: P<0.05 (F=35.35, p =0.01), TW: P<0.05 (F=556.72, p =0.00) and GY: P < 0.05(F = 19.025, p = 0.001), explaining a significant portion of the variability in DF (34.5%), PH (41.92%), DM (37.83), PL (44.94%), FL (32.49%), FW

(33.77%), PDL (38.32%), NT (19.89%), PW (33.58%), BY (42.55%), HI (14.22%), FY (50.16%), TW (68.01%) and GY (24.94%) respectively.

Residuals: Residuals represented a relatively small portion of the variability in most traits, DF (2.95%), DM (5.44%), PH (29.28%), PL (10.84%), FL (16.08%), PDL (16.04%), NT (69.57%), PW (19.31%), BY (10.12%), HI (28.38%), FY (11.35%) and GY (11.75%) of the variability, while the overall model effectively explained the observed data DF (Total SS = 11250.64), DM (Total SS =939.25), PH (Total SS = 126744.36), PL (Total SS = 5671.64), FL (Total SS = 4033.18), FW (Total SS =14.59), PDL (Total SS = 6547.52), NT (Total SS = 225.97), PW (Total SS =82.81), BY (Total SS = 2269.39), HI (Total SS = 14857.05), FY (Total SS = 7243.76), TW (Total SS = 15.54) and GY (Total SS = 6294.28).

In the AMMI model, we simplify the interaction between genotypes and environments (GEI) into three main components: PC1, PC2, and PC3, each accompanied by a significance level at $P < 0.05$. PC1 emerges as the dominant influence of these axes, encapsulating the majority of variation. It illuminates a substantial proportion in DF (48.8%), DM (47.4%), PH (47.8%), PL (43.5%), FL (47.6%), FW (61.10%), PDL (40.9%), NT (61.9%), PW (46.20%), BY (46.20%), HI (55.80%), FY (51.7), TW (87.90%) and GY (54.5) of the overall variability, as evidenced by its associated sum of squares SSPC1 = DF (1698.994), DM (2294.69), PH (13400.61), PL (537.89), FL (441.03), FL (320.97), FW (16.71), PDL (571.45), NT (26.26), PW (1896.97), BY (1896.97), HI (1721.96), FY (687.95), TW (0.78) and GY (623.11). Following, PC2 upholds significance by contributing in DF (34.9%), DM (34.3%), PH (33.3%), PL (34.2%), FL (34.6%), FW (22.50%), PDL (36.9%), NT (27.2%), PW (38.70%), BY (38.70%), HI (31.30%), FY (35.2%), TW (9.00), and GY (28.7%)to the variance, with its sum of squares SSPC2 = DF (1217.15), DM (1657.29), PH (9330.43), PL (423.18), FL

(320.97), FW (6.15), PDL (514.58), NT (11.55), PW (1588.94), BY (1588.94), HI (966.49), FY (468.00), TW (0.08) and GY (327.82) reflecting its impact. The third axis, PC3, adds a further layer of understanding, explaining In DF (16.3%), DM (18.3%), PH (19.00%), PL (22.4), FL (17.8%), FW (16.40%), PDL (22.2%), NT (10.8), PW (15.00%), BY (15.00%), HI (12.90%), FY (13.1%), TW (3.10%) and GY (16.8%)of the variation and represented by its sum of squares SSPC3 = DF (566.41), DM (885.80) PH (5327.88), PL (276.84), FL (164.57), FW (4.49), PDL (310.22), NT (4.58), PW (22.85), BY (616.99), HI (398.39), FY (173.84), TW (0.03) and GY (192.54).

To build the most accurate AMMI model, it's common to use the first two PCAs, according to Gauch and Kang (1996) and Yan and Rejcan (2000). Additional interaction principal components mostly contained irrelevant information and did not aid in predicting validation observations (Mekonnen & Mohammed, 2010). Therefore, the interaction between the 30 genotypes and 4 environments in this study was forecasted using the first two principal components of genotypes and environments. The model effectively explained the genotype × environment interaction (Yan and Rajcan, 2000). Similar studies reported by Ghazvini et al. (2018) documented that GEI's primary and secondary Principal Components (PCs) contributed 49.49% and 22.50%, respectively, accounting for 71.60% of the GEI's variability. Kilic (2014) reported that IPCA 1 captured 40.42% of the interaction variation in 17.85% of the degrees of freedom. IPCA 2 explained an additional 20.66% of GEI variation. IPCA 1 and IPCA 2 were highly significant ($P < 0.01$) and contributed to 61.07% of the total GEI. Hagos and Abay (2013) reported that combined, the first and second IPCAs accounted for 85.77% of the grain yield variability in the ten tested genotypes across five locations.

Table 4.11.1 AMMI analysis for Days to flowering of 30 genotypes evaluated in 4 environments

Source	Df	Sum Sq	Mean Sq	F value	Pr(>F)	significant levels	Proportion	Accumulated
ENV	3	47.04	15.68	6.12	0.02	significant	41.8	
REP(ENV)	8	20.50	2.56	1.79	0.08	non-significant	18.21	
GEN	29	3885.79	133.99	93.58	0.00	significant	34.5	
GEN: ENV	87	3482.56	40.03	27.96	0.00	significant	30.9	
PC1	31	1698.99	54.81	38.28	0.00		48.8	48.8
PC2	29	1217.15	41.97	29.31	0.00		34.9	83.7
PC3	27	566.42	20.98	14.65	0.00		16.3	100
Residuals	232	332.19	1.43				2.95	
Total	446	11250.64	25.23					

Table 4.11.2 AMMI analysis for Days to maturity of 30 genotypes evaluated in 4 environments

Source	Df	Sum Sq	Mean Sq	F value	Pr(>F)	significant levels	Proportion	Accumulated
ENV	3	76.29	25.43	3.79	0.06	significant	0.44	
REP(ENV)	8	53.69	6.71	1.66	0.11	non-significant	0.31	
GEN	29	6537.81	225.44	55.69	0.00	significant	37.83	
GEN: ENV	87	4837.78	55.61	13.74	0.00	significant	27.99	
PC1	31	2294.69	74.02	18.28	0.00		47.40	47.4
PC2	29	1657.29	57.15	14.12	0.00		34.30	81.7
PC3	27	885.80	32.81	8.10	0.00		18.30	100
Residuals	232	939.25	4.05				5.43	
Total	446	17282.59	38.75					

Table 4.11.3 AMMI analysis for Plant Height of 30 genotypes evaluated in 4 environments

Source	Df	Sum Sq	Mean Sq	F value	Pr(>F)	significant levels	Proportion	Accumulated
ENV	3	10506.20	3502.07	148.15	0.0	significant	8.29	
REP(ENV)	8	189.11	23.64	0.81	0.6	non-significant	0.15	
GEN	29	53137.75	1832.34	62.58	0.0	significant	41.93	
GEN:ENV	87	28058.94	322.52	11.01	0.0	significant	22.14	
PC1	31	13400.61	432.28	14.76	0.0		47.80	47.8
PC2	29	9330.44	321.74	10.99	0.0		33.30	81
PC3	27	5327.89	197.33	6.74	0.0		19.00	100
Residuals	232	6793.43	29.28				5.36	
Total	446	126744.36	284.18					

Table 4.11.4 AMMI analysis for Panicle Length of 30 genotypes evaluated in 4 environments

Source	Df	Sum Sq	Mean Sq	F value	Pr(>F)	significant levels	Proportion	Accumulated
ENV	3	19.06	6.35	3.93	0.05	significant	0.34	
REP(ENV)	8	12.94	1.62	0.61	0.77	non-significant	0.23	
GEN	29	2549.12	87.90	33.18	0.00	significant	44.95	
GEN: ENV	87	1237.93	14.23	5.37	0.00	significant	21.83	
PC1	31	537.90	17.35	6.55	0.00		43.50	43.50
PC2	29	423.18	14.59	5.51	0.00		34.20	77.60
PC3	27	276.85	10.25	3.87	0.00		22.40	100.00
Residuals	232	614.66	2.65				10.84	
Total	446	5671.64	12.72					

Table 4.11.5 AMMI analysis for Flag Leaf Length of 30 genotypes evaluated in 4 environments

Source	Df	Sum Sq	Mean Sq	F value	Pr(>F)	significant levels	Proportion	Accumulated
ENV	3	182.05	60.68	12.45	0.00	significant	4.51	
REP(ENV)	8	38.99	4.87	1.74	0.09	non-significant	0.97	
GEN	29	1310.29	45.18	16.16	0.00	significant	32.49	
GEN: ENV	87	926.58	10.65	3.81	0.00	significant	22.97	
PC1	31	441.04	14.23	5.09	0.00		47.60	47.60
PC2	29	320.97	11.07	3.96	0.00		34.60	82.20
PC3	27	164.57	6.10	2.18	0.00		17.80	100.00
Residuals	232	648.70	2.80				16.08	
Total	446	4033.18	9.04					

Table 4.11.6 AMMI analysis for Flag Leaf Width of 30 genotypes evaluated in 4 environments

Source	Df	Sum Sq	Mean Sq	F value	Pr(>F)	significant levels	Proportion	Accumulated
ENV	3	3.20	1.07	4.02	0.05	significant	2.84	
REP(ENV)	8	2.13	0.27	4.23	0.00	significant	1.89	
GEN	29	38.04	1.31	20.87	0.00	significant	33.77	
GEN: ENV	87	27.36	0.31	5.00	0.00	significant	24.28	
PC1	31	16.71	0.54	8.57	0.00		61.10	61.10
PC2	29	6.15	0.21	3.37	0.00		22.50	83.60
PC3	27	4.49	0.17	2.65	0.00		16.40	100.00
Residuals	232	14.59	0.06				12.95	
Total	446	112.67	0.25					

Table 4.11.7 AMMI analysis for Peduncle Length of 30 genotypes evaluated in 4 environments

Source	Df	Sum Sq	Mean Sq	F value	Pr(>F)	significant levels	Proportion	Accumulated
ENV	3	161.96	53.99	12.86	0.00	significant	2.47	
REP(ENV)	8	33.58	4.20	0.93	0.49	non-significant	0.51	
GEN	29	2509.29	86.53	19.12	0.00	significant	38.32	
GEN: ENV	87	1396.26	16.05	3.55	0.00	significant	21.33	
PC1	31	571.46	18.43	4.07	0.00		40.90	40.90
PC2	29	514.58	17.74	3.92	0.00		36.90	77.80
PC3	27	310.23	11.49	2.54	0.00		22.20	100.00
Residuals	232	1050.18	4.53				16.04	
Total	446	6547.52	14.68					

Table 4.11.8 AMMI analysis for No. of tillers per plant of 30 genotypes evaluated in 4 environments

Source	Df	Sum Sq	Mean Sq	F value	Pr(>F)	significant levels	Proportion	Accumulated
ENV	3	15.82	5.27	3.62	0.06	non-significant	7.00	
REP(ENV)	8	11.66	1.46	4.92	0.00	significant	5.16	
GEN	29	44.94	1.55	5.23	0.00	significant	19.89	
GEN: ENV	87	42.40	0.49	1.64	0.00	significant	18.76	
PC1	31	26.26	0.85	2.86	0.00		61.90	61.90
PC2	29	11.55	0.40	1.34	0.12		27.20	89.20
PC3	27	4.58	0.17	0.57	0.96		10.80	100.00
Residuals	232	68.75	0.30				30.43	
Total	446	225.97	0.51					

Table 4.11.9 AMMI analysis for Panicle Width of 30 genotypes evaluated in 4 environments

Source	Df	Sum Sq	Mean Sq	F value	Pr(>F)	significant levels	Proportion	Accumulated
ENV	3	2.13	0.71	5.50	0.02	significant	2.57	
REP(ENV)	8	1.03	0.13	1.87	0.06	non-significant	1.25	
GEN	29	27.80	0.96	13.91	0.00	significant	33.58	
GEN: ENV	87	17.93	0.21	2.99	0.00	significant	21.65	
PC1	31	12.12	0.39	5.67	0.00		67.60	67.60
PC2	29	3.97	0.14	1.98	0.00		22.10	89.70
PC3	27	1.84	0.07	0.99	0.48		10.30	100.00
Residuals	232	15.99	0.07				19.31	
Total	446	82.81	0.19					

Table 4.11.10 AMMI analysis for Biological Yield of 30 genotypes evaluated in 4 environments

Source	Df	Sum Sq	Mean Sq	F value	Pr(>F)	significant levels	Proportion	Accumulated
ENV	3	2327.71	775.90	74.25	0.00	significant	10.38	
REP(ENV)	8	83.60	10.45	1.07	0.39	non-significant	0.37	
GEN	29	9544.88	329.13	33.65	0.00	significant	42.55	
GEN: ENV	87	4102.90	47.16	4.82	0.00	significant	18.29	
PC1	31	1896.97	61.19	6.26	0.00		46.20	46.20
PC2	29	1588.94	54.79	5.60	0.00		38.70	85.00
PC3	27	616.99	22.85	2.34	0.00		15.00	100.00
Residuals	232	2269.39	9.78				10.12	
Total	446	22431.376	50.29457					

Table 4.1.11 AMMI analysis for Harvest index of 30 genotypes evaluated in 4 environments

Source	Df	Sum Sq	Mean Sq	F value	Pr(>F)	significant levels	Proportion	Accumulated
ENV	3	2136.78	712.26	26.21	0.00	significant	14.38	
REP(ENV)	8	217.43	27.18	1.50	0.16	non-significant	1.46	
GEN	29	2112.67	72.85	4.01	0.00	significant	14.22	
GEN: ENV	87	3086.84	35.48	1.95	0.00	significant	20.78	
PC1	31	1721.96	55.55	3.06	0.00		55.80	55.80
PC2	29	966.49	33.33	1.83	0.01		31.30	87.10
PC3	27	398.39	14.76	0.81	0.74		12.90	100.00
Residuals	232	4216.49	18.17				28.38	
Total	446	14857.05	33.31					

Table 4.11.12 AMMI analysis for Fodder yield per plant of 30 genotypes evaluated in 4 environments

Source	Df	Sum Sq	Mean Sq	F value	Pr(>F)	significant levels	Proportion	Accumulated
ENV	3	106.54	35.51	12.83	0.00	significant	1.47	
REP(ENV)	8	22.14	2.77	0.78	0.62	non-significant	0.31	
GEN	29	3633.24	125.28	35.35	0.00	significant	50.16	
GEN: ENV	87	1329.80	15.29	4.31	0.00	significant	18.36	
PC1	31	687.95	22.19	6.26	0.00		51.70	51.70
PC2	29	468.00	16.14	4.55	0.00		35.20	86.90
PC3	27	173.85	6.44	1.82	0.01		13.10	100.00
Residuals	232	822.24	3.54				11.35	
Total	446	7243.77	16.24					

Table 4.11.13 AMMI analysis for Test weight of 30 genotypes evaluated in 4 environments

Source	Df	Sum Sq	Mean Sq	F value	Pr(>F)	significant levels	Proportion	Accumulated
ENV	3	3.05	1.02	5572.70	0.00	significant	19.65	
REP(ENV)	8	0.00	0.00	0.28	0.97	non-significant	0.01	
GEN	29	10.57	0.36	556.72	0.00	significant	68.01	
GEN: ENV	87	0.88	0.01	15.49	0.00	significant	5.68	
PC1	31	0.78	0.03	38.21	0.00		87.90	87.90
PC2	29	0.08	0.00	4.20	0.00		9.00	96.90
PC3	27	0.03	0.00	1.52	0.05		3.10	100.00
Residuals	232	0.15	0.00				0.98	
Total	446	15.54	0.03					

Table 4.11.14 AMMI analysis for grain yield per plant of 30 genotypes evaluated in 4 environments

Source	Df	Sum Sq	Mean Sq	F value	Pr(>F)	significant levels	Proportion	Accumulated
ENV	3	1473.95	491.32	111.56	0.00	significant	23.42	
REP(ENV)	8	35.23	4.4	1.38	0.20	non-significant	0.56	
GEN	29	1758.61	60.64	19.02	0.00	significant	27.94	
GEN: ENV	87	1143.48	13.14	4.12	0.00	significant	18.17	
PC1	31	623.12	20.1	6.31	0.00		54.50	54.50
PC2	29	327.82	11.3	3.55	0.00		28.70	83.20
PC3	27	192.55	7.13	2.24	0.00		16.80	100.00
Residuals	232	739.51	3.19				11.75	
Total	446	6294.28	14.11					

4.9 AMMI stability biplot-1

An appealing characteristic of the AMMI model lies in its ability to generate valuable visual depictions known as biplots (Gabriel, 1978), which contribute to the understanding of Genotype by Environment Interaction (GEI). IPCA scores for a genotype show how stable it is across environments (Purchase, 1997). Biplots are valid when the first two IPCAs explain most of the interaction variation and are often used to interpret AMMI results. However, breeders may need more than two PCA axes for complex models, especially when stability and high yield across various conditions are sought (Hanamaratti *et al.* 2009).

AMMI stability biplot-1displays IPCA1 scores for both genotypes and environments, plotted against the different traits in the foxtail millet dataset. Genotypes are denoted by numerical markers in blue, while environments are indicated by green lines. These environments are typically represented as interconnecting axes originating from their respective averages, signifying the trait averages within those environments. In the biplot, there's a broken vertical line at the center, representing the experiment's grand mean and a solid horizontal line at IPCA1 axis score = 0. IPCA1 was very important and explained interaction patterns better than other axes. The x-coordinate shows the main effects (means), while the y-coordinate represents the interaction effects (IPCA1). Genotypes and environments positioned to the right of this line exhibit superior yields to the overall mean, while those on the left side demonstrate yields below the overall mean. The intersection of this axis with the vertical axis divides the biplot into four quadrants. The quadrant II and IV are more potential than quadrant I and III.

In the AMMI biplots, Days to 50% flowering (Fig 4.7.1(a)) reveals 15 genotypes (G11, G8, G21, G22, G10, G19, G12, G14, G23, G16, G9, G6, G18, G17, and G4) and two environments (E4 and E2), positioned to the right of the grand mean.

Days to maturity (Fig 4.7.2a) reveals 16 genotypes (G10, G9, G21, G24, G26, G5, G20, G18, G3, G1, G13, G27, G14, G4, G23, and G16) and three environments (E1, E2 and E3), positioned to the right of the grand mean. Plant height (Fig 4.7.3(a)) reveals 18 genotypes (G26, G20, G22, G25, G24, G30, G21, G2, G28, G5, G29, G9, G18, G17, G27, G23, and G1) and one environment (E1), positioned to the right of the grand mean. Panicle length (Fig 4.7.4(a)) reveals 16 genotypes (G14, G2, G1, G10, G17, G8, G18, G30, G29, G26, G22, G9, G28, G23, G21, and G25) and two environments (E1 and E3), positioned to the right of the grand mean. Flag leaf length (Fig 4.7.5(a)) reveals 16 genotypes (G27, G21, G8, G25, G22, G2, G24, G23, G15, G1, G18, G29, G16, G28, G5, and G14) and one environment (E2), positioned to the right of the grand mean. Flag leaf width (Fig 4.7.6(a)) reveals 14 genotypes (G28, G27, G26, G8, G6, G7, G29, G9, G19, G12, G22, G16, G18, and G15) and two environments (E1 and E4), positioned to the right of the grand mean. Peduncle length (Fig 4.7.7(a)) reveals 12 genotypes (G22, G25, G15, G18, G2, G29, G28, G24, G1, G8, G5, and G6) and one environment (E1), positioned to the right of the grand mean. No. Of tillers per plant (Fig 4.7.8(a)) reveals 15 genotypes (G7, G4, G13, G6, G15, G16, G18, G25, G8, G14, G2, G11, G17, G29 and G22) and one environment (E1), positioned to the right of the grand mean. Panicle width (Fig 4.7.9(a)) reveals 13 genotypes (G25, G22, G12, G19, G18, G30, G6, G28, G8, G9, G29, G5, and G23) and one environment (E1), positioned to the right of the grand mean. Biological yield (Fig 4.7.10(a)) reveals 10 genotypes (G19, G21, G7, G18, G23, G1, G5, G8, G3, G22, and G25) and one environment (E1), positioned to the right of the grand mean. Harvest index (Fig 4.7.11(a)) reveals 13 genotypes (G16, G23, G14, G25, G20, G28, G12, G21, G30, G27, G22, G24, and G7) and one environment (E1), positioned to the right of the grand mean. Fodder yield per plant (Fig 4.7.12(a)) reveals 16 genotypes (G13, G21, G5, G19, G6, G4, G17, G18, G8, G25, G11, G9, G7, G22,

G3, and G1) and two environments (E1 and E4), positioned to the right of the grand mean. Test weight (Fig 4.7.13(a)) reveals 13 genotypes (G6, G5, G20, G11, G12, G15, G4, G21, G13, G24, G28, G2, and G1) and one environment (E1), positioned to the right of the grand mean. Grain yield per plant (Fig 4.7.14(a)) reveals 16 genotypes (G13, G21, G5, G19, G6, G4, G17, G18, G8, G25, G11, G9, G7, G22, G3, and G1) and one environment (E1), positioned to the right of the grand mean. The genotypes are presented on the right of the grand mean; those are identified as high-yielding, whereas their counterparts with lower yields were on the left side of the grand mean.

Furthermore, in the high-potential environments found were DF (E2), DM (E1), FL (E2), FW (E1), NT (E1), BY (E1), HI (E1), FY (E4 and E1), TW (E1) and GY (E1) in quadrant II, indicated by high positive IPCA1 values. At the same time, environments DF (E4), DM (E2 and E3), PH (E1), PL (E1 and E3), FW (E4), PDL (E1) and PW (E1) were found in quadrant IV to have negative IPCA1 values but high yielding.

Conversely, the least productive environments, DF (E3), PH (E4), PL (E2), FL (E4 and E3), FW (E3), PDL (E2), NT (E2 and E3), BY (E2 and E3), HI (E2 and E3), FY (E2 and E3), TW (E2, E4 and E3) and GY (E2, E4 and E3) were situated in quadrant III, with negative IPCA1 values, While environments, DF (E1), DM (E4), PH (E2 and E3), PL (E4), FL (E1), FW (E2), PDL (E3 and E4), NT (E4), PW (E2, E3 and E4), BY (E4), HI (E4), were located at quadrant I but positive IPCA1 values.

In AMMI biplots, quadrant I have genotypes DF (G26, G28, G2, G24, G15, G5 and G13), DM (G12, G19, G22, G2, G28, G17, and G11), PH (G15, G16, G6, G13, G14, G8, and G11), PL (G3, G12, G4, G13, G20, G5, G7, G15, and G24), FL (G4, G26, G6, G9, G19, G30 and G7), FW (G3, G4, G5, and G30), PDL (G30,

G14, G21, G7, G12, G13, G10, and G11), NT (G27, G12, G5, G19, G23, and G3), PW (G4, G20, G15, G14, G16, G10, G17, G11, G13, G21, and G2), BY (G24, G27, G28, G4, G6, G12, G10, and G16), HI (G6, G13, G4, G11, G10, G2, G8, G9, G5, G26, G29, and G18), TW (G17, G7, G19, G16, G10, G14, G8, G23, G25, and G22), FY (G16, G24, G2, G12, G28, G10, and G27) and GY (G24, G27, G28, G4, G16, G15, G10, and G12).

Quadrant III includes genotypes, DF (G11, G8, G21, G22, G10, G19 and G12), DM (G8, G7, G5, G15, G25, G29, and G30), PH (G3, G4, G10, G12, G7, and G19), PL (G6, G16, G11, G19, and G27), FL (G13, G10, G20, G3, G12, G17, and G11), FW (G1, G24, G2, G21, G10, G14, G13, G20, G25, and G11), PDL (G16, G20, G19, G17, G9, G26, G23, G4, G3, and G27), NT (G26, G28, G10, G9, G21, G20, G30, G1, and G24), PW (G1, G24, G7, G3, G27, and G26), BY (G15, G13, G2, G30, G29, G14, G26, G7, G20, and G11), HI (G3, G1, G17, G19, and G15), TW (G27, G30, G29, G3, G26, G18, and G9), FY (G23, G30, G29, G14, G26, G15, and G20) and GY (G29, G6, G7, G13, G30, G14, G26, G2, and G11).

Quadrant I: Genotypes in this quadrant are characterized by high positive values on the first principal component (PC1). They are highly responsive to environmental variations, which can be a disadvantage in practical agriculture.

- **Non-Adaptability:** Genotypes in this quadrant are often considered non-adaptive because they exhibit highly variable performance across different environments. They may excel in a few specific conditions but perform poorly or unpredictably in most other situations. This lack of adaptability makes them less suitable for widespread cultivation, as their performance cannot be relied upon.

- **Low Yielding:** Since these genotypes are not well-suited to a broad range of environments, they are more likely to have lower average yields compared to genotypes that are more stable and adaptive.

Quadrant IIII: Genotypes in this quadrant are characterized by negative values on the first principal component (PC1). This means they have highly responsive to environmental variations.

- **Non-Adaptability:** Like Quadrant I, genotypes in Quadrant III are considered non-adaptive because they exhibit variable performance across environments. They have low average performance but may occasionally perform well in specific conditions.
- **Low Yielding:** Genotypes in this quadrant have low average yields, which makes them unsuitable for cultivation as they do not provide consistently high yields across a range of environments.

In practical agriculture and plant breeding, stability and adaptability are desirable traits in a genotype. Genotypes that consistently perform well across a wide range of environments are preferred because they provide more predictable and reliable yields. Genotypes in Quadrants I and II may have specific niche applications or may be used in specialized breeding programs to improve their adaptability, but they are generally not suitable for widespread cultivation due to their variable and low-yielding nature.

Quadrant II comprises genotypes, DF (G30, G25, G20, G1, G27, G29, G7 and G3), DM (G10, G9, G21, G24, G26, G5, G20, and G18), PH (G26, G20, G22, G25, G24, G30, G21, G2, and G28), PL (G14, G2, G1, G10, G17, G8, G18, and G30), FL (G3, G4, G5, and G30), FW (G28, G27, G26, G8, G6, G7, G29, G9, G19, and G12), PDL (G22, G25, G15, G18, G2, G29, and G28), NT (G7, G4,

G13, G6, G15, G16, G18 and G25), PW (G25, G22, G12, G19, G18, and G30), BY (G19, G21, G7, and G18), HI (G16, G23, G14, G25, G20, and G28), TW (G6, G5, G20, G11, G12, G15, G4, and G21), FY (G13, G21, G5, G19, G6, and G4) and GY (G21, G9, G17, G18, G3, and G19).

Quadrant IV contains genotypes, DF (G14, G23, G16, G9, G6, G18, G17, and G4), DM (G3, G1, G13, G27, G14, G4, G23, and G16), PH (G5, G29, G9, G18, G17, G27, G23, and G1), PL (G29, G26, G22, G9, G28, G23, G21, and G25), FL (G22, G2, G24, G23, G15, G1, G18, G29, G16, G28, G5, and G14), FW (G22, G16, G18, and G15), PDL (G24, G1, G8, G5, and G6), NT (G8, G14, G2, G11, G17, G29 and G22), PW (G6, G28, G8, G9, G29, G5, and G23), BY (G15, G13, G2, G30, G29, G14, G26, G7, G20, and G11), HI (G12, G21, G30, G27, G22, G24, and G7), TW (G13, G24, G28, G2, and G1), FY (G17, G18, G8, G25, G11, G9, G7, G22, G3, and G1) and GY (G8, G23, G22, G25, G5, and G1).

IPCA values close to zero, indicates significant stability with minimal GEI interaction and in this study, DF (G14, G23, G16, and G9), DM (G3, G1, and G13), PH (), PL (G18 and G30), FL (G14 and G25), FW (G12, G17 and G18), PDL (G24 and G28), NT (G18, G16 and G25), PW (G13 and G18), BY (G18, G17 and G5), HI (G28 and G1), TW (G21 and G13), FY (G13, G17 and G18) and GY (G8, G9, G21, and G22).

Quadrant II: Genotypes in this quadrant are characterized by positive values on the first principal component (PC1) axis.

- **Stability:** Genotypes in Quadrant II have low sensitivity to changes in environmental conditions. They consistently perform well or at least adequately across different environments. This stability is a desirable trait in agriculture because it ensures that the genotype's

performance remains reliable, regardless of variations in environmental factors such as weather, soil, or management practices.

- **Adaptability:** The stable genotypes in Quadrant II are considered adaptive because they maintain their performance without exhibiting extreme fluctuations in different environments. They can be grown in a wide range of conditions and still provide satisfactory yields.

- **High Yielding:** Genotypes in Quadrant II are characterized by their ability to achieve relatively high average yields across various environments. Their combination of stability and high yields makes them suitable for widespread cultivation, as they are likely to consistently provide satisfactory harvests.

Quadrant IV: Genotypes in this quadrant are characterized by high negative values on the first principal component (PC1).

- **Stability:** Genotypes in Quadrant IV are also stable across different environments, similar to those in Quadrant II. They exhibit consistent performance and are less affected by environmental variations.

- **Adaptability:** Genotypes in Quadrant IV are considered adaptive because they perform well across a wide range of environments. Their high adaptability means they are suitable for cultivation in diverse geographic locations and under various conditions.

- **High Yielding:** Genotypes in Quadrant IV are known for their high average yields. They not only exhibit stability but also consistently achieve high yields across different environments. This combination

of adaptability and high yield potential makes them excellent candidates for widespread cultivation.

In practical agriculture and plant breeding, genotypes that combine stability, adaptability, and high yields are highly sought after. They provide a reliable source of production in varying conditions and help minimize the risk associated with environmental fluctuations. Genotypes in Quadrants II and IV of the AMMI biplot are regarded as valuable for their consistent and high-yielding performance across diverse environments, making them suitable choices for cultivation and crop improvement programs.

4.10 AMMI-2 stability Biplot

The AMMI-2 stability Biplot plotted IPCA1 scores for both genotypes and environments against IPCA2 scores for genotypes and environments. This model uses the first two interaction axes of genotype and environment scores (Vargas and Crossa, 2000). It helps understand genotype-environment interactions and reveals which genotypes perform best in specific conditions (Li *et al*. 2006). Genotypes near the center of the biplot are considered more stable, as per Purchase (1997).

The AMMI-2 stability biplots provide insights into the distribution of variation for various traits. For days to flowering, PC1 and PC2 capture 48.8% and 34.9% of the total variation (83.7%). In the case of days to maturity, PC1 and PC2 capture 47.4% and 34.3% of the total variation (81.7%). Plant height exhibits PC1 at 47.8% and PC2 at 33.3% of the total variation (81.1%). Panicle length is characterized by PC1 at 43.5% and PC2 at 34.2% of the total variation (77.7%). Flag leaf length demonstrates PC1 at 47.6% and PC2 at 34.6% of the total variation (82.2%). Flag leaf width yields to PC1 at 61.1% and PC2 at 22.5% of the total variation (83.6%). Peduncle length displays PC1 at 40.9% and PC2 at 36.9%

of the total variation (77.8%). The number of tillers per plant exhibits PC1 at 61.9% and PC2 at 27.2% of the total variation (89.1%). Panicle width is particularly well-represented by PC1 at 67.6% and PC2 at 22.1% of the total variation (89.7%). For biological yield, PC1 and PC2 represent 46.2% and 38.7% of the total variation (84.9%). Harvest index shows notable representation with PC1 at 55.8% and PC2 at 31.3% of the total variation (87.1%). In the case of test weight, PC1 and PC2 are overwhelmingly dominant at 87.9% and 9.0% of the total variation (96.9%). Fodder yield per plant is well-represented with PC1 at 51.7% and PC2 at 35.2% of the total variation (86.9%). Lastly, grain yield per plant is effectively captured by PC1 at 54.5% and PC2 at 28.7% of the total variation (83.2%). All traits AMMI-2 biplots represented in Fig 4.7.1(b, c)-4.7.14(b, c)

In the AMMI 2 biplot, the environmental scores are joined to the origin by side lines. Sites with short spokes do not exert strong interactive forces. Those with long spokes exert strong interaction. In this AMMI Biplot-2, all environments *viz* E1, E2, E3 and E4 are connected to the origin. Among these environments in DF, PL, FY and GY (E2 and E3), PH (E4 and E2), FL, FW (E1 and E2), PDL, PW, TW (E3 and E4), DM (E1 and E3) and NT, BY, HI (E3 and E2) are exhibits short spokes, indicating limited interaction strength, while DF, PL, FY and GY (E1 and E4), PH (E1 and E3), FL, FW (E4 and E3), PDL, PW, TW (E2 and E1), DM (E2 and E4) and NT, BY, HI (E4 and E1) are display long arrows, indicating strong interaction forces. Polygonal biplot is used 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.

In days to 50% flowering Genotypes G5, G7, G3, G4, G18, G9, G21, G22, G19, G12 and G24 were located at the farthest distance and formed a polygon. As a result, the polygon in this study has seven vertexes and two equality lines that divide the biplot for days to 50% flowering into nine sectors, of which all the environments are connected to the origin. In E4 G5, G25 are the vertex genotypes, respectively, while G9, G18 is the vertex genotype in E2 and G12 in E1. These vertex genotypes were shown to be the highest performers in their respective contexts.

In days to maturity genotypes G5, G10, G12, G9, G6, G3, G1, G13, and G5 were located at the farthest distance and formed a polygon. As a result, the polygon in this study has 10 vertexes and no equality lines that divide the biplot for days to maturity into 10 sectors, of which all the environments are connected to origin. In E4 G10 and G12 are the vertex genotypes, respectively, while G11 and G9 are the vertex genotype in E2 and G1 in E3.

In plant height study, genotypes G4, G3, G5, G11, G16, and G15 were positioned at the maximum distance and formed a polygon with 6 vertices. Consequently, the polygon in this study has 6 vertices and does not have any equality lines that divide the biplot for plant height into 6 sectors. In E4, G4 is the vertex genotype, while in E2 and E3, G15 and G11 respectively are the vertex genotypes. Similarly, G3 is the vertex genotype in E1. These vertex genotypes have demonstrated superior performance in their respective contexts. Environments in quadrants II and IV (E2 and E3) have higher potential compared to quadrants I and III (E4 and E1), which represent low potential environments.

In panicle length study, genotypes G25, G26, G14, G3, G23, and G22 were positioned at the maximum distance and formed a polygon with five vertices. Consequently, the polygon in this study has five vertices and one equality line

dividing the biplot for test weight into six sectors. In E2, G25 and G22 represent the vertex genotypes, while in E1, G23 is the vertex genotype, and in E4, G3 is the vertex genotype, and in E3, G26 is the vertex genotype. These vertex genotypes have shown to be the top performers in their respective contexts. Environments in quadrant IV (E4) have higher potential compared to quadrants I, II, and III (E1, E2, and E3), representing a low potential environment.

In Flag leaf length study, genotypes G22, G2, G29, G6, G4, G27, G24 were positioned at the maximum distance and formed a polygon with 7 vertices. As a result, the polygon in this study has 7 vertices and no equality lines that divide the biplot for flag leaf length into 7 sectors. In E4, G24 represents the vertex genotype, while in E2 and E3, G6 and G4 respectively are the vertex genotypes. Similarly, G2 is the vertex genotype in E1. These vertex genotypes have shown to be the highest performers in their respective contexts. Environments in quadrants II and IV (E1 and E2) have higher potential compared to quadrants I and III (E3 and E4), which represent low potential environments.

In flag leaf width, genotypes G22, G20, G18, G12, G6, G28, and G26 were located at the maximum distance and formed a polygon with five vertices. Consequently, the polygon in this study has five vertices and two equality lines dividing the biplot for flag leaf width into seven sectors. In E4, G18 and G12 are the vertex genotypes, and similarly, in E2 and E3, G18 and G12 respectively are the vertex genotypes. Also, in E1, G22, G20, and G26 represent the vertex genotypes. These vertex genotypes have demonstrated superior performance in their respective contexts. Environments in quadrants II and IV (E1 and E2) have higher potential compared to quadrants I and III (E3 and E4), which represent low potential environments.

In peduncle length study, genotypes G26, G27, G9, G23, G15, G30, G22, and G28 were positioned at the maximum distance and formed a polygon with eight vertices. Consequently, the polygon in this study has eight vertices and two equality lines dividing the biplot for panicle width into eight sectors. In E1, G26 and G27 represent the vertex genotypes, while in E3 and E4, G30 and G22 respectively are the vertex genotypes. These vertex genotypes have shown to be the top performers in their respective contexts. Environments in quadrant II and IV (E3, E4, and E2) have higher potential compared to quadrant III (E1), representing a low potential environment

In number of tillers per plant, genotypes G22, G24, G8, G27, and G14 were positioned at the maximum distance and formed a polygon with four vertices. Consequently, the polygon in this study has four vertices and one equality line dividing the biplot for the number of tillers per plant into five sectors. In E3 and E2, G22 represents the vertex genotype, while in E4 and E1, G27 and G8 respectively are the vertex genotypes. These vertex genotypes have demonstrated to be the top performers in their respective contexts. Environments in quadrant II and IV (E4 and E1) have higher potential compared to quadrants I and III (E3 and E2), representing low potential environments.

In panicle width, genotypes G26, G27, G9, G23, G15, G30, G22, and G28 were positioned at the maximum distance and formed a polygon with eight vertices. Consequently, the polygon in this study has eight vertices and two equality lines dividing the biplot for panicle width into eight sectors. In E1, G26 and G27 represent the vertex genotypes, while in E3 and E4, G30 and G22 respectively are the vertex genotypes. These vertex genotypes have shown to be the top performers in their respective contexts. Environments in quadrant II and IV (E3, E4, and E2)

have higher potential compared to quadrant III (E1), representing a low potential environment.

In biological yield per plant, genotypes G11, G1, G4, G27, G9, and G3 were positioned at the maximum distance and formed a polygon with six vertices. Consequently, the polygon in this study has six vertices and one equality line dividing the biplot for biological yield into seven sectors. In E1, G24 represents the vertex genotype, while in E3 and E2, G11 and G3 respectively are the vertex genotypes. These vertex genotypes have shown to be the top performers in their respective contexts. Environments in quadrant II and IV (E1 and E4) have higher potential compared to quadrant I and III (E2 and E3), representing a low potential environment.

In harvest index, genotypes G7, G3, G16, G11, and G5 were positioned at the maximum distance and formed a polygon with five vertices. Consequently, the polygon in this study has five vertices and no equality line dividing the biplot for harvest index into five sectors. In E1, G16 represents the vertex genotype, while in E4 and E3, G7 and G5, G11 respectively are the vertex genotypes. These vertex genotypes have shown to be the top performers in their respective contexts. Environments in quadrant II and IV (E3, E2, and E1) have higher potential compared to quadrant I and III (E4), representing a low potential environment.

In fodder yield per plant study, genotypes G3, G24, G27, G4, G1, G14, G20, and G22 were positioned at the maximum distance and formed a polygon with six vertices. Consequently, the polygon in this study has six vertices and no equality line dividing the biplot for fodder yield per plant into six sectors. In E1, G24 represents the vertex genotype, while in E4, G4 and G27 are the vertex genotypes. Similarly, in E2 and E3, G3, G22, and G20 respectively are the vertex genotypes. These vertex genotypes have shown to be the top performers in their respective

contexts. Environments in quadrant II and IV (E4 and E1) have higher potential compared to quadrant I (E3 and E2), representing a low potential environment.

In test weight, genotypes G9, G18, G4, G7, G17, and G11 were positioned at the maximum distance and formed a polygon with six vertices. Consequently, the polygon in this study has six vertices and no equality line dividing the biplot for test weight into six sectors. In E2, G4 represents the vertex genotype, while in E1, G17 and G11 respectively are the vertex genotypes. Similarly, in E4 and E3, G9 and G18 respectively are the vertex genotypes. These vertex genotypes have shown to be the top performers in their respective contexts. Environments in quadrant II (E1) have higher potential compared to quadrants I and III (E3, E4, and E2), representing a low potential environment.

In grain yield per plant Genotypes G1, G11, G9, G24 and G27 were located at the farthest distance and formed a polygon. These five rays divide the biplot into five sectors, and the all environments are connected to the origin. Thus, 2 environments, E3 and E2 fell into similar sector, and the vertex genotype for this sector isG11 suggesting that this genotype achieve ideal performance in those specific environments. Similarly, 1 environment, E4fell into single sector, and the vertex genotype for this sector was G27 while E1 fell into single sector, and the vertex genotypes for this sector were G24 and G9. Conversely, genotypes situated in sections without associated environments are less favourable for cultivation across the studied conditions. According to this figure 4, G2, G25, G14, G15, G20, G23, G18 and G16 and were close to the centre and were considered to have high grain yield stability. Remain genotypes are exhibit’s medium to instability.

4.11 WAAS biplot

In contrast to the AMMI model, which primarily focuses on the first IPC (Interaction Principal Component), the WAAS biplot offers a broader perspective by considering scores from all IPCs when examining the relationship between mean performance and WAAS. This approach enables a comprehensive assessment of Genotype-Environment Interaction (GEI) variation, particularly when identifying stable genotypes (Taleghani *et al.* 2023). Within this biplot, a central vertical line represents the overall mean of the respective traits across four environments. Genotypes and environments positioned to the right of this line display superior means compared to the overall mean, while those on the left side demonstrate yields below the overall mean. Simultaneously, a central horizontal axis denotes the mean of the WAAS scores, and the intersection of this axis with the vertical axis divides the biplot into four quadrants. WAASB can assist breeders and agronomists in making the right choices when picking or suggesting genotypes. Additionally, the simultaneous selection index, WAASBY, will be valuable when selection needs to account for various preferences in terms of stability and average performance. We also explore some advantages over existing statistics. WAAS biplot of all yield traits represented at Fig 4.8.

The biplot's four quadrants simplify the classification of genotypes based on their suitability for different environments. In the first quadrant, genotypes such as in DF:G7, G15, G22, G19, G13, and G12, DM: G6, G7, G8, G11, G22, G13, G19, and G12, PH:G3, G4, and G2, PL: G6, G4, and G3, FL: G11, G12, G26, G6, and G4, FW:G11 and G23, PDL: G4, G7, G11, G3, and G27, NT:G27, G24, and G12, PW: G7, G14, G3, G15, G27, and G26, BY:G7, G11, G4, G27, and G24, HI:G5, G11, and G3, FY: G20, G27, and G24, TW: G26, G19, G7, G17, G18, and G9 and GY:G24, G27, G11, and G28show higher WAAS values but lower means

compared to the overall mean. This indicates their vulnerability to fluctuating conditions and instability in the yield traits across various environments, leading to below-average performance. Environments E3 and E1 in DF, DM and PL: E4 and E2, FW in E3, PH, FL, PDL, NT, IW, BY, HI, FY, TW and GY in E3, E2 and E4 also fall into this quadrant, suggesting they have limited potential for crop performance.

The second quadrant of the biplot showcases genotypes like in DF: G5, G3, and G24, DM: G3, G9, G21, G1, and G10, PH: G5 and G11, PL: G9, G26, G14, G23, G25, and G22, FL:G2, G24, G22, and G27, FW:G22, G28, G27, G26, G8, G6, and G7, PDL: G22 and G24, NT: G17, G22, and G29, PW: G29, G5, and G30, BY:G9, G19, G3, and G1, HI:G24 and G7, FY: G5, G9, G22, G7, G4, and G3, TW:G24, G6, G28, G1, and G2 and GY:G1, G5, G19, and G3,which demonstrate both high WAAS values and performance above the overall mean yield. The presence of E2 and E4 in DF, E3 and E1 in DM and PL, E1 and E4 in FW, PH, FL, PDL, NT, IW, BY, HI, FY, TW and GY in E1 in this quadrant also suggests that this environments holds promise for achieving good trait performance with these genotypes.

Genotypes DF:G30, G11, G28, and others, DM: G15, G2, G29, G28, G17, and G30, PH: G15, G16, G13, G14, G10, G12, G7, G8, G19, and G6, PL: G12, G20, G7, G11, G24, G5, G16, and G15, FL: G19, G7, G20, G3, G9, G17, G10, and G13, FW: G20, G25, G3, G1, G5, G4, G21, G13, G24, G14, G2, and G10, PDL: G10, G23, G12, G19, G26, G16, G13, G9, G30, G20, G17, G21, and G14, NT: G1, G5, G7, G20, G19, G30, G21, G10, G14, G9, G23, G3, G26, and G28, PW: G20, G16, G4, G24, G1, G10, G21, G11, G17, BY: G20, G12, G10, G29, G28, G14, G30, G6, G26, G23, G13, G2, G16, and G15, HI:G10, G17, G4, G13, G18, G6, G29, G1, G8, G2, G15, G9, G19, G26, and G12, FY:G10, G12, G14, G29,

G30, G28, G23, G26, G15, and G16, TW: G16, G29, G30, G23, G10, G14, G8, G27, G25, and G22 and GYG4, G30, G29, G12, G26, G20, G16, G2, G6, G7, G13, G14, G15, and G10 are found in the third quadrant of respective traits biplot. They have lower WAAS values, suggesting stability and minimal responsiveness to environmental changes. However, this group also exhibits relatively lower performance values. The genotypes in the third quadrant are characterized by their consistency and resistance to environmental variations, as indicated by their low WAAS values. This means they are less influenced by changing conditions, making them stable options. However, their lower performance values imply that they may not achieve exceptionally high trait performance, even under favorable circumstances.

Fourth quadrant, genotypes like DF: G26, G25, and G23, DM:G24, G5, G25, G4, G27, G18, G16, G14, G26, G23, and G20, PH:G27, G22, G9, G18, G25, G26, G29, G30, G20, G23, G24, G17, G2, G1, G21, and G28, PL:G29, G2, G28, G1, G21, G8, G10, G17, G18, and G30, FL: G8, G21, G23, G29, G18, G28, G16, G15, G25, G1, and G5, FW: G29, G19, G16, G12, G9, G15, G18, and G17, PDL:G6, G18, G15, G25, G2, G1, G29, G8, G5, and G28, NT: G11, G4, G13, G6, G8, G18, G15, G16, G2, and G25, PW:G22, G23, G25, G28, G12, G6, G8, G9, G6, G19, and G18, BY:G22, G5, G8, G17, G18, G21, and G25, HI:G16, G22, G28, G30, G23, G14, G21, G25, G27, and G20, FY:G19, G6, G1, G11, G17, G2, G13, G21, G8, and G18, TW:G3, G5, G13, G21, G20, G12, G11, G15, and G4 and GY: 22, G17, G8, G23, G18, G21, and G25.These genotypes have lower WAAS values but higher mean values compared to the overall mean. Genotypes in the fourth quadrant demonstrate stability and resilience to environmental variations, as indicated by their lower WAAS values. Their higher mean values above the overall mean signify that they consistently perform well across diverse conditions, making them valuable choices for cultivation.

In general, the WAAS biplot categorizes genotypes based on their stability and performance. Genotypes with WAAS values close to zero are considered the most stable. For instance, in DF: G12, G6, G21, G9, G4, and G18, DM:G6, G3, G15, and G24, PH: G15 and G27, PL:G9, G12, G29, G2, and G28, FL: G11, FW:G11, G6, G7, and G20, PDL: G10 and G6, NT: G17, G1, G4, and G5, PW: G7, G5, G20, and G22, BY:G7, G9, G19, G20, and G22, HI:G5, G16, and G22, FY: G20, G5, G10, and G19, TW: G26, G24, G6, and G3 and GY:G10, G15, G13, G6, G7, and G8 exhibit low GEI (Genotype-Environment Interaction) and high stability. However, the ideal genotypes are those with WAAS values close to zero and yields trait means higher than the overall mean.

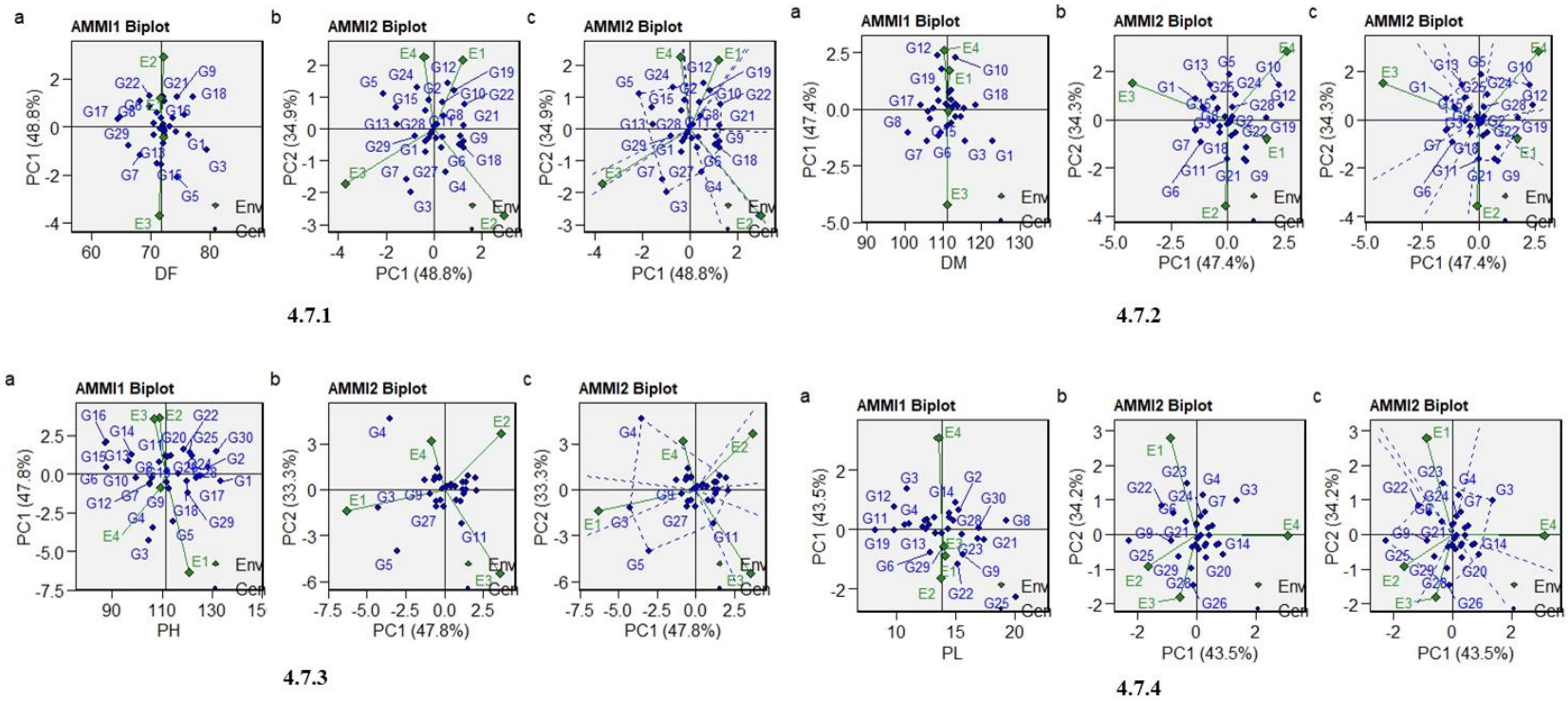


Fig 4.7.1-4.7.4(a). AMMI-1 biplot analysis of IPCA 1 score versus grain yield of 30 genotypes under four environmental conditions, (b) AMMI-2 biplot analysis of IPCA 1 score versus IPCA 2 score of 30 genotypes under four environmental conditions and (c) Polygon view of AMMI-2 biplot based on symmetrical scaling for which-won-where pattern of 30 genotypes under four environmental conditions of days to flowering, days to maturity, plant height and panicle length.

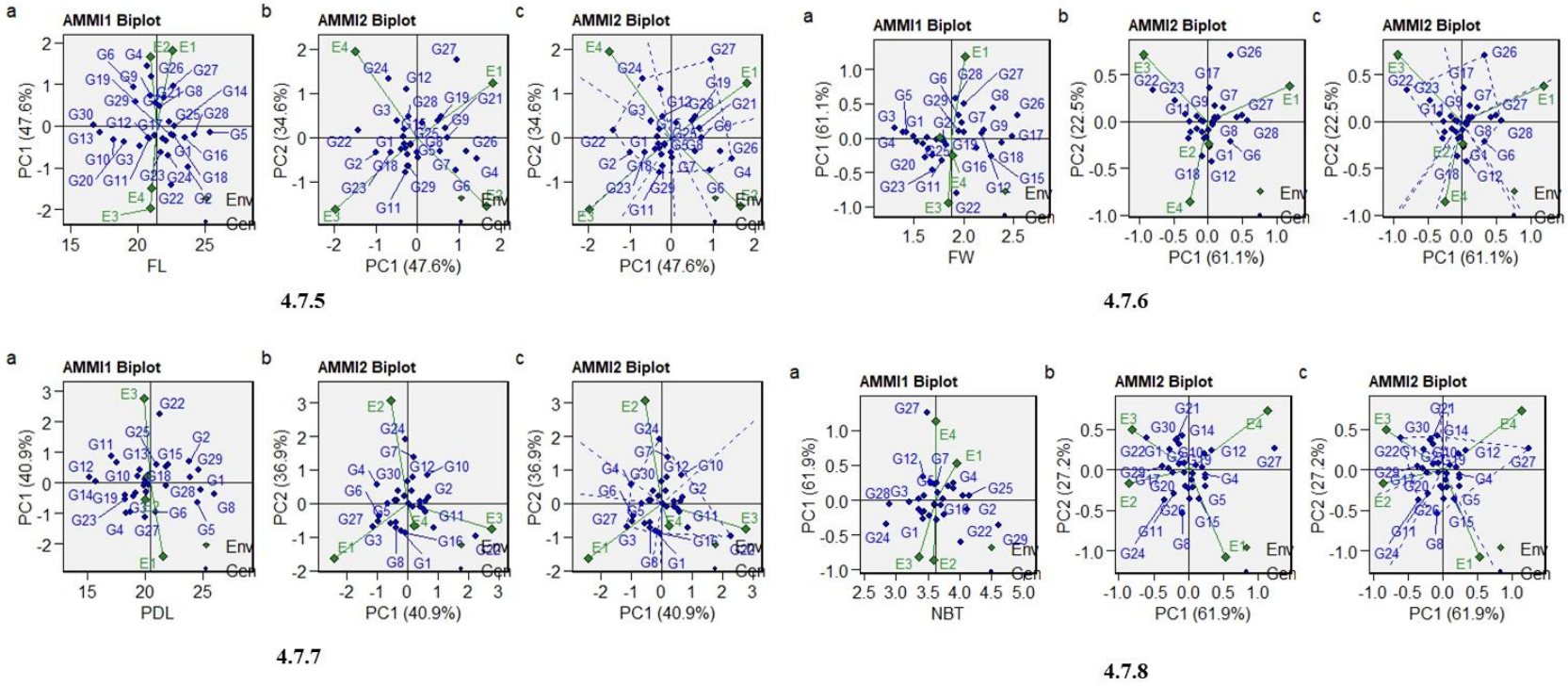


Fig 4.7.5-4.7.8(a). AMMI-1 biplot analysis of IPCA 1 score versus grain yield of 30 genotypes under four environmental conditions, (b) AMMI-2 biplot analysis of IPCA 1 score versus IPCA 2 score of 30 genotypes under four environmental conditions and (c) Polygon view of AMMI-2 biplot based on symmetrical scaling for which-won-where pattern of 30 genotypes under four environmental conditions of flag leaf length, flag leaf width, peduncle length and No. of tillers per plant.

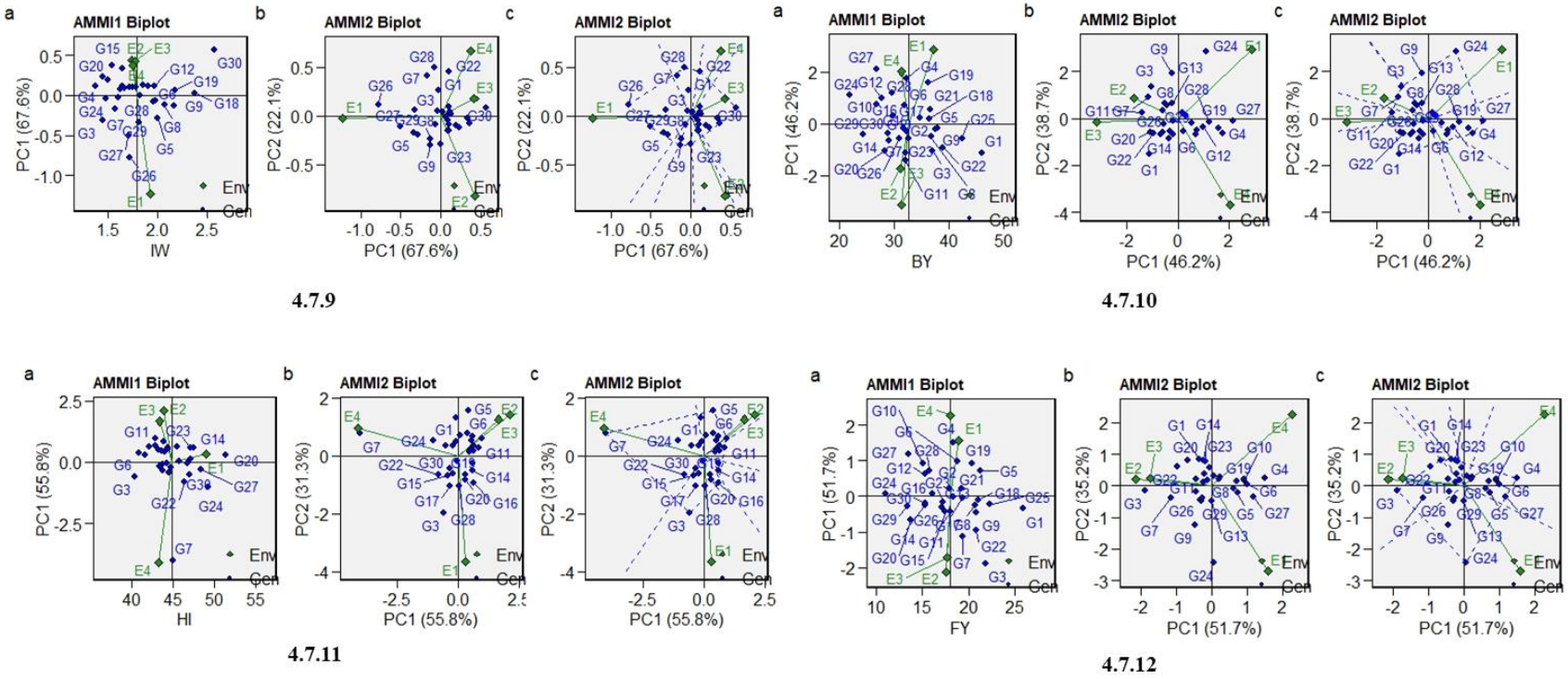


Fig 4.7.9-4.7.12(a). AMMI-1 biplot analysis of IPCA 1 score versus grain yield of 30 genotypes under four environmental conditions, (b) AMMI-2 biplot analysis of IPCA 1 score versus IPCA 2 score of 30 genotypes under four environmental conditions and (c) Polygon view of AMMI-2 biplot based on symmetrical scaling for which-won-where pattern of 30 genotypes under four environmental conditions of panicle width, biological yield, harvest index and fodder yield per plant.

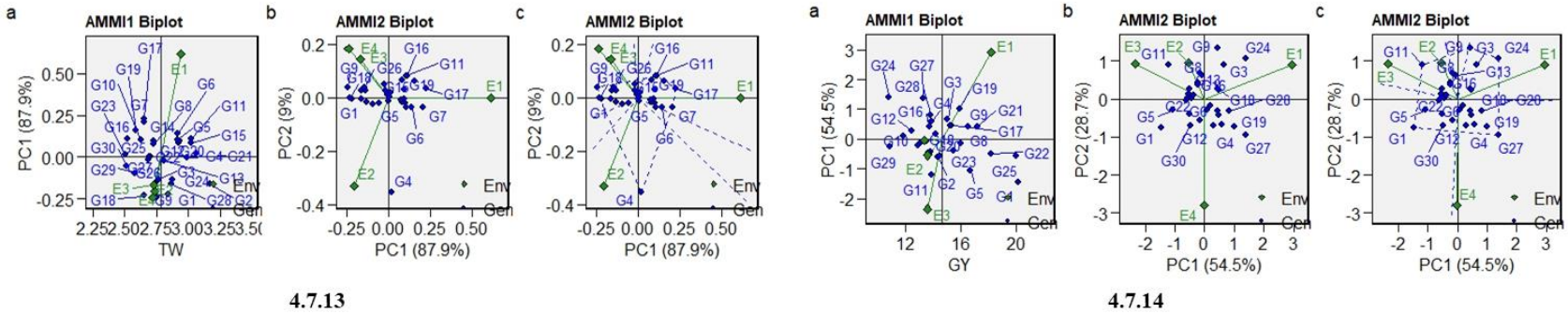


Fig 4.7.13-4.7.14(a). AMMI-1 biplot analysis of IPCA 1 score versus grain yield of 30 genotypes under four environmental conditions, (b) AMMI-2 biplot analysis of IPCA 1 score versus IPCA 2 score of 30 genotypes under four environmental conditions and (c) Polygon view of AMMI-2 biplot based on symmetrical scaling for which-won-where pattern of 30 genotypes under four environmental conditions of test weight and grain yield per plant.

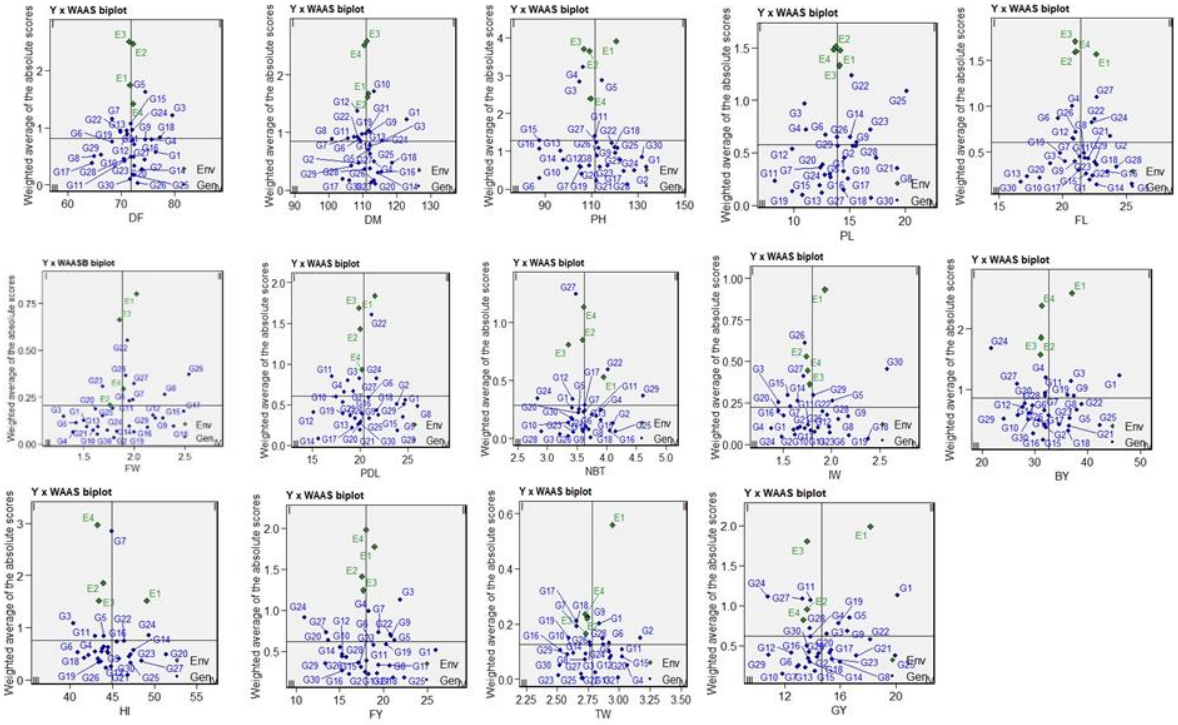


Fig 4.8. Mean performance vs. WAAS biplot from AMMI model for yield traits.

4.12 AMMI stability value (ASV)

The Additive Main effects and Multiplicative Interaction (AMMI) model is a statistical method used to analyse multi-environment trials (MET) data in agricultural research, particularly in plant breeding. It's employed to evaluate the genotype-by-environment interaction (GEI) in such trials. In the context of AMMI, the AMMI Stability Value (ASV) is a measure used to assess the stability of genotypes across different environments. It is a quantitative indicator that helps in identifying genotypes that perform consistently well across diverse environments or those that are stable in their performance. The ASV is calculated based on the interaction principal component analysis (IPCA) scores obtained from the AMMI analysis. The formula for ASV involves taking the sum of squares of IPCA1 (the first principal component) scores for each genotype and then dividing it by the total sum of squares of IPCA1 scores for all genotypes. The lower the ASV, the more stable and consistent the genotype is across environments is a useful tool for plant breeders and researchers to identify genotypes that perform well in a wide range of environments, aiding in the selection of superior and stable genotypes for further breeding programs or recommendations.

Days to 50% flowering, the genotype G26 has demonstrated the highest stability, as evidenced by its ASV score of 0.061, which ranks it first in terms of stability. Following closely are G30 (ASV = 0.171, Rank = 2), G11 (ASV = 0.203, Rank = 3), G25 (ASV = 0.265, Rank = 4), and G23 (ASV = 0.0335, Rank = 5), all of which are recognized as environmentally stable genotypes. Days to maturity, G20 stands out as the most environmentally stable genotype, achieving the top position with an ASV of 0.158. Following closely are G23 (ASV = 0.178, Rank = 2), G30 (ASV = 0.191, Rank = 3), G16 (ASV = 0.200, Rank = 4), and G5 (ASV = 0.228,

Rank = 5). Plant height, G28 is the most environmentally stable genotype, achieving the top position with an ASV of 0.185. Following closely are G21 (ASV = 0.276, Rank = 2), G6 (ASV = 0.618, Rank = 3), G2 (ASV = 0.708, Rank = 4), and G17 (ASV = 0.820, Rank = 5). Panicle length, G30 exhibits the highest environmental stability, securing the top position with an ASV of 0.138. Following closely are G13 (ASV = 0.188, Rank = 2), G27 (ASV = 0.262, Rank = 3), G18 (ASV = 0.303, Rank = 4), and G19 (ASV = 0.304, Rank = 5). Flag leaf length, G13 emerges as the most environmentally stable genotype, securing the top position with an ASV of 0.268. Following closely are G5 (ASV = 0.270, Rank = 2), G14 (ASV = 0.338, Rank = 3), G25 (ASV = 0.352, Rank = 4), and G30 (ASV = 0.448, Rank = 5). Flag leaf width, G30 emerges as the most environmentally stable genotype, securing the top position with an ASV of 0.096. Following closely are G2 (ASV = 0.162, Rank = 2), G24 (ASV = 0.181, Rank = 3), G19 (ASV = 0.210, Rank = 4), and G5 (ASV = 0.213, Rank = 5).

Peduncle length, G14 emerges as the most environmentally stable genotype, securing the top position with an ASV of 0.037. Following closely are G28 (ASV = 0.217, Rank = 2), G20 (ASV = 0.239, Rank = 3), G21 (ASV = 0.379, Rank = 4), and G17 (ASV = 0.401, Rank = 5). No. of tillers per plant, G30 emerges as the most environmentally stable genotype, securing the top position with an ASV of 0.096. Following closely are G2 (ASV = 0.162, Rank = 2), G24 (ASV = 0.181, Rank = 3), G19 (ASV = 0.210, Rank = 4), and G5 (ASV = 0.213, Rank = 5). Panicle width, G18 emerges as the most environmentally stable genotype, securing the top position with an ASV of 0.099. Following closely are G24 (ASV = 0.142, Rank = 2), G19 (ASV = 0.203, Rank = 3), G2 (ASV = 0.224, Rank = 4), and G6 (ASV = 0.227, Rank = 5).

Biological yield, G15 stands out as the most environmentally stable genotype, securing the top position with an ASV of 0.239. Following closely are G18 (ASV = 0.343, Rank = 2), G16 (ASV = 0.367, Rank = 3), G17 (ASV = 0.593, Rank = 4), and G2 (ASV = 0.642, Rank = 5). Harvest index, G21 emerges as the most environmentally stable genotype, securing the top position with an ASV of 0.200. Following closely are G12 (ASV = 0.503, Rank = 2), G26 (ASV = 0.520, Rank = 3), G19 (ASV = 0.694, Rank = 4), and G27 (ASV =0.706, Rank = 5). Fodder yield per plant, G18 emerges as the most environmentally stable genotype, securing the top position with an ASV of0.225. Following closely are G16 (ASV = 0.328, Rank = 2), G21 (ASV =0.368, Rank = 3), G25 (ASV = 0.351, Rank = 4), and G2 (ASV = 0.424, Rank= 5). Test weight, G22 emerges as the most environmentally stable genotype, securing the top position with an impressively low ASV of 0.032. Following closely are G25 (ASV = 0.040, Rank = 2), G21 (ASV = 0.066, Rank = 3), G23(ASV = 0.141, Rank = 4), and G27 (ASV = 0.171, Rank = 5). Grain yield perplantG10 emerges as the most environmentally stable genotype, securing the top position with a low ASV of 0.34. Following closely are G15 (ASV = 0.38, Rank = 2), G7 (ASV = 0.57, Rank = 3), G29 (ASV = 0.61, Rank = 4), G6 (ASV = 0.62, Rank = 5), and G13 (ASV = 0.63, Rank = 6).

Table 4.12. AMMI stability value (ASV) of yield and yield related traits in 30 foxtail millet genotypes over four environments

	DF		DM		PH		PL		FL		FW		PDL	
GEN	ASV	ASV_R	ASV	ASV_R	ASV	ASV_R	ASV	ASV_R	ASV	ASV_R	ASV	ASV_R	ASV	ASV_R
G1	0.606	8	2.150	27	1.03	8	0.720	15	0.473	9	0.275	9	0.871	19
G2	0.967	13	0.740	11	0.71	4	0.898	18	1.409	24	0.163	2	0.793	17
G3	2.409	29	1.978	24	6.24	29	1.994	29	0.765	16	0.413	14	1.200	25
G4	1.527	17	0.719	10	6.84	30	1.149	23	2.032	29	0.229	7	1.249	26
G5	3.173	30	1.863	21	5.95	28	0.529	11	0.270	2	0.213	5	0.733	14
G6	1.547	18	1.871	22	0.62	3	1.184	24	1.483	25	0.909	24	1.114	22
G7	2.284	27	2.026	25	1.13	10	0.731	16	0.823	17	0.617	19	1.396	27
G8	0.700	9	1.501	16	1.07	9	0.498	10	0.761	15	1.164	26	0.830	18
G9	1.779	23	2.095	26	1.38	14	1.123	22	0.996	22	0.340	12	0.492	9
G10	0.984	14	3.441	30	0.95	7	0.558	13	0.461	8	0.249	8	1.119	23
G11	0.231	3	1.644	18	2.77	25	0.354	6	0.897	18	0.901	23	1.187	24
G12	1.650	20	3.356	29	1.19	12	1.002	20	1.157	23	0.460	18	0.788	16
G13	2.178	26	1.770	20	1.36	13	0.189	2	0.269	1	0.449	17	0.476	7
G14	0.548	7	0.557	7	1.83	20	1.273	25	0.334	3	0.280	10	0.037	1
G15	2.312	28	1.557	17	2.93	26	0.437	8	0.452	7	0.730	21	0.682	13

G16	1.527	16	0.200	4	2.96	27	0.401	7	0.450	6	0.419	15	0.889	21
G17	0.744	10	0.229	5	0.82	5	0.485	9	0.505	10	0.364	13	0.402	5
G18	1.820	24	0.718	9	1.52	16	0.304	4	0.721	14	0.422	16	0.582	10
G19	1.674	21	2.417	28	0.87	6	0.305	5	0.920	19	0.210	4	0.735	15
G20	0.437	6	0.158	1	1.72	17	0.796	17	0.604	12	0.771	22	0.239	3
G21	1.749	22	1.903	23	0.28	2	0.598	14	0.941	21	0.229	6	0.380	4
G22	1.946	25	1.645	19	2.40	24	1.696	28	1.946	28	2.196	30	2.677	30
G23	0.334	5	0.179	2	1.14	11	1.542	27	0.939	20	1.300	27	0.881	20
G24	1.637	19	1.172	14	1.76	19	0.550	12	1.633	26	0.181	3	1.915	29
G25	0.265	4	1.232	15	2.02	22	2.904	30	0.352	4	0.695	20	0.660	12
G26	0.062	1	0.328	6	1.74	18	1.487	26	1.643	27	1.152	25	0.492	8
G27	0.875	12	0.846	13	1.38	15	0.262	3	2.189	30	1.371	28	1.449	28
G28	0.772	11	0.609	8	0.19	1	1.014	21	0.553	11	1.547	29	0.218	2
G29	1.147	15	0.759	12	1.89	21	0.997	19	0.719	13	0.287	11	0.469	6
G30	0.172	2	0.192	3	2.04	23	0.139	1	0.449	5	0.097	1	0.637	11

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), No. of tillers per plant (NBT), Panicle width (PW), Biological yield (BY), Harvest index (HI), Test weight (TW), Fodder yield per plant (FY), Grain yield per plant (GY), AMMI Stability value (ASV), Ranking (R).

Table 4.12. AMMI stability value (ASV) of yield and yield related traits in 30 foxtail millet genotypes over four environments

	NBT		PW		BY		HI		FY		TW		GY	
GEN	ASV	ASV_R	ASV	ASV_R	ASV	ASV_R	ASV	ASV_R	ASV	ASV_R	ASV	ASV_R	ASV	ASV_R
G1	0.139	1	0.282	6	2.016	27	1.322	22	0.992	17	2.160	27	2.879	30
G2	0.020	10	0.225	4	0.642	5	1.253	21	0.424	5	1.561	24	1.147	19
G3	0.125	18	0.970	24	1.846	24	2.219	29	2.774	30	1.299	19	1.536	22
G4	0.207	23	0.348	11	2.185	28	1.211	20	2.231	28	0.394	7	1.295	21
G5	0.031	6	0.899	23	0.717	9	1.744	26	1.095	19	1.022	16	2.042	25
G6	0.043	9	0.227	5	1.093	17	1.040	13	1.455	24	1.370	21	0.623	5
G7	0.072	13	0.651	21	1.621	22	7.178	30	1.719	26	2.012	26	0.575	3
G8	0.043	8	0.446	16	0.878	12	0.937	9	0.534	8	0.751	9	0.740	7
G9	0.270	24	0.487	17	1.954	26	0.851	8	1.400	23	2.367	30	1.571	23
G10	0.143	20	0.368	14	1.030	15	1.519	24	1.363	22	0.994	15	0.342	1
G11	0.014	19	0.362	13	1.686	23	1.815	27	0.649	12	1.076	18	2.453	27
G12	0.021	3	0.350	12	1.237	18	0.503	2	0.906	16	0.816	10	0.889	12
G13	0.120	17	0.298	8	0.702	7	1.158	17	0.486	7	0.225	6	0.633	6
G14	0.110	16	1.034	25	1.055	16	1.176	18	0.878	15	0.946	14	0.847	9
G15	0.953	30	1.125	27	0.240	1	1.008	12	0.678	13	0.820	11	0.388	2

G16	0.277	25	0.610	20	0.367	3	1.438	23	0.328	2	1.047	17	0.860	10
G17	0.070	12	0.322	10	0.594	4	1.206	19	0.578	9	2.212	28	0.977	14
G18	0.080	14	0.100	1	0.343	2	0.814	7	0.225	1	2.264	29	0.919	13
G19	0.649	29	0.204	3	1.928	25	0.695	4	1.350	21	1.531	23	2.067	26
G20	0.280	26	0.717	22	1.383	20	0.973	11	1.253	20	0.906	12	1.073	18
G21	0.387	28	0.313	9	0.666	6	0.201	1	0.368	4	0.067	3	0.864	11
G22	0.028	5	0.569	19	1.287	19	1.559	25	1.523	25	0.032	1	1.048	16
G23	0.089	15	0.295	7	0.898	13	1.103	15	0.804	14	0.141	4	0.740	8
G24	0.041	7	0.143	2	3.145	30	1.913	28	2.430	29	1.318	20	2.875	29
G25	0.027	4	0.385	15	0.708	8	0.716	6	0.351	3	0.041	2	1.071	17
G26	0.060	2	2.363	30	0.767	11	0.521	3	0.643	10	1.405	22	0.996	15
G27	0.151	21	1.555	28	2.548	29	0.707	5	1.759	27	0.172	5	2.790	28
G28	0.316	27	0.547	18	1.450	21	1.041	14	1.063	18	1.580	25	1.589	24
G29	0.185	22	1.047	26	0.758	10	1.103	16	0.647	11	0.940	13	0.619	4
G30	0.066	11	1.752	29	0.941	14	0.950	10	0.474	6	0.530	8	1.152	20

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), No. of tillers per plant (NBT), Panicle width (PW), Biological yield (BY), Harvest index (HI), Test weight (TW), Fodder yield per plant (FY), Grain yield per plant (GY), AMMI Stability value (ASV), Ranking (R).

4.13 Best linear unbiased prediction (BLUP)

Best Linear Unbiased Prediction (BLUP) is a statistical method widely used in genetics and breeding to assess the genetic merit of individuals or genotypes while considering various sources of variability (Zhang *et al.* 2010). The key advantage of BLUP over AMMI lies in its ability to provide more robust and stable estimates of genotype performance across different environments, particularly in the presence of complex GEI. While AMMI is valuable for studying GEI patterns, it can be sensitive to noisy or unbalanced datasets, leading to less reliable predictions (Balzarini, 2002). The BLUP method estimates the average performance of genotypes in mixed models with high efficiency. Therefore, it can fill the gap of AMMI regarding the analysis of LMM structure (Taleghani *et al.* 2023).

The likelihood ratio test showed highly significant effects ($p < 0.05$) for both genotype and interaction in this experiment for all traits. This significance of genotype-environment interaction (GEI) indicates that different genotypes respond differently in different environments, each having its own strengths and weaknesses. Therefore, in such situations, using the BLUP method can lead to better and more reliable results (Taleghani *et al.* 2023).

In the analysis employing Best Linear Unbiased Prediction (BLUP) for the all yield traits within in this genetic population, several critical parameters were determined and represented at Table 13 and Figure 4.9.

The phenotypic variance, which represents the total variability in the traits, was estimated to be highest in PH (252.84%), followed by BY (45.73%), DM (35.38%), HI (27.05%), PDL (14.24%), FY (16.62%), PL (12.64%), GY (10.46%), FL (8.29%), NT (0.44%), FW (0.23%), TW (0.03%), PW (0.17%), and

the lowest in DF (22.12%). These percentages reflect the extent of observed variation in the traits. The heritability estimates for DF (35%), FL (34%), FW (36%), NT (19%), PW (35%), HI (11%), and GY (37%) indicate a relatively limited genetic influence on the variation in these traits. This suggests that a smaller proportion of the total variation in these traits is attributed to genetic factors. In other words, for these traits, the observed variation is influenced to a lesser extent by an individual's genetic makeup and is influenced more by environmental factors or random effects. In contrast, the heritability estimates for DM (40%), PH (49%), PL (48%), PDL (41%), BY (51%), and FY (55%) suggest a moderate genetic influence on the variation in these traits. This indicates that a more significant portion of the variation in these traits is determined by genetic factors. In other words, individuals with certain genetic characteristics are more likely to express similar traits for DM, PH, PL, PDL, BY, and FY, making them more heritable.The heritability of the TW (88%), suggesting a high genetic influence on the variation of this trait.Higher heritability values suggest a stronger genetic influence.

The coefficient of determination for genotype-versus-environment interaction effects revealed notable influence for the following traits: DF (0.581), DM (0.486), PH (0.387), PL (0.305), FL (0.316), FW (0.365), PDL (0.270), NT (0.142), PW (0.258), BY (0.272), HI (0.213), FY (0.235), TW (0.095), and GY (0.317). These values underscore the significant role played by the interplay between genetic factors and the environment in shaping each respective trait. The heritability of the genotypic mean was remarkably high for DF (70.13%), DM (75.3%), PH (82.4%), PL (83.8%), FL (76.4%), FW (76.0%), PDL (81.5%), NT (68.6%), PW (78.5), BY (85.7%), FY (87.8%), TW (97.2%), and GY (78.3%), underscoring the strong genetic influence on the average performance of these

traits. For HI, the heritability of the genotypic mean was 51.3%, signifying a moderate genetic impact on the average performance of this trait.

The BLUP analysis demonstrated a commendable accuracy in genotype selection, with accuracy scores of DF (83.74%), DM (86.8%), PH (90.8%), PL (91.5%), FL (87.4%), FW (87.2%), PDL (90.3%), NT (82.8%), PW (88.6%), BY (92.6%), HI (71.6%), FY (93.7%), TW (98.6%), and GY (88.5%). This reflects the effectiveness of BLUP in identifying and selecting genotypes with desirable traits.Additionally, the high correlation between genotypic values across diverse environmental conditions were observed at DF (0.900), DM (0.809), PH (0.769) and TW (0.828), illustrating the high genetic stability of these traits. Moderate correlation between genotypic values across diverse environmental conditions were observed at PL (0.593), FL (0.484), FW (0.571), PDL (0.459), PW (0.399), BY (0.560), FY (0.525) and GY (0.510), suggest the moderate genetic stability of these traits. Limited correlation between genotypic values across diverse environmental conditions were observed at NT (0.171) and FY (0.241), illustrating the limited genetic stability of these traits.The population displayed substantial genetic diversity in these traits, as indicated by the genotypic coefficient of variation for DF (3.89), DM (3.38), PH (10.06), PL (17.85), FL (7.92), FW (15.33), PDL (11.87), NT (8.20), PW (13.90), BY (14.84), HI (3.92), FY (16.80), TW (0.17), and GY (13.58). Additionally, the residual coefficient of variation and coefficient of variation for these traits was as follows: DF (1.66, 2.33), DM (1.81, 1.87), PH (4.85, 2.07), PL (11.72, 1.52), FL (7.81, 1.01), FW (13.33, 1.15), PDL (10.42, 1.13), NT (15.00, 0.54), PW (14.57, 0.95), BY (9.58, 1.55), HI (9.43, 0.41), FY (10.44, 1.60), TW (0.91, 6.71), and GY (12.19, 1.11). These values highlight the significant genetic diversity in the population, with variation both at the genotypic and residual levels across these traits.

In a study encompassing 30 different genotypes, a striking observation emerged, revealing that 14 specific genotypes, namely G10, G15, G30, G12, G13, G11, G28, G19, G22, G6, G7, G29, G8, and G17 exhibited a significantly lower mean value for the variable "days to 50% flowering" than initially predicted. Notably, within this group, genotypes G17 and G8 stood out as they exhibited the lowest predicted mean values for this crucial parameter. A salient observation emerge, revealing that 14 specific genotypes, namely G10, G15, G30, G12, G13, G11, G28, G19, G22, G6, G7, G29, G8, and G17, exhibited a significantly lower mean value for the variable "days to maturity" than initially predicted. Notably, within this group, genotypes G17 and G8 stood out as they exhibited the lowest predicted mean values for this crucial parameter. Among this diverse set of genotypes, 12 of them, namely G8, G4, G19, G7, G12, G3, G10, G14, G13, G6, G16, and G15, exhibited plant heights that lower predicted means. However, what truly stands out are genotypes G17 and G8, as they boasted the lowest predicted mean values for plant height.

Among the 30 genotypes under study, it is noteworthy that 16 of them displayed Panicle length values exceeding the initially predicted mean values. These exceptional genotypes, namely G26, G29, G18, G10, G1, G17, G14, G22, G2, G28, G9, G23, G30, G21, G8, and G25, outperformed expectations in terms of Panicle length. Notably, G17 and G8 emerged as the standout contenders, boasting the highest predicted mean values for Panicle length. Out of 30, 16 of them exhibited Flag leaf lengths that exceeded their initially predicted mean values. Specifically, these genotypes include G8, G23, G15, G21, G1, G24, G25, G29, G22, G18, G27, G14, G16, G2, G28, and G5. Notably, within this group, G5 and G28 stood out with the highest predicted mean values for Flag leaf length. Out of the 30 genotypes assessed, 15 genotypes exhibited Flag leaf widths that surpassed their originally predicted mean values. These noteworthy genotypes

include G28, G22, G6, G29, G7, G19, G27, G16, G12, G9, G15, G8, G18, G17, and G26. Particularly noteworthy within this subset were G17 and G26, as they displayed the highest predicted mean values for Flag leaf width. Among the 30 genotypes investigated, 12 of them displayed Peduncle lengths exceeding their initially predicted mean values. These specific genotypes are G6, G25, G22, G24, G18, G15, G2, G28, G5, G29, G1, and G8. Notably, within this group, G1 and G28 emerged as standout performers, boasting the highest predicted mean values for Peduncle length.

Out of the 30 genotypes analyzed, 14 genotypes exhibited a No. of tillers per plant that exceeded the initially predicted mean values. These specific genotypes include G17, G7, G6, G8, G18, G11, G13, G15, G4, G22, G16, G2, G25, and G29. Notably, among this group, G29 and G25 stood out with the highest predicted mean values for No. of tillers per plant. Among the 30 genotypes assessed, 13 genotypes demonstrated Panicle widths that exceeded their initially predicted mean values. These specific genotypes include G29, G23, G25, G22, G28, G12, G6, G5, G8, G9, G19, G18, and G30. Notably, within this group, G30 and G18 stood out with the highest predicted mean values for Panicle width. Among the 30 genotypes examined, 12 of them exhibited biological yields surpassing their initially predicted mean values. These specific genotypes are G17, G19, G18, G21, G8, G3, G9, G5, G22, G25, G1, and G25. Notably, within this subset, G25 and G1 emerged as the top performers, boasting the highest predicted mean values for biological yield among all the genotypes studied.

Among the 30 genotypes under scrutiny, 12 of them exhibited Harvest indexes that exceeded their initially predicted mean values. These specific genotypes include G7, G16, G28, G22, G21, G30, G23, G25, G14, G27, G24, and G20. Remarkably, within this group, G24 and G20 emerged as the top achievers,

showcasing the highest predicted mean values for Harvest index among all the genotypes assessed. Among the 30 genotypes assessed, 13 genotypes exhibited Test weights that exceeded their initially predicted mean values. These specific genotypes include G13, G1, G28, G24, G6, G5, G12, G20, G21, G15, G11, G4, and G2. Remarkably, within this group, G25 and G1 emerged as the top performers, showcasing the highest predicted mean values for Test weight among all the genotypes studied. Within the pool of 30 genotypes examined, a total of 12 genotypes displayed Grain yields per plant that surpassed their originally predicted mean values. Specifically, these genotypes are G3, G18, G17, G23, G19, G8, G9, G5, G21, G22, G25, and G1. Notably, among this group, G25 and G1 emerged as the top performers, boasting the highest predicted mean values for Grain yield per plant among all the genotypes studied.

Similar findings were reported by several studies. Munda *et al.* (2023) identified stable genotypes in Curcuma by analyzing BLUPs& WAAS values associated with yield and yield traits. Koundinya *et al.* (2021) similarly reported the identification of stable genotypes in cassava using BLUPs& WAAS values, focusing on yield and yield traits. Taleghani *et al.* (2023) also reported the identification of stable genotypes in sugar beet based on BLUPs& WAAS values correlated with root traits. Furthermore, Rajabi *et al.* (2023) identified stable genotypes in sugar beet with a specific focus on root traits through BLUPs& WAAS values analysis. Additionally, Mishra et al. (2023) reported the identification of stable Valepotriate Specific Valerian Chemotypes using BLUPs& WAAS.

Table 4.13 Deviance analysis, estimated variance components and genetic parameters for different traits of 30 foxtail millet genotypes evaluated in 4 environments.

	Phenotypic variance	Heritability	$GEIr^2$	h^2mg	Accuracy	r_{ge}	CV_g	CV_r	CV ratio
Days to 50% flowering	22.128	0.354	0.581	0.701	0.837	0.900	3.893	1.665	2.339
Days to maturity	35.387	0.400	0.486	0.753	0.868	0.809	3.386	1.811	1.870
Plant height	252.845	0.498	0.387	0.824	0.908	0.769	10.062	4.854	2.073
Panicle length	12.649	0.485	0.305	0.838	0.915	0.593	17.855	11.729	1.522
Flag leaf length	8.292	0.347	0.316	0.764	0.874	0.484	7.926	7.813	1.014
Flag leaf width	0.230	0.362	0.365	0.760	0.872	0.571	15.335	13.337	1.150
Peduncle length	14.241	0.412	0.270	0.815	0.903	0.459	11.874	10.424	1.139
No. of tillers per plant	0.449	0.197	0.142	0.686	0.828	0.177	8.204	15.008	0.547
Panicle width	0.177	0.354	0.258	0.785	0.886	0.399	13.909	14.579	0.954
Biological yield	45.739	0.514	0.272	0.857	0.926	0.560	14.848	9.580	1.550
Harvest index	27.057	0.115	0.213	0.513	0.716	0.241	3.929	9.493	0.414
Fodder yield per plant	16.624	0.551	0.235	0.878	0.937	0.525	16.802	10.448	1.608
Test weight	0.033	0.886	0.095	0.972	0.986	0.828	6.173	0.919	6.716
Grain yield per plant	10.464	0.378	0.317	0.783	0.885	0.510	13.583	12.190	1.114

$GEIr^2$= Coefficient of determination for the genotype-vs-environment interaction effects, h2mg= heritability of the genotypic mean, r_{ge}= correlation between genotypic values across environments, CV_g= genotypic coefficient of variation, CV_r= residual coefficient of variation and CV= coefficient of variation

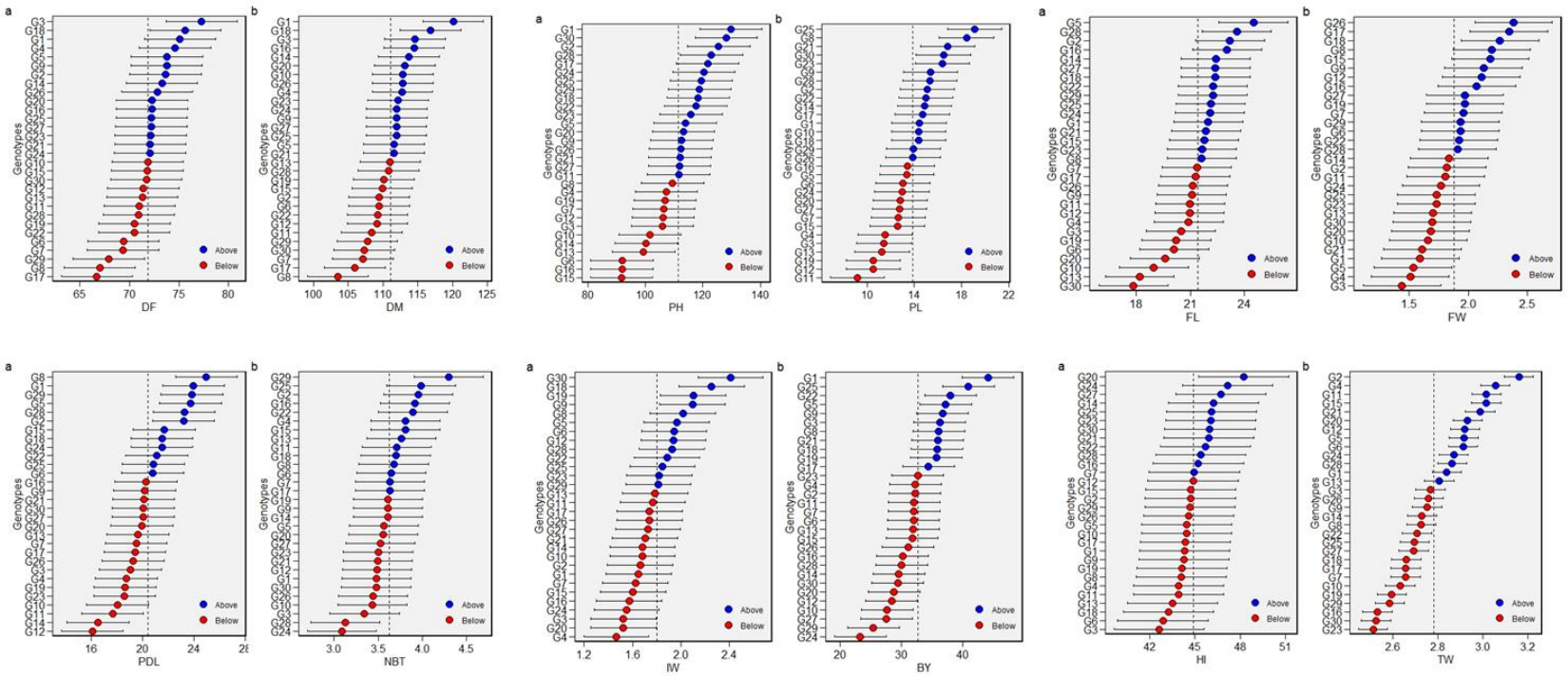


Fig 4.9 Best linear unbiased predilection mean values of 30 foxtail millet genotypes for yield traits.

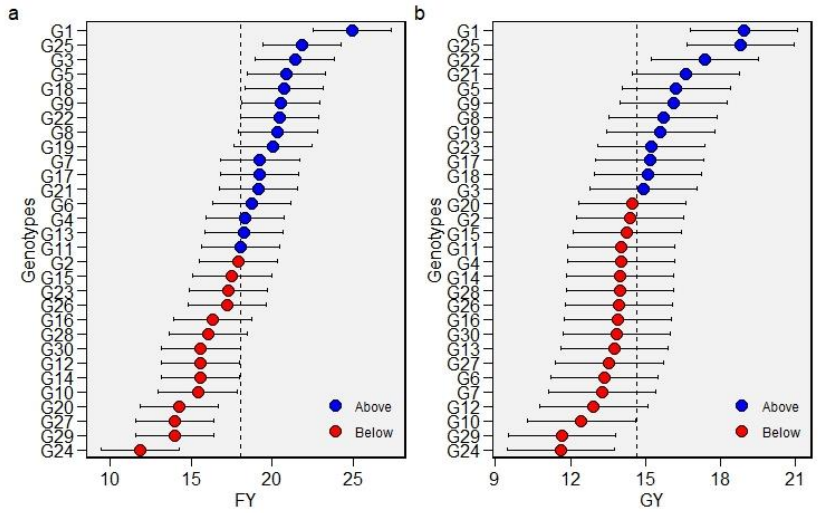


Fig 4.9 Best linear unbiased predilection mean values of 30 foxtail millet genotypes for yield traits.

4.14 GGE biplot graphical analysis.

Every year, variety trials are carried out in all regions for major crops. 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 is unbalanced and incomplete data due to changing genotypes over years. Two strategies are used: 1) Analysing yearly and summarizing results; 2) Evaluating consistency of patterns in grouping test locations and genotypes across years (Yan *et al*. 2002).

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 (Yan et al. 2005), but it doesn't condense the biplot invalid (Yan *et al*. 2007). As noted by Yang et al. (2009), 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).

4.14.1 The mean vs 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 AEA (The average environment axis) 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 (Yan, 2001). The AEC (average environment coordination) 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 (average environment coordination) point outward from the origin and indicate higher instability for the genotypes, regardless of the direction (Yan, 2001). 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 (Kaya *et al*. 2006).

In this study, all locations are on the same side of the AEC in DF (Figure 4.10.1), DM (Figure 4.10.2), PH (Figure 4.10.3), PL (Figure 4.10.4), FL (Figure 4.10.5), FW (Figure 4.10.6), PDL (Figure 4.10.7), NBT (Figure

4.10.8), PW (Figure 4.10.9), BY (Figure 4.10.10), HI (Figure 4.10.11), FY (Figure 4.10.12), TW (Figure 4.10.13) and GY (Figure 4.10.14) 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 genotypesof 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, (fromG11-G24) FY, (from G3-G23) TW and (from G20-G24)) GY exhibits belove 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 (Yan *et al.* 2002). 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 discardedrespective 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 (Yan *et al*. 2002).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 toachieve the highest yield in trials (with the longest vector among all genotypes) and complete stability, placing it precisely on the AEA (Yan *et al*. 2002). 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.

4.14.2 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 4.11.1- Figure 4.11.14 shows that G3 in DF, G1 and G18 in DM, G1in 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 arepositionedat the center of the concentric circles, is an ideal genotype due to its higher yield and stability compared to the other genotypes.

4.14.3 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 (Yan et al. 2007). 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 are perpendicular to the sides of the polygon or their extensions. In the GGE biplot DF: (Figure 4.12.1) genotypes G3, G18, G9, G21, G22, G6, G8, G17, G29, and G5, DM: (Figure 4.12.2) G12, G8, G7, G1, G3 and G10, PH: (Figure 4.12.3) G1, G30, G3, G5, G16, G15, and G6, PL: (Figure 4.12.4) G25, G23, G26, G8, G4, G11, and G12, FL: (Figure 4.12.5) G8, G26, G17, G22, G23, G3 and G28, FW: (Figure 4.12.6) G3, G23, G22, G17, G26, G8 and G28, PDL (Figure 4.12.7) G29, G27, G22, G28, and G24, NBT: (Figure 4.12.8) G29, G27, G22, G28, and G24, PW; (Figure 4.12.9) G15, G30, G18, G3, G26, G20 and G4, BY (Figure 4.12.10) G1, G3, G7, G24, G19, G4, and G27 , HI: (Figure 4.12.11) G20, G14, G23, G7, G10, G11, G6 and G3, FY (Figure 4.12.12) G1, G3, G24, G27 and G4, TW: (Figure 4.13.13) G2, G1, G6, G11, G16, G23, G30, G18 and G9 and GY: (Figure

4.12.14) 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 eight sectors through seven vertexes and one equality line, and the environments fall into two of these sectors. In contrast, the DM Biplot has five vertexes and no equality lines, resulting in the biplot being divided into five sectors, with the environments allocated into two of them. The PH Biplot involves six vertexes and one equality line, dividing the biplot into seven sectors, with two sectors accommodating the environments. Similarly, the PL Biplot and FL Biplot, both having seven vertexes, divide the biplot into seven sectors with two sectors housing the environments, but without equality lines. The FW Biplot utilizes five vertexes and two equality lines, dividing the biplot into seven sectors, and two sectors include the environments. In the PDL Biplot, five vertexes and one equality line create six sectors, with the environments falling into two of them. The NBT Biplot and PW Biplot both employ five vertexes but with different arrangements of equality lines, resulting in the biplot being divided into five sectors and environments falling into two of them. The BY Biplot, with seven vertexes and no equality lines, divides the biplot into seven sectors, and one of these sectors houses the environments. The HI Biplot, with five vertexes and one equality line, divides the biplot into six sectors, and two sectors accommodate the environments. Similarly, the FY Biplot with five vertexes but no equality lines divide the biplot into five sectors, and one sector includes the environments. In contrast, the TW Biplot utilizes eight vertexes and no equality lines, resulting in the biplot being divided into eight sectors, with two sectors accommodating the environments. Lastly, the GY Biplot, utilizing seven vertexes and no equality lines, divides the biplot into seven sectors, with the environments falling into two 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.

4.14.4 Discriminativeness 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 (as mentioned by Tariku *et al.* in 2017). 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 Yan and Kang (2002). 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 Yan and Kang (2002).The concepts of discriminativeness and representativeness in GGE biplots are crucial for identifying ideal environments that can effectively distinguish between genotypes. The use of average environmental coordinates (AEC) and test environments helps us visualize Environments-I, II, III, and IV more effectively and representation at Biplots (Figure. 4.12.1-4.13.14)

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 FYand 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.

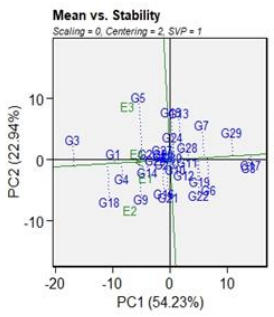
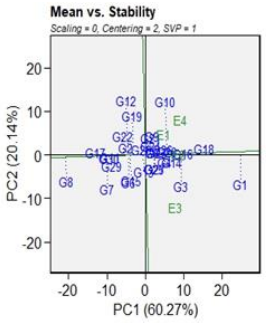


Fig 4.10.1



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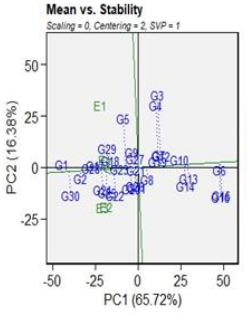


Fig 4.10.3

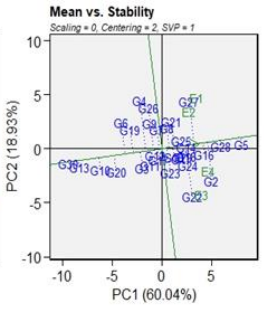


Fig 4.10.4

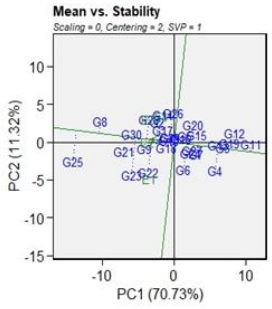
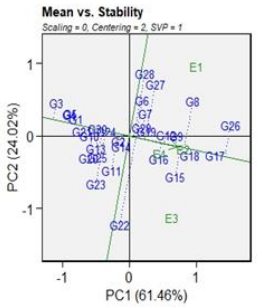


Fig 4.10.5



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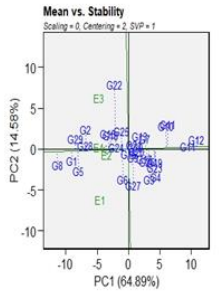


Fig 4.10.7

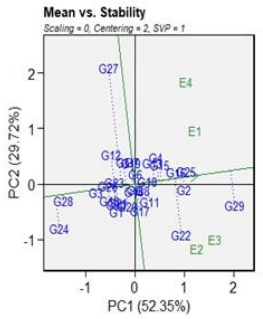


Fig 4.10.8

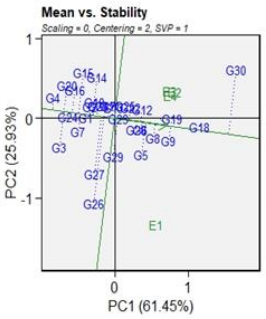


Fig 4.10.9

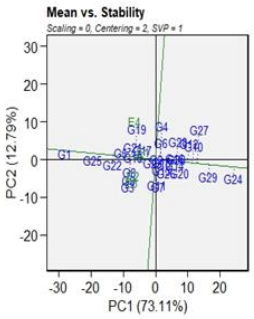


Fig 4.10.10

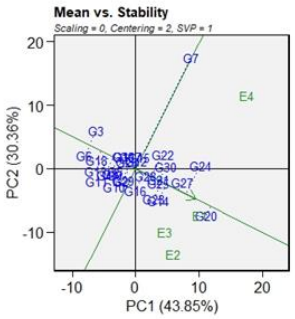


Fig 4.10.11

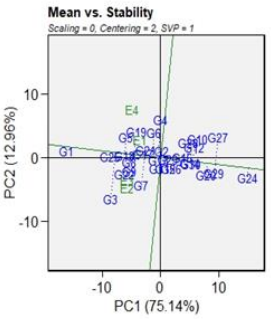
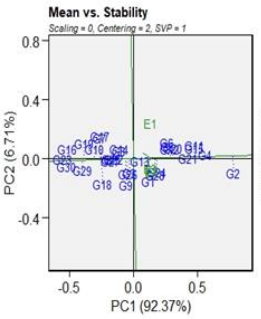


Fig 4.10.12



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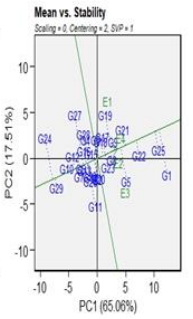


Fig 4.10.14

Fig 4.10.1-4.10.14 Average environment coordination (AEC) views of the GGE-biplot based on environment-focused scaling for the means performance and stability of genotypes for yield traits.

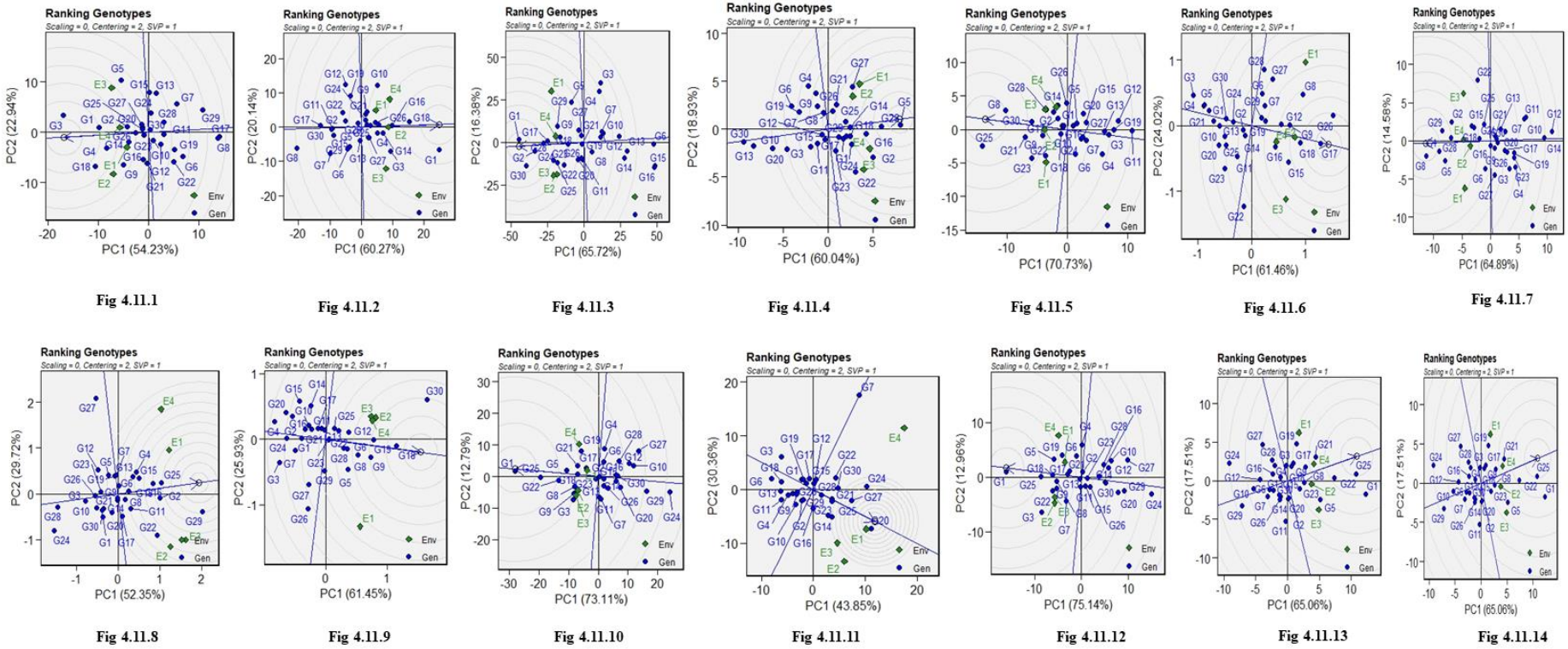


Fig 4.11.1 Fig 4.11.2 Fig 4.11.3 Fig 4.11.4 Fig 4.11.5 Fig 4.11.6 Fig 4.11.7

Fig 4.11.8 Fig 4.11.9 Fig 4.11.10 Fig 4.11.11 Fig 4.11.12 Fig 4.11.13 Fig 4.11.14

Fig 4.11.1-4.11.14 GGE-biplot based on genotype-focused scaling for comparison the genotypes with the ideal genotype for yield traits

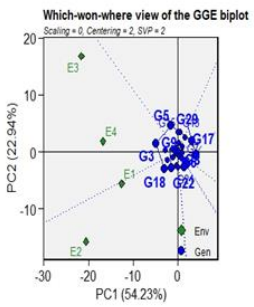


Fig 4.12.1

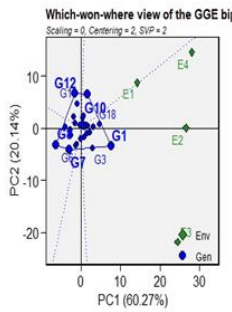


Fig 4.12.2

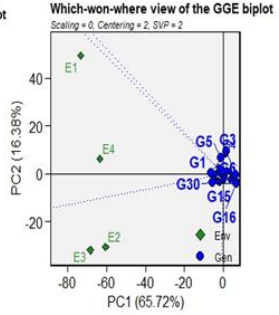


Fig 4.12.3

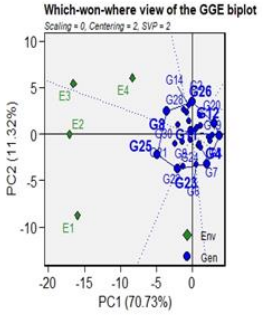


Fig 4.12.4

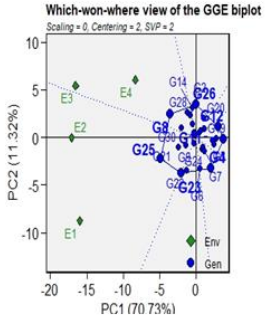


Fig 4.12.5

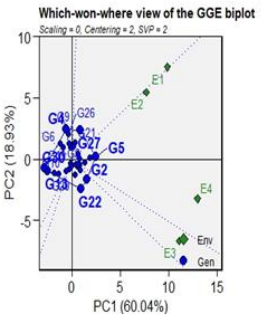


Fig 4.12.6

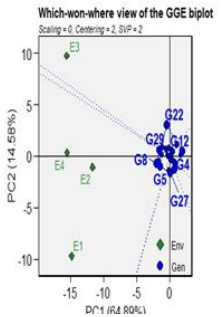


Fig 4.12.7

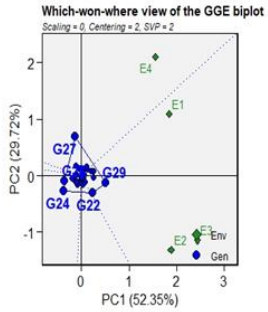


Fig 4.12.8

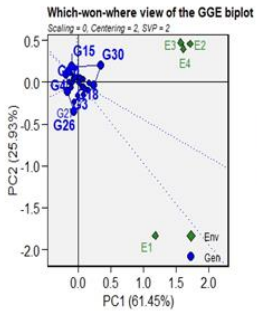


Fig 4.12.9

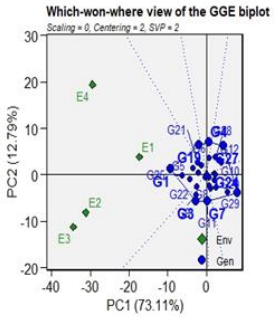


Fig 4.12.10

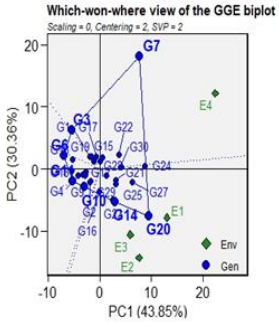


Fig 4.12.11

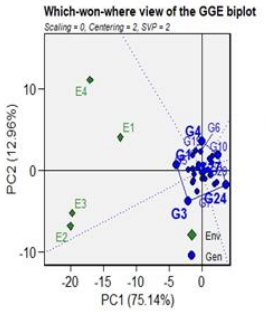


Fig 4.12.12

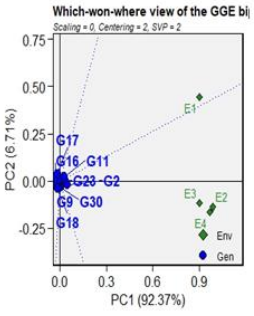


Fig 4.12.13

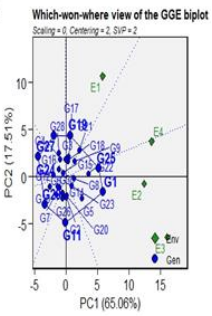


Fig 4.12.14

Fig 4.12.1-4.12.2. Polygon views of the GGE-biplot based on symmetrical scaling for the which-won-where pattern for genotypes and environments for yield traits.

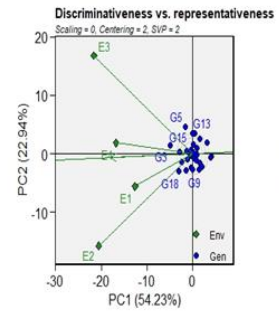
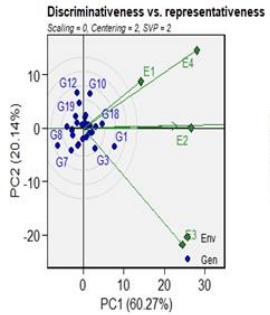


Fig 4.13.1



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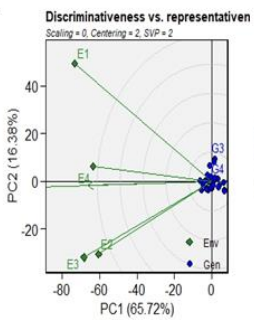

Fig 4.13.3

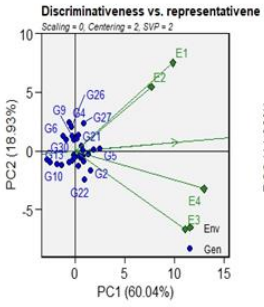

Fig 4.13.4

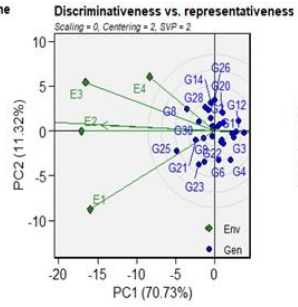

Fig 4.13.5

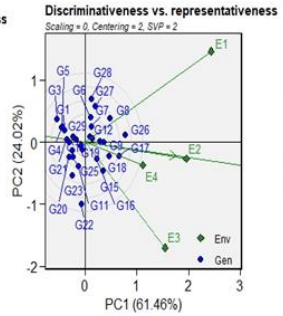

Fig 4.13.6

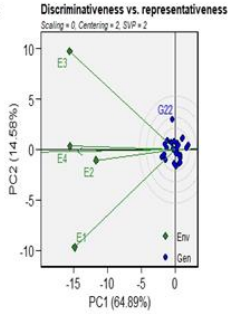

Fig 4.13.7

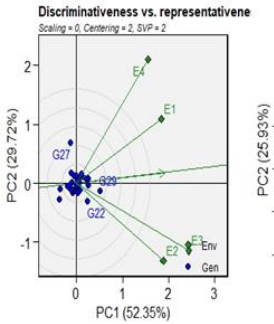

Fig 4.13.8

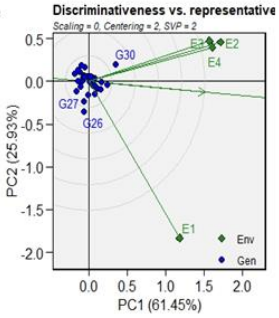

Fig 4.13.9

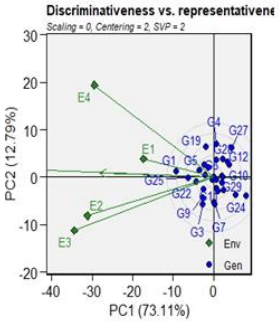

Fig 4.13.10

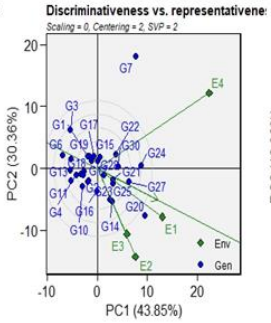

Fig 4.13.12

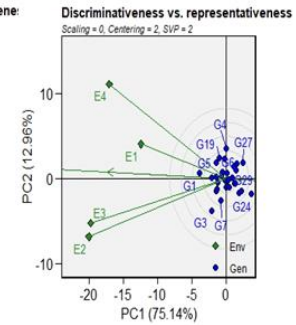

Fig 4.13.12

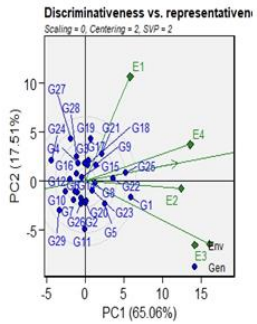

Fig 4.13.13

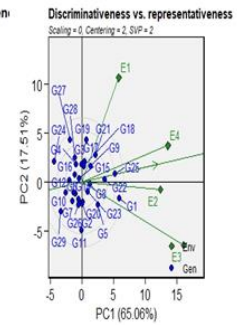

Fig 4.13.14

Fig 4.13.1-4.13.14. The GGE biplot 'Discriminativeness vs. Representativeness' pattern for genotype comparison with ideal genotype showing G+G×E interaction effect of 30 foxtail millet genotypes under four environments for yield traits.

4.15 Genotype Ranking Depending on the Number of Retained Interaction Principal Component Axis

Figure 4.14, illustrates how genotype rankings for stability shift with the number of IPCAs employed in WAASB estimation. Notably, the inclusion of IPCAs significantly impacts genotype ranking, particularly when up to three IPCAs are used (see Fig. 4.14). The dendrogram on the left side of Figure 4.27 facilitates the identification of groups of genotypes with similar stability performance. For instance, when considering four or more IPCAs, genotypes G10, G15, G13, G7, and G6 exhibit the lowest WAASB values, ranking as the first, second, third, four and five most stable, respectively (also evident in Fig. 4.14). One of the most pronounced changes is observed in the case of genotype G2. When the first and second IPCAs are used in WAASB estimation, G2 is ranked as the 21st and 13th most stable, respectively. However, with more than three IPCAs, G2 emerges as the ninth most stable (Fig. 4.14).

4.16 Identification of similarly responded genotypes

We used IPCA I and IPCA II scores within the GGE framework to examine how genotypes interacted with the environment. To simplify our findings, we performed cluster analysis on these scores for the early kharif-late kharif of 2022 and the early summer-late summer of 2023, focusing on grain yield per plant. This helped group genotypes with similar responses together, making it easier to understand than interpreting the complex biplot. We established an 80% similarity threshold for clustering genotypes using Ward's minimum variance technique. The results, presented in Table 4.14 and Fig 4.15, showed that we categorized 30 genotypes into 4 distinct responsive clusters.

In Cluster-2, there were 12 genotypes, all exhibiting a 45.02% similarity in their response to environmental conditions for grain yield per plant. Cluster-1 had 4 genotypes with a 45.70% similarity in their responses. Similarly,

Cluster-3 contained 6 genotypes with an 18.52% resemblance in this aspect. Notably, Cluster-4 included 8 genotypes with a negative similarity index (-1.208), indicating a highly diverse response pattern, as confirmed by the graphical representation. This highlights the usefulness of calculating similarity index values to identify genotypes that respond similarly to environmental factors for specific traits.

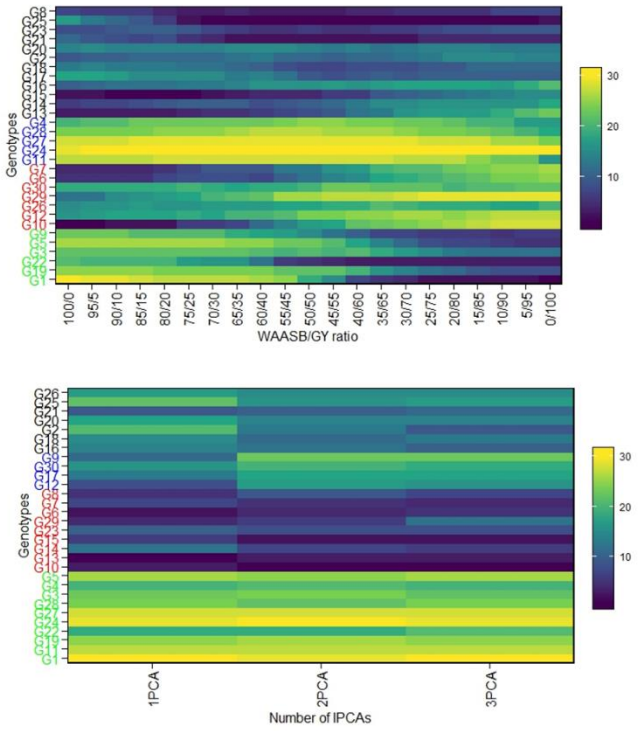

Fig 4.14 Heatmap showing the ranks of 30 genotypes in relation to the number of interaction principal component axes (IPCA) used in the weighted average of absolute scores for the best linear unbiased predictions (BLUPs) of the genotype-vs.-environment interaction (WAASB) estimation.

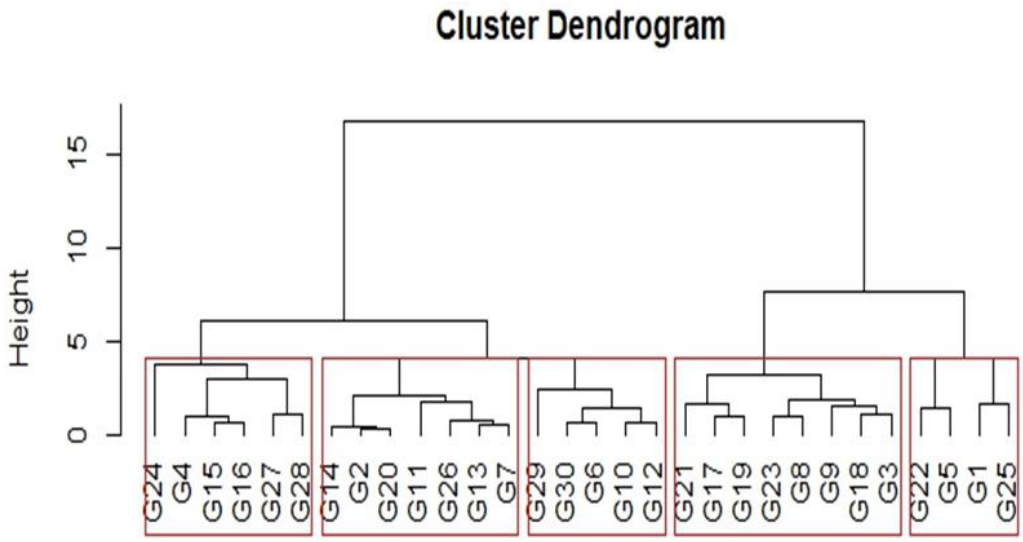

Fig 4.15. Clustering the similarly responding genotypes into different similarity groups based on Ward's minimum variance technique in 30 foxtail millet genotypes.

Table 4.14. Clusters Similarity Distance

Clusters	No. of genotypes	Similarity	Distance
1	6	45.701	4.09
2	7	45.028	4.14
3	5	18.523	6.13
4	8	-1.208	7.62
5	4	-122.505	16.75

4.17 Multi-trait stability index (MTSI)

We calculated the Multi-Trait Stability Index (MTSI) based on data from 14 different traits, and you can see the results in Figure 4.16. We ranked the genotypes from highest to lowest MTSI values. The genotypes with the highest MTSI values are at the center of the circle, and those with the lowest values are on the outermost circle. We marked some genotypes with red dots because they were chosen due to their MTSI values, with a selection intensity of 20%. The black dots represent genotypes that were not selected.

Interestingly, G17 secured the top rank, followed by G18, G21, and G14, indicating that these are the most desirable and stable genotypes. Additionally, genotypes like G16, G2, G20, G29, G8, and G13 are clustered closely to this circle, suggesting they might have interesting attributes worth exploring in future investigations.

The selected genotypes showed higher average values across all traits, which aligns with our goals. Overall, choosing these genotypes resulted in a favorable selection differential across all traits. The details of this selection differential for the mean of variables and the MTSI scores of the selected genotypes can be found in Tables 4.15.

Sharifi *et al*. (2021) and Koundinya et al. (2021) have previously emphasized the usefulness of the Multi-Trait Stability Index (MTSI) in helping plant breeders select superior genotypes across different traits using data from multiple environments. Similarly, Zuffo *et al.* (2020) used MTSI to identify stable soybean genotypes capable of withstanding drought and salinity stresses. These studies support our findings, highlighting the effectiveness of MTSI in pinpointing top-performing genotypes.

Table 4.15. Prediction of selection differential for studied traits based on MTSI index.

VAR	Factor	Xo	Xs	SD	SD%	h2	SG	SG%	sense	goal
BY	FA 1	32.65	34.12	1.48	4.52	0.86	1.26	3.87	increase	100
FY	FA 1	18.02	18.75	0.73	4.08	0.88	0.65	3.58	increase	100
GY	FA 1	14.65	15.39	0.74	5.04	0.78	0.58	3.95	increase	100
FL	FA 2	21.40	22.17	0.77	3.57	0.76	0.58	2.73	increase	100
FW	FA 2	1.88	2.06	0.18	9.49	0.76	0.14	7.21	increase	100
PDL	FA 2	20.41	19.16	-1.25	-6.15	0.81	-1.02	-5.01	increase	0
NBT	FA 2	3.63	3.60	-0.03	-0.75	0.69	-0.02	-0.51	increase	0
PL	FA 3	13.88	15.43	1.55	11.15	0.84	1.30	9.35	increase	100
DM	FA 4	111.11	112.29	1.17	1.06	0.75	0.88	0.80	increase	100
IW	FA 4	1.80	1.86	0.06	3.09	0.79	0.04	2.43	increase	100
DF	FA 5	71.88	71.95	0.07	0.10	0.70	0.05	0.07	increase	100
PH	FA 5	111.47	113.40	1.92	1.73	0.82	1.59	1.42	increase	100
HI	FA 5	44.91	44.95	0.04	0.10	0.51	0.02	0.05	increase	100

Xo original value, Xs selected value, SD selection differential, SD perc selection differential in percentage, h^2 broad sense heritability, SG selection gain, SG Perc selection gain percentage

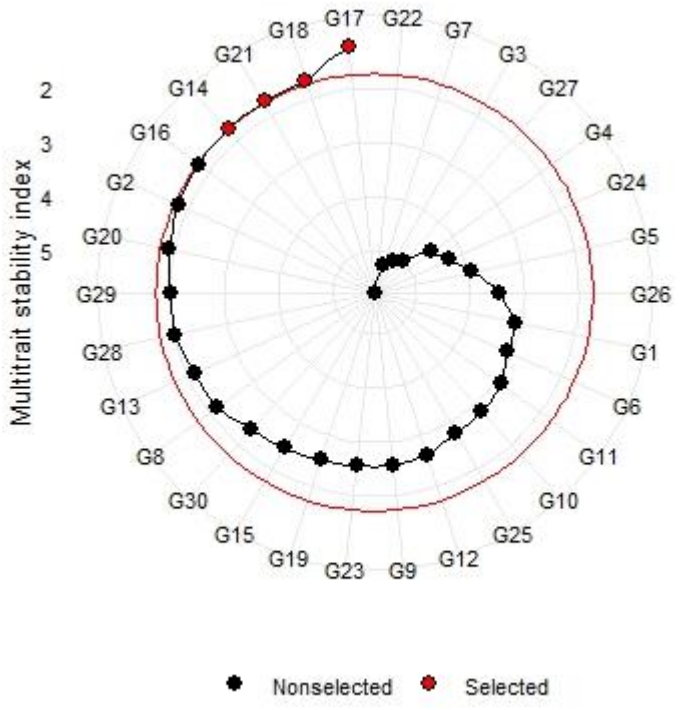

Fig 4.16. Ranking of 30 foxtail millet genotypes in ascending order based on MTSI index.

4.18 Selection of genotypes based on MGIDI index and genetic gain

Table 4.15 shows the MGIDI index values, which indicate how stable the genotypes performed. Out of the 30 genotypes we evaluated, only five of them—G25, G5, G1, G22, and G2—stood out with excellent characteristics, marked as red dots in Figure 4.30. G2, in particular, was very close to the selection cutoff point.

The MGIDI index helped us identify genotypes with the traits we desired. Most traits showed a positive selection gain, which means they were favourable for breeding purposes. However, there was an exception with flag leaf width, which had a negative gain of -7.83per cent. On the positive side, we observed significant gains in traits like fodder yield per plant (19.30 per cent),

biological yield (18.00 per cent), grain yield per plant (12.70 per cent), and panicle length (9.93 per cent). The details of this selection differential for the mean of variables and the MGIDI scores of the selected genotypes can be found in Tables 4.16 and Fig 4.17.

Table 4.16. Prediction of selection differential for studied traits based on MGIDI index.

VAR	Factor	Xo	Xs	SD	SD%	h2	SG	SG%	sense	goal
BY	FA1	32.65	40.59	7.94	24.32	0.74	5.86	17.96	increase	100
HI	FA1	44.91	45.18	0.27	0.59	0.27	0.07	0.16	increase	100
FY	FA1	18.02	22.32	4.30	23.85	0.81	3.48	19.32	increase	100
GY	FA1	14.65	18.04	3.39	23.14	0.55	1.86	12.70	increase	100
DF	FA2	71.88	73.19	1.31	1.82	0.72	0.94	1.31	increase	100
DM	FA2	111.11	113.65	2.54	2.28	0.74	1.88	1.69	increase	100
FW	FA2	1.88	1.66	-0.22	-11.61	0.67	-0.15	-7.83	increase	0
IW	FA2	1.80	1.84	0.04	2.22	0.66	0.03	1.46	increase	100
PH	FA3	111.47	121.17	9.70	8.70	0.75	7.30	6.55	increase	100
PL	FA3	13.88	15.64	1.76	12.70	0.78	1.38	9.93	increase	100
FL	FA4	21.40	22.92	1.51	7.08	0.65	0.98	4.58	increase	100
PDL	FA4	20.41	22.64	2.23	10.94	0.71	1.58	7.76	increase	100
NBT	FA4	3.63	3.74	0.11	3.08	0.41	0.05	1.26	increase	100

Xo original value, Xs selected value, SD selection differential, SD perc selection differential in percentage, h2 broad sense heritability.

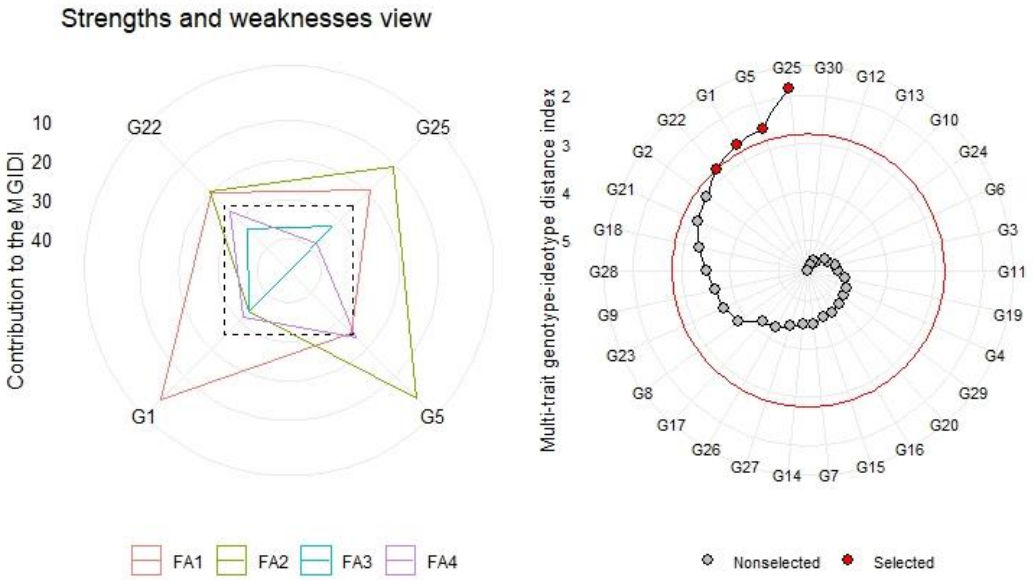

Fig 4.17. Ranking of 30 foxtail millet genotypes in ascending order based on MTSI index.

4.19 Micronutrient analysis

4.19.1 Calcium content

In the realm of genetic diversity, these scores reveal the intriguing spectrum of calcium levels among different genotypes. At the lower end of the scale, we find G30 with a modest calcium score of 0.331 ppm, followed closely by G2 with a score of 0.635 ppm, G17 with a score of 0.747 ppm, G14 with a score of 0.742 ppm, and G20 with a score of 1.041 ppm. These genotypes represent the end of the spectrum where calcium uptake appears to be comparatively limited. On the flip side, the highest calcium accumulators make an appearance in the form of G22 leading the pack with a robust score of 3.161 ppm, closely trailed by G16 with a score of 3.616 ppm, G27 with a score of 2.996 ppm, G21 with a score of 2.549 ppm, and G4 rounding up the top five highest genotypes with a solid score of 2.344 ppm.

4.19.2 Magnesium content

Analyzing the magnesium content in various genotypes provides insight into the diverse levels of this essential mineral. On the lower end of the spectrum, G30 stands out with the lowest magnesium content, measuring at 2.379 parts per million (PPM), followed by G17 at 4.488 PPM, G18 at 10.887 PPM, G2 at 8.15 PPM, and G28 at 13.423 PPM. These genotypes reflect a more constrained magnesium uptake compared to the higher-ranking genotypes. Conversely, at the higher end of magnesium accumulation, G3 commands the top position with an impressive 35.793 PPM, showcasing a robust magnesium presence. G6 follows closely with 27.879 PPM, trailed by G4 at 26.374 PPM, G27 at 27.539 PPM, and G22 at 24.196 PPM. These genotypes exhibit a remarkable capacity for magnesium absorption, shedding light on the genetic factors influencing mineral uptake in plants.

4.19.3 Iron content

Examining the iron content across various genotypes sheds light on the diversity of this vital mineral. At the lower end of the spectrum, G30 emerges with the lowest iron content at a mere 0.329 parts per million (PPM). Following closely, G21 showcases a modest iron presence at 1.433 PPM, while G25 and G11 stand at 1.367 PPM and 1.913 PPM respectively, highlighting their relatively lower iron absorption. G15 also falls into this category with an iron content of 1.753 PPM. On the flip side, the genotypes with the highest iron accumulation are particularly noteworthy. G3 takes the lead with a substantial iron content of 26.16 PPM, signifying a robust iron absorption capacity. G23 follows closely with 7.972 PPM, displaying a notable iron presence, while G8 and G7 exhibit iron contents of 12.373 PPM and 8.101 PPM respectively. G16 rounds up the top five highest genotypes with a respectable iron content of 6.121 PPM.

4.19.4 Zinc content

Analyzing the zinc content within various genotypes unveils a notable variance in this essential mineral. At the lower end of the spectrum, G30 exhibits the lowest zinc content at a mere 0.076 parts per million (PPM), underscoring a limited zinc absorption capacity. Following suit, G17 presents a slightly higher zinc content at 0.242 PPM, while G26, G24, and G20 demonstrate zinc levels of 0.454 PPM, 0.544 PPM, and 0.614 PPM, respectively. These genotypes depict a trend of lower zinc absorption. Conversely, at the higher end of zinc accumulation, G16 takes the lead with a substantial zinc content of 7.851 PPM, showcasing a robust zinc uptake. G18 closely follows with 3.167 PPM, demonstrating a notable zinc presence, while G23 and G5 exhibit zinc contents of 2.591 PPM and 1.256 PPM, respectively. G1 rounds up the top five highest genotypes with a respectable zinc content of 1.107 PPM.

4.19.5 Protein content

Analyzing the protein content across different genotypes provides valuable insights into their nutritional composition. On the lower end of the spectrum, G4 stands out with the lowest protein content at 0.25 grams per 100 grams (g/100g), emphasizing a relatively lower protein composition. Following closely, G11 and G19 both display slightly higher protein content at 0.26 g/100g, while G13 and G8 show protein levels of 0.28 g/100g and 0.29 g/100g respectively. These genotypes depict a trend of lower protein concentration. Conversely, at the higher end of protein accumulation, G2 and G17 take the lead with a substantial protein content substantial protein content of 0.42 g/100g, showcasing robust protein levels. G3 followsclosely at 0.41 g/100g, highlighting a notable protein presence, while G6 and G7 exhibitprotein contents of 0.35 g/100g and 0.38 g/100g respectively.

Table 4.17 Micro nutrient compounds

	ca	Mg	Fe	Zn	Protein
G1	1.922	14.703	4.236	1.107	0.360
G2	0.635	8.150	2.265	1.078	0.420
G3	1.088	35.793	26.160	0.856	0.410
G4	2.344	26.374	4.106	0.698	0.250
G5	1.183	18.188	2.709	1.256	0.370
G6	1.209	27.879	4.747	0.894	0.350
G7	1.071	18.822	8.101	0.728	0.380
G8	2.068	23.387	12.373	1.008	0.290
G9	1.217	19.524	2.947	0.900	0.350
G10	1.988	23.844	4.038	0.689	0.370
G11	1.390	15.194	1.913	0.618	0.260
G12	1.423	18.290	2.820	0.647	0.340
G13	1.126	19.019	3.544	0.658	0.280
G14	0.742	14.730	3.069	0.788	0.340
G15	1.819	18.300	1.753	1.011	0.290
G16	3.616	23.793	6.121	7.851	0.410
G17	0.747	4.488	3.250	0.242	0.420
G18	1.206	10.887	2.064	3.167	0.340
G19	1.329	16.544	2.526	0.736	0.280
G20	1.041	18.576	1.433	0.614	0.370
G21	2.549	21.662	1.508	0.666	0.340

G22	3.161	24.196	3.606	0.716	0.360
G23	2.317	20.629	7.972	2.591	0.340
G24	1.266	14.222	3.003	0.544	0.320
G25	1.626	17.935	1.367	0.628	0.330
G26	1.958	14.736	2.462	0.454	0.380
G27	2.996	27.539	1.586	0.817	0.340
G28	1.107	13.423	1.562	0.588	0.370
G29	1.807	15.250	2.873	0.812	0.360
G30	0.331	2.379	0.329	0.076	0.380

ca= Calcium content, Mg= Magnesium content, Fe= Iron content, Zn= Zinc content

DISCUSSION

Foxtail millet (*Setaria italica*) is an important cereal crop, particularly in regions with challenging environmental conditions like Nagaland, India. Understanding the role of genetic variability, genetic diversity, AMMI analysis, GGE Biplot study, and BLUPs (Best Linear Unbiased Predictors) in foxtail millet can greatly benefit agricultural research and production in this ecosystem.

Nagaland's climate and topography are diverse, ranging from sub-tropical to temperate, and there is substantial variation in soil types. Understanding genotype-environment interactions through AMMI and GGE Biplot studies is essential for selecting adaptable varieties. Foxtail millet is a staple crop in Nagaland, and genetic diversity can help develop varieties with improved resilience to pests, diseases, and changing climate conditions.BLUPs can optimize breeding efforts, ensuring that the foxtail millet varieties developed are not only high-yielding but also well-suited to the specific needs of farmers in the region.

In conclusion, the role of genetic variability, genetic diversity, AMMI analysis, GGE Biplot study, and BLUPs in under this study provide information about foxtail millet research in Nagaland's ecosystem is vital for improving agricultural productivity, sustainability, and food security in this region with its unique and challenging environmental conditions. These tools and techniques enable researchers and breeders to make informed decisions to develop and deploy foxtail millet varieties that can thrive in this diverse ecosystem.

Assess the variation and mean performance of yield and yield components.

There was significant variation observed in the pooled analysis of variance for the 14 traits across the 30 foxtail millet genotypes in the four environments. This information provides valuable insights for breeders to make informed decisions

on genotype selection, trait prioritization, and targeted breeding strategies. The aim is to develop foxtail millet varieties with improved performance, stability, and adaptability across different environments. Among the yield traits, the coefficient of variation (CV) ranged from flag leaf width (17.21) to test weight (2.23). Ataei *et al.* (2020) conducted a combined analysis of variance for measured traits in six foxtail millet genotypes across 12 different environments. They observed highly significant main effects of the environment and significant genotype by environment interaction effects ($p < 0.01$) for all studied traits. Zhang *et al.* (2023) reported significant effects of genotype (G), environment (E), and their interaction (G×E) based on AMMI ANOVA ($p < 0.01$) for 12 foxtail millet cultivars grown in eight different environments. Sanjana Reddy *et al.* (2021) conducted a combined analysis of variance across environments and found highly significant differences among genotypes for all recorded traits in foxtail millet. Ataei *et al.* (2020) reported the coefficient of variation (CV) for six foxtail millet genotypes across 12 different environments. The CV ranged from 0.05 for days to flowering to 0.14 for seed yield. In this research, significant divergence was observed among genotype-environment interactions and genotype effects. This indicated the presence of diverse environments with different genotypes and high yield potential. Genotype-environment interaction (GEI) in a wide range of environmental trials can be categorized into two types: crossover and non-crossover interactions. Non-crossover interaction represents consistent yield performance of tested accessions across multiple environments, while crossover interaction signifies changes in genotype rankings across diverse environments. Plant breeders can select specific genotypes for particular environments or choose adaptable genotypes for diverse environmental conditions when predictable components influence GEI (Dehghani *et al.* 2006). However, when GEI is influenced by unpredictable factors, it becomes essential to develop stable

genotypes that consistently perform well across multiple environments (Kang *et al.* 1991). To better understand and interpret GEI, analyzing yield stability across various locations and seasons can enhance reproducibility and heritability of evaluated traits Becker and Leon(1988).

Variance component analysis

According to Sivasubramanian and Madhavamenon (1973), when the values range from 0 to 10%, the proportion of GCV and PCV is considered low. When the values range from 10 to 20%, it is considered moderate, and when the values go over 20%, it is considered high. However, the coefficient of variation is more reliable when comparing trials, as it is not affected by the measurement unit. In this experiment, the phenotypic variance values for all traits are higher than the genotypic variance. Similar to previous studies by Ayesha *et al.* (2019) abd Sharma *et al.* (2018), it suggests that trait expression is influenced by the environment. Understanding the variability in yield traits is crucial for plant breeders. Traits with low variability provide stability and predictability, aiding effective breeding planning. Traits with medium variability require careful monitoring and management for optimal performance. Traits with high variability offer opportunities for selection and breeding, as well as the need for adaptable management practices to maximize productivity. By considering the variability of these traits, researchers, and breeders can make informed decisions regarding crop selection, breeding strategies, and agricultural management practices. This knowledge can contribute to the development of resilient and high-yielding crop varieties.

Heritability percentage indicates how much a trait is influenced by genetics. According to Johnson *et al.* (1955), low heritability is between 0 and 30%, moderate heritability is between 30 and 60%, and high heritability is above 60%.

Breeders can use high heritability traits to select superior genotypes based on observable characteristics. On the other hand, low heritability suggests that environmental factors have a greater impact on the trait, making selection based on such traits futile. Emphasized that high heritability does not always lead to higher genetic advancements. Therefore, heritability should be considered along with genetic advancement for more reliable outcomes. Genetic advance ranges from modest (0-10%) to moderate (10-20%) and high (>20%). In our study, yield components showed moderate to high heritability and genetic advance, except for days to flowering and days to maturity, indicating medium to high environmental influences on these traits. Similar observations were reported by Kumar *et al.* (2015), Kavya *et al.* (2017), and Nandini *et al.* (2016). Understanding the heritability of these yield traits is crucial for effective breeding and selection strategies. High heritability traits allow targeted genetic improvements, while medium heritability traits require a balanced approach considering both genetics and environment. Low heritability traits may benefit from specific management practices to optimize their performance under certain environmental conditions.

Correlation co-efficient

It is important to identify traits that are strongly and positively correlated when selecting genotypes. Emphasize the significance of understanding trait variation and inter-correlations for successful selection in crop improvement. In this study, significant positive associations were found between grain yield per plant and traits such as days to 50% flowering, days to maturity, plant height, panicle length, flag leaf length, peduncle length, biological yield, and fodder yield per plant at both genotypic and phenotypic levels. Traits like number of basal tillers and panicle width showed positive associations only at the phenotypic level. Similar findings were reported by Ayesha *et al.* (2019) and Amarnath *et al.*

(2018). Total tiller numbers per plant positively correlated with grain yield per plant at the phenotypic level, as higher tiller numbers contribute directly to yield by providing more stalks. While most of field conditions this trait performance purely depends on agronomic practices. Flag leaf area showed a positive association with grain yield per plant, possibly due to increased assimilates accumulation from a larger photosynthetic area, as supported by Jyothsna *et al.* (2016). Panicle length and width were also positively associated with grain yield per plant, as larger panicles result in more grains, contributing directly to yield, as supported by Kavya *et al.* (2017). Days to flowering and maturity directly affects the grain yields per plant because they influence the plant's reproductive phase and overall growth cycle. This has been supported by Tyagi *et al.* (2011). Early flowering and shorter maturity duration lead to a longer grain-filling period, resulting in improved grain development and higher grain yield per plant. Therefore, differences in the timing of flowering and maturity can greatly impact the final grain yield, as also supported by Kavya *et al.* (2017).

Path coefficient

By employing path coefficient analysis, it was possible to uncover both the direct and indirect effects of each component on grain yield. This approach revealed nuances that were not apparent through traditional correlation analysis, highlighting the significance of a comprehensive and multi-dimensional perspective in understanding yield and its component traits. The results indicated that the examined components, including biological yield, harvest index, flag leaf width, and number of basal tillers, had substantial direct effects on grain yield per plant at both the genotypic and phenotypic levels. These findings present promising avenues for the development of effective selection indices aimed at enhancing foxtail millet yield. Earlier studies by Sapkal *et al.* (2019), Ayesha *et*

al. (2019), Amarnath *et al.* (2018), Kavya *et al.* (2017c), Karvar *et al.* (2021), and Jyothsna *et al.* (2016) found that specific traits like days to flowering, number of tillers, ear head length, finger number, panicle length, test weight, plant height, flag leaf blade length, and 1000-grain weight have positive direct effects on grain yield in foxtail millet. These findings provide valuable information for selecting high-yielding genotypes and improving grain yield through breeding programs.

Genetic Diversity by Mahalanobis' D^2 Statistic

Mahalanobis' D^2 statistics, also known as Mahalanobis Distance, measures the distance between a data point and a cluster of data points in a multivariate space. It considers both the mean and covariance of the data, enabling the assessment of similarity or dissimilarity between a data point and a cluster based on multiple variables at once. This powerful tool finds applications in plant breeding, including identifying similar genotypes, selecting diverse parental lines, evaluating germplasm performance, and developing improved crop varieties with desirable traits for enhanced productivity and sustainability (Yogeesh *et al*. 2015).

In this study, Mahalanobis' D^2 Statistic was utilized to group the genotypes into clusters, considering their similarities and differences in various traits across four environmental datasets and pooled data as well. In the first environment, 30 genotypes were grouped into nine clusters based on their similarities using the Tocher method. Similarly, in environment-2, the genotypes were clustered into six clusters, in environment-3, they formed seven clusters, in environmental-4, they were categorized into ten clusters, and in the pooled environmental combination, they resulted in five clusters. Mahalanobis' D^2 Statistic was employed to facilitate the clustering process, taking into account the multivariate traits and their respective distances to establish meaningful groupings (Gangurde *et al*. 2016).

The observed variation in the number of clusters across environments can be attributed to the influence of different environmental conditions on the expression of traits in the genotypes. Environmental factors such as temperature, humidity, soil type, and photoperiod can significantly impact the phenotypic expression of traits in plants. As a result, genotypes that exhibit similar trait profiles in one environment may show different trait patterns in another environment, leading to the formation of distinct clusters.

This variability in clustering indicates that certain genotypes may perform better in specific environmental conditions, while others may be more adaptable and perform consistently across diverse environments. Understanding how genotypes respond to different environments is crucial for plant breeding and crop improvement. It allows breeders to identify genotypes with broad adaptability and stability across multiple environments, as well as those with specific strengths in particular conditions.

Various studies have utilized Mahalanobis' D2 statistics to assess genetic diversity in different crop species under diverse environmental conditions. Shinde *et al.* (2013) estimated the genetic distance for 41 finger millet genotypes from various geographical areas and found that they could be grouped into seven clusters using D^2 statistics. Swamynatham *et al.* (2020) utilized D^2 clustering to group genotypes into sixteen clusters. Additionally, Singh *et al.* (2020) distributed 22 rice genotypes into six clusters using D^2analysis. These studies demonstrate the versatility and significance of Mahalanobis' D2 statistics in assessing genetic diversity and clustering genotypes based on multiple traits, providing valuable insights for crop breeding and improvement programs.

Cluster distance in Mahalanobis' D^2 Statistic refers to the distance between clusters of data points in a multivariate space. It measures the dissimilarity or

similarity between different groups of data points based on their mean vectors and covariance matrices. The cluster distance helps to identify how distinct or similar the clusters are, providing insights into the genetic divergence or similarity between groups of genotypes in plant breeding. Inter-cluster distance quantifies the dissimilarity between different groups of genotypes, while intra-cluster distance measures the variability or spread of data points within each cluster.

In the four environments studied, the foxtail millet genotypes showed varying intra-cluster distances. Cluster-VI exhibited the highest intra-cluster distance (14.26) in Environmental-1. In Environmental-2, cluster-III had the highest intra-cluster distance (12.31). In Environmental-3, cluster-I exhibited the highest intra-cluster distance (14.25) among all clusters. In Environmental-4, cluster-I had the highest intra-cluster distance (8.13), while the pooled environmental analysis, Cluster-I had the highest intra-cluster distance (8.13).

Parental selection is a crucial step in plant breeding, aiming to identify diverse and superior genotypes for hybridization. In Environmental-1, Cluster-VI with five genotypes and Cluster-III in Environmental-2 with six genotypes have the highest intra-cluster distances (14.26 and 12.31, respectively). Similarly, in Environmental-3, 4, and the pooled combination, Cluster-I with 24, 18, and 26 genotypes, respectively, exhibits the highest intra-cluster distances. These findings indicate that the genotypes within these clusters possess greater genetic diversity, encompassing a broader range of desirable traits. Opting for parents from these clusters can significantly increase the likelihood of producing hybrid progeny with enhanced performance and adaptability in breeding programs. Variety development aims to create new cultivars with specific traits. Selection of these clusters have heights inter cluster distance respective environmental, suggesting a considerable genetic variation within this cluster. Selecting

genotypes from this cluster for breeding programs can help in developing diverse and distinct varieties with a broader range of traits and Utilizing parents from this cluster in hybridization can lead to increased heterozygosity and potentially improved performance in the hybrid offspring. The selection of clusters for different breeding purposes is driven by the genetic diversity and variation observed within the clusters. Clusters with higher intra-cluster distances offer more genetic divergence, making them suitable for parental selection, hybridization, and crop improvement strategies, while clusters with unique traits are preferred for variety development to create distinct and specialized cultivars. By strategically choosing clusters based on their genetic characteristics, plant breeders can optimize their breeding programs to develop improved and resilient foxtail millet varieties to meet various agricultural challenges.

The inter-cluster distances provide insights into the genetic relationships and relatedness among clusters. Larger inter-cluster distances suggest greater dissimilarity and differentiation between clusters, indicating distinct and genetically diverse groups. On the other hand, smaller inter-cluster distances suggest closer genetic relationships and similarities between clusters, possibly sharing common traits or ancestry.

The differences in inter-cluster distances among the environments can be attributed to variations in the genetic makeup and traits of the foxtail millet genotypes in each environment. Environmental conditions, such as soil type, climate, and management practices, can lead to diverse genetic expressions in different locations, resulting in distinct cluster formations. In this environment-1, the inter-cluster distances range from 35.09 to 11.25. Clusters VIII and IX have the highest inter-cluster distance (35.09), followed by clusters VII and IX (34.99), indicating significant genetic differentiation between these clusters. The presence

of diverse genotypes from different geographical regions in this environment might contribute to the significant genetic differentiation observed between clusters. Foxtail millet genotypes adapted to diverse geographical conditions might have distinct traits, resulting in the formation of genetically dissimilar clusters.

Environmental-2: The inter-cluster distances in this environment range from 22.94 to 11.71. Clusters III and IV display the maximum inter-cluster distance (22.94), followed by clusters II and V (21.72). The genotypes in this environment may have some level of geographical overlap with those in Environmental-1, leading to some similarity in cluster patterns. However, the different environmental conditions still contribute to variations in genetic relationships among clusters. Environmental-3: Inter-cluster distances in this environment vary from 25.56 to 10.59. Cluster I and VII exhibit the highest inter-cluster distance (25.56), followed by clusters VI and VII (25.00). Similar to Environmental-2, there might be some geographical overlap with previous environments, but unique environmental factors lead to distinctive genetic relationships and cluster formations. Environmental-4: The inter-cluster distances in this environment range from 21.35 to 6.46. Cluster II and X have the maximum inter-cluster distance (21.35), followed by clusters V and X (20.61). The genotypes in Environmental-4 may have their unique geographical origins and adaptations, contributing to differences in cluster formations and genetic relationships. Pooled Environmental Analysis: The inter-cluster distances in this analysis range from 8.75 to 6.01. Cluster III and V exhibit the highest inter-cluster distance (8.75). The pooled analysis includes genotypes from various geographical regions and environmental conditions. As a result, the pooled data may show smaller inter-cluster distances compared to some individual environments due to the broader representation of genotypes.

In summary, geographical distribution plays a significant role in shaping the genetic diversity and relationships among foxtail millet genotypes in different environments. Geographical factors can lead to the presence of distinct genotypes with specific adaptations, resulting in diverse cluster formations and inter-cluster distances. The environmental conditions in each specific region further influence the genetic expression of these genotypes, leading to variations in intra-cluster distances as well. By considering the geographical distribution and environmental factors, researchers and breeders can better understand the genetic relationships among foxtail millet genotypes and make informed decisions for crop improvement and breeding programs tailored to specific regions and environments.

Several studies have assessed genetic divergence in various millet genotypes using Mahalanobis' D2 statistic. Cluster III in foxtail millet (Ayesha and Babu, 2019), Clusters II and IX in Indian Italian millet (Amarnath *et al*. 2019), and Clusters IV and V in little millet Suryanarayana and Sekhar(2018) displayed the highest inter-cluster distances, indicating significant genetic diversity. These clusters are suitable for inter-varietal hybridization to obtain desirable recombinants. Additionally, clusters with high intra-cluster distances, such as Cluster I in foxtail millet (Thippeswamy *et al*. 2018), Cluster VIII in finger millet (Devaliya *et al*. 2017), and Cluster II in foxtail millet (Gangurde *et al*. 2016), offer diverse genotypes within the cluster and are potential candidates for hybridization to enhance yield and performance.Kumari and Singh (2015) grouped 35 finger millet genotypes into six clusters using Tocher's method. Cluster IV exhibited the highest intra-cluster distance, followed by cluster II and cluster I, indicating genetic variations within these clusters. Clusters IV and VI showed the maximum inter-cluster distance, highlighting their high genetic diversity.

In Mahalanobis' D2 Statistic, the percentage contribution to genetic diversity is represented by the eigenvalues associated with the principal components used in the analysis (Do Rego *et al*. 2003). The eigenvalues provide information about the amount of variance explained by each principal component. When conducting cluster analysis using Mahalanobis' D2 Statistic, the data is transformed into a multidimensional space, and the first few principal components are selected to represent the most significant sources of variation in the data (Babnik *et al*. 2008). The eigenvalues associated with these principal components indicate the proportion of total variance explained by each component. These percentages represent how much of the total genetic diversity in the data is attributed to each principal component. The higher the percentage contribution of a component, the more important it is in explaining the genetic variation among the genotypes (Rao,1964). Understanding the percentage contributions helps researchers prioritize the most influential components and focus on the key sources of genetic diversity in their analysis.

In this study, in Environmental-1 plant height is dominance of contributing to genetic divergence may indicate its strong influence on the overall variability observed in this environment.In Environmental-2, test weight played the most significant role in the total genetic divergence (31.03%), being ranked first 135 times. In Environmental-3, test weight had the highest contribution to the total genetic divergence (53.56%), ranked first 233 times. In Environmental-4, test weight had the greatest contribution to the total genetic divergence (36.78%), ranked first 160 times. In the pooled environmental analysis, test weight showed the highest contribution to the total genetic divergence (22.30%), ranked first 97 times.

Test weight consistently emerged as a significant contributor to genetic divergence in all environments, indicating its importance in shaping the observed variability. Other traits such as days to flowering, days to maturity, and plant height also played crucial roles in certain environments, emphasizing their impact on the overall genetic diversity. Understanding the reasons behind the diversity of these traits provides valuable insights for crop improvement strategies and targeted breeding efforts to develop foxtail millet varieties with desirable traits and enhanced adaptability in diverse environmental conditions.

Kumari and Singh (2015) reported those days to 50% flowering, days to maturity, and grain yield per plant played the most significant roles in genetic divergence, indicating potential for improvement in these traits. Yogeesh *et al.* (2015) observed that seed yield exhibited greater diversity compared to days to 50% flowering, plant height, and length of inflorescence. Sao et al. (2016) identified days to maturity and days to 50% flowering as the major contributors to genetic divergence. Singh *et al.* (2016) reported that inflorescence length, flag leaf blade length, basal tillers number, and panicle exertion had the most significant influence on genetic divergence, suggesting scope for improvement in these characteristics. Devaliya *et al.* (2017) found that iron content contributed the most to genetic divergence, followed by main ear head length, harvest index, test weight, and number of productive tillers per plant, while calcium content, days to maturity, grain yield per plant, and straw yield per plant had low contributions to divergence. Suryanarayana and Sekhar (2018) observed that grain yield, days to 50% flowering, and plant height were the primary contributors to total divergence. Thippeswamy *et al.* (2018) reported that the number of tillers per meter row length and 1000 seed weight made the highest contributions to divergence. Amarnath *et al.* (2019) found that culm branches followed by 1000

grain weight contributed the most to total divergence, suggesting the feasibility of improvement through these traits.

AMMI analysis

AMMI, which stands for Additive Main Effects and Multiplicative Interaction, is a statistical method used for analyzing data from multi-environment trials (METs) in agricultural research. It helps to understand how different crop varieties interact with their environments, aiding in the selection of stable and adaptable cultivars. AMMI is valuable for optimizing resource allocation, guiding hybridization, accelerating breeding, and improving traits to meet market demands.

The analysis of variance conducted within the AMMI model yielded several notable insights. First and foremost, it became evident that environmental factors exerted a substantial influence on the studied traits, accounting for a significant portion of the observed variability. Remarkably, replicated environments showed minimal impact on the traits, implying a remarkable consistency in the performance of genotypes across diverse settings. Genotypes themselves emerged as pivotal contributors to the observed variance, underscoring their critical role in shaping the traits under study. Furthermore, the interaction between genotype and environment demonstrated a significant influence on trait variability, emphasizing the need to consider this intricate relationship in crop breeding and management. Lastly, the relatively modest contribution of residuals to variability highlighted the effectiveness of the AMMI model in explaining the observed data. The AMMI model simplifies the genotype-environment interaction into three main components: PC1, PC2, and PC3. PC1 had the most significant influence, explaining the majority of the variation in the traits. PC2 and PC3 also contributed to the variance but to a lesser extent.

To build the most accurate AMMI model, it's common to use the first two PCAs according to Gauch and Kang (1996). Additional interaction principal components mostly contained irrelevant information and did not aid in predicting validation observations (Mekonnen & Mohammed, 2010). Therefore, the interaction between the 30 genotypes and 4 environments in this study was forecasted using the first two principal components of genotypes and environments. The model effectively explained the genotype × environment interaction. Similar studies reported by Ghazvini et al. (2018) documented that the primary and secondary Principal Components (PCs) of the GEI contributed 49.49% and 22.50%, respectively, combining to account for 71.60% of the GEI's variability. Kilic, (2014) reported IPCA 1 captured 40.42% of the interaction variation in 17.85% of the degrees of freedom. IPCA 2 explained an additional 20.66% of GEI variation. Both IPCA 1 and IPCA 2 were highly significant ($P < 0.01$) and together contributed to 61.07% of the total GEI. Hagos and Abay (2013) reported Combined, the first and second IPCAs accounted for 85.77% of the grain yield variability in the ten tested genotypes across five locations.

In the context of this study and its AMMI Biplot-1, IPCA values near zero signify significant stability with minimal Genotype by Environment Interaction (GEI) interaction. Several traits and genotypes in the study displayed this desirable trait of stability. Genotypes such as G14, G23, G16, and G9 in Days to 50% flowering (DF), G3, G1, and G13 in Days to Maturity (DM), G18 and G30 in Plant Height (PH), G14 and G25 in Panicle Length (PL), G12, G17, and G18 in Flag Leaf Width (FW), G24 and G28 in Peduncle Length (PDL), G18, G16, and G25 in No. of Tillers per Plant (NT), G13 and G18 in Panicle Width (PW), G18, G17, and G5 in Biological Yield (BY), G28 and G1 in Harvest Index (HI), G21 and G13 in Test Weight (TW), G13, G17, and G18 in Fodder Yield (FY), and G8, G9, G21,

and G22 in Grain Yield (GY) demonstrated significant stability with minimal GEI interaction.

This is a valuable finding for plant breeding and agriculture, as these genotypes and traits can provide reliable and consistent performance across various environmental conditions. Farmers and breeders can prioritize these stable genotypes to ensure more predictable and higher yields. This study highlights the importance of stability as a desirable trait in crop genotypes, as it helps mitigate the risks associated with varying environmental factors. By focusing on the identified stable genotypes, agricultural practices can be optimized for greater productivity and efficiency.

WAAS and BLUPs

Genotypes with WAAS values close to zero are considered the most stable. For instance, in DF: G12, G6, G21, G9, G4, and G18, DM:G6, G3, G15, and G24, PH: G15 and G27, PL:G9, G12, G29, G2, and G28, FL: G11, FW:G11, G6, G7, and G20, PDL: G10 and G6, NT: G17, G1, G4, and G5, PW: G7, G5, G20, and G22, BY:G7, G9, G19, G20, and G22, HI:G5, G16, and G22, FY: G20, G5, G10, and G19, TW: G26, G24, G6, and G3 and GY:G10, G15, G13, G6, G7, and G8 exhibit low GEI (Genotype-Environment Interaction) and high stability.

The likelihood ratio test showed highly significant effects ($p < 0.05$) for both genotype and interaction in this experiment for all traits. This significance of genotype-environment interaction (GEI) indicates that different genotypes respond differently in different environments, each having its own strengths and weaknesses. Therefore, in such situations, using the BLUP method can lead to better and more reliable results (Taleghani *et al.* 2023).

Similar findings were reported by several studies. Munda *et al.* (2023) identified stable genotypes in Curcuma by analyzing BLUPs& WAAS values associated with yield and yield traits. Koundinya *et al.* (2021) similarly reported the identification of stable genotypes in cassava using BLUPs& WAAS values, focusing on yield and yield traits. Taleghani *et al.* (2023) also reported the identification of stable genotypes in sugar beet based on BLUPs& WAAS values correlated with root traits. Furthermore, Rajabi *et al.* (2023) identified stable genotypes in sugar beet with a specific focus on root traits through BLUPs& WAAS values analysis. Additionally, Mishra et al. (2023) reported the identification of stable Valepotriate Specific Valerian Chemotypes using BLUPs& WAAS.

The mean v_s stability biplots revels, (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 ideal genotypes at respective traits.Ranking genotypes biplots revels, G3 in DF, G1 and G18 in DM, G1in 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 arepositioned at the center of the concentric circles, is an ideal genotype due to its higher yield and stability compared to the other genotypes.A previously similar study was conducted in yield and yield related traits in different crops, and significant results are reported by Sharma *et al.* (2020) in melon, Kendal *et al.* (2016) in triticale, and Kendal e*t al.* (2019) in barley.

SUMMARY AND CONCLUSION

SUMMARY AND CONCLUSIONS

The present study entitled “Stability and Genetic Diversity Analyses in Foxtail Millet [*Setaria italica* (L.) P. Beauv.] Genotypes” was carried out at the experimental farm (Genetics and Plant Breeding) of School of Agricultural Sciences (SAS), Medziphema Campus, Nagaland, from the *Zaid* season of 2022 to the *Rabi* season of 2023. The study was conducted in four different Environment conditions, with variations in sowing dates, and aimed to achieve the following objectives:

1. Preliminary screening of genotypes for genetic variation.
2. To estimate genetic variation and genetic diversity among selected genotypes.
3. To evaluate the genotype × environment interaction using AMMI and GGE biplot for stability of foxtail millet genotypes.
4. To estimate BLUPs for identification of superior genotypes.

We obtained a collection of one hundred foxtail millet germplasm including four check verities, from the Indian Institute of Millets Research (IIMR), Hyderabad. These samples were evaluated during the *Zaid* season in 2022. Based on the results of this evaluation, we identified the top 30 (29+1 check) genotypes that showed the highest grain yield in foothills of Nagaland. These 30 selected genotypes were used in our study to assess genetic variability, diversity, and stability across different environments in foot hills of Nagaland region.

The experiment was conducted using randomized complete block design (RCBD) with three replications at all environments. RCBD was chosen because the fertility of the experimental sites varied. Each replication consisted

of 30 plots or beds, each measuring 1 meter by 1 meter. There was a gap of 10 centimeters between each bed, and the spacing between individual plants within a bed was 10 centimeters. The distance between rows was 22.5 centimeters. The replications were separated from each other by a distance of 30 centimeters. The total size of the experimental plot was 30 meters by 5 meters, with 30 centimeters of space before the first replication and 30 centimeters of space after the third replication. In total, there were 90 beds across all environments. Throughout the experiment, recommended agricultural practices were followed.

The observations were recorded on 14 quantitative characters based on descriptions and guidelines provided by PPV&FR, 2001 (DUS). For each character, data were gathered from five randomly sampled plants within each genotype and replication. The observations were recorded on 1) Days to 50 per cent flowering (DF), 2) Days to maturity (DM), 3) Plant height (PH), 4) Panicle length (PL), 5) Flag leaf length (FL), 6) Flag leaf width (FW), 7) Peduncle length (PDL), 8) Total tiller numbers per plant (NT), 9) Panicle width (PW), 10) Biological yield (BY), 11) Harvest index (HI), 12) Test weight(TW), 13) Fodder yield per plant (FY) and 14) Grain yield/plant (GY).The measurements for biological yield, harvest index, test weight, fodder yield per plant, and grain yield per plant were verified in the laboratory after the harvest, while the remaining traits were measured directly in the field.

The pooled analysis of variance (ANOVA) was used to examine the interactions between different genotypes and environments. 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 ($p \leq 0.05$) in terms of the environment, genotype, and genotype-environment interaction.

Among the different genotypes G17 recorded the lowest number of days to reach 50 percent flowering (64.57) while G3 had the highest (79.58) across all environments. The grand mean value for this trait was 71.88 with a coefficient of variation (CV) of 5.08 %. G8 exhibited the lowest number of days to maturity (101.00) while G1 had the highest (122.99) with a grand mean value of 111.11 and a CV of 3.88 %. G15 had the shortest plant height (87.53 cm) while G1 had the tallest (133.60 cm) with a grand mean value of 111.47 cm and a CV of 9.30 %. G11 had the shortest panicle length (8.29 cm) while G25 had the longest (20.13cm) with a grand mean value of 13.88 cm and a CV of 15.69 %. G30 had the shortest flag leaf length (16.73cm) while G5 had the longest (25.47cm) with a grand mean value of 21.40 cm and a CV of 8.80 %. G26 had the narrowest flag leaf width (2.54 cm) while G3 had the widest (1.30cm) with a grand mean value of 1.88 cm and a CV of 17.21 %. G12 had the shortest peduncle length (15.12cm) while G8 had the longest (26.01cm) with a grand mean value of 20.41cm and a CV of 11.33 %. G29 had the lowest number of basal tillers (4.62) while G24 had the highest (2.84) with a grand mean value of 3.63 and a CV of 11.11 %. G24 had the lowest biological yield (21.75g) while G1 had the highest (46.04g) with a grand mean value of 32.64 g and a CV of 12.18 %. G3 had the lowest harvest index (40.43 %) while G20 had the highest (51.39 %) with a grand mean value of 44.91 % and a CV of 7.66 %. G24 had the lowest fodder yield per plant (10.97g) while G1 had the highest (25.91g) with a grand mean value of 18.02g and a CV of 12.52 %. G30 had the lowest test weight (2.52g) while G2 had the highest (3.17g) with a grand mean value of 2.79 g and a CV of 2.23%. G24 had the lowest grain yield per plant (10.78g) while G1 had the highest (20.14g) with a grand mean value of 14.65g and a CV of 14.28%. Based on the mean performance across all traits, G1 exhibited the best overall performance among the evaluated genotypes.

In this experiment, some traits exhibited low variability (<10%), indicating consistent and stable performance. These traits, such as "days to 50% flowering" (GCV: 3.89, PCV: 4.65), "days to maturity" (GCV: 3.39, PCV: 3.90), "harvest index" (GCV: 3.93, PCV: 5.49), "flag leaf length"(GCV: 7.92, PCV: 9.06), "test weight" (GCV: 6.13, PCV: 6.23), and "Number of basal tillers" (GCV:8.21, PCV: 9.91), consistently reached their respective developmental stages within a narrow range of time. On the other hand, several traits demonstrated moderate variability (10-20%), indicating moderate fluctuations in their measurements. Traits such as "plant height" (GCV: 10.06, PCV: 11.09), "peduncle length" (GCV: 11.87, PCV: 13.16), "panicle width" (GCV: 13.90, PCV: 15.69), "grain yield per plant" (GCV: 13.56, PCV: 15.33), "biological yield" (GCV: 14.85, PCV: 16.05), "flag leaf width" (GCV: 15.35, PCV: 17.60), "fodder yield per plant" (GCV: 16.80, PCV: 17.93), and "panicle length" (GCV: 17.85, PCV: 19.50) exhibited slight variations but generally remain within an acceptable range.

Heritability, expressed as a percentage, provides valuable information about the degree to which genetic factors contribute to the variation of a trait. Test weight (96.80%) exhibited high heritability, meaning that genetics largely determine the weight of the grains. Similarly, "Fodder yield per plant" (87.80%), “grain yield per plant” (78.30%), and "Biological yield" (85.60%) also have high heritability, suggesting that genetic factors significantly contribute to the crop's yield potential. "Plant height" (82.40%), "Panicle length" (83.80%), "Flag leaf length" (76.40%), "Flag leaf width" (76.10%), "Peduncle length" (81.40%), days to 50% flowering (70.10%), days to maturity (75.30%), panicle width (78.50%), and number of basal tillers (68.60%) also demonstrated high heritability. On the other hand, traits with medium heritability are influenced more by Environment factors than genetic factors. "Harvest index" (51.30%) was medium heritability, indicating that

variations in this trait are primarily influenced by non-genetic factors such as management practices and Environment conditions.

The genetic advance of yield traits provides valuable information about the potential for improvement through breeding efforts. Traits with high genetic advance values indicate significant progress and potential for substantial improvement through targeted breeding programs. For example, traits like "Fodder yield per plant" (32.44) and "Panicle length" (33.67) showed high genetic advance suggesting that these traits can be significantly enhanced through focused breeding strategies. Similarly, "Biological yield" (28.29) and "Flag leaf width" (27.58) also demonstrated high genetic advance indicating the potential for substantial genetic improvements in crop productivity and leaf characteristics. Traits such as "Peduncle length" (22.07), "Panicle width" (25.36), and "Grain yield per plant" (24.73) exhibited high genetic advance values offering opportunities for targeted selection and accelerated genetic improvement. Traits like "Plant height" (18.82), "Test weight" (12.43), "Number of basal tillers" (14.00), and "Flag leaf length" (14.27) demonstrated moderate genetic advance values indicated moderate progress and potential for further improvement. On the other hand, traits with low Genetic Advance values indicated slower progress and limited potential for significant improvement through genetic selection alone. Traits such as "Days to 50% flowering" (6.71), "Days to maturity" (6.05), and "Harvest index" (5.80) exhibited low genetic advance, suggesting that improving these traits may require a more comprehensive approach that considers other factors such as management practices and Environmental influences.

Traits such as fodder yield per plant, panicle length, biological yield, flag leaf width, peduncle length, panicle width, and grain yield per plant showed high heritability coupled with high genetic advance indicating that they are strongly influenced by genetic factors and can be improved through traditional breeding

methods. These traits predominantly exhibited additive gene action. Traits *viz,* plant height, test weight, number of basal tillers, and flag leaf length exhibit high heritability coupled with moderate genetic advance implies both additive and non-additive gene actions. These results suggested that genetic improvement can be achieved through traditional breeding methods, as well as, by harnessing non-additive gene interactions. On the other hand, traits such as days to 50 per cent flowering and days to maturity have high heritability but low genetic advance. This suggests that their improvement through selection and breeding might be limited. This could be due to the involvement of non-additive gene actions, where gene interactions play a larger role than individual genes. The medium heritability and low genetic advance observed in traits like harvest index indicate that their expression is strongly influenced by environment factors and involves non-additive gene action.

Grain yield per plant was positively and significantly associated with various traits. These included days to 50 per cent flowering (r_g: 0.232*, r_p: 0.238**), days to maturity (r_g: 0.276**, r_p: 0.257**), plant height (r_g: 0.331**, r_p: 0.312**), panicle length (r_g: 0.513**, r_p: 0.356**), flag leaf length (r_g: 0.190*, r_p: 0.297**), peduncle length (r_g: 0.278**, r_p: 0.236**), biological yield (r_g: 0.924**, r_p: 0.889**), and fodder yield per plant (r_g: 0.868**, r_p: 0.756**). These associations were observed at both the genotypic and phenotypic levels. The number of basal tillers (r_g: 0.022^{NS}, r_p: 0.225*) and panicle width (r_g: 0.131^{NS}, r_p: 0.218*) also showed positive and significant associations, but only at the phenotypic level.

Path analysis results indicated that biological yield had the greatest direct effect on grain yield per plant (r_g=2.093, r_p=1.956), followed by harvest index (r_g=0.0915, r_p=0.0987), flag leaf width (r_g=0.0150, r_p=0.0013), and number of base tillers (r_g=0.0056, r_p=0.0053) at both the genotypic and phenotypic levels. At the genotypic level, days to flowering (r_g=0.0329) and peduncle length

(r_g=0.0036) showed a positive direct effect. Panicle length showed a positive direct effect at the phenotypic level on grain yield per plant. These characteristics can be used to develop an effective selection index for improving the yield of foxtail millet.

In the present study, we observed 30 foxtail millet genotypes in four different environments. The results of the D^2 analysis confirmed the presence of high genetic diversity among the genotypes. We found that there were many differences in the traits among these genotypes. In the first environment, 30 genotypes were grouped into nine clusters based on their similarities using by Tocher method, followed by six clusters in environment-2, seven clusters in environment-3, ten clusters in Environment-4 and five clusters in the pooled Environment combination.

In Environment-1, the foxtail millet genotypes exhibited a broad range of intra-cluster distances, spanning from 0.00 to 14.26. Cluster-VI displayed the highest intra-cluster distancecomprising five genotypes. In Environment-2, the intra-cluster distances ranged from 0.00 to 12.31. Cluster-III displayed the highest intra-cluster distance (12.31) among all clusters, consisting of six genotypes. In Environment-3, the intra-cluster distances varied from 0.00 to 14.25. Cluster-I exhibited the highest intra-cluster distance (14.25) among all clusters, comprising 24 genotypes. In Environment-4, the intra-cluster distances ranged from 0.00 to 8.13. Cluster-I had the highest intra-cluster distance (8.13) and included 18 genotypes. In the pooled Environment analysis, the inter-cluster distances ranged from 4.59 to 0.00. Cluster-I had the highest intra-cluster distance (8.13) and comprised 26 genotypes.

In Environment-1, the inter-cluster distances ranged from 35.09 to 11.25. Clusters VIII and IX showed the maximum inter-cluster distance (35.09), followed by clusters VII and IX (34.99). in Environment-2, the inter-cluster distances ranged from 22.94 to 11.71. Clusters III and IV exhibited the

maximum inter-cluster distance (22.94). In Environment-3, the inter-cluster distances ranged from 25.56 to 10.59. Cluster I and VII showed the maximum inter-cluster distance (25.56). In Environment-4, the inter-cluster distances ranged from 21.35 to 6.46. Clusters II and X exhibited the maximum inter-cluster distance (21.35). Finally, in the pooled Environment analysis, inter-cluster distances ranged from 8.75 to 6.01. Clusters III and V displayed the maximum inter-cluster distance (8.75).

In Environment-1, plant height had the highest contribution to the total genetic divergence (48.74%), appearing 212 times in the first rank. In Environment-2, test weight played the most significant role in the total genetic divergence (31.03%), being ranked first 135 times. In Environment-3, test weight had the highest contribution to the total genetic divergence (53.56%), ranked first 233 times. In Environment-4 (Table 24), test weight had the greatest contribution to the total genetic divergence (36.78%), ranked first 160 times. In the pooled Environment analysis, test weight showed the highest contribution to the total genetic divergence, ranked first 97 times.

Since the error variance in different trials was similar, we used the AMMI model to analyze the additive effects yield traits. We found that the environment significantly affected all these traits at the 1% probability level, showing differences among the experimental environments. The genotype had a significant effect on all the studied traits at the 1% probability level. This means that the different genotypes had varying results for yield traits. Additionally, GEI was also significant for all the traits at the 1% probability level, leading to variations in how genotypes performed in different environments for all the studied traits.

Ideal Genotypes of different agronomic traits based on AMMI Biplot-1, WAAS and Mean vs stability biplots			
Traits	**AMMI Stability Biplot-1**	**WAAS**	**Mean v_s stability biplots**
Days to 50 per cent flowering	G14, G23, G16, and G9	G12, G6, G21, G9, G4, and G18	G1 and G4
Days to maturity	G3, G1, and G13	G6, G3, G15, and G24, PH: G15 and G27	G16 and G18
Plant height (cm)	G23 and G28	G15 and G27	G1, G2, G28 and G17
Panicle length (cm)	G18 and G30	G9, G12, G29, G2, and G28	G9, G30, G8
Flag leaf length (cm)	G14 and G25	G11	G28 and G5
Flag leaf width (cm)	G12, G17 and G18	G11, G6, G7, and G20	G18 and G17
Peduncle length (cm)	G24 and G28	G10 and G6	G28 and G1
No. of tillers per plant	G18, G16 and G25	G17, G1, G4, and G5	G29
Panicle width (cm)	G13 and G18	G7, G5, G20, and G22	19 and G9
Biological yield (g)	G18, G17 and G5	G7, G9, G19, G20, and G22	G1, G25, G22 and G5
Harvest index (%)	G28 and G1	G5, G16, and G22	G20
Fodder yield per plant(g)	G21 and G13	G20, G5, G10, and G19	G18 and G17
Test weight	G13, G17 and G18	G26, G24, G6, and G3	G21 and G22
Grain yield per plant(g)	G8, G9, G21, and G22	G10, G15, G13, G6, G7, and G8	G21 and G22

The likelihood ratio test showed highly significant effects ($p < 0.05$) for both genotype and interaction in this experiment for all traits. This significance of genotype-environment interaction (GEI) indicated that different genotypes responded differently in different environments, each having its own strengths and weaknesses.

Among the 30 genotypes studied in BLUPs, there were remarkable variations in key agronomic traits. Sixteen genotypes exceeded the initially predicted mean values for Panicle length, with G17 and G8 demonstrating exceptional performance in this regard. Additionally, sixteen genotypes surpassed the predicted mean values for Flag leaf length, where G5 and G28 showed as standout contenders. Notably, fifteen genotypes exhibited Flag leaf widths that exceeded their predicted mean values, with G17 and G26 standing out as top performers. Moreover, twelve genotypes displayed Peduncle lengths above the predicted mean values, and G1 and G28 emerged as standout performers. In terms of No. of tillers per plant, fourteen genotypes exceeded their predicted mean values, with G29 and G25 being notable standouts. Furthermore, thirteen genotypes demonstrated Panicle widths beyond their predicted mean values, with G30 and G18 showcasing top performance. In the context of biological yields, twelve genotypes exceeded predicted mean values, with G25 and G1 emerging as top performers. Additionally, twelve genotypes had Harvest indexes that exceeded their predicted mean values, where G24 and G20 achieved the highest scores. Furthermore, thirteen genotypes displayed Test weights beyond the predicted mean values, with G25 and G1 as top performers in this category. Lastly, twelve genotypes had Grain yields per plant surpassing predicted mean values, with G25 and G1 emerging as the top contenders in this respect.

Ranking genotypes biplots reveled, G3 in DF, G1 and G18 in DM, G1in 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 centre of the concentric circles, is an ideal genotype due to its higher yield and stability compared to the other genotypes.

MTSI revealed, G17 secured the top rank, followed by G18, G21, and G14, indicating that these are the most desirable and stable genotypes. Additionally, genotypes like G16, G2, G20, G29, G8, and G13 are clustered closely to this circle, suggesting they might have interesting attributes worth exploring in future investigations. MGIDI index values, which is used for genotype selection based on mean performance and stability. Out of the 30 genotypes we evaluated, only five of them *viz.*, G25, G5, G1, G22, and G2 stood out with excellent characteristics, marked as red dots in Figure 4.30. G2, in particular, was very close to the selection cut-off point.

Conclusions

The current study analyzed data from multiple environments to find out the ideal genotypes for foxtail millet cultivation in Nagaland. We employed various stability analysis methods and compared their results. Our findings indicated Environment E1, representing the timely *kharif* season, as the ideal environment for foxtail millet cultivation in Nagaland. This means that planting during this season is most favourable for good yields. Moreover, we identified specific genotypes that consistently performed well in this region. These genotypes, namely G1, G22, G25, and G21, exhibited stable and reliable performance across different conditions. Our findings are region-specific, centred around a particular area of Nagaland, and may not necessarily represent the entirety of the region. Despite this localized focus, we identified genotypes which showed stable and reliable performance across varied conditions in this particular region. This conclusion is based on a rigorous analysis of multi-Environment data, which provides practical guidance for farmers and cultivators in Nagaland looking to optimize their foxtail millet production.

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APPENDICES

Plate 4.1. Plant pigmentation

Plate 4.2. Leaf: Colour

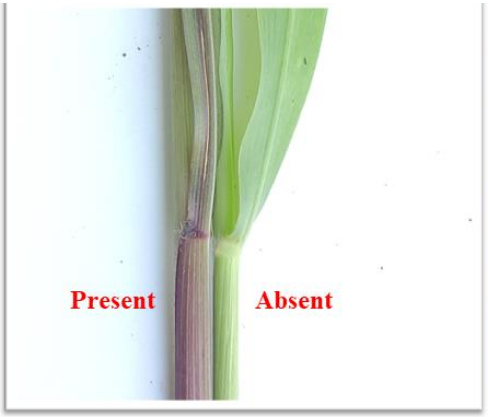

Plate 4.3. Plant pigmentation at auricle

Plate 4.5. Inflorescence: Bristles

Plate 4.4. Inflorescence: Shape

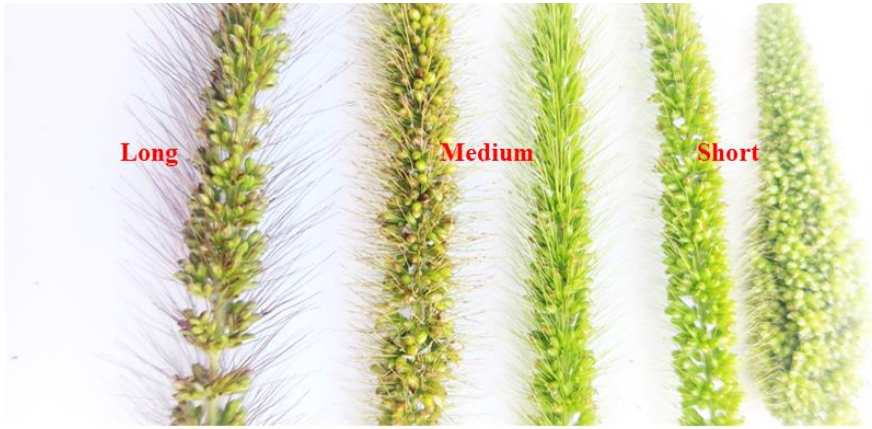

Plate 4.6. Inflorescence: Length of bristles

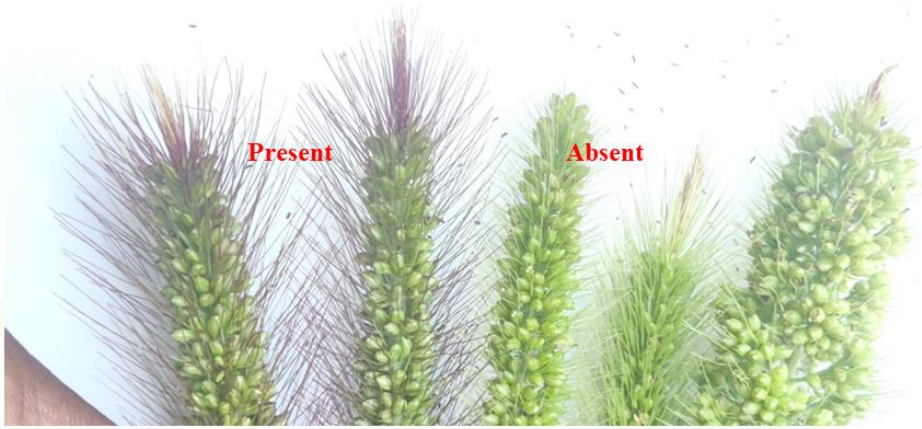

Plate 4.7. Inflorescence Apical: Sterility

Plate 4.8. Inflorescence: Lobes

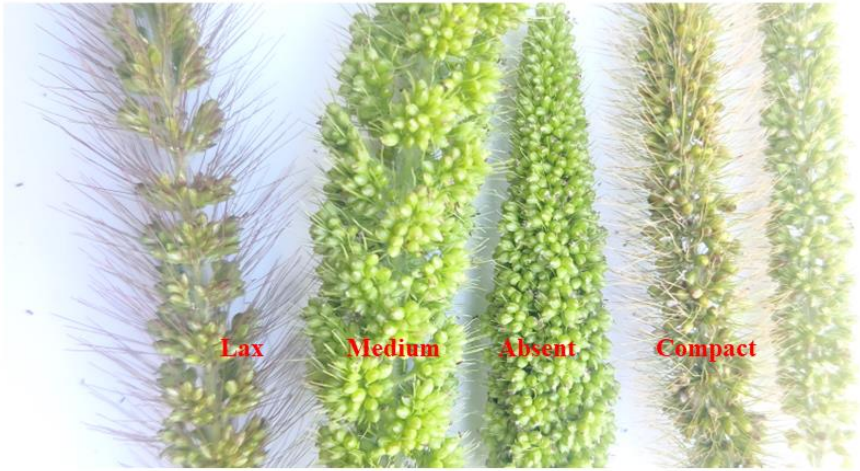

Plate 4.9. Inflorescence: Compactness

Plate 4.10. Field view at flowering stage

Plate 4.11. Overall, Field view of different stages of crop