Genetic Diversity in Finger Millet Collections for Agro-Morphological, Nutritional Traits, and its Seed Exchange Systems in Tigray, Ethiopia

Fikre Hagos Abay (PhD candidate)

Mekelle University

Mekelle, Ethiopia

November, 2024

Genetic Diversity in Finger Millet Collections for morpho-agronomic, nutritional Traits, and its Seed Exchange Systems in Tigray, Ethiopia

A PhD Dissertation Submitted to

The Department of Dryland Crop and Horticultural Science

Presented in Partial Fulfillment of the Requirements for the Degree of Doctor of Philosophy in Plant Breeding and Seed Systems.

Fikre Hagos Abay (PhD Candidate)

Advisors:
Yemane Tsehaye (PhD)

Dejene Kassahun (PhD)

Mekelle University

Mekelle, Ethiopia

November 2024

DEDICATION

This piece of work is wholeheartedly dedicated to my young nephew the martyr Shambel Negasi, whose precious life has been paid for peace and stability and he was my source of inspiration and strength when I thought of giving up, who continually provided me his moral and emotional support. Without his love and support this research would not have been made possible. May his soul rest in peace, Amen!

BIOGRAPHICAL SKETCH

The author was born on 22 August 1986 from his father Hagos Abay and mother Hatsey Gebray in Mereblehe Wereda at a place called Rama, Central Zone of Tigray region, Ethiopia. After completing his high school, he joined the Haramaya University's College of Agriculture in 2006 and had successfully completed his BSc in Plant sciences in 2008. Then he served as a unit farm manager at the Middle Awash enterprise private cotton farm in the Afar region of Ethiopia from 26 September 2009 to April 10, 2010. After that, he re-joined the Haramaya University to advance his educational career in 2012 and has successfully completed his MSc in Plant Breeding. After completing his MSc study, he was employed by the Debretabor University's College of Agriculture under the Department of Plant Sciences and served as a lecturer, researcher, supervisor and focal person for ISSD and JICA projects until 30 August 2014. After that, he joined Aksum University and took the responsibilities of teaching courses and students' supervision until he has joined Mekelle University for his PhD study. During his tenure at Aksum University, he contributed to the development of research strategies for the Department and Published results of research in articles and/or books. Currently, he is pursuing his PhD in Plant Breeding and Seed System at Mekelle University, Department of Dryland Crop and Horticultural Sciences.

SCHOOL OF GRADUATE STUDIES

MEKELLE UNIVERSITY COLLEGE OF DRYLAND AGRICULTURE AND NATURAL RESOURCES
DEPARTMENT OF DRYLAND CROP AND HORTICULTURAL SCIENCES

As thesis research, advisors we hereby certify that we have read and evaluated the thesis prepared under our direction **Fikre Hagos Abay** entitled **"Genetic Diversity in Finger Millet Collections for morpho-agronomic, nutritional Traits, and its Seed Exchange Systems in Tigray, Ethiopia"** We recommend that it be accepted as fulfilling the PhD thesis requirements.

PhD candidate Signature date
Fikre Hagos 14/11/2024
Major advisor Signature date
Yemane Tsahaye (PhD) 02/11/2024
Co- advisor Signature date

Dejene Kassahun (PhD) 13/11/2024

As members of Board of Examiners of the PhD thesis Open Defense Examination, we certify that we have read and evaluated the thesis prepared by **Fikre Hagos Abay** entitled **"Genetic Diversity in Finger Millet Collections for morpho-agronomic, nutritional Traits, and its Seed Exchange Systems in Tigray, Ethiopia** and recommended that the thesis be submitted as fulfilling the thesis requirements for the Degree of Doctor of Philosophy in plant breeding and Seed System

Addis Abraha (PhD) 20/03/2025
Internal Examiner Signature Date
Hailay Mahari (PhD) 20/03/2025
Internal Examiner Signature Date
Beyene Demtsu (PhD) ____________ ____________
External Examiner Signature Date
Lijalem G.wahid (PhD) 20/03/2025
PG coordinater signature Date
Wendim yigzaw (PhD) 20/03/2025
Department Head Signature Date

ACKNOWLEDGMENTS

The successful completion of this dissertation is a testament to the immense support I received from numerous institutions and individuals who truly deserve heartfelt recognition. I am deeply grateful to everyone who contributed in various ways to the achievement of this work.

First and foremost, I owe a profound debt of gratitude to my principal supervisor, Dr. Yemane Tsehaye. His meticulous supervision, insightful guidance, critical feedback, and unwavering support and hospitality have been indispensable. I would not have completed this work without his boundless advice and encouragement throughout my study. It has been a true privilege to work under his expert guidance.

I also extend my sincere thanks to my co-supervisor, Dr. Dejene Kassahun, for his professional and friendly supervision. His prompt feedback, excellent co-supervision, crucial theoretical and practical insights, and consistent assistance and encouragement have been deeply appreciated throughout my research.

I am thankful to Mekelle University for providing essential facilities for my research, and I appreciate the Ethiopian Biodiversity Institution for supplying the finger millet accessions used in this PhD study. My heartfelt thanks also go to Aksum University for awarding me the fellowship that enabled me to pursue my doctoral studies in Plant Breeding and Seed Systems at Mekelle University.

My gratitude extends to the staff members of Shire-Maitsebri and Axum Agricultural Research Centers of the Tigray Agricultural Research Institute (TARI), whose support was crucial for the successful completion of my field research. I am also appreciative of the technical and administrative support provided by the College of Agriculture and the Department of Dryland Crop and Horticultural Sciences at Mekelle University.

On a personal note, I must express my deepest thanks to my beloved wife, Kidan Kiros, for her love, care, and patience, which have been a constant source of strength. Her understanding and resilience in managing our young children through both good and challenging times have been invaluable. I am also grateful to my children, Kidus, Bethlehem, and Muse, who have endured my absence during their early years with remarkable patience. You are my sunshine, and I cherish every moment with you. I also extend my heartfelt appreciation to my brothers, Shawsh Hagos, Gebreslassie Kiros, Biruh Zeferu, and Hadush Hagos, as well as my sisters, Biraha, Silas, Almaz, and Zemeda, for their constant encouragement and support. My sincere thanks also go to my colleagues, Fisaha Amaha, Geray Hagos, Dr. Gebregergis T/mariam, Dr. Mengistu W/mariam and Abraha Arafaine for their moral support and strength during difficult times.

For those whose names have not been mentioned here, I apologize for the oversight. Every step of this journey, including the completion of this study, has been guided by the will of my Almighty God.

TABLE OF CONTENTS

LIST OF TABLES

Chapter Two

Chapter Three

Chapter Four

Chapter Five

LIST OF FIGURES

Chapter Two

Chapter four

Chapter five

APPENDICES

Chapter Two

Chapter Three

Chapter Four

Chapter Five

ACRONYMS AND ABREVIATIONS

AMMI	Additive main effect plus multiplicative interaction
AEC	Average-Environment Coordination
ANOVA	Analysis of variance
ATA	Agricultural Transformation Agency
ATC	Average-Tester Coordination
BLUP	Best Linear Unbiased Predictor
CSA	Central Statistical Agency of Ethiopia
CV	coefficient of variation
DTF	days to flowering
DTM	days to maturity
E	environment
EBI	Ethiopian Biodiversity Institute
FAO	Food and Agricultural Organization
Fe	Iron
G	genotype
GEI	genotype by environment interaction
GGE	genotype main effect and genotype by environment interaction
GY	grain yield
LSD	least significant difference
m.a.s.l	meter above sea level
Max.	maximum
min.	minimum
NIR	near infrared spectroscopy
NSPP	Number of seeds per plant
PCA	principal component analysis
PH	plant height
PVS	participatory varietal selection
Std	standard deviation
TSW	thousand seed weight
Zn	Zinc

ABSTRACT

Finger millet, despite being one of the most neglected and underutilized crops worldwide, serves as an important food source for millions of poor farmers in Africa. This study examined 200 finger millet accessions collected from different regions of Ethiopia and other African countries, including Eritrea, Zambia and Zimbabwe obtained from the Ethiopian Biodiversity Institute. The experiment was carried out using a 20 x10 lattice design across three locations and over two growing seasons, in 2019 and 2020. Data were collected for quantitative traits, including grain yield, 1000 seed weight, tiller number per plant, finger number per panicle, finger length and width, plant height and days to maturity; qualitative traits such as seed pericarp persistent, glume color, seed color, finger branching, and ear shape; and nutritional traits including protein, starch, calcium (Ca), magnesium (Mg), iron (Fe) and zinc (Zn) contents. The study also involved 160 respondents to analyze seed social network. The analysis of variance for quantitative traits showed highly significant ($P \leq 0.01$) variations among the tested genotypes. Three mega-environments were identified from the six tested environments, the first included Rama 2019 and Rama 2020, the second included Maiaini 2019 and Maiaini 2020, and the third included Zana 2019 and Zana 2020. Based on grain yield and other target traits, the GGE approach selected genotypes 203246 (21), 100022 (4), and 100020 (3) for Rama; 234184 (175), 229736 (114), and 233759 (143) for Maiaini; and 100022 (4), 203246 (21), and 229736 (114) for Zana. According to the frequency analysis of qualitative traits, all phenotypic classes, including seed pericarp persistence, glumes color, seed color, finger branching, and ear shape were observed across all countries of origin and altitude classes. However, the most frequent traits observed were non-seed persistence (46%), purple glume color (39%), black seed color (39%), and open ear shape (47%). Notably, brown seed color and persistent seed were absent in Zambia and Benishangul collections, respectively. The chi-square test showed significant ($p \leq 0.05$), highly significant ($p \leq 0.01$), and non-significant variations for the five qualitative traits across different countries. All the four qualitative traits, except for finger branching showed a high Shannon diversity index ($H' \geq 0.74$) across various regions and altitude classes. However, the seed color showed a medium Shannon diversity index for Eritrea collections ($H' = 0.65$). In terms of protein content, it ranged from 5.15 to 9.35% with the highest value obtained from accessions 203574 and the lowest from 203358. The study found a minimum variation in starch content among different finger millet genotypes, with values ranging narrowly from 72% to 75% and an average of 72.99%. A similar trend was observed for moisture content.

On the other hand, there was a considerable variation among genotypes for mineral contents, including Ca (139 to 431mg/100g), Mg (120.85 to 525.50 mg/100g), Fe (3.4 to 30.68 mg/100g), and Zn (0.11 to 4.89 mg/100g). Notably, high concentrations of Ca, Mg, Zn, and Fe were found in genotypes 234160, 203259, 203257, and 203262, respectively. Genotypes 234184, 100020, and 203246 exhibited impressive levels of Fe (28.16 mg/100g), Zn (3.15 mg/100g), and Ca (407 mg/100g), along with high grain yields of 3368, 4112, and 3693 kg ha^{-1}, respectively. A survey of finger millet growing households revealed that out of the participants, 145 (90.4%) cultivated landraces (referred to as farmers' varieties or FVs), while 16 (10%) grew improved varieties. Seed exchange primarily occurred between neighbors and relatives, with a higher seed flow rate observed within villages compared to outside. Seven farmers in central and six in the Northwest zones of Tigray played vital roles in the seed network as key players. Therefore, the promising genotypes that demonstrated high-yield production and stability in this study should be further tested in multiple environments alongside the released finger millet varieties to verify their superiority and adaptability.

Key words: Genetic Diversity, African Finger Millet Collections, Quantitative and Qualitative Traits, Seed Exchange Systems

ኣሕፅሮት

ዳጉሳ ብዙ ጥቅም ያለው ሰብል ሆኖ ሳለ ምርታማነቱ በተለያዩ ችግሮች ምክንያት እጅግ ዝቅተኛ ነው። የተለያዩ የዳጉሳ ዝርያዎችን ብዝሃነትና ተለያይነት ማጥናት እና የምርት ማነቆ የሆኑትን ችግሮች ማወቅ የተሻለ ምርት ሊያስገኙ የሚችሉ ዝርያዎችን ለመምረጥ ያስችላል። የጥናቱ ዋና ዓላማ ከኢተዮጲያ ብዝሀ ህይወት ኢንስቲትዩት የተገኙ 200 የዳጉሳ ዝርያዎችን በማይዓይኒ፣ ራማና መደባይ-ዛና ለሁለት ዓመት ማለትም በ 2011 ና 2012 ዓ/ም የዘር ወቅት በሲምፕል ላቲስ ኣሰራር በሁለት ድግግሞሽ ተዘርተው የተገመገሙ ሲሆን ያላቸውን የዝርያ ተመሳሳይነት፣ ብዝሃነት እና ስብጥር ምን እንደሚመስል ለማወቅ ነበር። የተወሰዱ ናሙናዎች፣ ምርትና ተያያዝነት ያላቸው ባህርያት፣ ኳሊቴቲቭ ትሬት፣ ኑትሪሽናል ትሬትና የአከባቢ የዘር ስርጭት ስርዓት ምን እንደሚመስል ለማወቅ ነበር። የተወሰዱ ናሙናዎች| ምርትና ተያያዝነት ያላቸው ባህርያት፣ ኳሊቴቲቭ ትሬት፣ ኑትሪሽናል ትሬትና የአከባቢ የዘር ስርጭት ስርዓት ምን እንደሚመስል ቃለ መጠየቅ በማድረግ የመሳሰሉ ናቸው።መረጃዎችን ለመተንተን ጥቅም ላይ የዋሉት አኖቫ፣ ጇጇኢ|አሚ ባይፕሎት፤ ክላስተር እና ፕሪንሲፓል ኮምፖነንት የትንተና አይነቶች ናቸው። በዚህ መሰረት በጥናት ላይ የተካተቱት ሁሉም ባህሪያት በዝርያዎች መካከል ከፍተኛ የሆነ *($P \leq 0.01$)* ልዩነት መኖሩን ያሳያል። የኳንቲታቲቭ ባህርያት ሙከራ የተደረጉባቸው 6ቱ አከባቢዎች ባላቸው ተመሳሳይ የባህርያት ምዘና ወደ ሶስት ጠበዋል። ለምሳሌ ራማ 2011 እና ራማ 2012 በአንድ ጎራ የተመደቡ ሲሆን፣ ማይዓይኒ 2011 ና ማይዓይኒ 2012 በሁለተኛ ጎራ ተመድበዋል። የተቀረው ዛና 2011 እና ዛና 2012 ደግሞ በሶስተኛ ጎራ ተመድበዋል። ከተሞከሩ ዝርያዎች እነኚህ 203246 (21)፣ 100022 (4) እና 100020 (3) ከራማ ሲሆኑ፣ 234184 (175)፣ 229736 (114) እና 233759 (143) ከማይዓይኒ እና፣ 100022 (4), 203246 (21) እና 229736 (114) ከዛና ናቸው። ስለዚህ እነዚህ ኮድ የተሰጣቸው ዝርያዎች ከሁሉም የተሻለ ምርትና ተዛማጅ ባህርያት ውጤት አሳይተዋል። በሀገሮችና በምድር ከፍታ ያለው የኳሊታቲቭ ባህርያት ትንተና እንደሚያሳየው በቀላሉ የማሽት ባሀሪ፣ ቀጥ ያለ የዳጉሳ ራስ፣ ወይንጠጅ የሽፋን ህብርና ጠይም የዘር ህብር በሁሉም የዘር ኣምራች አገሮችና የተሰበሰቡበት የምድር ከፍታ ከፍተኛ የብዝሃነት ባህሪ አሳይተዋል። በዚህ መሰረት ናን ፐርሲስተንት፣ ፐርፕል የሕብር ሽፋን፣ ጥቁር የዘር ሕብርና ቀጥ ያለ የራስ ቅርፅ በሁሉም አገር፣ ክልልና የቦታ ከፍታ በከፍተኛ መጠን የታየ ሲሆን ቡናማ የዘር ሕብር ከዛምብያ፣ ፐርሲስተንት የዘር ሽፋን ከበንሻንጉል ክልል ደግሞ ካልታዩ የዳጉሳ ባህርያት ናቸው። ካይ ስኴር ቴስት ትርጉም ያለው ተለያይነት ($p \leq 0.05$)፣ ከፍተኛ ትርጉም ያለው ተለያይነት ($p \leq 0.01$)፣ እንዲሁም ትርጉም የሌለው ተላያይነት በኣምስቱ የስነ-ምግባራዊ የዳጉሳ ባህርያት በአገራት ያለው ልዩነት ያሳያል። ከጣት ቅርንጫፍ ውጪ የተቀሩት ኣምስቱ ምርጥ የዳጉሳ ባህርያት ከፍተኛ ሻኖን ዳይቨርሲቲ በአገራት፣ ክልሎችና የከፍታ ቦታዎች ከ($H' \geq 0.74$) በላይ የሚያሳይ ቢሆንም የዘር ህብርና የጣት ቅርንጫፍ ግን በኤርትርያ መካከለኛ የሻኖን ዳይቨርስቲ ኣሳይተዋል። የፕሮቲን ይዘት ከ 5.15 እስከ 9.35% ነበር፣ ከፍተኛ የፕሮቲን ይዘት ከጀኖታይፕ 203574 የተገኘ ሲሆን፣ ዝቅተኛ ደግሞ ከጂኖታይፕ 203358 ነበር። የስታርችና የዘር የእርጥበት ይዘት በሁሉም የዳጉሳ ዝርያዎች የነበረ ልዩነት ዝቅተኛ ነው። በሌላ በኩል ከፍተኛ ልዩነት በካልሲየም (ከ 139 እስከ 431 ሚሊ ግራም/100 ግራም)፣ ማግኒዝየም (120.85 እስከ 525.50 ሚሊ ግራም/100ግራም)፣ ብረት (4.06 እስከ 30.68 ሚሊ ግራም/100ግራም) እና እንዲሁም ዚንክ (0.11 እስከ 4.89 ሚግ/100ግራም) በዳጉሳ ዝርያዎች የታየ ሲሆን ከፍተኛ በካልሲየም፣ ማግኒዝየም፣ ዚንክ እና ብረት ከጂኖታይፕ 234160፣ 203259፣ 203257፣ 203262ን በቅደም ተከተል ተገኝተዋል። በዘር ስርጭትና ልውውጥ ስርዓት የተደረገ ጥናት እንደሚያሳየው በጥናቱ ከተካተቱት 160 አባዎራዎች 145 (90.4%) የሚያህሉ ነባር (የራሳቸው) ዝርያ የሚጠቀሙ ናቸው ሲሆን 16 (10%) ደግሞ የተሻሻለ ዝርያ የሚጠቀሙ ናቸው። በጎራባብትና ዘመዳሞች መካካል የሚደረግ የዘር

ልውውጥ ከፍተኛ እንደነበር ጥናቱ ያሳያል። ከአከባቢ ወጭ ይልቅ በመንደር ውስጥ የሚደረግ የዘር ስርጭት የበለጠ ነበር። እነዚህ ገበሬዎች ለምሳሌ ‘AT26’ ፣ ’AY11’፣ ’AY13’፣ ’AY25’፣ ’EM08’፣ ’MR03’ እና ’MR14’ ከማእከላዊ ዞን እንዲሁም, ’AR18’፣ AR19’፣ ’BR33’ ፣ ’BR33’፣ ’DA15’፣ ’MT37’ እና ’MT39’ ከሰሜን ምዕራብ ዞን ዋነኛ የዘር ስርጭት ሰንሰለት ቦታ ከያዙ ናቸው። ስለዚህ በዚህ ጥናት ለምርት, ለተሻለ የማእድንና የፕሮቲን ይዘት የተመረጡ የዳጉሳ ዝርያዎች እንደ እጩ ተወስዶው በቀጣይ ከተለቀቁ ዝርያዎች በመወዳደር በሁሉም ለዳጉሳ ተስማሚ የሆኑ ቦታዎች ተጨማሪ ምርምር ሊደረግባቸው ይገባል።

ቁልፍ ቃላት: ዳጉሳ፣ የእህል ምርት፣ የእህል ጥራት ባህሪያት፣ የሻነን ልዩነት መረጃ ጠቋሚ፣ የዘር ፍሰት

ፅሚቕ ኣሕፅሮት

ዳጉሻ ሓደ ካብ ኣብ መላእ ዓለም ዕሸሸ እተባህለን ብዙሕ ዘይተሰረሐሉን እኽሊ እኳ እንተ ኾነ ነቶም ኣብ ኣፍሪቃ ዝነብሩ ብሚልዮናት ዝቑፀሩ ድኻታት ሓረስቶት ግና ኣገዳሲ እኽሊ ምግቢ እዩ። ካብ እተፈላለየ ዞባታት ኢትዮጵያ ዝተኣከቡ 200 ዝኣኽሉ ዓሌታት ዳጉሻ ኸምኡውን ካብ እተፈላለዩ ዓድታት ኣፍሪካ (ኤርትርያ፣ ዛምብያን ዚምባብወን) ዝተረኽቡ እንትኾኑ እዚ ፈተነ እዚ ኣብ 2011 ከምኡውን 2012 ዓ/ም እንትኸውን ኣብ ሰለስተ ቦታታት ብላቲስ (20 x10) ብእተሰርሐ ንድፌ ዝተኻየደ ኢዩ። ብዛዕባ ዝተፈላለየ ባህርያት እቶት እኽሊ፣ ምህርቲ ነፍሲወከፍ ተኽሊ፣ 1000 ክብደት ዘርኢ፣ ቍጽሪ ኣጻብዕቲ ዳጉሻ፣ ንውሓት ኣፃብዕቲ፣ ስፍሓት ኣፃብዕቲ፣ ቍመት ኣትክልትን መዓልትታትን ክሳዕ ብስለት) ዚገልፅ ሓበሬታ ተኣኪቡ እዩ። መጠን ትሕዝቶ ፕሮቲን፣ ስታርች፣ ካልኦት ናይ ሚነራል ትሕዝቶ ዚገልፅ ሓበሬታ እውን ተኣኪቡ እዩ። ከምኡ’ውን ማሕበራዊ መራኸቢ ዘርኢ ኣብ 160 ሰባት መፅናዕቲ ተገይሩሎም እዩ። ብዛዕባ እተፈላለየ ባህርያት እተገብረ መፅናዕቲ ከም ዚሕብሮ ኣብ መንጎ እቲ ዝተገበረ መፅናዕቲ ኣዝዩ ኣገዳሲ ፍልልይ (P≤0.01) ኣሎ። በዚ መሰረት እቶም ሽዱሽተ መፅናዕቲ ዝተኻየደሎም ቦታታት ኣብ ሰለስተ ሜጋ ኣከባቢ ዝተመደቡ እንትኾኑ፣ ንኣብነት ራማ 2011ን ራማ 2012ን ኣብ ናይ መጀመርታ ሜጋ ኣከባቢ፣ ማይዓይኒ 2011ን ማይዓይኒ 2012ን ኣብ ካልኣይ ሜጋ-ኣከባቢ (ንኡስ ዞባ)፣ ከምኡ’ውን ዛና 2011ን ዛና 2012ን ኣብ ሳልሳይ ሜጋ ኣከባቢ ተመቒሎም። ጀኖታይፕስ 203246 (21)፣ 100022 (4)ን 100020 (3)ን ካብ ራማ¥ ጂኖታይፕስ 234184 (175)፣ 229736 (114)ን 233759 (143)ን ካብ ማይዓይኒ¥ ጂኖታይፕስ 100022 (4)፣ 203246 (21)ን 229736 (114)ን ድማ ካብ ዛና ካብ ካልኦት ዝሓሸ ምህርቲ ዘመዝገቡ ዓሌታት ዳጉሳ እዮም። ብመሰረት ናይ ዳጉሻ ቡሉፅ ባህርያት ስርጭት አብ ዝተመረፁ ናይ አፍሪካ ሃገራት፣ አብ ዝተመረፁ ናይ ኢትዮጵያ ክልላት እተገብረ መፅናዕቲ ኩሎም ዓይነት ብሉፃት ባህርያት ማለት (ፐሪካርፐ ፐርሲስተንስ፣ ጉሉምስ ሕብሪ፣ ናይ ዘርኢ ሕብሪ፣ ቅርንጫፍ አፃብዕቲ ዳጉሳን፣ ቅርፂ ርእሲ ዳጉሻን ኣብ ኵለን ሃገራት መበቊልን ብራኽን ተራእዩ ኢዩ። በዚ መሰረት ናን ፐርሲስተንት፣ ፐርፐል ሕብሪ ሽፋን፣ ፀሊም ናይ ዘርኢ ሕብሪ፣ ቀጥ ዝበለ ናይ ርእሲ ቅርፂን፣ ዳርጋ አብ ኩለን መበቊል ሃገራት፣ ክልላትን ከፍታ ቦታን ብዝለዓለ መጠን ዝተራአየ እንትኸውን ቡናማ ናይ ዘርኢ ሕብሪ ካብ ዛምብያ፣ ፐርሲስተንት ናይ ዘርኢ ሽፋን ካብ በንሻንጉል ክልል ካብ ዘይተራአዩ ባህርያት ዳጉሳ እዮም። ፓይ ስኴር ቴስት ኣገዳሲ (p≤0.05)፣ ልዑል ኣገዳስነት ዘለዎ (p≤0.01) ከምኡ’ውን ኣገዳስነት ዘይብሉ ኣብተን ሽዱሽተ ናይ ስነ-ምግባራዊ ባህርያት ዳጉሻ አብ ሞንጎ ሃገራት ዘሎ አፈላላይ የርኤና ኣሎ። ብዘይካ ጨንፈር ኣጻፃዕቲ እተን ዝተረፋ ሓሙሽተ ብሉፅ ባህርያት ዝለዓለ ሻኖን ዳይቨርሲቲ ኣብ ሃገራት፣ ክልላትን በረኽቲ ቦታታትን ልዕሊ (H’ ≥ 0.74) ዜርኢ እኳ እንተ ኾነ ሕብሪ ዘርእን ጨንፈር ኣጻብዕቲን ግና ኣብ ኤርትርያ ማእኸላይ ሻኖን ዳይቨርስቲ እዩ ነይሩ። ትሕዝቶ ፕሮቲን ካብ 5.15 ክሳዕ 9.35% እዩ ነይሩ¥ እቲ ዝለዓለ ትሕዝቶ ፕሮቲን ከኣ ካብ ጂኖታይፕ 203574 ተመዝጊቡ፣ እቲ ዝተሓተ ኸኣ ካብ ጂኖታይፕ 203358 እዩ። እቲ ብዛዕባ ስታርች ዚገልፅ ትሕዝቶ ኣብ ግምት ዘይኣቱ እዩ ነይሩ። ዳርጋ ኣብ ኩሎም ዓሌታት ንኡስ ኣፈላላይ እዩ ኣርእዩ። ከምኡ’ውን መጠን ጠሊ ተመሳሳሊ ዝንባለ ከም ዘለዎ ተራእዩ እዩ። ብተወሳኺ ልዑል ኣፈላላይ ኣብ ሞንጎ ዓሌታት ዳጉሻ ካልሲየም (ካብ 139 ክሳዕ 431 ሚሊ ግራም/100 ግራም)፣ ማግኒዝየም (120.85 ክሳዕ 525.50 ሚሊ ግራም/100ግራም)፣ ሓፂን (4.06 ክሳዕ 30.68 ሚሊ ግራም/100ግራም) ከምኡ’ውን ዚንክ (0.11 ክሳብ 4.89 ሚግ/100ግራም) ናይ ኣፋላላይ ትሕዝቶ ዝነበሮ እንትኸውን እቲ ዝበለፀ ካልሲየም፣ ማግኒዝየም፣ ዚንክ፣ ከምኡውን ሓፂን ካብ ጂኖታይፕ 234160፣ 203259፣ 203257ን 203262ን ብቀደም ተኸተል ይርከብ። ብመሰረት እቲ ብዛዕባ ምንጪ ዘርእን ናይ ዘርኢ ልውውጥ ስርዓትን ዝተገብረ መፅናዕቲ ካብቶም ጠቕላላ ኣብዚ መፅናዕቲ ዝተኻተቱ 160 ስድራቤታት እቶም 145 (90.4 ሚእታዊት) ናይባዕሎም ዓሌት

ዝጥቀሙ እንትኾኑ 16 (10%) ድማ ዝተመሓየሸ ዓሌት ይጥቀሙ። መብዛሕትኡ ግዜ ኣብ ሞንጎ ጐረባብትን ኣዝማድን ዝግበር ናይ ዘርኢ ልውውጥ ካብ ምስ ካልኦት ዝግበር ልውውጥ ዝለዓለ ግደ ነይርዎ። ኣብ ውሽጢ እታ ቍሸት ዝውሕዝ ዝነበረ መጠን ዘርኢ ምስ ናይ ካብ ቁሸት ወፃኢ ዘሎ ፍሰት ምቅይያር ዘርኢ እንትነፃፀር እቲ ዝለዓለ አብ ቁሸት ውሽጢ ዝግበር ምልውዋጥ ነይሩ። እዞም ሓረስቶት እዚኣቶም ማለት’ውን AT26፣ ’AY11’፣ ’AY13’፣ ’AY25’፣ ’EM08’፣ ’MR03’ን ’MR14’ን ካብ ማእኸላይ ዞባ ከምኡ’ውን ’AR18’፣ AR19’፣ ’BR33’፣ ’BR33’፣ ’DA15’፣ ’MT37’ን ’MT39’ን ካብ ሰሜናዊ ምዕራብ ዞባ ሓደ ኻብቶም ኣብቲ መርበብ ዘርኢ ኣገዳሲ ቦታ ዝነበሮም ቀንዲ ሰባት እዮም ነይሮም። ስለዚ እቲ ኣብዚ መፅናዕቲ እዚ ብዙሕ ምህርቲ ኽም ዚፈሪን ርግኣት ከም ዚህልዎን ዜርኢ ተስፋ ዚህብ ዓሌት ዳጉሻ ከም ሕፁይ መጠን ኣብ እተፈላለየ ኽባቢ ምስቶም ዝወፁ እተፈላለዩ ዓይነታት ዳጉሻ ኹይኑ ተወሳኺ መርመራ ኺግበረሎም ኣለዎ።

ቀንዲ ቓላት፡- ዳጉሻ፣ ምህርቲ እኽሊ፣ ብሉፅ ባህርያት እኽሊ፣ ጂጂኢ፣ ሻኖን ዳይቨርሲቲ፣ ስርዓት ዘርኢ ምቅይያር

CHAPTER ONE: OVERALL VIEW OF THE DISSERTATION

1. INTRODUCTION

1.1 Background

Finger millet (*Eleusine coracana* (L.) Gaertn) (2n = 4x = 36) is a vital small grain cereal grown in eastern and southern Africa, where it contributes significantly to food security and subsistence agriculture due to its high nutritional and cultural value (Dida et al., 2008). It is a key component of traditional low-input, cereal-based farming systems (Wolie et al., 2013) and is also extensively cultivated in Southern Asia, including India, Myanmar, Sri Lanka, Bhutan, and China (Upadhyaya et al., 2004). Finger millet stands out for its superior nutritional quality compared to most other cereals, being rich in proteins, fiber, and essential minerals like calcium and iron, which are crucial in combating malnutrition and anemia in regions where it is a staple food (Babu et al., 2006). Adapted to a wide range of environmental conditions, finger millet thrives in diverse agro-ecological zones, including higher elevations and both dry and rain-fed conditions, often being grown by smallholder farmers and considered as a food source for the less affluent populations (Kumar et al., 2019).

Morphological descriptors, which include various observable traits of finger millet accessions, have been extensively used in diversity studies (Negi et al., 2017). These descriptors encompass both qualitative and quantitative traits. Comprehensive evaluation of these traits, along with grain nutrient quality and their interrelationships, is crucial for conserving and improving high-quality collections of finger millet (Da-zhong et al., 2019). For instance, genetic diversity assessments have been conducted to explore the divergence among 35 finger millet genotypes based on fourteen morphological traits using Mahalanobis distances (Negi et al., 2017). Damtie et al. (2019) employed ANOVA, cluster analysis, and principal component analysis to examine Ethiopian finger millet genotypes, analyzing maximum, minimum, mean values, standard deviations, and variation coefficients of quantitative traits. Additionally, Dasanayaka and Kaluthanthri (2017) conducted a diversity analysis focusing on qualitative traits, using frequency distributions. These qualitative traits, assessed visually, are essential for differentiating varieties and advancing genetic improvement (Kumar et al., 2019).

The diversity observed in traits such as seed color, ear shape, pericarp persistence, lodging susceptibility, growth habit, and glume color is critical for advancing genetic improvements and effective use in crop improvement programs (Tesfaye and Mengistu, 2017). Therefore, the primary objective of this research was to assess the genetic variability among finger millet collections and identify promising accessions based on both quantitative and qualitative traits, including nutritional attributes like iron, zinc, calcium, magnesium, and protein content, for crop improvement programs.

1.2. Research Problem, Questions, Hypotheses and Objectives

1.2.1. Research problem

Despite the extensive morphological and genetic diversity among finger millet genotypes, their application in breeding programs remains limited in many countries, including Ethiopia. This is largely due to the little attention given to characterization, evaluation, and pre-breeding activities for this crop. Several factors contribute to Ethiopia's low finger millet productivity relative to its potential yield, including biotic and abiotic stressors and socioeconomic constraints. It is crucial to systematically document and address these challenges to guide future production efforts and improve variety development and release (Gebreyohannes et al., 2021).

Dietary deficiencies in essential minerals, such as iron (Fe), zinc (Zn), magnesium (Mg), and calcium (Ca), can lead to severe negative outcomes, including learning disabilities in children, increased morbidity and mortality, reduced worker productivity, and high healthcare costs in developing countries like Ethiopia (Karak et al., 2012). Farida et al. (2022) also highlighted that deficiencies in protein and micronutrients, particularly iron and zinc, are serious health issues. In Ethiopia, finger millet is a significant cereal crop predominantly cultivated by smallholder farmers (Admasu and Belete, 2023). It is mainly grown in the Tigray, Oromia, Benishangul-Gumuz, Southern Nations, Nationalities, and People’s, as well as the Amhara regions. However, finger millet productivity is low due to factors such as lack of improved varieties, diseases and pests, inappropriate seed and fertilizer application, moisture stress in dry areas, and limited research focus on the crop (Admasu and Belete, 2023). Although Ethiopia is a center of finger millet genetic diversity, its productivity remains below potential, with an average yield of less than 2.4 tons per hectare compared to a potential of 6 tons per hectare (Gebreyohannes et al., 2021).

1.2.2. Research questions

Ethiopia is recognized for its substantial genetic diversity in finger millet, but efforts to improve this resource for enhancing yield and nutritional has been limited. Additionally, the country faces challenges related to dietary diversity. Evaluating and selecting a diverse range of finger millet genotypes could be an effective approach to genetic improvement, addressing climate variability in marginal areas, and enhancing food fortification. To address these issues, the current study aimed to answer the following key research questions:

- ✓ Is the performance of the collected genotypes consistent across different temporal and spatial conditions for grain yield and other traits? How does genotype performance vary across different locations and years?
- ✓ What is the extent of genotype-by-environment interaction (GEI) among these genotypes and environments?
- ✓ Are certain environments more effective than others at distinguishing genotype performance?
- ✓ Do genotypes differ in their quantitative and nutritional traits?
- ✓ Either there are existing seed exchange mechanisms and seed flow networks among local finger millet producers?

1.2.3. Significance of the study

Finger millet is nutritionally rich, offering calcium (0.38%), protein (6–13%), dietary fiber (18%), carbohydrates (65–75%), and minerals (2.5–3.5%) (Arjun et al., 2014; Chandra et al., 2016). This composition positions it as a valuable crop for enhancing nutritional security (Hiremath et al., 2018). Developing and selecting high-nutrient finger millet genotypes could play a significant role in addressing food insecurity and malnutrition at the regional, national, and household levels in Tigray, Ethiopia. Diversifying food production with such crops, particularly traditional ones like finger millet, presents a promising strategy for improving household food security. Minerals, essential for physiological functions in both plants and humans, are vital dietary components. The human body requires over 22 minerals from a balanced diet, with key elements including phosphorus (P), potassium (K), calcium (Ca), magnesium (Mg), iron (Fe), zinc (Zn), copper (Cu), and manganese (Mn) (Karak et al., 2012).

In Ethiopia, finger millet is primarily grown as a marginal crop but is the third most significant crop in yield production in the northwestern and central Tigray region, following sorghum and teff (Hailegebrial et al., 2017). Traditionally, it is used to make a popular local beverage known as 'Siwa' in Tigrigna or '*Tella*' in Amharic. This beverage, deeply rooted in Tigray's culture, is prepared for holidays, weddings, and religious ceremonies. Additionally, it provides an income source for many women, with a cup typically sold for 15 Ethiopian birr, though prices can vary from 10 to 25 birr based on quality. On average, a household who engaged in income generation can produce around 140 liters (210 cups of '*Siwa*') every three days, and consumers consider it a great energy source (as per elder insights). The byproduct of this drink, called '*Hatella*' in Tigrigna or '*Atella*' in Amharic, is also valuable as feed for animals, including cows, oxen, and goats, aiding their recovery and providing nutrition. Farmers view it as comparable to '*Fruska*,' a commercial animal feed used by local small-scale fattening farms. Beyond these uses, the stalks of finger millet are repurposed as livestock feed, construction material, and fuel (Gebreyohannes et al., 2021).

In summary, finger millet holds substantial benefits in terms of nutrition, health, local beverages, and animal feed compared to other cereals. Despite these advantages, however, the crop remains underutilized and lacks sufficient recognition. This study, therefore, aims to address this gap by evaluating the genetic diversity of various finger millet accessions sourced from African countries, assessing their quantitative, qualitative, and nutritional traits. Additionally, it will explore seed distribution channels and exchange practices among local farmers.

1.2.4. Study Objectives

1.2.4.1. General Objectives

The overall objective of the research was to assess the genetic diversity of finger millet *ex situ* collections via quantitative, qualitative, nutritional traits, and seed exchange systems.

1.2.4.2. Specific objectives

I. Evaluation of African finger millet *ex situ* collections for quantitative traits under rainfed growing conditions.
II. Characterization of African finger millet collections for qualitative traits under rainfed growing conditions.
III. Evaluation of African finger millet collections grown under rainfed conditions for grain nutrient contents.
IV. Assessment of seed exchange network among finger millet growing farmers in Mereblehe and Asgede tsmbila Districts of Tigray.

1.2.5. Structure of the Study

A clearer clarification of an overall framework in which relevant components of the diversity analysis of African finger millet accessions and seed flow and exchange mechanism can be considerably used for research interventions of the crop. The research emphasized to overlook the genetic diversity of different finger millet accessions collected from African countries, more specifically from Ethiopia, Eritrea, Zambia, and Zimbabwe. These accessions were sourced from the Ethiopian Biodiversity Institute (EBI). The main framework of this study was to assess, evaluate and characterize quantitative, qualitative and nutritional traits. Furthermore, it sought to determine the interactions between genotype and environment (G x E) that affect grain yield and other important traits. By analyzing these interactions, the study aimed to identify the most stable genotypes with relatively high yields across tested environments. The analysis determined the representativeness and discriminating power of these environments. The study also explored the qualitative trait diversity in relation to the countries of origin and altitudinal classes of the accessions. It also examined the diversity of key nutritional components like protein, starch, Ca, Mg, Fe, and Zn contents of the accessions which could be valuable for future crop improvement program. Finally, this study examined the existence of social seed networks, focusing on seed sources, exchange mechanisms and roles of farmers (**nodal, non-nodal** and **connecto**r) within the network The insights could also inform strategies for local seed sector development, enhancing seed security, and promoting the dissemination of superior finger millet varieties.

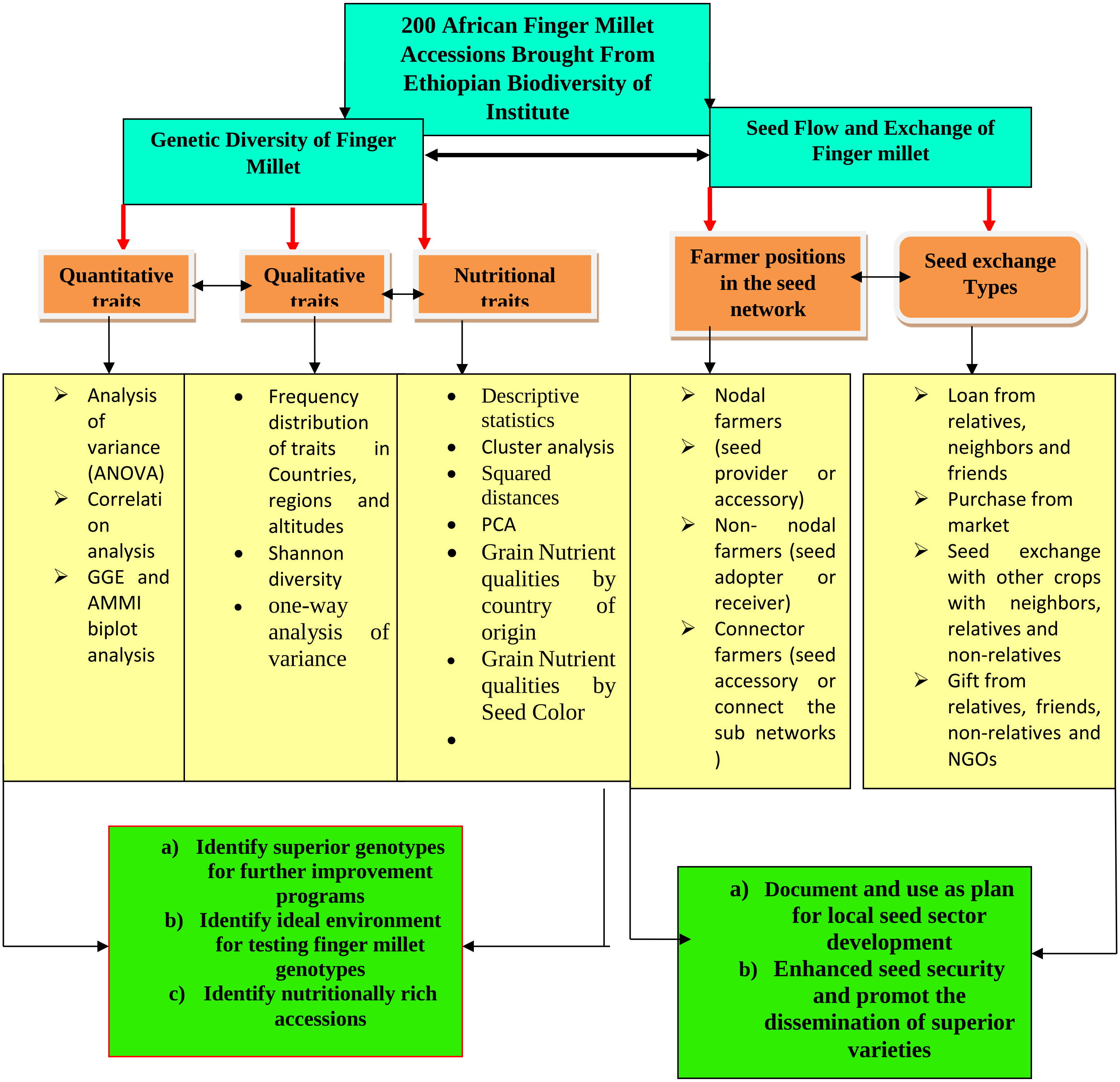


Figure 1.1: A Synthesis and Conceptual Framework of the study

2. MATERIAL AND METHODS

Plant Material: The study utilized 200 finger millet genotypes sourced from the Ethiopian Institute of Biodiversity (described in Chapter Two).

Study Site: The research was conducted at three locations; Rama, Maiaini, and Zana; over two growing seasons (2019 and 2020). Detailed descriptions of these sites are provided in Chapter Two.

Design: An alpha lattice design (20 x 10) with two replications was employed for the experimental setup.

Data Collected:

1. Quantitative Traits: Data on nine traits—grain yield, plant height, 1000 seed weight, number of fingers per panicle, number of tillers per plant, finger length, finger width, days to 50% flowering, and days to 75% maturity—were collected from five randomly selected and tagged plants per genotype and replication. This data pertains to the first research objective, which evaluated the performance of African finger millet genotypes under marginal growing conditions in Tigray, Northern Ethiopia (Chapter Two).

2. Qualitative Traits: Five qualitative traits, including seed pericarp persistence, finger branching, ear shape, glumes color, and seed color; were recorded from 5 randomly selected plants per genotype. This data supports the second research objective, which focused on the diversity of qualitative traits and the eco-geographical distribution of African finger millet collections (Chapter Three).

3. Grain Nutritional Traits:: The analysis of nutritional traits focused on evaluating iron (Fe), zinc (Zn), calcium (Ca), magnesium (Mg), moisture content, starch, and protein content. This assessment supports the third research objective, which aimed to explore the genetic diversity of nutritional traits in African finger millet collections (Chapter Four).

4. Seed flow and Exchange system: The fourth research objective focused on analyzing the seed flow and exchange systems of finger millet in Central and North Western Tigray. This involved collecting data on respondents' socioeconomic characteristics, seed exchange mechanisms, the roles farmers play in the seed flow process, and the transactions related to farmers' varieties**.**

.

3. RESULT

This dissertation presents four research objectives, each addressing different aspects of finger millet research.

1. Performance Evaluation: The first objective evaluated the performance of African finger millet accessions under the marginal growing conditions of Tigray, Northern Ethiopia. The two-year study (2019 and 2020) revealed significant differences in grain yield and related traits among genotypes, as well as considerable environmental variation. This allowed the identification of high-performing genotypes across various environments (Chapter Two).

2. Qualitative Traits Diversity: The second objective investigated the diversity of qualitative traits and their eco-geographical distribution among African finger millet collections. Using methods such as percentage distribution, the Shannon diversity index, chi-square tests, and one-way ANOVA, the study analyzed qualitative traits across different regions, countries, and altitudes. The results highlighted a high degree of polymorphic diversity (Chapter Three)

3. Genetic Diversity for Nutritional Quality: The third objective assessed the genetic diversity of nutritional traits among African finger millet collections. Analysis of 200 finger millet accessions using near infrared spectrophotometry (NIR) revealed significant variation ($P<0.001$) in protein, starch, and mineral contents. This data provided valuable insights into the genetic diversity and trait relationships, which are crucial for developing successful breeding programs. Notable genotypes, such as 203574, 234160, 203259, 203262, and 203257, were identified for their superior protein, calcium, magnesium, iron, and zinc contents, respectively (Chapter Four).

4. Seed Flow Network Analysis: The fourth objective focused on the network analysis of finger millet seed flows in the Central and Northwestern Zones of Tigray. The study involved interviewing 160 household heads through snowball sampling, semi-structured questionnaires, and focus group discussions (FGDs). The research documented farmers' varieties, seed exchange mechanisms within and outside villages, and the role of farmers in the seed network, aiming to identify key farmers who play crucial roles in seed saving, exchange, and maintaining on-farm crop diversity (Chapter Five).

4. CONCLUSIONS AND RECOMMENDATION

Finger millet is a globally important millet species and a staple traditional food crop in various regions of Africa and Asia. In Africa, it is widely cultivated in countries such as Uganda, Tanzania, Ethiopia, Eritrea, Kenya, Rwanda, Burundi, Zimbabwe, Zambia, and Malawi. Understanding the genetic variability and diversity within finger millet germplasm, as along with the relationships between different traits, is vital for effective plant breeding programs. This study revealed significant genotype-by-environment (G x E) interactions, highlighting variability in the performance of finger millet genotypes across different environments. It also found high Shannon diversity in six qualitative traits: seed pericarp persistence, ear/glume color, seed color, finger branching, ear shape, and the number of grains per spike. Additionally, genotypes with superior nutritional traits, including high protein, calcium, iron, magnesium, and zinc content were identified. The research further highlighted the key roles farmers play in seed exchange and saving through informal seed flow channels, underscoring the importance of these practices in maintaining crop diversity and supporting food security.

5. REFERENCE

Admasu, S. and Belete, T. (2023). Finger millet (*Eleusine coracana* (l .) Gaertn) breeding , major production challenges and future prospects. *Journal of Agricultural Research Advances*, *02*(02); 33–39.

Arjun, D., Kumar, R., & Singh, C. (2014). Finger millet for nutritional security and source of food. *Advances in Food Science and Technology*, *2*(3); 184–190.

Babu, B.K.,Senthil, N., Gomez, S.M., Biji,K.R., Rajendraprasad, N.S., Kumar, S.S., and Babu, R.C. 2006. Assessment of genetic diversity among finger millet (Eleusine coracana L. Gaertn) accession using molecular markers. *Genetic Research and Crop Evolution* 54: 339-404

Chandra, D., Chandra, S., & Sharma, A. K. (2016). Review of Finger millet (*Eleusine coracana* (L .) Gaertn): A power house of health benefiting nutrients. *Food Science and Human Wellness*, *5*(3); 149–155.

Damtie, Y., Girma, F., Terfessa, A., & Demelash, H. (2019). Genetic Diversity and Heritability Estimates among Ethiopian Finger Millet (*Eleusine coracana*) (L.) Gaertn.) Genotypes for Yield and Its Contributing Traits at Assosa , Western Ethiopia Yaregal Damtie * , Firezer Girma , Alemu Terfessa and Habtamu De. *Asian Journal of Plant Science and Research*, *9*(2); 6–15.

Da-zhong, Z., Panhwar, R. B., Jia-jia, L. I. U., Xiang-wei, G., Ji-bao, L., & Min-, L. I. U. (2019). Morphological diversity and correlation analysis of phenotypes and quality traits of proso millet (*Panicum miliaceum* L .) core collections. *Journal of Integrative Agriculture*, *18*(5); 958–969.

Dasanayakal, P. N., & Kaluthanthri, D. V. S. (2017). Genetic Variability Characterization of Some Ex Situ Conserved Finger Millet (*Eleusine Coracana* (L.) Gaertn. Subsp. Coracana) Germplasm Accessions In Sri Lankausing Qualitative Morphological Markers. *International Journal of Advanced Research (IJAR)*, *5*(5); 1381–1389.

Dida, M. M., Wanyera, N., Harrison Dunn, M. L., Bennetzen, J. L., & Devos, K. M. (2008). Population Structure and Diversity in Finger Millet (*Eleusine coracana*) Germplasm. *Genetic Resources and Crop Evolution*, *1*(2); 131–141.

Farida Traoré, F., El-Baouchi, A., En-nahli, Y., Hejjaoui, K., Metougui, M. L., Hamwieh, A., Sohail, Q., Istanbuli, T., Boughribil, S., & Amri, M. (2022). Exploring the Genetic Variability and Potential Correlations Between Nutritional Quality and Agro-Physiological Traits in Kabuli Chickpea Germplasm Collection (*Cicer arietinum* L.). *Frontiers in Plant Science*, *13*(7); 1.14.

Gebreyohannes, A., Shimelis, H., Laing, M., Mathew, I., Odeny, D. A., & Ojulong, H. (2021). Finger Millet Production in Ethiopia : Opportunities , Problem Diagnosis , Key Challenges and Recommendations for Breeding. *Sustainability*, *13*(13463); 1–23.

Hailegebrial, K., Yiergalem, T., Alem, R., Redae, W., Desalegn, Y., & Welegerima, G. (2017). Yield performance and Adaptability of Finger millet landrace in North Western Tigray , Ethiopia. *World News of Natural Sciences*, *15*(October); 98–111

.

Hiremath, N., Geetha, K., Vikram, S. R., Nanja, Y. A. and, & Shivaleela, H. B. (2018). Minerals Content in Finger Millet [*Eleusine coracana* (L.) Gaertn]: A Future Grain for Nutritional Security. *International Journal of Current Microbiology and Applied Sciences*, *7*; 3448–3455.

Karak, T., Erdem, H., Baloch, F. S., Toklu, F., Eker, S., Kilian, B., & Ozkan, H. (2012). Diversity of Macro- and Micronutrients in the Seeds of Lentil Landraces. *The Scientific World Journal*; 1–9.

Kumar, A., Chawla, H. S., Jeena, A. S., & hit, R. (2019). Morphological Characterization of Finger Millet Germplasm Collected from Uttrakhand Hills for Qualitative Traits. *International Journal of Current Microbiology and Applied Sciences*, *8*(09); 2105–2109.

Negi, S., Kumar, V., & Bhatt, A. (2017). Genetic Diversity among Finger Millet [*Eleusine coracana* (L.) Gaertn] Genotypes for Yield and Its Contributing Traits. *International Journal of Current Microbiology and Applied Sciences*, *6*(8); 3332–3337.

Tesfaye, K., & Mengistu, S. (2017). Phenotypic characterization of Ethiopian finger millet accessions (*Eleusine coracana* (L.) Gaertn), for their agronomically important traits. *Acta Universitatis Sapientiae, Agriculture and Environment*, *9*(1); 107–118.

Wolie, A., Dessalegn, T., & Belete, K. (2013). Heritability, variance components and genetic advance of some yield and yield related traits in Ethiopian collections of finger millet (*Eleusine coracana* (L.) Gaertn.). *African Journal of Biotechnology, 12*(36); 5529–5534.

Upadhyaya, H.D., Gowda, C.L.L., Pundir, R.P.S., Reddy,V.G., Singh, S. (2004). Development of core subset of finger millet germplasm using geographical origin and data on 14 quantitative traits. *Genetic Resource and Crop Evolution*, 53; 679-685.

CHAPTER TWO
Evaluation of Finger Millet *Ex situ* Collections for Yield and its component traits Under Rainfed Growing Conditions of Tigray, Northern Ethiopia

ABSTRACT

Finger millet, though underutilized globally, serves as an important source of food for millions of poor farmers in Africa. This study evaluated 200 finger millet collections under the marginal/challenging production conditions of Tigray, Ethiopia, during 2019 and 2020 growing seasons. Using a 20×10 lattice design with two replications per location, data on various traits, including grain yield, plant height, 1000 seed weight, number of fingers per panicle, number of tillers per plant, finger length, finger width, days to 50% flowering, and days to 75% maturity were collected. These data were analyzed using Minitab software, with results presented as ANOVA tables, means, and bi-plots. Results showed highly significant (*P<0.01*) effects of genotype and genotype-environment interactions (G×E), which accounted for 65.9% and 26.2% of the variability, respectively, while the environment contributed only 5.8%. The average grain yield across genotypes ranged from 1773 kg ha^{-1} to 3749 kg ha^{-1}, with an average of 2549 kg ha^{-1}. Notably, high yields were recorded for genotypes 203246 (G21) and 234184 (G175), achieving 4138 $kgha^{-1}$ and 3986 $kgha^{-1}$, at Rama and Maiaini locations, respectively; genotype 234184 (G175) also performed well with a yield of 3368 kg ha^{-1} at Zana. Yield per plant (g) varied across locations, ranging from 5.5 to 6.5 at Rama, 4.1 to 9.6 at Maiaini, and 1.8 to 4.8 at Zana. A significant correlation between grain yield and 1000 seed weight was found observed, especially at Rama and Maiaini. Maiaini also recorded the highest mean performance for traits such as 1000 seed weight (2.6 g), plant height (85.8 cm), number of fingers per panicle (7.5 numbers), number of tillers per plant (0.2), finger length (10cm), and finger width (17.1 cm) compared to other locations. Therefore, the study highlights promising genotypes with high yield and stability, which could be valuable for future breeding efforts to enhance finger millet production.

Keywords: Finger millet, Grain yield, AMMI, GGE, Biplot

2.1. INTRODUCTION

Finger millet (*Eleusine coracana* (L.) Gaertn) is an allotetraploid (2n = 4× = 36) annual cereal crop consisting of two distinct subspecies; subsp. *coracana* (the cultivated finger millet) and subsp. *Africana* (the wild finger millet) (Dessalegn et al., 2019). It is widely cultivated in eastern Africa and south Asia. Finger millet is mostly considered a crop of poor farmers due to its adaptability to diverse environmental conditions, making it a potential food crop. It ranks third in importance among cereals in semi-arid and subtropical regions, following pearl millet (*Pennisetum glaucum*) and foxtail millet (*Setaria italica*) (Adugna et al., 2011). In Tigray, finger millet is characterized by three dominant colors—black, brown and white—each often associated with different culinary uses in the traditional finger millet production systems. The red-seeded type is commonly noted for its nutritional value (Negi et al., 2017), while the black-seeded type is commonly used for making a local drink known as "*Siwa*" (traditional alcoholic beverage) and its resistance to bird attack probably due to high tannin content, and the white-seeded variety, highly preferred for making high quality injera but more susceptible to bird attack (Tsehaye et al., 2006).

Finger millet is also predominantly Known for its climate resilience, gluten-free seeds, antioxidant properties, and rich in calcium and iron content, finger millet also boasts excellent malting qualities (Kumar et al., 2016). Despite such tremendous advantages, it remains underutilized in low-input agricultural systems in the Tigray region and elsewhere in the country, with productivity below potential due to technical and attitudinal constraints. Limited genetic resources in breeding programs have hindered the development of high-yielding, stable finger millet varieties. Genetic improvement depends largely on access to diverse genetic materials and genetic variability within the populations (Dhanapal and Selvi, 2008). Grain yield and other traits depend on genotype, environment, and their interaction (Phuke et al., 2017). Evaluating hundreds of local and exotic accessions under various conditions can help identify superior genotypes. Therefore, the present study was undertaken to evaluate the performance of finger millet accessions under a range of environments, analyze genotype-by-environment interaction, and identify stable, high-yielding accessions for the Tigray region. The objectives of this study were to evaluate the effects of genotypes, environments, and their interaction (genotype × environment) on grain yield and associated traits; identify superior genotypes; and recommend better performing genotypes for wide-scale production in the Tigray region.

2.2. MATERIALS AND METHODS

2.2.1. Plant material

A total of 200 finger millet accessions/collections (hereafter genotypes), were retrieved from the Ethiopian Biodiversity Institute (the National *ex situ* gene bank). The genotypes were collected from different regions of Ethiopia (n = 102), and other African countries mainly from Eritrea (n = 30), Zambia (n = 19), and Zimbabwe (n = 49). The collections from Zambia and Zimbabwe were donations that have been placed in the Ethiopian gene bank for long-term conservation and utilization purposes (Tsehaye, 2016). The Ethiopian accessions were collected from a wide altitudinal range (from 1000 to 2380 m.a.s.l) which represents the agro-ecological zones of finger millet growing areas of Ethiopia (Tsehaye, 2016).

2.2.2. Description of the experimental sites

Three potential finger millet growing areas in the Tigray region, namely, North-Western [Maiaini and Zana] and central zone of the Tigray region [Rama] were identified and selected for genotypes evaluation during 2019 and 2020 planting seasons. These sites are known for their suitability for finger millet production and serve as ideal sites for evaluating and characterizing new finger millet genotypes and other cereal crops like sorghum (Tsehaye *et al.*, 2006).

Maiaini is geographically located in the Tselemti district of Tigray, 85 km from Shire town, at 14°16'N latitude, 38°12'E longitude, and an elevation of 1450 m.a.s.l. It is bordered by Asgede Tsimbla, Welkait, Tanqua Abrgelle districts, and the Amara region to the north, west, east and south, respectively. The mean minimum and maximum annual temperature of the area is 16 °C (November–January) and 38 °C (February–May), respectively. Some of the major crops grown in the area include sorghum, finger millet, maize, chickpea and sesame (Gebregergs, 2020).

Zana is located in the Medebay (the then Medebay-Zana) district, geographically located at 38º 20′ E longitude, 14º 06′ N latitude, and an elevation of 1865 m.a.s.l. The average daily temperature ranges between 12ºc and 28ºc, with annual rainfall ranging from 500 to 900mm (Abrha et al., 2020).

Rama is located in the former district of Mereb lekhe, later named as Rama Adi-Arbate district, in the central zone of Tigray. It lies 35 km north of Adwa town and 7 km from the Tigray-Eritrea border, at 14°25′N latitude, 38°47′E longitude, and an elevation of 1385 m.a.s.l. The area is known for its fertile lowlands. A map indicating the study locations is presented below (Fig. 2.1).

2.2.3. Climate and soil of the experimental sites

The experimental sites are characterized by subtropical climate with low annual rainfall and frequent droughts. While some precipitation occurs from February to May (the *belg* season), most rain falls during June to September (the *kremt* season), which is followed by October to January (the *bega* dry season) as described in Figure 2.2. The mean annual temperature ranged from 18.6 to 32.0, 19.5 to 32.7, 10.6 to 23.1, 12.2 to 23.9, 14.3 to 33.8, 14.7 to 34.3^{0}C for Maiaini, Zana and Rama during 2019 and 2020 growing seasons, respectively. Further, the mean annual rainfall ranged from 1301.0 to 1685.1 mm, 1482.2 to 2095.0 mm and 510.1 to 1049.6 mm for Maiaini, Zana and Rama during 2019 and 2020 growing seasons, respectively. The soil type at Maiaini was verti-cambisol with a pH of 6.2.

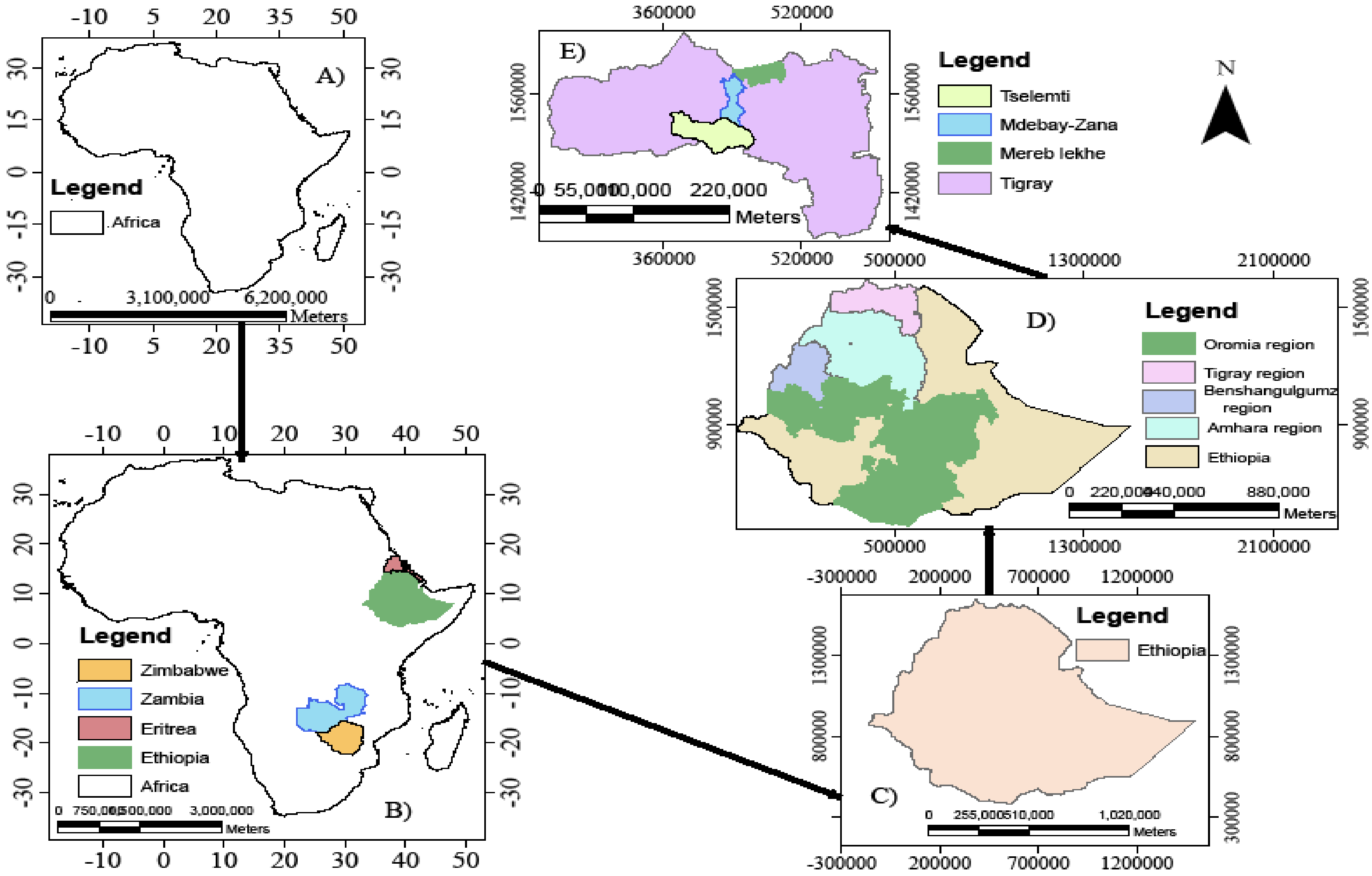


Figure 2 1. Map of the source regions and location of the testing areas in Tigray

2.2.4. Experimental design and layout

At each site, the genotypes were arranged using an alpha lattice design, consisting of 10 incomplete blocks (20 x 10) and replicated twice. Each genotype was planted in 7.5 m^2 plots, with two rows measuring 5 m in length. The inter-row spacing was set at 0.75 m, and the intra-row spacing was 0.1 m. The spacing between plots and replications were 0.5 and 1m, respectively. Seeds were sown along the rows at rate of 11.25 g/plot, equivalent to 15 kg/ha^{-1}, and later thinned to maintain the 0.1 m spacing between plants. Each experimental plot received a uniform basal dose of DAP fertilizer (100 kg/ ha) at the time of planting and Urea (100 kg/ha) in three stages: at planting, one month after planting, and at grain filling stage. Weeding and other management practices were uniformly applied across all experimental plots as per crop recommendations.

2.2.5. Data collected

Data were collected for a total of 9 quantitative traits (yield and associated traits) from five randomly selected and tagged plants per genotype and replication.

Finger number per panicle (FNPP): - The number of fingers per panicle was counted from five randomly selected plants and the average value was calculated for analysis.

Finger length (FL): - The length was measured, in centimeters, from the base to the tip of the longest finger at maturity stage for each of the five randomly tagged plants using a ruler.

Fingers width (FW): - Measured in millimeters (mm) across center of longest finger at maturity stage for each the five randomly selected plants.

Number of tillers per plant (NTPP): - Number of productive tillers per plant was counted from five randomly tagged plants at maturity.

Days to 50% Flowering (DTF): It was recorded as the number of days from sowing to the stage when 50% of the plants within each plot reach 50% flowering

Days to 75% maturity (DTM): -It was recorded as the number of days from sowing to the stage when 75% of the plants within each plot reach 75% of ears turned brown in color.

1000 Seed weight (TSW): - After harvest, 1000 seeds were counted and weighed in gram (g) on plot basis.

Grain yield per plot (GY): - Was determined on plot basis and converted to kg ha^{-1}

2.2.6. Statistical Data analysis

Analysis of variance (ANOVA) for all traits combined across locations was performed using Minitab software (Alvarado et al., 2015). The Best Linear Unbiased Predictor (BLUP) values were estimated from the full model (Genotype x Location x Year Interaction component [G x L x Y]) using a mixed model approach, where the genotype, year, and the G x L x Y interaction were treated as random effects, while replication, blocks nested within replication, and replication nested within locations were treated as fixed effects. The BLUP values estimated for each environment (Location by year component) were then used as an input for the Additive Main effects and Multiplicative Interaction (AMMI) as well as GGE-biplot analyses. These methods were employed to identify superior and stable genotypes and to determine the most discriminating locations in a multivariate platform.

Heritability Broad Sense (H^2) = $\left(\frac{\sigma 2g}{\sigma 2p}\right)$ x100

Where, $\sigma^2 g$ = genotypic variance and **$\sigma^2 p$** = phonotypic variance

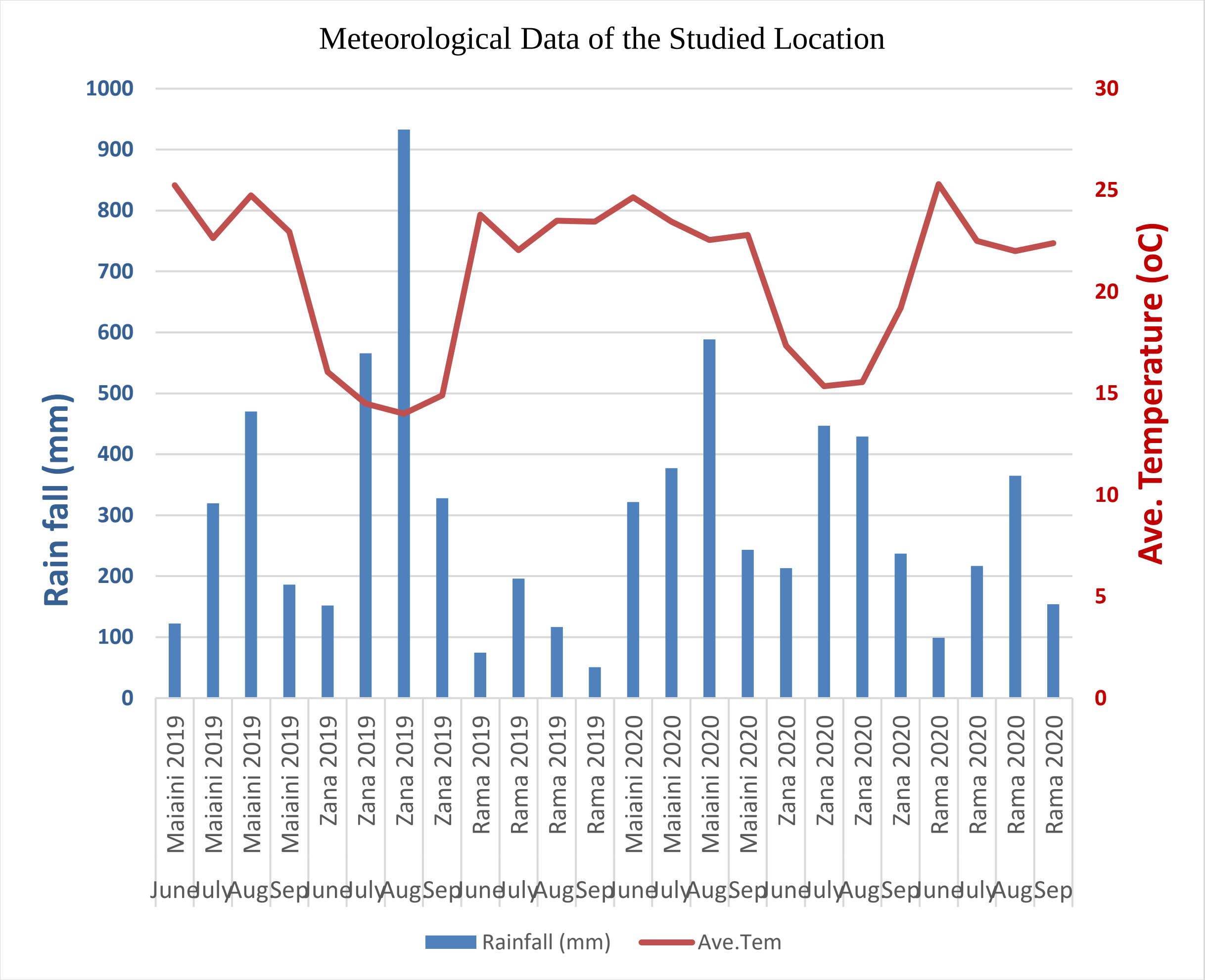


Figure 2 2. Meteorological Data from the experimental sites during the study periods.

2.3. RESULTS

2.3.1. Overall mean performance of the Genotypes for quantitative traits

The descriptive statistics for each trait considered in the present study, including the maximum and minimum mean values and the standard deviation, were calculated from the average data of each genotype to understand their performance across different environments (Table 2.1). In general, the genotypes depicted a wide range of diversity for all quantitative traits, resulting in significant variation in maximum and minimum mean values. For example, the average grain yield of the 200 tested genotypes ranged from 1773 kg ha^{-1} to 3749 kg ha^{-1}, with an overall mean of 2549 kg ha^{-1}, in this regard, genotypes 203246, 203263, 100022, 203339 and 203353 were identified as the top five high yielders with mean grain yield of 3986, 3981, 3969, 3900 and 3745 kg ha^{-1}, respectively (Appendix Table 2.7.5). In contrast, genotypes 234174, 203068, 234173, 203357 and 203063 were among the five lowest performing genotypes.

The TSW ranged from 1.9 to 2.8 g, plant height varied from 61.0 cm (genotype 203246) to 78.5 cm (genotype234823), the number of tillers per plant ranged from 0 to 1, finger number per panicle ranged from 4.5 (genotype 203258) to 8.0 (genotype 233601), finger length ranged from 5.1 (genotype 20335 to 10.7 cm (genotype 234160) and finger width ranged from 13.4 (genotype 235135) to 19.0 mm (genotype 203351). In this study, some genotypes like 203355, 234197, 234196, 233769, 233580, 203581 and 234255 matured earlier with their maturity dates ranged from 97 to 105 days. Genotypes 203557, 208725, 234180, 203350, 235135, 234184 and 203558 were categorized as late-maturing types (Table 2.1).

TSW (1000-seed weight), FNPP, (Finger number per panicle), FL (Finger length), DTF (Days to 50% flowering) and DTM (Days to 75% maturity) showed high ($H^2 > 60\%$) heritability (Table 2.1), these traits could be more reliable for selection in breeding improvement program of finger millet. In contrast, GY (grain yield), NTPP (number of tillers per plant), and FW (finger width) showed low (H2<50%) heritability indicated that these traits were largely influenced by environmental factors and difficult to improve through direct selection.

Table 2.1. The minimum, maximum, mean, and standard deviation values for the nine quantitative traits of finger millet genotypes

Trait	Min.	Max.	Ave./mean value	Std	Heritability% (H^2)
Grain yield (Kg ha^{--})	1773	3749	2549	481.0	46.8
1000-seed weight (g)	1.9	2.8	2.2	0.18	71.3
Plant height (cm)	61.0	78.5	69.9	3.21	54.5
Number of tillers per plant	0.0	1.0	0.5	0.07	24.0
Finger number per panicle	4.5	8.0	5.9	0.46	62.0
Finger length (cm)	5.1	10.7	8.6	1.20	75.4
Finger width (mm)	13.4	19.0	16.5	0.85	49.6
Days to 50% flowering	72.5	106.1	94	6.66	85.4
Days to 75% maturity	97	136	123	7.72	87.8

2.3.2. Analysis of Variance

The analysis of variance for the different locations—Rama, Maiaini, and Zana—are presented in Tables 2.2, 2.3, and 2.4. Apparently, highly significant variations ($P<0.01$) were observed among the finger millet genotypes for most of the traits across all locations. At Rama, traits such as GY, FL, FW, DTF, and DTM depicted a highly significant variation, while other traits such as TSW, PH, NTPP, and FNPP showed non-significant variation. In contrast, all traits showed a significant variation at both Maiaini and Zana. The genotype-by-year interaction also imposed highly significant ($P<0.01$) effects on most of the studied traits, except for DTF and DTM in Maiaini and Zana, and the DTF in Rama, which showed a non-significant variation (Tables 2.2, 2.3 and 2.4). This might be due to the erratic nature of rain-fail at these locations. The combined analysis of variance showed highly significant ($p<0.01$) differences in the mean sum of squares for all nine traits across genotypes, locations, genotype-by-location interaction, genotype-by-year interaction, and genotype x location x year interaction (Table 2.5). However, the effects of year and locations x year interaction depicted a non-significant variation for TSW, PH, and NTPP. The significant variation observed in other traits suggests considerable genetic variability, which can be exploited through further selection.

Table 2.2. Mean squares from the separate analysis of variance for nine quantitative traits in 200 finger millet genotypes at Rama during 2019 and 2020 cropping season

Source of variance	**df**	**Quantitative traits**								
		GY	**TSW**	**PH**	**NTPP**	**FNPP**	**FL**	**FW**	**DTF**	**DTM**
Acc.	199	1410542**	0.26866**	138.6**	1.1242**	3.0277**	10.523**	34.48**	299.75**	425.47**
Year	1	2011644**	1.02245ns	19929.1ns	4.3956ns	99.0528ns	321.058*	2824.89**	2771.40**	2914.66**
Acc.*Year	199	67875**	0.21205**	153.3**	1.1533**	2.3468**	9.312**	27.27**	1.18ns	1.35**
Rep(Year)	2	18064ns	0.18915ns	2804.5ns	11.6208ns	21.3575ns	22.454ns	32.16	1.00ns	0.47ns
Blc(Year, Rep)	36	7721ns	0.04131ns	241.7ns	1.3803ns	3.5557ns	2.150ns	10.03	1.10ns	0.94ns
									1.24	0.88
Error	362	7968	0.05007	67.9	0.6277	0.9159	2.701	8.19		
Total	799									
CV%		19.8	0.7	17.7	1.5	1.0	1.5	3.5	1.6	1.6
LSD (%)		3.3	8.8	10.6	64.8	14.0	16.6	18.2	1.2	0.8

Table 2.3. Mean squares from the separate analysis of variance for nine quantitative traits in 200 finger millet genotypes at Maiaini during 2019 and 2020 cropping season

Source of variance	**df**	**Quantitative traits**								
		GY	**TSW**	**PH**	**NTPP**	**FNPP**	**FL**	**FW**	**DTF**	**DT M**

Acc.	199	1776780**	1.00656**	330**	0.5803**	4.687**	12.955**	15.858**	258.65**	281.09**
Year	1	1069112**	1.32845**	104084**	0.5202*	536.609**	24.710**	453.758**	5000.00**	5000.00**
Acc.*Year	199	98433**	0.04635**	260**	0.2869**	2.801**	8.898**	9.759**	0.50ns	0.60ns
Rep(Year)	2	6657 ns	0.02623 ns	3715 ns	1.2841 ns	0.292 ns	20.925 ns	23.198 ns	0.02ns	11.90ns
Blc(Year, Rep)	36	7527 ns	0.03775 ns	176 ns	0.1093 ns	0.595 ns	1.753 ns	6.630 ns	8.29 ns	9.20 ns
Error	362	8230	0.03085	78	0.1345	0.953	1.637	4.712	10.84	12.80
Total	799									
CV%		7.9	0.3	11.2	0.8	2.4	4.4	4.5	3.7	4.0
LSD (%)		3.5	6.8	10.4	22.3	12.7	12.7	12.8	3.0	2.3

Table 2.4. Mean squares from the separate analysis of variance for nine quantitative traits in 200 finger millet genotypes at Zana during 2019 and 2020 cropping season

Source of variance	**df**	**Quantitative traits**								
		GY	**TSW**	**PH**	**NTPP**	**FNPP**	**FL**	**FW**	**50%F**	**75% M**
Acc.	199	903689**	1.00656**	330**	0.5803**	4.687**	12.955**	15.858**	258.65**	281.09**
Year	1	18698753**	1.32845**	104084**	0.5202**	536.609**	24.710**	453.758**	5000.00**	5000.00**
Acc.*Year	199	67216**	0.04635**	260**	0.2869**	2.801**	8.898**	9.759**	0.50ns	0.60ns
Rep(Year)	2	4876ns	0.02623ns	3715**	1.2841**	0.292ns	20.925**	23.198*	0.02ns	11.90ns
Blc(Year, Rep)	36	9693ns	0.03775ns	176**	0.1093ns	0.595ns	1.753ns	6.630ns	8.29ns	9.20ns
Error	362	7591	0.03085	78	0.1345	0.953	1.637	4.712	10.84	12.80
Total	799									
CV%		16.1	0.2	21.8	0.7	2.3	4.4	5.5	14.8	15.6
LSD (%)		3.7	8.3	18.7	26.4	26.4	24.0	12.5	6.9	5.8

KEY: df= degree of freedom, GY= Grain yield, YPP= Yield per plant, TSW= 1000 seed weight, PH = Plant height, NTPP =number of tiller per plant, Total tiller FNPP = finger number per panicle, FL = finger length, FW = finger width, 50%F = 50% flowering and 75%M = 75% maturity

Table 2.5. Mean squares from combined analysis of variance for nine quantitative traits in 200 finger millet genotypes

Source of variance	**df**	**Quantitative traits**								
		GY	**TSW**	**PH**	**NTPP**	**FNPP**	**FL**	**FW**	**50%F**	**75% M**
Acc	199	3027747**	0.711**	398**	0.744**	6.33**	28.65**	33.16**	671.9**	862.2**
Loc	2	17880156**	214.563**	368180**	285.777**	4096.11**	4009.44**	432.90**	63210.6**	3811.1**
Year	1	15307022**	0.007ns	129291**	8.320ns	86.16*	157.41*	3067.53**	10391.7**	14220.4**
Acc*Loc	398	521454**	0.393**	145**	0.600**	2.18**	3.99**	16.09**	133.4**	138.7**
Acc*Year	199	72142**	0.110**	367**	0.815**	4.31**	18.27**	23.21**	55.2**	59.1**
Loc*Year	2	3236243**	1.173**	10003ns	4.830ns	278.98**	132.87*	336.14**	11250.7**	21771.6**
Acc*Loc*Year	398	79459**	0.076**	138**	0.431**	1.73**	4.42**	13.86**	59.6**	63.6**
Rep(Loc, Year)	6	9866ns	0.080ns	3056ns	4.373ns	12.15ns	23.58*	18.49ns	1.3ns	5.2ns
Blc(Loc, Year, Rep)	108	8314ns	0.047ns	222ns	0.553ns	2.63ns	1.92ns	7.56*	15.1ns	15.3ns
Error	1086	7930	0.036	73	0.317	0.88	2.17	5.77	21.9	22.4

Total	2399									
CV%		13.3	8.4	12.3	8.6	15.9	16.8	14.5	7.6	8.0
LSD (%)		404.3	0.3	8.3	0.3	1.0	1.9	2.4	4.9	3.8

KEY: df= degree of freedom, GY= Grain yield, TSW= 1000 seed weight, PH = Plant height, NTPP =number of tiller per plant, Total tiller FNPP = finger number per panicle, FL = finger length, FW = finger width, DTF = 50% flowering and DTM = 75% maturity

2.3.3. Grain Yield

The AMMI analysis of variance was conducted to determine the effects of environment (location), genotype and their interactions on grain yield of the 200 African finger millet genotypes (Table 2.6). The main effects of environment (E), genotype (G), and G×E interaction, along with the first, second and third Principal Components (Table 2.6) were all highly significant ($P \leq 0.01$).

Genotype and G×E interaction had showed the largest effects, explaining 65.9% and 26.2% of the total variability, respectively, while the environment explained only 5.8% of the total sum of squares. The higher genotype-by-environment interaction variance for grain yield was mainly due to the first (IPCA-I) and second (IPCA-II) principal components, which accounted for 52.19 and 33.59% of the variation, respectively, collectively explaining 85.78% of the total variation (Table 2.6 and Fig. 2.3). A visual AMMI biplot was created based on the first and second principal component analyses (PCA) to provide insights into the correlations between testing environments and the stability of individual genotypes across the different tested environments (Fig. 2.3).

Table 2.6. AMMI analysis of variance for grain yield of finger millet genotypes tested across six environments in Tigray, Ethiopia

Source of variance	DF	SS	MSS	% contribution
Genotypes	199	327736220	1646916**	65.9
Environments	5	28729983	5745997**	5.8
Interactions	995	130548982	131205	26.2
IPCA 1	203	68126763	335600**	52.19
IPCA 2	201	43853286	218176**	33.59
IPCA 3	199	7950454	39952*	6.09
Residuals	392	10618479	27088	

Key: DF, degree of freedom; SS, sum Square; MSS, mean square value, ICCA, interaction principal component analysis

The significant contribution of the genotype indicated substantial genetic diversity, with much of the variation in grain yield attributed to differences among environmental means. This highlights the genotypes' strong ability to distinguish performance differences. The G × E interaction effect was four times higher (26.2%) than the environment (5.8%) effect, indicating a considerable variation in how genotypes respond to growing environments and the differential discriminating ability of the test environments.

2.3.3.1 Genotype Evaluation for the quantitative traits in Each Location

Among the three test locations, Maiaini emerged as the most conducive and productive location during both cropping seasons. This location recorded higher mean values for all traits studied, except for grain yield, NTPP, and DTF. The highest mean GY (2669 kgha^{-1}) was recorded at Rama followed closely by Maiaini (2596 kg ha^{-1}), while the lowest yield (2381kgha^{-1}) was obtained from Zana (Table 2.7).

Table 2.7. Summary of the minimum, maximum, and mean values for nine quantitative traits of finger millet genotypes across different locations.

Trait	**locations**								
	Rama			**Maiaini**			**Zana**		
	Min.	**Max.**	**mean**	**Min.**	**Max.**	**mean**	**Min.**	**Max.**	**mean**
Grain yield (Kg ha^{--})	1832	4138	2669	1411	3368	2596	1773	3749	2381
1000-seed weight (g)	2.4	2.8	2.5	1.7	4.1	2.6	1.1	2.4	1.6
Plant height (cm)	61.8	92.5	78.4	79.7	93.4	85.8	25	67.5	45.5
Number of tillers per plant	0.0	2.4	1.2	0.1	1.1	0.2	0.2	0.2	0.2
Finger number per panicle	6.2	7.5	6.8	6.2	9.1	7.5	3	3.7	3.3
Finger length (cm)	9.3	10.3	9.8	8.4	11.5	10	4.5	7.1	6.1
Finger width (cm)	13.1	17	15.6	14.5	19.2	17.1	16.3	17	16.7
Days to 50% flowering	62	104	88	66	112	89	80	112	104
Days to 75% maturity	87	139	120	103	139	124	98	133	124.5

The study revealed varied performance in yield and yield related traits across different environments. Table 2.7 presents the lowest and highest mean values for the 9 quantitative traits at each testing locations. Specifically, genotype 234174 (G169) showed a very low grain yield of 1832 kg ha^{-1} in Rama, genotype 203068 (G20) yielded 1411 kg ha^{-1} in Maiaini, and genotype 234174 (G169) produced 1773 kg ha^{-1} in Zana during the 2019 and 2020 growing seasons. On the other hand, the highest grain yield was obtained from genotype 203246 (G21) in Rama with average yields of 4138 and genotype 234184 (G175) in Maiaini with average yields of,3368 kg ha^{-1}. While genotype 100022 (G4) depicted the highest grain yield of 3749 kg ha^{-1} in Zana (Appendix tables.2.7.3, 2.7.4 and 2.7.5)

Miaini recorded high mean values for several traits, including TSW (2.6 g), PH (85.8 cm), FNPP (7.5 number), NTPP (0.2), FL (10cm), FW (17.1 cm). On average, Rama exhibited early maturity with DTF (88 days) and DTM (120 days), while Zana showed delayed maturity with both traits (104 and 125 days, respectively). Therefore, these findings suggest that genotypes with higher mean values for these traits might be valuable for further finger millet improvement programs.

2.3.4. AMMI Biplot Analysis

The AMMI Biplot analysis is one of the important tools to determine the relationships among testing environments and the performance of genotypes within each environment, aimed at identifying genotypes with either wide or specific adaptability for a specific trait. The angle formed between testing environments in the biplot measures/reflects their correlations. Accordingly, a < 90^0 angle formed across years at the same location indicates nosignificant variation in grain yield performance among finger millet genotypes when planted in the same location across different years (Fig. 2.3). On the other hand, angles >90^0 formed between locations indicate a strong but negative correlation, confirming that the testing locations should be treated as separate mega-environments for further evaluation and recommendations of finger millet genotypes.

Genotypes 102, 17, 15, 54, 75, and 101 performed better at the Rama location in both test years, while genotypes 52, 62, 61, and 71 displayed better performance at Maiaini across years. Additionally genotypes 116, 38, 86, 27 and 83 were identified as well-suited for the Zana location. The length of the environment vectors indicates the discriminating ability of the environments. Based on the present findings, Rama and Zana were the most discriminating locations, whereas Maiaini showed relatively less discriminative power during the 2019 and 2020 growing seasons

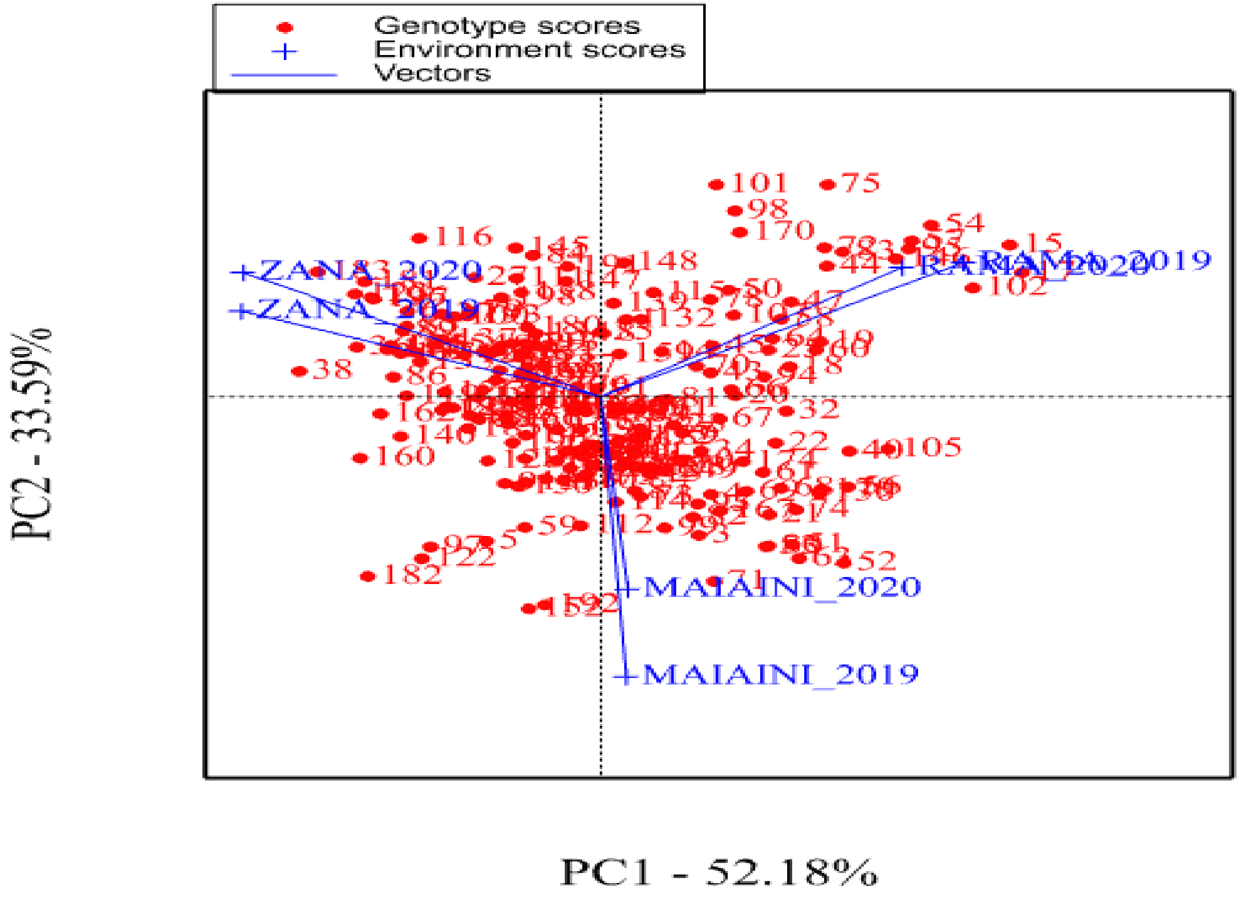


Figure 2 3 AMMI biplot depicting yield data for 200 African finger millet genotypes tested across three locations over two growing seasons in 2019 and 2020.

The distribution of finger millet genotype points in the AMMI biplot shows that genotypes located close to the origin demonstrate minimal genotype-by-environment interactions and are considered stable genotypes. On the contrary, genotypes positioned far from the origin, as shown in the AMMI biplot (Fig. 2.3), indicate instability and a high differential response to the different growing environments. Thus, genotypes with above-average grain yield performance across testing environments and positioned close to the biplot origin could be identified as stable and widely adapted. Conversely, genotypes with above-average performance but positioned far from the biplot, indicating instability and highly significant G × E interactions, may be suitable for selection in specific environments (Fig 2.3).

2.3.5. Correlation analysis

Separate correlation analyses for each test location are presented in Tables 2.8, 2.9 and 2.10 for Rama, Maiaini and Zana, respectively. In Rama, grain yield showed a positive and significant correlation with 1000 seed weight, finger number per panicle, and finger width, but it was negatively and significantly correlated with days to 50% flowering and days to 75% maturity. Additionally, 1000 seed weight was positively and significantly correlated with finger number per panicle and finger width. Finger length also showed significant positive correlations with finger number per panicle, finger width, days to 50% flowering and days to 75% maturity. Moreover, days to 75% maturity were significantly and positively correlated with days to 50% flowering (Table 2.8). In Maiaini, grain yield was positively and significantly correlated only with 1000 seed

Table 2 8. Correlations between traits across 200 finger millet genotypes in Rama during 2019 and 2020 growing season

Traits	**GY**	**TSW**	**PH**	**NTPP**	**FNPP**	**FL**	**FW**	**DTF**
TSW	0.46**							
PH	-0.10	-0.04						
NTPP	0.09	0.11	-0.02					
FNPP	0.37**	0.26*	0.08	0.12				
FL	0.05	0.12	0.06	0.06	0.23*			
FW	0.44**	0.31**	0.12	-0.07	0.16	0.25**		
DTF	-0.20*	-0.12	0.02	0.05	0.10	0.45**	-0.10	
DTM	-0.16*	-0.10	-0.01	0.03	0.12	0.45**	-0.09	0.98**

weight, while its correlation with days to 50% flowering and days to 75% maturity was negative but no-significant.

Table 2.9. Correlations between traits across 200 finger millet genotypes in Maiaini during 2019 and 2020 growing season

Traits	GY	TSW	PH	NTPP	FNPP	FL	FW	DTF
TSW	0.51**							
PH	-0.06	-0.07						
NTPP	0.10	0.09	-0.08					
FNPP	0.17	0.13	0.24*	0.19				
FL	-0.04	-0.03	0.23*	-0.04	0.23*			
FW	0.08	-0.05	0.19*	0.03	0.15	0.42**		
DTF	-0.15	-0.16	0.06	-0.04	0.03	0.03	-0.12	
DTM	-0.12	-0.14	0.13	-0.07	0.00	0.21*	-0.08	0.81**

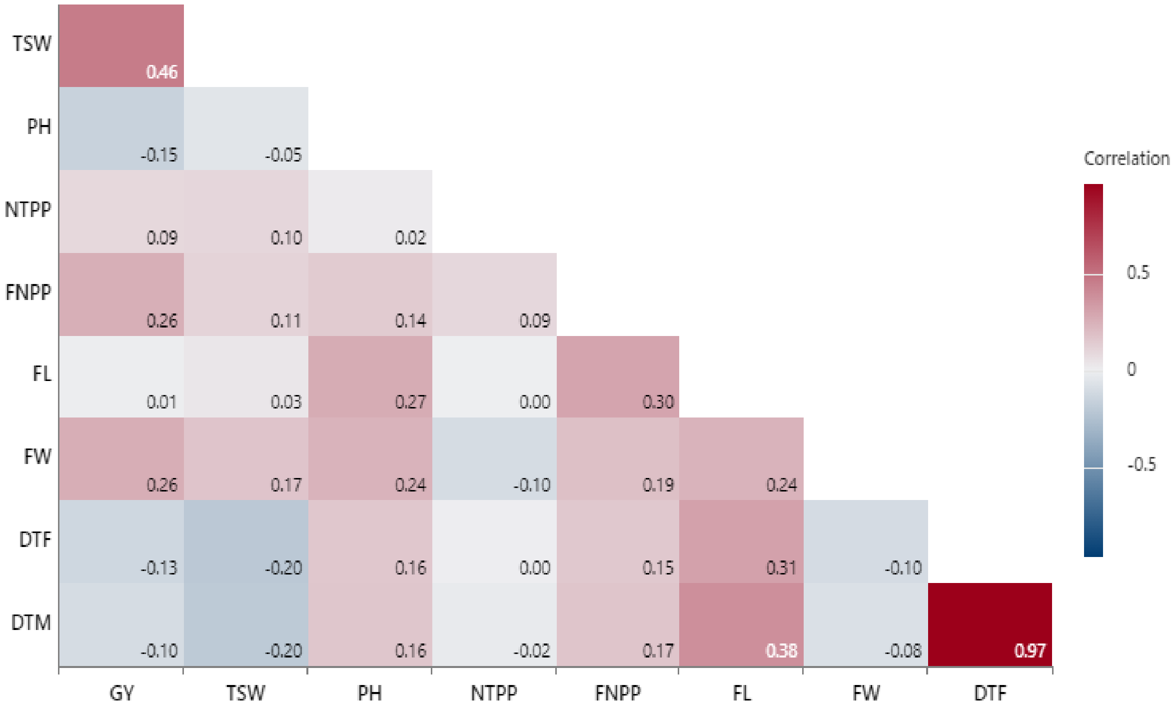
In this case, plant height was positively and significantly associated with finger number per panicle, finger length and finger width, similarly finger length was also associated with finger width and finger number per panicle (Table 2.9). The correlations of nine quantitative traits in Zana testing site showed that grain yield was non-significantly associated with all the traits under studied regardless of the positive or negative correlations. At this location, traits like finger length, finger width, days to 50% flowering and days to 75% maturity were positively and significantly associated with plant height and finger number per panicle (Table 2.10)

Table 2.10. Correlations between traits across 200 finger millet genotypes in Zana during 2019 and 2020 growing season.

Traits	**GY**	**TSW**	**PH**	**NTPP**	**FNPP**	**FL**	**FW**	**DTF**
TSW	-0.11							
PH	-0.15	-0.03						
NTPP	-0.07	0.06	0.10					
FNPP	0.01	-0.02	0.10	0.05				
FL	0.03	-0.01	0.25*	-0.05	0.28**			
FW	0.05	0.05	0.26*	-0.08	0.17	0.22*		
DTF	0.02	-0.13	0.19*	0.08	0.14	0.27*	-0.01	
DTM	0.02	-0.13	0.18*	0.07	0.15	0.28**	-0.02	0.99**

Estimates of the phenotypic correlation coefficients for all studied traits, based on combined BLUP analysis, and are presented in Table 2.11. Grain yield showed a positive and highly significant ($P<0.01$) phenotypic association with 1000-seed weight, finger number per panicle, and finger width. It was also positively, but not significantly ($P<0.05$), correlated with finger length and tiller number per plant. Conversely, grain yield had a negative, non-significant association with plant height, days to 50% flowering, and days to 75% maturity. Plant height exhibited a significant ($P<0.01$) correlation with finger length and width, and a significant ($P<0.05$) association with days to 50% flowering and days to 75% maturity. Additionally, finger length showed a strong positively correlation with finger width, days to 50% flowering and days to 75% maturity. The phonological traits (days to 50% flowering and days to 75% maturity) were highly and positively associated with each other. These traits showed a negative, non-significant interaction with grain yield, 1000 seed weight, and finger width.

Table 2.11. Correlations between traits across 200 finger millet genotypes for the overall locations



	GY	TSW	PH	NTPP	FNPP	FL	FW	DTF
TSW	0.46							
PH	-0.15	-0.05						
NTPP	0.09	0.10	0.02					
FNPP	0.26	0.11	0.14	0.09				
FL	0.01	0.03	0.27	0.00	0.30			
FW	0.26	0.17	0.24	-0.10	0.19	0.24		
DTF	-0.13	-0.20	0.16	0.00	0.15	0.31	-0.10	
DTM	-0.10	-0.20	0.16	-0.02	0.17	0.38	-0.08	0.97

Key: GY= Grain yield; TSW = 1000 seed weight; PH = plant height; TNPP = tiller number per plant; FNPP = finger number per panicle; FL = finger length of panicle; FW = finger width; DTF = days to 50% flowering and DTM = days to 75% maturity.

2.3.6. GGE Biplot Analysis

The GGE (genotypic main effect plus genotype-by-environment interaction) biplot is a valuable analytical tool for examining and visualizing the factors contributing to genotype × environment (GE) interactions for important traits. The GGE biplot analysis explained 89.22% of the total variation in Genotype-by-Environment interaction, with 72.09 and 17.13 of the variation explained by the first and second principal components (PCA1 and PCAII), respectively (Fig.2.4).

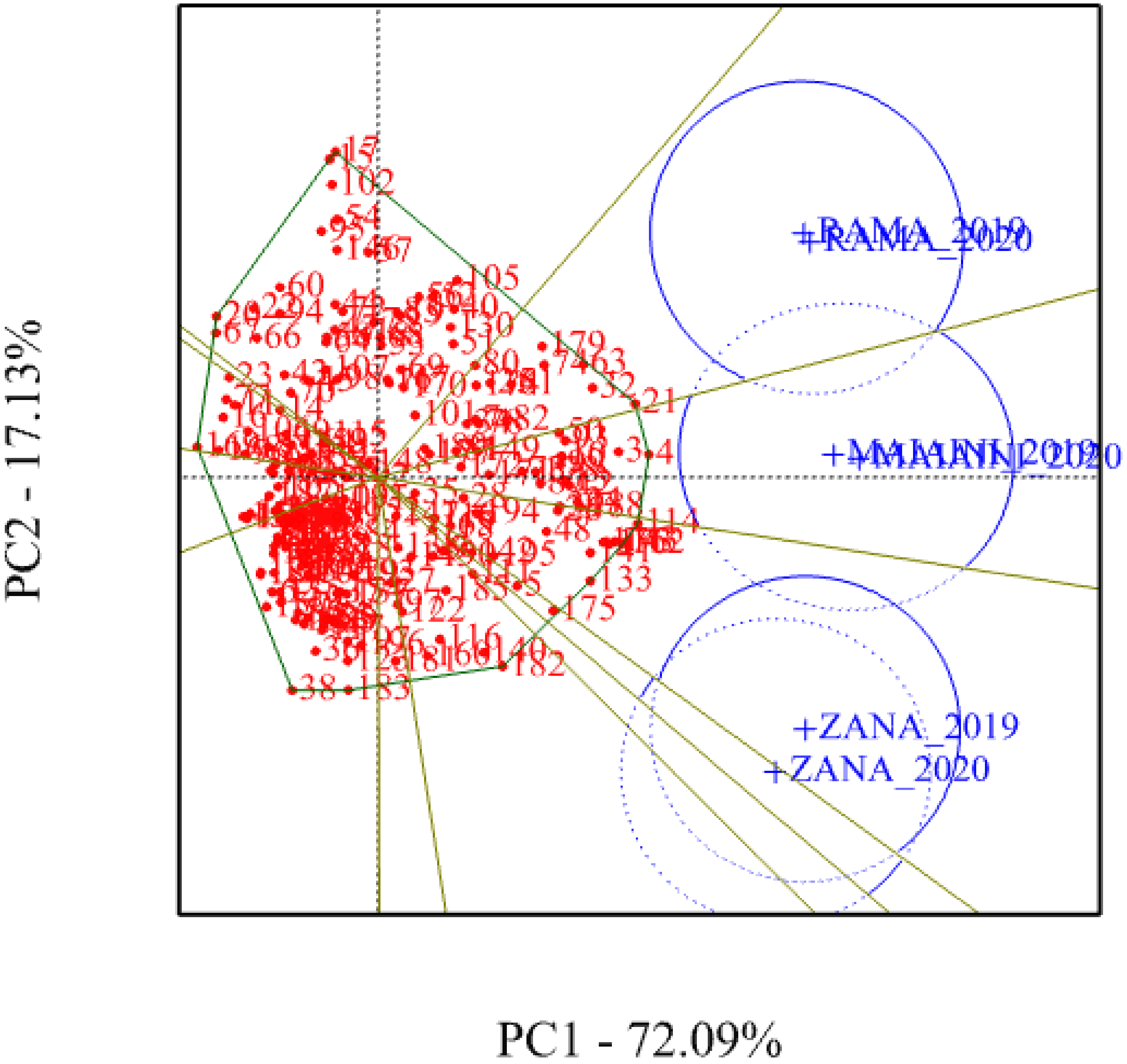


Figure 2 4. The “which-won-where” view of the GGE biplot to show which genotypes performed best in which environment.

The “which won where/what” analysis using the GGE biplot showed that the perpendicular lines divided the irregular polygon into thirteen sectors. A set of lines was drawn from the biplot origin, intersecting the sides of the polygon at right angles. In this analysis, the winning genotypes were placed at the vertices of each polygon sector, corresponding to a particular environment in the

GGE biplot. The biplot also showed the mean yield performance of genotypes for each respective location (Fig. 2.4). The vertex genotypes helped identify potential opportunities to subdivide the target environment into distinct mega-environments. As a result, the analysis classified the present target environments into three sectors (i.e., three mega-environments), revealing that genotype grain yield performance varied across environments. The environments Rama 2019 and Rama 2020 were grouped into one mega-environment, Maiaini 2019 and Maiaini 2020 into another, and Zana 2019 and Zana 2020 into a third.

Genotypes located at the vertices of the polygon, within their respective sectors, exhibited the highest yields for the environments associated with them. Genotypes that performed poorly in one environment were among the best-performing genotypes in the other environments. All other genotypes, contained within the polygon, had smaller vectors, indicating they were less responsive to the environmental interactions within that sector

2.3.6.1 Ranking Genotypes Based on Grain Yield Performance in Each Location

To rank the genotypes based on their yield performance in each environment, an average environmental coordinator (AEC) line was drawn through the biplot origin and the environment. This line helps to rank the genotypes along it (Fig. 2.5). Genotypes closest or nearest to the concentric circle had greater-than-average yield performance, while those farther from the AEC line exhibited lower-than-average yields. The AEC view of the GGE biplot was therefore helpful for evaluating genotypes based on their mean yield across environments.

The study revealed that genotypes 21 (203246), 4 (100022), 3 (100020), 114 (229736), 112 (229734), and 63 (203353) showed a clear yield advantage in Rama (Fig. 2.5a), similarly, genotypes 175 (234184), 114 (229736), 143 (233759), 133 (230136), 173 (234179), and 112 (229734) ranked among the top genotypes for higher yield in Maiaini (Fig. 2.5b). For the Zana location, genotypes 4 (100022), 21 (203246), 114 (229736), 112 (229734), 3 (100020), and 143 (233759 were closest to the AEC, indicating that these genotypes were the most representative and highest yielding in this particular environment (Fig. 2.5 c).

.

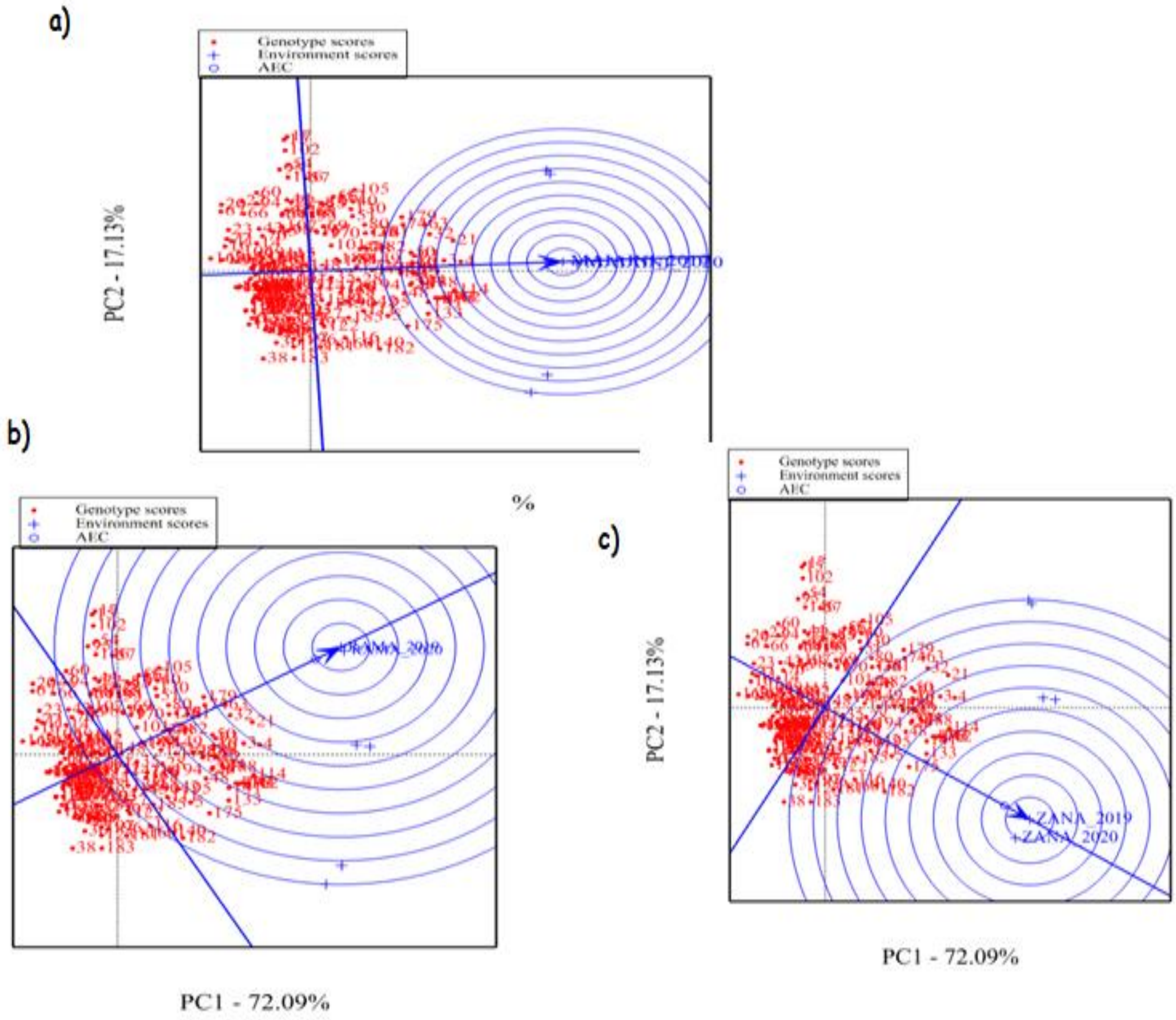


Figure 2 5. The average-environment coordination (AEC) view to rank genotypes relative to each testing location (the center of the concentric circles)

2.4. DISCUSSIONS

2.4.1. Variance Component

The analysis of variance (ANOVA) for grain yield (kg/ha) across each environment and combined results over years and locations revealed highly significant variations for genotype, environment, and the genotype-by-environment interaction (GEI) effects (Table 2.6). All components of variation, including environment (year and location), genotype, and GEI, were significant. Among these, the genotype effect accounted for the highest variance (65.9%), followed by GEI (26.2%) and environment (5.8%). Although the environment's variance was relatively low, GEI showed a notable contribution. These findings are consistent with similar studies, such as Anuradha et al. (2022), who reported a higher variance contribution from genotype in finger millet varieties. Likewise, Lakew et al., (2017) reported that the main effects of genotypes (G) and environments (E) accounted for 53.8% and 26.8% of the upland rice genotypes sum of squares, respectively. In contrast, a large proportion of total variation contributed by the environment was reported in finger millet in other studies (Adugna et al., 2011; Fentie et al., 2013; Lule et al., 2014; Meles et al., 2016; Seyoum et al., 2020). Similarly, Tolessa et al., (2013); Gedif and Yigzaw, (2014); Singamsetti et al., (2021); Mengesha et al., (2022) and Bayissa et al., (2023) showed GEI among the genotypes of bread wheat, field pea, maize, and potato, respectively.

2.4.2. Genotype by Environment Interaction

The analysis of stability and genotypic superiority for grain yield, using ANOVA and GGE biplot analyses, revealed significant differences ($P \leq 0.01$) in grain yield among the evaluated finger millet genotypes. Stability analysis provides basic information about the stability and superiority of a genotype. A genotype with high yield and high stability is recommended for the target environments and could be used to develop new, high-yielding cultivars by breeders. Genotypes 100020, 100022, and 229736 were identified as having both high yield performance and adaptability, making them ideal candidates for future use (Appendix table 2.7.2). This aligns with findings by Koutis et al., (2012), who reported significant yield performance differences among wheat genotypes tested in three locations across three growing seasons. Similarly, Khan et al.

(2023) noted that the grain yield performance of 16 wheat genotypes varied across three different locations.

The current study identified three distinct mega-environments, suggesting they might have dissimilar climate conditions. These mega-environments should be evaluated separately when recommending finger millet genotypes. The presence of genotype by environment interaction complicates the selection of superior genotypes, as it reduces the consistency between genotype and phenotype making it harder to identify the best performing genotypes. However, GEI remains an important tool for evaluating genotypes, either for broad mega-environments or specific ones, through the identification of crossover and non-crossover types of GEI (Jalata, 2011). Several studies (Yan & Tinker, 2006; Dhanapal & Selvi, 2008; Koutis et al., 2012; Fu-fu et al., 2014 and Mousavi et al., 2021) reported that wide obtuse angles in the GGE biplot indicate significant crossover interactions in GEI, leading to changes in genotype ranking across the tested environments. The identification of crossover GEI suggests the need to categorize environments into specific groups for further testing (Yan & Rajcan, 2014). Our results were consistent with the finding of Yan & Tinker (2006), who described mega-environments as regions that do not exhibit major crossover GE interactions. Likewise, through the use GGE biplot, Sood et al., (2016) identified two mega-environments for finger millet based on testing across four environments. Thus, our results suggest that closely related test environments (figure 2.3) may provide the same genotype information, potentially reducing testing costs. If two environments are consistently correlated over time, one of them could be dropped without losing much information (Scavo & Mauromicale, 2023).

Moreover, genotypes coded as 203246, 203263, 100022, 203339, and 203353 were among the top performers in Rama (E1 and E4), while genotypes 203246, 100022, 100020, 229736 and 229734 were top performers in Maiaini during 2019 and 2020 growing seasons. This inconsistency in genotype rankings across years indicates that these environments should be treated as independent mega-environments. Likewise, genotypes like 234184, 229736, 233759, 230136 and 234179 performed well in Zana (E3 and E6) during both years, suggesting the presence of cross-over GEI and the need for three different mega-environments.

2.4.3. Ranking of Genotypes

In this study, the ranking of the top five high-yielding and the bottom five lowest-yielding genotypes out of the 200 genotypes was based on BLUPs averaged across positively correlated environments, showing consistent rankings over years (Dessalegn et al., 2019). The performance of genotypes varied across the three study locations, necessitating independent rankings at each location over the years using AMMI analysis. As a result, Rama emerged as a superior testing site in 2019 and 2020 due to its high grain yields, selecting it as optimal for evaluating finger millet genotypes.

The GGE biplot (Figure 2.3) indicated the best-performing genotype(s) for specific environment and groups of environments, segmenting the plot into six sections and identifying three mega-environments. According to Yan et al. (2007), different sectors with different high-yielding cultivars indicate crossover interactions. The presence of significant G x E interaction indicated inconsistencies in the performance of maize genotypes across environments (Anley et al., 2013). Likewise, Lagat et al. (2018) emphasized the importance of genotype-by-environment interaction when it significantly alters genotype rankings across environments Dessalegn et al. (2019) noted that the genotype at the vertex of the polygon performs best in the environment falling within the sector.

Two methods, BLUP and GGE-based (Anuradha et al., 2022), were used to identify stable high-yielding genotypes. Variability in genotype performance across locations can be attributed to factors such as the genotype, soil fertility, temperature, and rainfall (intensity and duration), necessitating further investigation to understand the G x E interactions (Seyoum et al., 2020). Similarly, Lagat et al. (2018) reported that crop yield performance is a function of genotype, environment and genotype by environment interaction.

2.4.4 Correlations of traits

Correlation analysis is very crucial in order to provide clear information about the magnitude and level of relationship between traits. Grain yield, being a complex trait controlled by many genes, makes selection based solely on yield unreliable. Thus, selection of genotypes or breeding lines should be based on the association of grain yield with contributing traits (Adugna et al. 2011). This study used Pearson correlation coefficients with BLUPs for single and multiple locations to evaluate the relationship between grain yield and other quantitative traits like 1000 seed weight, plant height, tiller number per plant, finger number per panicle, finger length and width, days to 50% flowering, and days to 75%.

In Rama and Maiaini, negative correlations were found between grain yield and days to flowering and maturity, likely due to short period of rainfall durations, which are mostly from June to August. Thus, late flowering and maturing genotypes are vulnerable to yield losses and cannot escape the terminal drought. These traits, however, revealed a positive correlation of low magnitude in Zana, where rainfall extended up to the end of September. Adugna et al. (2011) found that late flowering, coinciding with blast fungal infections, reduced Plant height consistently and negatively correlated with grain yield across locations, possibly due to taller plants being more prone to lodging yield loss. In contrast to our results, Backiyalakshmi et al. (2021) reported a positive correlation between grain yield and plant height. However, grain yield was positively correlated with tiller number per plant, finger number per panicle, finger length and width, which is in line with the findings of Ganapathy et al. (2011). Da-zhong et al. (2019) also confirmed significant positive correlations between vegetative traits such as plant height, stem diameter, stem node number, and panicle length and yield in finger millet genotypes. Numerous studies emphasizing the relationships between grain yield and other important traits have been published, with associated traits being crucial when associated with high yield (Dhanapal & Selvi, 2008; Jifar et al., 2015; Yan et al., 2016; Yan & Frégeau-Reid, 2018; Merrick et al., 2020; Moeinizade et al., 2020; Woyann et al., 2020 and Mousavi et al., 2021). Thus, the superiority of a genotype should be judged by its overall yield performance in association with other target traits, rather than on individual traits alone.

2.5. CONCLUSION AND RECOMMENDATION

2.5.1 Conclusion

The significant variation observed among finger millet genotypes across different traits and locations highlights a strong genetic diversity within the crop. This diversity is crucial for plant breeding, as it indicates the potential for selecting genotypes adapted to specific environmental conditions. The considerable impact of G × E on grain yield, accounting for 26.2% of the total variation, emphasizes the importance of considering both genotype and environmental factors in yield performance. This variability in genotype responses across different environments underscores the need for multi-environment testing to ensure accurate evaluations. The IPCA revealed that the first two principal components explained most of the G × E interaction variance, indicating that a few key traits largely influence yield variability across environments. This insight can help streamline the focus in future analyses and selection criteria. The positive correlation of genotype performance within the same location across years (with angles < 90°) implies consistency over time. In contrast, the strong negative correlation between different locations (angles > 90°) indicates significant environmental differences, supporting the classification of these locations as separate “mega-environments” for genotype testing. This approach helps in recommending varieties best suited to specific environments. The findings suggest that finger millet genotypes need to be tailored to specific environmental conditions rather than aiming for broad adaptability across regions. Breeders should focus on selecting and recommending specific genotypes best suited for each identified mega-environment to optimize yield performance. In this study, genotypes 102, 17, 15, 54, 75, and 101 showed high yield performance in Rama location. Similarly, genotypes 52, 62, 61, and 71 were among the high-performing genotypes in Maiaini, while genotypes 116, 38, 86, 27 and 83 were identified as high yielders in Zana location over two years.

2.5.2. Recommendation

The promising genotypes identified for their high yield and stability in this study should undergo further testing across multiple environments together with the currently released finger millet varieties. This will allow for a comprehensive assessment of their overall performance in grain yield and other key traits before being used as benchmarks for evaluating new candidate entries. Furthermore, finger millet breeders should prioritize traits that show a positive and significant associations with grain yield, as these traits are crucial for further genetic improvement of the crop.

2.6. REFERENCE

Abrha, T., And, B. E., & Gebre, G. G. (2020). *Factors Affecting Onion Market Supply In Medebay Zana District , Tigray Regional State , Northern Ethiopia*. *Cogent Food and Agriculture*, 00: 171214 ; 1-14

Adugna, A., Tesso, T., Degu, E., Tadesse, T., Merga, F., Legesse, W., Tirfessa, A., Kidane, H., Wole, A., & Daba, C. (2011). Genotype-By-Environment Interaction And Yield Stability Analysis In Finger Millet (≪I≫Elucine Coracana≪/I≫ L. Gaertn) In Ethiopia. *American Journal Of Plant Sciences*, *02*(03); 408–415.

Alvarado, G., López, M., Vargas, M., Pacheco, Á., Rodríguez, F., Bur gueño, J., & Crossa, J..(2015) META-R (Multi Environment Trail Analysis with R for Windows) Version 6.03. *CIMMYT Research Data & Software Repository Network* 21; 1-14

Anley, W., Zeleke, H., & Dessalegn, Y. (2013). Genotype X Environment Interaction Of Maize (Zea Mays L .) Across North Western Ethiopia. *Journal of Plant Breeding and Crop Science* 5(9); 171–181.

Anuradha, N., Patro, T. S. S. K., Singamsetti, A., Sandhya Rani, Y., Triveni, U., Nirmala Kumari, A., Govanakoppa, N., Lakshmi Pathy, T., & Tonapi, V. A. (2022). Comparative Study Of AMMI- And BLUP-Based Simultaneous Selection For Grain Yield And Stability Of Finger Millet [Eleusine Coracana (L.) Gaertn.] Genotypes. *Frontiers In Plant Science*, *12*(January); 1–10.

Backiyalakshmi, C., Babu, C., Reddy, D. N., Padmakumar, V. P., Prasad, K. V. S. V., Azevedo, V. C. R., & Vetriventhan, M. (2021). Assessing Forage Potential Of The Global Collection Of Finger Millet (Eleusine Coracana (L.) Gaertn.) Conserved At The Icrisat Genebank. *Agronomy*, *11*(9); 1–20.

Bayissa, T., Mengistu, G., Gerema, G., Balcha, U., Feyisa, H., Kedir, A., Legese, Z., Asegid, D., Leta, T., & Jobe, T. (2023). Genotype × Environment Interaction Of Lowland Bread Wheat Varieties For Irrigation In Different Areas Of Oromia. *Wiley Onlinel Ibrary.Com/Journal/*; 2–10.

Da-Zhong, Z., Panhwar, R. B., Jia-Jia, L. I. U., Xiang-Wei, G., Ji-Bao, L., & Min-, L. I. U. (2019). Morphological Diversity And Correlation Analysis Of Phenotypes And Quality Traits Of Proso Millet (Panicum Miliaceum L .) Core Collections. *Journal Of Integrative Agriculture*, *18*(5); 958–969.

Dessalegn, K., Lule, D., Mengistu, G., Mamo, K., Birhanu, C., Chemeda, G., & Bedada, G. (2019). Genotype By Environment Interaction And Grain Yield Stability Of Ethiopian Black Seeded Finger Millet Genotypes. *African Crop Science Journal*, *27*(2); 281.

Dhanapal, A. P., & Selvi, B. (2008). Variability And Multivariate Analysis In Finger Millet (

Eleusine Coracana) Germplasm For Yield Characters. *crop research.,* 36(1, 2 & 3); 218-223

Fentie, M., Assefa, A., & Belete, K. (2013). Ammi Analysis Of Yield Performance And Stability Of Finger Millet Genotypes Across Different Environments. *World Journal Of Agricultural Sciences*, *9*(3); 231–237.

Fu-Fu, T. A. N. G., Ya-Fang, S. H. A. O., Ya-Ling, C. H. E. N., Chuan, T. O. N. G., & Jin-Song, B. A. O. (2014). *Genotype × Environment Interactions For Agronomic Traits Of Rice Revealed By Association Mapping*. 21(3); 133–141.

Ganapathy, S., Nirmalakumari, A., & Muthiah, A. R. (2011). Genetic Variability And Interrealtionship Analyses For Economic Traits In Finger Millet Germplasm. *World Journal Of Agricultural Sciences* 7(2); 185–188.

Gebregergs, T. (2020). Herbaceous Species Composition, Diversity And Biomass Of Communal Grazing Lands Under Exclosure Management In Northwestern Tigray Region Of Ethiopia. *I Nternational J Ournal Of Agriculture And Biosciences, Www.Ijagbi*(August); 325–332.

Gedif, M., & Yigzaw, D. (2014). Genotype By Environment Interaction Analysis For Tuber Yield Of Potato (Solanum Tuberosum L .) Using A GGE Biplot Method In Amara Region , Ethiopia. *Agricultural Sciences*, *5*; 239–249.

Jalata Zerihun. (2011). GGE-Biplot Analysis of Multi-Environment Yield Trials Of Barley (Hordeium Vulgare L) Genotypes In Southeastern Ethiopia Highlands. In *International Journal Of Plant Breeding And Genetics*, 5(1); 59–75).

Jifar, H., Assefa, K., & Tadele, Z. (2015). Grain yield variation and association of major traits in brown-seeded genotypes of tef [Eragrostis tef (Zucc .) Trotter]. *Agriculture and Food Security*, *4*(7); 1–9.

Khan, I., Gul, S., Khan, N. U., Fawibe, O. O., Akhtar, N., Rehman, M., Sabah, N., Tahir, M. A., Iqbal, A., Naz, F., Haq, I., & Rauf, A. (2023). *Stability Analysis Of Wheat Through Genotype By Environment Interaction In Three Regions Of Khyber Pakhtunkhwa , Pakistan*. *55*(449); 50–60.

Koutis, K., Mavromatis, A. G., Baxevanos, D., & Koutsika-Sotiriou, M. (2012). *Multienvironmental Evaluation Of Wheat Landraces By GGE Biplot Analysis For Organic Breeding*. *3*(1); 66–74.

Kumar, A., Metwal, M., Kaur, S., Gupta, A. K., Puranik, S., Singh, S., Singh, M., Gupta, S., Babu, B. K., Sood, S., & Yadav, R. (2016). Nutraceutical Value Of Finger Millet [Eleusine Coracana (L.) Gaertn.], And Their Improvement Using Omics Approaches. *Frontiers In Plant Science*, *7*(June); 1–14.

Lagat, N., Kimurto, P., Kiplagat, O., Towett, B., Jeptanui, L., Gatongi, I., Njogu, N., Ojulong, H., Manyasa, E., & Siambi. (2018). Evaluation Of Genotype X Environment Interaction And Stability Of Grain Yield And Related Yield Components In Pearl Millet (Pennisetum Glaucum (L.) R.Br.). *Journal of Experimental Agriculture International*, *21*(1); 1–18.

Lakew, T., Dessie, A., Tariku, S., & Abebe, D. (2017). Evaluation Of Performance And Yield Stability Analysis Based On AMMI And GGE Models In Introduced Upland Rice Genotypes Tested Across Northwest Ethiopia. *International Journal Of Research Studies In Agricultural Sciences, 3*(2)*;* 17-24

Lule, D., Fetene, M., De Villiers, S., & Tesfaye, K. (2014). Additive Main Effects And Multiplicative Interactions (AMMI) And Genotype By Environment Interaction (GGE) Biplot Analyses Aid Selection Of High Yielding And Adapted Finger Millet Varieties. *Journal Of Applied Biosciences*, *76*(1); 6291–6303.

Meles, B., Tesfay, M., Nigus, C., & Meles, K. (2016). Stability Analysis Of Finger Millet Genotypes In Moisture Stressed Areas Of Northern Ethiopia. *Journal of Natural Sciences Research*, *6*(3); 73–83.

Mengesha, G. G., Abebe, S. M., Tsakamo, Y. T., Issa, B. T., Mekonnen, A. A., Esho, A. G., Dojamo, T. S., & Halengo, M. M. (2022). Genotype By Environment Interaction Analysis For Fusarium Head Blight Response And Yield Performance Of Bread Wheat (Triticum Aestivum L .) In Southern Ethiopia. *Phytopathology Research*; 4–45.

Merrick, L. F., Glover, K. D., & Yabwalo, D. (2020). Use Of Genotype By Yield * Trait (GYT) Analysis To Select Hard Red Spring Wheat With Elevated Performance For Agronomic And Disease Resistance Traits. *Crop Breed Genet Genom*., *2(2); 1-18*

Moeinizade, S., Kusmec, A., Hu, G., Wang, L., & Schnable, P. S. (2020). *Multi-Trait Genomic Selection Methods For Crop Improvement*. *Genetics Investigation, 10; 1-15*

Mousavi, S. M. N., Bojtor, C., Illés, Á. And, & Nagy, J. (2021). Genotype by Trait Interaction (GT) in Maize Hybrids on Complete Fertilizer. *Plants*, 10; 1-16

Negi, S., Kumar, V., & Bhatt, A. (2017). Genetic Diversity Among Finger Millet [Eleusine Coracana (L.) Gaertn] Genotypes For Yield And Its Contributing Traits. *International Journal Of Current Microbiology And Applied Sciences*, *6*(8); 3332–3337.

Phuke, R. M., Anuradha, K., Radhika, K., Jabeen, F., Anuradha, G., Ramesh, T., Hariprasanna, K., Mehtre, S. P., Deshpande, S. P., Anil, G., Das, R. R., Rathore, A., Hash, T., Reddy, B. V. S., & Ashok Kumar, A. (2017). Genetic Variability, Genotype × Environment Interaction, Correlation, And GGE Biplot Analysis For Grain Iron And Zinc Concentration And Other Agronomic Traits In RIL Population Of Sorghum (Sorghum Bicolor L. Moench). *Frontiers*

In Plant Science, 8; 1–13.

Scavo, A., & Mauromicale, G. (2023). *Dissecting The Genotype × Environment Interaction For Potato Tuber Yield And Components*. *agronomy*, 13; 1-1*8*

Seyoum, A., Semahegn, Z., Nega, A., & Gebreyohannes, A. (2020). AMMI And GGE Analysis Of Gxe And Yield Stability Of Finger Millet [Eleusine Coracana (L.) Gaertn] Genotypes In Ethiopia. *International Journal Of Trend In Research And Development*, *6*(2); 2394–9333.

Singamsetti, A., Shahi, J. P., Zaidi, P. H., Seetharam, K., Vinayan, M. T., Kumar, M., Singla, S., Shikha, K., & Madankar, K. (2021). Genotype × Environment Interaction And Selection Of Maize (Zea Mays L.) Hybrids Across Moisture Regimes. *Field Crops Research*. 270; Article 108224

Sood, S., Patro, T. S. S. K., Karad, S., & Sao, A. (2016). Stability Of Finger Millet Genotypes Under Diverse Environments. *Indian Journal Of Genetics And Plant Breeding*, *76*(3); 369–372.

Tesfaye, K., Alemu, T., Argaw, T., & Villiers, S. De. (2023). *Evaluation Of Finger Millet (Eleusine Coracana (L .) Gaertn .) In Multi-Environment Trials Using Enhanced Statistical Models*. *PLoS ONE* 18(2); 1–17.

Tolessa, T. T., Keneni, G., Sefera, T., Jarso, M., & Bekele, Y. (2013). Genotype × Environment Interaction And Performance Stability For Grain Yield In Field Pea (Pisum Sativum L .) Genotypes. *International Journal Of Plant Breeding*, *7*(2); 116–123.

Tsehaye, Y., Berg, T., Tsegaye, B., & Tanto, T. (2006). Farmers' Management Of Finger Millet (Eleusine Coracana L.) Diversity In Tigray, Ethiopia And Implications For On-Farm Conservation. *Biodiversity And Conservation*, *15*(13); 4289–4308.

Woyann, L. G., Meira, D., Matei, G., Zdziarski, A. D., Dallacorte, L. V., Madella, L. A., & Benin, G. (2020). Selection Indexes Based On Linear-Bilinear Models Applied To Soybean Breeding. *Agronomy Journal*, *112*(1); 175–182.

Yan, W., & Frégeau-Reid, J. (2018). Genotype By Yield∗Trait (GYT) Biplot: A Novel Approach For Genotype Selection Based On Multiple Traits. *Scientific Reports*, *8*(1); 1–10.

Yan, W., Frégeau-Reid, J., Mountain, N., & Kobler, J. (2016). *Genotype And Management Evaluation Based On Genotype By Yield * Trait (GYT). Crop Breed Genet Genom*. Article 190002; 1–21.

Yan, W., & Rajcan, I. (2014). Biplot Analysis of Test Sites And Trait Relations Of Soybean In Ontario. *Crop Sciences* 42; 11-20

Yan, W., Rutger, J. N., Bryant, R. J., Bockelman, H. E., Fjellstrom, R. G., Chen, M., & Mcclung, A. M. (2007). Development and eval- uation of a core subset of the USDA rice germplasm collection. Crop Science, 47; 869–878

Yan, W., & Tinker, N. A. (2006). Biplot Analysis Of Multi-Environment Trial Data : Principles And Applications. *Canadian Journal of Plant Science*, 6; 623-645

.

CHAPTER THREE

Diversity of Qualitative Traits and Eco-Geographical Distribution of Ex-situ Finger Millet Collections

ABSTRACT

A total of 200 finger millet genotypes, collected from various regions and altitudes in Ethiopia, along with some introductions from Eritrea, Zambia, and Zimbabwe, were planted alongside two improved varieties to evaluate genetic diversity for qualitative traits. This experiment, conducted using a 10 x 20 lattice design at Maiaini during the 2019 and 2020 cropping seasons, utilized descriptors from the International Plant Genetic Resource Institute (IPGRI). Observations indicated that traits such as non-seed persistence, erect ear shape, purple glume color, and black seed color were commonly found across all regions, altitude classes, and countries of origin. Shannon diversity analysis revealed high diversity indices for genotypes from Zambia and Zimbabwe (H’ = 0.90 ± 0.05), with Benishangul Gumuz exhibiting the highest regional diversity for seed pericarp persistence and glume color (H’ = 0.99). Significant differences ($P \leq 0.05$) were found in seed pericarp persistence and highly significant differences ($P \leq 0.01$) in seed color between countries, while other traits showed no significant differences. Regionally, seed color exhibited significant differences ($P \leq 0.05$), with other traits showing non-significant variations. These findings emphasize the substantial genetic diversity in finger millet, the significance of farmer preferences, and the potential for further research and conservation. Understanding the geographical distribution of economically important traits and overall diversity is crucial for effectively utilizing these genetic resources to enhance productivity and environmental resilience in this vital crop..

***Key words**: Eleusine coracana, finger millet, qualitative traits, Shannon diversity index.*

3.1. INTRODUCTION

Finger millet (*Eleusine coracana* L. Gaertn) ($2n = 4x = 36$) is an important small grain cereal for food security and subsistence farming in eastern and southern Africa, valued for its high nutritional and cultural values (Dida et al., 2008). It plays a key role in traditional low-input cereal-based farming systems (Wolie and Dessalegn, 2011) and is also widely cultivated in Southern Asia, particularly in India, Myanmar, Sri Lanka, Bhutan, and China (Upadhyaya et al., 2004). Renowned for its superior nutritional quality compared to most cultivated cereals, finger millet is rich in protein, fiber, and minerals, most importantly calcium and iron, which greatly help in alleviating malnutrition and anemia in countries where it is dietary staple (Babu et al., 2006). The crop thrives in diverse agro-ecological zones and various environmental conditions, including dry and rain-fed areas, making it more adaptable than other tropical cereals. It is principally grown by small-holder farmers and is often regarded a poor man’s food (Kumar *et al.*, 2019).

In finger millet and most related wild species, morphological descriptors that include observable traits are commonly used in diversity studies. These descriptors, which include qualitative and quantitative traits, are vital for racial differentiation and varietal identification (Kumar *et al.*, 2019). Therefore diverse genetic resources in qualitative traits among finger millet genotypess like in seed color, panicle shape, perishable ability, lodging susceptibility, growth habit and glumes (ear) color are very crucial for the genetic advancement of finger millet, for their effective use in the crop improvement programmes (Tesfaye and Mengistu, 2017). In addition, qualitative traits are useful criteria for characterization of germplasm accessions, as they are stable expression. Further, if qualitative characters show association with yield components, it can serve as a marker in selection process (Das et al., 2017). Genetic resource conservation is aided by evaluating the genetic diversity of finger millet qualitative features across origin countries and altitude classes (Brhane et al., 2022). It contributes to the identification and conservation of distinct genetic traits found in various eco-geographical regions. The creation of core subsets of finger millet germplasm and an understanding of the crop's population structure are made possible by the research of genetic diversity across eco-geographical locations and designing successful breeding programs and conservation efforts requires knowledge of this kind. The primary objective of this research study was to investigate the pattern of genetic diversity among 200 finger millet accessions, categorized by their countries of origin and altitudinal class. These genotypes were collected from various regions of Ethiopia and three other African countries, representing different agro-ecological zones and conserved ex situ in the gene banks of the Ethiopian Biodiversity Institute (EBI). Understanding this diversity is essential for developing core germplasm subsets, elucidating population structures, and designing effective breeding and conservation programs.

3.1.1. General Objective

- ⇒ To assess the diversity and distribution of qualitative traits in finger millet genotypes across various countries of origin and altitude classes

3.1.2. Specific objectives

- ⇒ To estimate the level of diversity and identify the most important qualitative traits that contribute considerable variability across different countries of origin and altitude classes.
- ⇒ To evaluate the associations between qualitative traits and altitude classes in finger millets collected from different countries.
- ⇒ To Identify and document the variations in qualitative traits among different finger millet genotypes.

.

3.2. MATERIALS AND METHODS

3. 2.1. Experimental site

The 202 accessions were evaluated at one location with two years in Maiaini. The detailed information of this site is as described in chapter two.

3.2.2. Plant materials

A total of 200 finger millet accessions, (hereafter genotypes) collected from different regions of Ethiopia and other African countries (Eritrea, Zambia, and Zimbabwe), were obtained from the Ethiopian Institute of Biodiversity (Table 3.1.). These genotypes span altitudes from 1000 to 2380 m.a.s.l, representing Ethiopia's agro-ecological zones for finger millet cultivation. Two improved varieties, Mereb-1 and Tekeze-1 released from Aksum and Maitsebri agricultural research centers, were used as checks to evaluate the qualitative traits in the accessions..

Table 3.1. Number of finger millet genotypes collected from different African countries/regions and altitudinal classes.

No	**Country**		**Altitude class (m.a.s.l.)**			
		Region	**≤1500**	**1501-2000**	**≥2001**	**# of genotypes**
1	Ethiopia	Tigray	2	30	19	**51**
2	Ethiopia	Oromiya	2	9	10	**21**
3	Ethiopia	Amara	2	16	7	**25**
4	Ethiopia	Benishangul Gumuz	2	3	0	**5**
	Total		8	58	36	**102**
5	Eritrea		0	30	0	**30**
6	Zambia		11	8	0	**19**
7	Zimbabwe		49	0	0	**49**
	Sub-total		**68**	**96**	**36**	**200**
	Released varieties		**2**			**2**
	Grand total					**202**

3.2.3. Experimental design and layout

The details of this were described in Chapter Two, Section 2.2.4.

3.2.4. Data collection

Data on five qualitative traits (ear shape, finger branching, seed color, glume color, and pericarp persistence) were collected from 5 randomly selected individual plants per genotype (Table 3.2). The traits were assessed according to the International Plant Genetic Resources Institute (IPBGR, 1985) descriptor list for finger millet. Besides, color chart and visual examination using a 10× magnifying lens were used (Munsell, 1970).

Table 3.2. Phenotypic classes of the qualitative characters used for diversity study

Traits	No. of class	Code	classes
Ear shape	5	1	droopy
		2	Open
		3	Semi-compact
		4	Compact
		5	Fist-like
Finger branching	2	1	Present
		2	absent
Seed color	5	1	Black
		2	Red
		3	White
		4	Brown
		5	Orange
Glume (Ear) color:	4	1	Yellow-green
		2	Light-green
		3	Purple
		4	White
Pericarp persistent	3	1	Persistent
		2	Partially persistent
		3	Not persistent

The collection sites for each of the 200 genotypes, along with the two check varieties, were classified into the major agro-ecological zones of Ethiopia based on altitude. Of these, 70 genotypes, including the check varieties, were collected from areas at or below 1500 m.a.s.l., classified as lowland; 96 genotypes were from altitudes between 1501-2000 m.a.s.l., categorized as intermediate; and 36 genotypes were originally collected from 2001 m.a.s.l. and above, classified as highland. According to Ayana and Bekele (1998), the highland zones are mainly characterized by fertile soils and dense populations, the intermediate zones have good agricultural potential often with mixed farming systems, while the lowland zones tend to be more arid often facing challenges like drought.

3.2.5. Statistical analysis

The genotypes were stratified by country of origin, region, and altitudinal class. Trait frequency percentages were calculated using SPSS software packages v 20 (SPSS, Chicago, IL, USA), and chi-square tests were carried out using MINITAB software version 19 to test deviations from expected values. The Shannon-Weaver diversity index (H') was estimated and used to measure the phenotypic diversity among the genotypes for the studied traits. The index (H') was estimated on the frequency data as described by Hutcheson (1970) as follows:

$$\mathrm{H}' = -\sum_{\mathrm{i}=1}^{\mathrm{n}} \frac{\boldsymbol{pi}\ \mathbf{ln}\ \boldsymbol{pi}}{\mathbf{ln}\ \boldsymbol{n}}$$

Where ***n*** is the number of phenotypic classes for a character and ***Pi*** is the proportion of total entries (N) in the i^{th} class.

Descriptive statistics (**mean and standard error**) were estimated using PAST software, a one-way ANOVA tested differences in H’ across classifications (Table 3.2). The chi-square analysis was carried out to test deviations from the overall mean for countries of origin, regions, and altitude classes.

3.3. RESULTS

3.3.1. Frequency distribution of qualitative traits by country

The variation in pericarp persistence revealed the predominance of non-persistent types in genotypes collected from all countries, except Zimbabwe, which recorded higher frequency of partially persistent seeds (43%). Across regions in Ethiopia, no persistent type was observed in samples from Benishangul Gumuz (Table 3.4). The open type ear shape was predominant across all countries, with Ethiopia showing the highest frequency at 54%, followed by Eritrea (47%), Zimbabwe (36%), and Zambia (35%). In Ethiopia, droopy and semi-compact ear shapes were also common, while the fist-like ear shape was rare in Ethiopian (3%) and Zambian (7%) samples. This type was not observed in Eritrea, and droopy was the least frequent in Zimbabwe (Table 3.3).

Finger branching was observed in two phenotypic classes (present and absent) across all countries with minor proportional differences. For this trait, Zambia and Ethiopia exhibited slightly higher frequencies of the present type, which accounted for 55% and 51%, respectively, while Eritrea and Zimbabwe were dominated by the absent type (Table 3.3). The four phenotypic classes of ear (glume) color were observed in all countries, with purple being the most frequent, followed by white, except in Zimbabwe, where yellow-green was the most dominant. Eritrea and Zambia had the highest frequencies of purple glumes (42%), while light-green was least frequent color in all countries of origin (Table 3.3). A high proportion of black-seeded finger millet genotypes was observed in Eritrea (54%) and Ethiopia (46%). In Zambia, both black- and red-seeded were equally dominant at 32%, followed by orange seed type. In contrast, Zimbabwe’s genotypes were predominantly red-seeded (43%), followed by orange (30%) and Black (19%).

Table 3.3. Percentage distribution of five major qualitative traits among 200 genotypes collected from African countries, four Ethiopian finger millet-producing regional states, and two standard check varieties.

Country	No.	Pericarp persistence			Glumes color				Seed Color				
		P	PAP	NP	YG	LG	PP	WT	BK	RD	WT	BN	OG
Ethiopia	104	11	37	52	21	12	40	27	46	28	10	6	10
Eritrea	30	19	31	50	18	8	42	32	54	35	2	2	7
Zambia	19	23	33	44	13	4	42	41	32	32	12	0	24
Zimbabwe	49	24	43	33	29	12	34	25	19	43	4	4	30
Total	202	16	38	46	22	11	39	28	39	33	8	4	16

Country		Finger branch		Ear Shape				
	No	PT	AB	DR	OP	SM	CM	FL
Ethiopia	104	51	49	21	54	15	7	3
Eritrea	30	49	51	23	47	23	7	0
Zambia	19	55	45	19	35	18	21	7
Zimbabwe	49	48	52	10	36	17	24	14
Total	202	50	50	18	47	17	12	6

P = persistent, PAP = partially persistent, NP =not persistent, YG = yellow green, LG = light- green, PP = purple, WT = white, BK =black, RD = red, BN = brown, OG = orange, PT = present, AB = absent, DR = droopy, OP = open, SM =semi-compact, CM = compact, FL = fist-like

Table 3.4. Percentage distribution of five major qualitative traits among 200 genotypes collected from four Ethiopian finger millet producing regional states and two standard check varieties.

Region/Ethiopia	No.	Pericarp persistence			Glumes color				Seed Color				
		P	PAP	NP	YG	LG	PP	WT	BK	RD	WT	BN	OG
Amara regional state	25	11	43	46	24	10	46	20	50	31	11	2	6
Benishangul gumuz regional state	5	0	44	56	28	16	36	20	52	24	12	4	8
Oromiya regional state	21	18	35	47	12	11	45	32	35	34	19	6	6
Tigray regional state	53	8	35	57	22	13	36	29	48	24	6	9	13

total	104	11	38	52	21	12	40	27	46	28	10	6	10

	No.	**Finger branch**		**Ear Shape**				
Region/Ethiopia		**PT**	**AB**	**DR**	**OP**	**SM**	**CM**	**FL**
Amara regional state	25	56	44	16	54	17	9	4
Benishangul gumuz regional state	5	60	40	16	48	20	16	0
Oromiya regional state	21	53	47	7	46	25	15	7
Tigray regional state	53	46	54	30	58	9	2	1
total	104	51	49	22	54	15	6	3

Table 3.5. Percentage proportion of five major qualitative traits among 200 finger millet genotypes and two standard checks across three altitude classes.

		Pericarp persistence			**Glumes color**				**Seed Color**				
Altitude	**No.**	**P**	**PAP**	**NP**	**YG**	**LG**	**PP**	**WT**	**BK**	**RD**	**WT**	**BN**	**OG**
≤1500	70	23	40	37	25	9	36	30	23	40	6	3	28
1501-2000	96	13	36	51	19	11	41	29	48	30	8	5	9
≥2001	36	12	35	53	22	14	40	24	48	27	11	6	9
Total	202	16	37	46	22	11	39	29	39	33	8	5	16

		Finger Branching		Ear Shape				
Altitude	No	**PT**	**AB**	DR	**OP**	**SM**	**CM**	**FL**
≤1500	70	51	49	13	43	14	20	10
1501-2000	96	48	52	22	44	20	10	4
≥2001	36	54	46	21	62	12	5	0
Total	202	50	50	18	47	17	12	6

P = persistent, PAP = partially persistent, NP =not persistent, YG = yellow green, LG = light- green, PP = purple, WT = white, BK =black, RD = red, BN = brown, OG = orange,

PT = present, AB = absent, DR = droopy, OP = open, SM =semi-compact, CM = compact, FL = fist-like

All five seed color types were recorded in samples from all countries, except for brown seed color, which was absent in the Zambia collections (Table 3.3). The chi-square test showed significant ($p \leq 0.05$), highly significant ($p \leq 0.01$), and non-significant deviations for the five qualitative traits among countries compared to expectations (Table 3.6).

The observed and expected frequencies for finger branching across all countries were similar, with no significant deviations. In contrast, highly significant deviations were observed for seed pericarp persistence, glume color, seed color, and ear shape in Ethiopia and Eritrea. In Zambia, a high deviation was observed only for glume and seed color traits. In contrast, finger branching and ear shape did not exhibit significant deviations from expectations in Zimbabwe.

3.3.2. Regional Distribution of Traits

Table 3.4 presents the regional frequency distributions of five traits. Regionally, the most notable result for pericarp persistence was to the predominance of non-persistent types across all regions, followed by partially persistent types. Persistent types were generally less frequent across regions, with none observed in Benishangul Gumuz region. The distribution of glume color showed proportionate patterns throughout regions, with 12 out of 25 (46%) in Amhara, 10 out of 21 (45%) in Oromiya, 2 out of 5 (36%) in Benishangul Gumuz, and 19 out of 53 (36%) in Tigray having mostly purple glumes.The pattern of seed color in the regions was similar with the countries of origin, with black-seeded types being more frequent, followed by red seed types; while brown seed type was less frequent. The predominant phenotypic classes for finger branching and ear shape were largely observed in most regions, except for Tigray, where the open type was more common. The chi-square test showed significant regional differences in seed pericarp persistence and seed color, while Tigray and Amara regions showed highly significant differences in ear shape (Table 3.6).

3.3.3. Altitudinal Distribution of Traits

Among the 202 genotypes studied (Table 3.5), 28 out of 70 (40%) were classified as partially persistent types at altitudes below 1500 m.a.s.l., with traits such as purple glume (36%), red seeds (40%), finger branching (51%), and open ear shapes (43%). In this altitude class, non-persistent pericarp, white glumes, black seeds, and compact ear shapes were also observed. For the 96 genotypes collected from altitudes between 1501 and 2000 m.a.s.l., notable traits included non-persistent pericarp (51%), purple glumes (41%), black seeds (48%), absence of finger branching (52%), and open ear shapes (44%). The remaining 36 genotypes from altitudes of ≥2001 m.a.s.l. showed non-persistent pericarp (53%), purple glumes (40%), black seeds (48%), open ear shapes (62%), and finger branching (54%). The study noted that purple glumes and open ear shapes were consistent across altitudinal ranges, with higher dominance of purple glumes in the intermediate range and an increasing trend of open ear shapes with altitude (Table 3.5). Significant differences were found for all traits except finger branching (Table 3.6).

Table 3.6. Chi-square values for five qualitative traits across different countries, regions and altitude ranges.

	Qualitative traits				
	PP	**GC**	**SC**	**FB**	**ES**
country	x^2	x^2	x^2	x^2	x^2
Ethiopia	137.40**	85.98**	293.3**	0.069ns	30.53**
Eritrea	20.52**	40.56**	166.8**	0.027ns	15.36**
Zambia	6.34*	43.15**	35.16**	0.85ns	3.8*
Zimbabwe	13.53**	27.34**	136.65**	0.33ns	1.18ns
x^2	38.93**	27.2**	137.81**	1.26ns	7.53ns
region					
Amara	27.66**	34.00**	104.56**	1.8ns	8.71**
Benishangul	13.04**	2.36ns	18.8**	1ns	1.96ns
Oromia	13.03**	32.56**	44.38**	0.47ns	1.61ns
Tigray	93.11**	29.99**	150.38**	1.66ns	20.11**
x^2	14.24*	12.45*	25.70**	4.86ns	1.98ns
altitude					
≤1500	17.90**	56.08**	163.29**	0.29ns	7.73**
1501-2000	103.09**	98.28**	334.52**	1.01ns	23.41**
≥2001	47.1**	27.2**	110.44**	1.42ns	15.02**
x^2	26.45**	10.02NS	103.09**	2.7ns	2.6ns

a) PP = Pericarp persistence, GC = Ear (glumes) color, SC = Seed color, FB = finger branching, ES = Ear shape,

b) * Significant at 5 % level; ** significant at 1 % level; otherwise n.s, non-significant; x^2, chi-square

3.3.4. Shannon-Weaver diversity index (H') analysis

The Shannon-Weaver diversity index (H’) analysis revealed notable variations in diversity among the countries of collection. The highest diversity for seed pericarp persistence was observed in

Zimbabwe and Zambia (0.98), while the lowest was in Ethiopia (0.86), with an overall mean of 0.94. Glume color diversity was high across all countries of origin, though Zambia showed a relatively lower diversity estimate (0.82) compared to Zimbabwe (0.96), Ethiopia (0.94), and Eritrea (0.90). Genotypes collected from the studied countries demonstrated larger phenotypic diversity for seed color and ear shape (Table 3.7), with moderate differences between countries. Zambian had the highest diversity for both seed color (0.97) and ear shape (0.95), while Eritrea and Ethiopia demonstrated lower diversity indices (0.65 for SC and 0.77 for ES, respectively). Besides, Ethiopian and Zimbabwean genotypes exhibited intermediate diversity for seed color (Table 3.7). In contrast, the diversity for finger branching was low across all countries, likely due to the balanced proportions of phenotype classes for this trait. However, a high diversity index for ear shape (0.77 – 0.94) was calculated in all countries (Table 3.7).

Within Ethiopia, relatively high H’ values were observed for all traits across regions. Pericarp persistence had H’ values ranged from 0.82 in Tigray to 0.99 in Benishangul Gumuz. The highest H' values across regions were recorded for glume color and ear shape. Similar to the country-level analysis, finger branching showed low H' across all regions. According to Table 3.8, the pooled H' values across traits ranged from 0.85 for seed color to 0.94 for glumes color across countries, and from 0.78 for ear shape to 0.95 for glumes color across regions. This indicates a rich phenotypic variation in genotypes from various countries, regions, and altitudes, with H' values generally exceeding 0.78 across all traits.

Table 3 7. Estimation of Shannon-Weaver diversity indices (H') and standard error of mean (± SE) for five qualitative traits in finger millet genotypes categorized by countries of origin, regions, and altitude ranges.

	Qualitative traits					
Country	**PP**	**GC**	**SC**	**FB**	**ES**	**Mean±SD**
Ethiopia	0.86	0.94	0.84	0.69	0.77	0.85±0.04
Eritrea	0.94	0.90	0.65	0.70	0.88	0.84±0.05
Zambia	0.98	0.82	0.97	0.69	0.95	0.90±0.05
Zimbabwe	0.98	0.96	0.81	0.69	0.94	0.89±0.05
Mean	0.94	0.91	0.82	0.69	0.89	
	Qualitative traits					
Region/Ethiopia	**PP**	**GC**	**SC**	**FB**	**ES**	**Mean±SD**
Amara regional state	0.89	0.91	0.74	0.69	0.80	0.84±0.05
Benishangul gumuz regional state	0.99	0.99	0.84	0.69	0.95	0.88±0.05
Oromiya regional state	0.95	0.90	0.87	0.70	0.86	0.85±0.04
Tigray regional state	0.82	0.96	0.84	0.69	0.63	0.82±0.06
Mean	0.91	0.95	0.82	0.69	0.81	
	Qualitative traits					
altitude	**PP**	**GC**	**SC**	**FB**	**ES**	Mean±SD
≤1500	0.98	0.93	0.84	0.69	0.91	0.89±0.05
1501-2000	0.89	0.93	0.80	0.69	0.86	0.86±0.05
≥2001	0.87	0.95	0.83	0.69	0.75	0.84±0.04
Mean	0.89	0.94	0.82	0.69	0.84	

PP = Pericarp persistence, GC = Ear (glumes) color, SC = Seed color, FB = finger branching, ES = ear shape

Table 3.8. Estimation of mean Shannon-Weaver diversity indices (H') and standard error of mean (± SE) of the 5 qualitative traits of finger millet collections pooled over countries, regions and altitude.

Pooled data	**PP**	**GC**	**SC**	**FB**	**ES**	**Mean±SD**
country	0.93	0.94	0.85	0.92	0.87	0.90±0.02
altitude	0.93	0.94	0.85	0.86	0.87	0.89±0.02
region	0.87	0.95	0.85	0.91	0.78	0.87±0.03

3.3.5. Analysis of diversity

The one-way analysis of variance (ANOVA) for the non-normalized diversity index (H) of individual qualitative traits is presented in Table 3.9. Seed pericarp persistent and seed color were the only traits that revealed significant (P≤0.05) and highly significant (P≤0.01) differences between countries, respectively. However, the other traits revealed no significant differences across countries.

Table 3.9 Mean squares for variations across country, region and altitude classes from the one-way ANOVA of the diversity index (H')′ for individual traits.

	Between			**Between genotypes within**		
Traits	Country (df =3)	Region (df =3)	Altitude (df =2)	Country (df =198)	Region (df =198)	Altitude (df =199)
PP	0.003*	0.006	0.003	0.048*	0.051*	0.048*
GC	0.004	0.003	0.000	0.065*	0.059*	0.065*
SC	0.017**	0.003*	0.000	0.074*	0.087*	0.074*
FB	0.000	0.000	0.000	0.072*	0.025*	0.072*
ES	0.001	0.000	0.001	0.093*	0.057*	0.093*

***** significant at 0.05******significant at 0.01, df = degree of freedom

PP = Pericarp persistence, GC = Ear (glumes) color, SC = Seed color, FB = finger branching, ES = ear shape

As interpreted above, traits with a high diversity index (H') value offer ample opportunities for genetic improvement of finger millet through exploitation of these traits in breeding improvement.

Finger millet genotypes across various altitude ranges displayed high mean Shannon diversity (H') values for pericarp persistence (H' = 0.98) and glume color (H' = 0.95), while lower diversities were observed for finger branching (H' = 0.69) and seed color (H' = 0.80). There was a noticeable decrease in polymorphism for pericarp persistence and ear shape with increasing altitude, with H' values dropping from 0.98 to 0.87 and from 0.91 to 0.75, respectively, between lower altitudes (≤1500 m.a.s.l) and higher altitudes (≥2001 m.a.s.l) (Table 3.7). Genotypes from altitudes above 2001 m.a.s.l. exhibited higher diversity for glume color (H' = 0.95), while higher H' values for seed color (H' = 0.84) and ear shape (H' = 0.91) were more prevalent at lower altitudes ≤1500 m.a.s.l (Table 3.7). Seed color diversity was lower at altitudes between 1501-2000 m.a.s.l. In contrast, finger branching (H' = 0.69) showed consistent diversity across all altitude ranges, indicating this trait is relatively unaffected by altitude changes.

3.4. DISCUSSION

3.4.1 Distributions of Finger Millet Qualitative Traits across Countries, Regions in Ethiopia, and Attitude Ranges

Finger millet's adaptability to a wide range of agro-ecological zones enables it to be cultivated in different African countries and by farmers across a wide range of altitudinals. In the present study, the 202 African finger millet genotypes, including the check varieties (merb-1 and Tekeze-1), showed high diversity for seed pericarp persistence after harvesting. Genotypes with non-persistent seed pericarp were more abundant across the countries of origin and regions, except in Zimbabwe, where partially persistent types were more dominant. In terms of altitude, genotypes collected from lowland areas (≤1500 m.a.s.l.) were dominated by partially persistent seed pericarp, while those collected from altitudes between 1501-2000m.a.s.l and ≥ 2001m.a.s.l. were mostly characterized by intermediate, non-persistent seed pericarp types (Tables 3.3, 3.4, and 3.5). This pattern suggests that farmers prefer non-persistent finger millet genotypes, as these genotypes are easier to thresh compared to those with persistent seed pericarp, which are more challenging due to tightly bound seed coats (Tsehay and Kebebew, 2002; Yemane, 2016). Likewise, Kumar et al. (2019) reported that non-persistent types were dominant in finger millet germplasm collected from Uttrakhand Hills, constituting (76.08 %) of the total population. In contrast, Bezaweletaw et al. (2007) found persistent pericarp types predominating (91%) in the Tigray region. The same study showed that the partially persistence seed type dominate in most finger millet growing regions of Ethiopia with the non-persistence type was common in sampled from Gojam, Welega and Gamo Gofa. The widespread presence of non-persistent types in this study could potentially help in the development varieties with improved threshability and processing ease. Genotypes collected from regions such as Benishangul Gumuz and Tigray in Ethiopia, and from Eritrea, could be considered enter of concentration for this trait.

Finger branching, an important yield-related trait (Malambane and Jaisil, 2015; Dasanayake, 2017; Kumar et al., 2019; Benkaddour, 2023), showed varying frequencies across countries of origin. In Ethiopia and Zambia, genotypes with branching type were more common, while in Eritrea and Zimbabwe, non-branching types predominated. Regionally, genotypes collected from Amara, Benishangul Gumuz, and Oromia were more likely to be branching, while those from Tigray were mostly non-branching type. Despite some studies, such as Dasanayaka and Kaluthanthri (2017), who found lack of significant variability for branching in 42 finger millet genotypes, the phenotypic variation observed in this study presents a promising opportunity for finger millet breeders to develop high-yielding varieties by selecting for branching traits in larger populations.

Seed color variation was depicted among the 202 genotypes collected from different altitudinal ranges and African countries (Tables 3.3, 3.4, and 3.5). Overall, black was the dominant seed color (39%), followed by red (33%) and orange (16%), while white (8%) and brown (4%) colors were less infrequent. All types of seed colors appeared across all countries, regions, and altitudes, although brown seed color was absent in Zambian collections (Table 3.3). In Ethiopia, brown seed color followed by orange color was rare compared to the other colors, with similar frequency trend observed across altitude ranges (Table 3.4). Bezaweletaw et al. (2007) also reported the rarity of white colored seeds in Welega finger millet collections. On the other hand, Malambane and Jaisil (2015) reported the dominancy of brown seed color in their finger millet collections. The differences in seed color might be related to the yielding potential of the genotypes, with dark-colored (black) varieties often being more resilient to climate change and higher-yielding (Bezaweletaw et al., 2007; Reddy et al., 2009). Seed color also affects the market value, as black-seeded varieties typically fetch higher market prices than white or red varieties (Kebede et al., 2019). Seed color is one of the most important trait for quality and market acceptance, with farmers often using seed color for variety identification and even associating it with palatability, with lighter colors believed to be more palatable than darker ones (Malambane and Jaisil, 2015). The abundance of black and red seeds might reflect farmers' preference for these types, as black grain is used to make local drinks (e.g., 'Siwa', 'Tella', and 'Ferso' in Tigrigna, Amharic, and Afan Oromo languages, respectively) while red seeds are mainly preferred for making the local flat bread (injera), though both require fertile, well-drained soil (Yemane et al., 2006).

Finger millet farmers mostly divide their varieties mainly into five phenotypic classes based on ear shape. This trait is also important for differentiating pearl millet varieties (Upadhyaya et al., 2017). The frequency distribution of ear shape indicated that open-shaped panicles were most common across the studied countries. Overall, 47% of the genotypes had open panicles, followed by 18% droopy, 17% semi-compact, 12% compact, and 6% fist-like shapes (Table 3.3), with similar trends obtained across all regions and altitude ranges (Tables 3.4 and 3.5). These results align with Abdi et al. (2002), who reported that about 59% of their sorghum collections were open-panicle types. In addition, Dasanayaka1 and Kaluthanthri (2017) found four ear shape categories in their 42 finger millet study: semi-compact (68.0%), compact (19.0%), open (10.4%), and flat-like (2.6%). Tsehaye and Kebebew (2002) also reported higher frequencies of semi-compact and compact types of finger millets in the Gamogofa, Illubabor, and Welega regions of Ethiopia. Overall, the present study suggests that countries, regions, and altitude ranges with better distribution of phenotypic classes across various traits exhibit better diversity, which is important for improving finger millet varieties.

3.4.2. Estimation diversity

The diverse distribution of finger millet types across different countries, regions, and altitudinal ranges contributes significantly to the phenotypic diversity of finger millet populations. This variation highlights the importance of these areas for *in situ* conservation of finger millet germplasm, representing the genetic diversity of African countries. According to Bezaweletaw et al (2007), the Shannon-Weaver diversity index (H') for seed pericarp persistence ranged from 0.60 to 0.99. Lule et al. (2012) reported the highest diversity for ear shape in Eritrea (H' = 0.485) and the lowest in Zimbabwe (H' = 0.302). The diversity index (H') estimates across the three altitudinal classes showed varying degrees of polymorphism for most traits, indicating a broad range of variation within the genotypes (Derbew et al., 2013).

Qualitative traits are less influenced by environmental factors and tend to show high diversity due to genetic differences, making them important for successfully identifying desirable genotypes. Research by Devaliya et al. (2018) confirmed that genotypic variation exists among finger millet genotypes for qualitative traits, with variation documented across different countries of origin, collection regions, and altitude ranges by various scholars (Abubakar et al., 2019; Kumar et al., 2019; Bezaweletaw et al., 2007; Tsehaye and Kebebew, 2002). Additionally, Lule et al., (2012) reported that the highest diversity index was found at lower altitudes (among farmer varieties), followed by diversity within regions, among regions or countries, and within altitudes, with the least similarity observed among different altitudes. This suggests that intensive genetic collection and *in situ* genetic conservation efforts should focus more at lower altitudes. Furthermore, studies by Lule et al. (2012), Sapkota et al. (2016), and Yadav et al. (2018) emphasize the broad genetic variation observed among finger millet genotypes, highlighting the importance of this diversity for effective collection, conservation, and sustainable improvement of breeding programs. This information is vital for genetic exploitation and further research.

3.4.3. Statistical significance of Traits

The variation in qualitative traits like seed pericarp persistent, glume color, finger branching, and ear shape did not show statistical significance across the collection regions in Ethiopia. However, seed color displayed significant variation between regions, though no significant differences were found across altitude ranges. On the other hand, the real diversity was observed at the genotype level, where statistical differences were observed between genotypes within classification variables (Table 3.9). Previous studies by Bekele (1984), Negassa (1986), and Bechere et al. (1996) on Ethiopian wheat, as well as Tsehaye and Kebebew (2002) on finger millet, Geleta and Labuschagne (2005) on sorghum, Mengistu et al. (2015) on durum wheat, Addisu et al. (2018) on barley, Kefyalew et al. (2000) on tef, and Workeye (2002) on chickpea have all reported high diversity within regions. Across the collection of origin and altitude ranges, all these traits showed highly significant differences ($P < 0.001$) among the farmers' varieties of the aforementioned crops.

3.5 CONCLUSIONS AND RECOMMENDATIONS

3.5.1 Conclusions

Effective use of genetic resources requires an understanding of the diversity and geographic distribution of economically important traits. This study found significant variation in five qualitative traits among 202 finger millet genotypes from various nations and elevations. Common traits observed included black seed color, purple glume color, open ear shape, and non-persistent seed pericarp. In Zambia, both black and red seed colors were equally prevalent, while partially persistent seed pericarp and red seed color were more prevalent in Zimbabwe and lower elevations (≤1500 m.a.s.l.). Genotypes from Eritrea and Zimbabwe lacked finger branching, while those from Ethiopia and Zambia displayed higher frequencies of this trait. Finger branching was more common in all regions except Tigray. The Shannon diversity index proved to be an essential tool for assessing trait diversity among genotypes, especially when taking into account their altitude range and region of origin. The study showed a significant degree of variability in qualitative traits such as ear shape, glume color, seed color, and seed pericarp persistence, emphasizing the importance of conserving the genetic diversity of these traits in their natural habitats for future breeding initiatives and environmental adaptation. Qualitative traits, therefore, serve as valuable criteria for characterizing germplasm genotypes and can potentially be used as a marker in the selection process if correlated with yield components.

3.5.2. Recommendations

The genetic variation observed in African finger millet genotypes offers significant opportunities for selecting and developing varieties suitable for Tigray's diverse agro-climatic conditions. The findings of the study underscore the importance of the diversity found in traits such as seed pericarp persistence, glume color, seed color, ear shape, and grain number, particularly among samples from Ethiopia and Eritrea. This diversity indicates the crop's potential for adaptation and resilience to environmental challenges, highlighting its importance for future breeding and adaptation strategies.

3.6. REFERENCE

Abdi, A., Bekele, E., Asfaw, Z., & Teshome, A. (2002). Patterns of morphological variation of sorghum (*Sorghum bicolor (* L .) Moench) landraces in qualitative characters in North Shewa and South Welo , Ethiopia. *Hereditas, 172*; 161–172.

Abubakar, A., Falusi, O. A., Adebola, M. O., & Daudu, O. A. Y. (2019). Genetic diversity studies for morphological traits in pearl millet (Pennisetum glaucum L.) landraces of Northern Nigeria. *GSC Biological and Pharmaceutical Sciences, 7*(2); 060–070.

Addisu, F., Fantahun, W., & Shumet, T. (2018). Qualitative traits variation in barley (Hordeum vulgare L.) landraces from the Southern highlands of Ethiopia. *International Journal of Biodiversity and Conservation, 10*(5); 258–264.

Ayana, A., & Bekele, E. (1998). Geographical patterns of morphological variation in sorghum (Sorghum bicolor (L .) Moench) germplasm from Ethiopia and Eritrea : qualitative characters. *Hereditas*, 129; 195–205.

Babu, B.K.,Senthil, N., Gomez, S.M., Biji,K.R., Rajendraprasad, N.S., Kumar, S.S., and Babu, R.C. 2006. Assessment of genetic diversity among finger millet (Eleusine coracana L. Gaertn) accession using molecular markers. Genetic Research and Crop Evolution 54; 339-404

Bechere, E., Belay, G., Mitiku, D., & Merker, A. (1996). Phenotypic diversity of tetraploid wheat landraces from northern and north-central regions of Ethiopia. *Hereditas*, *124*(2); 165–172.

Bekele, E. (1984). Analysis of regional patterns of phenotypic diversity in the Ethiopian tetraploid and hexaploid wheats. *Hereditas, 100*, 131–154.

Benkaddour, R. (2023). *Characterization of Some Turkish Faba Bean (Vicia faba L.) Genotypes for Agro- morphological Traits*. *7*(1); 116–134.

Bezaweletaw, K., Sripichitt, P., Wongyai, W., & Hongtrakul, V. (2007). Phenotypic diversity of Ethiopian finger millet [Eleusine coracana (L.) Gaertn] in relation to geographical regions as an aid to germplasm collection and conservation strategy. *Kasetsart Journal - Natural Science*, *41*(1); 7–16.

Brhane, H., Haileselassie, T., Tesfaye, K., Ortiz, R., Hammenhag, C., Abreha, K. B., & Geleta, M. (2022). Novel GBS-Based SNP Markers for Finger Millet and Their Use in Genetic Diversity Analyses. *Frontiers in Genetics*, *13*; 1-17

Dasanayaka1, *P. N., & Kaluthanthri, D. V. S. (2017). Genetic Variability Characterization Of Some Ex Situ Conserved Finger Millet (Eleusine Coracana (L.) Gaertn. Subsp. Coracana) Germplasm Accessions In Sri Lankausing Qualitative Morphological Markers. *International Journal of Advanced Research (IJAR)*, *5*(5); 1381–1389.

Dasanayake, P. N. (2017). Characterization of Some ex situ Conserved Finger Millet (Eleusine coracana (L.)) Germplasm Accessions in Sri Lanka. *International Journal of Multidisciplinary Studies*, *3*(2); 141.

Derbew, S., Mohammed, H., & Urage, E. (2013). Phenotypic Diversity for Qualitative Characters of Barley (Hordeum Vulgare (L .)) Landrace Collections from Southern Ethiopia. *International Journal of Science and Research (IJSR)*, *2*(9); 34–40.

Devaliya, S. D., Singh, M., Intawala, C. G., & Bhagora, R. N. (2018). Genetic Variability Studies in Finger Millet (Eleusine coracana (L .) Gaertn . *Int. J. Pure App. Biosci.*, *6*(1); 1007–1011.

Dida, M. M., Wanyera, N., Harrison Dunn, M. L., Bennetzen, J. L., & Devos, K. M. (2008). Population Structure and Diversity in Finger Millet (Eleusine coracana) Germplasm. *Genetic Resources and Crop Evolution*, *1*(2); 131–141.

Geleta, N., & Labuschagne, M. T. (2005). Qualitative traits variation in sorghum (Sorghum bicolor (L .) Moench) germplasm from eastern highlands of Ethiopia. *Biodiversity and Conservation*, *14*; 3055–3064.

Hutcheson, K. (1970). A test for comparing diversities based on the shannon formula. *Journal of Theoretical Biology*, *29*(1); 151–154.

IPBGR. (1985). *Descriptors for finger millet* (p. 20).

Kebede, D., Dangnachew, L., Megersa, D., Chemeda, B., Girma1, M., Geleta, G., Gudeta, B., & Bako. (2019). Genotype by Environment Interaction and Grain Yield Stability of Ethiopian Black Seeded Finger millet Genotypes. *African Crop Science Journal*, *27*(2); 281–294.

Kefyalew, T., H. Tefera, K. Assefa and M. Ayele. 2000. Phenotypic diversity for qualitative and phenological characters in germplasm collection of tef (Eragrostis tef). *Genet. Resou. Crop Evol.* 47; 73-80.

Kumar, A., Chawla, H. S., Jeena, A. S., & hit, R. (2019). Morphological Characterization of Finger Millet Germplasm Collected from Uttrakhand Hills for Qualitative Traits. *International Journal of Current Microbiology and Applied Sciences*, *8*(09); 2105–2109.

Lule, D., Tesfaye, K., Fetene, M., & de Villiers, S. (2012). Inheritance and Association of Quantitative Traits in Finger Millet (Eleusine coracana Subsp. Coracana) Landraces Collected from Eastern and South Eastern Africa. *International Journal of Genetics*, *2*(2); 12–21.

Malambane, G., & Jaisil, P. (2015). Morphological variability for qualitative and quantitative traits in finger millet (Eleusine coracana L. Gaertn). *Journal of Advances in Agriculture*, *5*(1); 528–537.

Mengistu, D.K., Kiros, A.Y. & Pè, M. E. (2015). Phenotypic diversity in Ethiopian durum wheat (Triticum turgidum var. durum) landraces. The Crop Journal, 3 (3); 190-199.

Munsell. (1970). *The Munsell Book of Colour: Matte Collection*; 1–48.

Negassa, M. (1986). Patterns of Diversity of Ethiopian Wheats (Triticum spp.) and a Gene Center for Quality Breeding. *Plant Breeding*. 97; 147-162

Reddy, V.G., Upadhyaya, H.D., Godwa, C.L.L, Singh, S.(2009). Characterization of eastern African finger millet germplasm for qualitative and quantitative characters at ICRISAT.SAT *e Journal,*7(1); 1-9.

Sapkota, M., Pandey, M. P., Thapa, D. B., Yadav, M. K., & Ghimire, S. (2016). Diversity Assessment Of Foxtail Millet (Setaria Italica L . Beauv) Accessions Collected From Different Locations Of Nepal. *Int J Appl Sci Biotechnol (IJASBT), 4*(4); 483–488.

Tesfaye, K., & Mengistu, S. (2017). Phenotypic characterization of Ethiopian finger millet accessions (Eleusine coracana (L.) Gaertn), for their agronomically important traits. *Acta Universitatis Sapientiae, Agriculture and Environment*, *9*(1); 107–118.

Tsehaye, Y., & Kebebew, F. (2002). Morphological diversity and geographic distribution of adaptive traits in finger millet [Poaceae]) populations from Ethiopia. *Ethiopian Journal of Biological Sciences, 1*; 37–62.

Wolie A. and Dessalegn. T. 2011. Correlation and path coefficient analyses of some yield related traits in finger millet (Eleusine analyses of some yield related traits in finger millet (Eleusine coracana coracana (L.)Gaertn.) germplasms in northwest Ethiopia. (L.)Gaertn.) germplasms in northwest Ethiopia. African Journal of Agricultural Research 6(22); 5099-5105

Upadhyaya, H.D., Gowda, C.L.L., Pundir, R.P.S., Reddy,V.G., Singh, S. (2004). Development of core subset of finger millet germplasm using geographical origin and data on 14 quantitative traits. *Genetic Resource and Crop Evolution*, 53; 679-685.

Upadhyaya, Reddy K. N, M, I. A., Kumar, V., . M. K. G., Ramachandran, S., & Received: (2017). Geographical distribution of traits and diversity in the world collection of pearl millet [Pennisetum glaucum (L .) R . Br ., synonym : Cenchrus americanus (L .) Morrone] landraces conserved at the ICRISAT genebank. *Genetic Resources and Crop Evolution*, *64*(6); 1365–1381.

Workeye, F. 2002. Morphological and Biochemical Diversity in Chickpea (Cicer arietinum L.) Landraces of Ethiopia. M.Sc. thesis. Addis Ababa University; Addis Ababa

Yadav, R. K., Adhikari, A. R., Gautam, S. and, Ghimire, K. H., & | R. D. (2018). Diversity sourcing of foxtail millet through diversity assessment and on-farm evaluation. *Cogent Food & Agriculture*, *4*; 1–17.

Yemane, T. (2016). Establishing A Core Collection Of Finger Millet (Eleusine coracana [L .] Gaertn .) Ex Situ Holdings Of The .Ethiopian Genebank. *Journal of the Drylands*, *6*(2), 519–530.

CHAPTER FOUR

Genetic Diversity Assessment for Nutritional Traits of Ex-situ Finger Millet Collections

ABSTRACT

Finger millet plays a vital role in providing dietary and nutritional balance due to its high carbohydrate, energy, and nutrient content. Understanding the existing nutritional genetic diversity within finger millet collections is essential for initiating a successful breeding program. To evaluate and characterize the grain nutrient diversity of 200 finger millet collections from various African countries, an experiment was conducted over two years at three locations using a lattice (10 x 20) design. Statistically significant variations ($P<0.001$) were observed in protein, starch, and mineral contents among the genotypes. Notable differences were found in moisture content (7.9% to 12.4%), protein content (5.2% to 9.3%), calcium (139 to 431 mg/100g), magnesium (120.9 to 525.5 mg/100g), iron (4.06 to 30.68 mg/100g), and zinc (0.11 to 4.89 mg/100g). Correlation analysis revealed that iron (Fe) content was significantly and positively correlated with calcium (Ca), magnesium (Mg), and zinc (Zn) levels. Cluster analysis showed that the majority of genotypes were in cluster-I (73), while the fewest were in cluster-V (8). Magnesium (Mg), zinc (Zn), calcium (Ca), and moisture content accounted for 40.27% of the variation in the first principal component, while protein, starch, and iron contributed 17.51% to the second principal component. Genotypes 203574, 234160, 203259, 203262, and 203257 had higher protein, calcium, magnesium, iron, and zinc contents, respectively. Notably, all these high-ranking genotypes for nutrients, except one from Zimbabwe, were sourced from Ethiopia. The relationship between grain nutrient contents and geographical origin provides valuable insights for designing strategies to plan and collect nutrient-specific genotypes. Based on these findings, it is recommended to either use the identified genotypes with high nutritional compositions directly for cultivation or as parental lines in further hybridization programs to enhance finger millet.

Key words: finger millet, nutritional variability, PCA, and Seed Color

4.1. INTRODUCTION

Finger millet (*Eleusine coracana* (L.) Gaertn) is a stable food crop in arid and semi-arid parts of the world, valued for its exceptional nutritional content. including protein, calcium, magnesium, and iron (Luitel et al., 2020). It is a vital sources of energy, protein, fatty acids, minerals, vitamins, dietary fibre, and polyphenols (Amadou et al., 2013). In Africa, malnutrition caused by deficiencies in iron (Fe), zinc (Zn), and protein is a serious problem for pregnant women, lactating mothers, and pre-school children. Finger millet plays a significant role in alleviating this problem through its inclusion in balance diets (Upadhyaya et al., 2011; Pandian et al., 2017). Known for its drought resistant, finger millet is widely cultivated in the semi-arid tropics of Africa and Asia, contributing to food security and offering health benefits such as strengthening bones and teeth (Belay, 2023). Its nutritional richness has garnered increasing interest from food scientists, technologists, and nutritionists (Saleh et al., 2013). Finger millet is a rich source of mineral, vitamins, protein, and carbohydrates, important for human and animal consumption (Fred et al., 2021). Finger millet is primarily grown for its grain, used in traditional foods like '*Injera*' and local drinks, while its stalks are used for livestock feed and construction (Gebreyohannes et al., 2021)

Finger millet is one of the staple food cereal crops in the drought-prone areas of Ethiopia in general, and the Tigray region in particular, although it is considered relatively as a minor crop in the country (CSA, 2018). Its cultivation is mainly concentrated in lowland and mid-altitude areas, with occasional cultivation in some parts of the highlands for making the local drink known as '*Siwa*". Ethiopia is believed to be one of the centers of origin for finger millet, thanks to its wide range of altitudes, temperature extremes, rainfall, and different soil characteristics (Gebreyohannes et al., 2021).

Finger millet has calcium content 10-fold higher than all other cereals, seven times higher than rice, and even three times higher than milk (Das et al., 2017; Maharajan & Ceasar, 2022). It also contains the highest levels of calcium (344 mg %) and potassium (408 mg %) among all grains and millets (Vagdevi et al., 2023). It is a third important crop in north western and central part of Tigray following sorghum and teff (Hailegebrial et al., 2017) Despite its nutritional value, the consumption of finger millet in Ethiopia in general, and Tigray in particular, very low, with most of it used generating cash income (Gebreyohannes et al., 2021). In addition to its nutritional benefits, finger millet has health-promoting properties, such as anti-diabetic, anti-tumerogenic, atherosclerogenic, antioxidant, and antimicrobial effects (Devi et al., 2011), and it plays a vital role in wound healing, lowering blood sugar and cholesterol levels (Vagdevi et al., 2023). However, regardless of these benefits, the crop has not been prioritized for further genetic improvement and extensive utilization by breeders, researchers, and healthcare professionals in Ethiopia. Therefore, the current study was intended to evaluate and characterize the nutritional diversity of finger millet genotypes collected from different African countries, providing insights for breeders to exploit its genetic potential for nutritional and health benefits.

4.1.1. Objectives

⇒ To assess the genetic variability present within African finger millet collections, focusing on nutritional traits.

⇒ To identify specific genotypes with exceptional nutritional traits valuable for breeding programs or cultivation.

⇒ To provide guidance for future breeding programs to enhance nutritional traits in finger millet through targeted selection and breeding.

4.2. MATERIAL AND METHODS

4.2.1. Plant Material

The study used 200 genotypes obtained from the Ethiopia Institute of Biodiversity, evaluated during the 2019 and 2020 growing seasons.

4.2.2. Experimental Site and Design

The genotypes were planted at Maiaini, Zana, and Rama during the 2019 and 2020 growing seasons. These sites were selected for their potential for finger millet cultivation and their suitability for evaluating and characterizing both finger millet and other cereal crops like sorghum (Yemane et al., 2006). The geographic coordinates for Maiaini, Zana, and Rama are 14°16'N 38°12'E, 14°16'N 38°37'E and 14°22'N 38°48'E, respectively. The mean annual temperatures during the growing seasons ranged from 18.6°C to 32.1°C at Maiaini, 19.5°C to 32.7°C at Zana, and 10.6°C to 23.1°Cat Rama in 2019. In 2020, Maiaini, Zana, and Rama experienced mean annual temperatures between 12.2°C and 23.9°C, 14.3°C and 33.8°C, and 14.7°C and 34.3°C, respectively. The mean annual rainfall ranged from 1301.0 to 1685.1 mm for Maiaini, 2095.0 to 1482.2 mm for Zana, and 510.1 to 1049.6 mm for Rama during the same periods. The soil type at the experimental sites was verti-cambisol with a pH of 6.2. The study sites are approximately located 1002 km from Addis Ababa, the capital city of Ethiopia.

The genotypes were arranged in an alpha lattice design (10 x 20) with two replications. Each genotype was planted in a two row of 5 meters long, with a row-to-row spacing of 0.75 m and plant spacing of 0.1 m. Seeds were sown at a rate of 11.25 g per plot (15 kg per hectare), seedlings were thinned to maintain the 0.1-meter spacing between plants. A basal application of 46 kg of nitrogen (N) and 100 kg of phosphorus (P) per hectare was made, followed by a top dressing of 50 kg of nitrogen per hectare applied 30 days after sowing (DAS). All experimental plots were kept free of weeds and insect pests.

4.2.3. Grain nutrient determination

The nutrient content in grains was assessed for all genotypes tested across the three sites. Pooled grain samples were collected from each location in clean cloth bags, carefully cleaned to prevent contamination with dust and metal particles, and sent to the nutritional analysis laboratory at Mekelle University. The analysis was performed using a near-infrared spectrophotometer (DA

720), and estimated the nutritional traits such as iron (Fe), zinc (Zn), calcium (Ca), magnesium (Mg), moisture content (%), starch (%), and protein content (%).Each genotype sample (450g) placed in a sample cup was scanned twice with the NIR machine, and the average values were recorded.

4.2.4. Data analysis

The results obtained were reported as mean values ± standard error of mean. Significant tests were done using t-test in IBM-SPSS. Pearson's correlation coefficients were used to assess associations among the parameters. Cluster analysis was conducted on the standardized data using the Ward Linkage method and Squared Euclidean Distance in MINITAB v19. Discriminant analysis (DA) was conducted to validate the groups created by the cluster analysis. Principal component analysis (PCA) was performed using a correlation matrix to define the existing patterns of variation among populations using Past4.0 software.

4.3. RESULTS

4.3.1. Variability in Protein and Starch

Statistically significant (P<0.001) variations were observed in protein, starch, and mineral contents among the 200 finger millet genotypes (Table 4.1). The protein content ranged from 5.15 to 9.33%, with a mean value of 6.43%. The highest protein content was found in genotype 203574 (9.33%), followed by genotypes 203067 (9.00%), 203351 (8.21%), 212694 (8.20%), and 100002 (8.16%). In contrast, genotypes 203358, 234184, 233582, 234195, and 203585 exhibited lower protein content, ranging from 5.15 to 5.47% (Appendix 4.7.2). Starch content showed minimal fluctuation among the studied genotypes, ranged from 72 to 75%, with a mean of 72.99%. A similar trend was observed in moisture content.

Table 4.1: Descriptive statistics for all the nutritional traits of Finger millet genotypes

Variable	MC%.	Prt%	Ca (mg/100g)	Mg (mg/100g)	Zn (mg/100g)	Fe (mg/100g)	Str%
Max	12.42	9.33	431.00	525.50	4.89	30.68	75.00
Min	7.89	5.15	139.00	120.85	0.11	3.40	72.00
Mean	11.20	6.43	247.70	265.61	1.11	7.86	72.99
SE	0.04	0.06	4.88	6.09	0.05	0.37	0.04
SD	0.50	0.79	69.08	86.11	0.77	5.17	0.54
CV	4.47	12.23	27.89	32.42	69.39	65.86	0.75
T-test	0.000	0.000	0.000	0.000	0.000	0.000	0.000

Trait: Ca =calcium; Fe = iron; Mg = magnesium; Zn = zinc; MC = moisture content; Prt =protein content; Str = starch content

The genotype 203574, which had the highest protein content, was sourced from Zimbabwe, while the genotype 203358 from Ethiopia had the lowest protein content. In contrast, genotypes 203343, 234172, and 203250, all from Ethiopia, exhibited high starch content (75%). On the other hand, lower starch content was most commonly observed in the genotypes from Eritrea finger millet genotypes, followed by those from Ethiopia. Zambian genotypes showed a lower frequency of starch content, with Zimbabwean genotypes exhibiting the least frequency of low starch content (Appendix table 4.7.2).

4.3.2. Variabilities for Mineral Elements

Significant variation was observed in all mineral contents across the finger millet genotypes. Calcium (Ca) content varied significantly ($P<0.001$) among genotypes collected from four African countries, with levels ranging from 139 to 431 mg/100g and a mean of 247.70 mg/100g (Table 4.1). Similarly, magnesium ranged from 120.85 to 525.50 mg/100g, zinc from 0.11 to 4.89 mg/100g, and iron from 4.06 to 30.68 mg/100g (Table 4.1). The genotypes with the highest levels of calcium (Ca), magnesium (Mg), zinc (Zn), and iron (Fe) were 234160, 203259, 203257, and 203262, respectively, all sourced from Ethiopia (Appendix 4.7.3-4.7.6). Conversely, genotypes 100002, 208726, 229738, and 230139 showed lower levels of calcium, magnesium, zinc, and iron, respectively. Specifically, genotype 229738 had low magnesium and zinc content, while genotype 203262 consistently demonstrated high levels of magnesium, zinc, and iron. Genotype 203257 also showed high magnesium and zinc contents, and was obtained from Ethiopia. The top 30 and bottom 5 genotypes for calcium, magnesium, zinc, and iron were identified (Appendix Tables 4.7.3-4.7.6).

4.3.3. Association between Variables

Table 4.2 presents the correlation analysis for seven nutritional traits across 200 finger millet genotypes and two check varieties. Protein content showed weak and non-significant negative correlations with all traits. Similarly, starch showed very weak and non-significant correlations with all minerals and protein. Calcium (Ca) exhibited a strong and significant positive correlation with zinc (Zn) content ($r = 0.62$, $P<0.01$). Magnesium demonstrated moderate and significant correlations with zinc ($r = 0.46$, $P<0.05$) and iron ($r = 0.42$, $P<0.05$). Moisture content was positively and significantly associated with calcium ($r = 0.45$, $P<0.05$), magnesium ($r = 0.45$, $P<0.05$), and zinc ($r = 0.55$, $P<0.01$), but had weak associations with iron and starch ($r = 0.13$, $P>0.05$). Iron content had a moderate correlation with zinc content, suggesting that breeding programs focused on enhancing either zinc or iron content could be beneficial for improving finger millet.

Table 4.2. Pearson's correlation coefficients showing pair-wise association among the nutritional traits in Finger millet collections**.**

Variable	**Moisture**	**Protein**	**Calcium (Ca)**	**Magnesium (Mg)**	**Zinc (Zn)**	**Iron (Fe)**
Moisture						
Protein	-0.06					
Calcium (Ca)	0.45*	-0.01				
Magnesium (Mg)	0.45*	-0.20	0.28			
Zinc (Zn)	0.55**	-0.06	0.62**	0.46*		
Iron (Fe)	0.13	-0.31	0.35	0.42*	0.39	
Starch	0.13	-0.26	0.28	0.16	0.23	0.12

**. Correlation is significant at the 0.01 level (2-tailed).

*. Correlation is significant at the 0.05 level (2-tailed).

4.3.4. Cluster Analysis

The cluster analysis grouped the 200 finger millet genotypes and two standard check varieties into six clusters (Table 4.6). A dendrogram was created using Euclidean distances based on protein and mineral content (Table 4.6). The clusters varied in size, with cluster V having the fewest genotypes (8) and cluster I containing the most (73) (Tables 4.3 and 4.6). Cluster I included all 49 Zimbabwean genotypes, along with 20 from Ethiopia and 4 from Zambia. Clusters II and III predominantly comprised genotypes from Ethiopia and Eritrea, respectively. In cluster IV, 16 out of the 17 genotypes were from Ethiopia, with only one from Eritrea. Clusters V and VI were exclusively made up of Ethiopian genotypes (Appendix Table 4.7.1). Across all clusters, moisture content, protein percentage, and starch content showed limited variation. Moisture content ranged from 10.43% in cluster II to 11.85% in cluster VI, while protein content varied from 5.8% in cluster V to 7.20% in cluster I (Table 4.3).

Table 4.3. Means of Finger millet nutritional traits across six clusters.

cluster	**MC%**	**Prt%**	**Ca (mg/100g)**	**Mg (mg/100g)**	**Zn (mg/100g)**	**Fe (mg/100g)**	Starch%
I (73)	11.20	7.20	242.91	238.93	0.98	5.71	72.83
II (51)	10.43	6.27	166.79	165.83	0.33	5.10	72.52
III (26)	11.41	5.82	252.13	285.44	1.01	6.48	73.06
IV (17)	10.85	5.83	243.63	192.39	0.72	5.16	74.45

V (8)	11.19	5.80	253.07	357.48	1.17	16.33	73.16
VI (27)	11.85	6.42	359.29	350.09	3.11	12.86	73.17

Table 4.4. Squared distances between clusters (Mahalanobis Distance, D2).

Clusters	I	II	III	IV	V	VI
I	-					
II	12.91	-				
III	9.51	13.09	-			
IV	29.89	28.41	23.19	-		
V	20.80	27.18	10.57	36.49	-	
VI	32.80	64.95	35.21	75.91	33.40	-

Genotypes in cluster II consistently showed lower concentrations in all parameters except in protein: moisture (10.43%), calcium (166.79 mg/100g), magnesium (165.83 mg/100g), zinc (0.33 mg/100g), iron (5.10 mg/100g), and starch (72.52%). In contrast, genotypes in clusters V and VI showed higher mineral contents (Fig 4.1). For instance, cluster V had high levels of magnesium (357.48 mg/100g) and iron (16.33 mg/100g), while cluster VI contained elevated moisture (11.85%), calcium (359.29 mg/100g) and zinc (3.11 mg/100g). Cluster III mostly comprised genotypes with moderate levels of calcium (252.13 mg/100g), magnesium (285.44 mg/100g), zinc (1.01 mg/100g), and starch (73.06%) (Table 4.3). Notably, genotypes in cluster IV were distinguished by their high starch content (Fig 4.1).

Table 4.4 displays the squared distances between clusters, reflecting the degree of genetic dissimilarity or diversity based on nutritional traits. The largest squared distance was observed between cluster IV and VI, followed by cluster II and VI, and cluster IV and V, with values of 75.91, 64.95, and 36.49, respectively. In contrast, smaller squared distances were noted between cluster I and III, cluster III and V, cluster I and II, and cluster II and III, with values of 9.51, 10.57, 12.91, and 13.09, respectively.

4.3.4.1. Principal component analysis (PCA)

Principal Component Analysis (PCA) was employed to examine the patterns of variation and relationships among the six nutritional traits (Table 4.5). The first five principal components (PCs) accounted for 94.5% of the total variability. PC1 explained 41.4% of the variation, with zinc (0.484), calcium (0.465), iron (0.443) and magnesium (0.428) showing the highest positive loadings. PC2, which accounted for 19.3% of the variation, was most influenced by protein, calcium and zinc (positive loading) and starch (negative loading). PC3 explained 15.3% of the variation, with starch showing the highest positive loading, and iron and magnesium having the highest negative coefficients. The nutritional traits with the highest positive and negative loadings for the remaining principal components are highlighted in bold in Table 4.5. Together, the first two PCs accounted for 60.7% of the total variation in nutritional traits among the 200 finger millet genotypes and two check varieties from four African countries.

Table 4.5. Principal component analysis of nutritional traits in finger millet genotypes

Variable	PC1	PC2	PC3	PC4	PC5	PC6
Prt	-0.238	**0.766**	0.076	0.148	**0.545**	0.179
Ca	**0.465**	**0.366**	**0.357**	-0.263	-0.07	-0.67
Mg	**0.428**	0.009	**-0.465**	0.725	0.123	-0.244
Zn	**0.484**	**0.379**	-0.004	-0.005	**-0.515**	**0.597**
Fe	**0.443**	-0.135	**-0.408**	-0.552	**0.531**	0.178
Str	0.336	-0.343	**0.695**	0.28	**0.368**	**0.269**
Eigen value	2.48	1.16	0.92	0.61	0.51	0.33
Individuals %	41.40%	19.30%	15.3%	10.1%	8.4%	5.5%
Cumulative %	41.4%	60.7%	76.0%	86.1%	94.5%	100%

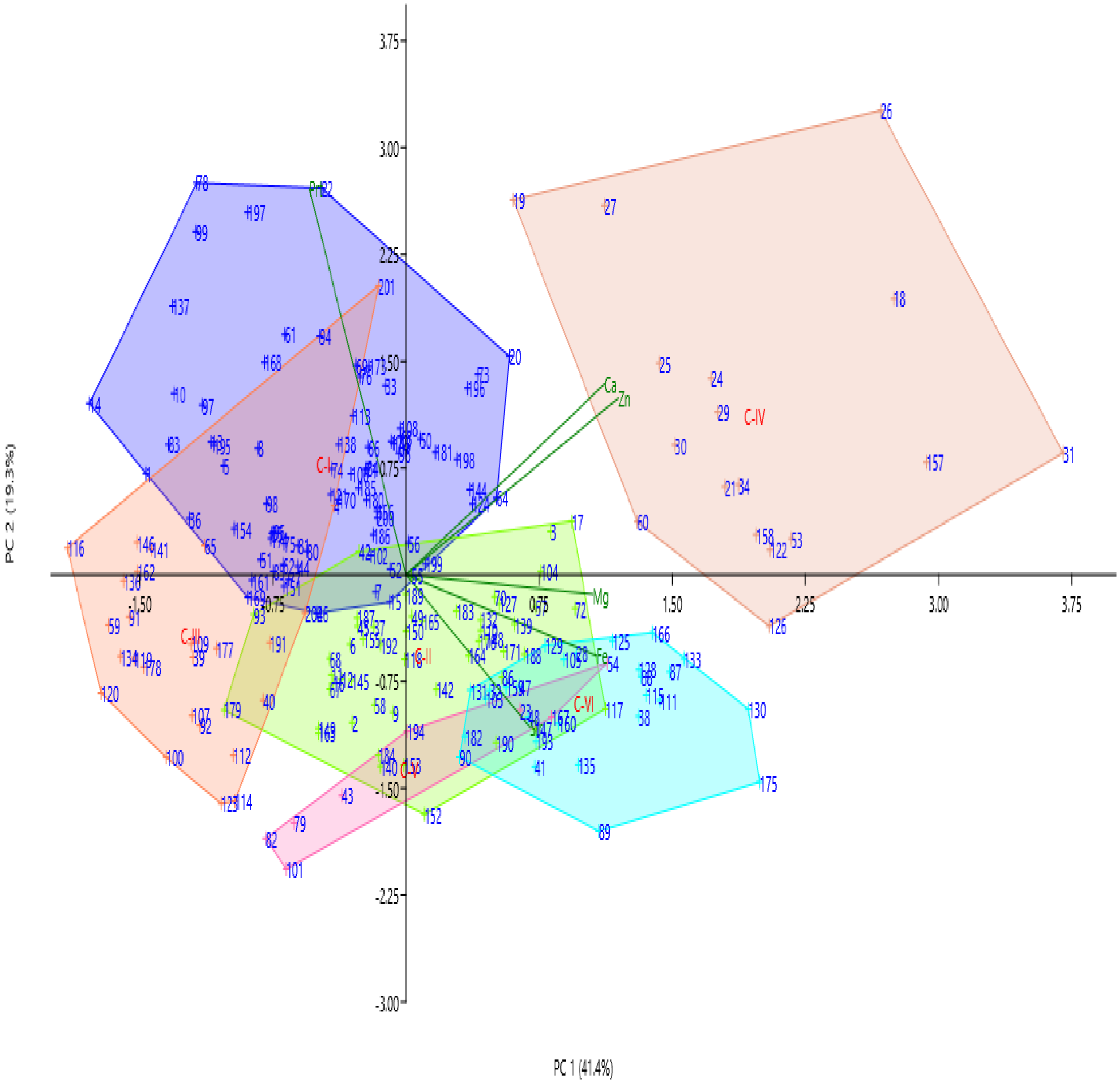


Figure 4.1. Biplot of the 200 finger millet genotypes and two check varieties for nutritional traits based on the first and second principal components.

4.4. DISCUSSION

4.4.1. Variability in Protein and Starch

The genetic variability observed in protein content within this study presents a promising opportunity for selecting high-protein genotypes in breeding programs. However, the variability in starch content among the African finger millet collections was not significant. The chemical composition of finger millet generally shows that the total carbohydrate (starch) content falls between 72% and 79.5% (Pragya et al., 2017). Evaluating the diversity in protein and starch contents directly impacts the enhancement of finger millet quality through breeding. Figure 4.2 illustrates the top 10 and bottom 5 genotypes from the 200 finger millet genotypes and two check varieties. Similarly, Vadivoo et al. (1998) reported a broad range of protein content among 36 finger millet genotypes.

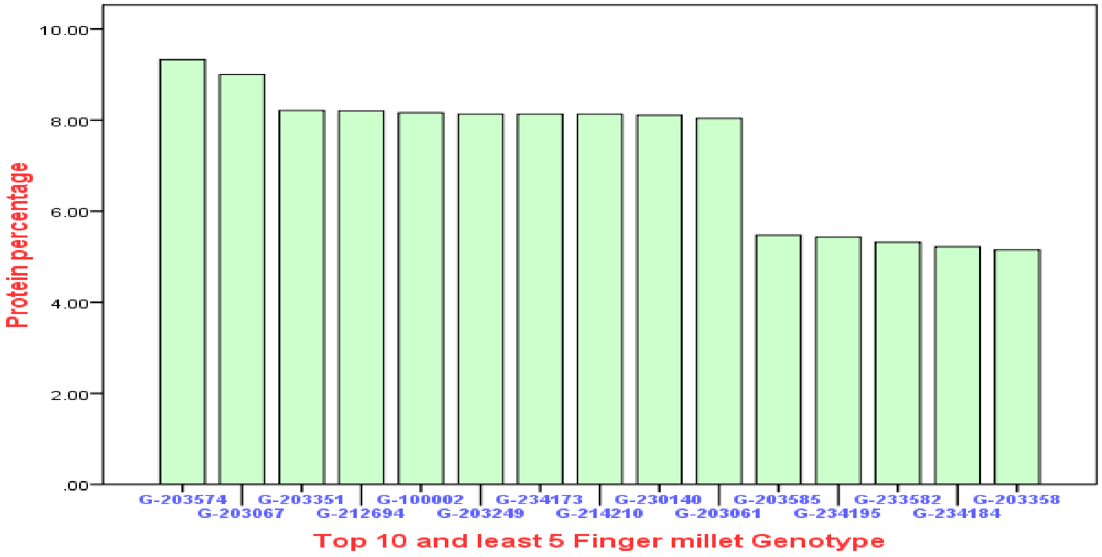


Figure 4 2. The top ten and bottom five finger millet genotypes based on protein percentage.

Research on the genetic diversity of protein content in finger millet genotypes has been limited, although protein is the second most important component of finger millet grains, following carbohydrates (Luitel et al., 2020). The protein content range observed in the present study (5.15% to 9.35%) aligns with findings from other studies. For instance, Arjun et al. (2014) reported a protein range of 5.6% to 12.7%, while Pragya et al. (2017) found protein levels ranging from 5.6% to 12.7%, with an average of 7%. Similarly, Vadivoo et al. (1998) found protein content ranging from 6.7% to 12.3%, with a mean of 9.7%, from the analysis of 36 genotypes. Other studies, such as Bachar et al. (2013), indicated that finger millet typically contains around 7% protein, whereas Amadou et al. (2013) reported up to 11%. Chethan & Malleshi (2018) noted that protein content in finger millet ranged from 5% to 8%. Additionally, Barbeau & Hilu (1993) reported a range of 7.5% to 11.7% in ten cultivars, including wild and regional varieties. Similarly, a study of Ethiopian landraces found protein content between 6.26% and 10.5% (Admassu et al., 2009). Chandra et al. (2016) reviewed studies indicating a protein range of 6% to 13%. These findings confirm the presence of substantial variation in protein content among finger millet genotypes, consistent with the current study.

4.4.2 Mineral Variability

The present investigation highlighted significant variation in mineral compositions among finger millet genotypes, indicating the potential to identify candidates for future breeding programs. Analysis of finger millet collections revealed substantial genetic diversity in grain contents of iron (Fe), zinc (Zn), calcium (Ca), and magnesium (Mg). Identifying genotypes rich in these minerals and assessing their genetic diversity is crucial for developing micronutrient- and protein-dense finger millet cultivars, addressing malnutrition in target populations. Previous research supports the observed variability. For example, Upadhyaya et al. (2011) found considerable variation in finger millet grain nutrients in their Indian study, with ranged for Fe (21.71–65.23 mg/kg), Zn (16.58–25.33 mg/kg), Ca (1.84–4.89 g/kg), and protein (6.00–11.09%). El-Beltagi et al. (2021) reported high variability in nutritional compositions, including iron, calcium, and zinc, among thirty wheat genotypes. Similarly, Depar an Rajpar (2011) observed significant variation in Fe, Zn, Cu, and Mn concentrations among different rice genotypes.

Amadou et al. (2013) noted millets for their exceptional calcium, dietary fiber, polyphenols, and protein content, with variability depending on the cultivar. Gerrano et al. (2018) also found considerable variation in nine mineral contents of cowpea genotypes. Furthermore, Shimelis & Rakshit (2005) reported that local finger millet varieties had superior iron content compared to improved dry bean varieties and other cereals like wheat, maize, and sorghum. Additionally, Admassu et al. (2009) highlighted that the calcium content of finger millet varieties is 5 to 30 times higher than that of other cereals, including sorghum (30 mg/100g), tef (140 mg/100g), barley (47 mg/100g), maize (6 mg/100g), and wheat (49 mg/100g).

The present study found a wide range of zinc content (0.11 to 4.89 mg/100g) among the 200 African finger millet collections and two check varieties. Admassu et al. (2009) reported zinc concentrations ranging from 0.97 to 2.56 mg/100g across nine finger millet genotypes, emphasizing zinc's role in immune function, enzyme activation, and growth. Zinc deficiency is prevalent in Africa and Asia, and supplementing plant-based foods with zinc can help alleviate malnutrition (Admassu, 2008).

The observed variability in mineral, protein, and carbohydrate content among the finger millet genotypes presents valuable opportunities to select genotypes with high levels of iron (Fe), calcium (Ca), zinc (Zn), magnesium (Mg), protein, and starch. These traits can be incorporated into breeding programs to develop varieties with both high nutritional density and desirable agronomic traits.

4.4.3. Relationship among nutritional traits

Calcium (Ca) and magnesium (Mg) levels showed significant positive correlations with iron (0.35* & 0.42*) and zinc (0.62** & 0.46*), respectively. Additionally, zinc (Zn) had a positive correlation with iron (0.39*). Upadhyaya et al. (2011) reported weaker or non-significant correlations between grain yield and Fe, Zn, Ca, and protein contents, although they observed statistically significant but weaker correlations between Fe and Zn, as well as Fe and protein. This underscores how grain yield is either positively or negatively associated with the mineral, protein, and starch contents of finger millet genotypes. These findings suggest the need for breeders to focus on genotypes that combine high levels of essential nutrients with high grain yield potential. Several studies (Hussain et al., 2010; Bachar et al., 2013; Győri, 2017; Anteneh et al., 2019; Anuradha et al., 2020; Arag et al., 2022; Goredema et al., 2023) emphasized the importance of integrating high micronutrient densities with high yield potential in crop breeding programs.

The present results indicated a negative and non-significant correlation between protein content and all other nutritional traits, except for starch, which had a positive but weak correlation. Vadivoo et al. (1998) observed a negative and significant association between protein content and calcium, whereas Badigannavar et al. (2015) reported a positive correlation between protein content and copper and zinc, but a negative correlation with magnesium. Significant correlations between some mineral elements and total protein content have been noted in cowpea genotypes (Gerrano et al., 2018). These results suggest the possibility of selecting genotypes with multiple desirable traits, such as high iron and zinc, which can be improved together in breeding programs. This is supported by the findings from Goredema et al. (2023) and Upadhyaya et al. (2011), who reported a positive and highly significant correlation between grain zinc and iron, suggesting that these traits can be enhanced simultaneously. Correlations among traits may arise from genetic linkage, pleiotropic effects, or environmental influences (Karak et al., 2012). Therefore, understanding the extent of these correlations is crucial for breeding programs aimed at meeting the needs of farmers and consumers.

4.4.3.1. Cluster analysis

The present study categorized the seven nutritional traits into six distinct clusters (Tables 4.3 and 4.6), allowing breeders to pinpoint and select elite genotypes with desired traits, thereby facilitating more focused breeding efforts. This clustering also revealed genotypes with similar nutritional profiles, providing insights into the relationships between different traits. For example, genotypes in cluster V, which have high iron and magnesium levels, and those in cluster VI, which exhibited high calcium and zinc contents, could be targetedfor efficient breeding that combine high mineral levels with desirable yield characteristics. Additionally, the present study identified diverse squared distances between clusters, indicating that breeders might consider selecting parent lines from clusters with larger squared distances to enhance genetic diversity and reduce inbreeding depression. This approach could lead to hybrids with broader genetic backgrounds, improving the resilience and adaptability of new varieties.

Table 4.2. Cluster analysis of protein and nutrients content in finger millet genotypes

No, Cluster	**No.genotypes**	**Genotypes**	**Ca (mg/100g)**		**Mg (mg/100g)**		**Zn (mg/100g)**		**Fe (mg/100g)**	
			Min.	Max.	Min.	Max.	Min.	Max.	Min.	Max.
1	73	100002, 100023, 100025, 100027, 100041, 100072, 203061, 203062, 203068,203249, 203268, 203281, 203282, 203323, 203330,203339, 203340, 203341, 203345, 20335,203352, 203353, 203354, 203356,203359, 203557, 203569, 203570, 203571, 203572, 203573, 203574, 203576, 203577, 203581 203582, 203583, 211504, 211506, 212462, 212694, 213228, 214210, 229724, 229728, 229730, 229735, 230124, 230127, 230140, 230141, 233759, 233765, 234151, 234155, 234159, 234166, 234173, 234174, 234176, 234178, 234179, 234183, 234190, 234191, 234196, 234197, 234210, 234822, 234823, 234824, 234825 and 235135	138.5	399.5	125.1	416.9	0.2	1.6	4.3	15.7
2	51	100013, 100020, 100024, 100028, 100063, 100065, 203063, 203065, 203283, 203321,203324, 203338,203344, 203346, 203347, 203357,203358, 203556, 203558, 203584, 211029, 229726, 229732, 230105, 230118, 230130, 230135, 233580, 233582, 233601, 233769, 234147, 234148, 234149, 234150, 234153, 234154, 234157, 234168, 234169, 234170, 234177,	150.0	406.5	130.4	400.3	0.2	1.5	4.3	17.2

		234185, 234188, 234193,234195, 234198, 234201, 234204, 234205, and 234207								
3	26	100022, 203285, 203286, 203349, 203355, 208726, 208730, 215798, 229729, 229731, 229734, 229736, 229738, 230121, 230123, 230126, 230137, 230139, 233584, 233891, 234167, 234186, 234187, 234206, Mereb-1 and tekeze-1	145.0	306.0	120.9	231.9	0.1	2.7	3.4	10.1
4	17	203066, 203067, 203246, 203251, 203256, 203257, 203258, 203260, 203261, 203262, 203280, 203342, 203350, 230125, 230129, 234160 and 234162	284.5	431.0	243.5	456.0	1.6	4.9	4.6	30.7
5	8	203250, 203322, 203343, 203575, 203578, 215802, 234172 and 234209	152.0	371.5	123.6	231.9	0.3	1.5	4.3	6.1
6	27	203259, 203263, 203284, 203320, 203336, 203337, 203585, 203586, 208446, 208725, 229725, 229727, 229733, 229737, 230128, 230131, 230132, 230133, 230134, 230136, 230138, 234164, 234165, 234171,234184, 234192 and 234208	189.5	371.5	215.3	525.5	0.7	1.5	9.1	28.2

El-Beltagi et al. (2021) noted that genotypes within the same cluster tend to share similar characteristics with less variability. Similarly, Badigannavar et al. (2015) used cluster analysis based on Euclidean distance to categorize germplasm lines and varieties, finding high-yielding lines with improved micronutrient profiles grouped into the same cluster. Bachar et al. (2013) grouped 30 finger millet accessions into three clusters based on their mineral, fiber, protein, and ash contents. Fred et al. (2021) also identified distinct clusters among finger millet accessions. Hiremath et al. (2018) found that hierarchical clustering of finger millet germplasm aids in identifying optimized lines with higher mineral content. In the present study, cluster I exhibited the highest mean protein content, while clusters V and VI had the highest mineral contents. Therefore, genotypes from these clusters could be selected as parents for breeding programs to enhance both protein and mineral composition.

4.4.3.1.1. Principal Component Analysis

According to Anteneh et al. (2019), principal components (PCs) with eigenvalues greater than one and component coefficients exceeding ±0.3 are deemed significant and valuable. As shown in Table 4.5, the first principal component (PC1) accounted for a substantial portion of the total variance (40.27%), followed by the second principal component (PC2) with 17.51%, and the third component (PC3) with 13.52%. The first principal component was primarily influenced by magnesium (Mg), zinc (Zn), calcium (Ca), and moisture content. The second principal component was notably affected by protein, starch, and iron, while the third component was predominantly shaped by starch, iron (Fe), and magnesium (Mg). These findings indicate the importance of these nutritional traits in differentiating between finger millet genotypes. They also aid in identifying clusters of genotypes with similar nutritional traits (Fig 4.1), facilitating informed decision-making in breeding programs and genotype selection based on optimal trait combinations. In line with the present study, previous studies have confirmed that principal component analysis (PCA) effectively reveals significant nutritional variability among genotypes of pearl millet, finger millet, wheat, and chickpea (Felix et al., 2015; Chandra et al., 2016; Gerrano et al., 2018; Anteneh et al., 2019; Kumari and Singh, 2020; Govindaraj et al., 2020; El-Beltagi et al., 2021; Honnappa et al., 2023). Additionally, Mahendran et al. (2015) and Farida et al. (2022) demonstrated the use of PCA in analyzing both morphological and nutritional traits in chickpea germplasm, while Mahmood et al. (2018), Chafoor et al. (2003), and Upadhyaya et al. (2007) emphasized the contribution of multiple principal components in explaining the variability of various agronomic and nutrient traits.

4.4.4. Nutrient qualities by country of origin

Different regions often exhibit unique environmental conditions, soil types, and farming practices, which can result in varied grain qualities among finger millet genotypes. This study assessed the nutritional traits of 202 finger millet genotypes from four African regions. The findings revealed that Ethiopian genotypes had lower calcium (Ca), zinc (Zn) and iron (Fe) concentrations compared to genotypes from Zimbabwe and Eritrea, which had higher levels of these minerals. Additionally, Zimbabwean and Ethiopian genotypes showed higher magnesium content, while those from Zambia had lower magnesium levels (Fig. 4.3). Besides, higher variations in calcium (Ca) and protein content were observed across the countries. In contrast, no significant regional differences were found in starch and moisture contents. These findings provide valuable insights for breeding programs aimed at enhancing these traits, helping farmers choose the most suitable genotypes for their local conditions to improve crop yield, quality, and productivity. Our findings align with those of Fred et al. (2021), who reported regional variations in nutrient concentrations, although no single region consistently yielded genotypes with superior nutrient profiles. Gerrano et al. (2018) similarly observed high calcium (Ca) levels in cowpea genotypes from South and West Africa. The correlation between grain nutrient content and geographical origin offers valuable insights for developing strategies to collect germplasm with specific nutrient profiles (Upadhyaya et al., 2011). Additionally, studies by Hilu and de Wet (1976), Dida et al. (2008), and Barbeau and Hilu (1993) reported that the greatest diversity in grain nutrient content is likely found in Africa and Asia, the primary and secondary centers of origin for finger millet. They also reported significantly higher calcium content (515 mg/100 g) in Ethiopian finger millet compared to that from Kenya (401 mg/100 g) and India (375 mg/100 g), suggesting that geographical origin may influence the nutrient composition of finger millet due to variations in soil mineral enrichment, impact of temperature, rainfall and altitude on nutrient uptake at different collection sites.

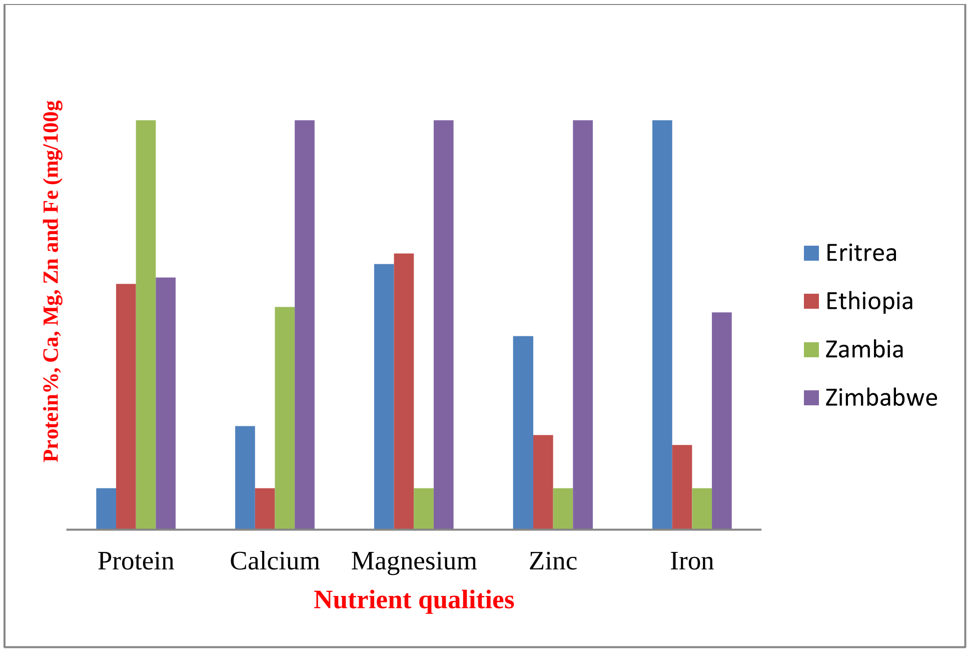
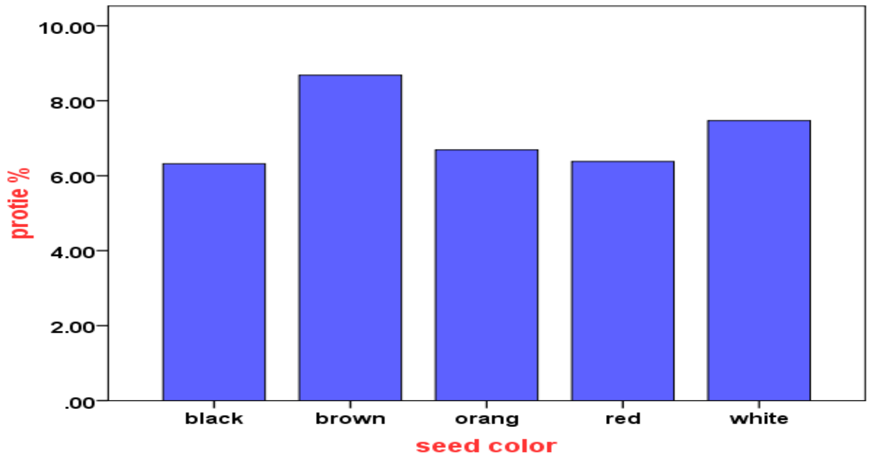


Figure 4 3. protein percentage, and mineral content of grains across different countries of origin for 200 finger millet genotypes and two check varieties.

4.4.5. Nutrient Qualities by Seed Color

The current study revealed that nutrient contents of finger millet, such as calcium (Ca), magnesium (Mg), zinc (Zn), and iron (Fe) vary with the seed color (see Fig. 4.5). Specifically, the brown seeds showed higher concentrations of calcium iron, and zinc. Besides, the orange seeds depicted higher concentration of magnesium while the white seeds with high concentration of zinc. In contrast, the black seeds tend to have lower levels of calcium iron, and zinc compared to brown seed color. Additionally, white seeds exhibit higher zinc content compared to black and red seeds. However, moisture, protein, and starch contents do not differ with seed color variations. The protein percentage by seed color is illustrated in Figure 4.4. Vadivoo, et al. (1998) found that white-seeded finger millet had higher protein content but moderate calcium levels compared to brown-seeded types. Similarly, Das et al. (2017) observed that white-seeded varieties generally have higher protein content compared to brown-seeded varieties, though protein content shows more variation among the brown-seeded types.



.

Figure 4 4. Protein percentage ranges among different seed colors of 202 finger millet genotypes.

The seed coat of finger millet is rich in various nutrients such as phenolic compounds, dietary fiber, minerals, and vitamins (Chandra et al., 2016; Kumar et al., 2016). According to Chethan and Malleshi (2018), the phenolic content and antioxidant activity in finger millet vary with seed color, brown seeds showing higher polyphenol content than white seeds. Xiang et al. (2019) also noted that finger millet grains with colored seeds (brown, red, or reddish) have higher levels of phenolic compounds than white seeds. For instance, orange seeds had an average Ca content of 250.6 mg/100 g compared to 284.2 mg/100 g in brown seeds. Black seeds contained 253.0 mg/100 g magnesium (Mg), whereas brown seeds had 220.3 mg/100 g. Additionally, brown seeds contained 1.39 mg/100 g zinc (Zn) compared to 1.03 mg/100 g in orange seeds. The highest average iron content was found in orange seeds at 9.30 mg/100 g, while the lowest was in white seeds at 6.53 mg/100 g.

Fred et al., (2021) also reported a correlation between seed color and nutrient concentration, with darker-colored grains generally exhibiting higher nutrient levels. Similarly, Depar and Rajpar (2011) emphasized the importance of seed size and color as crucial factors in determining dietary nutrition. These findings suggest that seed color can significantly affect various nutritional attributes, such as protein percentage, carbohydrate concentration, and mineral content.

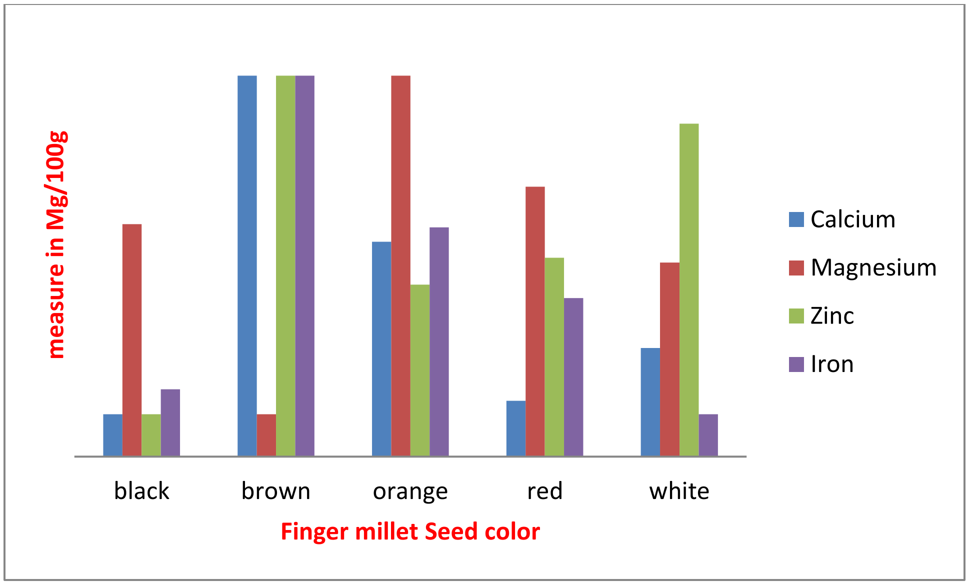


Figure 4 5. Mineral content in the grains of 200 finger millet genotypes based on seed color.

Understanding these factors is essential for developing varieties with desirable nutritional traits for specific applications. Additionally, seed color can influence consumer preferences and market value, with certain colors being more appealing or culturally significant. Thus, studying the grain composition of different seed colors can help researchers and breeders in creating varieties that meet consumer demands, potentially leading to achieve higher market prices.

4.5. CONCLUSION AND RECOMMENDATION

4.5.1. Conclusion

Finger millet remains a vital staple food for millions of poor people in Africa, including Ethiopia, and Asia. Due to its high carbohydrate, energy, and nutritional content, it plays an essential role in balanced diet. Understanding the existing genetic diversity within finger millet genotypes and the relationships between different traits is essential for effective plant breeding program. The current study highlighted significant diversity in the grain nutrient qualities among African finger millet collections, including protein, calcium, magnesium, iron, and zinc content. The top-ranked genotypes for protein, calcium, magnesium, zinc, and iron were 203574, 234160, 203259, 203257, and 203262, respectively. Notably, most of the highest-ranking genotypes were from Ethiopia, except for the top protein genotype from Zimbabwe. Conversely, the lowest-ranking genotypes for these traits included 203358, 100002, 229738, Tekeze-1, and 229738, respectively.

The cluster analysis in the study revealed that the most desirable grain quality traits are found in specific clusters. For example, Cluster V is exhibited high levels of magnesium (Mg) and iron (Fe), while Cluster VI contained genotypes with elevated levels of calcium (Ca), magnesium (Mg), zinc (Zn), and iron (Fe). These findings provide a clear path for selecting genotypes with the best combination of these traits. The principal component analysis (PCA) revealed patterns of variation and relationships among the seven grain quality traits, PC1 (40.27%) and PC2 (17.51%) together explaining 57.78% of the total variability, with calcium (0.442), magnesium (0.415), and zinc (0.493) contributing most to PC1, while protein and starch had the highest influence on PC2.

The study also revealed that the grain quality traits of finger millet genotypes varied by region and seed color. For instance, both Ethiopian and Zimbabwean genotypes had high levels of magnesium (Mg), but Ethiopian genotypes had lower zinc (Zn) and iron (Fe) concentrations. in contrast, Eritrean and Zimbabwean genotypes showed higher levels of zinc and iron levels, while Zambian genotypes had lower magnesium content. Seed color also impacted grain composition, with brown and orange seeds having higher calcium and iron concentrations but lower magnesium levels, while brown and white seeds showed higher zinc content compared to black and red seeds. However, moisture, protein, and starch contents did not vary with seed color. In general, this study provides valuable information for finger millet breeders regarding the existing genetic diversity of the crop, aiding in effective utilization and management of genetic resources.

4.5.2. Recommendation

Based on the findings of this study, it is recommended that finger millet genotypes with high nutritional content be considered for either direct cultivation or used as parent lines in hybridization programs. Integrating conventional breeding methods with molecular breeding techniques could accelerate the development and release of new varieties, significantly shortening breeding cycles. Assessing genetic diversity in terms of protein, starch, and mineral content will be instrumental in developing high-yielding finger millet varieties with enhanced nutritional value. While national breeding programs for finger millet have primarily emphasized on agronomic traits such as yield, drought tolerance, and disease resistance, nutritional quality has often been overlooked. Thus, breeding efforts should be redirected towards enhancing local varieties that are rich in grain nutrients. Overall, this study emphasizes that finger millet grains are a significant source of minerals, especially calcium, and could be incorporated into composite flour technology to enhance the nutritional quality and consumer acceptance of various food products. Further research is needed to explore the amino acid profiles of finger millet proteins, its phytochemical composition, and its digestibility.

4.6. REFERENCE

Admassu, S. (2008). Variability in Phytochemicals, Á-Galactosides, Sucrose Composition and *in vitro* Protein Digestibility of Common Bean (*Phaseolus vulgaris* L.) Varieties. *East African Journal of Sciences*, *2*(1); 45–54.

Admassu, Shimelis, Teamir, M., & Alemu, D. (2009). Chemical Composition Of Local And Improved Finger Millet [Eleusine Corocana (L .) Gaetrtin] Varieties Grown In Ethiopia. *Ethiop J Health Sci.*, *39*(7); 1–8.

Amadou, I., Gounga, M. E., & Le, G. W. (2013). Millets: Nutritional composition, some health benefits and processing - A review. *Emirates Journal of Food and Agriculture*, *25*(7); 501–508.

Anteneh, D., Mekbib, F., Tadesse, T., & Dessalegn, Y. (2019). *Genetic Diversity among Lowland Finger Millet (Eleusine coracana (L) Gaertn) Accessions*. *29*(2); 93–108.

Anuradha, N., Patro, T., Triveni, U., & Rao, P. J. (2020). *Heritability and trait association in finger millet [Eleusine coracana (L .)*. *9*(4); 768–771.

Arag, L. De, Kessiane, T., & Freitas, T. (2022). *Evaluation of adaptability and stability for iron , zinc and protein content in cowpea genotypes using GGE biplot approach*. *8;* 0–9.

Arjun, D., Kumar, R., & Singh, C. (2014). Finger millet for nutritional security and source of food. *Advances in Food Science and Technology*, *2*(3); 184–190.

Bachar, K., Mansour, E., Ben Khaled, A., Abid, M., Haddad, M., Ben Yahya, L., El Jarray, N., & Ferchichi, A. (2013). Fiber Content and Mineral Composition of the Finger Millet of the Oasis of Gabes Tunisia. *Journal of Agricultural Science*, *5*(2); 219–226.

Badigannavar, A., Girish, G., Ramachandran, V., & Ganapathi, T. R. (2015). Genotypic variation for seed protein and mineral content among post-rainy season-grown sorghum genotypes. *CJ*, *4*(1); 61–67.

Barbeau, W. E., & Hilu, K. (1993). Protein , calcium , iron , and amino acid content of selected wild and domesticated cultivars of finger millet Protein , calcium , iron , and amino acid content of selected wild and domesticated cultivars of finger millet. *Plant Foods for Human Nutrition*, *43*; 97–104.

Belay, F. (2023). *Performance Evaluation of Finger Millet (Eleusine coracana L . Gaertn) Varieties in Dry Land Areas of Northern Ethiopia*. *4*(1); 2–7.

Central Statistical Agency (CSA). Agricultural sample survey,(2018) Report on area and production of crops (Private peasant holdings, main season). Statistical Authority, Addis Ababa, Ethiopia. Statistical Bulletin. 5;:446

Chandra, D., Chandra, S., & Sharma, A. K. (2016). Review of Finger millet (Eleusine coracana (L .) Gaertn): A power house of health benefiting nutrients. *Food Science and Human Wellness*, *5*(3); 149–155.

Chafoor, A., Gulbaaz, F. N., Afzal, M., And, M. A., & M.Arshad. (2003). *inter-relationshi between sds-page and agronomic traits in chickpea (Cicer arietinum L.)* (pp. 613–624).

Chethan, S., & Malleshi, N. G. (2018). Finger millet polyphenols : Optimization of extraction and the effect of pH on their stability. *Food Chemistry 105*; 862–870.

Das, R., Pandravada, S. R., Harikrishnan, P. J., & Agriculture, C. (2017). *Estimation Of Grain Nutrient And Their Association With Grain Yield In Finger Millet [Eleusine Coracana (L .) Gaertn]*. *17*(1); 241–246.

Depar, N., Rajpar, I. Memon1, M. Imtiaz1 and Zia-ul-hassan (2011). *Mineral nutrient densities in some domestic and exotic rice genotypes*. *J. Agri., Agril. Engg., Vet. Sci*.,.27(2); 134-142

Devi, P. B., Vijayabharathi, R., Sathyabama, S., Malleshi, N. G., & Priyadarisini, V. B. (2011). Health benefits of finger millet (Eleusine coracana L.) polyphenols and dietary fiber: A review. *Journal of Food Science and Technology*, *51*(6); 1021–1040.

Dida, M. M., Wanyera, N., Harrison Dunn, M. L., Bennetzen, J. L., & Devos, K. M. (2008). Population Structure and Diversity in Finger Millet (Eleusine coracana) Germplasm. *Genetic Resources and Crop Evolution.* 1(2); 131–141

El-Beltagi, H. S., Basit, A., Ullah, I., Ullah, I., Mohamed, H. I., & Alqurashi8, R. M. (2021). *Assessment Of Biochemical Diversity , Estimation Of Mineral Composition And Nutritional Status In Different Wheat (Triticum Assessment Of Biochemical Diversity , Estimation Of Mineral Composition And Nutritional Status In Different Wheat (Triticum aesti.. Fresenius Environmental Bulleti 30(7A); 9490-9507*

Farida Traoré, F., El-Baouchi, A., En-nahli, Y., Hejjaoui, K., Metougui, M. L., Hamwieh, A., Sohail, Q., Istanbuli, T., Boughribil, S., & Amri, M. (2022). Exploring the Genetic Variability and Potential Correlations Between Nutritional Quality and Agro-Physiological Traits in Kabuli Chickpea Germplasm Collection (Cicer arietinum L.). *Frontiers in Plant Science*, *13*(7); 1.14.

Felix, K., Paul, K., Paul, O., Bernard, T., Lillian, J., Ojulong, H., & Nicholas, L. (2015). Multivariate analysis of nutritional diversity of selected macro and micro nutrients in pearl millet (Pennisetum glaucum) varieties. *African Journal of Food Science*, *9*(3); 103–112.

Fred, O. H., Sheunda, P., Kibuka, J., Kumar, A., Rathore, A., Manyasa, E., & Ajaku, D. (2021). *Characterization of finger millet germplasm for mineral contents : Prospects for breeding*. *12*; 33–44.

Gebreyohannes, D., Shimelis, H., Laing, M., Mathew, I., Odeny, D. A., & Ojulong, H. (2021).

Finger Millet Production in Ethiopia: Opportunities, Problem Diagnosis, Key Challenges and Recommendations for Breeding. *Sustainability, 13*(13463), 2–23.

Gerrano, A. S., Rensburg, W. S. J. Van, Venter, S. L., Shargie, N. G., Amelework, B. A., Shimelis, H. A., Maryke, T., Shegro, A., Rensburg, W. S. J. Van, Venter, S. L., Shargie, N. G., Amelework, B. A., Shimelis, H. A., & Labuschagne, M. T. (2018). Selection of cowpea genotypes based on grain mineral and total protein content. *Acta Agriculturae Scandinavica, Section B — Soil & Plant Science*, *0*(0); 1–12.

Goredema, N., Ndhlela, T., Biljon, A. Van, Kamutando, C. N., Cairns, J. E., Baudron, F., & Labuschagne, M. (2023). *Genetic Variation of Zinc and Iron Concentration in Normal , Provitamin A and Quality Protein Maize under Stress and Non-Stress Conditions*. *plants.12;270*

Govindaraj, M., Yadav, O. P., Rajpurohit, B. S., Kanatti, A., Rai, K. N., & Dwivedi, S. L. (2020). Genetic Variability, Diversity and Interrelationship for Twelve Grain Minerals in 122 Commercial Pearl Millet Cultivars in India. *Agricultural Research*, 9(5);106.

Győri, Z. (2017). Evaluation of the mineral content of winter wheat. *MOJ Food Processing & Technology Short*, *4*(4); 122–123.

Hailegebrial, K., Yiergalem, T., Alem, R., Redae, W., Desalegn, Y., & Welegerima, G. (2017). Yield performance and Adaptability of Finger millet landrace in North Western Tigray , Ethiopia. *World News of Natural Sciences*, *15*(October), 98–111.

Hilu, K. W., & de Wet, J. M. J. (1976). Domestication of Eleusine coracana. *Economic Botany*. https://doi.org/10.1007/BF02909728

Hiremath, N., Geetha, K., Vikram, S. R., Nanja, Y. A. and, & Shivaleela, H. B. (2018). Minerals Content in Finger Millet [Eleusine coracana (L .) Gaertn]: A Future Grain for Nutritional Security. *International Journal of Current Microbiology and Applied Sciences*, *7*; 3448–3455.

Honnappa, M., Mannur, D. M., Padmashree, R., S, U. B. B., Muttappa, H., & Archana, K. A. (2023). *Multivariate Analysis for Grain Yield and Nutritional Quality Traits of Green Seeded Chickpea (Cicer arietinum L .) Genotypes derived from Desi and Kabuli (GKB-10 × MNK-1): Initial Efforts for Green Seeded Chickpea Bio-fortification*. *15*(3); 313–325.

Hussain, A., Larsson, H., Kuktaite, R., & Johansson, E. (2010). *Mineral Composition of Organically Grown Wheat Genotypes : Contribution to Daily Minerals Intake.. Iinternational Journal of Environmental Research and Public Health,* 7; 3442-3456

Karak, T., Erdem, H., Baloch, F. S., Toklu, F., Eker, S., Kilian, B., & Ozkan, H. (2012). Diversity of Macro- and Micronutrients in the Seeds of Lentil Landraces. *The Scientific World Journal*, 1–9.

Kumar, A., Metwal, M., Kaur, S., Gupta, A. K., Puranik, S., Singh, S., Singh, M., Gupta, S., Babu, B. K., Sood, S., & Yadav, R. (2016). Nutraceutical value of finger millet [Eleusine coracana (L.) Gaertn.], and their improvement using omics approaches. *Frontiers in Plant Science*, *7*(June); 1–14.

Kumari, S., & Singh, S. K. (2020). *Assesment Of Genetic Diversity In Promising Finger Millet [Eleusine Coracana (L .) Gaertn] Genotypes*. *Genetics and Plant Breeding.10(2); 825-830*

Luitel, D. R., Siwakoti, M., & Jha, P. K. (2020). Nutrients in finger millet and soil at different elevation gradients in Central Nepal. *CABI Agriculture and Bioscience*; 1–10.

Maharajan, T., & Ceasar, S. A. (2022). Finger Millet (Eleusine coracana (L .) Gaertn): Nutritional Importance and Nutrient Transporters. *Critical Reviews in Plant Sciences*, *0*(0); 1–31.

Mahendran, R., Veerabadhiran, P., & S. R., Raveendran4, M., & Center. (2015). Principal Component Analysis of Rice Germplasm Accessions under High Temperature Stress. *International Journal of Agricultural Science and Research (IJASR)*, *5*(3); 355–360.

Mahmood, M. T., Ahmad, M., Ali, I., Hussain, M., Latif, A., & Zubair, M. (2018). Evaluation of Chickpea Genotypes for Genetic Diversity through Multivariate Analysis. *Journal of Environmental and Agricultural Sciences*, *15*(June); 11–17.

Pandian, S., Sivasankar, C., Muthuramalingam, P., & Ramesh, M. (2017). *An Amazing Nutritional Value in Wonderful Finger Millet Makes This "The Most Lovable Food Crop" to the World*. *3*(October); 34–36.

Pragya, U. D., Pradesh, V. E., & Singh, T. K. (2017). Chemical composition of finger millet of food and nutritional security. *Internationa Scholars Journals*, *5*(8); 1–8.

Saleh, A. S. M., Zhang, Q., Chen, J., & Shen, Q. (2013). Millet grains: Nutritional quality, processing, and potential health benefits. *Comprehensive Reviews in Food Science and Food Safety*, *12*(3); 281–295.

Shimelis, E. A., & Rakshit, S. K. (2005). Proximate composition and physico-chemical properties of improved dry bean (Phaseolus vulgaris L.) varieties grown in Ethiopia. *Lebensmittel-Wissenschaft Und-Technologie(Lwt)*, *38*(4); 331–338.

Upadhyaya, H. D., Dwivedi, S. L., Gowda, C. L. L., & Singh, S. (2007). Identification of diverse germplasm lines for agronomic traits in a chickpea (Cicer arietinum L.) core collection for use in crop improvement. *Field Crops Research*, *100*(23); 320-326.

Upadhyaya, H. D., Ramesh, S., Sharma, S., Singh, S. K., Varshney, S. K., Sarma, N. D. R. K., Ravishankar, C. R., Narasimhudu, Y., Reddy, V. G., Sahrawat, K. L., Dhanalakshmi, T. N., Mgonja, M. A., Parzies, H. K., Gowda, C. L. L., & Singh, S. (2011). Genetic diversity for grain nutrients contents in a core collection of finger millet (Eleusine coracana (L.) Gaertn.) germplasm. *Field Crops Research*, *121*(1); 42–52.

Vadivoo, A. S., Joseph, R., & Ganesan, N. M. (1998). Genetic variability and diversity for protein and calcium contents in finger millet (Eleusine coracana (L.) Gaertn) in relation to grain color. *Plant Foods for Human Nutrition*, *52*(4); 353–364.

Vagdevi, A., Trupthi, S., Pandey, M., & Bharath, N. (2023). *Nutritional qualities , processing and health benefits of finger millet (Eleusine coracana L .)*. *12*(1), 1291–1297.

Xiang, J., Apea-Bah, F. B., Ndolo, V. U., Katundu, M. C., & Beta, T. (2019). Profile of phenolic compounds and antioxidant activity of finger millet varieties. *Food Chemistry*, *275*(April); 361–368.

Yemane T., T. Berg, B. Tsegaye, T. Tanto, (2006) 'Farmers' management of finger millet (Eleusine coracana L.) diversity in Tigray, Ethiopia and implications for on-farm conservation', *Biodiversity and Conservation*, 15(13); 4289–4308

CHAPTER FIVE:

Analysis of Finger Millet Seed Systems in Central and North Western Zones of Tigray, Northern Ethiopia

ABSTRACT

The northwestern and central regions of Tigray are crucial for finger millet cultivation, with farmers predominantly relying on local seed systems and traditional varieties. This study aimed to investigate the sources of finger millet seeds and analyze their flow among farmers in these regions of Northern Ethiopia. Data were collected through semi-structured interviews with 160 respondents from eight villages: Adiyemano, Aditseneke, Endamariam, and Mereb in the central zone, and Debreabay, Birhan, Mitekli, and Araada in the northwestern zone. According to demographic analysis the majority of respondents in Asgedetsimbla were over 50, while 55% of respondents in Mereb were between 28 and 50 years old. Based on educational levels, 54.3% respondents in Asgedetsimbla had education beyond elementary school, while 52.5% of respondents in Mereb were illiterate. Approximately 90.4% of the respondents reported using farmer varieties for cultivation. Seed acquisition methods in the study area included exchanging with neighbors, receiving seeds from relatives, using saved seeds, purchasing seeds from markets, and obtaining seeds through loans. Accordingly, 122 households (76.3%) obtained seeds through exchanges with neighbors, 59 (36.9%) from relatives, 44 (27.5%) used saved seeds, 32 (20%) made purchases from markets, and 15 (9.4%) accessed seeds through loans. Seed flows were more common within villages than between them. The structure of the seed exchange network was influenced by factors such as the number of farmer varieties, reliance on personal relationships, geographic locations, and cultural aspects. Social network analysis identified key farmers with the most direct connections, including AT24, AYII, EM08, MR19, AR13, BR33, DA19, and MT11, who were located in both the central and the northwestern zone villages. This study offers valuable insights for crop breeders on the dissemination of improved finger millet varieties and their impact on seed systems in these regions.

Keywords: Social seed network, Connectors, Nodal farmers, On-farm conservation, Farmer varieties

5.1. INTRODUCTION

Seeds are crucial for maintaining genetic diversity and ensuring agricultural productivity, but Ethiopian agriculture faces a significant challenge due to lack of certified seeds for improved varieties. This shortage results in an uneven distribution of high quality seeds among farmers (Labeyrie et al., 2016). To address this issue, farmers in Ethiopia often rely on informal seed exchange networks. These networks facilitate the distribution of local or introduced finger millet varieties through methods, such as gifting, swapping, bartering, purchasing, and selling, all outside the commercial and formal seed sectors (Coomes et al., 2015). Informal seed systems differ from formal ones, which are typically managed by companies or public institutions (Biemond et al., 2013). Many farmers do not purchase seeds annually; instead, they use seeds saved from previous harvests due to financial constraints or a traditional belief in avoiding seed-related expenses for subsistence farming. Over 90% of farmers save their own finger millet seeds, predominantly local varieties (Devkota et al., 2014). Similarly, Samberg et al. (2013) found that around 90% of the seeds planted each year in Ethiopia come from farmers’ own saved stocks. Local markets also serve as an important alternative source of seeds for farmers with limited access, enabling them to buy and sell surplus produce, grains, and seeds (Rodier & Struik, 2018; Sperling & Mcguire, 2010).

Farmers in subsistence agricultural systems obtain seeds from four main sources: their own saved seeds, gifts or exchanges with other farmers, purchases from local markets, and government agricultural extension services. A study by Abay et al. (2011) on the social networks of finger millet seeds revealed that 61.5% of seeds are saved from previous harvests, 63.1% come from exchanges with neighbors, 40.8% from exchanges with relatives, and 56.9% are obtained from markets. Local farmers typically exchange seeds through networks involving relatives, neighbors, or friends, often within the same ethnic group (Song et al., 2019). Despite its significance, finger millet has been largely neglected by Ethiopian crop researchers and remains an overlooked crop, mainly grown by farmers in drought-prone areas. Consequently, farmers rely heavily on informal seed systems to fulfill their seed needs, particularly in remote areas where access to other seed sources is limited.

Nodal and connector farmers are crucial for maintaining the steady flow of information within social seed networks. They contribute to enhancing the genetic diversity of local crop varieties

(Samberg et al., 2013; Song et al., 2019; Abay et al., 2011). Social ties, including kinship alliances, are essential for seed exchange and information sharing, ensuring equitable access to seeds, especially during low-yields years (Badstue et al., 2006; Ricciardi, 2019; Abay et al., 2011). Factors such as gender, age, kinship ties, geographical distance, and the exchange of goods and information, along with a farmer's position within the network, play significant roles in strengthening social networks and improving seed access to the farmers (Ricciardi, 2019). This study aimed to examine and document the social networks that govern the flow and exchange of finger millet local varieties. Better understanding these networks can help breeders accelerate the adoption of improved crop technologies and identify key farmers (nodal and connector) who can sustain and enhance local crop varieties.

5.1.1. Objectives

⇒ To investigate and map the exchange, distribution, and management of finger millet seeds within the Central and Northwestern Zones of Tigray.

⇒ To study the seed resource and exchange mechanisms among different farmer groups.

⇒ To determine and understand the major roles and influence of farmers in seed flow network.

5.2. MATERIALS AND METHODS

5.2.1. Preparation

Before the seed survey, three activities were carried out at the household level. First, consultations were held with zonal and district agricultural officials to assist the selection of study districts. Second, a Participatory Rural Appraisal (PRA) was conducted to understand the importance of finger millet in the selected districts. Third, key informants were interviewed, and focus group discussions (FGDs) were conducted to gather basic information and document knowledge about the local seed system.

5.2.2. Study sites

The survey was carried out in the north-western and central zones of Tigray, Ethiopia, focusing on one district and four villages from each zone, selected for their significance in finger millet production and consumption (Mereblehe and Asgede Tsimbila). In these areas, subsistence agriculture is the primary livelihood strategy, with households selling any surplus crops at local markets. These areas are among the most food-insecure and impoverished in Tigray. Detailed background information on the study sites is provided in Table 5.1.

5.2.3. Household seed system survey

The study was conducted from October 2019 to November 2020. A total of 160 household heads were interviewed using a semi-structured questionnaire, with additional insights gathered through focus group discussions (FGDs). Snowball sampling, an effective method widely used for social network analysis (Subedi et al., 2003), was employed to select participants. The questionnaire was initially prepared in English and then translated into Tigrigna, the primary local language.

The survey followed a three-step process. The first step involved a reconnaissance survey and discussions with agricultural experts, community leaders, and elders to gather background information on finger millet cultivation in the study areas. In the second step, 24 experienced finger millet farmers, mostly male, were purposefully selected for their knowledge and involvement in technology adoption. These farmers, referred to as first-batch farmers, acted as the entry points for the social network analysis in the northwestern and central Tigray. In-depth interviews with these first-batch farmers were conducted, addressing questions such as: (a) From whom do you usually obtain finger millet seed? (b) From whom did you get finger millet seed in the last growing season?

(c) To whom do you usually give seed? (d) To whom did you give seeds during the last growing season? (e) Who usually asks you for seed? These first-batch farmers identified at least 56 seed exchange partners.

In the third step, 56 of these partners, now referred to as second-batch farmers, were interviewed using the same semi-structured questionnaire. However, only 40 second-batch farmers were asked to name their seed exchange partners, as five had already been interviewed in the first step and 11 were unavailable for various reasons. These second-batch farmers identified 180 additional farmers, referred to as third-batch farmers. Out of these 180, 96 were interviewed, while the remaining 84 were not due to resource constraints.

5.2.4. Data analysis

The seed source data were analyzed to understand seed flows within and between villages as well as among different individuals. The total number of seed exchanges across all 160 households was calculated as the exchange count. Seed network analysis and mapping were carried out using UciNet version 6.21 (Borgatti et al., 2002). Data were entered into a spreadsheet, coded in VNA format, and analyzed with NetDraw (version 2.087) software. In this analysis, farmers were treated as nodes, with their characteristics such as sex, age, education, and religion considered as node attributes. Seed exchange methods (e.g., exchange, gift, purchase) and crop varieties involved were used as tie data. Centrality measures were applied to generate network maps to identify key nodal farmers and their connections.

The analysis focused on three centrality measures: degree centrality, closeness centrality, and betweenness centrality (Abay et al., 2011). Degree centrality indicates the number of direct connections a household has with others; a higher degree suggests greater connectivity. Closeness centrality measures how close a household is to all other households; a lower value sigifies more direct connections. Betweenness centrality reflects the number of shortest paths passing through a household; a higher value indicates more significant indirect connections.

Table 5.1. Characterization of study sites for analyzing social seed networks in Tigray, Ethiopia (2019-2020).

District	**village**	**Altitude (masl)**	**Average annual rainfall (mm)**	**Predominant crop**	**No. households interviewed**
Central tigray					
Mereblekhe	Mereb	1371	510.8 mm	FM, S ,GN & T	20
	E/mariam	1371	510.1 mm	FM, S ,GN, M & T	20
	aditseneke	1452	1045.6 mm	FM, S ,, M & T	20
	adiyemano	1450	1054.7 mm	FM, S ,, M & T	20
North west Tigray					
Asgede tsimbla	D/abay	2300	1408.6	FM, S , & T	20
	Birhan	2258	1409.2	FM, S , & T	20
	Maitekli	1895	1506.4	FM, S , & T	20
	Ar’ada	1896	1506.4	FM, S ,& T	20

m.a.s.l., metres above sea level; FM, finger millet; S, sorghum; GN, Groundnut; T, teff; M, maize
Source: wereda agricultural offices

5.3. RESULTS

5.3.1 Demographic characteristics of the respondents

Table 5.2 presents the demographic characteristics of the respondents. In Merebleke Wereda, 77.5% of the respondents were male, while 22.5% were female. In contrast, Asgedetsimbla Wereda had 92.6% male and 7.4% female respondents, reflecting the prevalence of male-headed households in these areas. Regarding age, 55% of respondents in Merebleke were between 28 and 50 years old, whereas 42% of in Asgedetsimbla were within this age range. Conversely, 45% of respondents in Merebleke were over 50 years old compared to 58% in Asgedetsimbla. The survey also assessed the educational status of the respondents. In Merebleke, 52.5% were illiterate, compared to 45.7% in Asgedetsimbla. Conversely, 47.5% of respondents in Merebleke and 54.3% in Asgedetsimbla had education beyond elementary level.

Table 5.2. Demographic profile of the respondents. Source: Field survey (2019-2020)

Variable	Mereblekhe	**Freq.**	**%**	Asgede tsimbila)	**Freq**	**%**
Sex						
Male		62	77.5		75	92.6
Female		18	22.5		6	7.4
Age (years)						
28-40		20	25.00		11	13.6
41-50		24	30.00		23	28.4
51-60		15	18.75		19	23.5
Above 60		21	26.25		28	34.5
Edu. status						
illiterate		42	52.5		37	45.7
elementary		26	32.5		27	33.3
secondary		7	8.75		11	13.6
Above secondary		5	6.25		6	7.4
No of respondent		**80**	**100**		**81**	**100**

5.3.2. Seed sources and flows

The study revealed that a majority of households growing finger millet (145 households or 90.4%) cultivate traditional farmer's varieties, while 16 households (10%) grow improved varieties (Table 5.3). These farmers primarily acquire their seeds through saving or exchanging them locally. The primary methods of seed acquisition reported by the interviewed households included exchanging seeds with neighbors, receiving seeds from relatives, using own-saved seeds, purchasing from local markets, and obtaining seeds through loans. Specifically, 122 households (76.3%) obtained seeds through exchanges with neighbors, 59 (36.9%) received seeds from relatives, 44 (27.5%) used own-saved seeds, 32 (20%) purchased seeds from local markets, and 15 (9.4%) accessed seeds through loans (Table 5.3).

The study found that seed exchange among farmers predominantly occurred within villages rather than between villages, likely due to stronger social connections with nearby neighbors and relatives. Conversely, seed purchases and access through loans were more common in the villages of ‘Aditseneke’, ‘Adiyemano’, and ‘Mereb’. This trend can be attributed to frequent drought conditions in these areas, making local markets a key source of seed acquisition in these communities (Table 5.3). In Endamariam and Aditseneke, exchanges of seed with relatives were more dominant than acquiring seeds from markets or loans. Analysis of seed flows between villages revealed that respondents from Mereb village were more active in exchanging seeds with both relatives (8 households) and non-relatives. However, seed acquisition through loans was rarely observed across the villages studied. This is likely due to the fact that most farmers tend to maintain closer relationships with their neighbors and relatives compared to non-relatives. Consequently, the seed exchange network was highly localized, with 87.5% of exchanges taking place between farmers within the same village and only 15.6% involving farmers from other villages (Table 5.3).

Table 5.3. Analysis of finger millet seed sources through social seed networks in eight study villages across two finger millet growing zones in Tigray, Ethiopia (2019-2020)

Seed sources analyzed number of farmer hh interviewed

	Central zone (merebleke weredas)				**Northwest zone (A/tsibla weredas)**				
Seed sources and flows	**Simret**		**Mihkaun**		**Debreabay**		**Mizan**		
	AT	**AY**	**MR**	**EM**	**DA**	**BR**	**MT**	**AR**	**total**
Number of hh	**20**	**20**	**20**	**20**	**20**	**20**	**20**	**20**	**160**
Finger millet cultivar available (hh)									
Farmer's variety	20	20	15	17	14	20	20	19	145
Improved variety	0	0	5	3	6	1	0	1	16
Seed origin (number of hh)									
Own	5	4	3	4	5	8	6	9	44
Exchange with neighbors	8	9	14	15	14	16	13	15	122
Exchange with relatives	9	12	13	14	12	11	13	10	59
Origin of seed of those that exchange seed (number of hh)									
Within village	18	18	17	12	18	20	19	18	**140**
Outside village	5	1	2	9	3	1	2	2	**25**
Type of exchange when exchanged within village (hh)									
Exchange with relatives	5	3	5	9	2	7	3	4	**38**
Purchase from market	2	4	2	1	0	1	1	1	**12**
Access through loan	4	3	1	0	0	0	0	0	**8**
Type of exchange when exchanged between village (hh)									
Exchange with relatives	4	1	2	8	3	1	1	1	**21**
Barter with non-relatives	3	1	1	5	2	1	2	1	**16**
Purchase from market	4	3	3	3	2	1	3	1	**20**
Access through loan	3	3	1	0	0	0	0	0	**7**

AT, adi tseneke; AY, adi yemano; MR, mereb; EM, endamariam; DA, debre abay; BR, birhan; MT, maitekli; AR, arada

5.3.3. Analysis of centrality data

The degree of centrality scores presented in Table 5.4 show that farmers within the seed social network occupy various roles, identified as nodal, connector, and accessory positions. The centrality analysis indicated that a farmer might hold one or more of these roles simultaneously. For instance, farmers with high closeness centrality were typically in nodal positions and maintained strong connections. Key examples from the central zone include farmers such as 'AT26', 'AY11', 'AY13', 'AY25', 'EM08', 'MR03', and 'MR14' (Fig 5.1a-b), as well as 'AR18', 'AR19', 'BR17', 'BR33', 'DA15', 'MT37', and 'MT39' from the north-west zone (Fig 5.1c-d). These farmers played crucial roles in facilitating seed access and flow within their communities. Other farmers were identified as holding multiple roles, such as being both nodal and connector, nodal and accessory, or connector and accessory, or even solely fulfilling one specific position within the seed network. This distribution of roles aligns with the findings from the survey (Table 5.4).

The centrality data revealed that farmers with the highest number of direct connections were 'AYII', 'EM08', 'MR14', 'AY25', and 'MR19' from Central, as well as 'BR33', 'MT11', 'AR13', 'AR19', and 'DA19' from north-Western. These farmers, located in the villages of 'Aditseneke', 'Adiyemano', 'Endamariam', and 'Mereb' in the central zone, and 'Araada', 'Brhan', 'Debreabay', and 'Maitekli' in the northwest zone, were central to the seed network (Table 5.4). Additionally, the centrality analysis identified farmers such as 'AT22', 'AY19', 'AY31', 'MR19', 'AR13', 'BR35', 'MT03', and 'MT05' as having significant harmonic closeness within the network. These individuals play a crucial role in managing or influencing seed flows and information about the availability of local varieties, which is essential for the timely and adequate distribution of seeds among farmers growing finger millet. Farmers who are more centrally positioned within the network tend to have better awareness and access to seed sources, particularly compared to those located farther from the core. This proximity facilitates more frequent seed exchanges, especially within villages where farmers are with one another or within families (such as between parents, siblings, aunts, uncles, and other relatives). As a result, seeds are preserved and circulate among farmers year after year.

Table 5.4. Identification of key farmer households in the social seed network occupying central positions as nodal or bridging farmers based on centrality scores, in two finger millet-growing zones in Tigray, Ethiopia, 2021.

Farmer household[a]	**Nodal data calculated on the basis of network analysis**				**Position in network**[b]
	Village	**Degree centrality**	**Betweenness centrality**	**Harmonic closeness centrality**	
Central Zone					
AT17	Aditseneke	1.944			N
AT22	Aditseneke	1.597	0.202		NC
AT24	Aditseneke	3.333		0.818	NA
AT26	Aditseneke	2.431	0.481	0.818	NCA
AT29	Aditseneke	2.569			N
AY11	Adiyemano	4.375	0.237	0.818	NCA
AY13	Adiyemano	1.042	0.162	0.817	NCA
AY19	Adiyemano		0.216	0.818	CA
AY 25	Adiyemano	3.681	0.023	0.817	NCA
AY31	Adiyemano	2.569	0.054		NC
EM08	E/mariam	4.028	0.286	0.818	NCA
EM09	E/mariam	3.264		0.817	NA
EM25	E/mariam	2.292		0.817	NA
EM28	E/mariam			0.816	A
EM33	E/mariam	2.222		0.818	NA
MR03	Mereb	3.264	0.304	0.818	NCA
MR14	Mereb	3.819	0.236	0.818	NCA
MR16	Mereb			0.633	A
MR19	Mereb	3.403	0.233		NC
MR22	Mereb	2.083			N

Northwest Zone					
AR13	Araada	6.389	0.225		NC
AR18	Araada	2.778	0.346	0.817	NCA
AR19	Araada	6.250	0.319	0.818	NCA
AR25	Araada	3.333			N
AR40	Araada	3.403		0.818	NA
BR06	Birhan	1.806			N
BR17	Birhan	2.986	0.234	0.704	NCA
BR28	Birhan	2.014			N
BR33	Birhan	7.292	0.278	0.825	NCA
BR35	Birhan	1.667	0.207		NC
DA15	D/abay	4.722	0.403	0.825	NCA
DA19	D/abay	5.278		0.825	NA
DA20	D/abay	1.806			N
DA23	D/abay			0.824	A
DA32	D/abay	1.944			N
MT03	Maitekli	4.575	0.171		NC
MT05	Maitekli	2.500	0.148		NC
MT11	Maitekli	6.806		0.818	NA
MT37	Maitekli	2.222	0.434	0.818	NCA
MT39	Maitekli	2.917	0.434	0.817	NCA

---

[a] The Smbol ‘Ay11’ means the code for the household Ay11 in the data file.

[b] N, nodal farmer; C, connector farmer; A, access farmer; combinations such as NC means a farmer that is characterized as both nodal and connecter, NCA, means a farmer that is characterized as nodal connecter and accessory

Tables 5.4 and 5.5 present the harmonic closeness centrality measures for farmer households that played key roles in accessing seeds within the network. Active participants included ‘AT24’, ‘AY19’, ‘EM09’, ‘EM25’, ‘EM28’, ‘EM33’, ‘MR16’, ‘AR40’, ‘DA19’, ‘DA23’, and ‘MT11’.

These farmers were skilled at identifying specific local finger millet varieties and knew who in their family or close circles could provide them. Among the various local finger millet varieties, black-seeded types were most frequently exchanged both within and beyond villages. This preference is likely due to the higher yields, better market value, and preference for black-seeded varieties, which are used to make a traditional drink called '*Siwa*'. The exchange of seeds within the network helps preserve these varieties. If a close family member conserves a variety, it is easy for farmers to access it, saving time ensuring seed quality that is suited to local conditions.

The network analysis revealed varying roles among the 160 farmers interviewed. Of these, 15 farmers held roles in all three centrality measures—nodal, connector, and access farmers—within the seed network. Additionally, 10 farmers held both nodal and connector positions, 11 were both nodal and cloth access farmers, and 3 were both connector and access farmers. Some farmers had only one type of centrality role: 11 were solely nodal, 6 were only connectors, and 5 were exclusively access farmers (Table 5.5). Overall, 61 farmers were actively involved in seed exchanges, which helped build trust among them. Seeds obtained from family members or local sources were more likely to remain within the region, as they were well-suited to the local conditions. The study emphasized the importance of networks among friends, family, and acquaintances in seed acquisition.

5.3.4. Analysis of network map

Fig. 5. 1 (a, b, c, and d) presents the network map generated from the social network analysis, which illustrates key nodal farmers and seed flow patterns based on degree centrality. Various network maps can be created using different variables, such as members' gender, religion, education, and age. The size of each node on the map represents the degree centrality of households crucial to the network's functionality. Green nodes specifically indicate female household heads that play a significant role in seed circulation within the network. These network maps are valuable for identifying key farmers—those who are central to the social community—and visualizing the exchange of finger millet farmers' varieties among farmers, which supports the preservation of crop genetic diversity. By combining visual maps (Fig 5. 1; a, b, c, and d) and mathematical scores (Table 5.5), farmers are categorized as nodal, connector, or access farmers, and the network is

classified as either large or small. These classifications highlight the importance of these networks in informal seed systems and in the conservation of agricultural biodiversity within the community. The network maps displayed several key variables, including the positions of connector, nodal, and access farmers, the flow and direction of seed/varieties, and the types of crop varieties being exchanged. Larger nodes represent nodal farmers who play a major role in seed exchange and maintain numerous direct or indirect connections within the community.

The network maps revealed both large and small networks within the community. A large seed network consists of many interconnected farmers, while a small network involves fewer connections. Additionally, sub-networks within the larger network are shaped by social factors such as marriage, kinship, holidays, funerals, and religious activities.

The maps also highlighted the role of female farmers in seed flow, particularly in the central zone villages of Mereb, Endamariam, Aditseneke, and Adiyemano, where female participation is more prominent. In contrast, female involvement was less prominent in villages of the northwest zone. From the network maps, one can identify who provides and receives seeds, how the flow occurs, and which seeds/varieties are being exchanged. For example, Figures 1 (a, b, c, and d) show that farmers BR06, BR33, BR35, DA15, DA23, AR13, AR19, MT03, MT11, AY04, AY19, AT24, AT26, MR01, MR03, and MR19 are the top seed providers. Notably, DA23 and MR19, who are female farmers, hold significant positions in the network.

Table 5.5. Characterization of farmer households and villages occupying various positions in the social seed network for finger millet in Tigray, Ethiopia, 2021.

Type[b]	No. of farmers	Number of farmer households that occupied specific positions in the Finger millet seed networks[c]								
		Household code[a]	Central				North west			
			AT	**AY**	**MR**	**EM**	**DA**	**BR**	**MT**	**AR**
NCA	15	AT26, AY11, AY13, EM08, MR03, MR14, DA15, BR33, MT37, MT39, AR18, AR19, MR01, AT07 and MT30	2	2	3	1	1	1	3	2
NC	10	AT22, MT03, MT05, AR13, MR19, BR17, BR35, MR34, MR37 and AR17	1	-	3	-	-	2	2	2

NA	11	AT24, AY25, EM09, EM25, EM33, DA19, MT11, AR40, DA25, BR38 and BR03	1	1	-	3	2	2	1	1
CA	3	AY19, MR03 and AY04	-	2	1	-	-	-	-	-
N	11	AT17, AT29, AY31, MR22, DA20, DA32, BR06, BR28, AR25, EM28 and DA11	2	1	1	1	3	2	-	1
C	6	MT07, EM32, EM27, MR37, MR15 and AY28	-	1	2	2	-	-	1	-
A	5	EM28, MR16, DA23,BR24 and DA07	-	-	1	1	2	1	-	-
Total of farmer households, identified per village			**6**	**7**	**11**	**8**	**8**	**8**	**7**	**6**
Percentage of interviewed households, identified per village (%)			**30**	**36.8**	**61.1**	**42.1**	**40**	**40**	**33.3**	**27.3**

[a] The symbol 'AT26'means the code for the farmer household AT26 in the data file.

[b] N, nodal farmer; C, connector farmer; A, access farmer; combinations such as NC means a farmer who is characterized as both nodal and connecter.

[c] AT, Aditseneke (20); AY, adiyemano (19); MR, mereb (18); EM, endamariam (19); DA, debreabay (20); BR, Birhan (20); MT, maitekli (21) and AR, araada (22).

5.4. DISCUSSION

5.4.1 Socio-Demographic Characteristics

Most of the respondents (55%) in Merebleke were below the age of 50 years old. In contrast, above 50 years old (58%) were in Asgedetsimbla. This suggests that Asgedetsimbla had a relatively higher percentage of elderly individuals compared to Merebleke, possibly due to factors such as limited healthcare access, malnutrition, and harsh environmental conditions, which can lead to higher rates of illness and mortality among older population (Abebaw et al., 2023). Additionally, the demographic trend in Asgedetsimbla may be influenced by limited land availability for younger farmers, as much of the land is controlled by older individuals. The higher illiteracy rate in Merebleke (52.5%) could be attributed to its more remote location near the Eritrean border, making access to education more challenging compared to Asgedetsimbla (45.7%), which is closer to the main road between Shire and Gondar, providing better access to educational resources. Education plays a crucial role in the adoption of new agricultural technologies, including improved seeds, which affect production and productivity (Zegeye et al., 2001). Formal education enhances farmers' ability to comprehend and implement new agricultural practices and risks, positively influencing the adoption of innovations and boosting technical efficiency (Asfaw & Admassie, 2004; Mamo et al., 2018).

5.4.2. Seed Exchange mechanisms and their impact on building social networks

Farmers continue to grow local and farmer’s varieties of finger millet due to their resilience to climate changes. This study found that more than 87.8% of farmers in the entire study area grow finger millet using farmer’s varieties, while only 4.5% cultivate local varieties (Table 5.3). Basically, farmer’s finger millet varieties are categorized in to five types based on their seed clour: black, brown, purple, red and white. As a result of this phenotypic variation, farmers have a tendency to prefer the seed color they are more accustomed to, leading them to typical grow only one or two types at home. This, in turn, forces them to seek additional seeds primarily from their neighbors and relatives rather than relying on their own saved seeds. Seed acquisition through loans or purchases represented a smaller proportion of the total seed access. This finding is in line with the findings of Song *et al*. (2019), which shows that finger millet seeds are primarily sourced and exchanged with neighbors and relatives. Similar patterns were observed for finger millet and maize varieties in Nepal, where seed varieties were predominantly obtained via seed exchange systems with neighbors and relatives (Devkota *et al*., 2014). Most studies on farmer seed exchange systems have demonstrated that a high level of exchange between neighbors and kinship networks positively contribute to the flow of genetic diversity in crops (Labeyrie et al., 2016; Rodier & Struik; 2018; Ricciardi, 2019; Song et al., 2019).

In Tigray, Ethiopia, more than 80% of the farmers rely on informal seed exchange channels for acquiring seeds, regardless of the crop they cultivate (Abay *et al*., 2011). The study found that seed exchange primarily occurs within villages of the entire study, rather than between villages. When exchanges happen between villages, they tend to involve relatives. This highlights the stronger social interactions that take place within villages compared to between villages, leading to the development of robust social networks at the village level. The formation of these networks is informed by several factors, such as marriage, relationships between neighbors and friends, and kinship and religious ties. Besides, informal seed systems contribute to building social links among farmers in the community via seed sharing, exchanges, selling or purchasing. Hence, seed exchange in small-scale farming plays a crucial role in promoting seed-driven social networks. Sharing seeds among smallholder farmers enhances the development of these social seed-networks (Davies *et al*., 2022).

5.4.3 Implication of Seed source and flows

The recent seed flow study has provided valuable insights into how seeds are distributed and exchanged within and beyond villages. The research highlighted the critical role of seed exchange in enhancing genetic diversity within farming communities. Since farmers' varieties are typically well-suited to their specific environmental conditions, this exchange is vital for collecting and preserving diverse finger millet germplasm, which is essential for future breeding and maintaining locally adapted traits. The study by Devkota et al. (2014) found that seed exchange was more common within villages than with neighboring villages. Within villages, exchanges more frequently took place between neighbors, followed by exchanges with relatives (Table 5.3). This finding aligns with Abay et al. (2011), who reported that while farm-saved seeds were the primary source for farmers, neighbors played a crucial role in seed provision. Similarly, Samberg et al.

(2013) found that 55% of 302 analyzed barley fields used seeds saved from the previous year, with 70% of farmers sourcing their seeds from neighbors.

Further research by Labeyrie et al. (2016) confirmed that the majority of seed exchanges occur among relatives. In line with this, Rodier and Struik (2018) reported that seed exchanges were predominantly confined to village boundaries. The demand for locally adapted seeds that meet farmers' specific needs drives the popularity of local finger millet varieties. These varieties are particularly valued for their role in producing traditional foods. For example, black-seeded finger millet is commonly used for making '*Siwa*,' a local drink preferred by over 80% of the population in the Tigray region of Ethiopia, while red and white-seeded finger millet varieties are used for preparing '*Injera*' (Tsehaye et al., 2006; Tesfaye & Mengistu, 2018). This study corroborates findings from several other studies (Nagarajan et al., 2007; Abay et al., 2011; Samberg et al., 2013; Song et al., 2019), which also reported that farmers primarily relied on saving seeds, exchanging with neighbors and relatives, and purchasing from markets, with seed exchange being more prevalent within villages than between villages.

5.4.4. Characterization of seed network members

Understanding the roles of farmers within seed networks through centrality measures is crucial for assessing their influence on seed access and distribution. This analysis provides valuable insights into each farmer's position within the network, helping to identify the most effective strategies for maintaining on-farm crop diversity, sharing genetic resources, promoting seed flow, and implementing breeding or seed interventions. A farmer with nodal positions included (AT17, AT29, MR22, AR25, BR06, BR28, DA20 and DA32) in this study showed only degree of centrality (Table 5.4). This confirmed that farmers with high degree of centrality might not necessarily have high betweenness or closeness centrality, and vice versa. Seed network roles include various types such as nodal, connector, and closeness, or combinations thereof, all of which affect a farmer's access to seeds (Mcewan et al., 2021).

Social seed network analysis offers valuable insights for researchers, breeders, seed distributors, and those involved in seed business development. This information helps them take informed steps to support participatory crop improvement, local variety dissemination, and seed distribution.

BR33 (7.29), MT11 (6.81), AR13 (6.39), AR19 (6.25), DA19 (5.28), AY11 (4.38), EM08 (4.03), MR14 (3.82), AY25 (3.68), and MR19 (3.40) were among the farmers who were selected from the existing social seed network with the highest degree of centrality for this study.

Identifying influential farmers within the network can enhance the community's access to diverse finger millet farmers' varieties adapted to challenging environmental conditions such as drought, diseases, and logging issues. Coomes et al. (2015) showed that weak social networks are more vulnerable to these adverse conditions due to limited access to locally adapted seeds, while stronger networks provide better resilience. Additionally, centrality in seed exchange networks plays a crucial role in conserving local farmers' varieties and traditional knowledge, which is vital for preserving agro-biodiversity (Tsehaye et al., 2006; Song et al., 2019). In Southern and Northwestern Ethiopia, households are intricately connected through complex seed exchange networks (Samberg et al., 2013; Rodier & Struik, 2018). Understanding these relationships is crucial for designing effective intervention strategies and targeting conservation efforts.

5.4.4.1. Nodal Farmers and Their Characteristics

Using NetDraw computations, it is possible to identify key farmers who play a crucial role in informal seed systems and agro-biodiversity management within their communities. These key farmers, typically occupying nodal positions, are central to the efficient distribution of seeds. By understanding which farmers are most connected, seed distributors—such as donors, NGOs, research institutions, and breeders—can more effectively introduce and disseminate new varieties. Typically, nodal farmers are older, wealthier, and more influential, giving them the capacity to sustain their networks and control resources. This, in turn, promotes local seed distribution and enhances genetic diversity. Our findings confirm that certain farmers have higher centrality measures, making them pivotal in facilitating the flow of finger millet farmers' varieties and maintaining agricultural biodiversity on farms. As indicated in Table 5.4 and Fig 5.1. a, b, c and d, seed network positions such as nodal, bridging, or connector roles, as along with accessory and closeness positions, significantly influence a farmer's access to seed within the finger millet-growing community.

The study also revealed a gender disparity, with men typically holding more significant nodal positions in seed exchange networks compared to women, which impacts their access to seeds. This is consistent with previous studies (McGuire, 2008; Devkota et al., 2014; Poudel et al., 2015;

Rodier & Struik, 2018; Ricciardi, 2019; Otieno et al., 2021; Llamas-Guzmán et al., 2022), which found that men are generally more involved in seed exchanges. In many villages in Tigray, men are heads of households and are responsible for farm-related activities, while women focus on domestic responsibilities. However, Llamas-Guzmán et al. (2022) identified some women who also play significant nodal roles and are responsible for conserving a wide range of seeds.

The present survey indicates that households in prominent nodal positions possess considerable knowledge of finger millet farmers' varieties and often source seeds from outside their villages to distribute within, as well as share seeds from within their villages to other areas. Supporting and training these nodal households in seed cleaning and multiplication could further boost crop genetic diversity. Therefore, seed exchange network analysis is a valuable tool for managing on-farm genetic diversity and enhancing the flow of finger millet farmers' varieties within communities. Properly engaging and mobilizing nodal farmers could improve the distribution of new crop varieties, strengthening food security. As key sources of seed information and custodians of crop diversity, nodal farmers are critical for achieving sustainable food and nutrition security.

5.4.4.2. Connector Farmers and Their Characteristics

Betweenness centrality measures the role of a farmer in connecting other members within a seed exchange network. Households identified as connectors in such networks play a crucial role in managing the flow of both information and seeds within the community. These farmers are central to the network's conservation and circulation of seeds, ensuring its continuity and sustainability. Connectors serve as intermediaries, linking farmers who are not directly connected but are connected through a third farmer. This bridging function is essential for the movement of seeds and genetic materials within and across networks. Studies have shown that connector farmers significantly impact the longevity of seed exchange networks by linking different sub-networks, helping to maintain these networks over time (Poudel et al., 2015; Devkota et al., 2014). If these key connectors leave farming, migrate, or pass away, the network could be disrupted, as they connect distinct sub-groups within the community.

The current study identified several key connector farmers from various villages, including BR33, BR06, BR17, DA15, DA23, DA19, and DA20 from Debreabay; MT30, MT11, MT03, MT39, and

MT37 from Mizan; AT22, AT26, AT24, AT29, AT07, AY04, AY19, AY11, AY13, AY25, and AY31 from Simret; and MR01, MR03, MR14, EM09, EM33, EM08, EM32, EM25, and EM28 from Mihkaun. Strengthening and empowering these farmers through targeted training and participatory approaches in seed variety selection and exchange systems can significantly enhance the resilience and reach of the network. Such an approach also supports the preservation and improvement of finger millet farmers' varieties, which are often overlooked by researchers and agricultural development programs. These findings align with previous research, which emphasizes the importance of understanding seed exchange pathways and identifying key farmers to design effective strategies for managing on-farm crop genetic diversity (Abay et al., 2011; Poudel et al., 2015; Song et al., 2019).

5.4.4.3 Access farmers (harmonic closeness) and their characteristics

Harmonic closeness is a key centrality measure used to describe a household's ability to access seed sources within a social seed network. This metric reflects how quickly and easily a household can access seeds from other members in the network. Farmers with high harmonic closeness are better positioned to facilitate the rapid transfer of seeds, as their proximity within the network allows for more efficient seed access and sharing. Conversely, farmers with lower harmonic closeness have limited access to seed sources.

Seed sharing within a community relies heavily on the closeness of farmers who are better positioned to access available seed varieties. This accessibility promotes seed saving, harvesting, and sharing among smallholder farmers, thereby strengthening relationships within the seed network and contributing to a more secure food system (Davies et al., 2022). Such accessibility not only supports direct seed exchanges but also contribute to the overall seed distribution process, enabling the movement of seeds through multiple connections.

Furthermore, accessible farmers play a crucial role in fostering social-ecological sustainability and helping communities in adapting to changing climate conditions. Households with high accessibility to other members of the seed network actively promote the movement of seed varieties, both directly and indirectly. Without these key accessible farmers, many seed varieties could be lost, disrupting the structure and functioning of the seed exchange network.

Numerous studies have shown that the movement of planting materials, including seeds and cuttings, is significantly influenced by the harmonic closeness of farmers within the network (McGuire, 2007; Abay et al., 2011; Samberg et al., 2013; Coomes et al., 2015; Pautasso, 2015; Ricciardi, 2019; Llamas-Guzmán et al., 2022; Davies et al., 2022; Kifle et al., 2022; Nduwimana et al., 2022; Abebaw et al., 2023). When farmers are widely dispersed, they may struggle with information gaps regarding seed sources, which can lead to seed insecurity and reliance on poorly adapted or unhealthy seeds.

5.4.5. Enrichment of genetic diversity of finger millet varieties

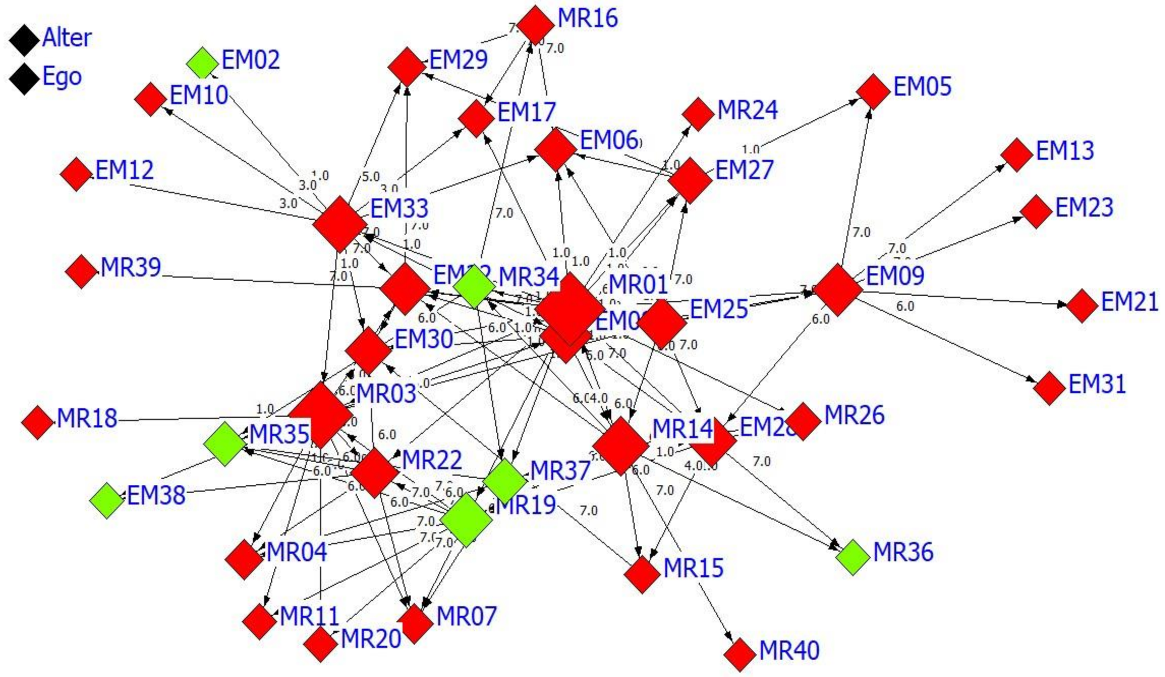
Genetic diversity in crops can be significantly enhanced through seed exchange networks among farmers, which facilitate the circulation of various crop varieties and are widely recognized as a valuable method for conserving this diversity (Llamas-Guzmán et al., 2022). Despite this, the improvement of finger millet farmers' varieties has been largely neglected by Ethiopian crop researchers (Tesfaye and Mengistu, 2017; Reddy et al., 2009; Fetene et al., 2010). As a result, farmers in Ethiopia, particularly in the central and northwest zones of Tigray, continue to cultivate local finger millet farmers' varieties. Although these farmers' varieties yield less than improved varieties, they are better adapted to local environmental conditions, require minimal agricultural inputs, and are resistant to diseases and drought. They also perform well in low-fertility soils found in marginal areas.

Different types of finger millet farmers' varieties are valued differently by farmers, depending on their specific needs. For example, some prefer varieties that are suited for making traditional drinks like '*Siwa*,' while others choose varieties for preparing *Enejera* or bread. This variation in preferences leads to a wide range of finger millet farmers' varieties being cultivated within the community. Seed circulation through social seed networks can enhance the genetic diversity of these farmers' varieties, potentially benefiting further breeding and improvement efforts by researchers, agronomists, breeders, and agricultural developers.

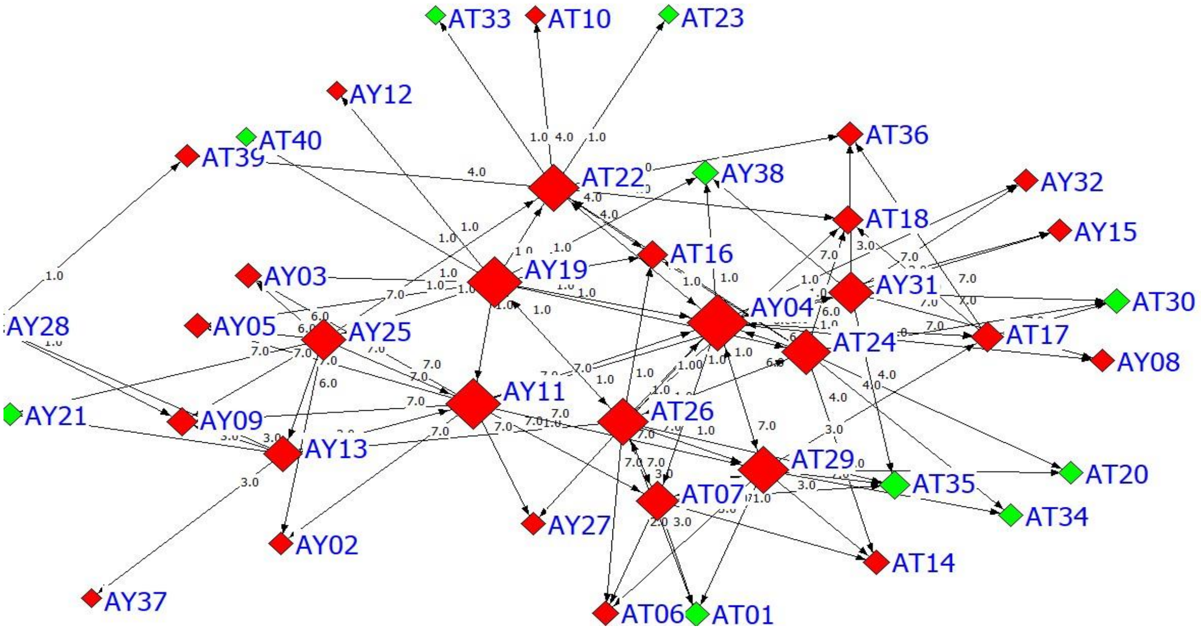
Analyzing social seed networks is a crucial approach for studying local seed systems and conserving finger millet farmers' varieties. The availability of these local seed varieties in farmers' hands is crucial for the *in-situ* conservation of finger millet. This genetic diversity is supported through social seed networks, as noted by Samberg et al. (2013) and Devkota et al. (2014). Nodal and connector farmers play a vital role in maintaining on-farm crop diversity by selecting and distributing seed varieties within their networks. Their ability to effectively manage seed flow ensures the adequate sharing of genetic material within the community (Seboka & Deressa, 2007).

The Tigray region, known for its rich genetic diversity, is considered a center of origin and diversification for finger millet (Tsehaye et al., 2006). This region serves as a valuable seed bank for future genetic improvement programs. This study identified and assessed the social seed network for finger millet in the surveyed villages and found that households in three key positions are crucial for seed flow and agro-biodiversity conservation within informal seed systems. These findings align with Devkota et al. (2014), who noted that most finger millet farmers save their own seeds, primarily local varieties, and play a significant role in conserving agro-biodiversity and ensuring food security.

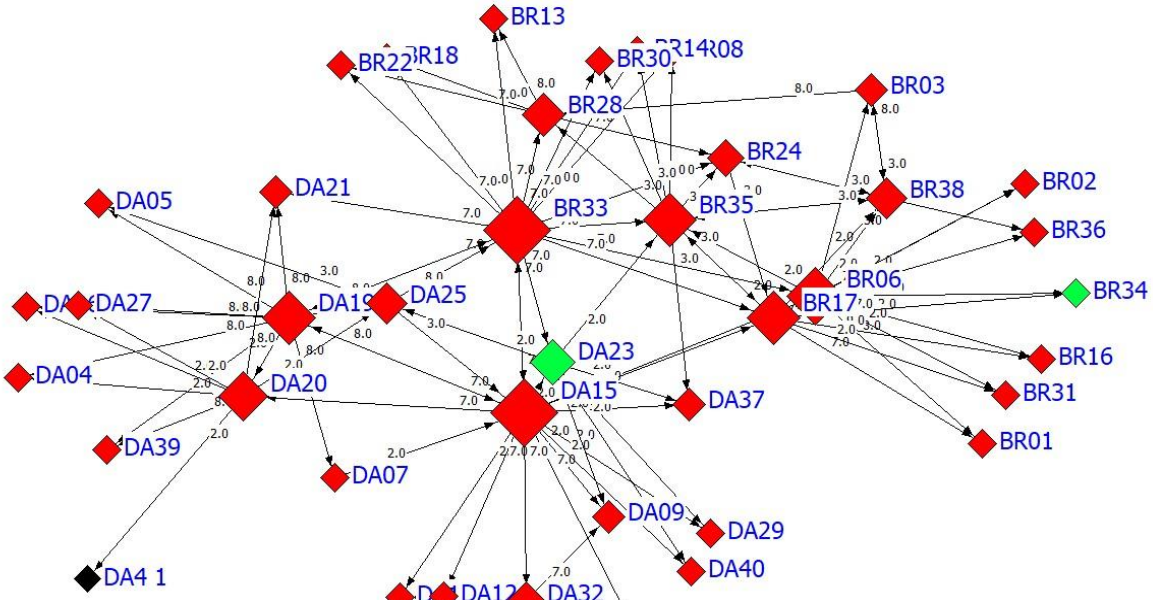
.



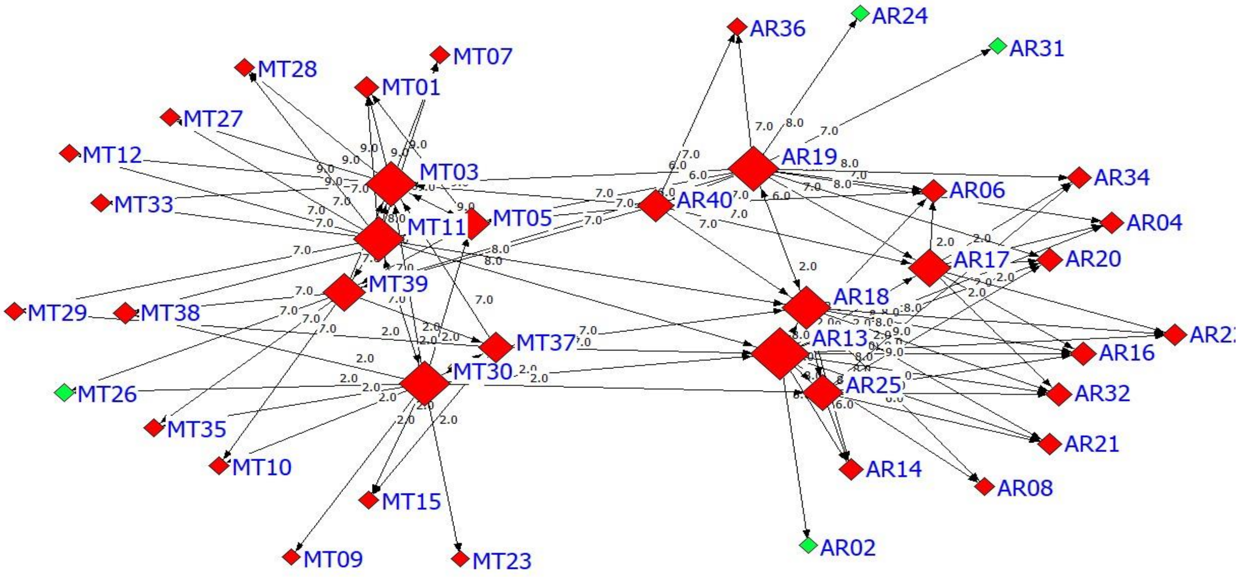
a)


AT33
AT10
AT23
AY12
AT40
AT39
AT36
AT22
AY38
AY32
AT18
AY15
AY19
AT16
AY03
AY31
AT30
AY28
AY05
AY25
AY04
AT24
AT17
AY08
AY11
AY21
AY09
AT26
AY13
AT29
AT20
AT35
AT07
AT34
AY27
AY02
AT14
AY37
AT06
AT01

b)


BR13
BR18
BR14
BR08
BR22
BR30
BR03
BR28
BR24
DA21
BR02
DA05
BR33
BR35
BR38
BR36
DA25
BR06
BR34
DA27
DA19
BR17
DA23
BR16
DA04
DA20
DA15
DA37
BR31
DA39
DA07
BR01
DA09
DA29
DA40
DA4 1
DA12
DA32
DA10

c)



d)

Figure 5.1. Farmers' social seed networks showing large networks, small networks, and sub networks in study villages. Node size is an indication for the degree centrality of the household; arrows indicate the direction of the seed flow; red node color represents the male household and green color represents the female household in the networks; the blue numbers indicate code for the households; letters indicated the name of kebeles used in the study (a = Mereb, b = Simret, c = Debreabay and d = Mizan), black numbers indicate the code for variety exchanged and mode of flow of the varieties (1 =Mereb-1, 2 =Tekeze-1, 3 = Tadese, 4 = Waliye, 5 = Hishey, 6 = Gobezay, 7 = Fanshoy, 8 = Zeritesfay and 9 = Arkibi and 1.0 = free, 2.0 = gift, 3.0 = exchange, 4.0 = purchase and 5.0 = loan). .

Studying social seed networks among finger millet farmers offers significant benefits to research institutions, agricultural extension services, seed-providing partners (such as NGOs), universities, and other stakeholders. Understanding these networks helps these organizations identify the most effective collaborators for disseminating knowledge and skills related to improved seed varieties and agricultural inputs. It also enables the development of targeted capacity-building programs for key farmers within these networks, strengthening their ability to maintain genetic diversity, ensure stable production, promote the use of diverse varieties, and mitigate risks such as crop failure, insect infestations, and diseases, ultimately contributing to food security.

Research has consistently shown that seed flow among farmers is crucial for conserving crop diversity. This diversity is essential for plant breeders and farmers to improve and adapt crops to changing climate conditions and future challenges (Mathur, 2012; Samberg et al., 2013; Shrestha, 2013; Devkota et al., 2014; Poudel et al., 2015). Consequently, traditional seed exchange systems for finger millet in the study area are highly localized, reflecting a rich presence of local varieties that are valuable for on-farm conservation and genetic improvement.

5.4.6. Enhancing the dissemination of new technologies

Analyzing the functional seed exchange network in small-scale farming is essential for identifying key individuals or households who play a significant role in facilitating the movement of genetic materials within the community. This analysis provides valuable guidance for local seed experts, agricultural extension services, and crop breeders by helping them support and train farmers in maintaining traditional seed exchange systems and building their capacity for seed selection. Understanding the existing seed networks and social relationships is crucial for recognizing the roles of nodal and connector farmers within these networks (Devkota et al., 2014).

Once these networks are understood, they can be leveraged as channels for introducing new technologies, such as improving crop yields, selecting specific plant traits, experimenting with new crops and varieties, or replacing lost or failed seeds. Furthermore, analyzing seed exchange networks can help develop effective seed dissemination strategies for local farmers and design participatory crop breeding programs involving influential farmers. Collaboration with these key farmers facilitates the creation of new varieties tailored to their needs and well-suited to the broader environmental context. Consequently, scaling up and disseminating new technologies through these established social seed networks can lead to more successful implementation and delivery to targeted beneficiaries (Fetene et al., 2010).

5.4.7. Local seed sector development

Social seed network analysis offers valuable insights by identifying households or farmers who can bolster local seed systems. This approach is instrumental in shaping interventions related to agricultural extension, seed dissemination, and seed business development. By improving informal seed network, these efforts can enhance seed security and bolster resilience to climate change (Fetene et al., 2010).

5.4.8. Social seed network analysis: final reflections on the tool

Social seed network analysis is a crucial method for understanding seed exchange within the broader framework of informal seed systems in smallholder farming communities. It sheds light on how social and cultural interactions among households create and sustain connections within their networks. By examining the complex patterns of seed transactions within a specific village, this tool helps identify the most influential farmers who shape and direct seed flow both within and between villages (Abay et al. 2011) . As discussed in this paper, the three centrality measures—, nodal, connector, and harmonic closeness—are essential for visualizing and understanding household positions within the social seed network (Ricciardi, 2019). These key households play a vital role in developing strategies for managing crop genetic diversity, creating new varieties, and supporting local farmers with new technologies and interventions.

5.5. CONCLUSION AND RECOMMENDATION

5.5.1. Conclusion

Among finger millet-growing households, 145 (90.4%) cultivate traditional finger millet varieties, while 16 (10%) grow improved varieties. Most farmers maintain strong relationships with their neighbors and relatives, contributing to a highly localized seed exchange network. Specifically, 87.5% of seed exchanges occur within the same village, with 15.6% taking place between farmers from different villages. Seed exchanges with neighbors are most common, followed by exchanges with relatives.

Centrality analysis of the seed network reveals patterns of seed exchange within and between villages. The analysis shows the crucial role of farmers who are central to the network,referred to as nodal farmers, in conserving finger millet varieties. Key nodal and connector farmers, such as those identified by codes like ‘AT26’, ‘AY11’, ‘AY13’, ‘AY25’, ‘EM08’, ‘MR03’, and ‘MR14’ in the central zone, and ‘AR18’, ‘AR19’, ‘BR17’, ‘BR33’, ‘DA15’, ‘MT37’, and ‘MT39’ in the northwest zone of Tigray, are vital in facilitating seed access within the network.

The survey indicates that this study provides valuable insights for crop breeders to evaluate the reach of their improved varieties. To address potential issues with seed distribution, breeders may need to collaborate with seed companies or distribution networks to enhance access and ensure that varieties reach the areas where they are needed. Additionally, understanding the centrality of farmers within the seed network is crucial for analyzing seed exchange patterns and flows, both within and between villages. The findings suggest that centrality measures at the household level are linked to families that conserve finger millet varieties. These central or nodal families typically preserve three to five traditional varieties and contribute significantly to the conservation of these crops. This extensive traditional knowledge is crucial for advancing finger millet seed systems, improving management and sustainability, and developing targeted strategies based on a comprehensive understanding of seed flow dynamics.

5.5.2 Recommendation

The current study on the social seed network for finger millet highlights potential issues and bottlenecks in seed flow that may affect the availability and quality of seeds. It also identifies opportunities to improve seed management and distribution. Based on these findings, strategies and interventions can be proposed to enhance the on-farm management of finger millet genetic resources, such as improving seed flow efficiency, supporting seed diversity, and ensuring access to high-quality seeds. These insights can support evidence-based policy-making and strategic planning for strengthening plant genetic resource management in target regions.

The study provides crop breeders a valuable opportunity to leverage these networks for promoting and expanding new seed varieties. It clarifies the structure and interaction processes within the seed exchange network, identifying key connector, nodal, and access farmers who are crucial in the exchange of different seed types. This information is vital for implementing effective participatory breeding programs.

Engaging with these central farmers can accelerate the circulation of improved seed varieties, contributing to the conservation and maintenance of agro-biodiversity. The findings also shed light on the factors influencing informal seed systems, allowing researchers, extension services, seed experts, governments, and local NGOs better understand and address the socio-economic, environmental, cultural, and familial aspects of these systems. This knowledge is essential for designing effective programs to introduce and distribute improved seed varieties to all farmers.

5.6. REFERENCE

Abay, F., De Boef, W., & Bjørnstad, Å. (2011). Network Analysis Of Barley Seed Flows In Tigray, Ethiopia: Supporting The Design Of Strategies That Contribute To On-Farm Management Of Plant Genetic Resources. *Plant Genetic Resources: Characterisation And Utilisation*, *9*(4), 495–505.

Abebaw, Y., Dawit, Y., Sisay, T., & Ayalew, D. (2023). Sources Of Bread Wheat (Triticum Aestivum L .) Seed In Northwest. *Discover Sustainability*.

Asfaw, A., & Admassie, A. (2004). The Role Of Education On The Adoption Of Chemical Fertiliser Under Different Socioeconomic Environments In Ethiopia. *Agricultural Economics*, *30*(December), 215–228.

Badstue, L. B., Bellon, M. R., Berthaud, J., Juárez, X., Manuel, I., Solano, A. M., Ramírez, A., Rosas, I. M., & Bellon, R. (2006). *Examining The Role Of Collective Action In An Informal Seed System : A Case Study From The Central Valleys Of Oaxaca , Mexico Examining The Role Of Collective Action In An Informal Seed System : A Case Study From The*. *34*(2), 249–273.

Biemond, P. C., Oguntade, O., Kumar, P. L., Stomph, T. J., Termorshuizen, A. J., & Struik, P. C. (2013). *Does The Informal Seed System Threaten Cowpea Seed Health ? 43*, 166–168.

Borgatti, S.P., Everett, M.G., Freeman, L.C., 2002. UCINET 6 for Windows: Software for Social Analysis. Analytic Technologies, Harvard, MA.

Coomes, O. T., Mcguire, S. J., Garine, E., Caillon, S., Mckey, D., Demeulenaere, E., Jarvis, D., Aistara, G., Barnaud, A., Clouvel, P., Emperaire, L., Louafi, S., Martin, P., Massol, F., Pautasso, M., Violon, C., & Wencélius, J. (2015). Farmer Seed Networks Make A Limited Contribution To Agriculture ? Four Common Misconceptions. *Journal Of Food Policy*, *56*, 41–50.

Davies, A. R., Rut, M., Feeney, J. K., & Davies, A. R. (2022). *Seeds Of Change ? Social Practices Of Urban Community Seed Sharing Initiatives For Just Transitions To Sustainability Sharing Initiatives For Just Transitions To Sustainability*. *May*.

Devkota, R., Khadka, K., Gartaula, H., Shrestha, A., Upadhya, D., Chaudhary, P., & Patel, K. (2014). Farmers' Seed Networks And Agro-Biodiversity Conservation For Sustainable Food Security: A Case From The Mid-Hills Of Nepal. *Biodivresity Watch*, *4*(July), 109–133.

Fetene, M., Okori, P., Gudu, S., Mneney, E. E., & Tesfaye, K. (2010). *Delivering New Sorghum And Finger Millet Innovations For Food Security And Improving Livelihoods In Eastern Africa*. *November*, 1-52.

Kifle, T., Tolossa, D., Shibru, A., & Alemu, D. (2022). *Analysis Of Seed System Actors : Roles , Responsibilities , And Linkages In Central Ethiopia*. *32*(2), 71–97.

Labeyrie, V., Thomas, M., Muthamia, Z. K., & Leclerc, C. (2016). Seed Exchange Networks, Ethnicity, And Sorghum Diversity. *Proceedings Of The National Academy Of Sciences Of The United States Of America*, *113*(1), 98 103.

Llamas-Guzm, L. P., Chavero, E. L., Rivera, H. R. P., & Casas, A. (2022). *Seed Exchange Networks Of Native Maize , Beans , And Squash In San Juan Ixtenco And San Luis Huamantla , Tlaxcala , Mexico*.

Mamo, T., Getahun, W., Chebil, A., Tesfaye, A., Debele, T., Assefa, S., & Solomon, T. (2018). *Technical Efficiency And Yield Gap Of Smallholder Wheat Producers In Ethiopia : A Stochastic Frontier Analysis*. *July*.

Mathur, P. N. (2012). Global Strategy For The Ex Situ Conservation Of Finger Millet And Its Wild Relatives. *New Delhi, Ondia: Biodiversity International, Sub-Regional Dffice for South Asia, NASC Complex, Pusa Campus;* 1–62.

Mcewan, M. A., Almekinders, C. J. M., Andrade-Piedra, J. J. L., Delaquis, E., Garrett, K. A., Kumar, L., Mayanja, S., Omondi, B. A., Rajendran, S., & Thiele, G. (2021). *" Breaking Through The 40 % Adoption Ceiling : Mind The Seed System Gaps ." A Perspective On Seed Systems Research For Development In One CGIAR*. *50*(1), 5–12.

Mcguire, S. J. (2007). *Vulnerability In Farmer Seed Systems : Farmer Practices In Eastern Ethiopia 1*. *61*(3) 211–222.

Nagarajan, L., Pardey, P., & Smale, M. (2007). Seed Systems And Millet Crops In Marginal Environments Of India: Industry And Policy Perspectives. *Quarterly Journal Of International Agriculture*, *46*(3), 263–288.

Nduwimana, I., Sylla, S., & Xing, Y. (2022). *Banana Seed Exchange Networks In Burundi – Linking Formal And Informal Systems*. *51*(3), 334-348.

Otieno, G., Zebrowski, W. M., Recha, J., & Reynolds, T. W. (2021). *Gender And Social Seed Networks For Climate Change Adaptation : Evidence From Bean , Finger Millet , And Sorghum Seed Systems In East Africa*.

Pautasso, M. (2015). *Network Simulations To Study Seed Exchange For Agrobiodiversity Conservation*. 145–150.

Poudel, D., Sthapit, B., & Shrestha, P. (2015). *An Analysis Of Social Seed Network And Its Contribution To On-Farm Conservation Of Crop Genetic Diversity In Nepal*. *2015*.

Reddy, V. G., Upadhyaya, H. D., Gowda, C. L. L., & Singh, S. (2009). Characterization Of Eastern African Finger Millet Germplasm For Qualitative And Quantitative Characters At ICRISAT. *Journal Of SAT Agricultural Research*, *7*(1), 1-9.

Ricciardi, V. (2019). Social Seed Networks : Identifying Central Farmers For Equitable Seed Access Social Seed Networks : Identifying Central Farmers For Equitable Seed Access. *AGSY*, *139*(October 2015), 110–121.

Rodier, C., & Struik, P. C. (2018). Nodal Farmers' Motivations For Exchanging Sorghum Seeds In Northwestern Ethiopia. *Sustainability (Switzerland)*, *10*(10), 1–15.

Samberg, L. H., Shennan, C., & Zavaleta, E. (2013). Farmer Seed Exchange And Crop Diversity In A Changing Agricultural Landscape In The Southern Highlands Of Ethiopia. *Human Ecology*, *41*(3), 477–485.

Seboka, B., & Deressa, A. (2007). Education And Extension Validating Farmers ' Indigenous Social Networks For Local Seed Supply In Central Rift Valley Of Ethiopia. *The Journal Of Agricultural*, *December 2014*, 37–41.

Shrestha, D. (2013). *MS 11: Special Issue On Community Food Security For Int J On Biodiversity Watch Farmers' Seed Networks And Agrobiodiversity Conservation For Sustainable Food Security: A Case From The Mid-Hills Of Nepal*. 1–32.

Song, Y., Fang, Q., Jarvis, D., Bai, K., Liu, D., Feng, J., & Long, C. (2019). Network Analysis Of Seed Flow, A Traditional Method For Conserving Tartary Buckwheat (Fagopyrum Tataricum) Farmers' varieties In Liangshan, Southwest China. *Sustainability (Switzerland)*, *11*(16).

Sperling, L., & Mcguire, S. (2010). *Understanding And Strengthening Informal Seed Markets*. *April*.

Subedi, A., Chaudhary, P., Baniya, B. K., Rana, R. B., Tiwari, R. K., Rijal, D. K., Sthapit, B. R., & Jarvis, D. I. (2003). Who Maintains Crop Genetic Diversity And How?: Implications For On-Farm Conservation And Utilization. *Culture And Agriculture*, *25*(2), 41–50.

Tesfaye, K., & Mengistu, S. (2017). Phenotypic Characterization Of Ethiopian Finger Millet Accessions (Eleusine Coracana (L.) Gaertn), For Their Agronomically Important Traits. *Acta Universitatis Sapientiae, Agriculture And Environment*, *9*(1), 107–118.

Tsehaye, Y., Berg, T., Tsegaye, B., & Tanto, T. (2006). Farmers' Management Of Finger Millet (Eleusine Coracana L.) Diversity In Tigray, Ethiopia And Implications For On-Farm Conservation. *Biodiversity And Conservation*, *15*(13), 4289–4308.

Zegeye, T., Taye, G., Tanner, D., Verkuijl, H., Agidie, A., & Mwang, W. (2001). *Adoption Of Improved Bread Wheat Varieties And Inorganic Fertilizer By Small-Scale Farmers In Yelmana Densa And Farta Districts Of Northwestern Ethiopia* (Issue June).

2.7. APPENDIX CHAPTER TWO

Appendix 2.7 1.Description of finger millet genotypes by country, region, zone, and woreda

country	region	Zone	Wereda	No. of entry
Ethiopia	Tigray	Eastern	Glomahda	1
Ethiopia	Tigray	Eastern	Gantafoshum	2
Ethiopia	Tigray	Central	Lalaymaychew	6
Ethiopia	Tigray	Central	Adwa	23
Ethiopia	Tigray	Central	Mereblehe	2
Ethiopia	Tigray	Central	Entcho	1
Ethiopia	Tigray	Central	Naeder adet	1
Ethiopia	Tigray	North west	Asgedetsimbla	4
Ethiopia	Tigray	North west	Tahtaykoraro	1
Ethiopia	Tigray	North west	Laelayadyabo	3
Ethiopia	Tigray	North west	Tahtayadyabo	4
Ethiopia	Tigray	North west	Medebayzana	3
Sub-total				**51**
Ethiopia	Amara	Semengonder	Gonderzuria	3
Ethiopia	Amara	Semengonder	Dembia	3
Ethiopia	Amara	Semengonder	Alefa	4
Ethiopia	Amara	Semengonder	Addiarkay	1
Ethiopia	Amara	Semengonder	Metema	1
Ethiopia	Amara	Debubgonder	Fogora	1
Ethiopia	Amara	Debubgonder	Este	1
Ethiopia	Amara	Debubgonder	Farta	1
Ethiopia	Amara	Mirabgojam	Bure	1
Ethiopia	Amara	Mirabgojam	Merawi	3
Ethiopia	Amara	Mirabgojam	Achefer	1
Ethiopia	Amara	Misrak gojam	Blbugn	1
Ethiopia	Amara	Bahirdar special	Bahirdar	3
Ethiopia	Amara	Agewawi	Dangela	1
Sub-total				**25**
Ethiopia	Oromia	Misrakwelega	Getu wayu	2
Ethiopia	Oromia	Misrakwelega	Limu	1
Ethiopia	Oromia	Misrakwelega	Jimma arjo	2
Ethiopia	Oromia	Misrakwelega	Diga leke	5
Ethiopia	Oromia	Misrakwelega	Nunu kumba	1
Ethiopia	Oromia	Mirabwelega	Gimbi	2
Ethiopia	Oromia	Mirabwelega	Sayo	4
Ethiopia	Oromia	Mirabwelega	Boji	2
Ethiopia	Oromia	Mirabwelega	Habro	1
Ethiopia	Oromia	Illubabor	Bedele	1

Sub-total				**21**
Ethiopia	B/shangul	Metekel	Mandura	1
Ethiopia	B/shangul	Metekel	Dibate	3
Ethiopia	B/shangul	Metekel	Dangur	1
Sub-total				**5**
Total				**102**

Eritrea	Not specified	Not specified	Not specified	30
Zambia	Not specified	Not specified	Not specified	19
Zimbabwe	Not specified	Not specified	Not specified	49
Sub-total	Not specified			**98**
Grand total				**200**

Appendix 2.7 2. BLUP mean of 10 traits ranked by grain yield (kg ha^{-1}) for the top 20 and bottom 10 out of 200 finger millet genotypes across combined environments.

G.code	Genotype	GY	YPP	TSW	PH	NTPP	FNPP	FL	FW	DTF	DTM
21	203246	3986	5.7	2.5	65.0	1.3	6.6	9.4	14.9	68	97
32	203263	3981	6.5	2.7	75.6	2.1	7.0	9.9	17.0	94	126
4	100022	3969	6.0	2.7	73.7	0.9	6.8	9.8	16.2	77	115
50	203339	3900	6.2	2.8	84.2	1.2	7.1	9.8	16.4	72	99
63	203353	3745	6.1	2.5	76.8	1.6	6.9	10.1	16.7	84	116
3	100020	3728	6.2	2.7	74.0	0.8	7.1	10.3	16.9	88	122
179	234188	3700	6.1	2.6	82.1	0.7	7.3	9.9	16.7	88	123
114	229736	3700	6.1	2.6	87.9	0.6	7.1	9.9	16.7	86	119
74	203570	3628	5.9	2.5	76.4	0.3	7.3	9.3	14.9	72	105
143	233759	3594	6.0	2.6	77.0	1.0	7.4	9.9	15.6	92	125
25	203256	3576	6.2	2.6	88.1	1.3	6.8	9.6	16.5	72	100
173	234179	3559	6.0	2.6	77.4	1.4	7.4	9.8	15.8	95	128
176	234185	3555	6.1	2.7	79.1	2.4	7.3	10.1	16.1	89	122
10	100041	3546	6.1	2.7	79.2	0.7	6.8	10.2	16.3	95	129
93	211029	3537	5.9	2.5	70.5	1.0	6.8	9.9	15.3	85	114

112	229734	3535	5.8	2.6	68.4	0.5	6.6	9.9	15.7	87	119
15	203062	3522	5.9	2.6	77.4	1.3	6.6	9.8	16.5	74	108
17	203065	3519	6.1	2.6	76.2	1.8	6.6	9.8	15.5	89	126
24	203251	3519	6.0	2.5	79.2	1.4	6.6	9.7	15.9	89	121
188	234201	3519	6.0	2.6	73.3	1.0	6.9	10.0	16.6	91	123
119	230121	1847	5.9	2.6	76.8	1.1	6.6	9.9	14.7	90	123
126	230129	1842	5.8	2.6	75.3	0.8	6.7	9.8	15.2	98	130
162	234167	1840	5.9	2.5	82.0	1.4	6.5	10.0	15.9	90	123
46	203330	1839	5.7	2.5	76.4	2.2	6.7	9.8	15.4	84	114
156	234159	1837	5.7	2.5	80.3	1.0	7.0	9.9	14.7	91	123
168	234173	1832	5.8	2.5	81.2	1.8	6.7	9.9	14.7	84	116
157	234160	1822	5.6	2.5	77.0	0.4	6.8	10.1	15.8	91	123
184	234195	1798	5.7	2.5	76.2	1.1	6.7	10.0	15.2	94	125
169	234174	1784	5.8	2.5	87.2	0.7	6.5	9.9	15.5	90	123
38	203284	1748	5.6	2.5	87.2	0.9	7.0	9.9	15.9	97	130

Appendix 2.7 3. BLUP mean of 10 traits ranked by grain yield (kg ha^{-1}) for the top 20 and bottom 10 out of 200 finger millet genotypes from the Rama site, combined over years.

G.code	Genotype	GY	YPP	TSW	PH	NTPP	FNPP	FL	FW	DTF	DTM
21	203246	4138	8.7	3.1	81.8	0.9	8.5	9.8	17.9	78	111
4	100022	4126	7.2	3.7	87.0	0.7	8.6	10.5	17.2	84	118
3	100020	4112	6.8	3.3	90.1	0.3	8.1	10.6	17.8	93	126
114	229736	4073	7.6	3.2	84.2	1.1	8.1	10.8	17.4	78	124
112	229734	4068	7.4	3.5	86.0	0.4	7.7	10.0	16.6	81	125
63	203353	4059	8.6	3.5	85.1	0.1	7.8	10.5	18.1	83	125
143	233759	3878	5.3	2.5	87.1	0.2	7.6	10.6	17.8	88	124
173	234179	3862	6.4	3.3	83.7	0.1	7.2	9.5	16.9	85	122
99	214210	3817	7.1	3.4	87.4	0.1	7.8	9.4	16.0	92	129
93	211029	3777	5.7	2.6	83.9	0.1	7.2	10.5	17.3	85	122
176	234185	3773	6.9	4.0	83.9	0.3	7.6	10.8	16.9	85	124
133	230136	3772	5.8	3.6	83.0	0.1	7.3	10.1	16.8	80	119
74	203570	3740	4.8	2.4	86.5	0.1	7.2	8.9	17.8	81	114
188	234201	3707	8.0	2.8	84.2	0.1	7.3	9.8	17.0	91	136
141	233584	3687	5.3	2.6	87.7	0.1	7.8	10.9	18.6	81	113

24	203251	3679	4.9	2.5	84.8	0.1	7.6	9.3	16.8	97	126
179	234188	3678	4.6	2.3	86.1	0.1	7.6	10.1	16.4	87	130
12	100065	3673	5.2	2.5	87.1	0.1	8.1	10.2	18.2	84	125
13	100072	3667	6.2	2.7	86.8	0.1	7.5	10.9	17.4	78	118
32	203263	3649	5.8	2.2	82.7	0.3	7.6	9.6	16.6	89	124
95	211506	1973	6.2	2.2	87.7	0.1	7.8	9.7	15.6	101	129
134	230137	1955	5.3	2.9	85.9	0.1	8.2	10.2	16.2	93	131
198	234824	1950	4.5	2.3	86.6	0.1	7.4	9.8	17.2	76	112
62	203352	1944	4.9	2.1	87.1	0.1	8.6	9.7	16.0	101	138
8	100027	1941	6.5	2.3	89.9	0.1	7.1	10.1	17.4	94	124
180	234190	1936	5.2	2.7	87.6	0.1	7.2	10.4	16.4	84	126
157	234160	1923	5.4	2.4	82.3	0.1	8.3	10.7	16.8	94	133
20	203068	1909	4.6	2.0	88.0	0.2	7.4	10.2	16.3	103	137
98	213228	1901	4.8	2.8	84.9	0.1	8.4	9.4	17.2	92	125
169	234174	1832	6.7	2.1	87.8	0.6	7.3	10.5	18.5	82	125

Appendix 2.7 4. BLUP mean of 10 traits ranked by grain yield (kg ha^{-1}) for the top 20 and bottom 10 out of 200 finger millet genotypes from the Maiaini site, combined over years.

G.code	Genotype	GY	YPP	TSW	PH	NTPP	FNPP	FL	FW	DTF	DTM
175	234184	3368	3.7	1.5	40.5	0.2	3.3	6.1	16.7	111	133
114	229736	3367	2.9	1.8	46.6	0.2	3.4	6.6	16.7	108	128
143	233759	3364	3.6	1.8	42.1	0.2	3.5	6.6	16.8	102	123
133	230136	3361	3.5	1.7	32.7	0.2	3.2	6.3	16.9	105	126
173	234179	3345	2.4	1.3	48.9	0.2	3.3	6.6	16.9	108	129
112	229734	3340	2.4	1.6	41.9	0.2	3.4	7.0	16.8	106	127
176	234185	3333	2.5	1.7	35.6	0.2	3.3	6.6	16.7	105	126
141	233584	3325	2.4	1.4	46.7	0.2	3.3	6.7	16.8	103	123
4	100022	3265	1.9	1.7	50.8	0.2	3.2	5.5	16.7	99	121
140	233582	3170	2.4	1.5	30.8	0.2	3.3	6.2	16.7	105	126
116	229738	3165	2.6	1.5	35.7	0.2	3.2	5.8	16.7	103	124
188	234201	3162	2.5	1.7	41.2	0.2	3.3	5.8	16.9	108	129
26	203257	3147	2.3	2.0	48.2	0.2	3.4	6.6	16.9	96	115
24	203251	3137	2.1	1.4	46.4	0.2	3.2	5.2	16.7	105	126
182	234192	3133	2.5	1.6	37.8	0.2	3.2	5.1	16.6	95	114

48	203337	3107	2.6	1.7	35.1	0.2	3.3	5.3	16.7	109	130
3	100020	3099	2.1	1.4	58.1	0.2	3.2	6.8	16.8	104	126
39	203285	3089	2.6	1.9	35.8	0.2	3.3	6.7	16.7	104	125
111	229733	3074	2.9	1.8	46.5	0.2	3.2	6.1	16.7	101	121
50	203339	3069	2.1	1.6	40.9	0.2	3.3	5.8	16.7	96	115
102	229724	1622	2.4	1.8	39.8	0.2	3.3	5.4	16.7	98	118
60	203350	1620	1.9	2.0	48.0	0.2	3.3	6.6	16.7	110	131
66	203356	1616	2.4	1.8	41.8	0.2	3.2	5.0	16.9	88	108
15	203062	1614	2.8	1.4	32.8	0.2	3.2	5.7	16.7	97	118
77	203573	1610	1.9	1.3	59.3	0.2	3.4	6.7	16.8	104	126
17	203065	1577	2.4	2.3	46.9	0.2	3.3	6.4	16.6	105	127
23	203250	1556	2.4	1.4	44.9	0.2	3.4	5.6	16.6	106	127
22	203249	1488	2.7	1.8	43.7	0.2	3.1	5.7	16.7	106	127
67	203357	1451	2.5	1.9	35.0	0.2	3.0	4.8	16.5	98	116
20	203068	1411	1.9	1.6	45.1	0.2	3.2	6.3	16.6	108	130

Appendix 2.7 5: BLUP mean of 10 traits ranked by grain yield (kg ha^{-1}) for the top 20 and bottom 10 out of 200 finger millet genotypes from the Zana site, combined over years.

G.code	Genotype	GY	YPP	TSW	PH	NTPP	FNPP	FL	FW	DTF	DTM
4	100022	3749	5.2	2.7	71.0	0.6	6.4	8.4	16.9	86.3	117
21	203246	3693	5.2	2.3	61.0	0.7	6.0	6.3	16.0	79.1	106
114	229736	3679	5.6	2.5	70.7	0.6	6.7	9.9	17.5	92.1	124
112	229734	3617	5.1	2.5	67.8	0.5	5.9	9.6	16.6	92.5	124
3	100020	3613	5.3	2.6	74.8	0.5	6.2	10.7	18.1	94.8	125
143	233759	3581	5.1	2.4	70.1	0.5	6.8	9.8	17.1	93.2	123
173	234179	3558	5.1	2.5	68.7	0.5	6.4	8.7	17.1	96.9	127
176	234185	3525	5.3	2.8	66.8	0.7	6.5	10.3	16.7	93.2	124
32	203263	3499	5.4	2.4	65.8	0.7	6.0	8.2	17.1	97.4	127
63	203353	3480	5.7	2.5	68.1	0.6	5.9	9.5	17.6	89.1	120
133	230136	3473	5.0	2.5	66.1	0.6	5.8	9.1	16.3	92.2	123
141	233584	3471	4.5	2.2	70.8	0.6	6.4	10.5	17.6	90.0	117
188	234201	3435	5.4	2.3	67.1	0.5	5.8	8.7	17.5	97.5	130
24	203251	3419	4.6	2.2	69.3	0.5	5.5	7.0	16.4	96.7	125
12	100065	3391	4.5	2.2	71.7	0.5	5.9	9.3	18.1	98.1	130

93	211029	3380	4.9	2.2	66.1	0.5	5.8	9.6	16.4	91.3	120
13	100072	3367	5.0	2.3	76.2	0.4	5.8	10.4	17.9	91.5	123
99	214210	3355	5.4	2.4	69.8	0.5	6.2	7.8	15.6	97.3	127
10	100041	3353	5.2	2.5	71.7	0.5	5.7	9.9	16.8	97.2	128
39	203285	3340	5.1	2.6	68.0	0.5	5.9	9.5	16.9	91.8	123
46	203330	1972	4.5	2.3	70.1	0.6	5.2	7.5	15.7	80.3	109
156	234159	1958	4.5	2.2	73.3	0.5	6.2	9.9	16.2	97.1	128
11	100063	1942	4.2	1.9	66.8	0.5	5.9	8.3	16.1	96.5	125
23	203250	1915	4.7	2.2	70.4	0.5	6.2	7.4	16.1	95.7	125
77	203573	1907	4.5	2.1	74.0	0.6	6.1	9.7	16.6	96.9	124
16	203063	1891	4.7	2.5	73.4	0.6	6.3	9.8	15.7	96.8	128
67	203357	1882	5.5	2.3	67.2	0.5	4.7	5.1	14.7	83.0	108
168	234173	1873	4.7	2.3	68.1	0.6	6.5	10.0	15.9	89.3	117
20	203068	1865	4.1	2.0	71.1	0.5	5.6	9.4	15.5	102.2	132
169	234174	1773	4.9	2.1	77.0	0.6	5.3	9.4	17.4	93.0	125

3.7. APPENDIX CHAPTER THREE

Appendix 3.7 1: Frequency distribution of five major qualitative traits of 202 germplasm samples collected from various African countries and four finger millet producing Ethiopian regional states.

Country	Region	No. of entries	Pericarp persistence			Glumes color				Seed Color				
			P	PAP	NP	YG	LG	PP	WT	BK	RD	WT	BN	OG
Ethiopia	Amara	25	14	54	57	30	12	57	26	64	39	15	0	7
	B.Gumuz	5	0	11	14	7	4	9	5	13	6	4	0	2
	Oromiya	21	19	37	49	13	12	47	33	39	37	23	0	6
	Tigray	53	22	93	150	58	35	95	77	143	67	18	0	37
Eritrea	-	30	29	47	74	27	12	63	48	84	53	2	0	11
Zambia	-	19	22	31	42	12	4	40	39	30	30	12	0	23
Zimbabwe	-	49	58	105	82	72	29	84	60	49	105	10	7	74
Total		202	164	378	468	219	108	395	288	422	337	84	7	160

Country	Region	No. of entries	Finger Branching		Ear Shape				
			PT	AB	DR	OP	SM	CM	FL
Ethiopia	Amara	125	70	55	21	67	21	11	5
	B.Gumuz	25	15	10	4	12	5	4	0
	Oromia	105	56	49	7	48	26	17	7
	Tigray	265	122	143	80	154	25	3	3
Eritrea	-	150	74	76	34	71	35	10	0
Zambia	-	95	52	43	18	31	19	20	7
Zimbabwe	-	245	118	127	24	87	41	59	34
Total		1010	507	503	188	470	172	124	56

4.7. APPENDIX CHAPTER FOUR

Appendix 4.7 1: Cluster analysis of 200 African finger millet accessions along with two check varieties.

clusters	**No of genotype within cluster**	**African countries**			
		Ethiopia	**Eritrea**	**Zambia**	**Zimbabwe**
I	73 (36.14%)	20	-	4	49
II	51 (25.25%)	27	9	15	-
III	26 (12.87%)	6	20	-	-
IV	17 (8.42%)	16	1	-	-
V	8 (3.96%)	8	-	-	-
VI	27 (13.37%)	27	-	-	-
Total	202	104	30	19	49

Appendix 4.7 2. Performance of the top 10 and bottom 5 finger millet genotypes based on protein percentage.

Gen	MC	**Prt**	Ca	Mg	Zn	Fe	Str	cluster	**C.code**
203574	10.94	**9.33**	271	126.40	0.73	5.42	73	1	ZIM
203067	11.63	**9.00**	290	408.75	1.63	11.45	73	4	ETH
203351	11.02	**8.21**	288	197.35	0.58	6.21	73	1	ETH
212694	10.89	**8.20**	192	197.35	0.56	5.46	73	1	ZIM
100002	11.72	**8.16**	139	215.45	0.19	5.46	73	1	ETH
203249	11.21	**8.13**	396	232.30	0.58	5.23	72	1	ETH
234173	10.92	**8.13**	270	197.25	0.49	5.92	73	1	ZIM
214210	11.66	**8.13**	313	125.30	0.71	4.38	72	1	ZIM
230140	11.34	**8.11**	223	197.35	0.72	4.60	72	1	ZIM
203061	10.24	**8.04**	148	215.40	0.21	4.59	72	1	ETH
203585	12.01	**5.47**	310	487.65	1.33	11.50	73	6	ETH
234195	10.85	**5.43**	225	297.30	0.51	5.88	73	2	ERI
233582	11.68	**5.32**	210	299.70	0.71	5.28	73	2	ETH
234184	11.21	**5.22**	290	370.55	1.34	28.16	73	6	ETH
203358	11.20	**5.15**	284	197.35	0.68	6.17	72	2	ETH

Appendix 4.7 3. Performance of the top 10 and bottom 5 finger millet genotypes based on Calcium (Ca) concentrations.

Gen	MC	Prt	**Ca**	Mg	Zn	Fe	Str	cluster	**C.code**
234160	11.85	6.04	**431**	303.35	3.03	28.14	73	4	ETH
100020	10.96	5.97	**407**	346.60	0.83	5.64	73	2	ZAM
234822	11.94	6.72	**400**	197.25	1.43	4.62	73	1	ZIM
230125	11.87	5.67	**399**	297.35	2.74	10.03	74	4	ETH
203249	11.21	8.13	**396**	232.30	0.58	5.23	72	1	ETH
203257	11.98	7.53	**395**	430.90	4.89	9.98	73	4	ETH
203260	12.42	6.13	**394**	430.90	2.67	5.41	73	4	ETH
203280	12.23	5.84	**394**	284.55	3.17	5.38	74	4	ETH
203342	11.33	6.08	**387**	246.95	2.68	17.91	74	4	ETH
203256	11.83	6.14	**386**	243.50	3.39	5.88	73	4	ETH
234187	9.97	6.07	**146**	215.20	0.13	4.27	72	3	ETH
208730	10.33	5.91	**146**	130.40	0.66	4.39	73	3	ERI
230121	10.29	5.87	**146**	125.35	0.62	4.35	72	3	ERI
230126	10.66	5.53	**145**	197.15	0.27	4.28	73	3	ETH
100002	11.72	8.16	**139**	215.45	0.19	5.46	73	1	ETH

Appendix 4.7 4 Performance of the top 10 and bottom 5 finger millet genotypes based on Magnesium (Mg) concentrations.

Gen	MC	Prt	Ca	**Mg**	Zn	Fe	Str	cluster	**C.code**
203259	11.43	6.23	205	**525.50**	1.28	10.93	73	6	ETH
229727	10.64	6.01	275	**487.75**	0.70	10.03	73	6	ETH
203585	12.01	5.47	310	**487.65**	1.33	11.50	73	6	ETH
203262	12.12	6.14	377	**456.00**	3.95	30.68	73	4	ETH
203257	11.98	7.53	395	**430.90**	4.89	9.98	73	4	ETH
203260	12.42	6.13	394	**430.90**	2.67	5.41	73	4	ETH
203066	12.01	6.85	382	**430.90**	3.93	17.18	73	4	ETH
229725	11.11	5.93	220	**428.20**	0.78	9.11	73	6	ETH
203062	10.81	6.71	153	**416.85**	1.19	4.87	73	1	ETH
203067	11.63	9.00	290	**408.75**	1.63	11.45	73	4	ETH
203575	10.65	5.61	184	**123.55**	0.52	5.30	74	5	ETH
215798	10.40	5.85	153	**120.90**	0.17	4.41	73	3	ERI
230123	10.34	5.81	147	**120.90**	0.16	4.36	72	3	ERI
208726	10.33	6.93	154	**120.85**	0.14	4.44	73	3	ERI
229738	10.27	6.90	154	**120.85**	0.11	4.40	72	3	ERI

Appendix 4.7 5: Performance of the top 10 and bottom 5 finger millet genotypes based on .zinc (Zn) concentrations.

Gen	MC	Prt	Ca	Mg	**Zn**	Fe	Str	cluster	**Code**
203257	11.98	7.53	395	430.90	**4.89**	9.98	73	4	ETH
203262	12.12	6.14	377	456.00	**3.95**	30.68	73	4	ETH
203066	12.01	6.85	382	430.90	**3.93**	17.18	73	4	ETH
203256	11.83	6.14	386	243.50	**3.39**	5.88	73	4	ETH
234162	11.50	5.90	285	343.95	**3.25**	17.87	73	4	ETH
203280	12.23	5.84	394	284.55	**3.17**	5.38	74	4	ETH
203258	12.13	7.94	305	408.65	**3.16**	4.65	73	4	ETH
203246	11.43	6.16	360	247.10	**3.15**	10.05	74	4	ETH
203251	12.18	6.23	385	377.10	**3.09**	5.85	73	4	ETH
234160	11.85	6.04	431	303.35	**3.03**	28.14	73	4	ETH
215798	10.40	5.85	153	120.90	**0.17**	4.41	73	3	ERI
230123	10.34	5.81	147	120.90	**0.16**	4.36	72	3	ERI
208726	10.33	6.93	154	120.85	**0.14**	4.44	73	3	ERI
234187	9.97	6.07	146	215.20	**0.13**	4.27	72	3	ETH
229738	10.27	6.90	154	120.85	**0.11**	4.40	72	3	ERI

Appendix 4.7 6: Performance of the top 10 and bottom 5 finger millet genotypes based on iron (Fe) concentrations.

Gen	MC	Prt	Ca	Mg	Zn	**Fe**	Str	cluster	**Code**
203262	12.12	6.14	377	456.00	3.95	**30.68**	73	4	ETH
234184	11.21	5.22	290	370.55	1.34	**28.16**	73	6	ETH
234160	11.85	6.04	431	303.35	3.03	**28.14**	73	4	ETH
230133	11.07	5.75	296	377.10	1.32	**28.10**	73	6	ETH
230136	11.16	5.84	300	343.90	1.48	**22.33**	73	6	ETH
230129	11.54	5.57	285	343.95	2.74	**21.85**	73	4	ETH
229733	11.39	5.69	278	370.55	1.31	**20.82**	73	6	ETH
203284	11.30	5.47	274	303.35	1.50	**20.80**	73	6	ETH
229737	11.18	5.82	268	377.10	1.24	**20.80**	73	6	ETH
208725	11.11	5.80	210	247.05	0.67	**18.28**	73	6	ETH
100041	11.29	7.79	160	262.45	0.79	**4.28**	72	1	ETH
234187	9.97	6.07	146	215.20	0.13	**4.27**	72	3	ETH
229731	10.80	6.68	153	199.90	0.30	**4.11**	73	3	ERI
230139	10.76	6.64	146	197.35	0.28	**4.06**	72	3	ETH
tekeze-1	10.45	5.47	182	213.2	1.81	**3.4**	72	3	ETH

5.7. APPENDIX CHAPTER FIVE

Appendix 5.7 1: Cultivation practices for improving finger millet by farmers in eight study villages across two finger millet-growing zones in Tigray, Ethiopia, during 2019-2020.

Seed sources and flows	**Farmers' method for improving finger millet production hh interviewed**								
	Central zone (merebleke wereda)				**Northwest zone (A/tsibla wereda)**				
	Simret		**Mihkaun**		**Debreabay**		**Mizan**		
	ATS	AY	MR	EMR	DA	BR	MT	AR	**total**
Number of HHs	20	19	18	19	20	20	20	20	**156**
Source of information for seed seeking (hh)									
local funeral ceremonial	5	13	8	6	15	14	13	12	**86**
wedding dowry	2	4	2	2	3	1	3	8	**25**
Local meetings	10	0	9	0	4	10	14	9	**56**
Blessing churches	12	5	10	15	6	4	1	12	**65**
holidays (epiphany)	6	9	8	10	9	11	6	8	**67**
Time of Seed Selection for next planting (hh)									
Mark at field	6	8	4	2	9	6	4	2	**41**
Harvesting time	14	10	12	14	16	16	13	11	**106**
Threshing time	2	0	1	0	1	3	0	0	**7**
From storage	10	15	16	10	9	5	7	9	**81**
Basis for seed selection (hh)									
Seed vigority	8	6	5	6	8	6	7	4	**50**
Tillering capacity	2	0	3	1	2	4	5	1	**18**
Panicle size	12	14	13	12	16	15	17	14	**113**
Plant height	3	2	1	4	1	2	0	0	**13**
Time of sowing for good germination capacity (hh)									

Sowing before onset of rainfall	10	9	11	6	8	5	4	10	**63**
Sowing after 1st shower of rainfall	15	16	15	17	14	12	14	9	**112**
Sowing immediately after onset of rainfall	1	0	0	0	2	3	2	3	**11**
Frequency of cultivating finger millet crop (hh)									
annually	18	13	12	11	10	11	12	11	**98**
Once per two years	2	6	6	8	9	9	7	9	**56**
Once per three years	0	0	0	0	1	0	1	0	**2**
Type of Cropping system used for finger millet cultivation (hh)									
Mono-cropping	0	0	0	0	0	0	0	0	**0**
intercropping	5	3	8	8	5	10	9	9	**57**
Crop rotation	15	15	10	11	15	10	11	11	**98**
Type of planting method used for finger millet cultivation (hh)									
broadcasting	20	19	14	17	19	20	18	20	**147**
Row spacing	0	0	4	2	1	0	2	0	**9**
drilling	0	0	0	0	0	0	0	0	**0**
Constraints of finger millet production as ranked by farmers (hh)									
Drought	2	6	5	2	6	4	4	3	**32**
pests	13	15	16	12	16	14	15	13	**114**
Lack of seeds (lack of improved variety)	10	11	9	10	14	13	15	16	**98**
termites	8	10	7	8	13	12	8	13	**79**
Late maturity	0	1	0	1	2	3	2	1	**10**

ATS, adi tseneke; AY, adi yemano; MR, mereb; EMR, endamariam; DA, debre abay; BR, birhan; MT, maitekli; AR, arada; hh, household