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Phenotypic characterization of okra (*Abelmoschus esculentus* (L).Moench) accessions collected from Humera, Tigray, Northern Ethiopia.

By

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A Thesis

Submitted in Partial Fulfillment of the Requirements for the

Masters of Science Degree in Horticulture

College of Dry land Agriculture and Natural Resources,

Department of Dry land Crop and Horticultural Science

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DECLARATION

I, Mehari Kassie Beyene, hereby submit my dissertation for consideration by the Dryland Crop and Horticultural Science Department within the College of Dryland Agriculture and Natural Resources at Mekelle University. This dissertation, entitled Phenotypic Characterization of Okra (*Abelmoschus esculentus* (L.) Moench) Accessions from Tigray at Humera, Northern Ethiopia, is presented in partial fulfillment of the requirements for the degree of Master of Science in Horticulture.

I affirm that this thesis is the result of my own original research and efforts. I declare that no similar study has been published by any other individual that I might have copied, and at no stage this work will be published without my consent and that of the Dryland Crop and Horticultural Science Department.

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BIOGRAPHY OF THE AUTHOR

Mehari Kassie Beyene was born on May 29, 1980, in Mekelle City. He completed his primary and secondary education at Hatsey Yohannes preparatory School in 1998 E.C., he joined Mekelle University to pursue a Bachelor's degree in Horticultural Sciences, graduating in 2000 E.C. After graduation, he worked as a crop production expert at the Tigray Bureau of Agriculture and Rural Development later he worked Tigray Agricultural Research Institute (TARI) under Humera Agricultural Research Center (HuARC) where he gained valuable experience in crop production.

In 2013 E.C., he began his Master's degree study in Horticulture at the Department of Dryland Crop and Horticultural Sciences College of Dryland Agriculture and Natural Resources, Mekelle University. During this time, he developed a strong interest in plant phenotypic characterization, particularly in okra (*Abelmoschus esculentus*), and conducted research on the phenotypic characterization of okra accessions from Tigray, Northern Ethiopia.

Mehari Kassie has presented his research findings at several conferences and workshops. He is passionate about agricultural development, crop improvement, and food security, and he plans to continue contributing to research in these areas.

DEDICATION

I dedicate this thesis manuscript to the memory of my mother and my wife, Tunsue Haftu and Rahile Mesfen respectively.

Table of Contents

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ABSTRACT

This research investigated the phenotypic traits of 72 okra(Abelmoschus esculentus (L.) Moench) accessions from Tigray, Northern Ethiopia, to evaluate their genetic variability and breeding potential. The study aimed to estimate phenotypic and genotypic variability, assess broad-sense heritability of selected traits, and explore phenotypic associations among measured traits. Although okra has been cultivated for generations in Tigray, particularly in the western region, there has been minimal systematic effort to evaluate the variability among local okra accessions for plant breeding. The research Conducted at the Humera Research Center and My-Weyini, the study utilized in alpha lattice design to assess growth, phonological, and yield-related traits. The analysis focused on identifying performance differences between accessions using two-way ANOVA in R software (version 4.4.1), revealing significant variability among accessions, particularly for key traits such as fruit number, single fruit weight, and yield per plant. Notably, accessions Bereket4, Hillegin10, Maikadra1, and AdiGoshu9 demonstrated exceptional yield performance, while early-maturing accessions like Hillegin19, Hillegin16, and AdiGoshu12 exhibited favorable traits for breeding.

The Genotypic Coefficient of Variation (GCV) and Phenotypic Coefficient of Variation (PCV) were calculated for 72 quantitative traits, revealing PCV values between 21.63% and 53.09% and GCV values from 17.50% to 48.54%. This significant variability indicates a strong potential for genetic improvement through selection. The narrow gap between GCV and PCV values for most traits highlights that genetic differences among genotypes primarily drive the observed variability. Heritability estimates ranged from 29.18% to 91.40%, with traits like the number of branches per plant (91.40%) and fruit diameter (86.89%) exhibiting high heritability, thereby enhancing their reliability for selection.

Qualitative traits also demonstrated considerable diversity, with 43% of the accessions classified as small in height and 97% exhibiting an angular fruit shape. Most of the accessions (44%) fell into the medium maturity category, supporting staggered harvesting and market availability. The prevalence of smooth stem texture (67%) and green fruit color (89%) underscores traits that could be prioritized in breeding programs for structural integrity and consumer appeal.

Clustering analysis identified groups of accessions based on key traits, with Cluster 7 showing the highest yield and fruit number per plant. In contrast Cluster 4 displayed the shortest time to flowering and maturity. Strong correlations among plant height, fruit dimensions, and yield-related traits provide *critical insights for selecting high-heritable traits for breeding. The results emphasize the importance of leveraging both genotypic and phenotypic variability to enhance okra productivity. Crossbreeding high-yielding accessions with early-maturing ones from different clusters can optimize yield and maturity times. This study establishes a foundational resource for developing improved okra varieties and promoting sustainable agricultural practices in Tigray.*

Key words: *Agronomic traits; Early maturing; Genetic improvement; Genetic variability; Resilience; Selection; Okra genotypes*

CHAPTER ONE: INTRODUCTION

1.1. Background Information

Okra (*Abelmoschus esculentus L. Moench*) is a widely cultivated crop in tropical and subtropical regions, prized for its tender fruits consumed as vegetables. Originally classified under the genus Hibiscus, it was later reassigned to the genus Abelmoschus due to its distinct morphological and taxonomic traits (Aladele et al., 2008). Ethiopia is regarded as a center of origin for okra, and historical evidence suggests that the crop spread to North Africa, the Mediterranean, Arabia, and India by the 12th century BC (Simmone et al., 2004; Sathish and Eswar, 2013; Getachew, 2001; Dandena, 2010).

Okra has a promising production potential in Tigray, Ethiopia. By addressing the challenges related to agronomic practices, pest and disease management, water availability, and market access, and by leveraging the opportunities for research, farmer education, and infrastructure development, okra can contribute significantly to the region's food security, economic development, and nutritional well-being.

In Ethiopia, Tigray stands out as a region where okra cultivation has been preserved through traditional farming systems. Farmers in western Tigray, particularly the Kunama ethnic group and communities near the Sudanese border, have a long-standing tradition of cultivating okra. These farmers exchange seeds with neighboring Sudan, contributing to local crop diversity and adaptation (Dandena, 2010). However, despite the rich cultural and agricultural heritage associated with okra in the region, scientific research on the crop remains minimal.

Okra plays an essential role in nutrition, income generation, and crop diversification. Its resilience to harsh environmental conditions makes it a suitable crop for regions experiencing erratic rainfall patterns and other climatic challenges. However, the full potential of okra remains unrealized in Ethiopia due to the absence of systematic studies on its phenotypic and genetic variability. Characterizing these traits is critical for identifying promising accessions that can be used in breeding programs to enhance yield, drought tolerance, and disease resistance.

Okra is a nutritional gem, packing a punch of essential nutrients into a low-calorie package. It's an excellent source of dietary fiber, crucial for healthy digestion, blood sugar regulation, and even heart health. This fiber, along with okra's mucilage (the "slimy" substance), can contribute to lowering cholesterol levels. Okra also provides a good dose of vital vitamins and minerals. It's rich in Vitamin

K, essential for blood clotting and bone health, and Vitamin C, a powerful antioxidant that boosts the immune system. Folate (Vitamin B9), crucial for cell growth and development, especially during pregnancy, is another valuable nutrient found in okra. Additionally, okra offers potassium, important for maintaining healthy blood pressure, and magnesium, which plays a role in numerous bodily functions. Beyond these vitamins and minerals, okra boasts antioxidants that protect cells from damage, further enhancing its health benefits. In short, okra is a nutrient-dense vegetable that contributes to overall well-being.

1.2. Problem Statement and Justification

Although okra has been cultivated for generations in Tigray, particularly in the western region, there has been minimal systematic effort to evaluate the variability among local okra accessions for plant breeding. Farmers, including the Kunama ethnic group and those near the Sudanese border, preserve crop diversity through traditional seed exchange practices (Dandena, 2010). However, the absence of research on the genetic and phenotypic variability of these accessions limits opportunities for developing improved varieties suited to the region's diverse agro-ecological conditions.

This lack of comprehensive research hinders the identification of essential agronomic traits, such as yield, drought tolerance, early maturity, and resilience under changing climatic conditions, which are critical for breeding programs. Without proper characterization, valuable genetic resources may remain untapped, depriving farmers of improved varieties that could enhance productivity and strengthen food security in the region.

Given these challenges, a systematic study of the phenotypic variability of okra accessions in Tigray is crucial. Such research will provide data to support plant breeding programs aimed at improving yield, adaptability, and resilience in response to changing climatic conditions. Unlocking the genetic potential of local okra accessions will benefit farmers in Tigray and contribute to Ethiopia's broader agricultural development goals.

1.3. Objectives

1.3.1. General Objective

- To assess the phenotypic diversity and characterize the morphological traits of okra (Abelmoschus esculentus (L.) Moench) accessions collected from Tigray Northern Ethiopia.

1.3.2. Specific Objectives

- To characterize okra accessions from Tigray using phenotypic traits.
- To estimate the broad-sense heritability of selected traits of okra accessions.
- To estimate phenotypic associations among measured traits of okra accessions.
- To estimate the genetic variability of accessions using genotypic and phenotypic variances and coefficients of variation.
- To identify superior okra accessions with desirable traits such as high yield, desirable pod characteristics, and early maturity for improved cultivation.

1.4. Hypothesis of the Study

There is significant phenotypic and genotypic variability among okra accessions from Tigray.

1.5. Significance/Importance of the Study

This study is essential for identifying superior traits in okra accessions through the characterization of phenotypic variability. Valuable traits such as high yield and early maturity will be identified, facilitating crop improvement and adaptation to the environmental conditions of Tigray and similar regions.

The findings will also support the development of breeding programs by providing vital information on the variability and heritability of key traits. This information is crucial for selecting promising genotypes that can be used to develop improved okra varieties suited to the agro-climatic conditions of Tigray and Ethiopia more broadly.

In addition, the study will contribute to the conservation of indigenous genetic resources through the systematic documentation of okra diversity. Preserving local germplasm is essential for maintaining genetic diversity, which underpins the long-term sustainability of breeding programs.

Improved okra varieties developed from this research will have direct economic and food security benefits. These varieties will increase farmers' income through higher yields and access to better market opportunities. Additionally, increased productivity will contribute to enhanced food security in the region.

Finally, the study will provide a foundation for future research by offering baseline data on the phenotypic characteristics of okra accessions. It will encourage further scientific exploration of okra and other underutilized crops, paving the way for long-term agricultural development initiatives.

1.6. Scope and Limitation of the Study

1.6.1. Scope of the Study

The study focuses on the phenotypic characterization of 72 okra accessions collected from different areas of Tigray, Ethiopia. It assesses growth, phenological, and yield-related traits, such as plant height, fruit number per plant, and single fruit weight. The experiment was conducted at two locations, My-Weyini and the Humera Research Center, representing different agro-ecological zones.

The study employs an alpha-lattice design with two replications to ensure accurate variability estimation while minimizing environmental influences. Data collected will help evaluate genetic variability, heritability, and phenotypic correlations among the traits, with the goal of supporting plant breeding efforts.

1.6.2. Limitations of the Study

The study faces several limitations. One major limitation is geographical coverage. Since the accessions are limited to Tigray, the findings may not fully represent the diversity of okra in Ethiopia or other regions. As a result, the conclusions drawn from this study may be region-specific and may not be directly applicable to other areas.

Another limitation is the number of experimental replications. Due to resource constraints, the experiment was conducted with only two replications, which may reduce the precision and reliability of the results. A higher number of replications would have improved the accuracy of the findings, especially for traits influenced by environmental variability.

The study is also limited by its focus on phenotypic traits. Since genotypic data was not collected, the analysis is restricted to morphological characteristics, which may not fully capture the genetic variability among accessions. A more comprehensive study integrating genotypic data would provide deeper insights into the genetic potential of the accessions.

Environmental factors such as rainfall and temperature fluctuations during the growing season may also influence the expression of certain traits. These variations could impact the performance of accessions and introduce additional variability into the results, potentially complicating the interpretation of findings.

Finally, time and resource constraints posed challenges to the study. The limited duration of the experiment restricted the amount of data that could be collected, which may affect the comprehensiveness of the analysis. Similarly, resource limitations constrained the scope of data collection and experimentation, influencing the depth of the study.

CHAPTER TWO: REVIEW OF LITERATURE

2.1 Origin and its diversity, Distribution, Production, and Importance of okra plant

2.1.1 Origin and Distribution

Okra (*Abelmoschus esculentus L.*) was initially classified under the genus Hibiscus within the Malvaceae family, but it was later separated into the distinct genus Abelmoschus based on floral morphology and taxonomic studies (Ogunbor, 2020). Although there is debate over its exact origin, okra is believed to have originated in regions such as India, Ethiopia, West Africa, and tropical Asia (Zeven & Zhukovsky, 1975; Vidhi, 2023). The species thrives across tropical and subtropical zones, with notable cultivation in Africa, India, and the Americas. In West Africa, A. esculentus is particularly suited to the Sudano-Sahelian zone, though it also grows in smaller quantities in forested regions, suggesting ecological adaptation to different climates (Siemonsma, 1982).

Two main hypotheses exist regarding the origin of okra: the Asian origin and the Ethiopian origin. Some authors support the theory that A. tuberculatus, a wild relative, originated in northern India, specifically Uttar Pradesh (Tripati et al., 2011). In contrast, others argue that ancient cultivation in East Africa, along with the presence of A. ficulneus, points to Ethiopia or northern Egypt as the domestication site, though conclusive evidence is lacking (Rao et al., 2019). Southeast Asia is also considered a center of diversity due to the overlapping distribution of both cultivated and wild species in that region (Waalkes, 1966; Vredebregt, 1991). Linguistic evidence from Sanskrit, where okra is referred to as tindisha and gandhamulla, further supports the idea of its Asiatic origin (Patil et al., 2015).

In India, eight species of Abelmoschus have been identified, with A. esculentus being the only cultivated species, and others, such as A. moschatus, grown for aromatic seeds (Tripati et al., 2011). These wild species occupy diverse habitats, ranging from semi-arid areas to the lower Himalayas, Western and Eastern Ghats, and northeastern regions of India, showcasing the plant's adaptability across phytogeography zones.

2.1.2 Historical Spread and Global Cultivation

Historical records indicate that okra was cultivated by the ancient Egyptians as early as the 12th century BCE and later spread across North Africa and the Middle East (Ogunbor, 2020). The Arabic word bamya was used to describe the plant, indicating that it may have been introduced to Egypt from

Ethiopia or Arabia (Axe, 2021). French colonists likely brought okra to the Americas, where it was cultivated as early as 1658 in Brazil and Suriname (Liqui, 2023). By the 18th century, it had spread to the southern United States, with Thomas Jefferson documenting its presence in Virginia by 1781.

2.1.3 Global Production of Okra

India leads the world in okra production, accounting for approximately 61% of global output with 6.87 million tonnes as of 2022. Nigeria and Mali also play significant roles, contributing substantially to global production, which reached 11.2 million tonnes that year. Okra is cultivated across several tropical and subtropical regions due to its importance in agriculture and food security, especially in South Asia and West Africa. Other notable producers include Sudan and Ghana, though at smaller scales compared to India and Nigeria (FAO, 2022).

Table 1: ten top Countries by Production of Okra in 2022

Rank	Country	Production(Tonnes)	Acreage(Hectare)	Yield
1	India	6,873,000	550,000	124,964
2	Nigeria	1,911,819	1,911,037	10,004
3	Mali	764,089	59,464	128,496
4	Pakistan	308,638	25,261	122,180
5	Sudan	295,869	26,739	110,651
6	Cote d'Ivoire	183,833	65,195	28,197
7	Iraq	88,843	14,014	63,396
8	Bangladesh	85,233	12,270	69,465
9	Egypt	79,503	5,441	146,125
10	Cameroon	77,632	30,153	25,746

Source: FAOSTAT (2023)

These countries accounted for the majority of global okra production in that year.

2.1.4 Okra Production in Ethiopia

Okra (Abelmoschus esculentus) is an important vegetable crop in Ethiopia, where it is believed to have originated. Despite its significance, okra production in Ethiopia faces several challenges and has not yet reached its full potential.

Production Areas: Okra is primarily cultivated in the western and southwestern lowlands of Ethiopia, including regions like Gambella, Benishangul Gumuz, and the western lowlands of Tigray.

Okra is mainly grown from local landraces, with limited adoption of improved varieties. Traditional farming practices are commonly used, which may not be optimized for high yields. Okra is valued for its immature pods, which are consumed fresh or cooked. The seeds can also be used to extract oil, comparable to other oil crops like palm and soybean. Additionally, in some regions, the leaves are used for food and medicinal purposes.

Compared to other crops, okra has received little research attention in Ethiopia. This has resulted in a lack of improved varieties and optimized production practices.

There is a lack of comprehensive data on okra production area and productivity in Ethiopia, making it difficult to assess the current status and track progress. Despite its nutritional value and versatility, okra is considered an underutilized crop in Ethiopia. Its potential for contributing to food security and nutrition is not fully realized.

Ethiopia is considered a center of origin for okra, indicating a rich genetic diversity of the crop within the country. This diversity can be utilized for developing improved varieties with desirable traits such as high yield, disease resistance, and nutritional quality. Okra is a nutritious vegetable, rich in vitamins, minerals, and fiber. Promoting okra consumption can contribute to improving the nutritional status of Ethiopians. Okra has the potential to be a significant cash crop for farmers in Ethiopia. Increasing production and market access can enhance income generation and rural development.

Increased research efforts are needed to characterize and evaluate okra germplasm, develop improved varieties, and optimize production practices. This will require collaboration among researchers, breeders, and farmers.

2.1.5 Importance of Okra

1 Health Benefits: Okra, also known as ladyfinger, is a nutrient-rich fruit often consumed as a vegetable. It is packed with essential vitamins (A, C, and K), minerals like magnesium and calcium, fiber, and antioxidants, making it highly beneficial for overall health. Okra supports digestion by preventing constipation, regulates blood sugar levels, lowers cholesterol, and promotes cardiovascular health. Its high vitamin C content strengthens the immune system, while vitamin A enhances vision and protects against eye-related conditions. Additionally, okra aids in weight management, improves skin texture, and supports bone health. With anti-inflammatory properties, it can help reduce the risk of chronic diseases such as arthritis and heart disease. Okra is a versatile food that contributes to well-being, making it a valuable addition to a balanced diet.

2 Food Securities: Okra provides essential nutrients in regions where other food sources might be limited, helping combat malnutrition. Its adaptability to tropical climates makes it a reliable crop during unfavorable conditions, thus supporting local food systems.

3 Macroeconomic and Market Impact: Okra contributes to local economies by generating income for farmers through fresh markets and processed products (like dried okra or seeds for oil). In global markets, countries like India have capitalized on the export potential of okra, supporting trade and agriculture-based economies. Ethiopia, too, has the opportunity to tap into the increasing demand for okra in international and regional markets (FAO, 2022).

2.2. Climatic Adaptability and Agro-Climatic Requirements of Okra

Okra (Abelmoschus esculentus) thrives under a variety of climatic conditions, but it performs optimally in tropical and subtropical regions with warm temperatures, well-distributed rainfall, and plenty of sunshine. The crop prefers silty to sandy loam soils with good drainage and organic content (Department of Agriculture, 2017). It germinates well in soil temperatures above 16°C, but colder conditions significantly hinder seed sprouting. Furthermore, okra is a short-duration crop, making it well-suited for areas with limited growing seasons.

Agro-Climatic Requirements

Temperature: Okra grows best in temperatures between 21°C and 30°C. It can tolerate heat but becomes susceptible to physiological stress above 35°C, which can affect pod quality and yield. The crop is highly sensitive to frost, limiting its cultivation in temperate areas with even mild winters (Tropical Agricultural Research, 2012).

Rainfall and Water Management: While okra is drought-tolerant, sufficient moisture is necessary during the flowering and pod development stages to ensure high yield. Inadequate water during critical growth phases can reduce pod size and overall productivity. Okra can benefit from light irrigation in dry spells, but excessive moisture can lead to root diseases, requiring well-drained soil.

Soil and pH Levels: The crop tolerates a pH range of 5.5 to 8.0 but performs best in slightly acidic to neutral soils (5.8 to 6.5). Fertile soils with good organic matter content improve okra's growth and productivity. Heavy clay soils should be avoided unless well-drained, as waterlogging negatively impacts the plant (Department of Agriculture, 2017).

Adaptation to Abiotic Stresses and Climate Change

Okra's ability to withstand drought and tolerate a range of soil conditions makes it a resilient crop for varying agro-climatic zones. However, the impacts of climate change pose challenges to its productivity. Rising temperatures can accelerate plant growth but may reduce the quality and number of pods. Research indicates that a 1% increase in mean temperature could result in a 29% decline in okra yield, stressing the need for adaptive farming practices (Tropical Agricultural Research, 2012). Salinity is another abiotic stress that affects okra production, particularly in areas with poor water quality or salt-affected soils.

Cultural Practices for Optimal Growth

To enhance okra production under changing climatic conditions, farmers can adopt practices such as mulching to retain soil moisture, thinning to reduce competition, and regular weeding to minimize stress from pests and weeds. Timely irrigation, fertilization, and use of improved varieties also contribute to sustainable okra production.

In summary, okra is well-suited for tropical climates, with the ability to adapt to various environmental conditions. However, its sensitivity to frost, high temperatures, and water stress highlights the importance of efficient management practices to ensure consistent yield and quality. Addressing socio-economic constraints, such as limited access to inputs and scientific information, is crucial for promoting climate-resilient okra production systems (Tropical Agricultural Research, 2012).

2.3. Phenotypic and Genotypic Variability of Okra

The diversity of okra (Abelmoschus esculentus L.) plays a critical role in improving the crop's productivity through breeding programs. Assessing phenotypic and genotypic variability provides insights into the extent of diversity among accessions and helps breeders select promising lines for various environments

Genetic variability in okra has been extensively studied, revealing significant differences among various genotypes. Shujaat et al. (2014) highlighted the importance of genetic diversity, particularly for traits such as fruit yield and days to flowering, which are essential for effective selection in breeding programs. Similarly, Tesfa and Yosef (2016) used both morphological traits and molecular markers to demonstrate high levels of variability, suggesting that a combination of phenotypic and genotypic data could enhance breeding strategies. Jindal et al. (2018) also emphasized the role of genetic diversity in improving adaptability, further confirming its critical importance in developing resilient and high-yielding okra varieties. . Below is a detailed discussion of phenotypic variability, genetic diversity, and genotype-by-environment interaction in okra.

2.3.1. Phenotypic Variability

Phenotypic variability reflects the observable differences in morphological and agronomic traits among accessions, resulting from both genetic factors and environmental influences. Okra shows significant phenotypic diversity for traits such as plant height, fruit length, number of fruits per plant, fruit yield, and 100-seed weight. Studies indicate that the phenotypic coefficient of variation (PCV) is often higher than the genotypic coefficient of variation (GCV), suggesting that environmental factors contribute significantly to trait expression. For example, traits like plant height and fruit yield exhibit moderate to high phenotypic variability, making them essential targets for selection in breeding programs (The Pharma Innovation Journal, 2023; Alam et al., 2020).

Phenotypic assessments also help in characterizing accessions based on yield performance under stress and non-stress conditions. For instance, Gerrano et al. (2022) reported wide phenotypic variation in plant height and pod yield per plant across okra genotypes grown under drought-stressed and irrigated environments. This variation is critical in identifying high-performing accessions suitable for various climatic conditions (Alam et al., 2020).

2.3.2. Genetic Variability

Genetic diversity is essential for crop improvement, providing the raw material for breeding programs. Okra exhibits moderate to high genetic variability across several traits. Studies using molecular markers, such as Simple Sequence Repeats (SSR), have identified significant genotypic differences among accessions, which can be harnessed for hybridization. Gerrano et al. (2022) demonstrated that okra genotypes show genetic clustering, forming distinct groups based on their molecular and phenotypic profiles (Alam et al., 2020).

2.3.3. Genotype by Environment Interaction in Okra

Genotype-by-environment (G × E) interaction describes how different genotypes respond to varying environmental conditions. This interaction is a significant challenge for breeding programs, as the performance of okra genotypes can vary across locations and seasons. Several studies emphasize the importance of evaluating genotypes under multiple environments to select stable performers. Gerrano et al. (2022) found that okra accessions showed distinct responses to drought-stressed and non-stressed environments, with some genotypes performing well only under specific conditions Alam et al., 2020.

By studying G × E interactions, breeders can develop stable okra varieties that maintain high yields across diverse agro-climatic conditions. This strategy is particularly important for regions like Ethiopia, where climatic variability poses challenges to agricultural productivity.

Jindal et al. (2008) explored genotype-by-environment (G × E) interactions in okra, highlighting how environmental conditions impact the stability and performance of genotypes. Their study emphasized that traits such as fruit yield, plant height, and branching patterns showed variability across environments. They recommended that breeding programs should target stability in performance across both favorable and unfavorable conditions to ensure reliable yield. Selection should focus on traits directly linked to productivity, such as fruits per plant, for identifying stable genotypes with wide adaptability.

In summary, understanding the phenotypic and genotypic variability of okra is crucial for developing resilient and high-yielding varieties. High heritability and genetic advance in specific traits suggest promising opportunities for selection in breeding programs. Furthermore, assessing genotype-by-environment interactions ensures that breeders can recommend varieties with consistent performance across different environments (Gerrano et al., 2022; Alam et al., 2020).

2.4. Variation in Qualitative Characteristics of Okra Genotypes

Variation in qualitative traits plays a significant role in the characterization and identification of okra genotypes. A study examining forty okra genotypes revealed considerable diversity across several qualitative traits, including stem and fruit pubescence, fruit color, and the position of fruit on the main stem (Hindawi International Journal of Agronomy, 2021).

The study reported diverse stem pubescence, ranging from prickly, downy, glabrous, to slightly rough surfaces. The majority of the genotypes exhibited downy stems, followed by slightly rough, prickly, and glabrous forms, which were the least common. Similarly, variability in stem color was observed, with green being the most dominant, alongside other shades like purple, red-green, and yellowish-green (Hindawi, 2021). Petal color was more uniform across genotypes, with all forty accessions displaying yellow petals.

Fruit color, on the other hand, varied from green to purple-green and yellowish-green, with green fruits being the most prevalent. The position of fruits on the main stem also differed among genotypes, with most showing an erect fruiting habit, followed by horizontal and a few pendulous orientations. These qualitative traits are essential for breeders as they contribute to cultivar identification, consumer preference, and adaptability to environmental conditions (Gerrano et al., 2022; Sharma et al., 2016).

The observed diversity in qualitative traits can support the selection of specific genotypes for targeted breeding programs. This variability also offers the potential for developing varieties with improved market acceptance and stress tolerance (Alam et al., 2020). Furthermore, understanding qualitative trait variation helps in the conservation of okra genetic resources, promoting sustainable agricultural practices.

By identifying and utilizing accessions with desirable traits, breeding programs can develop cultivars with improved resilience and productivity. These findings underscore the importance of phenotypic evaluations alongside genotypic assessments to achieve comprehensive okra improvement strategies (Hindawi, 2021).

2.4 Qualitative Data Analysis

Qualitative data analysis in plant breeding is crucial for assessing categorical traits that define morphological diversity in crop genotypes. Traits such as Fruit Color, Fruit Shape, Maturity, Stem Texture, and Flower Color are central to describing phenotypic diversity, particularly in horticultural crops like okra, where these visual and structural characteristics significantly influence agronomic and consumer preferences (Anderson and Lee, 2021).

Qualitative data analysis enables breeders to characterize morphological traits and understand genetic variation within and across accessions. Unlike quantitative traits, which are continuous, qualitative traits are categorical and are often represented by frequency distributions. Bar charts, for instance, are commonly used to visualize the distribution of these categorical traits, providing a straightforward method to assess the prevalence of different phenotypes within a population (Rao et al., 2019).

In addition to aiding descriptive characterization, qualitative trait analysis can reveal genetic markers associated with particular traits. This can be particularly useful in selecting genotypes with desirable attributes, as well as in distinguishing between similar genotypes based on visible phenotypic differences (Martinez et al., 2023). Furthermore, assessing categorical traits supports genebank managers and breeders in the maintenance and improvement of crop collections, ensuring that key traits related to crop adaptability and market preference are preserved (Johnson et al., 2020).

R software is widely used in qualitative data analysis for plant characterization due to its ability to manage large datasets and generate visual summaries. The ggplot2 package, for example, is particularly effective for visualizing categorical data distributions through bar charts, while packages like dplyr facilitate efficient data manipulation, such as counting trait frequencies and calculating proportions (Sharma and Patel, 2021). These tools allow researchers to handle qualitative data in a reproducible and customizable manner, making it possible to efficiently explore trait diversity across numerous accessions.

CHAPTER THREE: MATERIALS AND METHODS

3.1. Study Area Description

The experiment was conducted at two distinct locations in Tigray: the Humera Research Center and My-Weyini Ranch, each offering unique environmental conditions to evaluate the performance of okra accessions.

Humera Research Center is situated at an elevation of 596 meters above sea level (amsl), with coordinates 14°17'11" N latitude and 36°36'35" E longitude. The region experiences a hot, semi-arid climate. During the cropping season, temperatures can reach 42°C in April and 33°C in August, with minimum temperatures fluctuating between 17.5°C in July and 22.2°C in May. Rainfall ranges from 563 mm to 888 mm annually, most of which occurs during the rainy season. The soil at this location is vertisol, with a clay to silty clay texture, and has a slightly acidic pH of 5.0 to 5.6, requiring careful management for optimal crop growth (Sahile et al., 2016).

My-Weyini Ranch, located approximately 100 kilometers from Humera, lies at 116 meters amsl, with coordinates 14°05'27" N latitude and 37°12'31" E longitude. This site experiences a cooler, slightly moist climate compared to Humera, with a maximum temperature of 36°C and a minimum of 17°C in July. The average rainfall is moderate, supporting plant growth during the cropping season. The soil at My-Weyini is also classified as vertisol, but with a silty clay to clay loam texture, which provides better drainage than the soil in Humera. The pH remains within the acidic range of 5.0 to 5.6 (Gebremedhin et al., 2019).

The two locations were chosen to assess genotype-by-environment interactions and ensure that the okra accessions are evaluated under different environmental conditions. This setup allows for identifying accessions with better adaptability, yield potential, and resilience to varying climatic factors, which is essential for developing improved varieties for the region. Evaluating okra accessions across these sites contributes to the broader goal of enhancing agricultural productivity in Tigray and supports sustainable crop breeding efforts (Haile et al., 2020).

3.2. Experimental Materials

The experiment utilized 72 okra accessions to assess variations in morphological traits. These genotypes originated from various locations:

- 19 accessions collected from Setit-humera (Hillegin)
- 7 accessions collected from adiabo(around sheraro)
- 16 accessions from Qfta-humera (AdiGoshu2)
- 15 collected from Qfta-humera (Maikadra)
- 12 accessions from Qfta-humera (Bereket)
- 1 released variety (Bamya Humera)
- 2 additional commercial varieties introduced from India(SOH 701 and SOH 714)

All accessions from Tigray were collected at varying altitudes between 576 and 1097 meters above sea level (m.a.s.l.). Details on these genotypes can be found in Table 2.

Table 2: accessions from Tigray were collected at varying altitudes

accession Code	Genotype Number	Regional state	District (werda)	Altitude(m. a.s.l.)	Geographic region
Maikadra1	1	Tigray	Qfta- humera	685	western
Maikadra2	2	Tigray	Qfta- humera	685	western
Maikadra3	3	Tigray	Qfta- humera	685	western
Maikadra4	4	Tigray	Qfta- humera	685	western
Maikadra5	5	Tigray	Qfta- humera	685	western
Maikadra6	6	Tigray	Qfta- humera	685	western
Maikadra7	7	Tigray	Qfta- humera	685	western
Maikadra8	8	Tigray	Qfta- humera	685	western
Maikadra9	9	Tigray	Qfta- humera	685	western
Maikadra10	10	Tigray	Qfta- humera	685	western
Maikadra11	11	Tigray	Qfta- humera	685	western
Maikadra12	12	Tigray	Qfta- humera	685	western
Maikadra13	13	Tigray	Qfta- humera	685	western
Maikadra14	14	Tigray	Qfta- humera	685	western
Maikadra15	15	Tigray	Qfta- humera	685	western
Hillegin1	16	Tigray	setit – humera	600	western

Hillegin2	17	Tigray	setit – humera	600	western
Hillegin3	18	Tigray	setit – humera	600	western
Hillegin4	19	Tigray	setit – humera	600	western
Hillegin5	20	Tigray	setit – humera	600	western
Hillegin6	21	Tigray	setit – humera	600	western
Hillegin7	22	Tigray	setit – humera	600	western
Hillegin8	23	Tigray	setit – humera	600	western
Hillegin9	24	Tigray	setit – humera	600	western
Hillegin10	25	Tigray	setit – humera	600	western
Hillegin11	26	Tigray	setit – humera	600	western
Hillegin12	27	Tigray	setit – humera	600	western
Hillegin13	28	Tigray	setit – humera	600	western
Hillegin14	29	Tigray	setit – humera	600	western
Hillegin15	30	Tigray	setit – humera	576	western
Hillegin16	31	Tigray	setit – humera	576	western
Hillegin17	32	Tigray	setit – humera	576	western
Hillegin18	33	Tigray	setit – humera	576	western
Hillegin19	34	Tigray	setit – humera	576	western
Bereket1	35	Tigray	Qfta- humera	694	western
Bereket2	36	Tigray	Qfta- humera	694	western
Bereket3	37	Tigray	Qfta- humera	694	western
Bereket4	38	Tigray	Qfta- humera	694	western
Bereket5	39	Tigray	Qfta- humera	694	western
Bereket6	40	Tigray	Qfta- humera	694	western
Bereket7	41	Tigray	Qfta- humera	694	western
Bereket8	42	Tigray	Qfta- humera	694	western
Bereket9	43	Tigray	Qfta- humera	694	western
Bereket10	44	Tigray	Qfta- humera	694	western
Bereket11	45	Tigray	Qfta- humera	694	western

Bereket12	46	Tigray	Qfta- humera	694	western
AdiGoshu1	47	Tigray	Qfta- humera	907	western
AdiGoshu2	48	Tigray	Qfta- humera	907	western
AdiGoshu3	49	Tigray	Qfta- humera	907	western
AdiGoshu4	50	Tigray	Qfta- humera	907	western
AdiGoshu5	51	Tigray	Qfta- humera	907	western
AdiGoshu6	52	Tigray	Qfta- humera	846	western
AdiGoshu7	53	Tigray	Qfta- humera	846	western
AdiGoshu8	54	Tigray	Qfta- humera	846	western
AdiGoshu9	55	Tigray	Qfta- humera	846	western
AdiGoshu10	56	Tigray	Qfta- humera	846	western
AdiGoshu11	57	Tigray	Qfta- humera	846	western
AdiGoshu12	58	Tigray	Qfta- humera	846	western
AdiGoshu13	59	Tigray	Qfta- humera	846	western
AdiGoshu14	60	Tigray	Qfta- humera	846	western
AdiGoshu15	61	Tigray	Qfta- humera	846	western
AdiGoshu16	62	Tigray	Qfta- humera	846	western
Adiabo1	63	Tigray	Sheraro		N/western
Adiabo2	64	Tigray	Sheraro		N/western
Adiabo3	65	Tigray	Sheraro		N/western
Adiabo4	66	Tigray	Sheraro		N/western
Adiabo5	67	Tigray	Sheraro		N/western
Adiabo6	68	Tigray	Sheraro		N/western
Adiabo7	69	Tigray	Sheraro		N/western
Bamya Humera	70	Tigray	Released variety	609	western
SOH 701	71	India	Registered C/ variety		India
SOH 714	72	India	Registered C variety		India

3.3. Experimental Design and Trial management

The field experiment utilized an alpha lattice incomplete block design to manage a large number of treatments (72) while ensuring plot uniformity. Seventy-two genotypes were randomized across two replicates (super block), each containing six incomplete blocks. Each block encompassed 12 experimental plots. These incomplete blocks, also known as sub-blocks, do not include all genotypes. Plot size measured 1.35 meters by 2.40 meters. Plant spacing was set at 45 centimeters between rows and 30 centimeters between plants within a row. This configuration resulted in 4 rows and 10 plants per plot. A separation of 1 meter was maintained between plots and 1.5 meters between blocks. Seeding involved planting three seeds per planting hill, with subsequent thinning to one plant per hill at the 3-4 leaf stage.

3.4 Data Collection

Five plants per plot were chosen randomly, excluding border plants at each end for consistency. These chosen plants were tagged for easy identification throughout the experiment. A strict data collection process aligned with the comprehensive descriptor list established for okra species in 1991 by the International Plant Genetic Resources Institute (IPGRI) guided the collection of essential information on various plant characteristics. This list served as a blueprint for the data collection process.

3.4.1 Quantitative Data Collection

The data collection focused on two key categories defined by IPGRI's descriptor list. The first category involved quantitative traits, which are precise measurements of physical plant characteristics. The focus was on five plants per row, leaving out the border plants at each end. Here are some specific quantitative data collected, listed in the order they were measured:

- **Days to Emergence (50%):** The number of days it took for half the seedlings in a plot to emerge above the soil, starting from the planting date, was carefully counted.
- **Plant Height (cm):** At final harvest, the height of five plants from the ground to the tip of the main stem was measured, following IPGRI's descriptor list. The average height was then recorded.
- **Stem Diameter (cm):** Calipers were used during final harvest to measure the diameter of the stem at the base for five plants. The average diameter was recorded, adhering to IPGRI's recommendations.

- **Number of Internodes**: As suggested by IPGRI, the total number of internodes per plant was counted at final harvest, and the average of five plants was calculated.
- **Internode Length (cm):** The length of the internodes between the fifth and sixth node was measured before the first harvest, following IPGRI's descriptor list.
- **Number of Branches per Plant:** At the last harvest, the number of branches on five plants per plot was counted, following IPGRI's guidelines. The average number of branches was then calculated.
- **Days to Flowering Stages:** Following IPGRI's descriptor list, the days from planting to when the first flower appeared (first flowering) and when 50% of plants in a plot were flowering (50% flowering) were recorded.
- **Days to Maturity:** The number of days from seedling emergence to when 90% of plants in a plot reached maturity was counted, as outlined by IPGRI.
- **Number and Weight of Dry Pods per Plant (g**): To determine the average number and weight of dry pods per plant, pods from five plants per plot were harvested, counted, and weighed following IPGRI's protocol.
- **Number of Ridges per Pod:** The average number of ridges on five dry pods per plot was calculated, following IPGRI's recommendations.

3.4.2 Qualitative Data Collection

While the provided information focused on quantitative data collection, IPGRI's descriptor list likely includes sections for qualitative data collection as well. These data focus on non-numerical observations of the plants. Here are some potential examples of qualitative data that could be collected following IPGRI's guidelines:

- **Plant Habit:** The overall growth pattern of the okra plants (bushy, upright, sprawling) was recorded.
- **Leaf Characteristics:** Qualitative descriptors were used for leaf size (large, small), shape (lobed, unlobed), color (dark green, light green), and surface texture (smooth, rough).
- **Flower Color and Size:** The color (yellow, white) and size (large, small) of the okra flowers were observed and captured.
- **Pod Characteristics:** Qualitative data on pod shape (straight, curved), color (green, red), surface texture (smooth, bumpy), and presence or absence of spines were collected.

By following IPGRI's descriptor list, a standardized and comprehensive dataset was created. This dataset can be compared to future studies and contribute valuable information to understanding and improving okra varieties.

3.5 Methods of Statistical Data Analysis

3.5.1. Quantitative data analysis

ANOVA and mean comparison

The alpha-lattice design is widely used in agricultural research for experiments with numerous treatments. By organizing plots into incomplete blocks, this design minimizes environmental variability and reduces experimental error, ensuring precise comparisons between treatments (Patterson & Williams, 1976). It is especially useful when testing many genotypes across diverse conditions, as it improves statistical power and efficiency.

In this study, data analysis involved two key components: ANOVA and post-hoc tests using R software (version 4.4.1). R provides several packages for implementing alpha-lattice designs, such as agricolae, which offers convenient tools for experimental designs and statistical tests (de Mendiburu, 2020).

Model-based Approach and Flexibility

The model-based approach adopted in this study allows for deeper exploration of treatment effects and interactions across the two experimental locations. This method incorporates replication, block, and location effects while capturing genotype-by-environment interactions, which are essential for breeding programs aiming to develop resilient cultivars. The flexibility of R software enables researchers to adjust the model structure to fit the specific requirements of alpha-lattice designs (Bates et al., 2015; Piepho et al., 2008).

Correlation among Quantitative Traits of Okra Accessions

This section examines the relationships between quantitative traits of okra accessions using Pearson correlation analysis. Pearson correlation measures the strength and direction of linear associations between continuous variables. Data analysis was performed using R software, employing packages like tidy verse, psych, and corrplot for data handling, statistical computations, and visualization.

A correlation significance test was conducted to identify statistically meaningful correlations. A custom function assigned significance stars based on p-values for easier interpretation of results:

The most common formula used to calculate the correlation coefficient between two quantitative traits (let's call them X and Y) is Pearson's correlation coefficient, denoted by r. It's calculated as follows:

$$r = \Sigma[(\mathrm{Xi} - \bar{X})(\mathrm{Yi} - \bar{Y})] / \sqrt{\ } [\Sigma(\mathrm{Xi} - \bar{X})^2 * \Sigma(\mathrm{Yi} - \bar{Y})^2]$$

Where:

r is the Pearson's correlation coefficient

Xi is the value of trait X for the ith accession

$\bar{X}$ is the mean value of trait X

Yi is the value of trait Y for the ith accession

$\bar{Y}$ is the mean value of trait Y

Σ represents the summation over all accessions (Field, 2013)

The correlation matrix, combined with significance levels, guides breeding programs by identifying traits with favorable associations for selection. Understanding these correlations helps breeders optimize trait combinations, ensuring improved yield and performance of future okra varieties.

This method provides robust insights into trait relationships, crucial for selecting genotypes that align with breeding goals.

Estimates of Variability Components: This study employed R software (version 4.4.1) to estimate variability components, including genotypic and phenotypic variance, heritability (H^2), and genetic advance (GA). These components provide insights into the genetic potential of okra accessions and their responsiveness to selection.

Broad-Sense Heritability (H^2): Broad-sense heritability (H^2) was calculated to measure the proportion of phenotypic variance attributed to genetic effects. High H^2 suggests greater genetic influence, making selection based on phenotypic traits more effective.

Formula: $H^2 = Vg / (Vg + Ve)$

Where: H^2 = Broad-sense heritability

Vg = Genetic variance (variance due to genetic factors)

Ve = Environmental variance (variance due to environmental factors)

Genetic Advance (GA) and Genetic Advance as a % of Mean (GAM): Genetic advance (GA) predicts the improvement expected after one selection cycle. GA expressed as a percentage of the mean (GAM) indicates how much a trait can be improved. Traits with high heritability and GA offer better prospects for genetic improvement.

Genetic Advance as a % of Mean (GAM):

$GAM = (GA / \bar{x}) * 100$ Where:

GAM = Genetic advance as a percentage of the mean

GA = Genetic advance (calculated above)

$\bar{x}$ = Mean of the original population

Clustering of Okra Accessions: This study employed R software (version 4.4.1) for hierarchical clustering of okra accessions, aiming to group genotypes based on their morphological traits. Hierarchical clustering is a powerful tool for identifying patterns and relationships within large datasets. The Unweighted Pair Group Method with Arithmetic Mean (UPGMA) and Euclidean distances were used to perform agglomerative clustering.

Mahalanobis Distance Analysis: Mahalanobis distance is a multivariate statistical measure used to determine the similarity between an observation and a dataset's centroid, accounting for correlations among variables. In this study, Mahalanobis distance was applied using R software to assess the divergence among okra accessions based on multiple traits. It is particularly useful for identifying distinct clusters and outliers in breeding programs.

Here's the formula for Mahalanobis Distance Formula:

The Mahalanobis Distance (D^2) between two vectors x and y is calculated as:

$D^2 = (x - y)^T S^{-1} (x - y)$ Where:

D^2 is the Mahalanobis Distance

x and y are the vectors representing the two points (observations) in multivariate space. These vectors contain the measurements of the different variables.

$(x - y)^T$ is the transpose of the difference vector (x - y). This is important for matrix multiplication.

S^{-1} is the inverse of the sample covariance matrix S. The covariance matrix describes how the variables relate to each other (De Maesschalck et al., 2000).

Principal Component Analysis (PCA): Principal Component Analysis (PCA) is a statistical technique used to reduce the dimensionality of a dataset while retaining as much variation as possible. In this study, PCA was employed to identify key traits contributing to the overall variability among okra accessions, using R software.While a full matrix representation is complex, a simplified way to express the core idea is:

$S v = \lambda v$ Where: S is the covariance matrix, v is an eigenvector, λ is an eigenvalue (R Core Team, 2023)

3.5.2. Qualitative Data Analysis

The qualitative data analysis focused on categorical traits of okra accessions, including variables like No Ridges, Stem Texture, Fruit Color, Fruit Shape, Maturity, Stem Pubescence, and Flower Color, totaling 13 categorical variables. These traits are essential for characterizing the morphology and developmental stages of okra accessions and provide valuable information for descriptive analysis and potential breeding selection. R statistical software was used for data analysis and visualization, leveraging. Several R packages were used to facilitate data manipulation and visualization:

ggplot2: This package was the primary tool for creating bar charts, which effectively illustrate the distribution of categorical traits. The flexibility of ggplot2 allows for customization of colors, labels, and themes to enhance data presentation.

reshape2: Used to reshape data into formats suitable for plotting. This package is particularly useful when transforming wide-format data into long-format, which is often required for ggplot2.

dplyr: Essential for data manipulation, dplyr enables efficient counting of categories, calculating proportions, and formatting data for visualization. It simplifies tasks such as filtering, summarizing, and grouping data.

Break Down: This package allows for deeper inspection of categorical data by breaking down results and simplifying the analysis, making it easier to interpret complex distributions.

CHAPTER FOUR: RESULTS AND DISCUSSION

4.1 Performance analysis (using ANOVA) of accessions

The analysis of variance (ANOVA) for the phenology, morphological, and yield-related traits of 72 okra accessions (Table 1) revealed highly significant differences ($P < 0.01$) among the genotypes for all traits. This indicates the presence of substantial genetic variability, which is crucial for selection in breeding programs aimed at improving these traits.

4.1.1 Phenological Trait

The analysis of variance indicated significant differences among the 72 okra genotypes for key phenological traits, such as days to emergence (mean square = 3.82, $p < 0.001$), days to 50% flowering (mean square = 584.64, $p < 0.001$), and days to first picking (mean square = 727.47, $p < 0.001$). The observed coefficient of variation (CV%) for these traits was moderate, suggesting that the differences are mainly due to genetic variation among the genotypes rather than environmental influences. This high level of genetic variability suggests that breeding for early or late maturation could be feasible within this set of genotypes.

The significant genetic variability observed in phenological traits, such as days to flowering and days to first picking, aligns with findings from similar studies, underscoring the diversity in maturity timing among okra genotypes. Mallesh et al. (2015) reported significant differences among 52 okra accessions in India for traits like days to first flowering, fruit set, and first harvest, suggesting that okra genotypes may exhibit a broad range of maturity timelines under different environmental conditions. Likewise, studies by Badiger et al. (2017) and Singh et al. (2017) found significant variations in days to first flowering and days to 50% flowering among diverse okra genotypes, confirming the existence of valuable genetic diversity in phenological characteristics.

Table 3: Mean squares from analysis of variance for growth traits of 72 okra genotypes

. Mean squares from analysis of variance for growth traits of 72 okra genotypes

Trait	Means	Replication(1)	Genotype (71)	Location	Replication:Block(11)	Genotypes:Location	Error(133)	CV%
Days to Emergency	7.02	2.00	3.82***	9.39**	1.01	0.23	1.01	14.34
days to 50% flowering	64.38	96.94	584.64***	2871.75***	61.86	28.30	42.48	10.12
Steam of diameter	1.61	0.27*	1.17***	10.87***	0.13*	0.02	0.06	14.68
Days first picking	73.66	0.65	727.47***	2070.84***	52.41	37.82	47.83	9.39
Plant height cm	144.98	628.90	5006.50***	1888.40**	278.30	190.20	225.50	10.36
No of branches	4.64	0.07	11.16***	73.51***	0.57*	0.97	0.50	15.22
Internode length	5.59	4.47*	12.44***	110.78***	2.19	1.40	1.39	21.11
pandicle length	1.98	2.85*	1.01***	13.28***	0.16	0.03	0.15	19.60
No_ridges	6.79	0.13	11.54***	2.00	2.64	0.70	1.53	18.21
Fruit_length	13.67	0.18	60.13***	39.41**	7.33	0.84	4.19	14.98
Fruit_diameter	1.57	0.33	1.14***	2.35***	0.13	0.04	0.10	20.17
Fruits plant	21.74	173.54	206.12 ***	636.59 ***	10.94	7.77	11.02	15.27
single fruit weight	31.94	9.51	124.49***	512.00***	48.99***	16.84	12.20	10.94
weight fruit per plant	241.26	1018.10	10059.50***	5179.30**	366.20	953.90	729.20	11.19
Esteemed yield hectare	126.83	440.52	3008.02***	1780.67**	96.74	210.48	162.46	10.05

Signifiance codes : 0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1 CV (%) = Coefficient of Variation in percent. Numbers in parenthesis represent degree of freedom for the respective source of variation.

In studies conducted in Nigeria, Nwangburuka et al. (2012) and Olayiwola et al. (2015) also observed significant differences in flowering time across various okra genotypes, further supporting the influence of genotype on phenological traits. This consistency across studies from different regions reinforces the potential to select okra varieties with tailored flowering and maturity timelines. In the Ethiopian context, selecting for variability in phenological traits could enable breeders to develop varieties that are well-suited to local growing conditions, potentially enhancing crop scheduling and optimizing yield.

The current findings, therefore, not only confirm that substantial phenological diversity exists within Ethiopian okra accessions but also highlight the relevance of these traits for breeding programs aiming to improve crop adaptability and productivity in variable climates.

4.1.2 Morphological Traits

The analysis of variance revealed significant differences among the 72 okra genotypes for key morphological traits, including stem diameter (mean square = 1.17, $p < 0.001$), plant height (mean square = 5006.50, $p < 0.001$), and the number of branches (mean square = 11.16, $p < 0.001$). The coefficients of variation (CV%) for these traits varied, indicating a mix of genetic and environmental influences, with traits such as plant height showing moderate variability (CV% = 10.36) while others, like the number of branches, had higher variability (CV% = 15.22).

The significant variability observed in morphological traits among the okra genotypes underscores the potential for selective breeding to enhance desired characteristics. For instance, the substantial differences in plant height and stem diameter are consistent with findings from previous studies, which highlighted the importance of these traits in determining the structural integrity and overall productivity of okra plants. Mihretu et al. (2014), Muluken et al. (2016), and Tesfa and Yosef (2016) have all documented significant variation in morphological traits within different okra accessions, supporting the notion that genetic diversity plays a critical role in trait expression.

Furthermore, research by Badiger et al. (2017) and Singh et al. (2017) also emphasized the significance of morphological traits, such as stem diameter and plant height, in okra breeding programs. Their findings align with the current study, which demonstrated that the observed differences in these traits could be effectively utilized in breeding strategies to develop high-yielding and resilient okra varieties.

The variability in morphological traits, particularly those with moderate to high coefficients of variation, suggests that there is considerable opportunity for genetic improvement. Selecting genotypes with desirable characteristics, such as optimal plant height and stem strength, could enhance resistance to lodging and improve yield potential. Overall, the findings highlight the importance of utilizing the existing morphological diversity within the okra germplasm to inform breeding programs aimed at developing varieties that can thrive in diverse Ethiopian agro-climatic conditions.

4.1.3 Yield-Related Traits

Yield-related traits demonstrated high levels of genotypic variability, indicating that these traits are strongly influenced by genetic factors (table 1). For instance, fruit length and fruit diameter showed significant mean squares of 60.13 ($p < 0.001$) and 1.14 ($p < 0.001$), respectively, while the number of fruits per plant (mean square = 206.12, $p < 0.001$) also showed considerable genetic diversity. The weight of fruits per plant (mean square = 10059.50, $p < 0.001$) and the esteemed yield per hectare (mean square = 3008.02, $p < 0.001$) exhibited substantial variation among genotypes, reflecting strong potential for yield improvement through selection.

The pronounced variability in yield-related traits, such as fruit length, diameter, and the number of fruits per plant, is highly beneficial for breeding high-yielding okra varieties. Fruit length and diameter are crucial for marketability, as consumer preference in Ethiopian markets often favors larger fruits with an appealing shape and size (Hailemariam & Mekonnen, 2022). This significant genotypic variation allows for the selection of genotypes that align with market demands, enhancing the economic viability of okra farming.

The strong genotypic influence on the number of fruits per plant and the weight of fruits per plant highlights the potential for achieving higher yields through genetic improvement. The substantial variability in esteemed yield per hectare also indicates that selecting genotypes with superior yield traits can have a major impact on productivity. Previous studies in Ethiopia have emphasized the importance of yield-related traits for ensuring food security and improving farmer incomes, particularly in regions where okra serves as a staple crop (Melese et al., 2023).

Overall, the high genetic variability in yield-related traits across these okra genotypes underscores the potential for breeding programs to improve productivity. By selecting high-yielding and market-preferred varieties, breeders can support Ethiopian farmers in achieving better yields and higher economic returns. The findings align with Teklay et al. (2020), who advocated for breeding strategies that prioritize yield enhancement and quality traits, ensuring that new varieties meet both productivity and consumer preferences.

The analysis of variance on the phenological, morphological, and yield-related traits of 72 okra genotypes showed significant genetic variability, indicating strong potential for improving okra varieties through selective breeding. The significant differences observed in phenological traits, such as days to emergence and days to flowering, suggest adaptability to Tigray's diverse growing environments, which is crucial for developing varieties suited to various agro-ecological zones. Notably, these traits also exhibited relatively low coefficients of variation (CV%), underscoring that observed phenotypic differences are largely attributable to genetic factors rather than environmental noise, which is favorable for reliable selection.

In morphological traits, such as stem diameter, plant height, and internode length, the substantial variability suggests that genotypes possess distinct structural characteristics that can enhance resilience and productivity. Traits with higher CV% values, like internode length and panicle length, indicate more environmental influence, suggesting that these traits may benefit from stabilization through breeding practices.

And also in Yield-related traits such as fruit size, fruit number per plant, and yield per hectare, showed high genetic variability, with significant potential for improving yield. The low to moderate CV% values associated with these yield traits imply that their phenotypic expression is relatively stable, making them dependable targets for selection. Furthermore, these traits align with consumer preferences for larger fruit size and high productivity, which are essential for meeting market demands and supporting Tigray farmers' economic outcomes.

Overall, the significant genetic diversity and manageable CV% values across key traits highlight the potential for developing high-yielding, resilient okra varieties tailored to Tigray's agricultural needs. By focusing on traits with lower CV% and strong genetic control, breeding programs can more reliably achieve improvements that contribute to sustainable agricultural development, food security, and economic gains for Tigray farmers even Ethiopian farmers.

4.2 Performance Analysis (Using Mean Values) of Accessions

The performance analysis of okra accessions revealed considerable variation in phenological and morphological traits, as well as yield-related characteristics, as presented in Table 2. This diversity indicates a rich genetic resource that can be harnessed for breeding programs aimed at improving okra production. The mean values of the traits underscore the potential for selecting superior accessions with desirable attributes. To further assess these differences, the Tukey test was employed to compare means among the accessions, highlighting significant variations in performance. Accessions demonstrating enhanced traits are vital for developing high-yielding cultivars that can adapt to different agro-ecological environments. Overall, this analysis contributes valuable insights into the genetic potential of okra accessions.

4.2.1 Phenological Traits

Days to Emergence: Significant variation was observed in the number of days to emergence among the okra accessions (Table 4). The time to emergence ranged from 5 days for the AdiGoshu9 accession to 9 days for the Maikadra10 accession. Accessions such as Maikadra10, Maikadra15, Hillegin11, Maikadra11, Maikadra4, Maikadra1, Hillegin4, and AdiGoshu14 exhibited longer emergence times of 8.5 to 9 days. In contrast, AdiGoshu9, Bereket6, and Bereket7 emerged the fastest at 5 days, followed closely by AdiGoshu12 (5.25 days), Hillegin3 (5.5 days), Bereket4 (5.75 days), and Adiabo5 (5.5 days). These accessions demonstrated quicker and more reliable germination compared to the check cultivars Bamya Humera (8.81 days) and SOH 714 (8.59 days).

Number of Days to 50% Flowering: The time to 50% flowering varied significantly among accessions, with flowering times ranging from 36.5 days in AdiGoshu9 to 82.5 days in Bereket7 (Table 4). Early flowering accessions included Hillegin19 (44.0 days), Hillegin16 (41.5 days), AdiGoshu12 (38.75 days), and AdiGoshu9 (36.5 days), which flowered significantly earlier than the check cultivars SOH 701 (63.5 days) and SOH 714 (74.25 days). Conversely, accessions such as Bereket7 (82.5 days), Maikadra11 (81.61 days), AdiGoshu13 (81.25 days), Maikadra15 (80.75 days), and AdiGoshu15 (80.0 days) exhibited the latest flowering times.

Number of Days to First Picking: The variation in the number of days to first picking among the okra accessions indicated a wide range of maturity rates (Table 4). Time to first picking ranged from 46.50 to 97.75 days. Early maturing accessions included AdiGoshu8 (53.00 days), Adiabo4 (53.00 days), AdiGoshu9 (48.25 days), Hillegin19 (47.50 days), Hillegin16 (47.25 days), and AdiGoshu12

(46.50 days), suggesting better adaptability and genetic performance. Most accessions were mid-season, maturing within 55 to 86 days, while a few genotypes, such as Bereket2 (97.75 days), Bereket7 (96.25 days), AdiGoshu13 (96.25 days), Maikadra11 (95.75 days), Maikadra15 (95.25 days), AdiGoshu15 (92.75 days), Hillegin4 (91.50 days), Bereket6 (91.50 days), and Adiabo5 (90.50 days), took longer to mature.

The observed variation in phenological traits among the okra accessions indicates significant potential for selection based on maturity characteristics. Early maturing accessions such as Hillegin19, Hillegin16, AdiGoshu12, and AdiGoshu9 showed advantages in regions with shorter growing seasons, allowing farmers to harvest earlier and prepare for subsequent crops. This aligns with findings from Kenaw et al. (2021), who noted that early maturity can mitigate risks associated with drought and late-season diseases. The selection of accessions for specific maturity classifications—early, medium, and late—can be strategically utilized to meet market preferences and environmental challenges.

Moreover, understanding local market demands for okra maturity is crucial. As indicated by Temam et al. (2019), consumer preferences can vary widely, and early maturing varieties may be favored for their culinary uses. The inclusion of these varieties in crop rotations not only improves soil health but also reduces pest pressures, enhancing overall productivity. Future research should focus on the genetic underpinnings of these traits, enabling the development of cultivars tailored to diverse farming systems and market needs.

The findings in this study corroborate with previous research; for example, Kenaw et al. (2021) reported variations in days to emergence (9.33 to 12 days) and flowering (55.35 to 75.91 days). Similarly, Muluken et al. (2021) highlighted delayed emergence and flowering in Ethiopian genotypes compared to commercial varieties, reinforcing the importance of local genetic resources in breeding programs (Mihretu et al., 2020; Pandey et al., 2021).

Table 4: Mean values of best ten okra accessions for phenology and growth traits evaluated at Humera

Trt No	accessions	Days to emergency	days to 50% flowering	Steam diameter	Days first pikcing
1	Bereket4	5.75^{bcd}	74.5000 ^{abcdefghij}	2.0900^{bcdefghij}	86.75 ^{abcdef}
2	Hillegin10	8.00^{abcd}	50.0000 ^{pqrstuv}	1.6500 efghijklm	62.75 ^{ijklmnopqr}
3	Maikadra1	9.00^{a}	55.7500 ^{jklmnopqrstuv}	1.1100 ^{mno}	63 ^{ijklmnopqr}
4	AdiGoshu9	6.00^{abcd}	74.7500 ^{abcdefghij}	1.7450^{cdefghijklm}	83 ^{abcdefghij}
5	Bereket10	6.50^{abcd}	74.0000^{abcdefghijkl}	3.7000^{a}	83.25 ^{abcdefghij}
6	AdiGoshu12	5.25^{cd}	38.7500 ^{uv}	1.3250 ^{lmno}	46.5 ^{r}
7	Hillegin6	6.50^{abcd}	51.0000 ^{opqrstuv}	2.4800 ^{b}	64.25 hijklmnopqr
8	AdiGoshu8	7.50^{abcd}	48.0000 ^{qrstuv}	0.8000 ^{o}	53 ^{Opqr}
9	Hillegin14	7.00 ^{abcd}	72.2500 ^{abcdefghijklmn}	2.3000 ^{bcdefg}	81.5 abcdefghijkl
10	AdiGoshu11	9.00^{a}	78.0000 ^{abcde}	1.1250 ^{mno}	83.5 ^{abcdefghi}

4.2.2 Morphological Traits

Stem Diameter: Significant differences ($p < 0.05$) in stem diameter were observed among the evaluated okra accessions, with measurements ranging from 0.78 cm in Bereket-6 to 3.70 cm in Bereket-10 (Table 4). This variation highlights the potential for genetic improvement of this trait, as thicker stems enhance plant stability and lodging resistance. Developing cultivars with optimal stem thickness is essential, but it should not compromise yield or fruit quality.

Plant Height: The studied okra accessions exhibited significant variation in plant height. Mean heights varied, with Hillegin13 reaching 208.81 cm, while Bereket6 measured 51.30 cm (Table 5). Similar variations were reported by Temam et al. (2019). The tallest accessions tended to have more branches and greater stem diameter, while the shortest accessions showed lower branching. A moderate variation (coefficient of variation = 10.36%) suggests potential for further selection based on height.

Number of Branches per Plant: The number of branches per plant varied significantly among the 72 okra accessions (table 5). Accessions with the highest average branches included AdiGoshu2 (7.20), Adiabo5 (7.18), and Bereket6 (7.16). An intermediate group averaged between 5.99 to 2.78

branches, while the fewest branches were observed in AdiGoshu5 (2.80) and Hillegin16 (2.78). This diverse genetic makeup presents opportunities for breeding programs targeting increased fruit production while considering plant manageability.

Internode Length and Pedicle Length: Significant differences ($p < 0.05$) in internode and pedicle lengths were found among okra genotypes. Internode length ranged from 2.27 cm in AdiGoshu8 to 9.85 cm in Bereket4, while pedicle length varied from 0.80 cm in Hillegin9 to 3.11 cm in Maikadra15 (Table 5). These variations indicate opportunities for genetic improvement, balancing plant architecture with traits affecting yield and harvesting efficiency.

Number of Locules: The comparison of locule numbers across the accessions showed significant variation, with the highest counts observed in accessions 21, 47, and 62, all having 11 locules. This trait can influence fruit development and yield.

The significant variation observed in stem diameter across the okra accessions underscores the potential for genetic improvement. Thicker stems can enhance plant stability, which is crucial for lodging resistance, particularly in regions prone to strong winds (Kenaw et al., 2021). Moreover, selection for stem diameter should consider trade-offs between plant robustness and the overall yield potential to avoid compromising fruit quality (Mihretu et al., 2020).

The observed variations in plant height and the number of branches per plant align with findings by Temam et al. (2019), who reported similar morphological diversity in okra accessions. Taller plants typically exhibit more branching, leading to higher fruit production. The moderate coefficient of variation suggests that selection for height and branching traits could enhance yield potential. For effective selection, breeders might consider the ideal height that maximizes sunlight exposure and minimizes shading of lower branches (Pandey et al., 2021).

The significant differences in internode and pedicle lengths indicate the potential for optimizing plant architecture, which is essential for harvesting efficiency. Accessions with longer pedicels may facilitate easier fruit harvesting, a vital consideration for commercial production (Mihretu et al., 2020). Furthermore, the number of locules directly influences fruit development and yield potential, making this trait a key target for selection in breeding efforts. Breeders should aim to develop varieties with higher locule counts to enhance fruit size and yield, aligning with market demands for larger fruits.

These findings collectively indicate that understanding the genetic variation within these traits can significantly impact breeding strategies aimed at improving okra production. Future research should focus on identifying the genetic basis of these traits to develop improved cultivars tailored to specific environmental conditions and market preferences.

Table 5: Mean values of best ten okra accessions for growth traits evaluated at Humera

Trt No	Accessions	Plant height cm	No of branches	Inter nod lentgh	pedL	Fruit length
1	Bereket4	206.895^{ab}	7.1425^{a}	9.845^{a}	$1.745^{efghijklmno}$	14.8425^{bcdefg}
2	Hillegin10	185.005^{Abcd}	7.135^{a}	9.775^{ab}	$1.8525^{cdefghijklmno}$	16.67^{Bcdefg}
3	Maikadra1	$158.075^{cdefghijklmnop}$	6.97^{ab}	$4.595^{efghijklmn}$	$1.795^{defghijklmno}$	7.9825^{jklm}
4	AdiGoshu9	191^{Abc}	7.04^{ab}	8.1175^{abcde}	$2.465^{abcdefghijkl}$	15.74^{bcdefg}
5	Bereket10	185.005^{Abcd}	7.135^{a}	9.775^{ab}	$1.8525^{cdefghijklmno}$	16.67^{Bcdefg}
6	AdiGoshu12	177.2325^{abcdef}	5.785^{abcd}	$7.2325^{abcdefghij}$	$1.8325^{defghijklmno}$	15.1475^{bcdefg}
7	Hillegin6	181.625^{abcd}	6.9575^{ab}	8.0675^{Abcdef}	$2.155^{abcdefghijklm}$	$13.9675^{cdefghij}$
8	AdiGoshu8	65.875^{R}	7.1125^{a}	2.265^{n}	1.3075^{Lmno}	20.48^{ab}
9	Hillegin14	$171.4725^{abcdefghijk}$	3.0975^{jklmno}	$7.3725^{abcdefghi}$	$2.69^{abcdefgh}$	$13.185^{defghijkl}$
10	AdiGoshu11	$131.03^{hijklmnopq}$	$5.1375^{abcdefghij}$	$4.3725^{ghijklmn}$	$1.8075^{defghijklmno}$	15.22^{bcdefg}

4.2.3 Yield Related Traits

Variation in Yield-Related Traits: The evaluated okra accessions exhibited considerable variation in yield-related traits (Table 5). Accessions such as Bereket4, Hillegin10, Maikadra1, AdiGoshu9, and Bereket10 demonstrated superior performance across multiple traits, including the number of green fruits per plant, weight of green fruits per plant, green fruit length, green fruit width, and overall fruit yield. Notably, AdiGoshu2 stood out for its exceptionally long fruit length, significantly exceeding other genotypes. Additionally, Hillegin10, AdiGoshu8, and Hillegin1 produced longer fruits, while the majority of genotypes (61) exhibited medium fruit lengths. A smaller group, including AdiGoshu4, Hillegin11, Maikadra3, Hillegin3, AdiGoshu13, AdiGoshu15, and Hillegin15, was categorized as short-podded.

Fruit Diameter: Significant variation ($p < 0.05$) in fruit diameter was observed among the okra accessions. Hillegin1 exhibited the largest diameter (2.74 cm), while AdiGoshu13 had the smallest

(0.62 cm). Genotypes such as Hillegin1 and SOH 701 displayed significantly larger fruit diameters compared to check cultivars Bamya Humera and SOH 714. Most genotypes fell into intermediate diameter categories, with no significant differences among them, though they outperformed Bamya Humera. A third group, including genotypes 55, 48, 22, and 67, exhibited the smallest diameters, similar to Bamya Humera but smaller than SOH 701 and SOH 714.

Fruit Length of Okra accessions: AdiGoshu2 (25.02 cm) and Hillegin10 (20.85 cm) exhibited the highest mean values for several traits, including the number of green fruits per plant, fruit weight, green fruit length, fruit width, and overall fruit yield. This suggests that their superior performance may be due to a combination of factors such as higher fruit count, increased weight, and longer fruit length, reflecting their genetic responsiveness to environmental conditions. Consumers tend to prefer longer and wider fruits with greater weight.

Number of Fruits per Plant: Significant variation in the number of fruits per plant was noted among the okra genotypes (Table 6). The number of fruits ranged from 7.75 in AdiGoshu40 to 33.81 in Maikadra10. Genotypes like Maikadra10, Hillegin5, Adiabo1, Maikadra9, and AdiGoshu6 produced significantly more fruits than the check cultivars Bamya Humera, SOH 701, and SOH 714. Conversely, genotypes 19, 54, 8, and 40 had significantly fewer fruits per plant compared to the checks.

Weight of Pods per Plant: Significant variation in pod weight per plant was observed among the okra accessions (Table 6). Pod weight ranged from 145.65 grams in Hillegin2 to 389.85 grams in Bereket4. Accessions such as Hillegin10, Maikadra1, Bereket10, AdiGoshu12, and Hillegin6 also exhibited higher pod weights, while Hillegin18 and Hillegin2 had lower weights.

Single Fruit Weight: A significant range in single fruit weight was observed among the okra accessions. Maikadra2 had the highest mean single fruit weight (41.77 g), followed by Bereket4 (40.33 g) and Maikadra1 (40.22 g). In contrast, Maikadra13, Bereket6, and Maikadra9 exhibited the lowest weights, at 20.07 g, 19.11 g, and 18.60 g, respectively.

Fruit Yield per Hectare: Significant variation in fruit yield per hectare was recorded among the okra accessions (Table). Yields ranged from 74.69 quintals in Hillegin2 to 206.25 quintals in Bereket4. Bereket4 exhibited the highest yield, followed by Hillegin10, Maikadra1, and AdiGoshu9, which also produced relatively high yields.

The substantial variation observed in yield-related traits among the evaluated okra accessions indicates considerable potential for genetic improvement (Muluken et al., 2020). Accessions such as Bereket4 and Hillegin10, which demonstrated exceptional performance, are vital for breeding high-yielding cultivars. The significant variation in traits such as the number of fruits per plant and overall fruit yield aligns with previous studies, which reported similar findings within Ethiopian okra germplasm (Tesfa & Yosef, 2019). Identifying superior accessions with desirable traits facilitates targeted breeding efforts aimed at enhancing productivity.

The results showed that AdiGoshu2's long fruit length significantly exceeded other genotypes, highlighting its potential for developing cultivars that cater to market demands for long-podded okra (Binalfew et al., 2020). Similarly, Hillegin1's larger fruit diameter can meet specific market preferences, indicating that accessions with larger diameters may be suited for processing applications (Kenaw et al., 2021). Understanding consumer preferences and market trends will be essential for guiding breeding strategies to ensure that new cultivars are both productive and market-oriented.

The variations in single fruit weight among the accessions underscore the importance of targeting specific market niches (Temam et al., 2020). Larger fruits, such as those from Maikadra2, may be valuable for fresh markets, while smaller fruits could fulfill different market needs. The significant differences in fruit yield per hectare recorded in this study emphasize the importance of further evaluation of accessions under diverse agro-ecological conditions to assess adaptability and yield stability (Mihretu et al., 2020).

Future research should focus on exploring the genetic basis of these traits to enhance our understanding and facilitate the development of high-yielding and resilient okra cultivars adapted to varying environmental conditions.

Table 6: Mean values of best ten okra accessions for growth traits evaluated at Humera

Trt No	Accessions	Fruit diameter	Fruits plant	single fruit wieghit	Weight fruits plant	Esteemed yield hectare
1	Bereket4	$8.5^{abcdefg}$	34.8725^{Abc}	40.325^{Abc}	389.8525^{A}	206.251^{A}
2	Hillegin10	6.25^{cdefg}	$29.66^{abcdefgh}$	40.8625^{Ab}	367.0325^{Ab}	193.9575^{Ab}
3	Maikadra1	5^{g}	35.9775^{ab}	40.2225^{abc}	344.0475^{abc}	181.575^{abc}
4	AdiGoshu9	5^{g}	34.4^{Abcd}	$37.4675^{abcdefg}$	$296.4525^{Bcdefgh}$	176.6925^{Abcd}
5	Bereket10	6.5^{bcdefg}	33.67^{abcde}	40.3275^{Abc}	333.195^{abcd}	175.7275^{abcde}
6	AdiGoshu12	5.5^{efg}	$27.6725^{abcdefghijkl}$	39.835^{abcd}	327.605^{abcde}	172.7175^{Abcdef}
7	Hillegin6	5.4^{efg}	36.6175 a	$35.5575^{abcdefghij}$	323.625^{Abcdef}	$170.5725^{abcdefg}$
8	AdiGoshu8	5.5^{efg}	11.1875^{Vwxy}	$26.9125^{hijklmnopqr}$	$311.3^{abcdefg}$	$163.9325^{Bcdefgh}$
9	Hillegin14	6.5^{bcdefg}	20.05 hijklmnopqrstuvw	31.3675 Abcdefghijklmno	$297.03^{bcdefgh}$	$156.245^{bcdefghi}$
10	AdiGoshu11	5.5^{efg}	$14.7575^{pqrstuvwxy}$	$31.6625^{abcdefghijklmn}$	$286.24^{bcdefghi}$	$150.4325^{cdefghij}$

4.3 Genetic variability of accessions using Genotypic and phenotypic variances

The genotypic and phenotypic variances for various traits of 72 okra genotypes were analyzed to understand the extent of genetic and environmental influences on the expression of these traits (Table 9). This analysis provides essential insights into genetic variability and helps identify traits that could be more stable or responsive to environmental factors.

4.3.1 Phenological Traits

Days to Emergence: The genotypic variance (1.51) was lower than the phenotypic variance (2.31), indicating a significant environmental influence on this trait.

Days to 50% Flowering: The genotypic variance was high (266.39) compared to the phenotypic variance (318.25), suggesting strong genetic control with some environmental influence.

Days to First Picking: This trait showed substantial genetic control with a genotypic variance of 336.67 against a phenotypic variance of 390.81.

The results for days to emergence highlight the considerable impact of environmental factors on this trait, as also noted by Adeoluwa and Kehinde (2011). While there is genetic control, the variation suggests that environmental conditions play a crucial role, especially in early establishment phases.

For days to 50% flowering, the significant genotypic variance indicates that breeding programs can effectively select for early flowering genotypes, supported by similar findings from Kumar et al. (2014). The genetic control observed for days to first picking aligns with Ehab et al. (2017), emphasizing the potential for selecting genotypes that can fruit earlier, thus enhancing productivity.

4.3.2 Morphological Traits

Stem Diameter: Both genotypic (0.53) and phenotypic (0.63) variances were low, indicating moderate genetic control with minimal environmental influence.

Plant Height: A high genotypic variance (2391.22) close to its phenotypic variance (2615.26) suggests strong genetic control with minimal environmental impact.

Number of Branches: The genotypic variance (5.08) was slightly lower than the phenotypic variance (6.08), indicating environmental influences alongside genetic factors.

Internode Length: This trait exhibited a genotypic variance of 5.25 and a phenotypic variance of 7.19, suggesting both genetic and environmental contributions.

Peduncle Length: The low genotypic variance (0.419) compared to the phenotypic variance (0.59) reflects limited genetic variability and a considerable environmental influence.

Number of Ridges: With a genotypic variance of 5.12 and a phenotypic variance of 6.43, moderate genetic control is evident, with environmental factors also playing a role.

The low variances in stem diameter imply stability across different environmental conditions, reinforcing the findings of Adeoluwa and Kehinde (2011). The significant genetic control over plant height indicates a promising trait for selection in breeding programs targeting height variability, as corroborated by Kumar et al. (2014).

In the case of the number of branches, the notable environmental influence suggests that external conditions might significantly affect branching patterns, aligning with findings from Ehab et al. (2017). The internode length's variability underscores the interplay between genetic and environmental factors, as noted in similar studies. The limited genetic variability in peduncle length indicates challenges in breeding for this trait, emphasizing the need for a targeted approach to enhance its expression.

4.3.3 Yield-Related Traits

Fruit Length: The phenotypic variance (31.76) was higher than the genotypic variance (28.37), indicating contributions from both genetic and environmental factors.

Fruit Diameter: The genotypic variance (0.52) was slightly lower than the phenotypic variance (0.61), suggesting moderate genetic control.

Number of Fruits per Plant: Both genotypic (96.63) and phenotypic (109.49) variances were high, indicating a strong genetic component.

Single Fruit Weight: The phenotypic variance (71.13) notably exceeded the genotypic variance (53.36), reflecting substantial environmental influence.

Weight of Fruits per Plant: High genotypic (4626.12) and phenotypic (5433.34) variances suggest robust genetic control with environmental influence.

Estimated Yield per Hectare: The genotypic variance (1409.57) was slightly lower than the phenotypic variance (1592.98), indicating contributions from both genetic and environmental factors.

The higher phenotypic variance in fruit length suggests a complex interaction of both genetic and environmental factors, aligning with findings from Adeoluwa and Kehinde (2011) regarding morphological stability. The moderate genetic control of fruit diameter indicates potential for selection but highlights the need to consider environmental conditions in breeding.

The high variances for the number of fruits per plant affirm the critical genetic basis for yield improvement, consistent with Kumar et al. (2014) on heritability in fruit traits. In contrast, the significant environmental influence on single fruit weight emphasizes the need for careful management of growing conditions to optimize fruit size, supported by Ethiopian studies by Adeoluwa and Kehinde (2011).

Lastly, the robust genetic control over the weight of fruits per plant indicates a promising trait for enhancing overall yield, while the estimated yield per hectare underscores the importance of both genetic and environmental factors in yield determination, as evidenced by previous research on okra yield dynamics (Ehab et al., 2017; Kumar et al., 2014).

4.4 Genetic variability of accessions using Genotypic and Phenotypic Coefficient of Variations

In plant breeding, understanding the variation within genotypes is essential for selecting superior individuals to enhance crop traits effectively. Two critical measures used to assess such variation are the Genotypic Coefficient of Variation (GCV) and the Phenotypic Coefficient of Variation (PCV). While GCV indicates genetic variability, PCV encompasses both genetic and environmental variations (Burton, 1952). A high GCV, close to PCV, implies substantial genetic control over a trait, thus showing greater potential for improvement through selection (Allard, 1960). In this study, GCV and PCV values for 72 quantitative traits of okra genotypes were calculated and summarized in Table 5. Figure 17 illustrates the distribution of these values across phenological, morphological, and yield-related traits, helping to identify traits with higher selection potential.

Table 7: the genotypic and phenotypic variances for various traits of 72 okra genotypes

Trait	Genotypic Variance	Phenotypic Variance

Days_to_emergency	1.51	2.31
daysto followering	266.39	318.25
Steam_diameter	0.53	0.63
Days_first_pikcing	336.67	390.81
Plant_height_cm	2391.22	2615.26
No_of_branches	5.0795	6.0787
Steam_diameter_cm	0.53	0.63
Inter_nod_lentgh	5.25	7.19
PedL	0.419	0.59
No_ridges	5.12	6.43
Fruit_length	28.37	31.76
Fruit_diameter	0.52	0.61
Fruits_plant	96.63	109.49
Fruit_weight	53.3597	71.1302
Weight_fruits_plant	4626.122	5433.3378
Esteemed_yield_hectare	1409.57	1592.98

4.4.1 Phenological Traits

The estimated GCV and PCV for phenological traits like days to 50% emergence and flowering displayed moderate variability, with PCV ranging from 21.63% to 30.42% and GCV from 18.54% to 25.12%. This moderate level suggests that these traits have a mix of genetic and environmental influence, aligning with Sivasubramanian and Madhavamenon's (1973) classification of moderate variability. Notably, the difference between PCV and GCV was generally below 5%, indicating that genetic factors predominantly drive these traits.

High GCV and PCV values observed for specific phenological traits, such as days to 50% flowering, align with findings by Yimam (2018) and Anteneh (2017), who reported similar moderate to high genetic variation in phenological traits among okra genotypes. These results underscore the potential for selecting genotypes with improved flowering times, essential for breeding programs aiming to optimize growth duration and adaptability (Muluken et al., 2016). However, traits with lower GCV and PCV values, like days to emergence, suggest limited genetic variability, which could impede progress through selection unless combined with favorable environmental conditions.

4.4.2 Morphological Traits

Morphological traits, including stem diameter, plant height, and the number of branches per plant, exhibited high GCV (22.5% to 48.54%) and PCV (25.4% to 53.09%) values. Traits such as plant height and the number of branches per plant had minimal differences between PCV and GCV values, suggesting limited environmental influence on these characteristics.

High GCV and PCV values in morphological traits reflect strong genetic variability, as also observed by Salesh et al. (2010) and Nwangburuka et al. (2012). The high genetic contribution to traits like plant height and branch number is promising for genetic improvement, as these characteristics are crucial for yield optimization and adaptability to diverse environments. Anteneh (2017) noted similar trends in morphological traits of okra, reinforcing the potential of morphological traits for effective selection in breeding programs. This supports the hypothesis that morphological traits can be improved through selection given their high heritability, minimal environmental impact, and significant genetic variance (Swati et al., 2014).

4.4.3 Yield-Related Traits

Yield-related traits such as single fruit weight, number of fruits per plant, and estimated yield per hectare displayed high GCV values (25.8% to 48.54%) and PCV values (30.12% to 53.09%), with a minor difference between the two coefficients for most traits. This indicates that these yield-related traits are primarily controlled by genetic factors rather than environmental conditions.

Traits with high GCV and PCV values, particularly those related to yield, highlight significant genetic variability, indicating promising potential for yield improvement through phenotypic selection (Bharathiveeraman et al., 2012; Melaku et al., 2020). These findings are consistent with Yimam (2018), who noted high genetic variance for yield-related traits, including single fruit weight and overall yield per hectare. Such traits, governed mainly by genetic factors, exhibit resilience to environmental fluctuations, making them valuable targets in breeding programs focused on yield enhancement.

In general, the high GCV and PCV values across most phenological, morphological, and yield-related traits underscore the substantial genetic variability among the okra genotypes, making them ideal candidates for selection. These findings align with previous research (Muluken et al., 2016; Anteneh, 2017) and emphasize the potential for breeding programs to exploit these traits for improved okra yield and adaptability.

4.5 Genetic variability of accessions using heritability and genetic advance

In plant breeding, heritability and genetic advance are vital indicators in understanding the potential for selecting desirable traits in crop improvement. Heritability in the broad sense (H^2) reflects the proportion of observed trait variation attributable to genetic differences among genotypes. Traits with high heritability tend to be more stable across environments, thus enhancing the effectiveness of selection. Genetic advance as a percentage of the mean (GAM) measures the expected progress from selection, indicating traits with significant potential for improvement through breeding (Johnson et al., 1955a). This study examined H^2 and GAM for 72 quantitative traits in okra genotypes, as shown in Table 10. Traits with high heritability and genetic advance can respond more favorably to selection, offering a foundation for enhancing okra accessions.

4.5.1 Phenological Traits

Phenological traits like days to 50% emergence days to 50% flowering, and days to first picking exhibited moderate to high heritability, ranging from 66% for days to emergence to 86% for days to first picking. High heritability combined with moderate GAM, such as 29.18% for days to emergence, indicates substantial genetic control but moderate selection gains. Consistent with Yimam (2018) and Melaku et al. (2020), traits with moderate heritability, like emergence, often require indirect selection methods due to environmental influence. The high heritability of flowering and picking times suggests genetic stability across environments.

Traits like days to emergence and flowering show moderate to high heritability but relatively lower GAM values, suggesting that while these traits are genetically stable, environmental factors might still play a role. Melaku et al. (2020) reported comparable findings, suggesting that traits with moderate heritability may benefit from indirect selection strategies to enhance yield and growth stability across different environments.

4.5.2 Morphological Traits

Morphological traits, including plant height, stem diameter, internode length, and fruit diameter, showed high heritability and GAM. For instance, plant height (91% heritability, 66.44% GAM) and stem diameter (85.91% heritability, 85.91% GAM) suggest a strong genetic basis, aligning with findings by Anteneh (2017) and Mihretu et al. (2014). High heritability in these traits indicates limited environmental impact, making direct selection effective for traits like plant height and stem diameter. Fruit diameter also showed similar stability, with high genetic advance (86.89%), indicative of the genetic potential for improving fruit quality traits through breeding.

High heritability values in plant height and stem diameter reflect their genetic determinism and stability across environments. Consistent with Anteneh (2017), the stability of morphological traits enables effective selection, especially for enhancing okra's structural growth and resistance to environmental stress. Such traits are crucial in improving plant architecture, influencing yield and adaptability.

4.5.3 Yield-Related Traits

Yield-related traits, including single fruit weight, total fruit weight per plant, and estimated yield per hectare, displayed high heritability and moderate to high GAM values. For example, the number of fruits per plant had a heritability of 88% and a GAM of 87.51%, reflecting high selection response potential. High heritability in yield traits is significant for productivity improvement, consistent with reports by Muluken et al. (2016) and Mihretu et al. (2014), who noted similar genetic stability in yield-related traits.

High heritability in yield-related traits suggests that okra productivity can be improved through selection based on phenotypic traits alone, given the minimal environmental influence. This aligns with Muluken et al. (2016), who also observed high heritability in yield traits, underscoring the effectiveness of selection in yield improvement programs. High GAM values for traits like the number of fruits per plant emphasize the genetic gain potential, promising better yield outcomes through targeted selection.

Figure 1: Genotypic and Phenotypic Coefficient of Variations for various traits of 72 okra genotypes

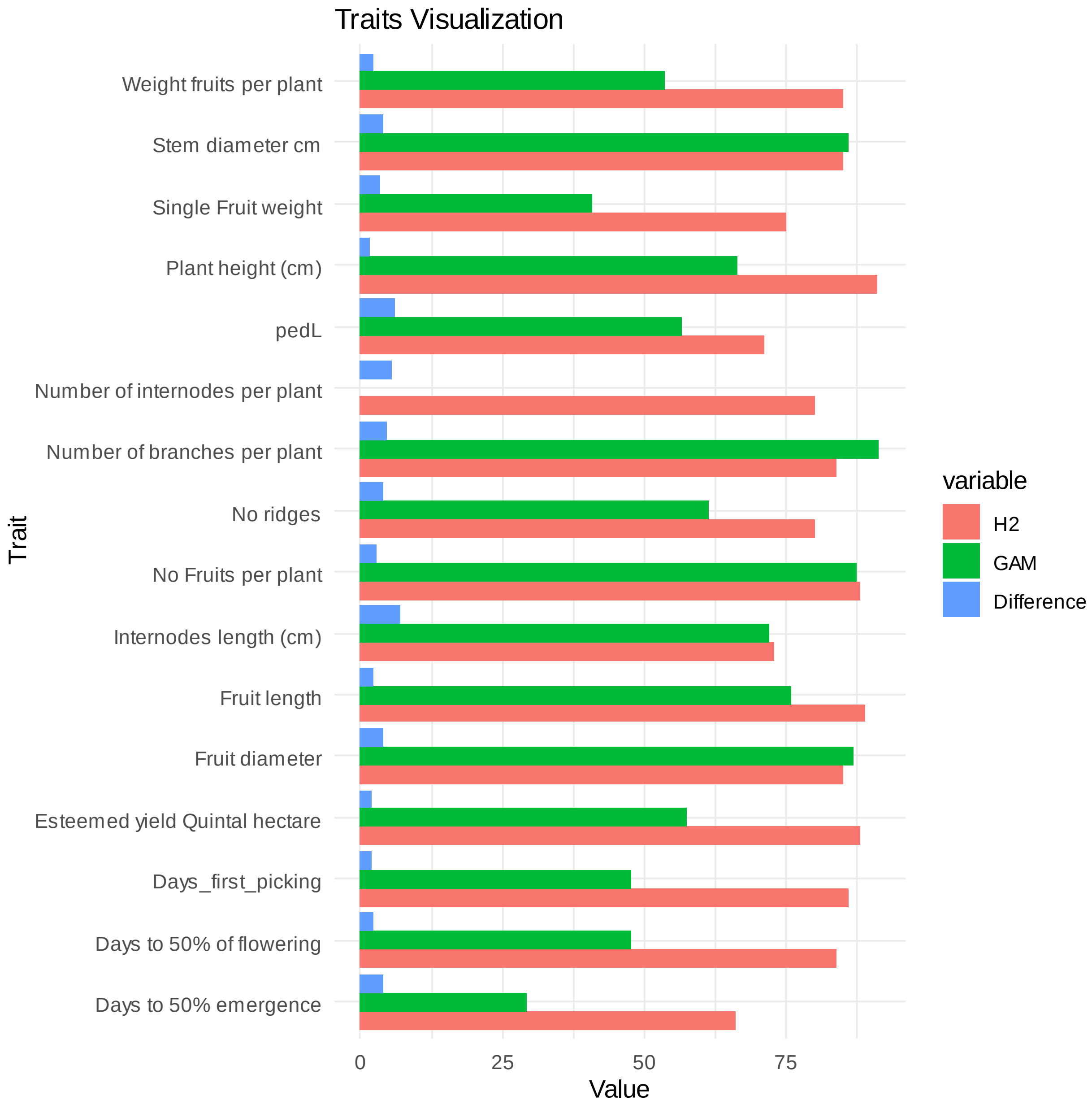

Table 8: Genetic variability components for 15 traits of 72 okra genotypes evaluated at humera in 2020

Trait	Grand Mean	GCV	PCV	H2	GA	GAM	Difference between PCV & GCV
Days to 50%emergence	7.02	17.50	21.63	0.66	2.05	29.18	4.12
Days to 50% of flowering	64.38	25.35	27.71	0.84	30.76	47.78	2.36
Days_first_pikcing	73.66	24.91	26.84	0.86	35.08	47.63	1.93
Plant height (cm)	144.98	33.73	35.27	0.91	96.32	66.44	1.54
Number of branches per plant	4.64	48.54	53.09	0.84	4.24	91.40	4.56
Steam_diameter_cm	1.61	45.34	49.30	0.85	1.39	85.91	3.96
Internodes length (cm)	5.59	41.00	47.99	0.73	4.03	72.17	6.98
PedL	1.98	32.63	38.75	0.71	1.12	56.61	6.12
No_ridges	6.79	33.30	37.33	0.80	4.16	61.21	4.02
Fruit_length	13.67	38.97	41.24	0.89	10.37	75.87	2.27
Fruit_diameter	1.57	45.83	49.79	0.85	1.37	86.89	3.96
No Fruits per plant	21.74	45.22	48.13	0.88	19.02	87.51	2.91
Single Fruit_weight	31.94	22.88	26.41	0.75	13.03	40.82	3.54
Weight fruits per plant	241.26	28.19	30.55	0.85	129.29	53.59	2.36
Esteemed yield Quintal hectare	126.88	29.59	31.46	0.88	72.75	57.34	1.87

PCV=Phenotypic Coefficient of Variation, GCV=Genotypic Coefficient of Variation, H2=Heritability in broad sense, GA=Genetic advance, GAM=Genetic Advance as Percent of Mean

4.6 Genetic Variability of Accessions Using Correlation Analysis

Understanding the genetic variability among okra accessions is essential for identifying desirable traits that can enhance productivity and adaptability. Correlation analysis provides insight into the relationships between various phenological, morphological, and yield-related traits, which can inform selective breeding efforts aimed at improving yield potential and resilience. In this study, correlation coefficients were calculated to assess the degree of association among key traits of the 72 okra accessions. This analysis helps reveal how certain traits influence others, providing a basis for selecting accessions with favorable characteristics for breeding programs.

Table 9 (Correlation traits of Okra Accessions with significance) and Table 10 (Correlation traits of Okra Accessions with values) summarize the genetic variability of these accessions, highlighting both significant and non-significant correlations among traits such as Days to Emergence, Stem Diameter, Plant Height, Fruit Diameter, Branch Number, and Esteemed Yield per Hectare. This information is crucial for identifying traits that contribute most significantly to yield, as well as for understanding how growth-related traits interact within the unique environmental conditions at the experimental sites.

4.6.1 Phenological Traits

Days to Emergence showed a positive correlation with Days to First Picking ($r = 0.03$, $p > 0.05$) and Plant Height ($r = 0.025$, $p > 0.05$), although these associations were weak and non-significant. A noteworthy positive correlation was found between Days to Emergence and Fruit Weight ($r = 0.145$, $p < 0.05$), suggesting that early-emerging plants may bear slightly heavier fruits.

Days to First Picking exhibited a highly significant positive correlation with Days to Flowering ($r = 0.913$, $p < 0.001$), indicating that accessions that flower earlier also tend to have early first fruit harvests. Additionally, Days to First Picking showed moderate, significant positive correlations with Number of Branches ($r = 0.211$, $p < 0.001$), Peduncle Length (PedL) ($r = 0.164$, $p < 0.01$), and Fruit Diameter ($r = 0.029$, $p > 0.05$), suggesting that early fruit picking may also be associated with traits contributing to yield.

The weak correlations between Days to Emergence and other phenological traits align with findings in broader okra studies, which often indicate that emergence time is loosely associated with other developmental stages (Sharma et al., 2021). However, the positive relationship with Fruit Weight implies that early germination might give plants a competitive advantage in fruit development, a trend also observed in certain tropical crop studies (Mishra & Khan, 2019). Ethiopian studies support these findings, with early-emerging okra plants often showing enhanced growth and yield potential (Tesfaye et al., 2022).

The strong correlation between Days to First Picking and Days to Flowering aligns with patterns in okra where early flowering accessions are linked to early harvesting (Adamu et al., 2020). The moderate positive associations between Days to First Picking and traits like Number of Branches and Peduncle Length suggest that earliness in fruit picking may enhance yield-related traits, aligning with findings from Ethiopian okra studies that link early maturity with increased branching and fruit size (Kassa & Gebretsadik, 2020). Furthermore, these correlations imply that selecting for early-flowering accessions can directly influence other yield-enhancing traits, contributing to more efficient breeding strategies.

4.6.2 Morphological Traits

Stem Diameter showed significant positive correlations with Plant Height ($r = 0.396$, $p < 0.001$), Internode Length ($r = 0.449$, $p < 0.001$), and Fruit Diameter ($r = 0.542$, $p < 0.001$). Thicker stems also correlated with a higher number of fruits per plant ($r = 0.47$, $p < 0.001$), although no significant association was found with Esteemed Yield per Hectare ($r = -0.013$, $p > 0.05$).

Plant Height was strongly positively correlated with Internode Length ($r = 0.65$, $p < 0.001$) and Stem Diameter ($r = 0.396$, $p < 0.001$), suggesting that taller plants generally have longer internodes and thicker stems. Additionally, Plant Height showed a significant correlation with the Number of Fruits per Plant ($r = 0.401$, $p < 0.001$) and Fruit Diameter ($r = 0.174$, $p < 0.01$), indicating that taller plants tend to produce larger fruits and more fruits, both of which contribute to higher yield.

Number of Branches exhibited high positive correlations with Fruit Weight ($r = 0.39$, $p < 0.001$), Weight of Fruits per Plant ($r = 0.435$, $p < 0.001$), and Esteemed Yield per Hectare ($r = 0.462$, $p < 0.001$), suggesting that plants with more branches generally bear more fruits and achieve higher yields, likely due to an increased number of fruit-bearing sites.

The positive correlations between Stem Diameter and traits like Plant Height and Fruit Diameter suggest that stem robustness plays a significant role in both structural support and fruit quality, supporting findings from broader okra research on the structural role of stem thickness (Liu et al., 2020). In Ethiopian contexts, similar trends have been observed, with thicker stems linked to increased plant height and fruit production (Girma & Abebe, 2019). Studies on related crops also highlight thicker stems as enhancing resilience and nutrient transport, which are important for yield improvement in challenging climates (Patel et al., 2018; Negash et al., 2021).

The strong correlations between Plant Height, Internode Length, and yield-related traits underscore the importance of these growth attributes in determining yield potential. The positive relationship between Plant Height and traits like Fruit Diameter and Number of Fruits per Plant aligns with studies where plant height was a predictor of yield attributes in various crops (Williams & Smith, 2021). Ethiopian okra research further supports these findings, showing that taller plants often exhibit both increased fruit size and quantity (Kassa & Gebretsadik, 2020).

The high positive correlations observed between Number of Branches and yield-related traits such as Fruit Weight and Esteemed Yield per Hectare affirm that branching patterns significantly influence yield. This trend has been widely documented, particularly in okra, where additional branches provide more fruiting sites, thereby enhancing yield (Yilma & Amare, 2018; Adekunle et al., 2020). Furthermore, the association between branching and yield-related traits aligns with Ethiopian studies that emphasize the importance of multi-branching varieties in achieving higher yields (Mesfin & Berhanu, 2023).

4.6.3 Yield-Related Traits

Fruit Length and Fruit Diameter were both significantly correlated with yield-related traits. Fruit Diameter had strong positive correlations with Number of Fruits per Plant ($r = 0.402$, $p < 0.001$) and Esteemed Yield per Hectare ($r = -0.171$, $p < 0.001$), whereas Fruit Length was moderately correlated with Number of Fruits per Plant ($r = 0.167$, $p > 0.05$), indicating that larger fruits generally contribute to higher yields.

Weight of Fruits per Plant was strongly correlated with Fruit Weight ($r = 0.371$, $p < 0.001$) and Esteemed Yield per Hectare ($r = 0.968$, $p < 0.001$), showing that fruit weight plays a major role in determining the overall yield per hectare.

Esteemed Yield per Hectare showed a strong positive correlation with yield-related traits such as Number of Branches ($r = 0.462$, $p < 0.001$) and Weight of Fruits per Plant ($r = 0.968$, $p < 0.001$), confirming that traits like branching and fruit weight are important yield determinants in okra accessions.

The correlation analysis revealed important relationships between growth, phenology, and yield-related traits in okra accessions. Traits like Number of Branches, Plant Height, and Stem Diameter had strong positive effects on yield-related traits, particularly Fruit Weight, Number of Fruits per Plant, and Esteemed Yield per Hectare. These findings highlight key traits that breeders can target for improving okra yield through phenotypic selection.

The significant positive correlations between Fruit Diameter and Number of Fruits per Plant, as well as with Esteemed Yield per Hectare, underscore the importance of fruit size and frequency in boosting overall yield in okra accessions. Larger fruit diameter correlating with increased yield aligns with findings from studies on okra and related crops, where fruit size is often directly linked to higher productivity (Singh and Reddy, 2019). In Ethiopian studies, such as those by Gebre and Melaku (2021), larger fruit dimensions have also been associated with higher yield outputs, emphasizing the potential of selecting for fruit size as a breeding strategy to enhance productivity.

The strong correlation between Weight of Fruits per Plant and both Fruit Weight and Esteemed Yield per Hectare highlights the role of fruit weight as a primary determinant of yield. This association indicates that accessions with heavier individual fruits contribute significantly to total productivity. These results are consistent with the findings of Kumar et al. (2020), who observed that selecting for higher fruit weight in okra breeding programs led to improved yields across different growing environments. Similar patterns were reported in Nigerian studies, where fruit weight was consistently linked to yield gains in various okra cultivars (Adekunle and Oyedele, 2020).

Esteemed Yield per Hectare also exhibited a strong positive relationship with branching traits, specifically with Number of Branches. This correlation suggests that a higher branching potential allows plants to produce more fruits, ultimately leading to higher yields. Studies in similar agro ecological contexts, including those by Ali et al. (2022), have shown that increased branching contributes to yield through enhanced fruit-bearing capacity. In Ethiopia, Yilma and Amare (2018) highlighted that the branching trait in okra positively influences productivity, making it a desirable trait in breeding programs aimed at yield improvement.

The overall positive correlations between growth traits (such as Plant Height and Stem Diameter) and yield-related traits further emphasize the importance of structural robustness in supporting yield potential. Robust plant height and thicker stems are often associated with resilience and enhanced nutrient transport, which are critical under challenging growing conditions. This aligns with the work of Negash et al. (2021), who found that structural traits support fruit production and yield under various environmental stresses, making them valuable traits for breeding programs in regions like Ethiopia.

Table 9 Correlation among Quantitative Traits of Okra Accessions with significance

	DE	DF	SD	DFP	PH	NoBr	IL	pedL	FR	FD	FP	FW	WFPP	EYP Ha
DE	1***	0.038	-0.015	0.03	0.025	-0.07	-0.081	0.067	-0.023	0.025	-0.043	0.145	-0.006	-0.028
DF	0.038	1***	0.142	0.913***	-0.079	0.156	-0.006	0.14	-0.325***	0.033	-0.031	0.001	0.039	0.039
SD	-0.015	0.142*	1***	0.121	0.396***	-0.135	0.449***	0.099	0.192.	0.542***	0.47***	0.066	-0.002	-0.013
DFP	0.03	0.913***	0.121*	1***	-0.065	0.211*	-0.035	0.164	-0.323***	0.029	-0.005	0.033	0.098	0.098
PH	0.025	-0.079	0.396***	-0.065	1***	-0.064	0.65***	0.088	0.058	0.174	0.401***	0.188.	0.122	0.129
NoBr	-0.07	0.156**	-0.135*	0.211***	-0.064	1***	0.085	0.107	-0.047	-0.276***	-0.022	0.39***	0.435***	0.462***
IL	-0.081	-0.006	0.449***	-0.035	0.65***	0.085	1***	0.175	0.097	0.144	0.354***	0.165	0.202*	0.207*
PedL	0.067	0.14*	0.099.	0.164**	0.088	0.107.	0.175**	1***	0.177	0.031	0.223**	0.25**	0.143	0.145
FL	-0.023	-0.325***	0.192**	-0.323***	0.058	-0.047	0.097	0.177**	1***	0.223**	0.167	0.062	0.007	0.011
FD	0.025	0.033	0.542***	0.029	0.174**	-0.276***	0.144*	0.031	0.223***	1***	0.402***	-0.037	-0.164	-0.171
FPP	-0.043	-0.031	0.47***	-0.005	0.401***	-0.022	0.354***	0.223***	0.167**	0.402***	1***	0.186.	0.183	0.197.
FW	0.145*	0.001	0.066	0.033	0.188**	0.39***	0.165**	0.25***	0.062	-0.037	0.186**	1***	0.371***	0.39***
WFPP	-0.006	0.039	-0.002	0.098.	0.122*	0.435***	0.202***	0.143*	0.007	-0.164**	0.183**	0.371***	1***	0.968***
EYP Ha.	-0.028	0.039	-0.013	0.098.	0.129*	0.462***	0.207***	0.145*	0.011	-0.171**	0.197***	0.39***	0.968***	1***

4.7 Genetic variability of accessions using principle component analysis (PCA)

4.7.1 Principal Component Analysis

The principal component analysis (PCA) of 14 quantitative traits across 72 okra genotypes is summarized in Table 12. Using the prcomp function in R, the traits were scaled to ensure equal contribution. PCA was conducted to reduce data dimensionality and to identify key components explaining most of the variance. The first five principal components (PCs) accounted for 74.97% of the total variance, indicating that the primary genetic information was concentrated within these dimensions: PC1: 22.71%, PC2: 20.85%, PC3: 15.18%, PC4: 8.70% and PC5: 7.53%.

These five PCs collectively explained the majority of the variation, confirming the adequacy of the PCA model in capturing the core traits of interest (Table 13). Selection of Principal Components (PCs): Two main criteria were applied to determine the number of principal components to retain for further analysis:

Kaiser-Guttman Criterion: The Kaiser-Guttman criterion (Kaiser, 1960) was used to select components with eigenvalues greater than 1. An eigenvalue greater than 1 indicates that a principal component explains more variance than a single original variable, thereby justifying its inclusion in the analysis. Based on this criterion, the first four PCs were retained, each with an eigenvalue exceeding 1, signifying that they capture substantial independent information.

Cumulative Variance Explained: In addition to the eigenvalue criterion, the cumulative variance explained by each PC was examined. The first five principal components accounted for over 87% of the total variance in the dataset, meeting the threshold commonly used in PCA analysis. Retaining these five PCs ensures that the majority of the dataset's variability is represented, balancing between data simplification and variance retention.

By applying these criteria, five PCs were selected, capturing the complex trait variability among the okra accessions. This selection enables a comprehensive analysis of the trait relationships while reducing dimensionality, facilitating clearer insights into the morphological and yield-related characteristics within the okra genotypes.

Traits such as internode length, estimated yield per hectare, fruit weight per plant, plant height, number of fruits per plant, days to maturity, and single fruit weight contributed significantly to PC1 (loading range: 0.319–0.400). In contrast, PC2 was primarily influenced by the number of branches, fruit weight per plant, and estimated yield per hectare, with loadings from 0.340 to 0.402. Fruit length and number of branches were major contributors to PC3 and PC4, while peduncle length and days to emergence were prominent in PC5.

The PCA identified five principal components with eigenvalues from 1.054 to 3.179, with the first four explaining 74.97% of the variance. This high cumulative variance supports that key traits are largely captured within these components, making PCA an effective tool for summarizing genotype variability. As noted in Demelie et al. (2022), a high percentage of explained variance in the first few components is characteristic of quantitative trait analyses in okra, allowing for efficient selection in breeding programs. Amoatey et al. (2021) similarly reported that the first three principal components accounted for 32.44%, 19.78%, and 9.68% of total variance, highlighting the substantial variability across okra genotypes.

In this study, the primary traits associated with PC1 and PC2 underscore the importance of these traits in genetic divergence, reflecting additive gene action, which can be advantageous in selection breeding. Mohammed et al. (2020) observed comparable trait contributions in PC1 and PC2, supporting the consistency of these results across okra studies. Traits like internode length, yield per hectare, and fruit weight per plant, being major contributors, are valuable indicators of genetic variation and potential targets for future genotype evaluation. Figure 2 the biplot of PCA1 and PCA2 shows the relationship between the genotypes and the traits in the first two principal components.

Figure 2: the relationship between the accessions and the traits in the first two principal components (PCA1 and PCA2)

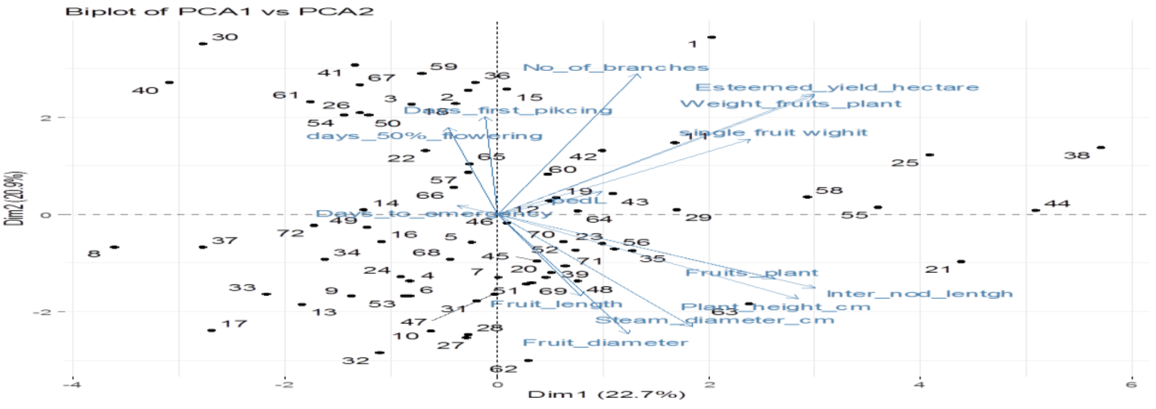

Table 10: the first five principal component axes for 14 quantitative traits of 72 okra accessions were evaluated at Humera in 2020.

Traits	pc1	PC2	PC3	PC4	PC5
Days_to_emergency	-0.05135	0.02640143	0.07943522	-0.66842903	0.489047704
days_50%_flowering	-0.06187	0.24868884	-0.59021761	-0.07365752	-0.053957653
Steam_diameter_cm	0.245227	-0.32187461	-0.30210777	0.06158774	-0.080577228
Days_first_pikcing	-0.0155	0.27920667	-0.57351233	-0.09546397	-0.113658412
Plant_height_cm	0.379392	-0.24124848	-0.09130667	-0.05960214	0.381397217
No_of_branches	0.177133	0.4020573	0.10180756	0.25880753	-0.077752147
Inter_nod_lentgh	0.400254	0.2115667	-0.0998074	0.16948131	0.225711195
PedL	0.132115	0.06459285	0.01307168	-0.57798854	0.492618605
Fruit_length	0.105725	-0.23257626	0.31213418	-0.08345962	-0.4806339
Fruit_diameter	0.164725	-0.34243859	-0.209644	-0.01401045	-0.137686197
Fruits_plant	0.349472	-0.18509775	-0.11352677	-0.09870416	-0.189755428
single fruit wighit	0.319224	0.21581391	0.14149521	-0.26961629	0.085735255
Weight_fruits_plant	0.397938	0.34034748	0.10123177	0.07278474	0.007022911
Esteemed_yield_per hectar	0.399357	0.34508615	0.10852737	0.08153212	-0.002951659
Eigenvalue	3.179421	2.919247299	2.125410341	1.218064127	1.054036378
percentage of variance	22.71015	20.85176642	15.18150243	8.70045805	7.52883127
cumulative percentage of variance	22.71015	43.56192	58.74342	67.44388	74.97271

PCA1 to PCA5 represented the first principal component axis to the five principal component axes

4.8 Clustering of accessions

4.8.1 Clustering of accessions through hierarchical clustering approach

The clustering analysis grouped the 72 okra accessions based on nine phenological and agronomic traits, using the Unweighted Pair-Group Method with Arithmetic Mean (UPGMA). A hierarchical clustering approach was applied to create a dendrogram (Figure 3), which categorized the accessions into nine distinct clusters. These clusters represent groups of accessions with similar trait profiles, allowing a visual and statistical understanding of genetic variation within the population.

A cut-off height was established to delineate nine main clusters, each containing different numbers of accessions:

Cluster 3 was the largest, comprising 44 accessions (61.11% of the total). This cluster may represent accessions with common agronomic and phenological characteristics.

Cluster 2 and Cluster 4 contained 16.67% and 6.94% of the accessions, respectively, indicating moderate commonality in traits among these groups.

The remaining clusters held fewer accessions, suggesting they possess unique or less common trait profiles.

Cluster analysis is a powerful tool in genetic studies, as it groups data points with similar characteristics and can identify genetic samples or accessions that share traits (Hair et al., 1995). In this study, the hierarchical clustering technique revealed nine distinct clusters, each indicating varying degrees of phenotypic similarity among the okra accessions. The presence of a large number of accessions in Cluster 3 suggests a substantial subset of the population with shared characteristics, possibly indicating core traits prevalent in the okra collection from this region.

This pattern of clustering aligns with findings from similar studies. For example, Muluken et al. (2015) identified ten main clusters among 25 okra genotypes, demonstrating genetic diversity through clustering. Mihretu et al. (2014) found five distinct clusters among okra collections from Gambella and Asossa, reflecting the diversity within Ethiopian okra accessions. Tesfa and Yosef (2016) grouped 50 okra accessions into four clusters based on regional data from Ethiopia's major production areas, while Anteneh (2017) classified 25 genotypes into seven clusters, noting that accessions from the same country often grouped together. In this study, six out of ten Indian varieties were clustered into two separate groups, corroborating Anteneh's observation that accessions from the same geographical origin often display genetic similarity.

Hierarchical clustering, as used here, provides a clear visualization of genetic relationships within the population (Everitt et al., 2011). The grouping of accessions with shared traits highlights key trait similarities and differences, aiding in identifying potential candidates for breeding programs focused on specific agronomic traits or stress resistance. The structure of these clusters can guide selective breeding by identifying core and unique genetic profiles within okra populations, a strategy valuable for conserving genetic resources and enhancing trait-based selection.

The diversity within and between clusters highlights potential genetic variability among the accessions. Accessions in smaller clusters with unique trait profiles might serve as important genetic resources, particularly in breeding programs aimed at developing new varieties with specialized characteristics. By identifying clusters with distinct traits, breeders can make informed decisions about which genotypes to cross for achieving desired phenotypic traits, ultimately contributing to crop improvement and yield optimization strategies.

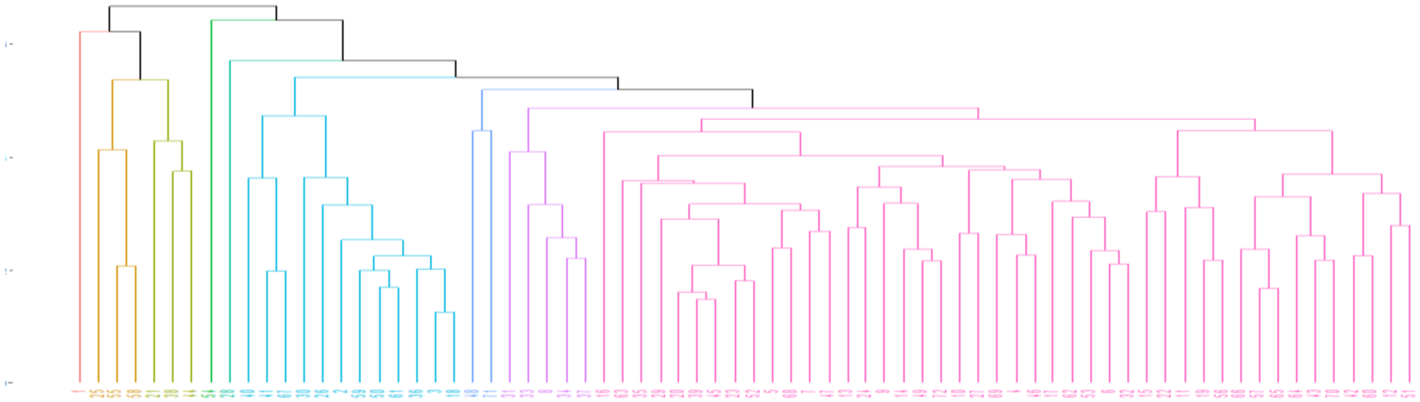

Figure 3: Dendrograms of Unweighted Pair Group Method with Arithmetic Mean Agglomerative Clustering

4.8.2 Cluster Means Analysis

The mean values of nine clusters for 16 fruit yield and fruit-related traits are presented in Table 11. The clusters reveal differences in key traits, such as days to emergency, days to 50% flowering, stem diameter, days to first picking, plant height, number of branches, internode length, fruit length, fruit diameter, number of fruits per plant, single fruit weight, weight of fruits per plant, and estimated yield per hectare.

Cluster I: Exhibits moderate days to emergency (7.42 days) and days to 50% flowering (53.33 days), suggesting a balanced growth rate. It shows a moderate stem diameter (1.58 cm) and plant height (183.54 cm), indicating robust vegetative growth. Higher values for fruit length (17.10 cm) and fruit diameter (7.75 cm) point to larger fruit sizes, though this cluster has a lower estimated yield per hectare (99.92).

Cluster II: This cluster shows longer days to 50% flowering (66.32 days) and days to first picking (73.80 days), indicative of slower maturation. It has moderate fruit characteristics and a slightly higher estimated yield per hectare (102.38).

Cluster III: Similar to Cluster I, this cluster has moderate growth patterns but shorter plant height (110.00 cm) and a lower estimated yield (83.79). The average number of fruits per plant is moderate (19.45), suggesting less prolific fruiting compared to other clusters.

Cluster IV: Characterized by longer days to 50% flowering (75.25 days) and days to first picking (87.15 days), indicating a slower growth cycle. Despite the smaller fruit size, it shows a significant number of branches (6.28) and a higher estimated yield per hectare (129.48).

Cluster V: Traits in this cluster resemble those of Cluster IV, with moderate growth rates and estimated yield (128.53). It is noted for having higher single fruit weight (31.59), suggesting potential for heavier fruits.

Cluster VI: Displays slightly longer days to 50% flowering (75.64 days) and smaller fruit sizes, but a high estimated yield per hectare (134.03).

Cluster VII: Characterized by moderate growth traits and the highest number of fruits per plant (33.27). It has the highest yield (182.50), suggesting high fruiting capacity.

Cluster VIII: Similar to Cluster I in terms of moderate growth traits, but with a higher estimated yield per hectare (145.74).

Cluster IX: Notable for having the quickest days to 50% flowering (48.00 days) and smallest plant height (65.88 cm). While the fruits are smaller, this cluster has a high estimated yield (163.93), indicating potential for early maturity and productivity.

The cluster analysis results reveal significant genetic variability among okra accessions, as evidenced by distinct trait patterns across the nine clusters. Genetic diversity in okra has been widely documented, with studies emphasizing the importance of such diversity for breeding programs aimed at enhancing yield, adaptability, and resilience (Getahun et al., 2020; Alemu et al., 2021). In Ethiopia, okra is an underutilized crop; thus, characterizing its genetic variability is crucial for improving local breeding initiatives (Tsegaye & Feyissa, 2018).

Clusters 1, 3, and 8, characterized by moderate growth rates and balanced yield-related traits, show adaptability to diverse environmental conditions. This aligns with the findings of Haile & Mohammed (2019), who reported that moderate growth patterns are often associated with resilience to climatic fluctuations in Ethiopian agro-ecological zones. Such clusters could be highly valuable for areas prone to environmental stress, as they display a balanced combination of yield and growth attributes, making them suitable for marginal areas.

Clusters 2, 4, 5, and 6, characterized by longer growth cycles and smaller fruit sizes, could be suitable for targeted breeding programs focusing on quality traits rather than rapid yield production. For instance, Gebremeskel et al. (2020) observed that traits like fruit size and maturation time are heritable and can be selectively bred to meet specific market demands. Similar findings by Osei & Danso (2017) in Ghana confirm that slow-maturing accessions may offer higher quality in fruit traits, aligning with consumer preferences in niche markets.

Clusters 7 and 9, with the highest estimated yield, underscore the potential for breeding high-yield okra varieties. Cluster 7, notable for the highest number of fruits per plant, and Cluster 9, characterized by quick maturation and high yield per hectare, indicate that these accessions could be optimal candidates for commercial production, especially in Ethiopia's fertile lowlands (Aklilu et al., 2022). Studies by Fekadu et al. (2021) highlight that quick-maturing, high-yield varieties could play a significant role in enhancing food security, especially in regions with short growing seasons or limited water availability.

International literature supports these findings, showing that high-yield clusters are also seen in okra breeding programs outside Ethiopia. For example, studies in India and Nigeria have identified clusters with similar traits, where high fruit yield and rapid maturity are prioritized for commercial cultivation (Patel et al., 2019; Nduka et al., 2020). Such similarities in trait patterns suggest that the genetic principles underlying okra productivity are consistent across diverse growing conditions, validating the applicability of these clusters for broader breeding programs.

The substantial genetic variability within these clusters also emphasizes the potential for cross-breeding. Genetic diversity studies on okra by Mulualem & Mesfin (2020) suggest that crossing accessions from high-yield and high-quality clusters could yield hybrids with enhanced productivity and resilience. This approach could be instrumental in Ethiopian okra breeding, where increased yield and adaptability are primary goals for food security and economic improvement.

4.8.3 Mahalanobis Distance Analysis

The Mahalanobis Distance Analysis is a statistical approach used to evaluate the similarity or dissimilarity between clusters in a dataset. This analysis accounts for correlations among variables, providing a robust measure for distinguishing clusters with complex trait interdependencies (Mahalanobis, 1936). In this study, k-means clustering identified nine distinct clusters of okra accessions based on phenotypic traits. Calculating the Mahalanobis distance between cluster centers helps us understand the degree of separation between groups, essential for effective trait characterization in breeding programs (Girma, 2018; Yilma et al., 2020).

The Mahalanobis distance matrix (Table 12) shows the squared distances between each pair of clusters, with significance levels indicated by p-values. Distances vary widely, reflecting distinct groupings among okra accessions based on their phenotypic traits. Key observations include:

Significant Distances: Clusters with substantial differences, such as Cluster 1 vs. Cluster 5 (distance = 105.81, $p < 0.001$) and Cluster 3 vs. Cluster 6 (distance = 145.42, $p < 0.001$), indicate highly divergent traits. These significant differences highlight clusters with unique trait combinations that could serve as a basis for selective breeding (Tesfaye, 2021; Mekonnen & Tadesse, 2022).

Table 11 Cluster means analysis of the nine clusters for 14 fruit yield and fruit related traits

Trait	cluster 1	cluster 2	cluster 3	cluster 4	cluster 5	cluster 6	cluster 7	cluster 8	cluster 9
Days_to_emergency	7.416667	6.977273	6.916667	6.2	6.894737	7.555556	6.5	7.46875	7.5
days_50%_flowering	53.33333	66.31818	53.91667	75.25	69.10842	75.63889	57.46	55.25	48
Steam_diameter_cm	1.575	1.967273	1.396667	1.33	1.693684	1.282222	1.914286	1.5275	0.8
Days_first_pikcing	61.04167	73.79545	59.625	87.15	78.93421	87.11111	68.18857	64.75	53
Plant_height_cm	183.5367	150.4573	110.0033	59.772	165.2374	128.7689	182.6086	135.1375	65.88
No_of_branches	3.888333	4.035455	3.271667	6.282	4.277368	4.991111	6.862857	4.29875	7.11
Inter_nod_lentgh	7.36	5.052727	4.22	3.362	6.422632	4.514444	7.795714	5.13875	2.27
PedL	1.816667	1.570909	2.128333	2.008	2.174737	2.086667	2.032857	2.045	1.31
Fruit_length	17.1	14.24182	14.69	13.484	12.00105	10.60889	15.02857	15.00625	20.48
Fruit_diameter	7.75	7.022727	6.916667	5.45	7.171053	5.75	6.821429	6.90625	5.5
Fruits plant	20.57833	23.49	19.45333	15.646	22.88684	17.03222	33.26714	19.54875	11.19
single fruit weight	29.495	30.32364	28.385	28.722	31.59211	33.70444	39.23	33.72875	26.91
Weight fruits plant	193.5083	194.8173	163.4733	247.35	245.5784	252.2289	340.26	277.5188	311.3
Esteemed yield hectare	99.91667	102.3773	83.79333	129.484	128.5279	134.0322	182.5	145.735	163.93

Non-significant Distances: Pairs such as Cluster 1 vs. Cluster 2 (distance = 7.96, $p = 0.89$) and Cluster 2 vs. Cluster 4 (distance = 16.43, $p > 0.05$) suggest similarity in trait profiles, possibly due to common environmental adaptation or genetic background. These clusters represent accessions with similar potential for agronomic performance under similar conditions (Girma, 2018).

The Mahalanobis distance analysis reveals both highly significant and non-significant differences among the nine clusters, implying varying levels of phenotypic diversity within the okra accessions studied. Accessions in significantly different clusters may possess unique traits valuable for breeding, particularly for enhancing yield, fruit quality, or resilience to environmental stressors.

For instance, the significant difference between Clusters 1 and 5 supports the presence of distinctive genetic variability, an essential factor for selecting superior genotypes for yield improvement (Addis et al., 2019). The non-significant distances among other clusters suggest similarities in trait expression, possibly linked to environmental adaptation mechanisms common among local accessions (Yilma et al., 2020; Mekonnen & Tadesse, 2022).

This analysis underscores the utility of Mahalanobis distance in identifying clusters with distinct trait profiles that align with the goals of okra breeding programs, especially in regions like Ethiopia where environmental adaptation is key (Tesfaye, 2021). Future research could integrate genetic data to deepen understanding of these phenotypic clusters and further validate these findings across different environments.

4.9 Qualitative Traits of Okra Accessions

The qualitative traits of okra (Abelmoschus esculentus) play a significant role in determining the plant’s appearance, adaptability, and marketability. These traits, which include stem texture, fruit shape, leaf color, and flowering characteristics, are important for agronomic performance and consumer preferences. In this study, I assessed the qualitative traits of 72 okra accessions from Tigray, Northern Ethiopia, to understand the genetic diversity within the region.

Table 12 Squared Distance between Groups (Mahalanobis distance matrix) or Mahalanobis Distance Analysis

	1	2	3	4	5	6	7	8	9
1	NA	7.96^{ns}	40.71**	29.95**	105.81**	124.08**	11.16^{ns}	46.53**	22.58**
2	7.96^{ns}	NA	26.27*	16.43^{ns}	73.91**	96.01**	24.28*	63.19**	9.57^{ns}
3	40.71**	26.27*	NA	28.74**	32.01**	145.42**	79.96**	139.43**	40.86**
4	29.95**	16.43^{ns}	28.74**	NA	76.37**	71.95**	49.25**	70.61**	10.00^{ns}
5	105.81**	73.91**	32.01**	76.37**	NA	208.33**	148.77**	251.27**	89.18**
6	124.08**	96.01**	145.42**	71.95**	208.33**	NA	140.96**	95.06**	56.86**
7	11.16^{ns}	24.28*	79.96**	49.25**	148.77**	140.96**	NA	33.37**	37.53**
8	46.53**	63.19**	139.43**	70.61**	251.27**	95.06**	33.37**	NA	57.41**
9	22.58**	9.57^{ns}	40.86**	10.00^{ns}	89.18**	56.86**	37.53**	57.41**	NA

Note: Chi-square (χ^2) = 22.362 at 5% and 27.688 at 1% probability levels. ** = highly significant at 1%, * = significant at 5%.

4.9.1 Maturity

The distribution of maturity stages among the okra accessions is shown in bar chart 5, with categories including "Very Early," "Early," "Medium," "Late," and "Very Late." The majority of accessions (69%) fell into the "Medium" maturity category. Smaller proportions were observed in the "Late" (7%), "Very Late" (7%), "Early" (6%), "Very Early" (6%), and "Late" (4%) categories.

The majority of accessions reached maturity at a moderate rate ("Medium"), indicating a stable and consistent maturation period. The smaller percentages of accessions that matured early or late show genetic variability in maturity, which could influence harvest timing and marketability. This variation in maturity may be critical in optimizing cultivation schedules, as different maturity stages may impact yield, marketability, and adaptability to different climatic conditions. Further research is needed to explore the genetic factors controlling maturity in okra.

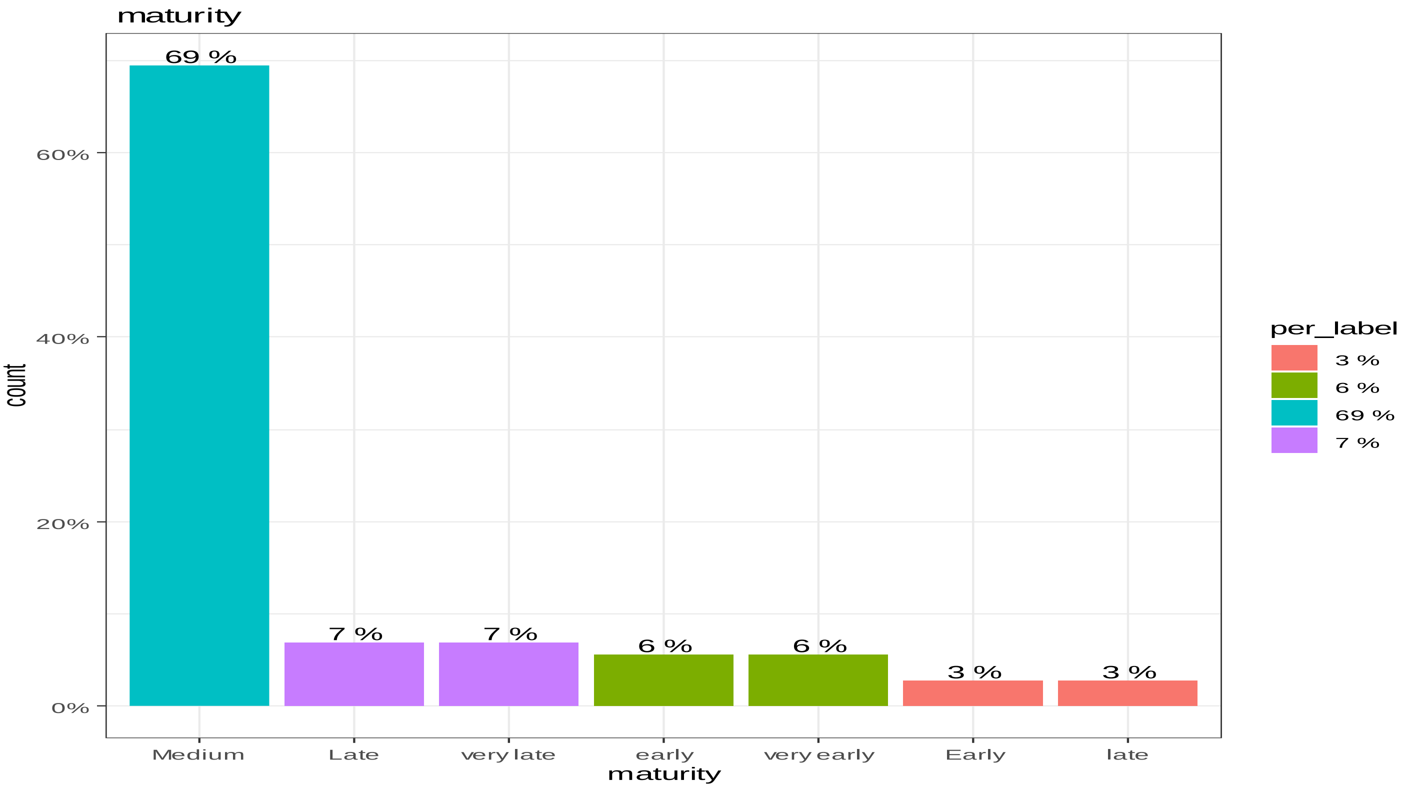

Figure 4: Maturity qualitative traits

4.9.2 Stem Texture

The R software display Bar chart 3 shows the distribution of stem texture, with 67% of the accessions having "Smooth" stems, while 33% exhibited "Slightly rough" stems.

The predominance of smooth stems in the study may suggest that smoothness is a favorable trait under the specific growing conditions tested, possibly aiding in handling during cultivation. This variation could be influenced by genetic factors or environmental adaptations, and further genetic studies could help clarify the significance of this trait in okra's growth and yield performance.

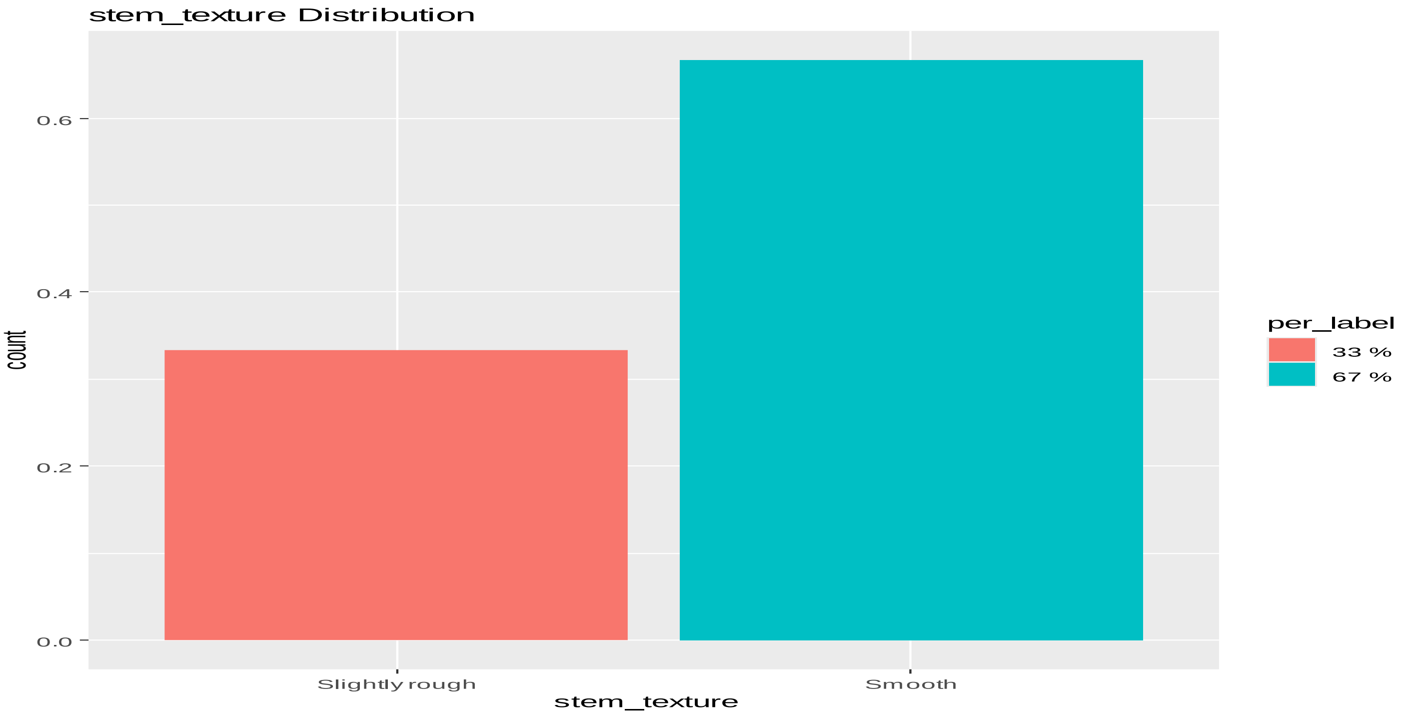

Figure 5: Stem texture qualitative traits

4.9.3 Stem color

The bar chart shows the distribution of okra accessions based on their stem color. Two categories are represented: green and red. This suggests that green-stemmed accessions are dominant among the okra population studied, with red-stemmed accessions forming a smaller proportion. The significant predominance of green-stemmed accessions (92%) compared to red-stemmed accessions (8%) could indicate that green stem color is either a more common trait in okra accessions from this region or is favored by the environmental conditions of the study location. Stem color in plants can be influenced by genetic factors, environmental adaptation, or selective breeding preferences by farmers. The green stem color might also be linked to other agronomically favorable traits such as higher yields, better stress tolerance, or consumer preference.

Further investigation could focus on the agronomic performance and adaptability of red-stemmed accessions. Though less frequent, red stem color may offer unique benefits, such as disease resistance or other desirable traits, which could be valuable for crop diversity and breeding programs. Evaluating the correlation between stem color and yield-related traits could provide insights into the practical significance of stem color variation in okra breeding.

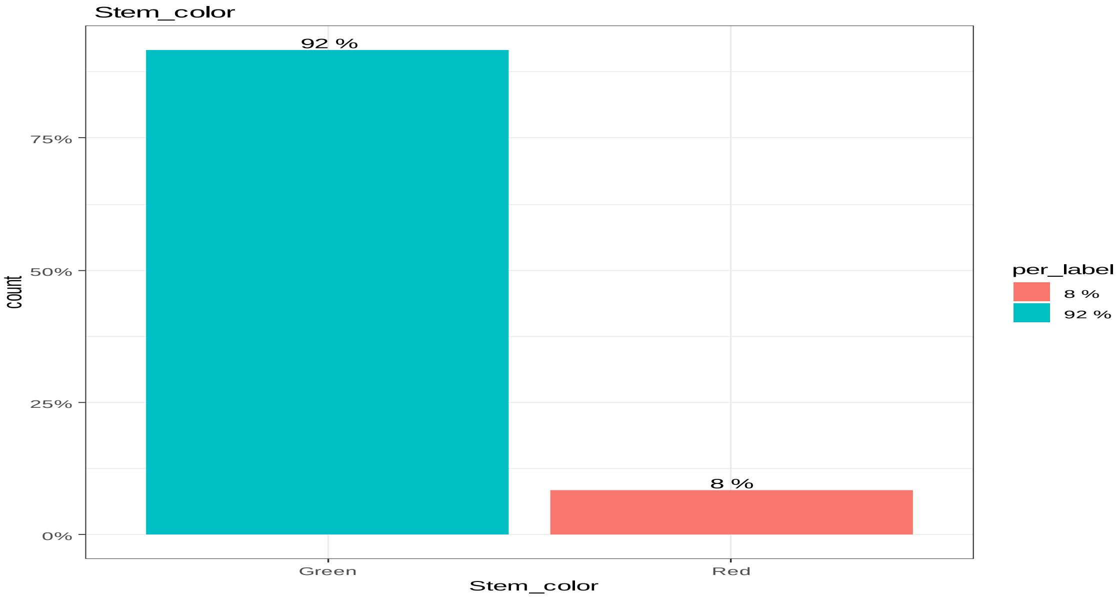

Figure 6: Stem color qualitative traits

Image 1: Stem color qualitative traits

Image 1 Red Stem color qualitative traits   Image 2 green Stem color qualitative traits

4.9.4 Internode Length (INL)

According to bar chart 4, the distribution of internode length was categorized into three classes: "Medium," "Short," and "Long." Most accessions (44%) exhibited a medium internode length, followed by 29% with short internodes and 26% with long internodes.

The prevalence of medium internode length suggests that this characteristic is stable and potentially advantageous for plant architecture, enabling optimal light interception and growth. The observed variation may be due to environmental factors or genetic diversity, and further analysis of its impact on plant architecture could inform breeding strategies aimed at improving growth patterns for specific environments.

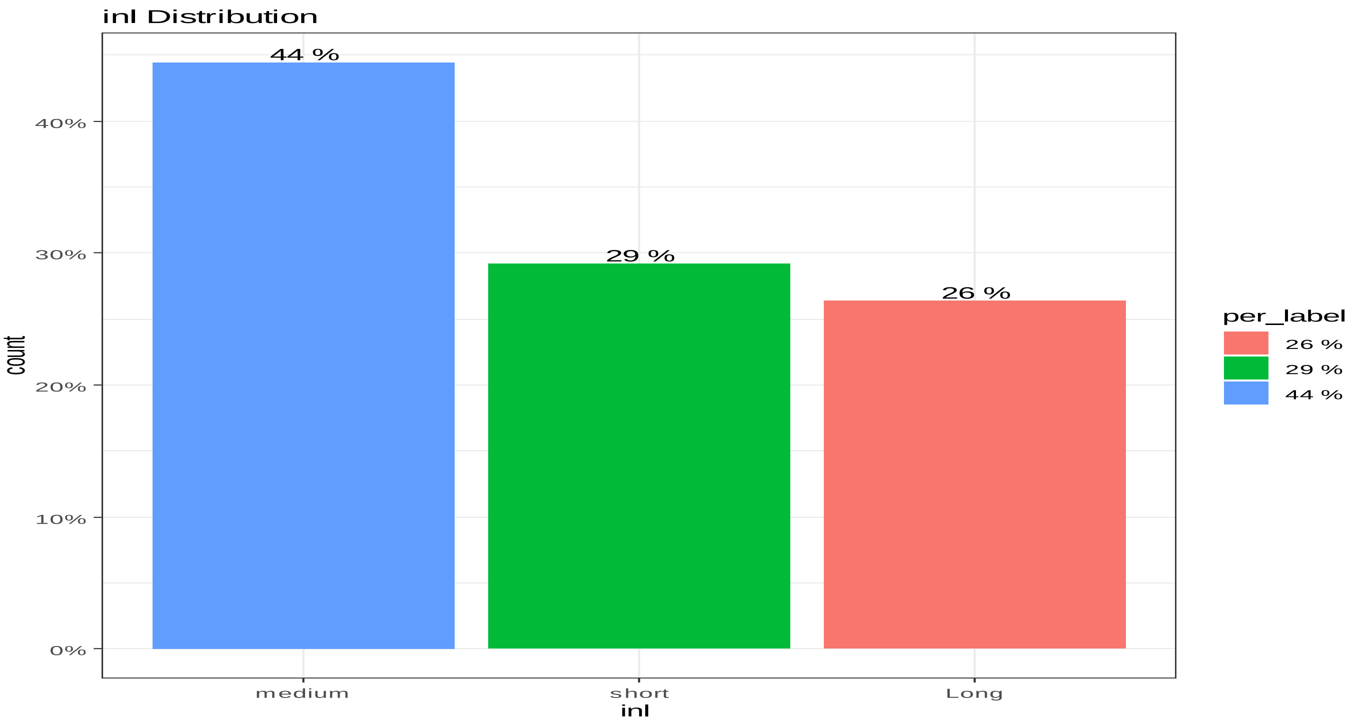

Figure 7: Internode length (inl) qualitative traits

4.9.5 Ridge Number (Fruit: Number of Locules)

The distribution of okra plants based on ridge number showed three categories: "Medium," "Many," and "Few." "Medium" ridges were most common (47%), followed by "Many" (46%) and "Few" (7%).

The high frequency of accessions with medium and many ridges could be due to the genetic makeup of the accessions or environmental influences. Understanding the significance of ridge number in terms of pod morphology and yield is essential, as it may influence factors like fruit development and market preferences. Further research is necessary to explore how the number of ridges affect yield and how this trait can be optimized for different growing conditions.

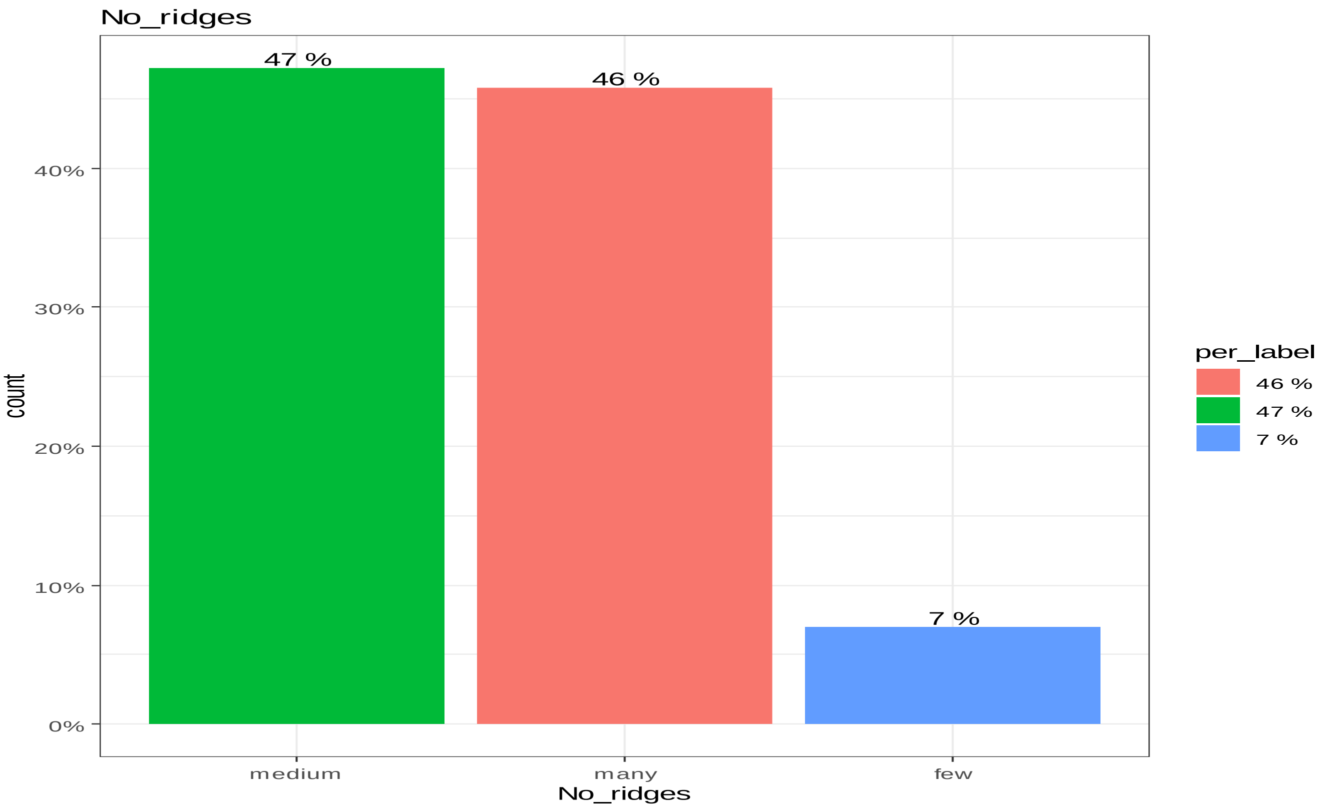

Figure 8 Ridge Number (Fruit: Number of Locules) qualitative traits

Image 2: Variation in number of locules qualitative traits among okra accessions

Image 2.1sex number of locules

Image 2.2 five number of locules

Image 2.3 nine number of locules

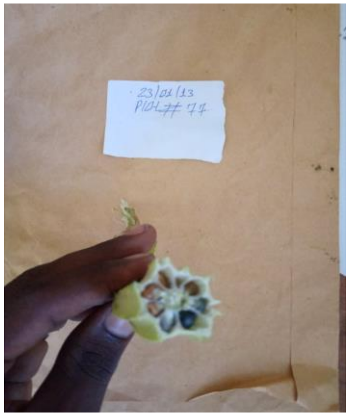

Image 2.4 eight numbers of locules

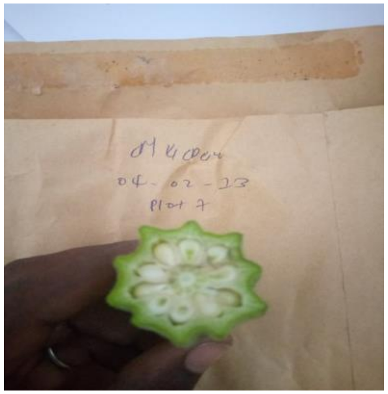

Image 2.5: 10 No. of locules

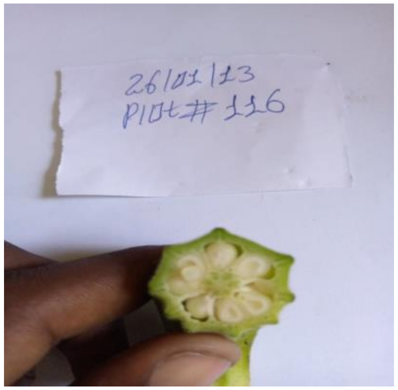

Image 2.6: 7 No. of locules

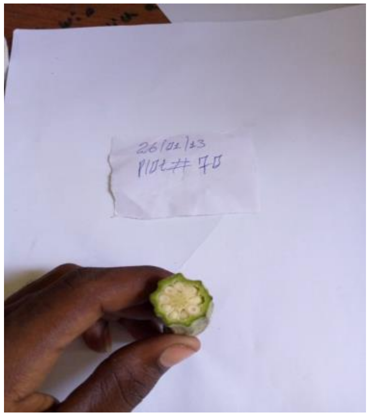

Image 2.7: 11 No. of locules

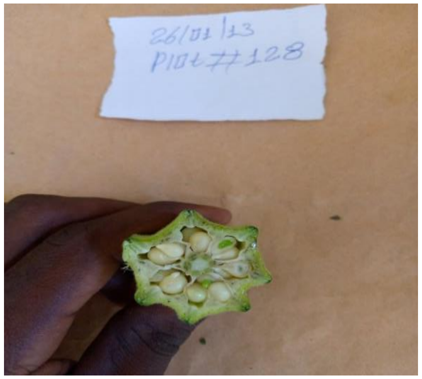

Image 2.8: 7 Nos. of locules

4.9.6 Fruit shape on top

Bar chart data shows that 97% of the accessions had "Angular" fruits, while only 3% had "Round" fruits. The predominance of angular fruits suggests that it is the more common fruit shape in the studied accessions. This could be due to genetic selection or environmental conditions. While "Round" fruits were rare, the genetic diversity in fruit shape may be useful for breeding programs focused on improving fruit quality and yield. Investigating the environmental and genetic factors influencing fruit shape could help in selecting suitable varieties for various market demands.

Figure 9: fruit shape on top qualitative traits

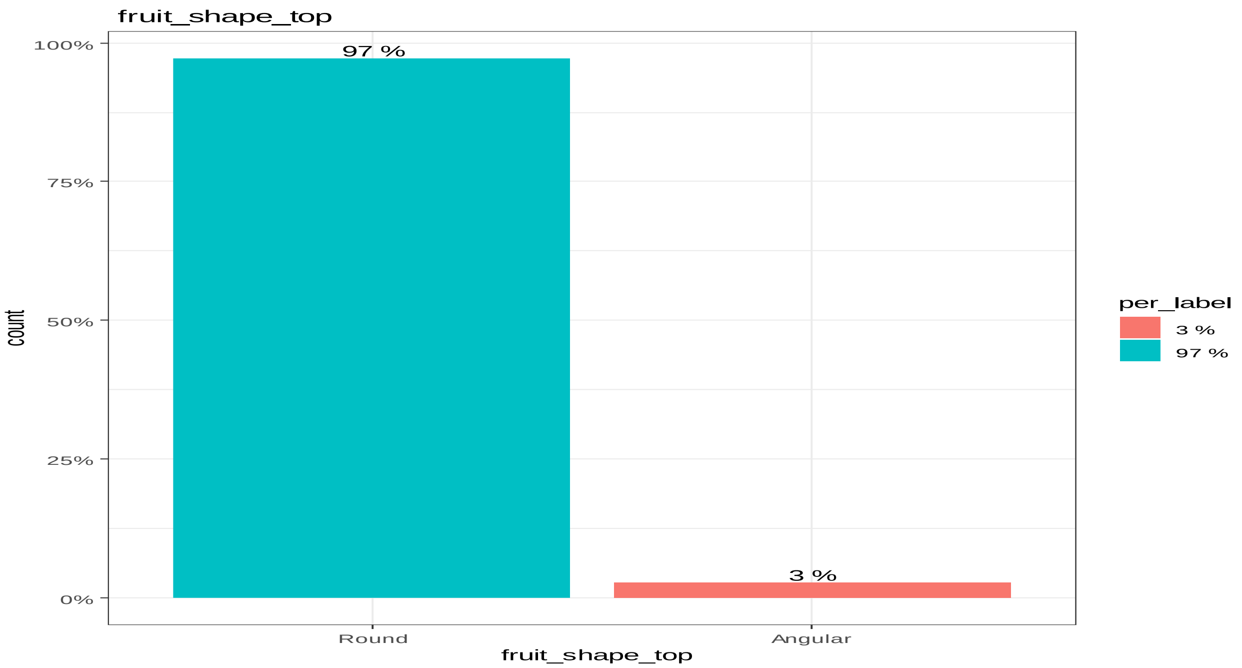

Image 3: fruit shape on top qualitative traits

Image 3.1 Round fruit shape

Image 3.2 Angular fruit shape

4.9.7 Fruit Shape

Analysis of Fruit Shape Distribution:

Based on the provided image, the most prevalent okra fruit shape is slender, accounting for 90% of the total population. This suggests that slender fruit shapes are the predominant morphological characteristic in the studied okra sample. The remaining 10% of the population is distributed among four other fruit shapes:

Genetic factors: The genetic makeup of the okra plants may favor the production of slender fruits.

Environmental factors: Factors such as soil conditions, climate, and cultivation practices can influence fruit shape development.

Selection pressure: Over time, selective breeding may have favored slender fruit shapes due to consumer preferences or other agronomic advantages.

While slender fruit shapes are the most common, the presence of other fruit shapes indicates genetic diversity within the okra population. This diversity can be exploited by breeders to develop new cultivars with desirable traits, such as improved yield, taste, or resistance to diseases.

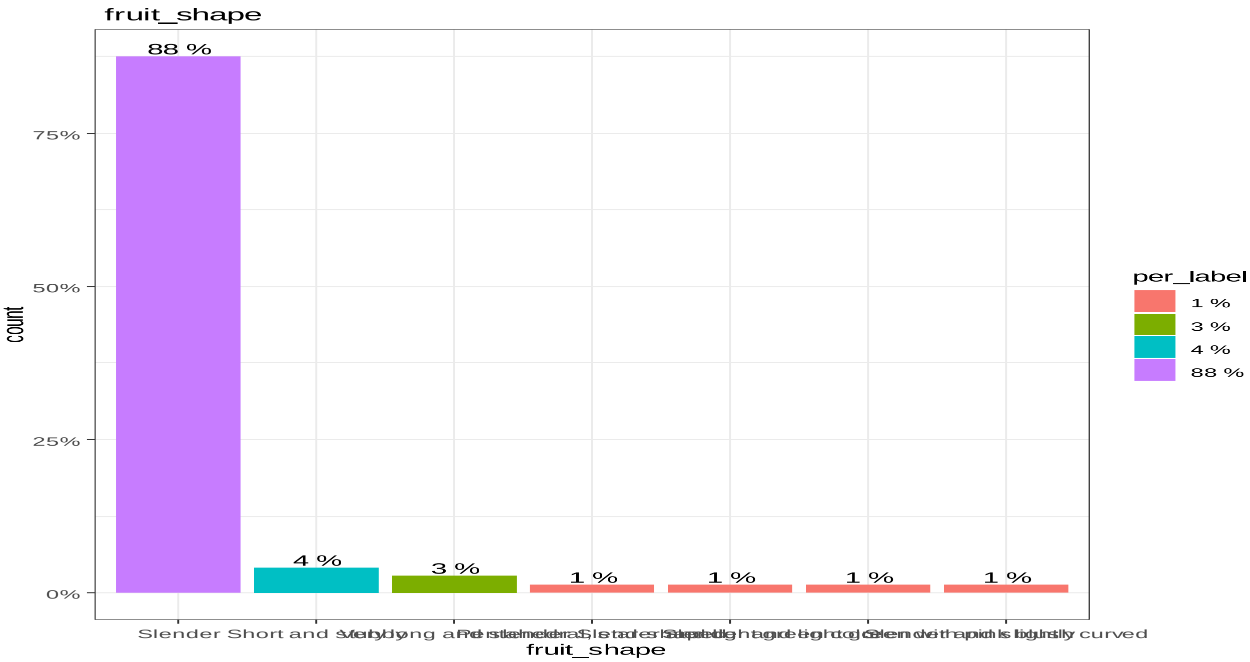

Figure 10 : Fruit Shape qualitative traites

Image 4 : Fruit Shape qualitative traits

Image 4.1 Very long and slender

Image 4.2 Star-shaped

Image 4.3 Slender and slightly curved

Image 4.4 Short and stubby

4.7.8 Fruit color

The R software gives a bar chart that displays the distribution of okra accessions based on fruit color. The data includes several categories of fruit color, and their corresponding percentages are as follows:

The majority of okra accessions have green fruit color (89%), while the remaining accessions exhibit various other fruit colors, each accounting for a very small percentage (1–3%).

The dominance of green fruit color (89%) among the okra accessions suggests that it is the most common or perhaps preferred trait in the population, likely due to natural selection, adaptation to local conditions, or consumer preference. Green fruit color may be associated with agronomical favorable traits, such as higher yield or quality, making it prevalent in the studied accessions.

The presence of other fruit colors, such as red, purple, and combinations of green with blushes or dark shades, though less frequent, could reflect genetic diversity within the okra population. These rare accessions may hold valuable traits such as tolerance to environmental stress, pest resistance, or unique market appeal.

Further studies could explore the relationship between fruit color and other morphological traits or yield components to assess the practical significance of color variation. Additionally, these diverse colors may be of interest in breeding programs aimed at increasing genetic diversity, developing new okra varieties, or catering to specific consumer preferences

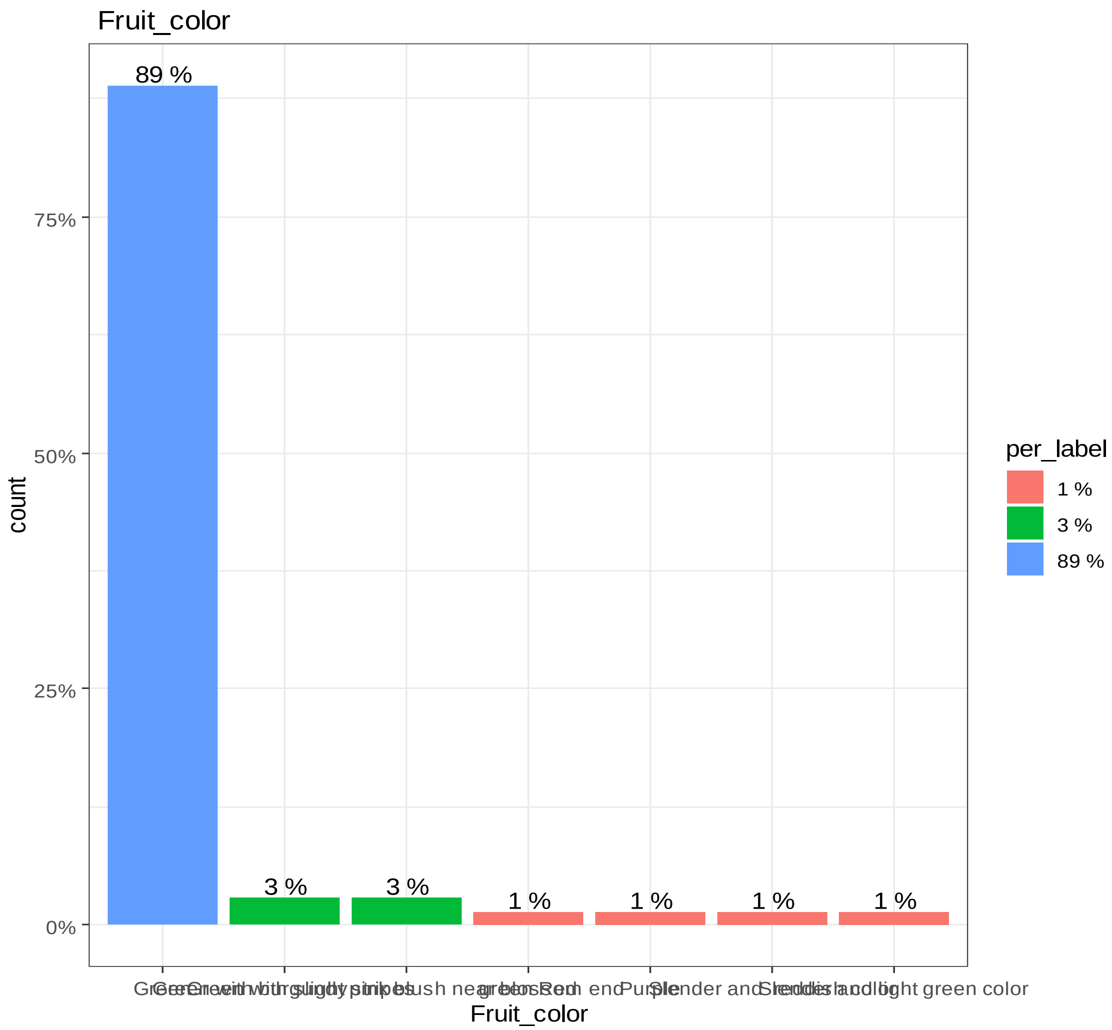

Figure 11 : Fruit color qualitative traits

Images 5 : Fruit color qualitative traits


Image 5.1 : green pod qualitative traits


Image 5.2 :   reddish-purple qualitative traits


Image 5.3 light green qualitative traits   +


Image 5.4 : dark green color qualitative traits


Image 5.5 : red color pod qualitative traits


Image 5.6 : purple pod qualitative traits


Image 5.7 Green qualitative traits


Image 5.8 Green with purple qualitative traits


Image 5.9 dark Red qualitative traits

4.9.9 Growth Habitat

The distribution of growth habitats showed that 58% of the accessions had a "Sparse" growth habit, 35% had a "Moderate" growth habit, and 7% had a "Bushy" growth habit.

The prevalence of sparse growth habits may offer advantages such as improved air circulation and disease resistance, but moderate growth types might lead to better yields due to balanced branching. The low occurrence of bushy growth suggests that such accessions may be less suited to the environmental conditions of the study site, possibly due to shading or competition. Further evaluation could help identify growth habits best suited to different environments and improve breeding programs aimed at optimizing plant structure.

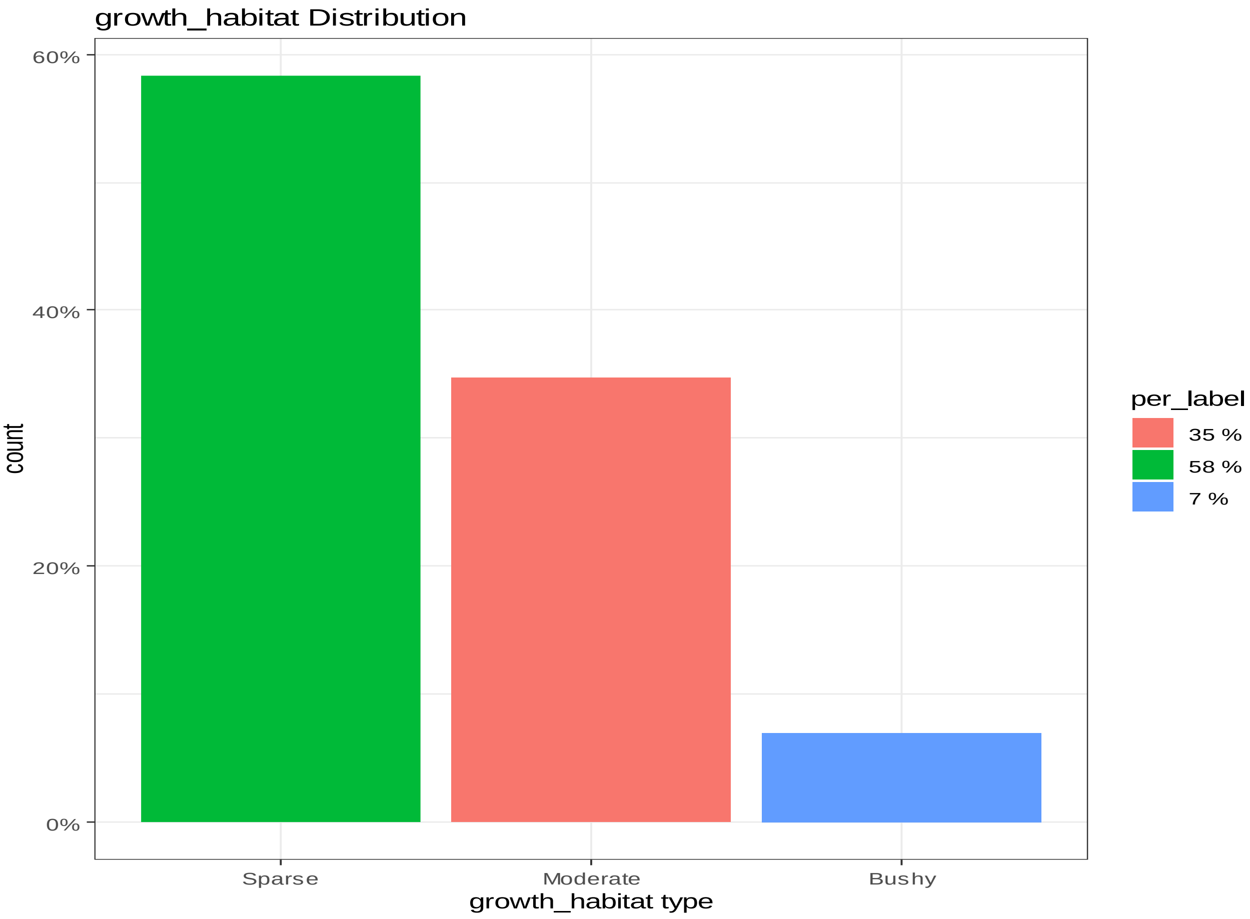

Figure 12: Growth habitat qualitative traits

4.9.10 Stem Pubescence

The distribution of stem pubescence types showed that 43% of accessions had "Moderate" pubescence, 29% had "Absent," 22% had "Sparse," and 6% had "Dense" pubescence.

Moderate pubescence was the most common trait, potentially providing a balance between plant protection and ease of handling. Absent pubescence in nearly a third of the accessions could indicate an advantage for cultivation practices that require less labor. The diversity in pubescence types suggests genetic variability that could be useful for breeding programs focused on pest resistance or environmental adaptability.

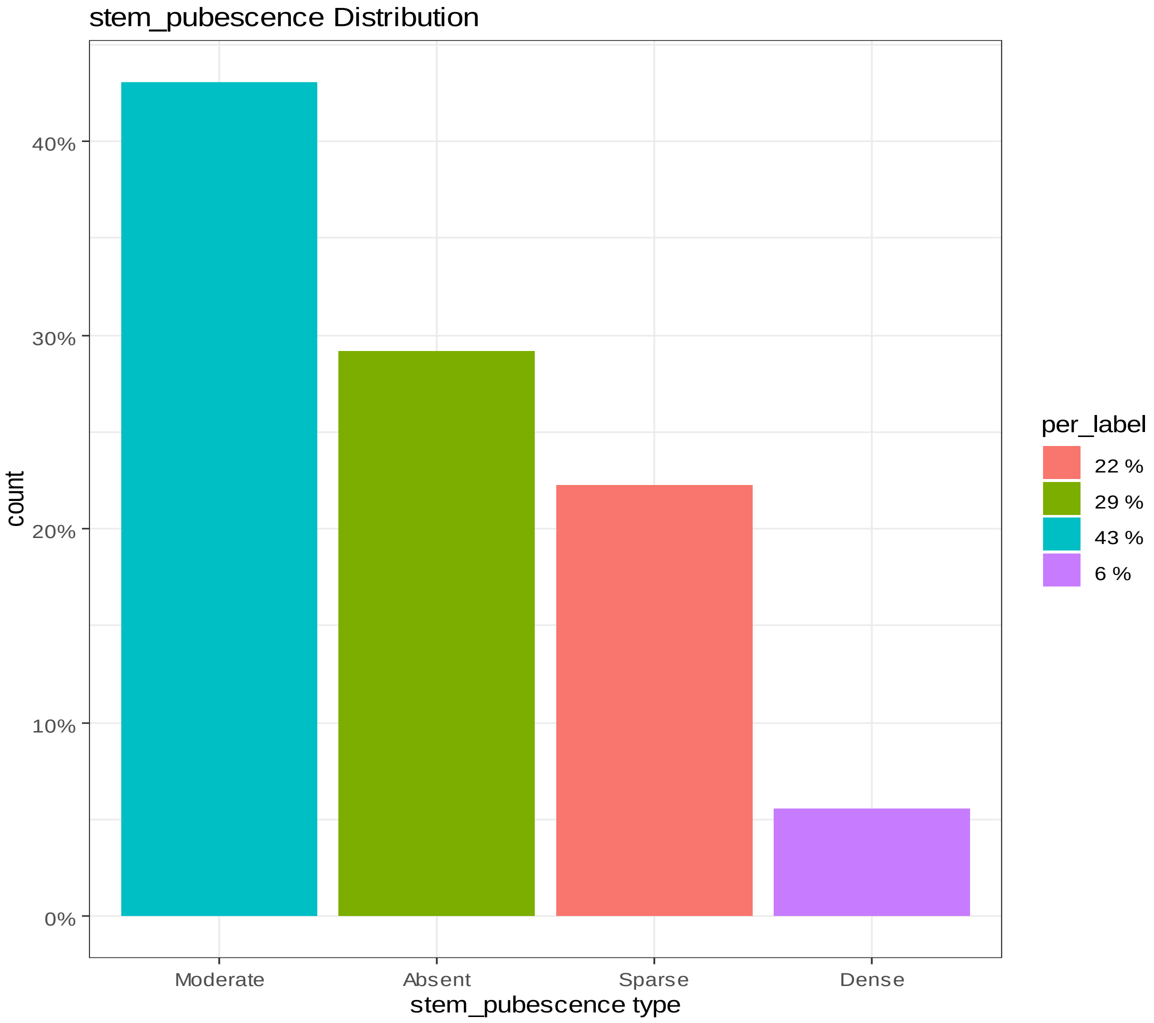

Figure 13 Stem pubescence qualitative traits

4.9.11 Color between Leaf Veins

Bar chart data indicated that 94% of accessions had "Green" coloration between leaf veins, with minor variations observed in the remaining 6%, including purple and pink hues.

The dominance of green coloration suggests that this trait is widely conserved, indicating healthy leaf function. The small proportion of accessions with other colors may reflect genetic diversity and could have implications for pest resistance or stress tolerance. Breeding programs could leverage these color variations for improved stress resilience or to meet specific market preferences.

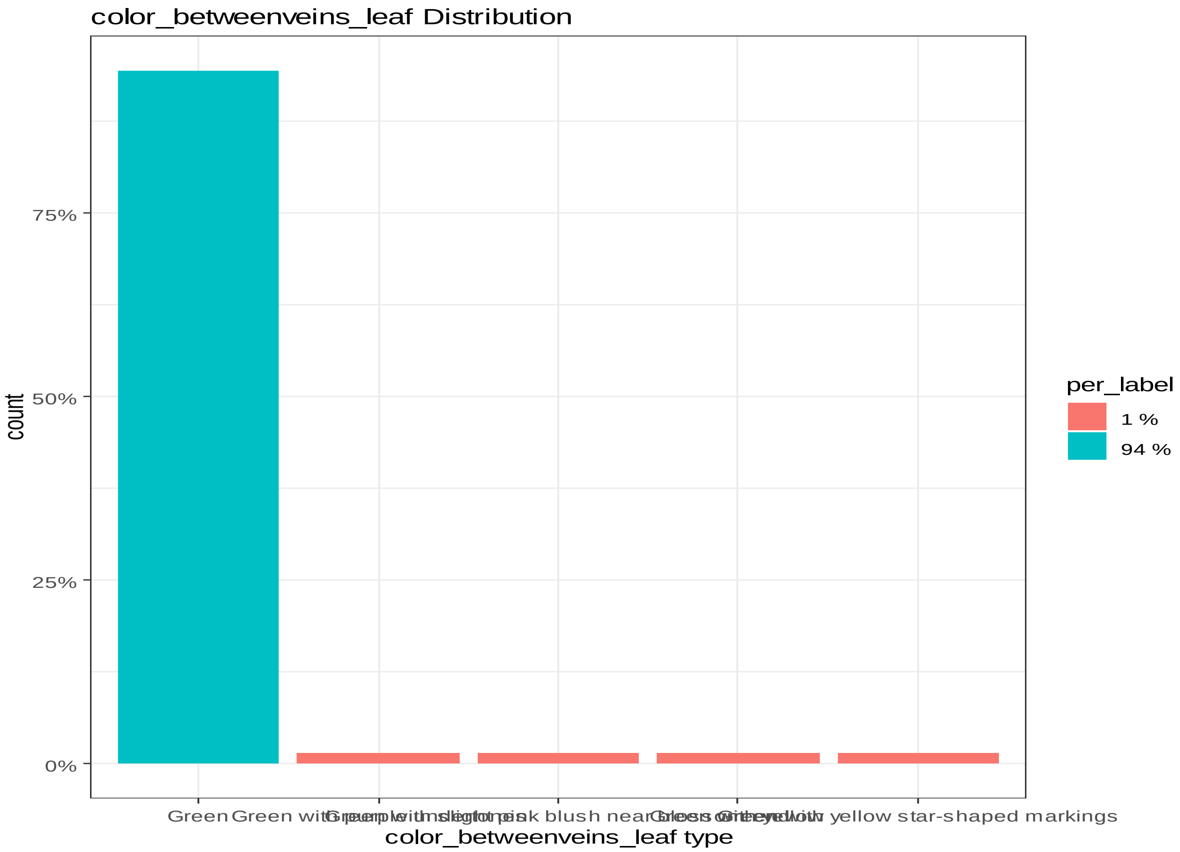

Figure 14 Color between leaf veins qualitative traits

4.9.12 Leaf Lobing Depth

The distribution of leaf lobing depth categorized plants as "Shallow" (89%), "Medium" (5%), and "Deep Lobes" (6%).

Shallow lobes were the most common among the accessions, likely reflecting the genetic makeup and environmental conditions. The presence of medium and deep lobes suggests that there is genetic diversity within the okra germplasm that could be explored for improving plant architecture or yield. Understanding the factors influencing leaf lobing depth could help in selecting okra varieties suited to different growing conditions.

The qualitative traits of okra accessions in this study, such as flower color, leaf shape, fruit color, and the presence of spines, exhibit significant diversity, reflecting the phenotypic variability within the genotypes. Previous studies in Ethiopia and elsewhere have emphasized the importance of such traits for breeding and selection purposes.

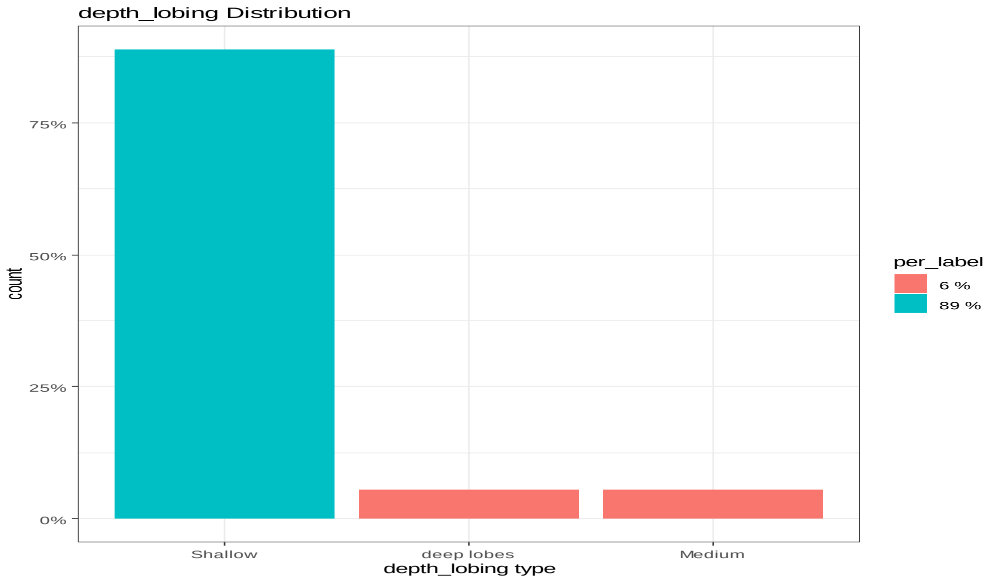

Figure 15: Depth Lobing qualitative traits

4.9.13 Flower Color Distribution:

As shown in the bar graph, the distribution of okra plants based on their flower color revealed five distinct categories: "Yellow with a dark red center," "Yellow," "Cream," "Yellow with a purple eye," and "Green." These categories were defined as categorized by the IPGR Descriptors (1991). The most common flower color was "Yellow with a dark red center," accounting for 40% of the total population. The second most common color was "Yellow," comprising 32% of the plants. A smaller percentage of plants exhibited "Cream" flowers (24%), "Yellow with a purple eye" (3%), and "Green" flowers (1%).

The predominance of "Yellow with a dark red center" and "Yellow" flowers in this study might be attributed to a combination of factors, including the genetic makeup of the okra varieties used, the prevailing environmental conditions, and the agronomic practices employed. Further research is needed to determine the specific factors that contribute to the variation in flower color and to identify the optimal flower color for different growing conditions and agronomic practices.

The qualitative analysis of okra morphological characteristics, specifically flower color, has revealed a diverse range of phenotypes. The most common flower colors in this study were "Yellow with a dark red center" and "Yellow." However, a significant proportion of plants exhibited other flower colors, including "Cream," "Yellow with a purple eye," and "Green." Understanding the factors that influence flower color can aid in the selection of suitable okra varieties for different growing conditions and the development of breeding programs aimed at improving ornamental value or other desirable traits.

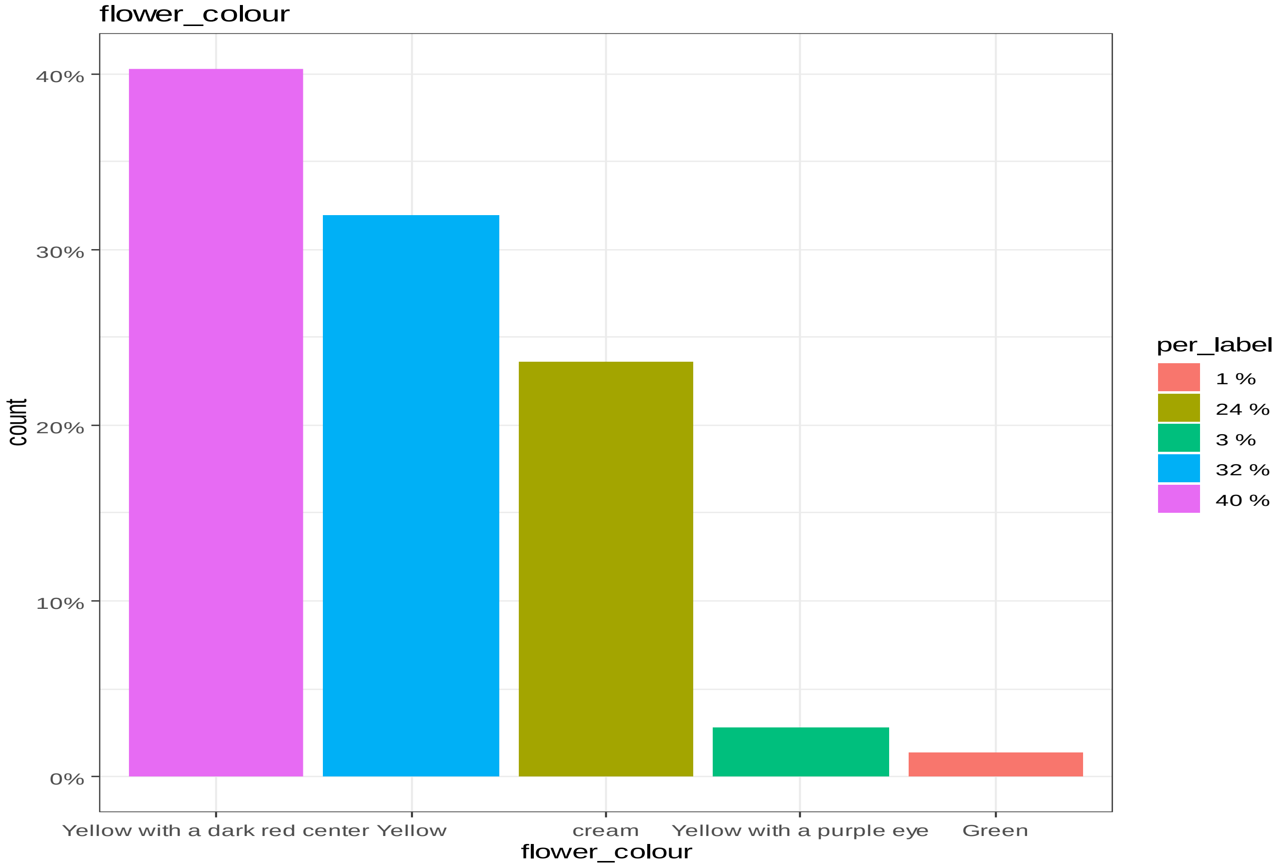

Figure 16: Flower Color qualitative traits

4.9.14 Spines on the stem

Figure 1 presents a bar chart illustrating the distribution of two distinct categories within the dataset: "Spineless" and "Spine." The results demonstrate a significant disparity in the prevalence of these categories.

The analysis reveals that the majority of observations (85%) belong to the "Spineless" category, while the "Spine" category comprises a smaller proportion (15%). This pronounced imbalance suggests potential biological implications, such as evolutionary adaptations or environmental factors influencing the observed distribution.

However, it is essential to consider potential biases in the dataset. The observed distribution might not accurately reflect the true proportions in the population. Further investigation is necessary to determine whether the results are representative or if they are influenced by sampling or data collection methods.

To gain a deeper understanding of the underlying factors, additional research should be conducted. This could involve analyzing the environmental conditions, genetic makeup, or morphological traits of the samples.

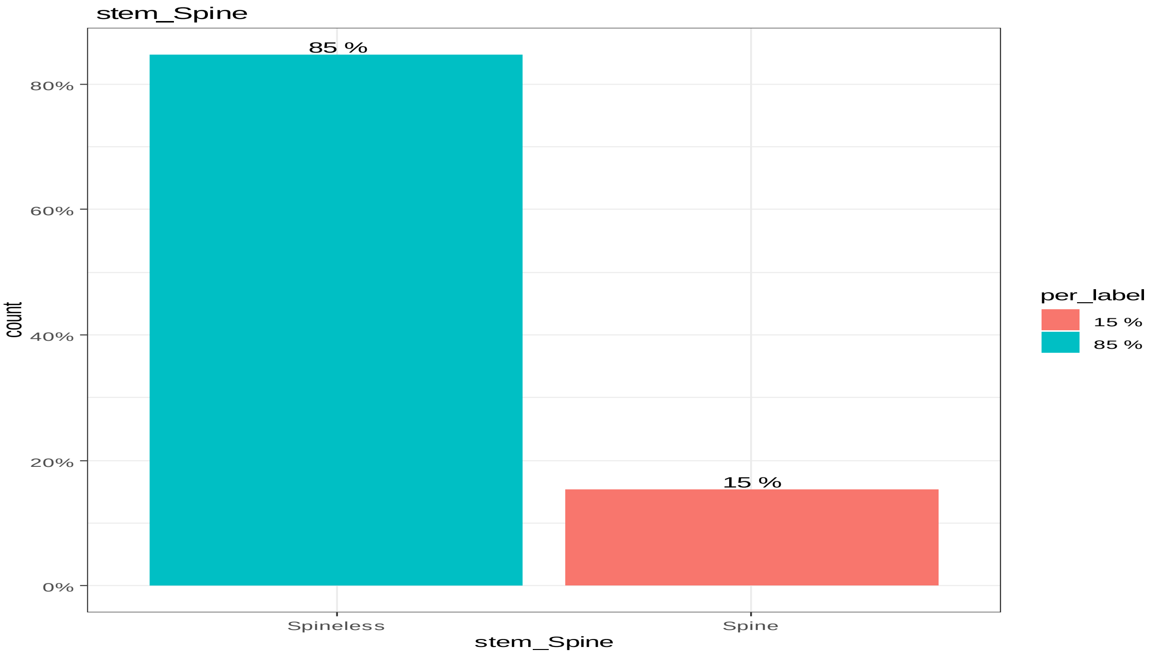

Figure 17: Spines on the stem qualitative traits

In the context of flower color, most okra accessions in this study exhibited white flowers, which are consistent with findings by Gashaw et al. (2020), who noted that white flowers are predominant in Ethiopian okra germplasm. However, some accessions exhibited yellow flowers, a trait associated with the introduction of exotic varieties and genetic variability. This finding supports the work of Tadesse et al. (2019), who observed variation in flower color among okra accessions from different agro-ecological zones in Ethiopia.

Fruit color, another key qualitative trait, was predominantly green across the accessions studied, but a few accessions had reddish or purple-tinged fruits. Similar color variation has been reported by Mulugeta et al. (2021), who observed that fruit color in okra can vary significantly depending on genotype and environmental factors. They noted that these color variations could influence market preferences, which may be a crucial aspect for future breeding programs in Ethiopia, particularly for improving the appeal of okra in local and export markets.

The presence of spines on the stem was another trait that exhibited variation. Some accessions were spine-free, while others had moderate to high spine density, which could affect both the ease of harvesting and pest resistance. This trait has been highlighted by Abdulkadir et al. (2019), who found that spine density is often correlated with pest resistance and may serve as an adaptive trait to enhance survival in certain environments. However, too many spines could make harvesting more difficult, as noted by Adhikari et al. (2022), which suggests that the balance between spine density and ease of harvest must be considered in breeding decisions.

Overall, these qualitative traits highlight the substantial diversity present in the okra accessions studied, supporting the idea that Ethiopia's okra germplasm has significant untapped potential for improvement through selective breeding.

CHAPTER FIVE: CONCLUSIONS AND RECOMMENDATION

5.1 Conclusion

This research characterized the phenotypic traits of 72 okra accessions from Tigray, providing valuable insights into their growth, phenology, and yield-related characteristics. Among the accessions, Bereket4, Hillegin10, Maikadra1, AdiGoshu9, Bereket10, and AdiGoshu12 excelled in key traits such as fruit number, single fruit weight, fruit weight per plant, and overall yield.

Several promising genotypes emerged with desirable high-yielding and early-maturing traits, notably Hillegin19, Hillegin16, AdiGoshu12, and AdiGoshu9. These accessions consistently demonstrated early emergence, 50% flowering, and early maturity.

Clustering analysis revealed significant genetic diversity among the accessions, highlighting distinct performances across clusters. Accessions in Cluster 7 exhibited exceptional traits, including the highest yield per hectare (182.5 kg/ha), the largest number of fruits per plant (33.27), and substantial single fruit weight (39.23 g). In contrast, Cluster 4 displayed desirable early-maturing traits, with a short duration to first picking (53 days) and 50% flowering (75.25 days).

Traits such as plant height, stem diameter, and fruit dimensions varied significantly among clusters, indicating opportunities for selection and improvement in breeding programs. The data suggest that crossing accessions from different clusters can yield genetically diverse recombination, enhancing the overall performance of new varieties. Specifically, combining high-yielding accessions from Cluster 7 with early-maturing accessions from Cluster 4 may optimize both yield and time to maturity.

This research underscores the importance of genetic diversity in improving okra production in Tigray. The findings lay a solid foundation for future breeding strategies aimed at developing superior varieties that address local agricultural needs and contribute to sustainable food security. Continued exploration of genetic recombination through targeted breeding will further enhance the agricultural viability of okra in the region.

The study also assessed correlations among various quantitative traits, revealing significant relationships that can guide breeding strategies. Days to emergence positively correlated with days to 50% flowering ($r = 0.913$, $p < 0.001$) and negatively with stem diameter ($r = -0.015$), indicating that early emergence does not adversely affect stem development. Furthermore, plant height correlated positively with fruit length ($r = 0.542$, $p < 0.01$) and the number of fruits per plant ($r = 0.47$, $p < 0.001$), suggesting that taller plants tend to produce larger and more numerous fruits. Fruit diameter also positively correlated with yield per hectare ($r = 0.401$, $p < 0.01$), underscoring the significance of fruit size in yield potential. Negative correlations, such as between stem diameter and the number of branches ($r = -0.079$), suggest potential trade-offs in resource allocation among traits that breeders should consider during selection.

The analysis of genotypic and phenotypic variances among the 72 okra genotypes revealed important insights into the variability of key traits. Traits such as plant height, days to flowering, and esteemed yield per hectare exhibited substantial genotypic variances, indicating a significant genetic component influencing these characteristics. For instance, plant height had the highest genotypic variance (2391.22), highlighting its potential for selection in breeding programs. In contrast, phenotypic variances were generally higher than genotypic variances for most traits, emphasizing the influence of environmental factors on trait expression. The close values of genotypic and phenotypic variances for traits like stem diameter and fruit diameter indicate that these traits are relatively stable across environments, making them reliable targets for selection.

The findings underscore the necessity of considering both genotypic and phenotypic variances when developing breeding strategies aimed at improving okra traits. By leveraging traits with high heritability, such as days to flowering and esteemed yield per hectare, breeders can enhance the productivity and adaptability of okra genotypes in Tigray. This study provides a foundational understanding that can guide future breeding efforts for optimizing okra production in the region.

The evaluation of genetic variability components for 15 traits of the 72 okra genotypes at Humera in 2020 highlighted significant findings. The grand means indicated a range of traits with varying genetic coefficients of variation (GCV) and phenotypic coefficients of variation (PCV). Traits such as the number of branches per plant (GCV = 48.54) and plant height (GCV = 33.73) demonstrated considerable genetic variability, suggesting strong potential for selection in breeding programs. High heritability values (H^2) for traits like days to 50% flowering (0.84) and esteemed yield (0.88) indicate that these traits are less influenced by environmental factors, making them reliable targets for genetic improvement. Additionally, the genetic advance (GA) values suggest significant potential for enhancing traits through selection, particularly in plant height and yield.

The analysis of the phenotypic qualitative traits of okra accessions reveals significant variability, demonstrating the diverse genetic potential within the studied population. In terms of plant height, the majority of accessions fall into the small (43%) and medium (22%) categories, indicating a predominance of shorter growth forms. This distribution may provide valuable insights for breeding programs focusing on optimizing plant height for both yield and ease of harvest.

Stem diameter exhibits a notable distribution, with a substantial percentage of accessions categorized as large (38%) and medium (43%), suggesting potential for selecting accessions with desirable stem thickness, which is important for plant support and fruit production. Additionally, the predominance of smooth stem texture (67%) over slightly rough (33%) indicates a preference for smoother varieties, which may appeal to both farmers and consumers.

The qualitative traits, such as fruit shape and color, also exhibit considerable variability. The majority of accessions are categorized as having an angular fruit shape (97%) and green fruit color (89%), highlighting common traits that may align with consumer preferences. However, the presence of diverse fruit shapes, including round and star-shaped varieties, offers exciting possibilities for market differentiation and consumer appeal.

Furthermore, the distribution of maturity categories shows a majority of accessions (44%) classified as medium maturity, which aligns with local growing conditions. The variation in flower color reveals diverse aesthetic traits, with a significant number of accessions exhibiting yellow flowers with a dark red center (40%), contributing to the visual appeal of okra plants.

Overall, the findings highlight the potential for selecting specific traits that enhance agricultural productivity and marketability. The rich diversity in both quantitative traits, such as plant height and yield-related characteristics, and phenotypic qualitative traits, including fruit shape and flower color, suggests ample opportunities for breeding programs to develop improved okra varieties tailored to the preferences of local farmers and consumers. This study underscores the importance of characterizing phenotypic qualitative traits in okra accessions, providing a foundational resource for future breeding efforts aimed at enhancing okra production in Tigray.

Overall, these findings provide a solid foundation for future breeding strategies, emphasizing the importance of focusing on traits with high genetic variability and heritability to optimize okra production in the region. The analysis revealed significant variability among the accessions, highlighting the potential for selecting superior genotypes for breeding programs. Key traits such as plant height, fruit number, and single fruit weight exhibited strong correlations with yield, underscoring their importance in breeding strategies aimed at enhancing productivity.

The findings also emphasized the critical role of genetic diversity in improving resilience against environmental challenges, pests, and diseases. This study’s results can guide future breeding efforts, focusing on accessions that perform well under local conditions and contribute to sustainable agricultural practices. Overall, the phenotypic characterization of okra accessions from Tigray provides a foundation for developing improved varieties that meet the needs of local farmers and enhance food security in the region. Continued research into the genetic basis of these traits, along with practical implementation of breeding recommendations, will further bolster the agricultural prospects for okra in Tigray.

5.2 Recommendation

Based on the findings of this research, several recommendations can enhance the breeding and cultivation of okra in Tigray: Prioritize the utilization of high-performing accessions identified in this study, such as Bereket4, Hillegin10, Maikadra1, AdiGoshu9, Bereket10, and AdiGoshu12. These accessions exhibit favorable traits, including high fruit number, increased single fruit weight, and overall yield, making them ideal candidates for breeding programs.

Incorporate early-maturing genotypes, particularly Hillegin19, Hillegin16, AdiGoshu12, and AdiGoshu9, into breeding strategies. These accessions consistently demonstrate early emergence and flowering, which can help optimize production cycles and enhance food security.

Utilize the genetic diversity identified through clustering analysis to inform breeding programs. Combining accessions from different clusters may lead to improved hybrids that enhance both yield and resilience to environmental stresses.

Emphasize traits with high heritability and significant correlations with yield, such as plant height, fruit number, and fruit diameter. By strategically selecting these traits, breeders can enhance the overall productivity and adaptability of okra genotypes in the region.

Continue investigating the correlations among quantitative traits to refine breeding strategies. Understanding the intricate relationships between traits will facilitate the selection of superior genotypes that are well-suited for local growing conditions.

Develop targeted breeding programs that focus on the identified traits with high genetic variability and heritability. This approach can optimize the development of improved okra varieties that meet the specific agricultural needs of Tigray.

Encourage sustainable farming practices that utilize improved okra varieties. This will not only enhance productivity but also contribute to the resilience of local farming systems against environmental challenges, pests, and diseases.

By following these recommendations, stakeholders can effectively enhance okra production in Tigray, contributing to the region's food security and agricultural sustainability. Continued research and collaboration among researchers, breeders, and farmers will be essential for the successful implementation of these strategies.

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APPENDIXES

Table 13: Mean values of 72 okra accessions growth traits evaluated at Humera

	Geno	Days to emergency	days to 50% flowering	Steam diameter	Days_first_pikcing
1	Maikadra1	8.50^{ab}	77.4650 ^{abcdefg}	0.7950^{o}	85.5675^{abcdefg}
2	Maikadra2	7.75 ^{abcd}	78.2500 ^{abcde}	1.1100^{mno}	83.5 ^{abcdefghi}
3	Maikadra3	6.25^{abcd}	77.2000 ^{abcdefg}	1.0500^{mno}	84.75 ^{Abcdefgh}
4	Maikadra4	9.00 ^{a}	74.5000 ^{abcdefghij}	2.2900^{bcdefgh}	81.75^{abcdefghijk}l
5	Maikadra5	7.25^{abcd}	65.5000 ^{abcdefghijklmnopqr}	1.8850^{bcdefghijkl}	71.5 ^{defghijklmno}
6	Maikadra6	6.00^{abcd}	57.5000 ^{hijklmnopqrstu}	2.0450^{bcdefghijk}	64.25 ^{Hijklmnopqr}
7	Maikadra7	7.25^{abcd}	74.5000 ^{abcdefghij}	1.9800^{bcdefghijkl}	82.25 ^{Abcdefghijk}
8	Maikadra8	6.75^{abcd}	54.2500 ^{mnopqrstuv}	0.8000^{o}	55.25 ^{Nopqr}
9	Maikadra9	6.00^{abcd}	74.7500 ^{abcdefghij}	1.7450^{cdefghijklm}	83 ^{abcdefghij}
10	Maikadra10	9.00^{a}	55.7500 ^{jklmnopqrstuv}	1.1100 ^{mno}	63 ^{ijklmnopqr}
11	Maikadra11	8.00^{abcd}	81.6075 ^{ab}	1.3150 ^{lmno}	95.75 ^{ab}
12	Maikadra12	7.75^{abcd}	51.5000 ^{opqrstuv}	1.4100 ^{jklmno}	55.25 ^{nopqr}
13	Maikadra13	7.25^{abcd}	59.5000 ^{efghijklmnopqrst}	1.8950^{bcdefghijkl}	65.25 ^{ghijklmnopqr}
14	Maikadra14	5.75^{bcd}	67.7500 ^{abcdefghijklmnop}	1.5550 ^{ijklmn}	76 ^{bcdefghijklmn}
15	Maikadra15	9.00^{a}	80.7500 ^{abcd}	1.5800^{hijklmn}	95.25^{abc}
16	Hillegin1	7.50^{abcd}	66.5000 ^{abcdefghijklmnopq}	2.5350 ^{b}	74.75 ^{cdefghijklmn}
17	Hillegin2	6.50^{abcd}	54.7500 ^{klmnopqrstuv}	1.5900^{ghijklmn}	65 ^{ghijklmnopqr}
18	Hillegin3	5.50^{bcd}	74.2500 ^{abcdefghijk}	1.1250^{mno}	80 ^{abcdefghijkl}
19	Hillegin4	7.00^{abcd}	66.7500 ^{abcdefghijklmnopq}	1.6800^{defghijklm}	91.5 ^{abcd}
20	Hillegin5	6.25^{abcd}	72.7500 ^{abcdefghijklmn}	1.9300^{bcdefghijkl}	80.5 ^{Abcdefghijkl}
21	Hillegin6	6.50^{abcd}	51.0000 ^{opqrstuv}	2.4800 ^{b}	64.25 ^{hijklmnopqr}

22	Hillegin7	8.25^{abc}	71.7500 ^{abcdefghijklmn}	1.1200 ^{mno}	81.25 ^{abcdefghijkl}
23	Hillegin8	6.50^{abcd}	72.7500 ^{abcdefghijklmn}	2.0450^{bcdefghijk}	82.75 ^{abcdefghij}
24	Hillegin9	7.50^{abcd}	55.5000 ^{jklmnopqrstuv}	2.2350 ^{bcdefghi}	62.75^{ijklmnopqr}
25	Hillegin10	8.00^{abcd}	50.0000 ^{pqrstuv}	1.6500 efghijklm	62.75 ^{ijklmnopqr}
26	Hillegin11	9.00^{a}	78.0000 ^{abcde}	1.1250 ^{mno}	83.5 ^{abcdefghi}
27	Hillegin12	6.75^{abcd}	56.5000 ^{ijklmnopqrstu}	1.4700 ^{jklmno}	63 ^{ijklmnopqr}
28	Hillegin13	7.50^{abcd}	54.0000 ^{mnopqrstuv}	1.9550^{bcdefghijkl}	64.75 ^{ghijklmnopqr}
29	Hillegin14	7.00 ^{abcd}	72.2500 ^{abcdefghijklmn}	2.3000 ^{bcdefg}	81.5 ^{abcdefghijkl}
30	Hillegin15	8.00 ^{abcd}	71.2500 ^{abcdefghijklmn}	0.8250 ^{o}	82.75 ^{abcdefghij}
31	Hillegin16	6.50^{abcd}	41.5000 ^{tuv}	1.1500 ^{mno}	47.25 ^{r}
32	Hillegin17	6.50^{abcd}	57.0000 ^{hijklmnopqrstu}	2.4350 ^{bc}	64.25 ^{hijklmnopqr}
33	Hillegin18	7.50^{abcd}	62.5000 ^{bcdefghijklmnopqrs}	1.5550 ^{ijklmn}	68.5 ^{fghijklmnop}
34	Hillegin19	6.75^{abcd}	44.0000 ^{stuv}	1.1000 ^{mno}	47.5 ^{qr}
35	Bereket1	6.25^{abcd}	76.5000 ^{abcdefgh}	2.3800 ^{bcd}	85 ^{Abcdefgh}
36	Bereket2	7.00^{abcd}	78.2500 ^{abcde}	1.0800 ^{mno}	97.75 ^{a}
37	Bereket3	7.50^{abcd}	51.0000 ^{opqrstuv}	0.8925 ^{no}	57.25 ^{Mnopqr}
38	Bereket4	5.75^{bcd}	74.5000 ^{abcdefghij}	2.0900^{bcdefghij}	86.75 ^{abcdef}
39	Bereket5	6.50^{abcd}	71.7500 ^{abcdefghijklmn}	2.3300 ^{bcde}	83.25 ^{abcdefghij}
40	Bereket6	5.00^{d}	77.7500 ^{abcdef}	0.7750 ^{o}	91.5 ^{Abcd}
41	Bereket7	5.00^{d}	82.5000 ^{a}	1.1000 ^{mno}	96.25 ^{Ab}
42	Bereket8	7.00^{abcd}	61.2500^{defghijklmnopqrs}	1.3250 ^{lmno}	76.5 ^{bcdefghijklm}
43	Bereket9	6.50^{abcd}	53.2500 ^{nopqrstuv}	1.5400 ^{ijklmn}	64.5 ^{hijklmnopqr}
44	Bereket10	6.50^{abcd}	74.0000^{abcdefghijkl}	3.7000^{a}	83.25 ^{abcdefghij}
45	Bereket11	6.50 ^{abcd}	70.0000 ^{abcdefghijklmno}	1.8700^{bcdefghijkl}	77.5 ^{abcdefghijklm}
46	Bereket12	8.00 ^{abcd}	75.0000 ^{abcdefghij}	1.9450^{bcdefghijkl}	84.5 ^{abcdefgh}
47	AdiGoshu1	6.75^{abcd}	75.5000 ^{abcdefghi}	1.8900^{bcdefghijkl}	84 ^{abcdefgh}
48	AdiGoshu2	7.75 ^{abcd}	54.2500 ^{mnopqrstuv}	1.4500 ^{jklmno}	63 ^{ijklmnopqr}

49	AdiGoshu3	6.25^{abcd}	$69.5000^{abcdefghijklmnop}$	$1.8950^{bcdefghijkl}$	$77.75^{abcdefghijklm}$
50	AdiGoshu4	7.50^{abcd}	$76.2500^{abcdefgh}$	1.1500^{mno}	$84^{abcdefgh}$
51	AdiGoshu5	7.50^{abcd}	46.5000^{rstuv}	$1.9150^{bcdefghijkl}$	$61.25^{lmnopqr}$
52	AdiGoshu6	6.50^{abcd}	$72.7500^{abcdefghijklmn}$	$2.2700^{bcdefgh}$	$81.25^{abcdefghijkl}$
53	AdiGoshu7	6.25^{abcd}	$72.5000^{abcdefghijklmn}$	$2.2300^{bcdefghi}$	$81.75^{abcdefghijkl}$
54	AdiGoshu8	7.50^{abcd}	48.0000^{qrstuv}	0.8000^{o}	53^{Opqr}
55	AdiGoshu9	5.00^{d}	36.5000^{v}	1.3500^{klmno}	48.25^{Pqr}
56	AdiGoshu10	6.50^{abcd}	$73.2500^{abcdefghijklm}$	1.3950^{jklmno}	$82^{abcdefghijkl}$
57	AdiGoshu11	7.50^{abcd}	46.5000^{rstuv}	1.1500^{mno}	58^{mnopqr}
58	AdiGoshu12	5.25^{cd}	38.7500^{uv}	1.3250^{lmno}	46.5^{r}
59	AdiGoshu13	6.50^{abcd}	81.2500^{abc}	1.1000^{mno}	96.25 ab
60	AdiGoshu14	8.50^{ab}	$58.2500^{fghijklmnopqrstu}$	1.4000^{jklmno}	$71^{Defghijklmno}$
61	AdiGoshu15	7.25^{abcd}	80.0000^{abcd}	1.1050^{mno}	92.75^{abc}
62	AdiGoshu16	7.00^{abcd}	$58.0000^{ghijklmnopqrstu}$	2.3100^{bcdef}	$65.25^{ghijklmnopqr}$
63	Adiabo1	7.50^{abcd}	$62.7500^{bcdefghijklmnopqrs}$	$1.9800^{bcdefghijkl}$	$70.75^{defghijklmno}$
64	Adiabo2	7.50^{abcd}	$50.2500^{pqrstuv}$	1.5400^{ijklmn}	$62.5^{jklmnopqr}$
65	Adiabo3	8.25^{abc}	$56.2500^{ijklmnopqrstu}$	1.0500^{mno}	$61.75^{klmnopqr}$
66	Adiabo4	8.25^{abc}	47.2500^{qrstuv}	1.100^{mno}	53^{Opqr}
67	Adiabo5	5.50^{bcd}	78.2500^{abcde}	1.4000^{jklmno}	90.5^{Abcde}
68	Adiabo6	7.00^{abcd}	$61.7500^{cdefghijklmnopqrs}$	1.4600^{jklmno}	$68.25^{fghijklmnopq}$
69	Adiabo7	7.75^{abcd}	$63.5000^{abcdefghijklmnopqrs}$	$1.9950^{bcdefghijkl}$	$70.25^{efghijklmno}$
70	Bamya Humera	7.50^{abcd}	$50.7500^{opqrstuv}$	$1.6500^{efghijklm}$	$65.25^{ghijklmnopqr}$
71	SOH 701	5.50^{bcd}	$54.5000^{lmnopqrstuv}$	$1.7150^{defghijklm}$	57.5^{mnopqr}
72	SOH 714	7.25^{abcd}	$72.7500^{abcdefghijklmn}$	$1.6050^{fghijklmn}$	$83^{abcdefghij}$

Cont... Mean values of 72 okra accessions growth traits evaluated at Humera

No	Geno	Plant_height_cm	No of branches	Inter_nod_lentgh	pedL	Fruit_length
1	Maikadra1	158.075^{cdefghijklmnop}	6.97^{ab}	4.595^{efghijklmn}	1.795^{defghijklmno}	7.9825^{jklm}
2	Maikadra2	132.45^{fghijklmnopq}	6.0975^{abcd}	4.94^{defghijklmn}	1.8925^{bcdefghijklmno}	7.9325^{jklm}
3	Maikadra3	155.5^{cdefghijklmnop}	5.5^{abcdefg}	4.84^{efghijklmn}	1.8^{defghijklmno}	7.105^{klm}
4	Maikadra4	154.525^{cdefghijklmnop}	3.425^{ghijklmno}	5.405^{defghijklmn}	1.5125^{ijklmno}	11.5325^{defghijklm}
5	Maikadra5	125.19^{lmnopq}	3.1525^{ijklmno}	6.25^{bcdefghijkl}	1.88^{bcdefghijklmno}	11.81^{defghijklm}
6	Maikadra6	150.635^{cdefghijklmnop}	2.9325^{lmno}	4.61^{efghijklmn}	2.0025^{abcdefghijklmn}	12.69^{defghijkl}
7	Maikadra7	173.055^{abcdefghij}	3.1125^{ijklmno}	5.9125^{cdefghijklm}	2.6525^{abcdefghi}	13.7125^{cdefghij}
8	Maikadra8	92.75^{qr}	3.355^{hijklmno}	2.925^{lmn}	1.8075^{defghijklmno}	14.25^{cdefghi}
9	Maikadra9	151.4425^{cdefghijklmnop}	2.8975^{lmno}	5.985^{cdefghijklm}	1.985^{abcdefghijklmn}	15.1375^{bcdefg}
10	Maikadra10	176.5^{abcdefg}	2.8225^{lmno}	6.0125^{cdefghijklm}	1.7025^{fghijklmno}	17.01^{bcdef}
11	Maikadra11	163.75^{abcdefghijklmn}	6.5^{abc}	6.9575^{abcdefghijk}	2.8925^{abcde}	17.145^{bcdef}
12	Maikadra12	173.875^{abcdefghi}	5.0775^{abcdefghijk}	6.9875^{abcdefghijk}	1.9075^{bcdefghijklmno}	8.25^{hijklm}
13	Maikadra13	151.725^{cdefghijklmnop}	3.08^{jklmno}	5.04^{defghijklmn}	1.455^{jklmno}	13.56^{defghij}
14	Maikadra14	115.3325^{pq}	5.41^{abcdefgh}	3.97^{Hijklmn}	1.435^{klmno}	14.805^{bcdefg}
15	Maikadra15	130.11^{hijklmnopq}	5.2375^{abcdefghi}	2.8975^{Lmn}	3.105^{a}	12.38^{defghijkl}
16	Hillegin1	91.595^{qr}	2.8525^{lmno}	2.53^{mn}	2.295^{abcdefghijklm}	19.8675^{abc}
17	Hillegin2	96.135^{qr}	2.93^{lmno}	4.035^{hijklmn}	1.2575^{mno}	13.6525^{defghij}
18	Hillegin3	160^{cdefghijklmnop}	6.085^{abcd}	4.915^{defghijklmn}	1.77^{defghijklmno}	7.015^{lm}

19	Hillegin4	143.835 ^{defghijklmnop}	3.545 ^{efghijklmno}	4.5825 ^{efghijklmn}	3.045 ^{ab}	15.8975 ^{bcdefg}
20	Hillegin5	169.9525 ^{abcdefghijklm}	2.19 ^{o}	7.41 ^{Abcdefgh}	1.635 ^{ghijklmno}	15.7175 ^{bcdefg}
21	Hillegin6	181.625 ^{abcd}	6.9575 ^{ab}	8.0675 ^{Abcdef}	2.155 ^{abcdefghijklm}	13.9675^{cdefghij}
22	Hillegin7	129.15 ^{ijklmnopq}	3.44 ^{ghijklmno}	4.225 ^{Ghijklmn}	2.615 ^{abcdefghij}	17.25 ^{bcdef}
23	Hillegin8	157.6875^{cdefghijklmnop}	3.3575 ^{hijklmno}	5.75 ^{defghijklmn}	1.9575^{abcdefghijklmno}	12.6025^{defghijkl}
24	Hillegin9	151.06 ^{cdefghijklmnop}	3.53 ^{fghijklmno}	5.735 ^{defghijklmn}	0.8 ^{O}	14.2725 ^{cdefgh}
25	Hillegin10	178.405 ^{Abcde}	6.9975 ^{ab}	6.9225 ^{abcdefghijk}	2.365 ^{abcdefghijklm}	20.8475 ^{ab}
26	Hillegin11	128.5 ^{jklmnopq}	3.4675 ^{ghijklmno}	4.1525 ^{Ghijklmn}	1.7625 ^{defghijklmno}	7.1125 ^{klm}
27	Hillegin12	176.4175 ^{abcdefg}	3.0675 ^{jklmno}	7.26 ^{abcdefghij}	1.795 ^{defghijklmno}	16.075 ^{bcdefg}
28	Hillegin13	208.8125 ^{a}	4.49 ^{cdefghijklmn}	9.3475 ^{Abc}	0.9175 ^{no}	16.6075 ^{bcdefg}
29	Hillegin14	171.4725 ^{abcdefghijk}	3.0975 ^{jklmno}	7.3725 ^{abcdefghi}	2.69 ^{abcdefgh}	13.185 ^{defghijkl}
30	Hillegin15	52.095 ^{r}	7.1175^{a}	2.875 ^{Lmn}	1.55 ^{hijklmno}	5.9525 ^{m}
31	Hillegin16	180.98 ^{abcd}	2.7775 ^{no}	8.0125 ^{abcdef}	2.4475 ^{abcdefghijkl}	17.045 ^{bcdef}
32	Hillegin17	122.315 ^{nopq}	2.13 ^{o}	4.525 ^{fghijklmn}	1.7475 ^{efghijklmno}	15.6475 ^{bcdefg}
33	Hillegin18	125.0675 ^{mnopq}	3.115 ^{ijklmno}	5.2025 ^{defghijklmn}	2.705 ^{abcdefgh}	13.0675^{defghijkl}
34	Hillegin19	129.5 ^{Ijklmnopq}	4.925 b^{cdefghijklm}	4.775 ^{efghijklmn}	2.4325 ^{abcdefghijkl}	15.3525 ^{bcdefg}
35	Bereket1	183.01 ^{abcd}	6.4575 ^{abc}	8.445 ^{abcd}	2.405 ^{abcdefghijklm}	13.215 ^{defghijk}
36	Bereket2	166.25 ^{abcdefghijklmn}	6.9325 ^{ab}	4.7075 ^{efghijklmn}	1.905 ^{bcdefghijklmno}	8.085 ^{ijklm}
37	Bereket3	94.2425 ^{qr}	3.1575 ^{ijklmno}	3.8425 ^{ijklmn}	2.8075 ^{Abcdefg}	16.17 ^{bcdefg}
38	Bereket4	206.895 ^{ab}	7.1425 ^{a}	9.845 ^{a}	1.745 ^{efghijklmno}	14.8425 ^{bcdefg}
39	Bereket5	150.5025^{cdefghijklmnop}	2.97 ^{klmno}	6.9675 ^{abcdefghijk}	1.8525 ^{cdefghijklmno}	13.23 ^{Defghijk}
40	Bereket6	51.3 ^{r}	7.1575 ^{a}	3.545 ^{klmn}	1.765 ^{defghijklmno}	8.1025 ^{Hijklm}

41	Bereket7	51.95 ^{r}	7.0975 ^{a}	4.0925 ^{hijklmn}	1.8125 ^{defghijklmno}	16.5625 ^{Bcdefg}
42	Bereket8	163.7 ^{abcdefghijklmn}	6.205 ^{abcd}	5.2125 ^{defghijklmn}	3.015 ^{Abc}	11.495 ^{efghijklm}
43	Bereket9	134.2225 ^{efghijklmnopq}	5.14 ^{abcdefghij}	5.495 ^{defghijklmn}	1.865 ^{cdefghijklmno}	13.8025 ^{Cdefghij}
44	Bereket10	185.005 ^{Abcd}	7.135 ^{a}	9.775 ^{ab}	1.8525 ^{cdefghijklmno}	16.67 ^{Bcdefg}
45	Bereket11	170.215 ^{abcdefghijklm}	3.02 ^{jklmno}	6.7675 ^{abcdefghijk}	2.1975 ^{abcdefghijklm}	12.955 ^{defghijkl}
46	Bereket12	160.0125 ^{cdefghijklmnop}	5.67 ^{abcde}	5.195 ^{defghijklmn}	1.715 ^{fghijklmno}	14.04 ^{Cdefghij}
47	AdiGoshu1	179.5875 ^{Abcd}	2.975 ^{klmno}	7.305 ^{abcdefghij}	1.605 ^{hijklmno}	11.415 ^{Fghijklm}
48	AdiGoshu2	183.45 ^{Abcd}	7.2025 ^{a}	7.71 ^{abcdefg}	2.32 ^{abcdefghijklm}	25.0175 ^{A}
49	AdiGoshu3	141.5625 ^{defghijklmnop}	3.5325 ^{fghijklmno}	2.995 ^{lmn}	1.7975 ^{defghijklmno}	12.0375 ^{Defghijklm}
50	AdiGoshu4	131.685 ^{ghijklmnopq}	5.3275 ^{abcdefgh}	5.0975 ^{defghijklmn}	1.8925 ^{bcdefghijklmno}	7.1225 ^{klm}
51	AdiGoshu5	156.3325 ^{cdefghijklmnop}	2.795 ^{mno}	7.345 ^{abcdefghi}	1.905 ^{bcdefghijklmno}	12.205 ^{defghijkl}
52	AdiGoshu6	172.2225 ^{Abcdefghij}	3.1225 ^{ijklmno}	6.055 ^{cdefghijklm}	2.0725 ^{abcdefghijklmn}	8.5775 ^{hijklm}
53	AdiGoshu7	152.37 ^{Cdefghijklmnop}	3.055 ^{jklmno}	5.315 ^{defghijklmn}	1.8025 ^{defghijklmno}	15.155 ^{bcdefg}
54	AdiGoshu8	65.875 ^{R}	7.1125 ^{a}	2.265 ^{n}	1.3075 ^{Lmno}	20.48 ^{ab}
55	AdiGoshu9	191 ^{Abc}	7.04 ^{ab}	8.1175 ^{abcde}	2.465 ^{abcdefghijkl}	15.74 ^{bcdefg}
56	AdiGoshu10	164.34 ^{Abcdefghijklmn}	2.97 ^{klmno}	6.845 ^{abcdefghijk}	2.9275 ^{abcd}	17.6925 ^{bcd}
57	AdiGoshu11	131.03 ^{hijklmnopq}	5.1375 ^{abcdefghij}	4.3725 ^{ghijklmn}	1.8075 ^{defghijklmno}	15.22 ^{bcdefg}
58	AdiGoshu12	177.2325 ^{abcdef}	5.785 ^{abcd}	7.2325 ^{abcdefghij}	1.8325 ^{defghijklmno}	15.1475 ^{bcdefg}
59	AdiGoshu13	130.15 ^{hijklmnopq}	5.8575 ^{abcd}	5.59 ^{defghijklmn}	1.5625 ^{Hijklmno}	7.0125 ^{lm}
60	AdiGoshu14	161.95 ^{bcdefghijklmno}	5.75 ^{abcd}	5.84 ^{cdefghijklm}	2.515 ^{Abcdefghijk}	8.475 ^{hijklm}
61	AdiGoshu15	117.7 ^{Opq}	6.515 ^{abc}	5.1725 ^{defghijklmn}	1.4625 ^{Jklmno}	5.9725 ^{m}
62	AdiGoshu16	175.06 ^{abcdefgh}	2.965 ^{klmno}	5.815 ^{cdefghijklmn}	1.7125 ^{Fghijklmno}	10.83 ^{ghijklm}

63	Adiabo1	170.4175 ^{abcdefghijkl}	3.175 ^{ijklmno}	9.6475 ^{ab}	2.355 ^{abcdefghijklm}	11.8175 ^{defghijklm}
64	Adiabo2	126.48 ^{klmnopq}	4.9525^{bcdefghijkl}	4.025 ^{hijklmn}	2.835 ^{Abcdef}	14.06 ^{cdefghij}
65	Adiabo3	130.7 ^{hijklmnopq}	5.63 ^{abcdef}	4.575 ^{efghijklmn}	1.9625 ^{abcdefghijklmno}	17.1025 ^{bcdef}
66	Adiabo4	129.925 ^{hijklmnopq}	3.14 ^{Ijklmno}	4.7775 ^{efghijklmn}	1.5075 ^{Ijklmno}	17.2125 ^{bcdef}
67	Adiabo5	51.9075 ^{r}	7.18 ^{a}	3.76 ^{jklmn}	2.6125 ^{Abcdefghij}	16.9375 ^{bcdefg}
68	Adiabo6	147.1525^{Cdefghijklmnop}	3.05 ^{Jklmno}	4.075 ^{hijklmn}	1.9075 ^{bcdefghijklmno}	17.2575 ^{bcdef}
69	Adiabo7	147.12 ^{cdefghijklmnop}	4.9175^{bcdefghijklm}	6.315 abcdefghijkl	1.3275 ^{Lmno}	15.9425 ^{bcdefg}
70	Bamya Humera	132.075 ^{fghijklmnopq}	4.1375^{defghijklmno}	4.225 ghijklmn	1.8 ^{defghijklmno}	17.655 ^{bcde}
71	SOH 701	150.5 ^{cdefghijklmnop}	7.1475 ^{a}	5.495 defghijklmn	1.415 ^{Klmno}	16.82 ^{bcdefg}
72	SOH 714	144.065 ^{defghijklmnop}	4.185 ^{defghijklmno}	3.45 klmn	1.445 ^{Jklmno}	15.4725 ^{bcdefg}

Images 6: okra plant on field experiment

Figure 6.1 Okra plants seedling stage

Figure 6.2 Okra plants fruit stage red type accessions

Figure 6.3 Okra plants vegitative stage

Figure 6.4 Okra plants fruit stage sample plot 2

Figure 6.5 Okra plants fruit stage plot sample 1

Figure 6.6 Okra plants fruit stage plot sample

Figure 6.7 fruit stage of okra green type

Figure 6.8 fruit stage of okra red type accessions sample 2

Figure 6.9: Okra plants field experiment sample1

Figure 6.9 Okra plants field experiment sample 2

Figure 6.5 Okra plants fruit stage plot sample 3