GENETIC DIVERSITY FOR AGRO-MORPHOLOGICAL AND NUTRITIONAL QUALITY TRAITS IN SORGHUM [*Sorghum Bicolor* (L) MOENCH] AND ITS SEED SYSTEMS IN TIGRAY NORTH ETHIOPIA

A PhD Dissertation

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A PhD Dissertation Submitted to

The Department of Dryland Crop and Horticultural Sciences

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

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Oct, 2023

DECLARATION

I hereby declare that this Ph.D. thesis **entitled''Genetic Diversity for Agro-morphological and Nutritional Quality Traits in Sorghum [*Sorghum bicolor* (L) Moench] and its Seed Systems of in Tigray, North Ethiopia**" is my original work and has not been presented for a degree in any other University, and all sources of material used for this dissertation have been duly acknowledged.

Name of student	signature	date
Shushay Welderufael Abrha	___________	____/____/______

This dissertation has been presented with the approval of the following examining board members:

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DEDICATION

This piece of work is dedicated to all Tigrayans who lost their life because of theTigray war and the longest siege in Tigray.

May their soul rest in peace

Amen

BIOGRAPHICAL SKETCH

The author was born on 16 December, 1985 in Wukro Maray Central Zone of Tigray, Ethiopia from His father Welderufeal Abrha and his mother Letensie Belay. He has been attended his elementary and secondary school at Wukro Maray primary and secondary school and his preparatory school at Axum comprehensive high school. Then after, he joined Haramaya University to attend his BSc in plant science on 2005/6. After successful completion of his BSc in 2008 he has been joined Haramaya University school of postgraduate in 2009 and completed his MSc study in Plant Breeding in 2011. His MSc thesis work was on Line x Tester Analysis of Maize (*Zea mays)* Inbred lines in Central Riftvalley of Ethiopia. Following successful completion of his MSc, Shushay has been appointed as a lecturer in Debretabor University until he was transferred to Adigrat University. After serving for four years, he has been joined Mekelle University in 2009 to pursue his PhD in plant breeding and seed system. His PhD thesis was entitled as Genetic Diversity for Agro-morphological and Nutritional Quality Traits in Sorghum [*Sorghum bicolor* (L) Moench] and its Seed Systems of in Tigray, North Ethiopia. He was also attended an international course in integrated seed sector development (ISSD) in 2015 at Wageningen University, The Netherlands and an international course on Modern maize breeding in 2018 in Ghent University, Belgium.

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I must thank my beloved wife Abrhet Gebremdedhin, for her love, care and patience, which have been always power to me. I appreciate your understanding, strength, and courage to overcome the hard task of nursing our very young kids in good and bad times. I am indebted to my children Nahom, Solik and Soliana who missed my care at their very early childhood and tolerated my absence. You are my sunshine, and I cannot get enough of you. I also thank my parents Letensie Belay and Welderufael Abrha and my brother Seifu W/Rufeal for their encouragement. And, for those whose names have not been mentioned in the acknowledgment page, my apology for the omission.

Every step in my life including completion of this study is by the will of my Almighty God.

ABBREVIATIONS

ATA	Agricultural transformation Agency
NRC	National research Center
AATF	African Agricultural Technology Foundation
CSA	Central Statistical Agency
EGS	Early Generation Seed
FAOSTAT	Food and Agricultural Organization
GYT	Genotype by Yield by Trait
GT	Genotype by Trait
GGE	genotype plus Genotype by Environment interactions
IPAD	International Production Assessment Division
LSB	Local Seed Business
META	Multi Environment Trail Analysis
NIRS	Near Infrared Spectrophotometers
OGTR	Office of the gene technology regular
SSNA	Social Seed Network Analysis

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GENETIC DIVERSITY FOR AGRO-MORPHOLOGICAL AND NUTRITIONAL QUALITY TRAITS IN SORGHUM [*Sorghum Bicolor* (L) MOENCH] **AND ITS SEED SYSTEMS IN TIGRAY NORTH ETHIOPIA**

EXECUTIVE SUMMARY

Sorghum [*Sorghum Bicolor* (L) moench] is one of the most important food crops in the arid and semi-arid regions of the world. Ethiopia is a center of origin, and diversity for sorghum where high genetic diversity of cultivated and wild forms has been reported. It is adapted to arid and semi-arid areas of the country in which recurrent drought and low soil fertility prevailes. Nontheless, the genetic diversity and varastility of Ethiopian sorghum germplasm has not been exploited to its potential. Information on the effects of genotype by environment interactions and genotype by yield by trait associations among various target traits is limited. Besides, seed system in general and the social, cultural in particular, and methodological dimensions that determine sorghum seed exchange mechanisms and seed sourcing, how the seed is exchanged among farmers and the assets that might sustain local seed exchanges and crop diversity are not exhaustively studied. Hence, collection, characterization and evaluation of sorghum germplasm is essential to exploit the genetic diversity useful for efficient breeding and conservation programs. The main objectives of this study were to evaluate the genetic diversity of sorghum genotypes for agro-morphological and nutritional quality traits, and to analyze the sorghum seed system in Tigray. One hundred and ten sorghum genotypes were evaluated in three locations (Tahtay Adaybo, Mereb Leke and Tselemti) of Tigray in the 2018 and 2019 cropping seasons. Each location and year were treated as an independent environment and designated as Tahtay Adyabo 2018 (En1), Mereb-Leke 2018 (En2), Tselemti 2018 (En3), Tahtay Adyabo 2019 (En4); Mereb-Leke 2019 (En5) and Tselemti 2019 (En6). Data on 13 qualitative traits were obtained from En1, whereas data on 12 quanitiative traits were obtained from all the six environments. In addition to the field experiments, data on seven nutritional quality traits were collected from each environment using Near Infrared Spectrophotometers (NIRS). To study the seed systems of sorghum in Tigray, a survey was conducted using a semi-structured questionnaire to collect information from 153 sorghum household farmers in six randomly selected villages: namely

Gezaadara, Medabe, Gezameker, Waekel, Munira and Gandostela. Farmers who had a major role in the sorghum seed exchange network were identified using social seed network analysis. The qualitative traits of sorghum were analysed using SPSS and PAST software whereas, the quanitative and nutritonal quality traits were analysed using META-R software. The GYT and GGE biplots were generated using Genstat software. The sorghum seed exchange, flow, factors that determine the seed exchange were analysed using SPSS, while the social seed network was analysed using UCINET and Netdraw software.

Results showed high genetic diversity of sorghum for qualitative traits, ranging from H′ = 0.33 for grain form to H′ 0.99 for grain plumpness with a mean of 0.83, which reveals huge diversity within the Farmers' varieties. The estimated H′ of each trait pooled over districts of origin, administrative zones, and altitude classes were high with an overall mean of 0.71, 0.74, and 0.70, respectively. The H′ pooled over traits within the districts of origin, administrative zone and altitude classes were high with an overall mean of 0.71, 0.74, and 0.69, respectively. The ANOVA computed in individual and across environments showed highly significant variations ($p < 0.001$) among the genotypes for all the traits studied. Likewise, the combined analysis showed strong significant variance ($p < 0.001$) for all traits studied due to genotype (σ^2g), genotype by environment interaction ($\sigma^2g \times e$) and environments (σ^2e) with the exception that variance due to environment (σ^2e) had significant variation ($p < 0.05$) for calcium content. This indicates that sorghum Farmers' varieties collected from Tigray harbor high genetic variation useful for the development and deployment of nutritionally enhanced and high-yielding sorghum varieties. The high broad-sense heritability ($H^2 > 0.6$) recorded in the present study for most of the traits studied indicates the possibility of effective selection among the genotypes.

The strong positive associations between some of the traits might be due to common and overlapping quantitative trait loci, suggesting that the traits can be improved concurrently through direct selection. The which won-where of the GGE biplot indicates the six testing environments can be grouped into two mega environments. En4 followed by En5 were identified as discriminative environments whereas, En6 followed by En2 were representative environments. Using the mean and stability view of the GGE biplot a high yielding genotypes **(**LR106, LR25, LR19, LR103, LR75, LR74, and LR16) were distinguished. The GYT biplots were instrumental

to rank genotypes based on yield trait combinations using ATC graph of the biplot and GYT superiority index, which is not applicable using the GT biplot. Accordingly, LR106 > LR25 > LR102 > LR12 > LR78 > LR103 > LR1 > LR74 > LR15 were best-ranked genotypes based on their level to combine grain yield and yield related traits, whereas LR12>LR23 > LR25 > LR106 > LR1 > LR27 > LR78 > LR6 > LR81 were best ranked genotypes based on their level to combine grain yield and nutritional quality traits.

Generally, the present study revealed that there is high genetic diversity of sorghum genotypes in Tigray. Further investigations of the genetic diversity of sorghum genotypes using combinations of morphological and molecular markers would be helpful for better understanding the magnitude and patterns of diversity along with its worth for breeding and conservation strategies. Careful attention is needed to different seed intervention strategies in Tigray including promotion of farmer-preferred sorghum varieties through quality declared seed systems and integrating the local seed systems with the formal seed systems.

Keywords: Genetic diversity, trait association, broad sense heritability, Seed netowrk

በትግራይ ሰሜናዊ ኢትዮጵያ የማሽላ [*Sorghum Bicolor* (L) Moench] አግሮ-ሞርፎሎጂካል እና የስነ-ምግብ ጥራት ባህሪዎች ዘረ-መል እና የዘር *ስርዓት*

የጥናታዊ ጽሑፍ ማጠቃለያ

ማሽላ በደረቃማ እና ከፊል ደረቃማ አካባቢዎች ከሚገኙ በጣም ጠቃሚ የምግብ ሰብሎች አንዱ ነው። ኢትዮጵያ ከፍተኛ የማሽላ የዘረ መል ልዩነት፣ የሰመረ እና የዱር ቅርጾች የተዘገበባት የማሽላ የትውልድ ማዕከል ነች። በሀገሪቱ ተደጋጋሚ ድርቅ፣ ዝቅተኛ የአፈር ለምነት በሆነባቸው ደረቃማ እና ከፊል ደረቃማ አካባቢዎች ጋር ተጣጥሟል። ቢሆንም፣ የኢትዮጵያ የማሽላ ዝርያዎች የዘረመል ልዩነትና ሁለገብነት አቅሙን ያህል ጥቅም ላይ አልዋለም። በአካባቢ መስተጋብር እና ባለው ምርትን ከ ስነ ምግብ ጥራት ትስስር ውጤት ላይ ያለው መረጃ በአጠቃላይ በሀገሪቱ በተለይም በትግራይ የተገደበ ነው። በተጨማሪም የማሽላ ዘር መለዋወጫ ዘዴዎችን እና የዘር ምንጮችን የሚወስኑት ማህበራዊ፣ ባህላዊ እና ዘዴያዊ ልኬቶች፣ በገበሬዎች መካከል ያለው የዘር ልውውጥ እንዴት እንደሚሰራ እና የአካባቢውን የዘር ልውውጦች እና የሰብል ብዝሃነትን ሊቀጥል የሚችል ሀብት በጥልቅ ኣልተጠናም። ስለሆነም የማሽላ ዝርያዎችነ መሰብሰብ ፣መለየት እና መገምገም ለተቀላጠፈ የዝርያ ማሻሻያ እና ጥበቃ ፕሮግራሞች ጠቃሚ የሆነውን የዘረ ምል ልዩነት ለመወሰን አስፈላጊ ነው። የዚህ ጥናት ዋና አላማዎች የማሽላ ዝርያዎች የአግሮ-ሞርፎሎጂ እና የስነ መግብ ጥራት ባህሪያትን የዘረመል ልዩነት መገምገም እና በትግራይ ውስጥ ያለውን የማሽላ ዘር ስርዓት መተንተን ነበር። በትግራይ 2018 እና 2019 የምርት ዘመን አንድ መቶ አስር የማሽላ ዝርያዎች በሶስት ቦታዎች (ታሕታይ አዳይቦ፣ መረብ ለኸ እና ፀለምቲ) በትግራይ ክልል ተገምግሟል። እያንዳንዱ ቦታ እና አመት እንደ ገለልተኛ አካባቢ ተደርገው ተወስደዋል። ታሕታይ ኣድያቦ 2018 (ኣከባቢ.1) ፣ መረብ-ለከ 2018 (ኣከባቢ 2) ፣ ጸለምቲ 2018 (ኣከባቢ.3) ፣ ታሕታይ አድያቦ 2019 (ኣከባቢ.4); መረብ-ለከ 2019 (ኣከባቢ 5) እና ጸለምቲ 2019 (ኣከባቢ 6) ። በ 13 የአይነት ባህሪያት ላይ ያለው መረጃ ኣከባቢ.1 የተገኘ ሲሆን, በ 12 መጠናዊ ባህሪያት ላይ ያለው መረጃ ከሁሉም ስድስቱ አከባቢዎች ተገኝቷል. ከመስክ ሙከራዎች በተጨማሪ NIRSን በመጠቀም ሰባት የስነ ምግብ ጥራት ባህሪያት መረጃ ከእያንዳንዱ አካባቢ ተሰብስቧል። በትግራይ ያለውን የማሽላ ዘር ሥርዓት ለማጥናት ከስድስት መንደሮች በዘፈቀደ የተመረጡ 153 የማሽላ አባወራ ገበሬዎችን ያሳተፈ በከፊል የተዋቀረ መጠይቅ በመጠቀም የዳሰሳ ጥናት ተካሄዷል። ማለትም ገዛአድራ ፣ መደቤ ፣ ገዛመቀር ፣ ዋዕከል ፣ ሙኒራ እና ጋንዶስተላ ናቸው ። በማሽላ ዘር መለዋወጫ አውታር ላይ ትልቅ ሚና የተጫወቱት አርሶ አደሮች በማህበራዊ የዘር ኔትወርክ ትንተና ተለይተዋል። የማሽላ የጥራት ባህሪያት SPSS እና PAST ሶፍትዌርን በመጠቀም የተተነተኑ ሲሆን የመጠን ባህርያት እና የስነ ምግብ ጥራት ባህሪያት በ META-R ሶፍትዌር ተንትነዋል። GYT እና GGE biplots የተፈጠሩት Genstatን በመጠቀም ነው። የማሽላ ዘር ልውውጥ፣ ፍሰት፣ የዘር ልውውጥን የሚወስኑ ምክንያቶች SPSSን በመጠቀም የተተነተኑ ሲሆን የማህበራዊ የዘር መረብ ደግሞ UCINET እና Netdraw ሶፍትዌርን በመጠቀም ተንትነዋል።

ውጤቶቹ እንደሚያሳዩት ከፍተኛ የዘረመል ልዩነት የኣይነት ባህሪያት ከ 0.33 ለእህል ቅርጽ 0.99 ለእህል ውፍረት በ 0.83 አማካኝ 0.83, ይህም በመሬት ውስጥ ያለውን ከፍተኛ ልዩነት ያሳያል። በትውልድ ወረዳዎች፣ ኣስተዳደር ዞኖች እና በከፍታ ደረጃዎች ላይ የተሰበሰበው የእያንዳንዱ ባህሪ H ' ከፍተኛ ሲሆን በአጠቃላይ 0.71 ፣ 0.74 እና 0.70 በቅደም ተከተል።

በትውልድ አውራጃዎች፣ ኣስተዳደር ዞኖች እና ከፍታ ደረጃዎች ውስጥ ያሉ ባህሪያት ላይ የተሰባሰበው የማሽላ ዝርያዎች በጠቅላላ 0.71፣ 0.74 እና 0.69 በቅደም ተከተል ከፍተኛ ነበር። በግለሰብ እና በአከባቢዎች የተሰላው ANOVA በጣም ጉልህ የሆኑ ልዩነቶች አሳይቷል ($p < 0.001$). እንደዚሁም, ጥምር ትንተና በጂኖታይፕ (σ^2g) ፣ በጂኖታይፕ እና አካባቢ መስተጋብር ውህደት (σ^2gxe) እና አከባቢዎች (σ^2e) ምክንያት ለተጠኑ ሁሉም ባህሪዎች ጠንካራ ጉልህ ልዩነት ($p <0.001$) አሳይቷል። አካባቢ (σ^2e) ለካልሲየም ይዘት ከፍተኛ ልዩነት ነበረው ($p < 0.05$). ይህ የሚያመለክተው ከትግራይ የሚሰበሰቡ የማሽላ ዝርያዎች በአመጋገብ የተሻሻሉ እና ከፍተኛ ምርት የሚሰጡ የማሽላ ዝርያዎችን ለማምረት እና ለማሰማራት የሚጠቅሙ ከፍተኛ የዘረመል ልዩነት አላቸው ። ለአብዛኛዎቹ የተጠኑ ባህሪያት በአሁኑ ጥናት ውስጥ የተመዘገበው ከፍተኛ ሰፊ-ስሜት ቅርስ ($H^2 > 0.6$) ዝርያዎች መካከል ውጤታማ የመመረጥ እድልን ያሳያል።

በአንዳንድ ባህሪያት መካከል ያለው ጠንካራ አዎንታዊ ግንኙነቶች በምክንያት ሊሆኑ ይችላሉ። የተለመዱ እና ተደራራቢ የመጠን ባህሪይ ሎሲ የሚጠቁመው በቀጥታ በመምረጥ ባህሪያቱ በአንድ ጊዜ ሊሻሻሉ እንደሚችሉ ይጠቁማል ። የGGE biplot ስድስቱ የሙከራ አካባቢዎች በሁለት ሜጋ አካባቢዎች ሊመደቡ እንደሚችሉ ያመለክታል። ኣከባቢ 4 በመቀጠል ኣከባቢ 5 እንደ አድሎአዊ አካባቢዎች ተለይተዋል፣ ኣከባቢ6 እና ኣከባቢ2 ተወካይ አካባቢዎች ናቸው። የGGE biplot ከፍተኛ ምርት የሚሰጡ ዝርያዎች (LR106፣ LR25፣ LR19፣ LR103፣ LR75፣ LR74 እና LR16) አማካኝ እና የመረጋጋት እይታን በመጠቀም ተለይተዋል። ATC እና GYT የላቀ ደረጃ መረጃ ጠቋሚን በመጠቀም በምርት ባህሪ ጥምር ላይ በመመስረት ጂኖታይፕን ደረጃ ለመስጠት መሳሪያ ነበሩ። በዚህ መሰረት LR106>LR25>LR102>LR12>LR78>LR103>LR1>LR74>LR15 በእነሱ ደረጃ ላይ በመመስረት የእህል ምርትን በማጣመር እና ተያያዥ ባህሪያትን በማዋሃድ የተሻሉ ነበሩ። የእህል ምርትን እና የስነ ምግብ ጥራት ባህሪያትን በማጣመር LR12>LR23>LR25>LR106LR>LR1>LR12 LR78>LR6>LR81 የተሻሉ ዝርያዎች ነበሩ።

ቁልፍ ቃላት፡ የዘረመል ልዩነት፣ የባህርይ ትስስር፣ ሰፊ የስሜት ውርስ፣ ማህበራዊ የዘር መረብ ፣

ናይ መሽላ [*Sorghum Bicolor* (L) Moench] ኣግሮ-ሞርፎሎጂካውን ስነ መዓዛን ባህርያት ዓልየታዊ ብዙሕነትን ስርዓት ዘርኢን ኣብ ትግራይ ሰሜን ኢትዮጵያ

መጠቃለሊ መጽናዕታዊ ጽሑፍ

መሽላ ኣብ ደረቕን ክፋል ደረቕን ከባቢታት ዓለም ካብ ዝርከቡ ኣገደስቲ ኣእካል መግቢ እዩ። ኢትዮጵያ ልዑል ጀነቲካዊ ብዙሕነት ዝለምዑን በረኻን መልክዓት መሽላ ዝተገለፀላ ማእኸል መበቀል፣ ከምኡ እውን ብዙሕነት እያ። ኣብ ደረቕን ፍርቂ ደረቕን ከባቢታት ሃገርና ዝላመድ ኮይኑ ተደጋጋሚ ድርቂ፣ ትሑት ልሙዕነት ሓመድን ዝሰፍሐሉ እዩ። እዚ ከምዚ ኢሉ እናሃለወ እቲ ኣብ ኢትዮጵያ ዝርከብ ዓልየታዊ ብዙሕነት መሽላ ክንዲ ዝድለ ኣብ ጥቅሚ ኣይዋዓለን። ሓበሬታ ኣብ መንጎ ዝተፈላለዩ ዓልየታዊ ባህርያትን ከባብያዊ ስነ ምህዳርን ዘሎ ምትእስሳርን ዘስዕቦ ፅልዋን ከማኡ እዉን ኣብ መንጎ ምህርትን ስነ መዓዛን ዘሎ ርክብ ኣብ ኢትዮጵያ ብሓፈሻ ኣብ ትግራይ ድማ ብፍላይ ድሩት እዩ። ብዘይካ'ዚ፣ ንኣገባባት ምልውዋጥ ዘርኢ መሽላን ምንጪ ዘርእን ዝውስኑ ማሕበራዊ፡ ባህላውን ኣገባባውን ሽነኻት፡ ኣብ መንጎ ሓረስቶት ዝካየድ ምልውዋጥ ዘርኢ ብኸመይ ይሰርሕ ከምዘሎን ኣብ ውሽጢ ዓዲ ንዝግበር ምልውዋጥ ዘርእን ዓልየታዊ ብዙሕነት ክቕጽል ዝኽእል ንብረትን ኣይፍለጥን። ስለዚ ንብቑዕ መደባት ዝራእቲ ምምሕያሽን ዕቃበን ዝጠቅም ዓልየታዊ ብዙሕነት ንምፍላጥ ምእካብ፣ ባህርያትን ምግምጋምን ኣገዳሲ እዩ። ቀንዲ ዕላማታት ናይዚ መፅናዕቲ ናይ መሽላ ኣግሮ-ሞርፎሎጂን ስነ መዓዛን ባህርያት ብዙሕነት ምግምጋም፣ ከምኡ እውን ኣብ ትግራይ ዘሎ ስርዓት ዘርኢ መሽላ ምትንታን እዩ ነይሩ። ኣብ ሰለስተ ቦታታት (ታሕታይ ኣድያቦ፣ መረብ ለኸን ፀለምቲን) ትግራይ ኣብ ወቕቲ ዕብየት 2018ን 2019ን ሚእትን ዓሰርተን ዓልየታት መሽላ ተገምጊሞም እዮም። ኣብዚ ነፍሲ ወከፍ ቦታን ዓመትን ከም ሓደ ፍሉይ ከባቢ እዩ ተታሒዙ። ንሳቶም ድማ ታሕታይ ኣድያቦ 2018 (ከባቢ1) ፡ መረብ-ለከ 2018 (ከባቢ2) ፡ ጸለምቲ 2018 (ከባቢ3) ፡ ታሕታይ ኣድያቦ 2019 (ከባቢ4) ፤ መረብ-ለኽ 2019 (ከባቢ5) ከምኡ'ውን ጸለምቲ 2019 (ከባቢ6) ። መረዳእታ ናይ 13 ዓይነታዊ ባህርያት ካብ ከባቢ1 ዝተረኽበ እንትኸውን፣ መረዳእታ ናይ 12 ብዝሒ ባህርያት ካብ ኩሎም ሽዱሽተ ከባቢታት ዝተረኽበ እዩ። ብዘይካ'ቲ ናይ ሜዳ ፈተነታት፡ ካብ ነፍሲ ወከፍ ከባቢ ብዛዕባ ሽውዓተ ስነ መዓዛ ዝምልከት NIRS ብምጥቃም፡ መረዳእታ ተኣኪቡ እዩ። ኣብ ትግራይ ዘሎ ስርዓት ዘርኢ መሽላ ንምፅናዕ ካብ ሽዱሽተ ቁሸታት ማለት ገዛዓድራ ፣ መዳበ ፣ ገዛመቀር ፣ ዋዕከል ፣ ሙኒራን ጋንዶስተላን ብዘይተሓሰበ መንገዲ ዝተመረፁ 153 ሓረስቶት መሽላ ገዛውቲ ዘሳተፈ ፍርቂ ቅርፂ ዘለዎ መሕተቲ ፅሑፍ ተጠቂምካ ዳህሳስ ተኻይዱ። ኣብ መርበብ ምልውዋጥ ዘርኢ መሽላ ዓብዪ ተራ ዝነበሮም ሓረስቶት ትንታነ ማሕበራዊ መርበብ ዘርኢ ብምጥቃም እዮም ተለልዮም። ዓይነታዊ ባህርያት መሽላ ብ SPSSን PASTን ሶፍትዌር ዝተተንተነ እንትኸውን፣ ብዝሕን መኣዛውን ፅሬት ባህርያት ድማ META-R ሶፍትዌር ተጠቒምካ ዝተተንተነ እዩ። እቶም GYTን GGEን ዝበሃሉ ባይፕሎት ብGenstat ሶፍትዌር እዮም ተሰሪሖዕም። ምልውዋጥ ዘርኢ መሽላ፣ ዋሕዚ፣ ምልውዋጥ ዘርኢ ዝውስኑ ረቛሒታት ብSPSS ዝተተንተኑ እንትኾኑ ማሕበራዊ መርበብ ዘርኢ ድማ ብUCINETን Netdraw ሶፍትዌርን ዝተተንተኑ እዮም።

ናይዚ መጽዕናቲ ውፅኢት ከምዘመልክቶ ልዑል ጀነቲካዊ ብዙሕነት መሽላ ብዙሕነት ዓይነታዊ ባህርያት ካብ 0.33 ንቅርፂ እኽሊ ክሳብ 0.99 ንስብሒ እኽሊ ብማእኸላይ 0.83 ከምዝኾነን እዚ ድማ ኣብ ውሽጢ ዓልየታት ዓብዪ ብዙሕነት ከምዘሎ ይሕብሩ። ኣብ ልዕሊ መበቀል ወረዳታት፣ ዞባታትን ክፍልታት ቁመትን ዝተገበረ ገምጋም H ' ናይ ነፍሲ ወከፍ ባህሪ ልዑል

ኮይኑ ሓፈሻዊ ማእከላይ ደረጃ 0.71 ፣ 0.74ን 0.70 ን ብቕደም ተኸተል እዩ። ኣብ ውሽጢ መበቖል ወረዳታ ፣ ዞባታትን ክፍልታት ቁመትን ኣብ ልዕሊ ባህርያት ዝተዋህለለ H ′ ልዑል ኮይኑ ሓፈሻዊ ማእኸላይ 0.71 ፣ 0.74 ፣ 0.69 ብቕደም ተኸተል እዩ። ኣብ ውልቀን ኣብ መላእ ከባቢታትን ዝተቐፀረ ANOVA ኣብ መንጎ ዓልየታት ንኹሎም ዝተፅንዑ ባህርያት ልዑል ትርጉም ዘለዎ ፍልልያት ($p < 0.001$) ኣርእዩ። ብተመሳሳሊ ፡ እቲ ውሁድ ትንተና ንኹሎም ብምኽንያት ዓልየታት (σ^2g) ፣ ምትእስሳር ዓልየታትን ከባብያዊ ምህዳርን (σ^2gxe) ፣ ከባቢታት ምህዳርን (σ^2e) ዝተጽንዑ ባህርያት ሓያል ትርጉም ዘለዎ ፍልልይ ($p < 0.001$) እዩ ኣርእዩ ብዘይካ ንትሕዝቶ ካልሲየም ብምኽንያት ከባቢ (σ^2e) ርኡይ ፍልልይ (< 0.05) ነይርዎ። እዚ ዘመላኽት ካብ ትግራይ ልዑል ምህርቲን ስነ መዓዛን ዝህቡን ናይ መሽላ ዓልየታት ክምዘለዉ የመልክት ። ኣብዚ መፅናዕቲ ንመብዛሕትኦም ዝተፅንዑ ባህርያት ዝተመዝገበ ልዑል ሰፊሕ ስሚዒት ውርሻ ($H^2 > 0.6$) ኣብ መንጎ ዓልየታት ውፅኢታዊ ምምራፅ ከምዝህሉ ዘመልክት እዩ።

ኣብ መንጎ ገለ ካብቶም ባህርያት ዘሎ ጽኑዕ ኣወንታዊ ምትእስሳር ብሰንኪ ልሙዳትን ዝተደራረቡን ብዝሒ ባህርያት ሎሳይ እቶም ባህርያት ብቐጥታዊ ምርጫ ብሓንሳብ ክመሓየሹ ከም ዝኽእሉ እዩ ዝሕብር. GGE biplot እቶም ሽዱሽተ ናይ ፈተነ ከባቢታት ኣብ ክልተ ሜጋ ከባቢታት ክጥርነፉ ከም ዝኽእሉ የመልክት። ከባቢ4ን ከባቢ5 ከም ኣድልዎ ዝፈጥሩ ከባቢታት ክለለዩ እንከለዉ፣ ከባቢ6ን ከባቢ2 ድማ ውክልና ዘለዎም ከባቢታት እዮም። ማእከላይን ምርግጋጽን ርእይቶ ናይ GGE biplot ልዑል ፍርያት ዘለዎም ዓልየታት (LR106, LR25, LR19, LR103, LR75, LR74, and LR16) ብምጥቃምፍሉያት ኮይኖም ነይሮም። እቶም ATCን GYT ደረጃ ጠቋሚን ብምጥቃምን ኣብ ውህደት ባህርያት ምህርቲ መሰረት ብምግባር ዓልየታት ንምስራፅ መሳርሒ ኮይኖም እዮም፣ እዚ ድማ GT biplot ተጠቒምካ ተግባራዊ ኣይኸውንን። በዚ መሰረት LR106 > LR25 > LR102 > LR12 > LR78 > LR103 > LR1 > LR74 > LR15 ምህርቲ እኽልን ምስ ምህርቲ ዝተኣሳሰሩ ባህርያትን ንምውህሃድ ብደረጅኦም መሰረት ዝበለፀ ደረጃ ዝረኸቡ ዓልየታት እንትኾኑ LR12>LR23 > LR25 > LR106 > LR1 > LR27 > LR78 > LR6 > LR81 ምህርቲ እኽልን ባህርያት ፅሬት ስነ መዓዛን ንምውህሃድ ብደረጃኦም መሰረት ዝበለፀ ደረጃ ዝተሰርዑ ዓልየታት እዮም።

መፍትሕ ቃላት፤ ዓልየታት ብዙሕነት፡ ምትእስሳር ባህርያት፡ ሰፊሕ ህዋሳዊ ውርሻ፡ ማሕበራዊ መርበብ ዘርኢ

LIST OF PAPERS

Published papers

1. Analysis of Sorghum Social Seed Network in Tigray, Northern Ethiopia (*African crop science journal* https://dx.doi.org/10.4314/acsj.v31i3.11)

2. Genotype by Trait (GT) and Genotype by Yield*****Traits (GYT) Analysis of Sorghum Farmers' Varieties in Tigray, Northern Ethiopia (Published in *journal of crop breeding, genetics and genomics* https://doi.org/10.20900/cbgg20230002

Papers in preparain for publication

1. Phenotypic diversity in sorghum [*Sorghum bicolor* (l.) Moench] farmers' varieties in Tigray, North Ethiopia
2. Genetic Variability and Genotype by Environment Interaction for Agro-morphological traits of Sorghum [*Sorghum bicolor* (L.) Moench] genotypes in Tigray, North Ethiopia
3. Genetic Diversity, Correlation and Genotype by Yield by Trait (GYT) Analysis of Grain Yield and Nutritional Quality Traits in Sorghum (*Sorghum bicolor* [L.] Moench) Genotypes in Tigray, North Ethiopia

CHAPTER ONE

1. General Introduction

1.1. Background and Justification of the Study

Sorghum [*Sorghum bicolor* (L) Moench; 2n = 2x = 20] belongs to the *Poaceae* family and Andropogoneae tribe (Harlan and de Wet, 1972). It is originated in Ethiopia and surrounding countries around 4000-3000 B.C. in Ethiopia and surrounding countries from wild forms (Ayana and Bekele (1998) and Dillon et al. (2007). Sorghumis the fifth most important cereal crop worldwide after maize, rice, wheat, and barley (FAOSTAT, 2021). United States, Nigeria, Mexico and Ethiopia are the world's leading sorghum producer countries (Statista, 2023). In Africa, sorghum is the fourth most widely cultivated cereal crop next to maize, rice, and wheat and second in area coverage after maize (FAOSTAT, 2021). It is a C4 photosynthetic crop serving as a major food security crop in sub-Saharan Africa and Asia supporting over 500 million people (Amelework et al., 2016; Mace et al., 2013). Sorghum is cultivated in a wide spectrum of geographic conditions starting from 400 to 3000 meters above sea levels and from semi-arid to humid regions (Geremew et al., 2004; Girma et al., 2020). Its inherent ability to give reasonable yield in relatively low soil fertility and moisture stress areas where other crops could survive least makes sorghum an excellent crop for smallholder farmers prevailing in the arid and semi-arid tropics of the world (Girma et al., 2020; Nida et al., 2019).

Sorghum is the most diversified crop having 28 domesticated species categorized into five basic races *i.e. bicolor, guinea, caudatum, dura* and *kafir* and ten hybrid races (Harlan and de Wet, 1972). Sorghum is the first fully assembled C4 crop using traditional Sanger sequencing and is considered as 'gold standard' reference due to its high percentage assembly (Boyles et al., 2019). The broad genetic base harbored mainly in sorghum farmers' varieties is essential for providing the gene pool necessary for the development and deployment of farmers' preferred varieties. Owing to its center of origin and diversity (Doggett, 1991) coupled with the diverse agro-ecologies, Ethiopia is a country endowed with high treasure of sorghum landrace diversities (Ayana and Bekele, 1998; Geleta and Labuschagne, 2005). As cited in other kinds of literature (Grenier et al., 2004; Hummer and Hancock, 2015), centers of origin are an important hotspot for generating new genetic variability essential for crop improvement and utilization programs. Previous studies on genetic diversity of Ethiopian sorghum germplasm (Abdi et al., 2002; Amelework et al., 2016; Ayana and Bekele, 1998; Geleta and Labuschagne, 2005; Gerrano et al., 2014; Girma et al., 2020) showed that there are high diversities of sorghum in the country. The Ethiopian sorghum gene pool has been contributing to global agriculture either for direct cultivation or as a source of important traits for various breeding objectives such as drought tolerance (Adugna, 2014), resistant to mold disease (Nida et al., 2019) and high lysine content (Singh and Axtell, 1973).

Most of the studies on sorghum diversity in Ethiopia were based on accessions from gene banks mainly on yield and agronomic traits with less emphasis given to the nutritional quality traits. Genetic diversity studies using genetic materials from ex-situ (Gene banks) have been reported to have limitations to maintain the patterns of evolutionary processes of crop genetic resources in their original habitats which may result to loss of genetic diversity and poor responses to newly emerged biotic and abiotic factors (Seboka and van Hintum, 2006; Thomas et al., 2011; Wang et al., 2016). Consequently, the importance of in-situ conservation strategy along with farmers' knowledge and practice, its complementarily with ex-situ conservation and relevance to maintain evolutionary forces within and between the different agricultural components is being recognized (Abay et al., 2009; Abdi and Asfaw, 2005; Thomas et al., 2011; Wang et al., 2016). In the country, there are still unexplored genetic diversities of Ethiopian sorghum germplasm which could be novel sources of various important traits (Cuevas et al., 2017; Girma et al., 2020). Moreover, the social, cultural, and methodological dimensions, features of seed exchanges among farmers and the assets that might sustain local seed exchanges and crop diversity the sorghum seed exchange mechanisms and seed sources are essential for efficient breeding programs and seed intervention strategies (Labeyrie etal, 2014; Wendmu et al., 2022).

Sorghum is well known for its multiple use such as source of food, fodder, fuel, bioethanol, alcoholic beverages and building materials (Adugna and Bekele, 2013). Sorghum is the second cheapest source of energy next to finger millet (Phuke et al., 2017) and its grains are good sources of various minerals, vitamins, carbohydrates and proteins essential for human well-being (Dicko et al., 2006; Kumar et al., 2015; Shegro et al., 2013) Besides, sorghum is gluten-free (Dicko et al., 2006), which makes it an excellent food crop for people who have gluten intolerance. Due to its high nutritional value, the market interest in sorghum grains is markedly growing worldwide (Angkuratipakorn et al., 2020).

In Ethiopia, sorghum is a multipurpose crop used for food, fuel, housing materials, fencing and livestock feed (Adugna and Bekele, 2013; McGuire, 2007). Sorghum ranked third in area coverage after teff and maize, and fourth in total production next maize, wheat and teff and cultivated by about 4.9 million smallholder farmers (CSA, 2022). In the 2021/22 growing season, Ethiopia produced 3.6 million metric tons from an area of 1.4 million hectares (CSA, 2022). It is mainly cultivated under rain-fed and low-input environments where acute shortage of food and malnutrition prevails. Ethiopian farmers grow diverse forms of sorghum varieties with over 95% of the area allocated for sorghum production covered by farmers' varieties (Adugna, 2014). The average yield of sorghum in Ethiopia is low as compared to its potential and production in other countries such as Egypt (5.4 t/ha), China (4.8 t/ha), the USA (4.6 t/ha) and Argentina (4.4 tons per hectare) (USDA, 2020). The low yield per hectare is attributed to various biotic and abiotic factors such as drought, poor soil fertility and Striga weeds (Amelework et al., 2016; Habte et al., 2020; Rebeka et al., 2013), genotype by environment interactions (Admas and Tesfaye, 2017; Worede et al., 2020) and low level of sorghum research investment in human, financial and material resources development and low input production systems (Mekbib, 2008).

Hence, further collection, characterization, evaluation and subsequent use of the genetic diversity of sorghum germplasm for breeding and conservation programs could significantly contribute to increased production and productivity of the crop. This demands a holistic and better understanding of the pattern of genetic diversity of the crop, the environment where it is growing and the social and cultural practices of the farmers (Labeyrie et al., 2014). The ways that crop diversity is shaped by social dynamics, especially among rural smallholders requires greater investigation (Kawa et al., 2013; Labeyrie et al., 2014) and it is useful to explore the patterns of seed exchange that influence farmers' use of and access to agricultural biodiversity, and the ways in which cultural, demographic, and agricultural changes have the potential to enhance or erode that diversity (Samberg et al., 2013). Thus, a proper understanding of the nature of seed sources and exchange mechanism among farming communities is essential to strengthening the capacity of seed production and distribution systems to ensure sustainability and longer-term impact by enhancing the facilities and increasing the capacity of key partners for systematic production and timely delivery of sufficient seed of farmer-preferred variety. In Tigray, one of the main sorghum-growing regions of Ethiopia (CSA, 2019) few information is avialable on the the genetic variation of agronomic and nutritional quality traits of farmers' varieties of sorghum and its seed systems. Therefore, this study was conducted with the following objectives.

1.2. Objectives

A. General Objectives

To assess the genetic diversity for agro-morphological and nutritional quality traits in sorghum (*Sorghum bicolor* (L.) Moench) genotypes and analyze sorghum seed system in Tigray.

B. Specific objectives

- To estimate the extent and patterns of phenotypic diversity of qualitative traits of sorghum genotypes according to their districts of origin, administrative zones, and altitude classes in Tigray
- To estimate genetic diversity, heritability and trait association, G×E interaction and stability of sorghum genotypes in different environments of Tigray
- To evaluate the genetic diversity, heritability and association of grain yield and nutritional quality traits of sorghum in Tigray
- To o explore the seed source and exchange mechanism and to identify nodal farmers who play a major role in the sorghum seed exchange networks in Tigray

1.3.Research hypothesis

In the present study the following hypotheses were tested:

- In areas of sorghum growing belts of Tigray, there are substantial genetic diversities of sorghum farmers’ varieties if assessed using phenotypic and nutritional quality traits
- Sorghum genotypes respond differently in different agro-ecologies of Tigray
- Subsistence smallholder farmers in Tigray use diiferent seed exchnge and sources of sorghum seeds in Tigray
- The social assets influnces the sorghum seed exchnge among farmers in Tigray

1.4.Conceptual framework

This research was framed with the concept that genetic diversity is essential prerquest for any breeding and conservation programs. The genetic diversity is determined by various biophysical factors such as farmers’ seed exchange and natural evoluationary forces. The genetic diversity contains varous target traits preffered by farmers, breeders and conservationists that can be detected using qualitative and quantitative traits evaluations and farmers’ seed network and flows as depicted in Figure 1.1.

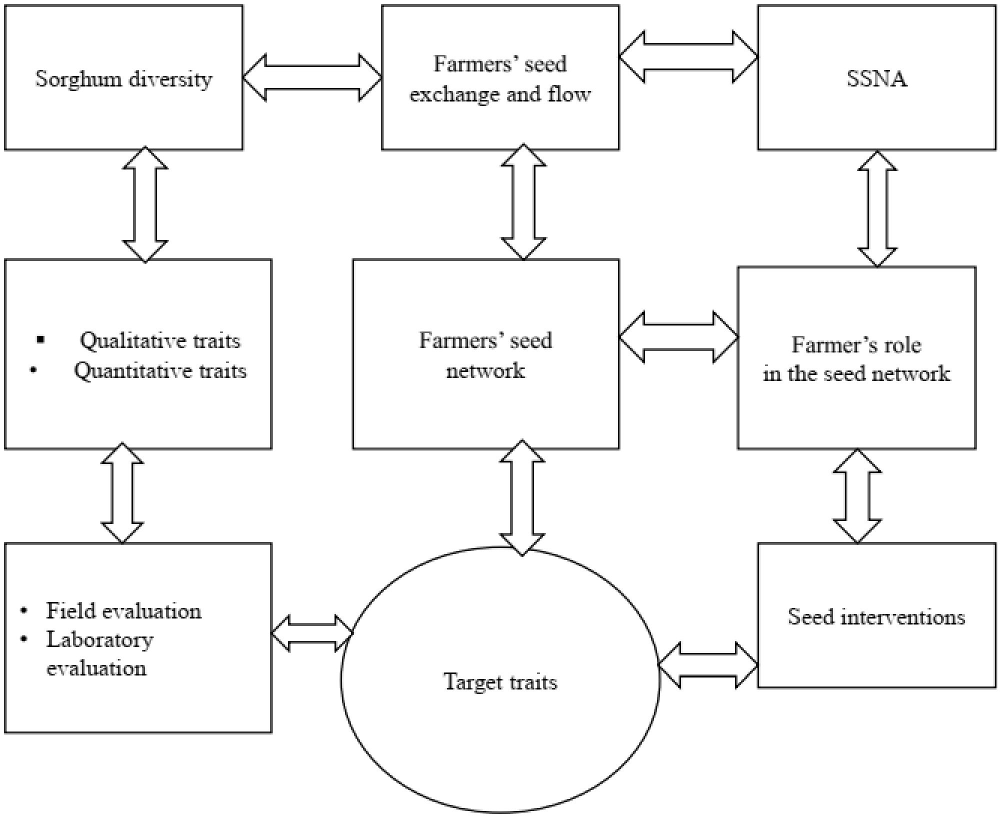

Figure 1.1. Conceptual framework of the study

1.5. Motivations (Integrations of the papers)

This research work was initatiated due to the fact that Ethiopia is endowed with high treasure of sorghum diversity of wild, weedy and cultivated sorghum which could be novel sources of various important traits. Besides, farmers have varied seed sources and exchange mechanisms, and cultivation and conservation strategies. This could be an opportunity to motivate policy attention, increase sorghum production and productivity, leading to increased household food security and improved livelihoods of farmers in arid and semi-arid areas like Tigray. Which in turn, demands thorough investigations of patterns of the available genetic diversities agro-morphological and nutritional quality traits along with the seed flow and exchange mechanisms and other determining factors.

Thus, we evaluate the genetic diversity of various qualitative, quanitiative and nutritional quality traits of sorghum genotypes along with the nature of sorghum seed exchange and flows in Tigray. This thesis was prepared according to the Mekelle University's draft on thesis writing guideline for postgraduate. It is comprised of seven interlinked chapters. The first chapter highlights the background, objectives and hypothesis of the study. The second chapter is aimed to review more about sorghum origin, taxonomy, genetic diversity, production constraints and seed systems. The third chapter explores the phenotypic diversity qualitative traits of sorghum genotypes taking their districts and zones of origin and altitude classes into consideration. Important insights about the diversity of 13 qualitative traits of sorghum are reported in this chapter. The fourth chapter explores the genetic diversity and genotype by environment interaction of sorghum genotypes for agro-morphological traits. In this chapter, genetic diversity, trait association, heritability of sorghum genotypes were investigated. Using the GGE biplots analysis, discriminative and representative environments and stable and high yielding genotypes were identified. The fifth chapter is the continuity of the forth chapter but it focuses on multi-trait analysis using the genotype by yield by trait (GYT) analysis approach using grain yield and yield related traits. The sixth chapter highlights the genetic diversity, trait association, heritability and multi-trait analysis of nutritional quality traits. In this chapter grain yield was included to determine the combining ability of nutritional quality traits with grain yield. The seventh chapter is about the social seed network of sorghum in Tigray which discloses the main seed exchange mechanisms and seed sources along with the main reasons motivate and of discourage of farmers to exchange sorghum seeds. Important insights on seed intervention strategies are also discussed.

1.6. Materials and Methods

1.6.1. Study sites, germplasm sources and experimental designs

To study the genetic diversity of sorghum in Tigray, a total of 110 sorghum genotype comprised of 108 sorghum landrace collections and two improved varieties were evaluated for 13 qualitative traits, 12 quantitative traits and seven nutritional quality traits. The farmers' varieties were collected from Raya Azebo (10 farmers' varieties), Mereb Leke (18 farmers' varieties), Asgede Tsimbla (14 farmers' varieties), Tselemti (10 farmers' varieties), Tahtay Adyabo (25 Farmers' varieties), Tsegede (6 farmers' varieties), Welkait (10 farmers' varieties), and Kafta Humera (15 farmers' varieties) (Figure 1.2). The districts are representative of four administrative zones of theTigray region which are Raya Azebo (southern zone), Mereb Leke (central zone), Asgede Tsimbla, Tahtay Adyabo, and Tselemti (northwestern zone), and Kafta Humera, Tsegede, and Welkait (western zone). For identification and retrieval purposes, information about the local name of the farmers' varieties, collection district, administrative zones, and altitude were recorded. In addition to this, collection numbers with the prefix LR were given for each of the Farmers' varieties (LR). For instance, LR1 was designated as landrace collection number one. Further details of the sorghum farmers' varieties are provided in Appendix 1. The improved varieties (Melkam and Dekeba) were obtained from Tigray Agricultural Research Institute (TARI). To collect the quantitative traits genotypes were planted in three locations (Tahtay Adyabo, Tselemti, and Mereb Leke) of Tigray in the 2018 and 2019 main growing seasons (Figure 1.3). Data on the 13 qualitative traits were obtained from the field experiment in Tahtay Adaybo in 2019.The agro-ecological description of the field experimental sites is given in Table 1.1.

The experimental layout was an alpha lattice design (Patterson and Williams, 1976) with two replications at each experimental site. On each plot, the seeds were sown in a single 5 meters long row. The spacing between rows and between plants within rows were 0.75 and 0.25 meters, respectively. The land was tilled twice-using traditional oxen-drawn plows and seedbeds were prepared using human power, and planting and harvesting were done manually. All other agronomic practices were applied as per the recommendations for the area. After harvesting at physiological maturity, panicles were sun-dried for 15 days. Thereafter, panicles from each plot were threshed, winnowed, and seeds packed.

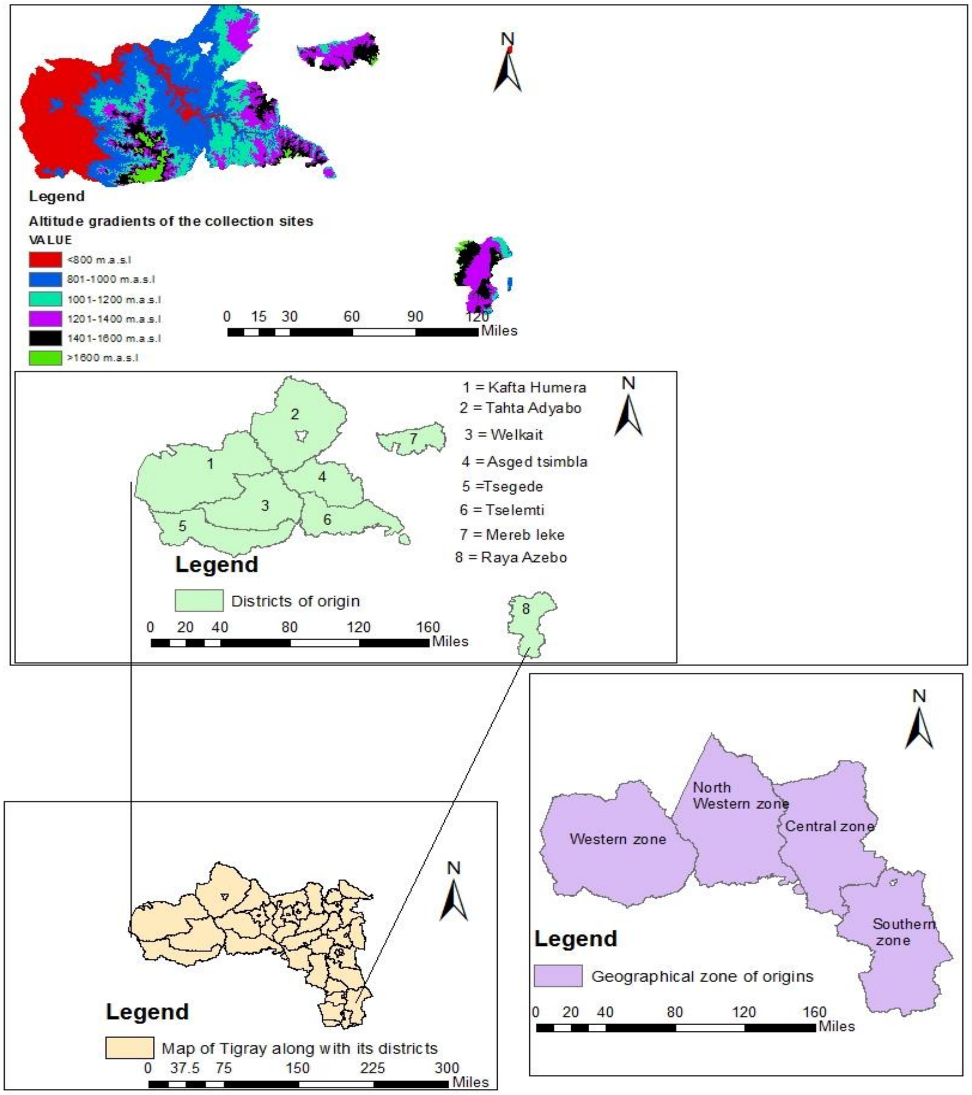

Figure 1.2. Map of the districts, zones and altitude classes from where the materials collected

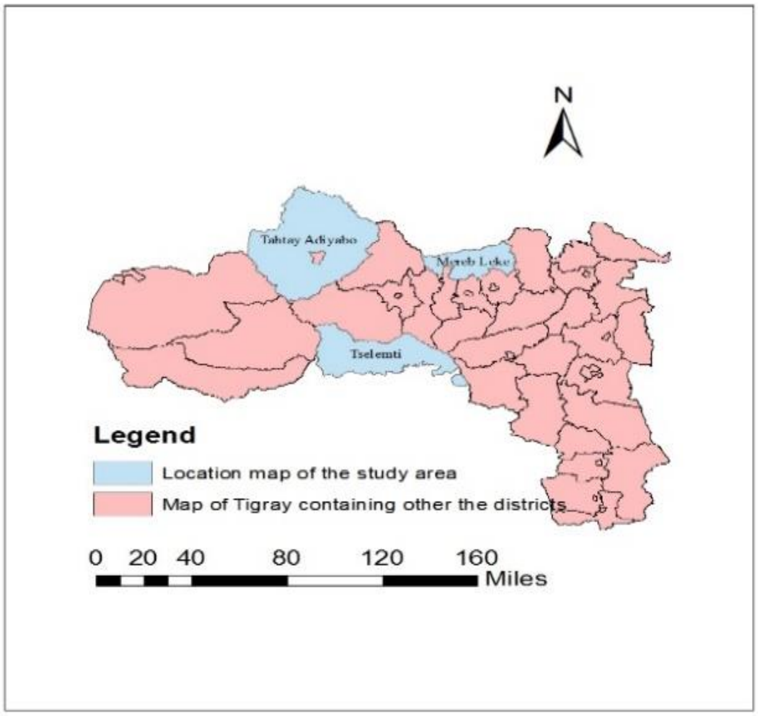

Figure 1.3. Location map of Tigray showing the experimental sites

Table 1.1. Agroecological and climatic data the experimental sites

Experimental site	Altitude m.a.s.l	Longitude	Latitude	Temperature (°C)		Rainfall mm/annum	
				2018	2019	2018	2019
Tahtay Adyabo	1025	37°45'E	14°24'N	20-35	20-37	677	1069
Mereb Leke	1395	38°47'E	14°23'N	14-34	15-34	510	1051
Tselemti	1450	38°10'E	13°41'N	19-32	20-33	1301	1685

Temperature and rainfall data were obtained from the Meteorological Agency of Ethiopia, Tigray office, Mekelle

The social seed network study was carried out in two districts of Tigray, namely, Raya Azebo and Tahtay Adyabo in northern Ethiopia. Raya Azebo is located in the Southern Zone of Tigray, while Tahtay Adyabo found in the northwestern Zone of Tigray (Figure 1.4). From Raya Azebo three villages *viz*: Waekel, Gandostela and Munira and from Tahtay Adyabo district, three villages namely Gezameker, Medabe, and Gezaadre were considered for the survey.

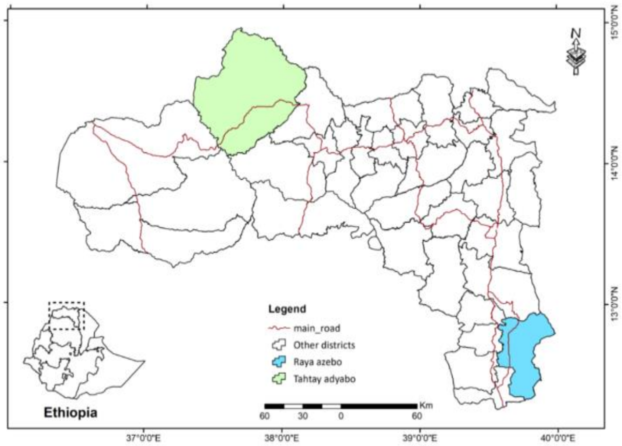

Figure 1.4. Map of Tigray showing the study districts for social seed network analysis of sorghum

1.7. Data Collection

Data were recorded on 13 qualitative traits (Table 1.2) using standard descriptors for sorghum (IBPGR, 1993). Besides, (Munsell, 1990) and visual examination using a 10× magnifying lens were used. Ten plants from each landrace were sampled to score the qualitative traits (five plants from each replication), which resulted in a total of 1100 plants.

Table 1.2. Qualitative traits, descriptors and codes used for phenotypic evaluations of sorghum genotypes in Tigray

Sn	Qualitative traits	Codes for the traits
1	Glume color:	(1) white group, (2) yellow group, (3) gray-orange, (4) red, (5) gray, (6) purple (7), black grey
2	Grain plumpness	(3) dimple, (7) plump
3	Glum hairiness	(1) hairiness, (2) middle, (3) hairless
4	Grain covering	(1) 1/4 grain covered, (3) 1/2 grain covered, (5) 3/4 grain covered, (7) grain fully covered, (9) glumes longer than the grain
5	Grain color	white (1), yellow (2), red (3), brown (4)
6	Grain form	(1) single-seeded, (2) twin seeded
7	Inflorescence exertion	(1) slightly-exerted, (2)exerted, (3) well-exerted (4), peduncle re-curved/ goose
8	Awns at maturity	(0) absent, (1) present
9	Inflorescence compactness	(1) very lax, (2) very loose, (3) very loose dropping primary branches, (4) loose erect, (5) loose drooping primary branches; (6) semi-loose erect primary branches, (7) semi-loose drooping primary branches, (8) semi-compact elliptic, (9) compact elliptic,(10) compact oval, (11) half broom corn, (12) broom corn
10	Endosperm texture	(1) completely corneous, (3) mostly corneous (5) intermediate (7) mostly starchy, (9) Completely starchy
11	Endosperm color	(1) white (2) yellow -grey
12	Shattering	(1) very low, 3 (low), (5) intermediate, (7) high, (9) very high
13	Thresh-ability:	(1) Thresh-able, (2) not thresh-able

Adapted from IBPGRI and ICRISAT (1993) Descriptors for Sorghum [Sorghum bicolor (L.) Moench

Data on agro-morphological traits such as days to 50% heading, days to 50% flowering days, days 50% to maturity, grain yield (quintal ha^{-1}), plant height (cm), panicle length (cm), leaf length(cm), leaf number, thousand seed weight (g), panicle weight (g) panicle width (cm) and leaf width (cm) were recorded (Table 1.3).

Table 1.3. Data collected on agro-morphological (quantitative) traits of sorghum in Tigray

SN	Data collected	Description of traits
1	Days to heading (DH)	Number of days from emergence to when 50% of plants have bear heading in a plot
2	Days to flowering (DF)	The number of days from planting to when approximately 50% of the plants in a plot reached flowering
3	Days to maturity (DM)	the number of days from planting to when seeds on 50% of the plants in a plot exhibited black layer on the lower third of the panicle.
4	Thousand seed weight (TGWT)	The weight of thousand seeds of sorghum in grams
5	Grain yield (GY)	Was obtained by converting grain yield/plot to hectare based expressed as quintal per hectar
6	Panicle length (Pnl)	The length of five randomly selected panicles from a plot was measured in cm and the average was taken as panicle length
7	Panicle width (Pnwd)	The length of five randomly selected panicles from a plot was measured in cm and the average was taken as panicle length
8	Panicle weight (Pnwt)	The length of five randomly selected panicles from a plot was measured in cm and the average was taken as panicle length
9	Plant height (PH)	The average length of five plants per plot measured from the base to the tip of the plant
10	Leaf length (LL):	The length of the third leaf from flag leaf of five randomly selected plants was measured and averaged.
11	Leaf width (Lwd)	The width of the third leaf from flag leaf of five randomly selected plants was measured and averaged.
12	Leaf number (LN)	Count of total number of leaves per plant (main stalk) of five randomly selected plants and averaged.

Data on nutritional quality traits were recorded using near infra-red spectroscopy (NIRS) method at Mekelle University. The nutritional quality traits such as protein, ash and starch content of the sorghum seeds were expressed in terms of percentages, whereas Fe, Zn, Ca and Mg concentrations were expressed in terms of parts per million (ppm).

Data on social seed network studied using, reconnaissance surveys and discussions with agricultural experts and community leaders to get important insights about sorghum cultivation in the areas. Then after, a total of 36 farmers (50% females) were selected as first group members and asked to list their seed exchange partners, what seed exchange mechanism they use while sharing seed, which variety of sorghum they exchange, factors that inspire and discourage them to exchange sorghum seeds, and the number of sorghum varieties they retain for further use. At this step, a total of 151 farmers (second group farmers) were listed by the first group farmers as their seed exchange partners. One hundred and seventeen of the second group farmers were asked to name their seed exchange partners. The number of second group farmers interviewed was reduced from 151 to 117 because 20 farmers were already interviewed during the first stage and the rest 14 farmers could not be available due to several reasons. The second group of farmers, in turn, list a total of 309 farmers as their seed exchange partners. Among these, 25 were the first group and 67 were among the second group farmers. The snowball sampling method was used through all the steps. The snowball sampling method has been an effective approach for social network analysis (Subedi et al., 2003). For the data on the socioeconomic of farmers, the number of varieties conserved per household, and on factors that motivate and discourage farmers to exchange sorghum seeds only the first and second-batch farmers' (a total of 153 farmers) were interviewed. The third group of farmers was not interviewed due to resource limitations. However, they were included in the seed networks, and seed sources and flow analysis based on the information obtained from the first and second group farmers as they are seed exchange partners.

1.8. Data Analysis

1.8.1. Qualitative traits

The 13 qualitative traits of sorghum were analysed for frequency percentages of each trait across districts, geographical zones, and altitude classes using SPSS software packages v 20. Additionaly, chi-square values were carried out to test the deviation of the observed frequency distributions of the traits from the expected values using the same software. Shannon-Weaver diversity index (H′)

was computed using the phenotypic frequencies to assess the phenotypic diversity for each trait for all the Farmers' varieties using PAST software v 3.22 (Hammer et al., 2001). This is provided as follows:

$$H' = -\sum_{i=1}^{K} Pi * ln\, Pi$$

Where 'Pi' is the proportion of i^{th} attribute state of the trait under consideration in the landrace and the signed sum indicates the summation over all the K attribute states of that trait. Each value of H' was standardized by dividing it by its maximum value, to keep the values in the range of 0–1.

This was done as $H' = H/H_{max}$

The altitudes were arbitrarily classified into six classes as 1 (< 800), 2 (801-1000), 3 (1001–1200), 4 (1201-1400), 5 (1401-1600), and 6 (>1600) meters above sea level. An arbitrary classification of altitudes has been also used by (Abdi et al., 2002). The Shannon-Weaver diversity indexes (H') was also arbitrary classified as very high (H'> 0.8), high (>0.6 H' ≤0.8), intermediate (>0.4 H' ≤ 0.6), low (> 0.2 H' ≤ 0.4), and very low (H' ≤ 0.2). Mengistu et al. (2015) also used subjective classifications of diversity index for durum wheat landraces. Analysis of variance of non-transformed H' was performed for all the characters across all districts of origin, geographical zones of origin, and altitude classes using a GenStat-18 statistical package. Moreover, principal components that explained at least 5% of the total variance and with an eigenvalue of at least 1 were retained.

1.8.2. Quantitative traits

The data collected on quantitative traits (12 agro-morphological and seven nutritional quality traits) were analyzed using linear mixed models in META-R software (Alvarado et al., 2015). Each location and year were treated as an independent environment. The mean performance, association among the traits, variances and heritability in individual environment (Tahtay Adyabo 2018, Mereb-Leke 2018, Tselemti 2018, Tahtay Adyabo 2019; Mereb-Leke 2019, and Tselemti 2019, hereafter referred as En1, En2, En3, En4, En5 and En6, respectively), and combined across the testing environments were analysed using the models implemented in lmer from package lme4 of R software. The formula and models used for this study are according to the description made by Alvarado et al. (2020).

The model for the analysis of variance in individual environments is given as

$$Y_{ijkl} = \mu + rep_i + block_k(rep_j) + gen_j + \varepsilon_{ijk}$$

Where Y_{ijk} = the trait of interest, μ = the mean effect, rep_i = the effect of the i^{th} replicate, $block_j$ (rep_i) = the effect of the j^{th} incomplete block within the i^{th} replicate, gen^k = the effect of the k^{th} genotype, ijk = the error associated with the i^{th} replication, j^{th} incomplete block and the k^{th} genotype.

For the combined analysis, new terms are added to the model for the individual environment as:

$$Y_{ijkl} = \mu + env_i + rep_j + rep_j(env_i) + block_k(env_i \times rep_j) + gen_j + env_j \times gen_j + \varepsilon_{ijkl}$$

Where env_i and $gnv_i \times gen_l$ = the effects of the i^{th} environment and the environment by genotype interaction, respectively.

Broad-sense heritability (H^2) in individual and overall environments were estimated using the formula:

$$H^2 = \frac{\sigma_g^2}{\sigma_g^2 + \sigma_e^2 / nr}, \text{ and}$$

$$H^2 = \frac{\sigma_g^2}{\sigma_g^2 + \sigma_{ge}^2/nEnvs + \sigma_e^2/(nEnvs \times nr)}$$

Where $\sigma^2{}_g$, $\sigma^2{}_e$, $\sigma^2{}_{ge}$, nr and $nEnvs$ = the genotype variance, error variance, genotype by environment interaction variance, number of replication and number of environments, respectively.

The least of significance differences (LSD) at 5% of significance was calculated as:

$$LSD = t(0.05, dfErr) \times ASED\ ,$$

Where t = the cumulative Student's t distribution, 0.05 = the selected α level (5%), dfErr = the degrees of freedom for error in the linear mixed model, and ASED = the average standard error of the differences of the means.

The coefficient of variation was calculated using the formula:

$CV(\%) = (\frac{\sqrt{MSE}}{Grandmean}) \times 100$, where MSE = the mean squared error.

1.8.3. GGE biplot analysis

Each year and each location was considered as a separate environment. When there was a significant difference in GE interaction, GGE biplot method was employed to analyze of GE interaction and to assess grain yield stability (Yan, 2001). The model for GGE analysis is given as

$$Y_{ij} - \mu - \beta_j = \sum_{k=1}^{k} \lambda_k \xi_{jk} \eta_{jk} + \varepsilon_{ij}$$

Where Y_{ij} = the mean yield of genotype i in environment j, μ = the grand mean, β_j = the main effect of environment j, λ_k = the singular value of K^{th} principal component (PC), ξ_{ik} = the eigen-vector of genotype i for $PC_{k,}$ η_{jk} = the eigen-vector of environment j for $PC_{k,}$ k = the number of PC axes retained in the model, and ε_{ik} = the residual associated with genotype i in environment j.

1.8.4. Genotype by Yield by Trait (GYT) analysis

GYT analysis was done following the steps described by (Yan and Frégeau-Reid, 2018). First, the genotype by trait (GT) two-way table was converted to GYT two-way table. This was done by multiplying grain yield by each nutritional quality trait (grain yield*starch, grain yield*protein, grain*ash content, grain yield*zinc, grain yield*iron, grain yield*calcium and grain yield*magnesium, hereafter, referred to as gy*sta, gy*pro, gy*ash, gy*Zn, gy *Fe, gy*Ca and gy*Mg, respectively. Thenafter, the GYT table was standardized **t**o mean zero and unity variance to minimize biases due to differences using the formula:

$$P_{ij} = \frac{T_{ij} - Tj}{S_j}$$

Where: P_{ij} = the standardized value of genotype *i* for a trait or yield-trait combination *j* in the standardized table, T_{ij} = the original value of genotype *i* for yield-trait combination *j* in the GYT table, T_j = the mean across genotypes for yield-trait combination *j*, and S_j = the standard deviation for yield-trait combination *j*.

The standardized GYT tables for each trait were used to generate biplots using Genestat software version 18th. The biplots were based on singular value decomposition of trait-standardized data (scaled by standard deviation, centered by tester-centered G+E and trait-focused symmetrical singular value partition). For clarity purposes, we use only the numbers of the genotype for GYT biplot constructions.

The following equation was used to construct the GYT biplot:

$$P_{ij} = (\alpha\lambda_1^{\alpha}\varsigma_{i1})*(\lambda_1^{1-\alpha}\Gamma_{1j}/d) + (d\lambda_2^{\alpha}\varsigma_{i2})*(\lambda_1^{2-\alpha}\Gamma_{2j}/d) + \varepsilon_{ij}$$

Where ς_{i1} and ς_{i2} = eigenvalues for PC1 and PC2, respectively, for genotype Γ_{1j}; Γ_{2j} = eigenvalues for PC1 and PC2, respectively for yield-trait combination (or trait) j, and ε_{ij} = residual from fitting the PC1 and PC2 for genotype i on yield-trait combination j; λ_1^{α} and λ_2^{α} = singular values for PC1 and PC2, respectively, and α = singular value partitioning factor. When α = 1 (i.e., SVP=1), the biplot is said to be genotype-focused and is suitable for comparing genotypes. When α = 0 (i.e., SVP=2), the biplot is said to be environment-focused and is suitable for visualizing correlations among environments. The scalar d is chosen such that the length of the longest vector among genotypes equals to that among environments; this is important for generating a functional biplot (Yan, 2014).

Data obtained on seed systems were analyzed using UCINET and Netdraw software package (Borgatti et al., 2002). While coding the data, farmers were considered as node data, whereas the seed exchange modes and the varieties under exchanged were used as tie data. The role of the farmers in the network was computed using degree and betweenness centrality measures as described by Abay et al. (2011). Descriptive statistics about the respondents' socioeconomic characteristics, seed exchange means, seed flow, sorghum varieties maintained per household, and motivations and daunt to exchange sorghum seed have been analyzed using SPSS 20.0 (SPSS, Chicago, IL, USA) software. Statistical differences were determined using the T-test.

1.9. Main Results and Discussions

The present study identified that high and comparable qualitative trait distributions among the sorghum Farmers' varieties. The H′ computed for individual qualitative traits varied from 0.33 for grain form to 0.99 for grain plumpness with a mean of 0.83, which reveals huge diversity within the Farmers' varieties. The estimated H′ of each trait pooled over districts of origin, administrative zones, and altitude classes were high with an overall mean of 0.71, 0.74, and 0.70, respectively. The H′ pooled over traits within the districts of origin, geographical zones, and altitude classes were high with an overall mean of 0.71, 0.74, and 0.69, respectively. On the basis of district origin, the highest (0.84) and the lowest (0.46) H′ values were recorded for the Tahtay Adyabo and Raya Azebo districts, respectively. When the geographical zones were considered, the highest (0.83) and the lowest (0.46) H′ values were recorded for the northwestern zone and southern zone, respectively. With respect to altitude classes, the highest (0.80) and the lowest (0.68) H′ value were recorded for 1001 m.a.s.l and >1600 m.a.s.l, respectively. Our finding confirmed the different degrees of higher variability of qualitative traits in Ethiopian sorghum gene pools reported so far (Abdi et al., 2002; Adugna and Bekele, 2013; Ayana and Bekele, 1998; Geleta and Labuschagne, 2005; Semere et al., 2023).

Several highly performing genotypes were distinguished for each trait studied that could be exploited as breeding parents or direct use. The analysis of variance computed in individual and across environments showed that highly significant variations p <0.001) among the genotypes for all the traits studied. Likewise, the combined analysis showed strong significant variance (P<0.001) for all traits studied due to genotype (σ^2g), genotype by environment interaction (σ^2 g x e) and environments (σ^2e) with the exception that variance due to environment (σ^2e) had significant variation (< 0.05) for calcium content. This indicates that farmers' varieties collected from Tigray harbor high genetic variation useful for the development and deployment of nutritionally enhanced and high-yielding sorghum varieties. This agrees with the report by Hummer and Hancock (2015) who noted that enormous variations are available in Farmers' varieties that are evolved in Vavilov centers of crop origin and diversity such as Ethiopia. High genetic variation of sorghum diversities collected from Tigray were also reported in recent study by Semere et al. (2023). The large genotype by environment interaction (σ^2 g x e) variance relative to the genotype variance indicates the need to select for trait stability in the target environment (Bashir et al., 2014; Andiku et al, 2022). The high level of genetic variation for various quantitative traits identified in the present study could be attributed to the genetic constitution of the genotypes, varied agro-ecologies and environmental conditions that could affect mineral uptake translocation and distribution. Gene flow between wild and cultivated relatives could be also a likely reason for the high genetic diversity in sorghum Farmers' varieties (Tesso et al., 2008). The present results support the high genetic diversity of various sorghum traits reported earlier (Badigannavar et al., 2016; Makebe and Shimelis, 2023; Phuke et al., 2017; Shegro et al., 2012).

In the individual environments high broad-sense heritability ($H^2 > 0.6$) were obtained for all traits studied except for leaf number and leaf length. Leaf length showed medium broad-sense heritability ($H^2 > 0.3 < 0.6$) in En1, En3 and En4, whereas leaf number showed lower broad-sense heritability ($H^2 < 0.3$) in En6 and medium broad-sense heritability in En5. Similarly, the across environment analysis showed the broad-sense heritability was higher ($H^2 > 0.6$) for all the traits studied except for protein and zinc which had moderate broad-sense heritability ($H^2 >0.3 <0.6$). The high broad-sense heritability recorded in the present study assured the possibility of effective selection among the genotypes. As in this study, high to medium heritability in sorghum germplasm has been also reported for various agronomic and nutritional traits by (Adedugba et al., 2023; Andiku et al., 2022; Phuke et al., 2017)**.**

Identification of sorghum genotypes having higher yield that combine important nutritional quality traits could play a pivotal role in reducing the widespread food and nutrition deficiencies, especially in the community deeply dependent on sorghum for their staple crop (Phuke et al., 2017). In the present study, both negative and positive significant associations between some of the traits were detected in the individual environments as well as in combined environments. The strong positive associations between traits might be due to common and overlapping quantitative trait loci (Kumar et al., 2016) suggesting that the traits can be improved concurrently through direct selection. The genotype by yield by trait (GYT) analysis showed that strong significant association between the traits studied. This is because all the yield by trait combinations have grain yield as a component that is the special feature of genotype by yield by trait (GYT) (Yan and Frégeau-Reid, 2018).

The GGE biplots displayed for grain yield showed the main effect of the genotypes (PC1) and the genotype by environment interaction effects (PC2) explains 79% of the total variations. The which won-where of the GGE biplot indicates the six testing environments can be grouped into two mega environments (En1 and En4 grouped to mega-environment one and, En2, En3, En5 and En6 grouped to mega-environment two). En4 followed by En5 were identified as discriminative environments whereas, En6 followed by En2 were representative environments. Using the mean and stability view of the GGE biplot high yielding genotypes (LR106, LR25, LR19, LR103, LR75, LR74, and LR16) were distinguished. The GYT biplot generated for grain yield and yield related traits showed about 96.4% (PC1 = 93.4%; PC2 = 3.0%) of the total variations, whereas the GYT biplot generated for grain yield and nutritional quality traits explores about 87.5% (PC1 = 78.3%; PC2 = 9.2%) of the total variation explained among the traits. The higher percentage of the total variation explained by the first two principal components indicates that the suitability of the biplots for further interpretations. The GYT biplots was instrumental to rank genotypes based on yield trait combinations using ATC graph of the biplot and GYT superiority index, which is not applicable using the GT biplot. Accordingly, LR106 > LR25 > LR102 > LR12 > LR78 > LR103 > LR1 > LR74 > LR15 were best ranked genotypes based on their level to combine grain yield and yield related traits, whereas LR12>LR23 > LR25 > LR106 > LR1 > LR27 > LR78 > LR6 > LR81 were best ranked genotypes based on their level to combine grain yield and nutritional quality traits. Our finding agrees with the earlier findings by (Merrick et al., 2020; Peixoto et al., 2022; Yan and Frégeau-Reid, 2018).

Farmers in Tigray aquire sorghum seeds mainly through exchanging seeds of different varieties, bartering, as gifts, purchasing from local markets using cash, and seed loans. This indicates sorghum farmers in Tigray are over-reliant on the informal seed exchange system. Similar finding was also reported in barley seed sources (Abay et al., 2011) and sorghum seed sources (Rodier and Struik, 2018) in Tigray. This could be due to the social and cultural customs of sharing seeds and the long history of cultivations of farmer-preferred local sorghum varieties (Wendmu et al., 2022). Majority (79%) of the sorghum seed exchanges took place between farmers living in the same village which suggests the sorghum seed network in Tigray was fairly active and hyper-localized. Farmers having bridging role and/or nodal role in sorghum seed and information exchange were identified as important entry points for seed effective intervention strategies in Tigray. Our finding is in line with the reports by Subedi et al. (2003) and Pautasso et al. (2013) who pointed out that nodal farmers are important hotspots for effective seed provision and maintenance of crop genetic diversity in their environment; and have better experience and exposure to information. On the contrary, Rodier and Struik (2018) concluded that seed distribution through nodal and/or brignig farmers could limit the introduction of new sorghum improved varietes, however they did not explain how these farmers are supposed to confine the transactions improved seeds.

The main reason for sorghum seed exchange in Tigray was embedded in the cultural norms in which the farmers strongly belief that seed belongs to the earth and thus should not be denied to any farmer and telling a lie about sorghum seed exchange is an act of disobedience to God. Social assets such as creating new and/or maintaining old friendships; the desire to help each other and increase production at the household and community also reportedly inspired many farmers to exchange sorghum seeds. This finding is similar with the reports by Rodier and Struik (2018). The farmers' awareness that seed exchange is important to boost sorghum production at the community level is a form of altruism, described as "the spirit of sharing (Kiptot and Franzel, 2014). On the contrary, respondents noted that in the process of seed exchange, they were often disadvantaged, because the seeds they in return got were of inferior quality to their seeds in terms of market value.

1.10. Conclusions and Recommendations

1.10.1. Conclusion

Thoughtful investigations of the extent and patterns of genetic diversity and trait association, heritability followed by identifications of high yielding and stable genotypes from the entire germplasm could contribute significantly in achieving efficient breeding and conservation programs. We evaluate a total of one hundred and ten sorghum genotypes in three locations of Tigray in 2018 and 2019 main growing seasons. The results of this study showed that high genetic diversities of qualitative traits and quantitative traits (agro-morphological and nutritional quality traits) of sorghum genotypes in Tigray that is essential for efficient breeding and conservation programs. The very high diversity across the districts, geographical zones, and altitude classes indicate the area could have specific sites to be considered as micro-centers and on-farm conservation. The high genetic diversity could be partly attributed to the countries tremendous variations in agro-ecologies and being center of origin and diversity for sorghum and smallholder farmers maintain large diversity of sorghum seeds for several purposes.

Most of the quantitative traits studied were also highly heritable ($H^2 > 0.6$) which assured the possibility of effective selection among the genotypes. The significant positive association between farmer-preferred traits suggests that the traits can be improved concurrently through direct selection whereas, the strong negative and unfavorable association between traits implies the need for growing and selection among large segregating populations to break the unfavorable association. The genotypes were also significantly ($p < 0.001$) affected by the genotype variance, environment variance and their interactions (GGE). The GGE biplots enable to identify high yielding and stable genotypes and discriminative and representativeness of the testing environments were also distinguished. Furthermore, various promising sorghum genotypes were identified for breeding programs based on (ATC) view of GYT biplot and overall superiority index (Mean SI) of the GYT analysis.

Our study shows that farmers in Tigray predominantly access sorghum seeds through informal seed systems to fulfill their seed requirements. Bartering and own saved seeds are the main seed sources for farmers. This study underscores the significance of social network analysis in describing the complexity of farmers' seed systems on-farm. Some farmers play a major role as nodal, bridging farmers, or a combination of activities within their seed network. Social, cultural, natural, human, and physical assets of the community are the most important driving assets for farmers to share seeds.

1.10.2. Recommendations

- The high performing genotypes for a specific trait/s of interest could be exploited as sources of breeding parents or direct use in sorghum improvement programs.
- The application of marker-assisted selection would be helpful for the selective introgression of targeted genes and genomic regions into the parental lines with high-yielding backgrounds to facilitate breeding activities.
- Further investigations of the genetic diversity of sorghum genotypes using combinations of morphological and molecular markers would be helpful for better understanding the magnitude and patterns of diversity along with its worth for breeding and conservation strategies.
- Careful attention is needed to different seed intervention strategies in Tigray including promotion of farmer-preferred sorghum varieties through quality declared seed systems and integrating the local seed systems with the formal seed systems.
- Efforts such as training farmers on seed selection, promoting nodal and bridging farmers to share their seed management and seed sharing experience, and awareness creation on the significance of seed exchange to farmers and extension workers could have a significant positive impact to smooth the informal seed system of sorghum in Tigray.

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CHAPTER TWO

Phenotypic Diversity in Sorghum [*Sorghum bicolor* (L.) Moench] **Farmers' Varieties for Qualitative Traits in Tigray, northern Ethiopia**

Abstract

In the present study, frequency distribution, Shannon–Weaver diversity index (H′), and multivariate methods were used to estimate the phenotypic diversity in 110 sorghum genotypes growing in Tigray taking their districts of origin, geographical zones, and altitude classes into considerations for qualitative. Results showed that high and comparable trait distributions among the sorghum genotypes. The H′ computed for individual traits varied from 0.33 for grain form to 0.99 for grain plumpness with a mean of 0.83, which reveals huge diversity within the Farmers' varieties. The estimated H′ of each trait pooled over districts of origin, zones, and altitude classes was high with an overall mean of 0.71, 0.74, and 0.70, respectively. Based on district of origin, the highest (0.84) and the lowest (0.46) H′ values were recorded for the Tahtay adyabo and Raya azebo districts, respectively. When the zones were considered, the highest (0.80±0.06) and the lowest (0.46) H′ values were recorded for the northwestern zone and southern zone, respectively. With respect to altitude classes, the highest (0.80) and the lowest (0.68) H′ value were recorded for 1001 m.a.s.l, and >1600 m.a.s.l, respectively. Disruptive selection is the most likely reason to maintain the huge diversity in the sorghum Farmers' varieties. The treasure of diversity suggests the potential for exploitation in sorghum improvement and conservation programs. The ANOVA showed that the mean squares due to H′ values within the districts, geographical zones, and altitude classes were significalntly variable for most of the traits studied. The difference in discriminating the Farmers' varieties within districts of origin, zones, and altitude classes demonstrate the phenotypic traits have different importance and contribution levels to the total variance explained.

Keywords: qualitative traits, diversity index, phenotypic frequency, principal components, Sorghum Farmers' varieties

2.1. Introduction

Sorghum [Sorghum bicolor (L) Moench; 2n = 2x = 20] belongs to the Poaceae family and Andropogoneae tribe (Harlan and de Wet, 1972). It is the fifth most important cereal crop worldwide after maize, rice, wheat, and barley (FAOSTAT, 2021). The crop is a C4 photosynthetic crop serving as a major food security crop in sub-Saharan Africa, supporting over 500 million people (Amelework et al., 2016). Sorghum is cultivated in a wide spectrum of geographic conditions starting from 400 to 3000 meters above sea levels and from semi-arid to humid regions (Girma et al., 2020). Its inherent ability to give reasonable yield in relatively low soil fertility and moisture stressed areas where other crops could survive least makes sorghum an excellent crop for smallholder farmers prevailing in the arid and semi-arid tropics of the world (Girma et al., 2020; Nida et al., 2019).

Ethiopia is one of the world's most important centers of origin and diversity of various crops, including sorghum (Vavilov, 1951). Owing to its center of origin and diversity (Doggett, 1991) coupled with the diverse agro-ecologies, the country is endowed with the high treasure of sorghum Farmers' varieties (Ayana and Bekele, 1998; Geleta and Labuschagne, 2005). As cited in other kinds of literature (Grenier et al., 2004; Hummer and Hancock, 2015), centers of origin are an important hotspot for generating new genetic variability essential for crop improvement and utilization programs. Likewise, the Ethiopian sorghum gene pool has been contributing to global agriculture either for direct cultivation or as a source of important traits for various breeding objectives such as drought tolerance (Adugna, 2014), resistant to mold disease (Nida et al., 2019) and high lysine content (Singh and Axtell, 1973)

Ethiopia is the 4rd sorghum-producing country worldwide after the USA and Nigeria and Mexico (Statista, 2023). However, the productivity (2.8 tons/ha) is very low as compared to its yield potential and other countries such as Egypt (5.4 tons/ha), China (4.8 tons /ha), the USA (4.6 tons/ha), and Argentina (4.4 tons/ha) (USDA, 2020). The reduced yield per hectare may partly result due to the effects of Striga weeds, poor soil fertility, diseases, and use of low-yielding local cultivars (Amelework et al., 2016) and low level of sorghum research investment (Mekbib, 2008).

Studying the overall patterns of genetic diversity along with the distribution of the genetic variability is useful for selecting appropriate parents for further use in breeding programs and designing effective conservation strategies. Morphological, biochemical, and molecular markers can be usedto study the genetic diversity of any crop. Molecular markers are considered more efficient to quantify genetic diversity than morphological and biochemical markers (Gerrano et al., 2014). However, qualitative traits are still relevant to exploring genetic diversity in several crops such as sorghum (Abdi, 2002; Ayana, and Bekele 1998; Geleta and Labuschagne, 2005), wheat (Eticha et al., 2005; Mengistu et al., 2015) and Finger millet (Tsehaye et al., 2006), because the traits are highly heritable, and can be applied without the need for sophisticated laboratory materials like the molecular markers (Eticha et al., 2005; Tsehaye et al., 2006).

In Ethiopia, high morphological diversities have been reported for sorghum (Abdi et al., 2002; Ayana and Bekele, 1998; Geleta and Labuschagne, 2005; Girma et al., 2020; Tesfaye, 2017), although the diversity is not exploited to its potential in breeding programs. Moreover, most of the studies conducted are based on accessions from ex-situ which might not retain co-evolution of biotic and abiotic stresses along with losing indigenous knowledge. The importance of in-situ conservation strategy along with farmers' knowledge and practice and its complementarity with ex-situ conservation is being recognized (Alvarez et al., 2005; Labeyrie et al., 2014; Seboka and van Hintum, 2006). Besides, there is limited information on the diversity of sorghum Farmers' varieties in Ethiopia, particularly in Tigray, northern Ethiopia. Therefore, this study aimed to evaluate the extent and patterns of phenotypic diversity of sorghum Farmers' varieties collected from Tigray taking their districts of origin, administrative zones, and altitude classes into considerations.

2.2. Material and Methods

2.2.1. Description of the study area and plant materials

Tigray Regional State of Ethiopia is located in the northern part of the country between $12^0$15'N-$14^0$15'N latitude and $36^0$28'E-$39^0$59'E longitude. About 53% of Tigray is lowlands, 39% medium and the rest eight percent is classified as highlands, and the altitude ranged from 500 meters above sea level in the northeast to almost 4000 in the southwest (Atakilte et al., 2001). Agriculture is the backbone of the economy of the region in which 65% of the land is under cultivation and more than 95% of the farmers are smallholder farmers. Cereal crops provide the major means of livelihood for the people. Of which, sorghum is the first crop in terms of area coverage (239,044 hectares) and production (7.2 million quintals) (CSA, 2019).

A total of 108 sorghum farmers' varieties (as named by farmers) were collected from eight main sorghum growing districts of Tigray during the 2017 growing season directly from the standing crop of farmers' fields (Figure 1.2). The farmers' varieties were collected from Raya Azebo (10 farmers' varieties), Mereb Leke (18 Farmers' varieties), Asgede Tsimbla (14 farmers' varieties), Tselemti (10 farmers' varieties), Tahtay Adyabo (25 farmers' varieties), Tsegede (6 farmers' varieties), Welkait (10 farmers' varieties), and Kafta Humera (15 farmers' varieties) (Figure 1.2). The districts are representative of four geographical zones of Tigray which are Raya Azebo (southern zone), Mereb Leke (central zone), Asgede Tsimbla, Tahtay Adyabo, and Tselemti (northwestern zone), and Kafta Humera, Tsegede, and Welkait (western zone). For statistical purpose the two improved varities were grouped with the collections from Tsegede district.

Sorghum farmers' varieties from each collection district were considered independent farmers' varieties. For identification and retrieval purposes, information about the local name of the Farmers' varieties, collection district, administrative zones, and altitude were recorded. In addition to this, collection numbers with the prefix LR were given for each of the farmers' varieties (LR). For instance, LR1 was designated as landrace collection number one. Further details of the sorghum farmers' varieties are provided in Appendix 1.

The farmers' varieties were planted in Tahtay Adyabo district situated at 14°24'N latitude, 37°45'E longitude, and an altitude of 1025 meters above sea level in the 2019 growing season. The experiment was arranged in alpha lattice design (Patterson and Williams, 1976) having two replications with rows of 5 meters per farmers' varieties. The distance between rows and plants was 0.75 meters and 0.25 meters, respectively. Planting was done manually making rows using a traditional hoe. UREA (100 kg/ha) and DAP (100 kg/ha) was applied as recommended for the area. Half of the UREA and full of the DAP were applied to the plots as a basal application in the planting rows during sowings. The remaining UREA was applied at the knee height stage.

2.2.2. Phenotypic evaluation

Data were recorded on 13 qualitative traits (Table 1.2) using standard descriptors for sorghum (IBPGR, 1993). Besides, Munsell color chart (Munsell,1990) and visual examination using a 10× magnifying lens were used. Ten plants from each landrace were sampled to score the qualitative traits (five plants from each replication), which resulted in a total of 1100 plants.

2.3. Statistical Analysis

Frequency percentages of each trait across districts, administrativel zones, and altitude classes were calculated using SPSS software packages v 20 (SPSS, Chicago, IL, USA). The chi-square values were also carried out to test the deviation of the observed frequency distributions of the traits from the expected values using the same software. Shannon-Weaver diversity index (H’) was computed using the phenotypic frequencies to assess the phenotypic diversity for each trait for all the Farmers’ varieties using PAST software v 3.22 (Hammer et al., 2001). This is defined as follows:

$$H' = -\sum_{i=1}^{K} Pi * ln\, Pi$$

Where ‘Pi’ is the proportion of i^{th} attribute state of the trait under consideration in the landrace and the signed sum indicates the summation over all the K attribute states of that trait. Each value of H’ was standardized by dividing it by its maximum value, to keep the values in the range of 0–1.

This was done as $H' = H/H_{max}$

The altitudes were arbitrarily classified into six classes as 1 (< 800), 2 (801-1000), 3 (1001–1200), 4 (1201-1400), 5 (1401-1600), and 6 (>1600) meters above sea level. An arbitrary classification of altitudes has been also used by Abdi et al. (2002). The Shannon-Weaver diversity indexes (H') was also arbitrary classified as very high (H' > 0.8), high (>0.6 H' ≤0.8), intermediate (>0.4 H' ≤

0.6), low (> 0.2 H' ≤ 0.4), and very low (H' ≤ 0.2). Mengistu et al. (2015) also used subjective classifications of diversity index for durum wheat Farmers' varieties. Analysis of variance of non-transformed H' was performed for all the characters across all districts of origin, administrative zones of origin, and altitude classes using a Genstat-18 statistical package. Moreover, principal components that explained at least 5% of the total variance and with an eigenvalue of at least 1 were retained.

2.4. Results

2.4.1. Phenotypic trait distributions

The percentage frequency distributions of the 13 qualitative traits are presented for districts of origin (Table 2.1), altitude classes (Table 2.2), and administrative zones (Table 2.3). Accordingly, 22.4% of the collected farmers' varieties had semi-compact elliptic followed by compact elliptic inflorescences (18%) and semi-loose erect primary branches (17%). A total absence of half broom corn and broom corn inflorescences were detected. Very lax inflorescences were found in Tahtay Adyabo and Tsegede; whereas compact oval inflorescences were found in geneotypes originated from Raya Azebo. And, slightly exerted (36%), exerted (30%) and well-exerted inflorescences (33%) with negligible (1%) peduncle re-curved inflorescences were identified concerning inflorescence exertions. Fifty-nine percent of the genotypes were observed to have awns at maturity and the rest 41% were detected to be awnless. Most of the farmers' varieties were exhibited low shattering (36%) followed by intermediate shattering (27%). Only 5% of the farmers' varieties had high shattering traits. With regard to thresh-ability, 91% of the Farmers' varieties are thresh-able; whereas the rest 9% are none thresh-able.

Concerning the size of grain covered by glumes at maturity, it was detected that 35%, 27%, and 21% of the grains were covered by 50%, 375%, and 25% glumes, respectively. Fully covered and glumes greater than grains were spotted in the rest 10% and, 8% of the genotypes, respectively. About 20%, 25%, and 20% of the glumes were white, yellow and, red groups, respectively.

The grain colors of the farmers' varieties were predominantly white (32%), yellow (26%), and red (26%). The frequency distributions of the glum hairiness of the farmers' varieties were found to be 42%, 37%, and 21% for hairy, middle hair and, hairless farmers' varieties, respectively. Regarding the grain forms, about 52% of the farmers' varieties were dimple; whereas 48% were plump seeds. Most of the farmers' varieties (44%) had intermediate endosperm texture followed by mostly starch endosperm texture which was 29%. White-colored endosperm texture was dominant (83%) than yellow-gray endosperm color (17%). Moreover, only 3% of the Farmers' varieties had twin (two) seeds.

Table 2.1. Phenotypic frequency percentages of 13 qualitative traits of sorghum farmers' varieties across districts of origin in Tigray

Districts of origin	Inflorescence compactness and shape													Grain covering					
	1	2	3	4	5	6	7	8	9	10	11	12	χ2	1	3	5	7	9	χ2
R/Azebo	0	0	0	8	8	22	10	12	0	34	2	4	62.6^{***}	14	66	20	0	0	48.6^{***}
M/Leke	0	6	3	12	15	13	9	27	15	0	0	0	51.1^{***}	17	41	17	17	9	51.8^{***}
A/Tsimbla	0	0	1	1	24	23	11	21	19	0	0	0	56.5^{***}	25	34	29	7	6	45.5^{***}
T/Adyabo	16	0	6	8	12	9	9	14	21	1	1	2	133^{***}	13	15	33	18	21	30.2^{***}
Tselemti	0	0	0	3	8	29	13	29	18	0	0	0	39.1^{***}	25	50	17	7	0	43.9^{***}
K/Humera	0	0	1	0	7	18	8	42	23	0	0	0	90.7^{***}	20	27	46	3	4	94.0^{***}
Welkait	0	0	10	10	4	15	35	16	10	0	0	0	41.5^{***}	21	45	29	5	0	32.3^{***}
Tsegede	24	0	0	0	0	3	5	18	50	0	0	0	25.8^{***}	43	23	10	0	25	35.5^{***}
Total	5	1	3	6	11	17	13	22	18	4	0	0		21	35	27	10	8	

Table 2.1 (continued)

Districts of origin	Shattering						Grain color							Grain form			Grain plumpness		
	1	3	5	7	9	χ2	1	2	3	4	5	6	χ2	1	2	χ2	3	7	χ2
R/Azebo	15	77	8	0	0	86.5^{***}	39	40	21	0	0	0	6.9^{*}	100	0	6.8^{*}	100	0	na
M/Leke	24	35	24	11	6	50.6^{***}	32	14	36	15	3	0	64.1^{***}	100	0	Na	10	90	115.2^{***}
A/Tsimbla	24	18	46	8	4	77.1^{***}	22	23	42	5	8	0	61.3^{***}	100	0	Na	61	39	7.1^{**}
T/Adyabo	19	20	23	24	14	8.9^{ns}	21	28	33	11	8	0	58.4^{***}	90	10	150^{***}	54	46	1.9^{ns}
Tselemti	5	44	40	12	0	51.2^{***}	36	31	20	7	5	0	41.8^{***}	90	10	73.6^{***}	38	62	41.8^{***}
K/Humera	27	53	18	2	0	80.9^{***}	53	22	13	10	2	0	119^{***}	80	20	54.0^{***}	33	67	16.0^{***}
Welkait	8	27	39	25	1	47.0^{***}	15	44	19	8	14	0	39.1^{***}	100	0	Na	86	14	51.8^{***}
Tsegede	33	23	20	5	20	36.2^{***}	40	15	0	25	10	10	72.6^{***}	100	0	Na	75	25	12.9^{***}
Total	19	36	27	12	5		32	26	26	9	6	0		97	3		52	48	

Table 2.1 (continued)

Districts of origin	Glum color								Endosperm color			Inflorescence exertion				
	1	2	3	4	5	6	7	χ2	1	2	χ2	1	2	3	4	χ2
R/Azebo	6	64	6	24	0	0	0	89.8***	90	10	64.0***	8	40	42	10	41.1***
M/Leke	12	21	14	27	6	11	9	10.53***	83	17	80.0***	28	37	36	0	2.53^{ns}
A/Tsimbla	15	18	11	44	4	6	1	123.5***	71	29	25.7***	3	64	34	0	77.4***
T/Adyabo	21	17	23	17	3	15	4	65.6***	75	25	63.5***	43	27	30	0	11.6**
Tselemti	25	12	25	19	13	3	4	39.2***	91	9	73.6***	18	49	33	0	15.2***
K/Humera	33	34	7	7	3	15	2	121.1***	93	7	112.0***	61	25	13	0	56.1***
Welkait	11	12	35	6	30	2	4	71.2***	84	16	46.0***	26	24	50	0	12.1**
Tsegede	6	64	6	24	0	0	0	37.8***	75	25	35.7***	55	40	5	0	5.6^{ns}
Total	20	25	16	20	7	8	4		83	17		30	36	33	1	

Table 2.1 (continued

Districts of origin	Threshability			Glum hairiness				Awns at maturity			Endosperm texture					
	1	2	χ2	1	2	3	χ2	0	1	χ2	1	3	5	7	9	χ2
R/Azebo	100	0	Na	10	44	46	24.5***	87	13	54.8***	0	0	42	58	0	2.6^{ns}
M/Leke	90	10	55.5**	41	37	22	10.5**	37	63	12.8***	1	15	41	36	8	107.6***
A/ Tsimbla	91	9	63.1**	36	63	1	78.3***	41	59	4.1*	1	4	49	42	4	152.1***
T/Adyabo	90	10	12.5***	72	18	10	171***	20	80	90.0***	12	20	50	18	0	84.3***
Tselemti	95	5	70.4***	20	62	18	40.2***	42	58	2.9^{ns}	1	9	57	24	9	110.3***
K/Humera	79	21	89.7***	51	32	17	25.1***	37	63	9.6***	0	41	49	9	0	40.3***
Welkait	93	7	33.3***	34	54	12	26.5***	33	67	11.5***	0	18	36	20	26	7.8**
Tsegede	100	0	35.7***	10	44	46	35.7***	50	50	12.9***	25	25	0	25	25	15.7**
Total	91	9		42	37	21		41	59		4	17	44	29	7	

***significant at P < 0.001; ** = Significant at P < 0.01, * = Significant at P < 0.05; ns = not significant, na = no valid chi-square tests.

Table 2.2. Phenotypic frequency percentages of 13 qualitative traits of sorghum farmers' varieties across altitude classes in Tigray

Altitude class (masl)	Inflorescence compactness													Grain covering					
	1	2	3	4	5	6	7	8	9	10	11	12	χ2	1	3	5	7	9	χ2
<800	8	0	0	0	1	8	17	33	33	0	0	0	66.1***	46	26	20	0	8	35.4***
8001-1000	5	0	6	6	14	7	11	24	24	0	1	3	113.6***	21	34	28	11	5	54.3***
1001-1200	7	0	4	5	13	20	15	17	18	1	0	0	138.2***	16	24	35	11	14	81.5***
1201-1400	0	0	0	0	0	40	8	33	20	0	0	0	23.8***	21	38	21	15	6	27.1***
1401-1600	0	11	6	13	14	12	12	16	16	0	0	0	5.2^{ns}	12	42	17	20	9	31.0***
>1600	0	0	0	11	16	13	10	24	5	18	1	2	81***	18	59	18	4	1	204***
Total	5	1	3	6	11	17	13	22	18	4	0	0		21	35	27	10	8	

Table 2.2 (continued)

Altitude class (masl)	Shattering						Grain color							Grain form			Grain plumpness		
	1	3	5	7	9	χ2	1	2	3	4	5	6	χ2	1	2	χ2	3	7	χ2
<800	19	55	18	2	7	104.5***	49	25	0	17	6	3	81.9***	83	17	53.3***	58	42	3.3^{ns}
8001-1000	11	20	44	19	6	82.2***	16	28	40	8	7	0	75.1***	100	0	Na	66	34	20.1***
1001-1200	23	30	24	16	7	61.2***	33	28	25	7	7	0	121***	91	9	271***	55	45	3.3^{ns}
1201-1400	14	24	50	11	1	68.5***	40	15	31	8	7	0	42.5***	90	10	65***	31	69	15.1***
1401-1600	33	33	10	16	8	28.1***	27	32	20	16	6	0	19**	100	0	Na	20	80	32.4***
>1600	19	55	18	2	7	248.5***	36	24	31	9	0	0	29.5***	100	0	Na	53	47	0.5^{ns}
Total	19	36	27	12	5		32	26	26	9	6	0		94	6		52	48	

Table 2.2. (continued)

Altitude class(masl)	Glum color								Endosperm color			Inflorescence exertion				
	1	2	3	4	5	6	7	χ2	1	2	χ2	1	2	3	4	χ2
<800	36	42	0	8	4	8	3	108.2^{***}	83	17	53.1^{***}	37	30	33	0	0.8^{ns}
8001-1000	12	13	31	29	13	1	2	108.2^{***}	75	25	46.5^{***}	26	44	30	0	9.5^{**}
1001-1200	25	22	15	16	5	12	3	116.1^{***}	81	19	154^{***}	39	32	29	0	5.1^{ns}
1201-1400	26	6	34	10	5	20	0	41.2^{***}	99	1	97^{***}	20	31	50	0	13.2^{**}
1401-1600	10	18	18	23	18	2	11	18.4^{**}	89	11	54.4^{***}	16	58	27	0	25.9^{***}
>1600	11	43	3	33	2	5	4	221^{***}	84	16	88^{***}	23	33	39	5	49.1^{***}
Total	20	25	16	20	7	8	4		83	17		30	36	33	1	

Table 2.2 (continued)

Altitude class(masl)	Threshability			Glum hairiness				Awns at Maturity			Endosperm texture					
	1	2	χ2	1	2	3	χ2	0	1	χ2	1	2	3	4	5	χ2
<800	91	9	53.3^{***}	17	20	63	48.8^{***}	65	35	10.8^{**}	8	43	3	28	17	62.2^{***}
8001-1000	89	11	46.5^{***}	44	44	12	40.5^{***}	34	66	20.2^{***}	6	12	43	23	17	78.5^{***}
1001-1200	90	10	104.5^{***}	59	34	6	171.7^{***}	27	73	85.5^{***}	5	18	56	21	0	235^{***}
1201-1400	90	10	65^{***}	40	41	20	8.3^{*}	38	62	6.1^{*}	0	30	29	32	10	12.5^{**}
1401-1600	87	13	17.8^{***}	47	33	20	9.6^{**}	30	70	14.4^{***}	2	7	62	24	4	144.2^{***}
>1600	92	8	134.7^{***}	15	49	36	34.9^{***}	67	33	22.9^{***}	0	1	42	53	5	154^{***}
Total	91	9		42	37	21		41	59		4	17	44	29	7	

*** = significant at P < 0.001; ** = significant at P < 0.01; * = Significant at P < 0.05; ^{ns} = not significant; na = no valid chi-square tests

Table 2.3. Percentage frequency of 13 qualitative traits of sorghum farmers' varieties across the administrative zone of origins in Tigray

Zone	Inflorescence compactness and shape													Grain covering					
	1	2	3	4	5	6	7	8	9	10	11	12	χ2	1	3	5	7	9	χ2
Southern	0	0	0	8	8	22	10	12	0	34	2	4	62.6***	14	66	20	0	0	48.6***
Central	0	6	3	12	15	13	9	27	15	0	0	0	51.1***	17	41	17	17	9	51.8***
N.western	8	3	5	15	18	10	20	19	1	0	1	0	307.5***	18	28	29	13	12	63***
Western	3	4	3	5	15	19	27	25	3	4	0	0	194***	29	32	31	3	5	142.9***
Total	5	1	3	6	11	17	13	22	18	4	0	0		21	35	27	10	8	

Table 2.3. (continued)

Zone	Shattering						Grain color							Grain form			Grain plumpness		
	1	3	5	7	9	χ2	1	2	3	4	5	6	χ2	1	2	χ2	3	7	χ2
Southern	15	77	8	0	0	86.5***	39	40	21	0	0	0	6.9*	100	0	6.8*	100	0	na
Central	24	35	24	11	6	50.6***	32	14	36	15	3	0	64.1***	100	0	Na	10	90	115***
N.western	18	25	32	17	8	78.9***	25	28	33	8	6	25	144.8***	92	8	350***	54	46	3^{ns}
Western	19	42	27	9	3	155.5***	42	26	12	11	8	1	221***	91	9	221***	56	44	5.4*
Total	19	36	27	12	5		32	26	26	9	6	0		94	6		52	48	

Table 2.3. (continued)

Zone	Glum color								Endosperm color			Inflorescence exertion				
	1	2	3	4	5	6	7	χ2	1	2	χ2	1	2	3	4	χ2
Southern	6	64	6	24	0	0	0	89.8***	90	10	64***	8	40	42	10	41.1***
Central	12	21	14	27	6	11	9	10.5**	83	17	80***	28	37	36	0	2.53^{ns}
N.western	19	16	20	26	6	10	3	141.3***	77	23	144.4***	27	41	32	0	14.9***
Western	31	27	15	8	11	7	2	156.8***	89	11	201.8***	42	27	31	42	13**
Total	20	25	16	20	7	8	4		83	17		30	36	33	1	

Table 2.3. (continued)

Zone	Thresh ability			Glum hairiness				Awns at Maturity			Endosperm texture					
	1	2	χ2	1	2	3	χ2	0	1	χ2	1	3	5	7	9	χ2
Southern	100	0	Na	10	44	46	24.5^{***}	87	13	54.8^{***}	0	0	42	58	0	2.6^{ns}
Central	90	10	55.5^{**}	41	37	22	10.5^{**}	37	63	12.8^{***}	1	15	41	36	8	107.6^{***}
N. western	74	27	108^{***}	51	41	7	156.4^{***}	29	71	83.3^{***}	7	14	52	25	3	380.5^{***}
Western	85	15	163.1^{***}	36	31	33	1.6^{ns}	45	55	3.1^{ns}	3	27	33	22	14	92.6^{***}
Total	91	9		42	37	21		41	59		4	17	44	29	7	

*** = significant at $P < 0.001$; ** = significant at $P < 0.01$; * = Significant at $P < 0.05$; ^{ns} = not significant, na = no valid chi-square tests

2.4.2. Estimation of diversity (H′)

The diversity index (H′) for the districts, zone and altitude classes are presented in Tables 2.4-2.6. The H′ pooled over traits within districts of origin varied from 0.84 ± 0.04 for farmers' varieties collected from Tahtay Adyabo to 0.46 ±0.08 for farmers' varieties collected from Raya Azebo with overall mean H′= 0.71±0.06 (Table 2.5). The within-district H′ depends on the indices of the measured traits. When the H′ of each trait was considered, farmers' varieties collected from Tahtay Adyabo showed very high diversity for most of the characters with the highest H′= 0.99 value for shattering and grain plumpness. On the other hand, grain form showed monomorphic in all the districts of origin (H′= 0.0) except in Kafta Humera, Tahtay Adyabo, and Tselemti). Besides, thresh-ability and grain plumpness were monomorphic (H′= 0.0) for the farmers' varieties collected from Raya Azebo (Table 2.4). The H′of each trait pooled over districts of origin varied from 0.21 ±0.11 grain forms to 0.87 ±0.06 awns at maturity with an overall mean of H′= 0.71±0.05.

The diversity index pooled over traits within altitude classes varied from 0.68 ±0.07 for farmers' varieties collected from altitude >1600 meters above sea levels to 0.80 ±0.04 for farmers' varieties collected from an altitude of 1001-1200 meters above sea levels with an overall mean H′= 0.74 ± 0.06 (Table 2.5). The H′of each trait showed that grain form had lower diversity (H′= 0.26) whereas grain plumpness had the highest diversity (H′= 0.99). The H′of each trait pooled over altitude classes varied from 0.26 for gran form to 0.91 for awns at maturity with an overall mean of 0.74±0.05. Diversity index pooled over traits within geographical zones showed that the farmers' varieties collected in the southern zone had intermediate variations (>0.4 H′ ≤6); whereas very high diversities (H′ >0.8) were scored from the farmers' varieties collected in the northwestern zone with an overall mean H′= 0.69±0.06 (Table 2.6). Farmers' varieties collected from the central and western zones showed high diversities (>0.6 H′ <0.8). When the diversity index of individual trait considered, the lowest mean diversities were obtained for grain form (H′= 0.23±0.13) with monomorphic (H′= 0.0) in southern and central zones; whereas the highest diversity was detected in the glum hairiness (H′= 0.91±0.04). Moreover, thresh-ability and grain plumpness were monomorphic in the farmers' varieties collected from the southern zone (Table 2.6). The diversity index of each trait pooled over geographical zones was varied from 0.13±0.13 for grain form to 0.91±0.04 for glum hairiness with an overall mean of 0.70±0.08.

Table 2.4. Shannon–Weaver diversity index (H’) for 13 qualitative traits of sorghum farmers’ varieties across districts of collections in Tigray

Districts	ICS	GRC	AM	TR	SH	GC	GF	ET	EC	GLC	IE	GP	GLH	Mean ± SE
R/Azebo	0.72	0.54	0.56	0.00	0.43	0.66	0.00	0.42	0.47	0.50	0.84	0.00	0.86	0.46±0.08
M/Leke	0.78	0.92	0.95	0.76	0.90	0.88	0.00	0.79	0.65	0.95	0.79	0.47	0.97	0.75±0.07
A/Tsimbla	0.68	0.88	0.98	0.64	0.83	0.86	0.00	0.63	0.86	0.80	0.55	0.96	0.66	0.72±0.07
T/Adyabo	0.86	0.96	0.72	0.96	0.99	0.92	0.51	0.77	0.81	0.92	0.78	0.99	0.70	0.84±0.04
Tselemti	0.65	0.74	0.98	0.47	0.70	0.87	0.44	0.71	0.44	0.90	0.74	0.96	0.85	0.73±0.05
K/Humera	0.59	0.79	0.95	0.51	0.67	0.77	0.72	0.58	0.35	0.80	0.66	0.92	0.92	0.71±0.05
Welkait	0.71	0.74	0.91	0.74	0.82	0.89	0.00	0.84	0.63	0.82	0.75	0.58	0.85	0.71±0.07
Tsegede	0.50	0.79	0.97	0.81	0.93	0.91	0.00	0.86	0.81	0.49	0.61	0.81	0.97	0.73±0.08
Mean ± (SE)	0.69 (0.04)	0.80 (0.05)	0.87 (0.06)	0.61 (0.10)	0.78 (0.06)	0.85(0.03)	0.21 (0.11)	0.70 (0.05)	0.63 (0.07)	0.77 (0.06)	0.72 (0.04)	0.71 (0.01)	0.85 (0.04)	

AM = awns at maturity, EC = endosperm color, ET = endosperm texture, GC = grain color, GF = grain form, GLC = Glum color, GP = grain plumpness, GRC = grain covering, ICS = Inflorescence compactness and shape, IE = inflorescence exertions, SH = shattering; TR = thresh-ability

Table 2.5. Shannon- Weaver diversity (H′) for 13 qualitative traits of sorghum farmers’ varieties across altitude classes in Tigray

Altitudes	ICS	GRC	AM	TR	SH	GC	GF	ET	EC	GLC	IE	GP	GLH	Mean± SE
<800	0.60	0.77	0.93	0.65	0.74	0.71	0.65	0.83	0.65	0.65	0.79	0.98	0.83	0.75 ±0.03
8001-1000	0.81	0.90	0.92	0.82	0.88	0.79	0.00	0.88	0.82	0.78	0.77	0.92	0.88	0.78 ±0.07
1001-1200	0.80	0.94	0.84	0.81	0.95	0.80	0.45	0.69	0.71	0.86	0.79	0.99	0.78	0.80 ±0.04
1201-1400	0.50	0.91	0.96	0.47	0.78	0.78	0.47	0.82	0.08	0.76	0.74	0.89	0.96	0.70 ±0.07
1401-1600	0.82	0.91	0.88	0.85	0.90	0.83	0.00	0.65	0.50	0.88	0.69	0.72	0.95	0.74 ±0.07
>1600	0.79	0.68	0.91	0.40	0.63	0.72	0.00	0.55	0.63	0.68	0.88	0.99	0.91	0.68 ±0.07
Mean ± (SE)	0.72 (0.06	0.85 (0.04)	0.91 (0.02)	0.66 (0.08)	0.81 (0.05)	0.77 (0.02)	0.26 (0.12)	0.74 (0.05)	0.56 (0.11)	0.77 (0.04)	0.78 (0.03)	0.92 (0.04)	0.88 (0.03)	

AM = awns at maturity, EC = endosperm color, ET = endosperm texture, GC = grain color, GF = grain form, GLC = Glum color, GP = grain plumpness, GRC = grain covering, ICS = Inflorescence compactness and shape, IE = inflorescence exertions, SH = shattering; TR = thresh-ability

Table 2.6. Shannon- Weaver diversity (H′) for 13 qualitative traits of sorghum farmers' varieties across adminstrative zones in Tigray

Zones	ICS	GRC	AM	TR	SH	GC	GF	ET	EC	GLC	IE	GP	GLH	Mean ± SE
Southern	0.72	0.54	0.56	0.00	0.43	0.66	0.00	0.42	0.47	0.50	0.84	0.00	0.86	0.46±*0.08*
Central	0.78	0.92	0.95	0.76	0.90	0.88	0.00	0.79	0.65	0.95	0.79	0.47	0.97	0.75±*0.07*
N.Western	0.82	0.96	0.87	0.83	0.95	0.83	0.4	0.79	0.78	0.92	0.78	0.99	0.82	0.83 ± *0.04*
Western	0.72	0.84	0.97	0.64	0.86	0.88	0.2	0.73	0.53	0.90	0.76	0.92	0.99	0.71 ± *0.04*
Mean ± (SE)	0.76 (0.02)	0.82 (0.10)	0.84 (0.09)	0.56 (0.19)	0.79 (0.12)	0.81 (0.06)	0.13 (0.13)	0.68 (0.10	0.61 (0.07)	0.82 (0.11)	0.79 (0.02)	0.6 (0.03)	0.91 (0.04)	

AM = awns at maturity, EC = endosperm color, ET = endosperm texture, GC = grain color, GF = grain form, GLC = Glum color, GP = grain plumpness, GRC = grain covering, ICS = Inflorescence compactness and shape, IE = inflorescence exertions, SH = shattering; TR = thresh-ability

The H' estimated for individual traits varied from 0.33 for grain form to 0.99 for grain plumpness with a mean of H′ = 0.83. All the traits showed very high diversity (H′ > 0.8) except for form and thresh-ability which were 0.33 and 0.72, respectively (Table 2.7). Partitioning of the phenotypic diversity into districts of origin, the geographical zone of origins, and altitude classes showed that about 85%, 92%, and 89% of the variations were explained within districts of origin, geographical zones of origin, and altitude classes, respectively (Table 2.7).

Table 2.7. Partitioning of the phenotypic diversity into within and between districts of origin, zones, and altitude classes of origin in Tigray

Traits	H'sp	H'w	Hw/H'sp	(H'sp-Hw)/H'Sp	H'z	H'/hsp	(H'sp-Hz)/H'sp	H'alt	H'alt/ H'sp	(H'sp-H'alt)/H'sp
ICS	0.82	0.69	0.84	0.16	0.72	0.88	0.12	0.72	0.88	0.12
GRC	0.92	0.8	0.87	0.13	0.84	0.92	0.08	0.85	0.93	0.07
AM	0.97	0.88	0.9	0.1	0.97	0.9	0.0	0.91	0.93	0.07
TR	0.72	0.61	0.85	0.15	0.64	0.89	0.11	0.66	0.92	0.08
SH	0.9	0.78	0.87	0.13	0.86	0.95	0.05	0.81	0.9	0.1
GC	0.92	0.85	0.92	0.08	0.88	0.96	0.04	0.77	0.84	0.16
GF	0.33	0.21	0.63	0.37	0.3	0.9	0.1	0.26	0.78	0.22
ET	0.83	0.7	0.85	0.15	0.73	0.88	0.12	0.74	0.89	0.11
EC	0.66	0.63	0.95	0.05	0.64	0.97	0.03	0.56	0.85	0.15
GLC	0.92	0.77	0.84	0.16	0.9	0.98	0.02	0.77	0.84	0.16
IE	0.82	0.72	0.88	0.12	0.76	0.93	0.07	0.78	0.95	0.05
GP	0.99	0.71	0.71	0.29	0.92	0.92	0.08	0.92	0.92	0.08
GLH	0.96	0.85	0.88	0.12	0.91	0.94	0.06	0.88	0.91	0.09
Mean	0.83	0.71	0.85	0.15	0.77	0.92	0.07	0.74	0.89	0.11

H'sp = diversity index for each trait computed from the entire data set, H'w, H'z, H'alt, = average diversity index of each character for the eight districts of origin, four zones and six altitude classes, respectively, H'w/H'sp = the proportion of diversity index within districts, H'z/H'sp = the proportion of diversity index within zones H'alt/H'sp = the proportion of diversity within altitude classes, (H'sp-H'w)/H'Sp, (H'sp-Hz)/H'sp and (H'sp-H'alt)/H'sp = the proportion of diversity between districts, between zones and altitude classes, respectively, in relation to the total variation. AM = awns at maturity, EC = endosperm color, ET = endosperm texture, GC = grain color, GF = grain form, GLC = Glum color, GP = grain plumpness, GRC = grain covering, ICS = Inflorescence compactness and shape, IE = inflorescence exertions, SH = shattering; TR = thresh-ability

The analysis of variance computed among traits within districts, geographical zones, and altitude classes is presented in Table 2.8. Within districts of origin, very strong significant variations ($p < 0.001$) were observed for traits such as grain covering, awns at maturity, grain color, endosperm type, glum color and grain form, and highly significant variations ($p < 0.01$) for traits such as grain plumpness and inflorescence compactness and shape. The rest of the traits showed no significant variations ($p > 0.05$).

When the mean squares of the traits within the geographical zones are considered, significant variations ($p < 0.05$) were detected for traits such as grain covering, awns at maturity, shattering, endosperm type, inflorescence exertions, and grain plumpness. Only glum color had highly significant differences ($p < 0.01$). The other traits had either non-significant variations or no valid statistical tests.

On the basis of the altitude classes, grain form showed a strongly significant difference ($p < 0.001$), grain covering and endosperm type showed highly significant difference ($p < 0.001$), inflorescence compactness and shape, shattering, endosperm color, inflorescence exertions, and grain plumpness had significant variations at $p < 0.05$.

Table 2.8. Mean squares from the ANOVA of H′ for individual traits of sorghum for districts of origin, administrative zones and, altitude classes in Tigray

	Mean squares		
Traits	Districts df =7)	Zones df =3)	Altitude df= 5)
ICS	0.036^{*}	0.005^{ns}	0.044^{*}
GRC	0.058^{***}	0.101^{*}	0.048^{**}
AM	0.084^{***}	0.103^{*}	0.002^{na}
TR	0.181^{ns}	0.213^{na}	0.049^{ns}
SH	0.103^{**}	0.168^{*}	0.056^{*}
GC	0.045^{***}	0.024^{ns}	0.002^{na}
GF	0.311^{***}	0.083^{ns}	0.217^{***}
ET	0.064^{*}	0.092^{*}	0.039^{**}
EC	0.085^{***}	0.046^{ns}	0.105^{*}
GLC	0.109^{***}	0.134^{**}	0.031^{*}
IE	0.022^{ns}	0.003^{*}	0.013^{ns}
GP	0.405^{**}	0.188^{*}	0.046^{*}
GLH	$0.022^{\ ns}$	0.007^{ns}	0.013^{ns}

df = degree of freedom, *** = significant at < P<0.001, ** = significant at P<0.01, * = significant at P<0.05; ns = not significant (P>0.05), AM = awns at maturity, EC = endosperm color, ET = endosperm texture, GC = grain color, GF = grain form, GLC = Glum color, GP = grain plumpness, GRC = grain covering, ICS = Inflorescence compactness and shape, IE = inflorescence exertions, SH = shattering; TR = thresh-ability

2.4.3. Principal component analysis (PCA)

The principal component analysis results to estimate the contributions of the characters for the total variations explained within districts of origin, geographical zones, and, altitude classes are presented in Table 2.9. Based on districts, traits such as inflorescence compactness and shape, grain covering, and awns at maturity were the most important traits contributing to principal component one (PC1) which explains about 47.7% of the total variance. Glume color and inflorescence exertion were the most important traits contributing to the second component (PC2) which has explained about 18.7% of the total variance. For the principal component three (PC3) which explained 15% of the total variance, grain plumpness was the most important contributing trait. Glum hairlines were found to be the most important contributing trait for the total variations explained by principal component four (PC4), which explains about 11.2% of the total variations.

The principal component analysis done to explore the variations among the geographical zones showed that only the first two principal components (PC1 and PC2) had an eigenvalue greater than one. Accordingly, traits such as grain covering, thresh-ability, shattering and, endosperm texture were the most contributing to the first principal component (PC1) which explains about 74.6% of the total variance. For the second principal component, which explains about 18.7%, glum hairiness was the most important contributing trait.

In the altitude classes, inflorescence compactness and shape and grain covering were the most important traits for the 44.6% variations explained by the PC1 whereas, endosperm color contributing trait for the PC2 which explains about 26% of the total variations. And, inflorescence exertion was the most important contributing trait for the 18.5% variations explained by the third principal component (PC3).

Table 2.9. Eigenvalues of the most important principal components (PCs) for variations districts of origin, adminsitraive zones of origin, and altitude classes in Tigray

	Eigenvectors								
	Districts of origin				Zones of origin		Altitude classes		
Traits	PC1	PC2	PC3	PC4	PC1	PC2	PC1	PC 2	PC 3
IC	0.96	0.07	-0.21	0.09	0.65	0.67	1.0	0.0	-0.1
GRC	0.96	0.08	-0.11	0.13	0.99	0.07	1.0	-0.2	-0.1
AM	0.95	0.00	-0.13	0.15	0.93	-0.38	0.9	0.1	0.3
TR	0.90	0.25	0.11	-0.03	0.99	0.03	0.9	0.3	0.3
SH	0.82	-0.12	-0.27	0.42	0.99	-0.01	0.9	-0.3	0.3
GC	0.76	-0.18	0.53	-0.26	0.93	-0.37	-0.7	0.6	-0.1
GF	0.66	0.09	-0.61	-0.41	0.62	0.54	-0.6	0.5	0.5
ET	0.63	-0.58	0.25	0.16	0.99	-0.05	0.1	0.9	0.1
EC	0.54	0.52	0.48	0.23	0.77	0.60	0.5	0.8	-0.4
GLC	0.08	0.99	-0.08	0.03	0.98	-0.15	-0.6	-0.7	0.0
IE	-0.46	0.68	-0.09	0.54	-0.90	0.29	-0.3	-0.3	0.8
GP	0.09	0.13	0.91	0.04	0.89	0.08	0.0	-0.7	-0.7
GLH	-0.23	-0.49	-0.09	0.80	0.25	-0.96	0.1	-0.4	0.7
Eigenvalue	6.2	2.4	1.9	1.5	9.7	2.4	5.8	3.4	2.4
Variance %	47.7	18.7	15.0	11.2	74.6	18.7	44.6	26.0	18.5
Cumulative%	47.7	66.4	81.4	92.6	74.6	93.3	44.6	70.6	89.1

AM = awns at maturity, EC = endosperm color, ET = endosperm texture, GC = grain color, GF = grain form, GLC = Glum color, GP = grain plumpness, GRC = grain covering, ICS = Inflorescence compactness and shape, IE = inflorescence exertions, SH = shattering; TR = thresh-ability

2.5. Discussions

2.5.1. Qualitative traits as markers to study genetic diversities

Thorough investigations of the extent of genetic diversity of any crop are considered groundbreaking to design effective breeding programs and conservation strategies. This can be estimated by morphological, biochemical, and molecular markers. The last one is considered more efficient to quantify genetic diversity than the morphological and biochemical markers (Gerrano et al., 2014). However, highly heritable morphological traits can be applied to study the diversity of crop germplasms without the need for sophisticated laboratory materials like molecular markers (Eticha et al., 2005).

In the present study, 13 qualitative traits of sorghum were used to investigate the extent and patterns of genetic diversity in Tigray northern Ethiopia. Large phenotypic diversity among the sorghum farmers' varieties in all the classifying variables (farmers' varieties, districts and admistrative zones, and altitude classes) were discovered. Our finding confirmed the different degrees of variability in Ethiopian sorghum gene pools reported so far (Abdi et al., 2002; Adugna and Bekele, 2013; Ayana and Bekele, 1998; Geleta and Labuschagne, 2005; Semere et al., 2023).

2.5.2. Qualitative traits distribution

Information regarding the phenotypic distribution of traits in certain districts, geographic zones, and/or altitude classes is useful to identify important traits for breeding objectives and choosing sites for in situ conservation that could be complementary to the ex-situ conservation programs. The present study showed that the frequency distributions of most of the traits were highly diverse across all the districts of origin, the geographical zone of origin, and altitude classes (Table 2.1-2.3). This implies that the farmers' varieties could be exploited for various breeding objectives and conservation strategies. The wide distribution of the inflorescence compactness and shape is an indication of the availability of different races of sorghum in the area. And, the higher proportion of the semi-compact elliptic and compact elliptic inflorescences implies that the race durra types are more dominant as compared to other races in the study area. Our finding agreed with the findings of Geleta and Labuschagne (2005) and Semere, et al. (2023). For traits such as grain form, single-seeded farmers' varieties were more predominant as compared to the twin seeded farmers' varieties. The twin seed farmers' varieties were detected in the farmers' varieties collected in Tahtay Adyabo, Tselemti, and Kafta Humera districts. A few numbers of sorghum accessions having twin seeds have been also reported by Ayana and Bekele, (1998) and Semere et al. (2023). For the endosperm-related traits, it was found that intermediate and mostly starchy endosperm textures were predominant, which has a direct advantage for milling quality. Similar results were also reported by Abdi et al. (2002) and Geleta and Labuschagne (2005). White-colored endosperm was dominant (83%) than yellow-gray endosperm color. On the other hand, we discovered a wide and fairly distribution for the other trait suggested that the possibility of selection of different traits of the sorghum farmers' varieties.

2.5.3. Estimates and analysis of phenotypic diversities

This study revealed that high phenotypic diversity of sorghum farmers' varieties is available within and between districts, geographical zones, and altitude classes. Estimated diversity (H′) for individual traits varied from 0.33 for grain forms to 0.99 grain plumpness with an average of H′= 0.83. Similar findings were reported erlier by Semere et al. (2023). The larger value of the mean of H′ suggested vast genetic diversity among the sorghum farmers' varieties which, in turn, strengthens Ethiopia is not only the center of origin but also the center of diversity for sorghum (Doggett, 1991). It also indicates that the Tigray region has specific sites to be considered as micro-centers and on-farm conservation. Besides, the mean diversity index H′ of each trait pooled over districts of origin, zones, and altitude classes were higher, which is an indication that the differences between districts, geographical zones, and altitude classes contributed strongly to the diversity of sorghum farmers' varieties. This might be partly due to the influences of diverse agro-ecologies and climatic conditions, and farmers' seed management to cope with the oscillations in rainfall patterns, suggesting that disruptive selection is the most likely reason to maintain the huge sorghum diversity in Tigray. This is in agreement with the findings of Teshome et al. (1997) who reported a wide array of diversity among 117 sorghum accessions from the north Shewa and south Welo areas of Ethiopia based on 14 morphological traits, and Grenier et al. (2004) cited high H′ of morphological traits within the region and geographical origins in their study on 2,017 Sudanese sorghum farmers' varieties. Abdi et al. (2002) discussed the importance of ecological heterogeneity and climatic variations for contributing extensive diversities of sorghum farmers' varieties. Adugna and Bekele, (2013) identified higher diversity in sorghum populations evaluated based on five geographic regions and eight agro-ecologies of Ethiopia and, they reported the sorghum populations collected from Tigray showed higher diversity (H′= 0.86) than others.

Furthermore, the partitioning of the phenotypic traits confirmed that the phenotypic diversities were more predominant within the classifying variables than beyond, which indicates the importance of local genetic diversity. Similar results were also found by Ayana and Bekele (1998) in their study on 415 sorghum accessions from Ethiopia and Eritrea. The significant difference in the traits between districts of origin, geographical zones, and altitude classes further validate the high treasure of sorghum diversities in Tigray northern Ethiopia.

2.5.4. Principal component analysis (PCA)

Studying the magnitude of genetic variability is important to exploit crop germplasm for trait improvement. PCA enable researchers to ascertain the pattern of diversity along with the contribution of each trait to the total variability (Tesfaye, 2017). Thus, plant breeders can apply PCA to evaluate the patterns of diversity of any crop under investigation. In the present study, it was possible to observe the districts of origin, geographical zones, and altitude classes were important in discriminating the morphological traits of sorghum farmers' varieties. The first principal components explained 47.7%, 74.6%, and 44.6% of the total variations for the traits within districts of origin, geographical zones, and altitude classes, respectively. The difference in discriminating the farmers' varieties within districts of origin, zones, and altitude classes demonstrate the phenotypic traits have different importance and contribution levels to the total variance explained. Akatwijuka et al. (2016), Ayana and Bekele (1998) and Hamidou et al.(2018) also discussed the importance of PCA to distinguish traits that contribute more to the total variations explained in sorghum germplasms.

2.6. Conclusions

Information on the extent and patterns of diversity is valuable in any crop improvement and conservation programs. In the present study, a high level of polymorphism was detected among sorghum farmers' varieties, districts of origin, geographical zone of origin, and altitude classes of Tigray, suggesting that disruptive selection is the most likely factor to maintain the diversity in sorghum farmers' varieties. The vast diversity of sorghum indicates that the potential for exploitation in sorghum breeding. From the conservation point of view, the very high diversity across the districts, geographical zones, and altitude classes indicates the area could have specific sites to be considered as micro-centers and on-farm conservation. Further investigations of the genetic diversity of sorghum farmers' varieties using combinations of morphological and molecular markers would be helpful for better understanding the magnitude and patterns of diversity along with its worth for breeding and conservation strategies.

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CHAPTER THREE

Genetic Variability, Genotype by Environment Interaction and Trait Associations for Agro-Morphological Traits of Farmers' Varieties of Sorghum [*Sorghum bicolor* (L.) Moench] in Tigray, Northern Ethiopia

Abstract

One hundred and ten sorghum genotypes were planted at three locations in Tigray in 2018 and 2019 main growing seasons to evaluate the genetic diversity and genotype by environment interaction and to select stable and high yielding genotypes using GGE biplots. Results showed that wide range and highly significant ($p < 0.001$) genotype mean performance in each environment as well as combined environments for all the grain yield and agro-morphological traits studied such as DF, DM, LL, LN, Lwd, PH, Pnwd, Pnht, Pnwt, Pnl, TGWT. Besides, highly significant variation ($p < 0.001$) among the tested genotypes for all the traits studied suggesting the presence of sufficient genetic diversity for selection. The strong significant positive association between some of the traits studied indicates that both the traits can be improved concurrently through direct selection. The which won-where biplot indicates the six testing environments can be grouped into two mega environments (En1 and En4 grouped to mega-environment one and, En2, En3, En5 and En6 grouped to mega-environment two). En4 followed by En5 were identified as discriminative environments whereas, En6 followed by En2 were representative environments. Using the mean and stability view of the biplot high yielding genotypes (LR106, LR25, LR19, LR103, LR75, LR74, and LR16) were distinguished. The GYT biplots was instrumental to rank genotypes based on their overall superiority of yield trait combinations using ATC graph of the biplot and GYT superiority index, which is not applicable using the GT biplot. Accordingly, LR106 > LR25 > LR102 > LR12 > LR78 > LR103 > LR1 > LR74 > LR15 were best ranked farmers' varieties. Hence, analysis of sorghum farmers' varieties based on multiple traits is crucial to develop superior varieties, and the details of this study are significant for thoughtful sorghum breeding programs.

Keywords: Broad-sense heritability, trait correlations, superior genotypes, GGE biplots, GYT biplot

3.1. Introduction

Sorghum (Sorghum bicolor [L.] Moench 2n=2x=20; family Poaceae), one of the five main cereal crops in terms of production and consumptions worldwide (FAOSTAT, 2021), is well known for its multiple use such as source of food, fodder and fuel, bioethanol, alcoholic beverages and building materials (Adugna and Bekele, 2013). It is well adapted to wide range of environmental condition and agro-ecological conditions ranging from the dry lowland areas of the semi-arid tropics to high rainfall and humid regions, as well as in the more temperate regions of the world (Girma et al., 2020). Its inherent ability to yield reasonably in relatively low soil fertility and moisture-stressed areas makes it an excellent crop for smallholder farmers, especially in the arid and semi-arid tropics (Mundia et al., 2019). USA, Nigeria, India, Ethiopia and Mexico are the leading sorghum producer countries worldwide (FAOSTAT, 2021). In Africa, sorghum is the fourth most widely cultivated cereal crop next maize, rice, and wheat and second in area coverage next to maize (FAOSTAT, 2021).

In Ethiopia, sorghum stands 4th crop in terms of production after maize, wheat and teff, and third in terms of area coverage next to teff and maize (CSA, 2022). In the 2021/22 growing season, Ethiopia produced 3.6 million metric tons from an area of 1.4 million hectares 2021/22). The yield of sorghum is low in Ethiopia as compared to its potential and other countries such as Egypt (5.4 t ha^{-1}), China (4.8 t ha^{-1}), the USA (4.6 t ha^{-1}) and Argentina (4.4 t ha^{-1}) (USDA, 2020). The lower yield may be partially attributed to the unavailability of farmer-preferred varieties for the diverse agro-ecologies of the country.

Broad genetic base is essential for effective utilization of germplasm for breeding and conservation programs. Farmers' varieties that are evolved in Vavilov centers of origin and diversity of crop plants often maintain wide genetic variability of crop germplasm (Hummer and Hancock, 2015). Ethiopia is center of origin and diversity of various crop including sorghum (De Wet and Harlan, 1971). Various research findings indicated high genetic diversity in Ethiopian sorghum germplasm that could be novel sources of various important traits (Adugna, 2014; Ayana and Bekele, 1998; Girma et al., 2020). There is still unexploited genetic diversity harbored in local farmers' varieties of sorghum in Ethiopia (Cuevas et al., 2017; Enyew et al., 2022; Girma et al., 2020). Cuevas et al.

(2017) identified various rare alleles in Ethiopian sorghum germplasm which could be novel sources important traits. The authors suggested that further efforts are required to discover and characterize the potentially useful undiscovered sorghum alleles. Collection and characterization of sorghum germplasm is a prerequisite to exploit the genetic diversity for efficient breeding and conservation programs. Nonetheless, identification of superior genotypes from the entire germplasm is influenced by genotype by environment interactions (Yan and Tinker, 2006). Genotype by environment interaction (GEI) effects slowdown the efficiency of plant breeding programs by reducing the association between phenotypic and genotypic values (Ceccarelli, 2015). It is more pronounced in arid and semi-arid areas because of the unpredictability of environmental conditions, which makes the identification and selection of superior varieties difficult (Ceccarelli, 2015). Theretofore, addressing the genotype by environment interaction effects (GEI) and determining the trait profile of crops is essential for effective utilization of genetic diversity, and to identify stable and superior genotypes.

The additive main effect and multiplicative interactions (AMMI) (Gauch 1992) and genotypic main effect plus genotype by environment interaction (GGE) biplots (Yan, 2001; Yan and Tinker, 2006) are effective tools to determine the stability and ranking of genotypes, and for identification of suitable mega environments (Gauch 1992; Yan, 2001; Yan and Tinker, 2006). Both models integrate principal component analysis (PCA) and biplot for the explanation of genotype by environment interaction (G×E). However, GE interaction has been only taken into account in AMMI analysis without considering the effects of genotype effects (Yan et al., 2007). The GGE biplot combines sources of variations due to genotype and genotype by environment interaction in multi-environment trails (Yan and Tinker, 2006). As a result, GGE biplot has been widely used to evaluate mean performance, stability of genotypes in various crops and discriminations of testing sites (Kang et al., 2006; Zhang et al., 2016). Recently, Yan and Frégeau-Reid (2018) introduced the genotype by yield * trait (hereafter, GYT) analysis as a new novel method to select genotypes based on multiple traits. Like the GT, the GYT is also based on the GGE biplot approach in which yield is a key trait, and the traits other than yield are judged based on their value to combine with yield. The GYT biplot analysis is instrumental to demonstrate the strengths and weaknesses of the genotypes graphically (Yan et al., 2019). Besides, this approach also provides a superiority index (SI) which allows for evaluating genotypes concerning multi-traits. The SI ranks genotypes by the mean of all traits (Yan and Frégeau-Reid, 2018). Since the development of GYT biplot method in recent years, it has been applied to evaluate genotypes of various crops such as wheat (Hamid et al., 2019; Kendal, 2019; Merrick et al., 2020), Barley (Karahan and Akgün, 2020; Kendal, 2020), Oat (Yan and Frégeau-Reid, 2018) and Sesame (Boureima and Abdoua, 2019). Although G×E interaction has been performed to assess the stability of improved varieties of sorghum using MET data (Admas and Tesfaye, 2017; Enyew et al., 2021; Worede et al., 2020) information is not aduquetely available on the stability of sorghum farmers’ varieties through the application of GGE biplot models in Tigray and research lacking on the genotype by yield by trait analysis sorghum genotypes using GYT methods. Thus, the objectives of this study were to evaluate genetic diversity, heritability and trait association, G×E interaction and identify superior sorghum genotypes in Tigray.

3.2. Materials and Methods

3.2.1. Experiment Materials and Multi-Environments

The experiment was conducted at three districts (Tahtay Adyabo, Tselemti, and Mereb Leke) of Tigray in the 2018 and 2019 growing seasons (Figure 1.3). Tigray is located in the northern part of Ethiopia between 12^{0}15’N-14^{0}15’N latitude and 36^{0}28’E-39^{0}59’E longitude (Table 1.1).

3.2.2. Experimental design and field evaluation

The experimental layout was an alpha lattice design with two replications at each experimental site. On each plot, the seeds were sown in a single 5 meters long row. The spacing between rows and between plants within rows were 0.75 and 0.25 meters, respectively. The land was tilled twice-using traditional oxen-drawn plows and seedbeds were prepared using human power, and planting and harvesting were done manually. All other agronomic practices were applied as per the recommendations for the area. After harvesting at physiological maturity, panicles were sun-dried for 15 days. Thereafter, panicles from each plot were threshed, winnowed, and seeds packed.

3.2.3. Data collection

Data were collected on various agromorphological traits such as days to 50% heading, days to 50% flowering days, days 50% to maturity, grain yield (quintal ha^{-1}), plant height (cm), panicle length (cm), leaf length(cm), leaf number, thousand seed weight (g), panicle weight (g) panicle width (cm) and leaf width (cm) (Table 1.3).

3.2.4. Data analysis

The data collected on grain yield and agromorphological traits of one hundred and eight sorghum farmers' varieties along with two improved varieties planted at three different locations of Tigray in the 2018 and 2019 growing seasons were analyzed using linear mixed models in META-R software (Alvarado et al., 2015). Each location and year were treated as an independent environment. Hence the mean performance, association among the traits, variances and heritability in individual environment (Tahtay Adyabo 2018, Mereb-Leke 2018, Tselemti 2018, Tahtay Adyabo 2019; Mereb-Leke 2019, and Tselemti 2019, hereafter referred as En1, En2, En3, En4, En5 and En6, respectively), and combined across the testing environments using the models implemented in lmer from package lme4 of R. The formula and models used for this study are according to the description made by Alvarado et al. (2020).

The model for the analysis of variance in individual environments the model is given as

$$Y_{ijkl} = \mu + rep_i + block_k(rep_j) + gen_j + \varepsilon_{ijk}$$

Where Y_{ijk} = the trait of interest, μ = the mean effect, rep$_i$ = the effect of the i^{th} replicate, block$_j$ (rep$_i$) = the effect of the j^{th} incomplete block within the i^{th} replicate, gen^k = the effect of the k^{th} genotype, ijk = the error associated with the i^{th} replication, j^{th} incomplete block and the k^{th} genotype.

For the combined analysis, new terms are added to the model for the individual environment as:

$$Y_{ijkl} = \mu + env_i + rep_j + rep_j(env_i) + block_k(env_i \times rep_j) + gen_j + env_j \times gen_j + \varepsilon_{ijkl}$$

Where env$_i$ and gnv$_i$ × gen$_l$ = the effects of the i^{th} environment and the environment by genotype interaction, respectively.

Broad-sense heritability (H^2) in individual and overall environments were estimated using the formula:

$$H^2 = \frac{\sigma_g^2}{\sigma_g^2 + \sigma_e^2 / nr}, \text{ and}$$

$$H^2 = \frac{\sigma_g^2}{\sigma_g^2 + \sigma_{ge}^2/nEnvs + \sigma_e^2/(nEnvs \times nr)}$$

Where σ^2_g, σ^2_e, σ^2_{ge}, nr and $nEnvs$ = the genotype variance, error variance, genotype by environment interaction variance, number of replication and number of environments, respectively.

The least of significance differences (LSD) at 5% of significance was calculated as:

$$LSD = t(0.05, dfErr) \times ASED\ ,$$

Where t = the cumulative Student's t distribution, 0.05 = the selected α level (5%), dfErr = the degrees of freedom for error in the linear mixed model, and ASED = the average standard error of the differences of the means**.**

The coefficient of variation was calculated using the formula:

$$CV(\%) = (\frac{\sqrt{MSE}}{Grandmean}) \times 100,$$ where MSE = the mean squared error.

3.2.5. GGE biplot analysis

Each year at each location was considered as a separate environment. When there was a significant difference in GE interaction, GGE biplot method was employed in Genstat software 18th edition to analyze of GE interaction and to assess grain yield stability (Yan, 2001). The model for GGE analysis is given as

$$Y_{ij} - \mu - \beta_j = \sum_{k=1}^{k} \lambda_k \xi_{jk} \eta_{jk} + \varepsilon_{ij}$$

Where Y_{ij} = the mean yield of genotype i in environment j, μ = the grand mean, β_j = the main effect of environment j, λ_k = the singular value of K^{th} principal component (PC), ξ_{ik} = the eigen-vector of genotype i for $PC_{k,}$ η_{jk} = the eigen-vector of environment j for $PC_{k,}$ k = the number of PC axes retained in the model, and ε_{ik} = the residual associated with genotype i in environment j.

3.2.6. Genotypes x Trait (GT) and Genotype x Yield x Trait (GYT) biplot analysis

The GT biplots were constructed as described by Yan and Rajcan, (2002) and Yan and Tinker, (2006) which is the same way as the GGE biplot except that environments are replaced by traits. It was generated from the GT table containing the mean performance of each trait of the genotypes. For clarity, we used only the numbers of the genotype. For example, LR1 was modified to 1; LR80 was replaced with 80; LR100 was replaced with 100, and so on for both GT and GYT biplot constructions.

The GYT analysis was done following the steps described by Yan and Frégeau-Reid (2018). First, GT two-way table was converted to GYT two-way tables **(**Appendix 3). For the number of days to heading (DH), days to flowering (DF) and days to maturity (DM), the GYT table was created by GY/DH, GY/DF and GY/DM, respectively. For the traits such as panicle weight (Pnwt), panicle length (Pnl), panicle width (Pnwd) and thousand seed weight (TGWT), the GYT table was created as GY*Pnwt, GY* Pnl, GY*Pnwd and GYT*TGWT, respectively. Then, the GYT table was standardized to mean zero and unity variance. The standardization was done to minimize bias that could arise from the difference in the units associated with the measured traits. This was done as:

$$\mathrm{P}ij = \frac{\mathrm{T}ij - \mathrm{T}j}{\mathrm{Sj}}$$

Where: P*ij* is the standardized value of genotype *i* for a trait or yield-trait combination *j* in the standardized table, T*ij* is the original value of genotype *i* for yield-trait combination *j* in the GYT table, T*j* is the mean across genotypes for yield-trait combination *j*, and S*j* is the standard deviation for yield-trait combination *j*.

The standardized GYT tables for each trait were used to generate the biplots using Genestat software 18th edition. The biplots were based on singular value decomposition of trait-standardized data (scaled by standard deviation, centered by tester-centered G+E and trait-focused symmetrical singular value partition.

3.3. Results

3.3.1. Mean performance and ranges of traits

The descriptive statistics (mean, range and standard deviation) of the traits studied are presented as location wise in Table 3.1. All the traits showed highly significant variation ($p < 0.001$) in mean performance in all the test environments. The longest average days to reach 50% flowering and maturity were 79 days (En1) and 121 days (En3), respectively, whereas the earlier average days to reach 50% flowering, and maturity were 66 days (En1) and 99 days (En1), respectively. Higher mean performance of genotypes for grain yield (31q ha^{-1}), leaf number (13 leaves/plant), leaf length (71.2 cm), leaf width (7.9 cm), plant height (240 cm), panicle length (25.5 cm), panicle width (10.6 cm), panicle weight (81.3 g) and thousand seed weight (34.2 g) were attained in En4, En1, En3, En1; En4, En3, En3 and En4, respectively. On the other hand, the lower mean performance of the genotypes for grain yield (25 q ha^{-1}), leaf number (9.7) leaves/plant), leaf length (60.1cm), leaf width (6.8 cm), plant height (2.2 meters), panicle length (18.8 cm), panicle width (7.0 cm), panicle weight (41.4 g) and thousand seed (22.6 g) weight were attained in En2, En4, En3, En2, En3, En2 and En5, respectively.

The average performance of the genotypes for all the traits across the six environments (three locations and two years) is presented in Table 3.3. The result showed that highly significant mean variation ($p < 0.001$) in all traits studied. The average days to reach 50% flowering and maturity were 74 days and 101 days, respectively and the ranges were 68.9 to 80 days and 102.9 to 119.5 days, respectively. The average grain yield, leaf number, leaf length, leaf width, plant height, panicle length, panicle width, panicle weight and thousand seed were 27.6 q ha-^{1}, 10.8 cm, 69.1cm, 7.2 cm 2.3 meters, 22.3 cm 8.4 cm, 60.3g and 28.1g, respectively, and the ranges were 15.3 to 41.9 qha^{-1}, 8.7 to 12.7 leaves/plant, 63.6 to 75.1 cm, 6.2 to 8.6cm, 170 to 280cm, 13.7 to 9.8cm, 6.7 to 9.9cm, 35.1 to 96.6g and 14. to 44.1g, respectively.

Table 3.1. Mean performance, range and standard deviation of sorghum genotypes in six individual environments in Tigray

	Environments											
	En1				En2				En3			
Traits	Mean	Max.	Min.	SD	Mean	Max.	Min.	SD	Mean	Max.	Min.	SD
DF	66.2[a]	76.8	58.1	4.0	69.1[a]	77.8	63.1	4.0	76.7[a]	88.2	63.4	5.7
DM	98.7[a]	113.4	83.6	6.2	102.7[a]	119.8	91.6	7.0	121.7[a]	156.9	96.0	17.1
LN	13.0[a]	16.3	9.3	1.2	10.2[a]	14.4	6.2	2.2	10.2[a]	16.2	6.2	2.1
LL	70.2[a]	80.3	52.2	4.3	70.6[a]	95.5	46.4	9.9	71.2[a]	78.9	65.1	3.0
Lwd	6.8[a]	9.9	5.5	0.7	7.0[a]	11.1	3.8	1.1	6.9[a]	9.7	5.6	0.7
PH	2.4[a]	2.9	1.7	0.3	2.3[a]	3.2	1.3	0.4	2.3[a]	2.9	1.5	0.3
Pnl	25.4[a]	35.2	15.6	4.3	18.8[a]	31.2	6.7	6.4	25.5[a]	39.5	9.6	4.4
Pnwd	8.5[a]	11.7	5.2	1.5	7.6[a]	13.8	4.5	1.7	7.0[a]	10.6	3.9	1.5
Pnwt	61.1[a]	115.6	26.4	16.5	41.4[a]	86.5	16.3	14.9	81.3[a]	144.0	52.4	13.8
Tswt	31.3[a]	46.9	6.5	8.3	23.6[a]	46.0	8.2	7.9	28.1[a]	43.9	9.1	6.4
GY	27.5[a]	43.6	8.5	7.0	24.4[a]	47.7	12.3	7.6	30.2[a]	48.0	12.5	8.1
		En4				En5				En6		
DF	75.8[a]	90.6	62.8	6.8	77.7[a]	89.6	66.7	4.8	79.4[a]	92.0	65.6	6.3
DM	109.0[a]	122.5	96.0	6.6	113.0[a]	131.4	96.5	8.3	114.4[a]	132.6	97.7	6.8
LN	9.7[a]	13.2	6.3	1.6	11.5[a]	13.6	9.1	1.0	10.5[a]	11.8	9.4	0.4
LL	70.8[a]	75.9	61.6	2.4	71.9[a]	83.6	62.2	4.7	60.1[a]	78.9	37.8	7.5
Lwd	7.4[a]	8.8	6.5	0.4	7.9[a]	8.9	7.1	0.4	7.3[a]	8.9	5.8	0.7
PH	2.4[a]	3.2	1.5	0.3	2.3[a]	3.1	1.2	0.4	2.2[a]	2.8	1.4	0.3
Pnl	21.7[a]	28.4	15.5	3.2	21.7[a]	33.3	10.3	4.7	20.9[a]	28.6	12.8	3.7
Pnwd	10.6[a]	18.6	6.3	2.1	8.3[a]	11.3	5.4	1.5	8.4[a]	12.1	3.7	1.7
Pnwt	63.9[a]	101.6	25.4	15.8	47.7[a]	93.4	22.3	15.4	66.5[a]	117.2	38.2	14.6
Tswt	34.2[a]	53.9	11.2	9.9	22.6[a]	50.2	5.6	8.9	28.7[a]	51.7	7.0	10.1
GY	30.4[a]	49.6	12.6	8.2	25.8[a]	46.3	10.5	8.1	27.3[a]	45.3	12.4	7.1

[a] = significant variations at p <0.001, DF, days to 50% flowering; DH, days to 50% heading; DM, days to maturity; GY, grain yield; LL, leaf length; Pht; LN, leaf number; LW, leaf width; PH, plant height; Pnht; panicle height; Pnwd, panicle width; Pnwt, panicle weight; TSWT, thousand seed weight.

3.3.2. Estimation of variance and broad-sense heritability

Table 3.2 demonstrates the variance and heritability of the traits studied in individual environment. The result showed that all the traits studied had highly significant variations ($p < 0.001$) in each environment. Higher genotype variance for days to 50% flowering, days to 50% maturity, leaf number, leaf length, leaf width, panicle length, panicle width, panicle weight thousand seed weight and grain yield in En1, En1, En3, En2, En2, En2, En5, En2, En4, En1, En6 and En3, respectively (Table 3.2). High broad-sense heritability ($H^2 > 0.6$) was attained in all the testing environments for all the traits except for leaf number and leaf length. Leaf length showed medium broad-sense heritability ($H^2 > 0.3 < 0.6$) in En1, En3 and En4, whereas leaf number showed lower broad-sense heritability ($H^2 < 0.3$) in En6 and medium heritability in En5 (Table 3.2).

The combined analysis of variance (pooled over six testing environments) displayed in Table 3.3 showed highly significant variance ($p < 0.001$) due to genotypes (σ^2g) and genotype by environment interaction (σ^2g x e) effects and environmental variance (σ^2e). The variance due to genotype by environment interaction effect was higher for all the traits studied except for grain yield in which the variance due to genotype was relatively higher than the σ^2g x e and σ^2e. As compared to the variance due to σ^2g and σ^2e, the variance due to σ^2g x e was higher for traits such as day to 50% maturity, leaf length, leaf number, plant height, panicle length and panicle width, whereas variance due to genotypes were higher in traits such as grain yield, thousand seed weight and panicle weight as compared to σ^2g x e and σ^2e. On the other hand, higher environmental variance was recorded in days to 50% heading, days to 50% flowering and panicle weight as compared to σ^2g x e and σ^2g (Table 3.3). The pooled analysis also showed higher broad-sense heritability ($H^2 > 0.6$) for all the traits studied except for leaf length which showed medium heritability.

Table 3.2. Heritability and Variance of sorghum genotypes in six individual environments in Tigray

	Environments														
	En1					En2					En3				
Traits	H^2	σ^2_g	*se*	LSD	CV	H^2	σ^2_g	*se*	LSD	CV	H^2	σ^2_g	*se*	LSD	CV
DF	0.99	16.7[a]	0.5	1.4	1.1	0.98	16.6[a]	0.5	1.4	1.0	0.98	33.2[a]	1.7	2.6	1.7
DM	0.96	40.1[a]	3.2	3.5	1.8	0.99	49.6[a]	1.4	2.4	1.2	0.99	295.9[a]	1.3	2.3	0.9
LN	0.74	1.9[a]	1.4	2.0	9.0	0.98	5.1[a]	0.2	0.9	4.3	0.92	5.0[a]	0.9	1.8	9.4
LL	0.5	38.2[a]	76.2	12.3	12.4	0.98	101[a]	3.3	3.6	2.6	0.4	22.6[a]	67.8	10.3	11.6
Lwd	0.65	0.7[a]	0.8	1.4	13.2	0.97	1.3[a]	0.1	0.5	3.9	0.62	0.7[a]	0.8	1.5	13.3
PH	0.79	760[a]	434.9	37.4	8.9	0.98	1377[a]	46.1	13.8	2.8	0.84	960.0[a]	392	36.1	8.6
Pnl	0.87	21.9[a]	6.2	4.7	9.9	0.94	43.7[a]	5.4	4.5	12.3	0.85	23.5[a]	8.6	5.4	11.4
Pnwd	0.87	2.4[a]	0.7	1.6	9.9	0.92	3.3[a]	0.5	1.4	9.6	0.76	3.0[a]	1.9	2.4	19.6
Pnwt	0.97	283[a]	14.9	7.5	6.3	0.99	227.5[a]	5.0	4.4	5.4	0.98	197.2[a]	8.5	5.7	3.6
TGWT	0.89	78.5[a]	18.6	8.5	13.8	0.98	64.8[a]	2.5	3.3	6.8	0.92	44.1[a]	7.4	5.2	9.7
GY	0.94	51.9[a]	6.5	4.9	9.3	0.96	60.1[a]	5.2	4.4	9.3	0.97	68.9[a]	4.1	4.0	6.7
	En4					En5					En6				
DF	0.97	47.8[a]	2.5	3.1	2.1	0.88	27.1[a]	7.4	5.2	3.5	0.93	42.9[a]	6.9	5.0	3.3
DM	0.97	45.9[a]	3.2	3.5	1.6	0.94	74.4[a]	9.3	5.9	2.7	0.86	54.5[a]	17.4	7.7	3.6
LN	0.82	3.1[a]	1.3	2.1	11.8	0.51	1.8[a]	3.5	2.6	16.3	0.25	0.8[a]	4.6	2.1	20.4
LL	0.41	14.1[a]	40.4	8.1	9.0	0.65	35[a]	37	9.8	8.5	0.95	60.1[a]	5.7	4.8	4.0
Lwd	0.59	0.3[a]	0.4	1.0	9.0	0.39	0.4[a]	1.1	1.3	13.6	0.68	0.7[a]	0.6	1.3	10.8
PH	0.82	1313[a]	563	42	10.1	0.89	1511[a]	400.6	37.6	8.7	0.82	941[a]	396.5	37	9.2
Pnl	0.72	14.2[a]	11.3	5.7	15.5	0.9	24.8[a]	5.6	4.4	10.9	0.87	15.6[a]	4.6	4.1	10.3
Pnwd	0.85	5.4[a]	2	2.6	13.2	0.85	2.7[a]	1.0	1.8	11.9	0.86	3.4[a]	1.1	1.9	12.5
Pnwt	0.95	265.1[a]	27.2	10.2	8.2	0.99	243.1[a]	6.6	5.1	5.4	0.99	217[a]	6.6	5.0	3.9
TGWT	0.97	101[a]	6.3	4.9	7.3	0.99	81.7[a]	1.8	2.7	5.9	0.98	104.4[a]	3.7	3.9	6.7
GY	0.97	69.5[a]	3.6	3.7	6.3	0.98	67.7[a]	2.8	3.4	6.4	0.97	52[a]	3.0	3.4	6.4

Table 3.3. Variance, broad –sense heritability, range and least of significant differences of sorghum genotypes across six environments in Tigray

Statistics	DF	DM	LN	LL	Lwd	PH	Pnl	Pnwd	Pnwt	TGWT	GY
H^2	0.70	0.60	0.60	0.50	0.70	0.70	0.80	0.60	0.90	0.90	0.90
σ^2_g	9.6 [a]	22.3 [a]	0.8 [a]	10.6 [a]	0.3 [a]	379.2 [a]	11.8 [a]	0.7 [a]	139.2 [a]	41.8 [a]	35.5 [a]
σ^2_{ge}	21.1 [a]	71.0 [a]	2.1 [a]	34.4 [a]	0.4 [a]	767.0 [a]	12.1 [a]	2.7 [a]	99.6 [a]	37.4 [a]	26.2 [a]
σ^2_e	27.5 [a]	69.0 [a]	1.4 [a]	19.3 [a]	0.1 [a]	44.8 [a]	6.7 [a]	1.5 [a]	200.6 [a]	19.5 [a]	5.3 [a]
SE	3.3	6.0	2.0	38.9	0.7	377.2	6.9	1.2	11.5	6.8	4.2
LSD	4.6	7.9	1.6	6.2	0.8	29.7	4.1	1.5	11.3	6.9	5.8
CV	2.4	2.2	13.1	9.0	11.2	8.5	11.8	13.1	5.6	9.3	7.5
Mean	74.0 [a]	101 [a]	10.8 [a]	69.1 [a]	7.2 [a]	2.3 [a]	22.3 [a]	8.4 [a]	60.3 [a]	28.1 [a]	27.6 [a]
Min.	68.9	102.6	8.7	63.6	6.2	170	13.7	6.7	35.1	14.1	15.3
Max.	80.0	119.5	12.7	75.1	8.6	280	29.8	9.9	96.6	44.5	41.9
SD	2.6	3.8	0.7	2.4	0.4	0.2	3.1	0.6	11.1	6.0	6.6

Where; H^2, heritability; [a] significant at $P<0.001$; [b] significant at $P<0.01$, DF, days to 50% flowering; DM, days to maturity; GY, grain yield; LL, leaf length; Pht; LN, leaf number; LW, leaf width; PH, plant height; Pnht; panicle height; Pnwd, panicle width; Pnwt, panicle weight; TSWT, thousand seed weight.

3.3.3. Phenotype correlation of traits

The correlation computed for the genotypes across all environments is presented in Table 3.4. Leaf length had strong significant positive association ($p < 0.001$) with plant height and panicle height. Traits such as days to maturity, leaf number, plant height, thousand seed weigh showed strong significant association ($p < 0.01$) with days to 50% flowering while leaf length and panicle width had significant positive associations with days to 50% flowering at $p < 0.001$ and $p < 0.05$, respectively. Days to maturity also had strong significant association ($p < 0.001; 0.01$) with plant height and panicle width, leaf number, leaf length and thousand seed weight. Plant height had strong significant positive association ($p < 0.001$ with panicle weight. The association of leaf number with plant height and thousand seed weight was significantly positive at $p < 0.01$ and $p < 0.05$, respectively. Leaf length had significant positive association with panicle length. Furthermore, strong significant positive association ($p < 0.001$) was detected among the yield and yield related traits such grain yield, panicle height, panicle length, panicle width, and thousand seed weight. Significant negative association ($p < 0.05$) was detected between leaf width and plant heigh.

Table 3.4. Coefficient of phenotypic correlation among traits of sorghum genotypes in Tigray

Traits	DF	DM	LN	LL	LW	PH	Pnl	Pnwd	Pnwt	TGWT
DF										
DM	0.83^{***}									
LN	0.52^{***}	0.27^{**}								
LL	0.20^{*}	0.2^{**}	0.18^{ns}							
LW	0.08^{ns}	0.12^{ns}	0.06^{ns}	-0.0						
PH	0.33^{***}	0.33^{***}	0.29^{**}	0.32^{***}	-0.17^{*}					
Pnl	0.012^{ns}	0.01^{ns}	0.07^{ns}	0.32^{***}	0.2^{*}	0.16^{ns}				
Pnwd	0.27^{**}	0.33^{***}	0.07^{ns}	0.09^{ns}	0.02^{ns}	0.16^{ns}	0.32^{***}			
Pnwt	0.06^{ns}	0.14^{ns}	0.12^{ns}	0.16^{ns}	0.06^{ns}	0.19^{**}	0.44^{***}	0.52^{***}		
TGWT	0.30^{***}	0.31^{**}	0.22^{*}	0.093^{ns}	0.07^{ns}	0.25^{ns}	0.43^{***}	0.58^{***}	0.83^{***}	
GY	-0.03^{ns}	0.01^{ns}	0.13^{ns}	0.17^{ns}	0.03^{ns}	0.12^{ns}	0.60^{***}	0.4^{***}	0.81^{***}	0.73^{***}

Abbreviations: ***, Significant variations at $p < 0.001$, **Significant at $P<0.01$; * Significant at $P<0.05$; ns, non-significant ($P>0.05$); DF, days to flowering; DM, days to maturity; GY, grain yield; Pnl; panicle lenght; Pnwd, panicle width; Pnwt, panicle weight; TGWT, thousand seed weight

3.3.4. GGE biplot analysis

The GGE biplots analysis for grain yield of sorghum genotypes are illustrated in Figure 3.1 A. The first two principal components explained about 63.4% (PC1) and 15.6 % (PC2) of the total variations, respectively. According to the explanations made by Yan and Tinker (2006) the angle of cosine between the vectors indicates the Pearson correlation between the traits. The cosine angles < 90^0 (acute angle), 90^0 (right angle), and >90^0 of the vectors indicate that positive correlations, no correlations and negative correlations between the traits, respectively. Accordingly, En2 and En3, En2 and En5, En2 and En6, En3 and En5, En3 and En6, En5 and En6, and En1 and En4 had positive association suggesting that less genotype by environment interaction effects. On the other hand, the obtuse angle between environments indicates negative association. En1 and En4 had negative association with En2, En3, En5, and En6 as indicated by the acute angle indicating that there has been interaction between genotype and environment (Adedugba et al., 2023).

The "which won where/what" of the genotypes is displayed in Figure 3.1 B. The perpendicular lines divide the biplot into ten polygon sectors containing the vertex genotypes (LR25, LR102, LR96, LR45, LR18 and LR92) which are displayed furthest away from the biplot origin. These genotypes are the best or the poorest genotypes in some or all environment, as they are the farthest genotypes from the biplot origin.

The discrimination and representativeness of environments are displayed in Figure 3.1 C. According to the explanations made by Yan and Tinker (2005) the small circle indicates the ideal environment. The arrow in the ideal environment locates the ideal center that the discrimination and representativeness of the environments. The vector length which is the absolute distance between environment and origin of the biplot measures the weakness and strength of the environment. The closer the environment to the origin of the biplot indicates the less discriminating environment and vice versa. The distance of the projections of the environments from the ATC axis measures representativeness, and the farthest the projection from the ATC axis indicates less representative of the environment and, vice versa. Accordingly, the discriminative ability of the environments was in the order of En4 > En5> En1> En3> En2 > En6, and the representatives of the environments was arranged as En6 > En2> En3> En5>En1 > En4.

The ATC view of the biplot shows the mean and the stability of the genotypes (Figure 3.1D). The line perpendicular to the ATA separates entries with below-average means (example: genotype LR8, LR1, LR47, LR40, LR86, LR50, LR52, LR49. LR45, LR24, and LR92) from those with above-average means (Example: LR106, LR25, LR19, LR103, LR75, LR74, and LR16). The nearest genotypes to the center of the horizontal line are the more stable genotypes (Example: LR103, LR3, LR105, LR68, LR11, LR2, and LR1) which implies less genotype by environment interaction effects; whereas the farthest genotypes (genotypes with long broken lines from the ATC) are the more unstable genotypes (example: LR106, LR56, LR102, LR15, LR57, LR18, LR89, andLR45) suggesting high genotype by environment interactions (Yan and Rajcan, 2002). On the other hand, genotypes far from the ideal center are not desirable, whereas genotypes displayed near/at the ideal center are considered as superior genotypes (Yan and Rajcan, 2002). Therefore, genotypes such as LR25, LR10, LR75 and LR 74 are superior genotypes while LR8, LR 40 and LR 86 are less performed farmers' varieties.

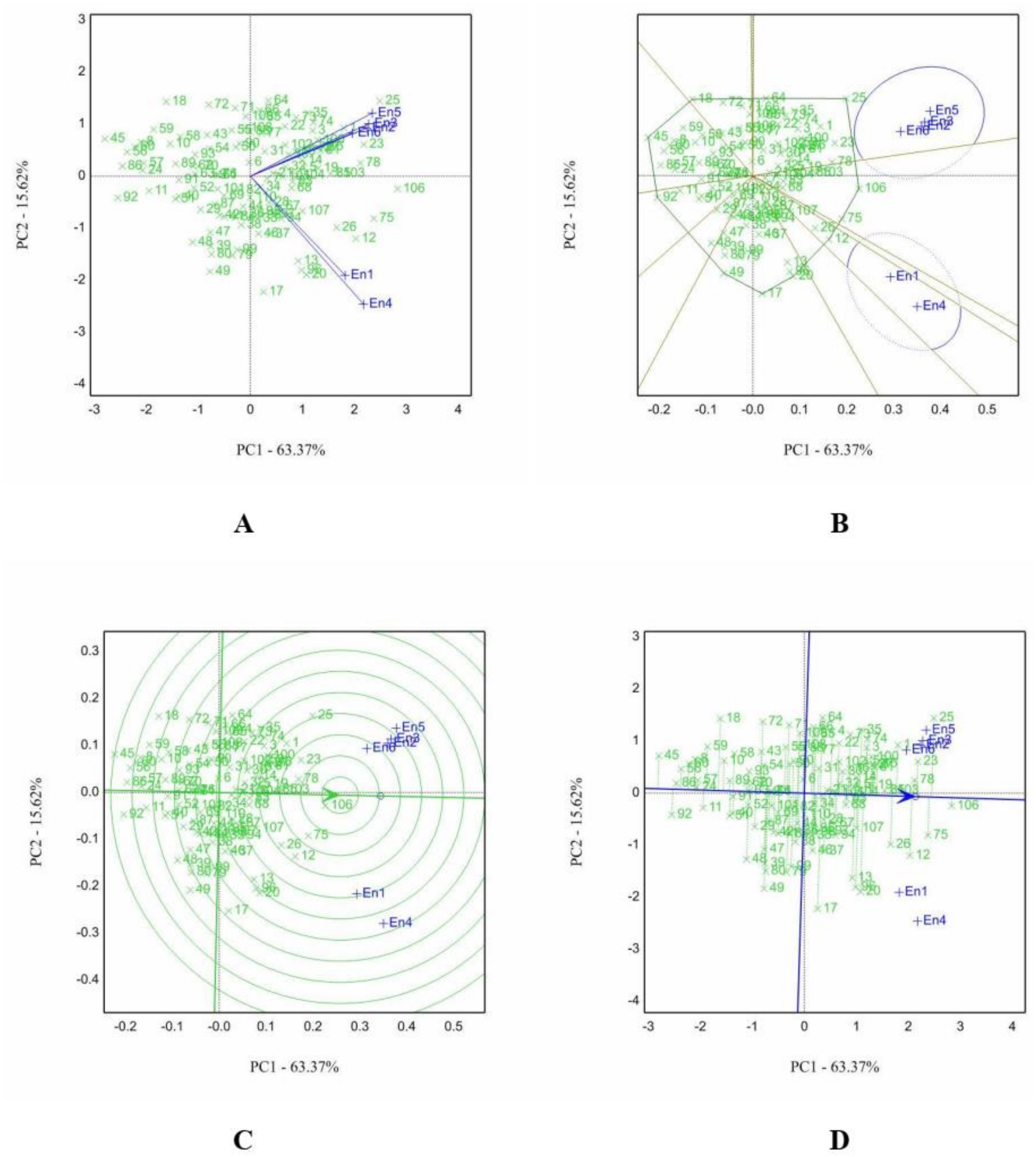

Figure 3.1. GGE biplots of sorghum genotypes in six environments of Tigray.

A = relationship among the environments, B = which one where/what of the genotypes, C = discriminative and representative of the environments, D = mean performance and stability of the genotypes

3.3.5. Genotype by Trait (GT) biplot

The GT biplot (Figure 3.2) generated from the GT data explores 77.6% of the total variations among the traits. The biplot shows a positive correlation of GY with Pnht, Pnwd, Pnwt and TGWT and, a negative correlation with DH, DF and DM. The angle between the vectors of the genotype i and trait j shows the value of the genotype for that trait (Yan and Tinker, 2006). Thus, it is possible to determine the trait profile of the farmers' varieties (the weakness and strength of the genotypes). Accordingly, LR106, LR12, LR102, LR23, LR75 and, LR14 revealed higher GY, Pnl, and Pnwt. Genotypes such as LR25, LR74 exhibited better TGWT and Pnwd. Genotypes such as LR56, LR58 and LR59 exhibited more to DH, DF, and DM indicating that the farmers' varieties are late maturing varieties.

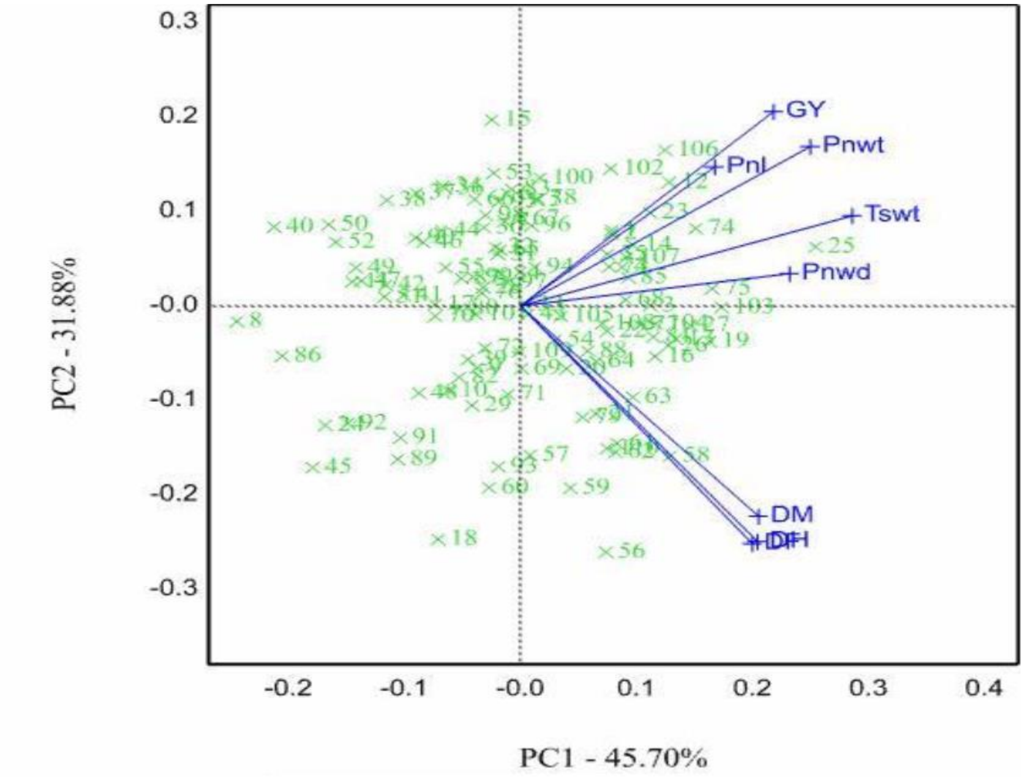

Figure 3.2. GT biplot of trait relationship of 108 sorghum farmers' varieties and two standard checks evaluated at three locations of Tigray in 2018 and 2019.

The numbers indicated the codes given for the farmers' varieties.

The "which won where/what" of the genotypes based on traits is displayed in Figure 3.3. The perpendicular lines divide the biplot into eight polygon sectors containing the vertex farmers' varieties (LR25, LR106, LR18, LR45, LR8, LR40, and LR15) which are displayed furthest away from the biplot origin. Vertex genotypes are winner genotypes for the trait placed within the corresponding sectors (Yan and Tinker, 2006). Genotypes and traits displayed in the same sector of the polygon indicate the genotypes have higher than the average value for a trait (Yan and Tinker, 2006). Thus, LR56, LR58, LR19, G59 had higher values for traits such as DM, DH, and DF while LR106, LR25, LR103, LR12, LR23, LR75, and LR74 had higher values for traits including GY, Pnl, Pwd, Pnwt and TGWT. Out of the eight sectors, only two had traits in their sectors which implied that the farmers' varieties in the other polygons were less desirable for the traits investigated.

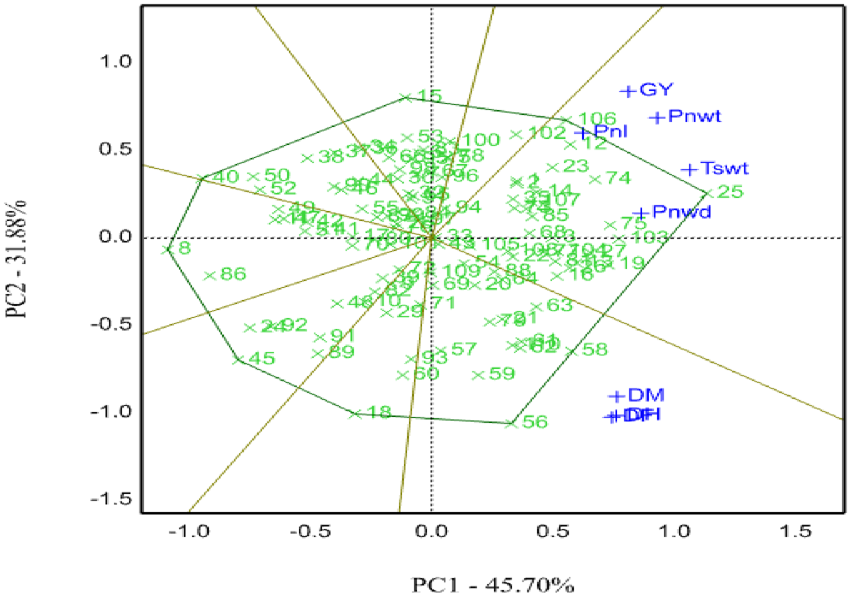

Figure 3.3. GT biplot showing which won where/what view of 108 sorghum farmers' varieties and two standard checks evaluated at three locations of Tigray in 2018 and 2019.

3.3.6. Genotype by Yield byTrait (GYT) biplots

The GYT biplot generated from the standardized GYT data displays about 96.4% (PC1 93.4% and PC2 3.0%) of the total variations explained among the traits (Figure 3.4). All the GYT biplots were interpreted following the explanations made by Yan and Frégeau-Reid (2018). The yield-trait combinations (GYT) displayed in Figure 3.4 demonstrate that there are positive correlations among all the traits. This is because the traits include grain yield in their component. The acute angle between the vectors of the farmers' varieties i and j also shows the value of the landrace. Accordingly, LR25 showed higher GY*TGWT, LR106 and LR23 showed higher GY*Pnl, LR73 and LR12 showed higher GY*Pwd, and LR103 and LR74 showed higher GY*Pwt.

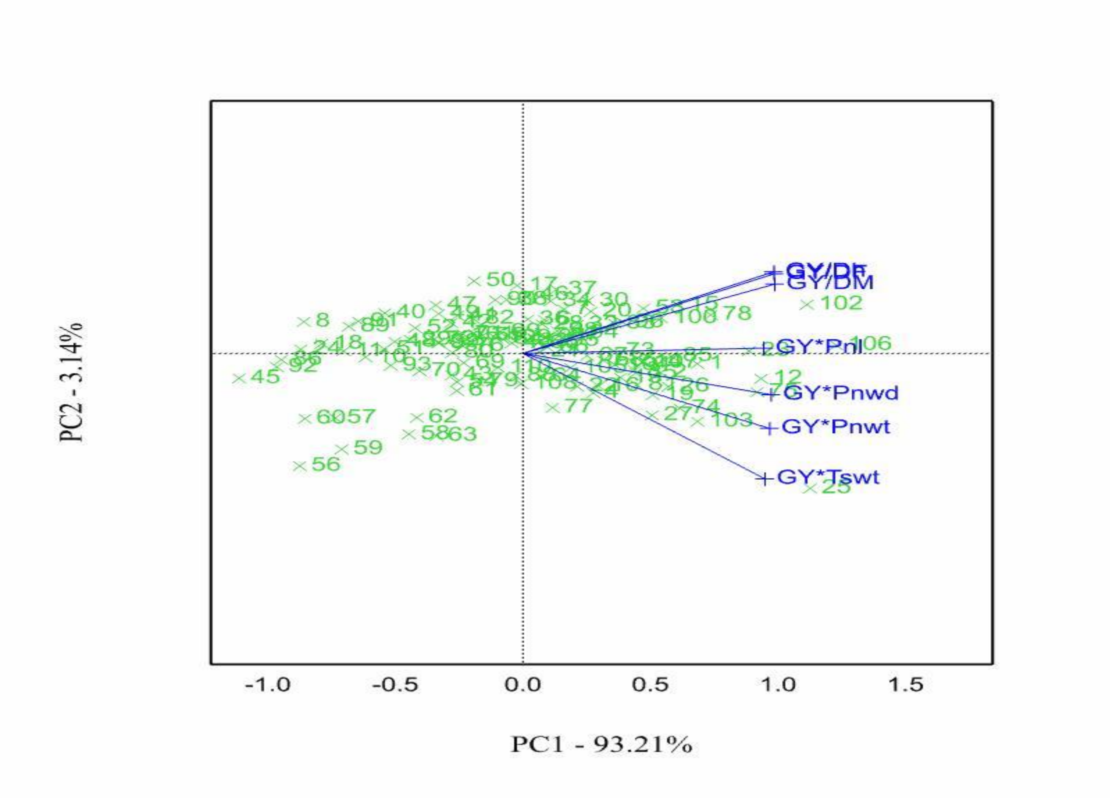

Figure 3.4. GYT biplot showing the relationship among the yield-trait combination of 108 sorghum farmers' varieties and two standard checks evaluated at three locations of Tigray in the 2018 and 2019 growing seasons.

Based on the "which won where/what" analysis (Figure 3.5), we address the following key points. The perpendicular lines divided the polygon into five sectors, the vertex farmers' varieties in each sector are indicated by the polygon peaks, and farmers' varieties that are desirable for a GYT are found in its sector as a group. Thus, farmers' varieties such as LR106, LR102, LR12, LR75, LR23, LR78 and LR26 are closely correlated with GY*Pwt GY*Pnl, GY*Pwd, GY*DM, GY*DF, and GY*DH. LR25 and LR27 are closely correlated with GY*TGWT. Farmers' varieties such as LR50, LR8, LR45 and LR56 did not correlate with any GYT combinations. Out of the five polygons, only two had traits in their sector.

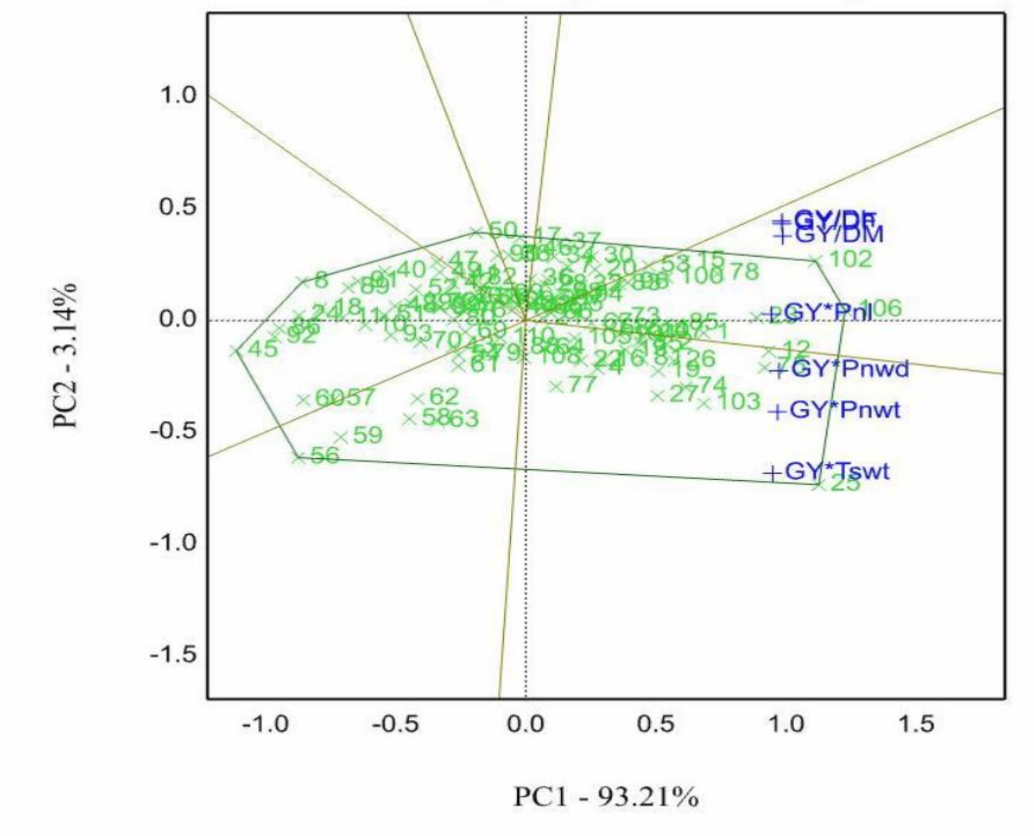

Figure 3.5 Which-won-where/what view of the GYT biplot of 108 sorghum farmers' varieties and two standard checks evaluated at three locations of Tigray in 2018 and 2019.

Figure 3.6 shows the ATC view of the GYT biplot generated from the standardized yield trait combination data. The small circle in the biplot indicates the average yield trait combinations and the line passes through the biplot origin and average yield trait combination is called the average tester axis (ATA) which is used to rank genotypes based on their overall superiority. Genotypes located close to ATA tend to have balanced trait profiles whereas those located far from the ATA in either direction have apparent strengths and/or weaknesses. From figure 3.6 the best ranked farmers' varieties include LR106> LR25> LR102 > LR12 > LR78 > LR103 > LR1> LR74 > LR15 whereas; farmers' varieties such as LR45, LR92, LR86, LR56, and LR24 were identified as the poorer genotypes. These results were confirmed by the superiority index generated from the yield-trait combinations (Table 3.5). LR106, LR102, LR are good in panicle length. Farmers' varieties such as LR25, LR75, LR103, and LR12 are good in TGWT, Pnwt, Pwd but poor in DH, DF and DM.

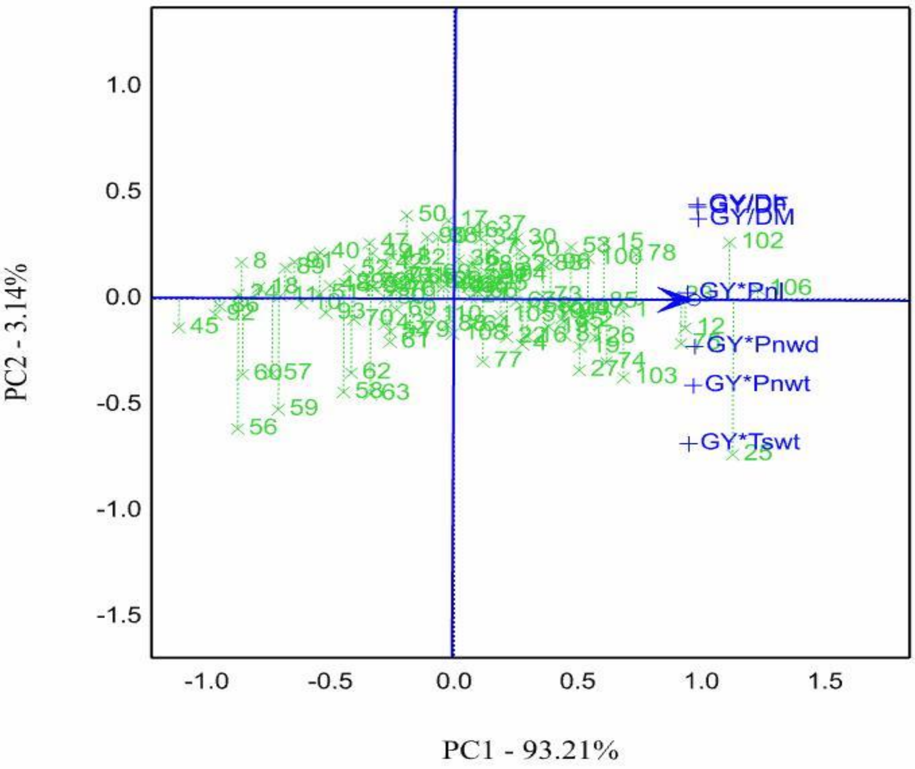

Figure 3.6. The Average Tester Coordination view of the genotype by yield*trait (GYT) biplot of 108 sorghum farmers’ varieties and two standard checks evaluated at three locations of Tigray in 2018 and 2019.

3.5. Top 20 and least 5 of sorghum genotypes in three locations of Tigray in the 2018 and 2019

Gen	GY/ DH	GY/ DF	GY/ DM	GY* Pwt	GY* Pnl	GY* Pwd	GY* TGWT	GY/ DH	GY/ DF	GY/ DM	GY* Pwt	GY* Pnl	GY* Pwd	GY* TGWT	mean (SI)
LR106	69.7	65.6	44.4	374.0	1148.7	416.2	173.9	3.5	3.5	3.6	3.3	2.7	3.1	3.0	3.2
LR 25	53.4	50.4	34.9	370.2	1020.8	358.5	173.9	1.5	1.5	1.7	3.2	2.0	2.1	3.0	2.2
LR 102	59.8	56.0	37.6	286.8	1155.9	334.6	136.3	2.3	2.3	2.3	1.9	2.7	1.7	1.8	2.1
LR 12	54.0	51.3	34.6	278.6	1020.7	348.4	141.7	1.6	1.6	1.7	1.7	2.0	1.9	1.9	1.8
LR 75	54.2	50.9	34.2	275.8	987.6	339.2	149.9	1.6	1.6	1.6	1.7	1.8	1.8	2.2	1.7
LR 23	54.8	51.5	34.5	268.7	962.5	355.0	128.9	1.7	1.7	1.6	1.6	1.7	2.0	1.5	1.7
LR 78	55.6	52.3	34.5	234.2	800.9	309.0	129.5	1.8	1.8	1.6	1.0	0.8	1.2	1.5	1.4
LR 103	49.6	46.9	31.3	302.7	830.9	315.4	130.7	1.0	1.1	1.0	2.1	1.0	1.3	1.6	1.3
LR 1	51.8	48.8	32.8	253.9	880.0	298.0	130.7	1.3	1.3	1.3	1.3	1.2	1.0	1.6	1.3
LR 74	48.0	45.2	30.1	256.9	963.8	311.9	126.1	0.9	0.9	0.8	1.4	1.7	1.3	1.4	1.2
LR 15	52.7	49.6	33.0	230.7	885.9	279.3	111.4	1.4	1.4	1.3	1.0	1.3	0.7	0.9	1.1
LR 85	49.7	46.8	31.8	221.6	894.3	304.9	120.8	1.1	1.1	1.1	0.8	1.3	1.1	1.2	1.1
LR 26	48.4	45.6	32.1	226.5	872.2	288.3	135.0	0.9	0.9	1.2	0.9	1.2	0.8	1.7	1.1
LR 100	50.4	47.6	31.5	224.2	972.7	266.5	108.2	1.2	1.2	1.0	0.9	1.7	0.4	0.8	1.0
LR 2	48.9	45.8	31.3	237.8	834.0	295.6	120.9	1.0	0.9	1.0	1.1	1.0	1.0	1.3	1.0
LR 19	46.9	44.5	29.8	246.0	811.9	327.6	111.9	0.7	0.8	0.7	1.2	0.9	1.5	1.0	1.0
LR 27	46.7	44.0	30.7	232.5	752.7	316.4	130.8	0.7	0.7	0.9	1.0	0.5	1.3	1.6	1.0
LR 107	47.6	44.9	29.6	222.2	900.5	291.8	109.6	0.8	0.8	0.7	0.8	1.3	0.9	0.9	0.9
LR 53	50.7	47.7	32.1	226.3	706.4	296.9	97.7	1.2	1.2	1.2	0.9	0.3	1.0	0.5	0.9
LR 14	47.6	44.6	29.3	222.8	885.1	308.0	104.4	0.8	0.8	0.6	0.8	1.2	1.2	0.7	0.9
LR 24	27.9	26.3	17.7	73.3	339.0	138.1	32.9	-1.6	-1.6	-1.7	-1.6	-1.7	-1.9	-1.6	-1.7
LR 56	24.0	22.7	15.3	95.1	273.5	159.5	63.7	-2.1	-2.1	-2.1	-1.2	-2.0	-1.5	-0.6	-1.7
LR 86	25.8	24.4	17.2	63.9	308.7	137.3	30.1	-1.9	-1.9	-1.8	-1.8	-1.8	-1.9	-1.7	-1.8
LR 92	25.3	23.8	15.9	60.8	379.2	130.2	29.8	-2.0	-2.0	-2.0	-1.8	-1.4	-2.0	-1.7	-1.8
LR 45	22.7	21.4	14.6	59.8	284.9	112.1	22.5	-2.3	-2.3	-2.3	-1.8	-1.9	-2.4	-2.0	-2.1

3.4. Discussions

Evaluation of the available genetic diversity of crop germplasm and subsequent utilization in crop improvement is helpful to achieve food security. Sorghum is one of the most important crop in arid and semiarid areas owing to its inherent ability to withstand adverse environmental condition even in areas where other cereals could not survive well. Thus, identification of superior sorghum genotypes from the entire sorghum germplasm could have significant contribution to accelerate plant breeding programs. Thus, determination of genetic diversity and heritability and its subsequent use for breeding and conservation program would have a great contribution for the current and future food security demands.

In the present study, several high yielding genotypes were found in each environment as well across environments. The high yielding attained in the present study may be attributed to the characteristic of farmers' varieties such as higher root to shoot ratio (Ali et al., 2009). The earlier genotypes to reach maturity can be used for crossing with the high yielding background. The wide range of genotype mean performance for all the traits studied indicates the possibility to distinguish among the genotypes. Our study agrees with the earlier findings (Andiku et al., 2022; Phuke et al., 2017; Tesso and Ejeta, 2011) who reported wide range of mean performance of various agro-morphological traits among sorghum genotypes. Location wise, the analysis of variance showed that highly significant variation among the genotypes for all the traits studied in all the environments suggesting the possibility of efficient selection. Similarly, the combined analysis of variance revealed that higher genotype variance, genotype by environment interaction variance and environmental variances. As it has been reported in other findings (Cuevas et al., 2017; Mekbib, 2008; Tesso and Ejeta, 2011), the higher variations among the sorghum genotypes may be attributed to the diverse agro-ecologies of the country.

The present study also revealed that highly significant variations due to genotype, genotype by environment interaction and environmental effects. The higher effects of genotype by environment interaction for most of the traits studied indicates that the traits are highly affected by the environmental factors and the dominant gene action controls the trait expression, whereas the higher genotype variance for traits such as grain yield and thousand seed weight indicate the relatively lower effects of environmental effects and additive gene action controls the expression of the traits. Similar to our finding Enyew *et al.*(2021) reported highly significant difference in yield and yield related traits among sorghum genotypes evaluated at three sites in Ethiopia. Gao et al. (2022) reported that higher environmental effect on sorghum cultivars grown in six environments of China. Many similar findings were also documented in other genotype by environment interaction studies on sorghum genotypes (Aruna et al., 2021; Rakshit et al., 2012).

Knowledge on the extent of heritability is essential for the success of plant breeding and conservation programs of crop improvement. For most of traits studied, higher broad-sense heritability was detected at each environment as well across environments. The higher broad-sense heritability of traits indicates that the traits are controlled by genetic factor to express the traits in the particular environment/s whereas the lower heritability indicates the higher influence the effect of environmental factors. This suggests the need for proper determination of the magnitude of GGE effects for efficient selection among genotypes. This finding agrees with the earlier reports by Adedugba et al. (2023) and Phuke et al. (2017).

Determination of the association among traits is essential to decide selection techniques. In the present study significant positive associations were detected for most of the traits. The positive association between yield and yield related traits suggests that selection can be done for both of the traits simultaneously. High number of leaves and/or leaf length resulted into late maturity of the genotypes. Genotypes with longer plant height were found to be late maturing and narrowed leaves. Longer plant height was also contributed to increased panicle weight. Late maturing varieties results in higher seed weight. Leaf number slightly increase/contribute to increased thousand seed weight. Leaf width slightly resulted in increased panicle length. Similar to the present finding, earlier studies detected positive association between agro morphological traits in sorghum (Girma et al., 2020; Subalakhshmi et al., 2019; Tesso and Ejeta, 2011) found positive association between grain yield and yield related traits such as thousand seed weight. The positive association between DF and DM, from the reported linkage between one of the height loci (Dw2) and the major photoperiod sensitivity locus, Ma1 (Lin et al., 1995).

Multi-environment trials are conducted for many of the major crops worldwide. This is to develop a variety suitable for a wide range of environments. A variety can be considered suitable when it shows a high yield with greater stability in a target environment. However, varietal evaluation is always determined by the genotype by environment interaction effects and undesirable associations of traits (Yan and Frégeau-Reid, 2018; Yan et al., 2007). Thus, evaluations of crop varieties across locations and over years are key activities in plant breeding programs to generate information for selection and recommended superior genotypes (Yan and Tinker, 2006). The effect of GGE can be exploited by selecting of genotypes for specific environment or eliminating by selecting genotypes for broad adaptations (Bashir et al., 2014). In the present study, one hundred and ten sorghum genotypes were evaluated in six testing environments to identify superior genotypes and ideal testing locations. The main effect of the genotypes (PC1) and the genotype by environment interaction effects (PC2) explains bout 79% of the total variations indicating the suitable of the biplot for further interpretation. The which won-where biplot indicates the six testing environments can be grouped into two mega environments (En1 and En4 grouped to mega-environment one and, En2, En3, En5 and En6 grouped to mega-environment two). Mega-environment delineation is useful to reduce redundancy of testing environments and cost of genotype evaluations (Yan and Tinker, 2006). Identification of representative and discriminative environment is useful for determinations of the trait profile of the genotypes. Accordingly, En4 followed by En5 were identified as discriminative environments whereas, En6 followed by En2 were representative environments. Using the mean and stability view of the biplot high yielding genotypes (LR106, LR25, LR19, LR103, LR75, LR74, and LR16) were distinguished.

Using GT biplot method, we demonstrate grain yield was positively correlated with yield-related traits such as panicle height, panicle weight, panicle width and thousand seed weight, and negatively correlated with traits such as days to heading, days to flowering and days to maturity. This implies that both positive and negative selections can be applied to deploy farmers' preferred varieties. Similar results were also reported by Mukondwa et al. (2021) in their study on GT association using 17 lines and three checks in Zimbabwe. We also found the GYT biplot approaches more promising because it ranks genotypes based on their worth in combining grain yield with other target traits alongside comprehensive visualization of the weakness and strength of genotypes. Our finding conforms with the discussion made by Yan and Frégeau-Reid (2018).

3.4.1. GT vs GYT Biplot analysis

In the study, we applied both GT and GYT biplot analysis to evaluate sorghum farmers' varieties that originated from Tigray North Ethiopia. The variations explained by the GT biplot were about 77.6% (Figure 2), whereas the variation explained by the GYT biplot was 96.4%. Based on the GT biplot, the correlation between the traits, and weaknesses and strength of the farmers' varieties were demonstrated. However, the GT biplot has limitations to make effective decisions on which landrace to be selected and recommended or avoided. As a result, low-yielding farmers' varieties might be selected if the other traits are superior. This is in line with the finding by (Yan and Tinker, 2005) who stated GT biplot analysis is important to identify traits useful for indirect selections and to evaluate the weakness and strengths of individual genotypes. In addition to the proper visualization of trait profile and association of the farmers' varieties, the GYT biplot was instrumental to ranking genotypes based on their overall superiority of yield trait combination using the ATC graph of the biplot, and GYT superiority index, which is not applicable using the GT biplot approach.

Farmers' varieties that combine grain yield with longer panicle length were considered superior farmers' varieties. Accordingly, LR106, LR102, LR23, LR25, LR12 and LR75 were identified as ideal farmers' varieties. Unlike the superior farmers' varieties identified using the GT biplot, the superior farmers' varieties identified using GYT are more significant because they are evaluated based on their ability to give higher yield along with combining other important traits meaning the farmers' varieties selected are at least high-yielding. The top 20 and five bottom farmers' varieties were listed in Table 4 using the GYT superiority index, and it confirms the GYT biplot is very effective to identify superior farmers' varieties. Our finding agreed with that of Kendal (2020), Yan and Frégeau-Reid (2018) and Yan et al. (2019) who reported that GYT biplot is an instrumental approach to evaluate genotypes based on their worth of higher yield with a combination of other breeding traits. The authors also cited that GT biplot is not much helpful to decide on cultivar evaluations and recommendations.

3.4.2. Implications for sorghum breeding programs

Effective utilization of the genetic variability of farmers' varieties for the selection and development of stable and superior genotypes is helpful to deploy farmers' preferred varieties. As discussed in other literature (Grenier et al., 2004; Hummer and Hancock, 2015), centers of origin are an important hotspot for generating new genetic variability essential for crop improvement and utilization programs. Likewise, the Ethiopian sorghum gene pool has been contributing to global agriculture either for direct cultivation or as a source of important traits for various breeding objectives such as sources of parental lines for hybrid development (Reddy et al., 2009), resistance to the green bug (Wu et al., 2006), drought tolerance (Adugna, 2014), resistance to mold disease (Nida et al., 2019), and high lysine content (Singh and Axtell, 1973). The Zera-zera landrace collected from Ethiopia has been extensively used for hybrid development (Reddy et al., 2004). In addition to the above, the present study identifies sorghum farmers' varieties outperform the standard checks evaluated based on both GT and GYT biplot approaches suggesting that the diversity of sorghum farmers' varieties in the country is not exploited to its potential in breeding programs. Therefore, the sorghum farmers' varieties that have been identified with combinations of important traits need to be included in breeding programmers.

3.5. Conclusions

Investigations of genetic diversity, trait association, heritability followed by identifications of high yielding and stable genotypes from the entire germplasm could contribute significantly in achieving efficient breeding and conservation programs. In the present study we found high genetic diversity of sorghum genotypes in Tigray essential for breeding programs. The mean performance of the genotypes was highly variable within and across environments for all the traits studied suggesting that the possibility to distinguish among the genotypes. Most of the traits studied were also highly heritable and the positive association between yield and yield related traits suggested that the genotypes can be improved simultaneously. The genotypes were also significantly ($p < 0.001$) affected by the genotype variance, environment variance and their interactions (GGE). The GGE biplots enable to identify high yielding and stable genotypes and discriminative and representativeness of the testing environments were also distinguished. The GYT analysiswas more efficient than the GT analysis in sorghum evaluations because it enables the breeder to select based on multiple trait combinations and simultaneously explores the strengths and weaknesses of the genotypes. These could also assist to developed farmers' preferred varieties and narrow the gap between varieties developed and target environments. Moreover, the results revealed that there is a high potential for sorghum farmers' varieties that could be utilized in sorghum breeding programs. Thus, further collection and detailed evaluation are important to exploit the potential thereby improving sorghum production and productivity in Arid and semi-arid areas of Ethiopia. Generally, there are many sorghum farmers' varieties being grown across a wide range of agro-ecologies of the region and they represent important resource for systematic sorghum improvement in Tigray. Thus, further collection and detailed evaluation are important to exploit the potential thereby improving sorghum production and productivity in arid and semi-arid areas of Ethiopia. The information generated form the present study could be a foundation for sorghum breeders and geneticists to effectively improve the crop.

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CHAPTER FOUR

Genetic Diversity, Correlation and Genotype by Yield by Trait (GYT) Analysis of Grain Yield and Nutritional Quality Traits in Sorghum (*Sorghum bicolor* [L.] Moench) Genotypes in Tigray, North Ethiopia

Abstract

Selecting sorghum genotypes with higher grain yield and nutritional quality is essential to tackle food insecurity and malnutrition in arid and semi-arid areas. Therefore, this study aimed to determine the genetic diversity, trait association and genotype by yield by trait (GYT) analysis and to select superior sorghum genotypes. One hundred and ten sorghum genotypes were evaluated at three locations in Tigray during the 2018 and 2019 growing seasons using alpha lattice design. Traits such as grain yield, protein, ash, starch, zinc, iron, calcium, and magnesium were profiled. Results showed that wide range and highly significant ($p < 0.001$) genotype mean performance in each environment as well as combined environments. Several out-performing genotypes were distinguished for each trait that could be exploited as breeding parents or direct use. This study further detected highly significant variation ($p < 0.001$) among the test genotypes for all the studied traits in individual environments and combined analysis suggesting the presence of sufficient genetic diversity for selection. The high broad-sense heritability ($H^2 > 0.9$) in all individual environments and moderate to high ($H^2 > 0.0.41 < 0.82$) in pooled environments recorded in the present study assured the possibility of effective selection among the genotypes. Besides, strong positive and negative associations were detected between some of the traits in individual and combined environments. The significant positive association between traits indicates that selection is possible for both of the traits simultaneously. Based on the GYT analysis we suggest ten promising sorghum genotypes for direct use or breeding programs in arid and semi-arid areas in general and in Tigray in particular.

Keywords: alpha lattice, mean performance; genotype variance, broad–sense heritability, nutritional grain quality

4.1. Introduction

Sorghum is the most diversified crop having 28 domesticated species categorized into five basic races *i.e. bicolor, guinea, caudatum, dura and kafir* and ten hybrid races (Harlan and de Wet, 1972). All the races of sorghum are grown across the diverse agroecological zones and farming systems of Ethiopia (Ayana and Bekele, 1998; Teshome et al., 1997). Sorghum is the first fully assembled C4 crop using traditional Sanger sequencing (Ayana and Bekele, 1998) and is considered as ‘gold standard’ reference due to its high percentage assembly (Boyles et al., 2019). The broad genetic base harbored mainly in sorghum farmers’ varieties is essential for providing the gene pool necessary for the development and deployment of farmers' preferred varieties. Hence, collection and assembly followed by thoughtful quantification of the genetic diversity of such a collection are essential for efficient crop improvement and conservation programs.

Ethiopian farmers grow diverse forms of sorghum varieties with over 95% of the area allocated for sorghum production covered by farmers’ varieties (Adugna, 2014) farmers’ varieties are heterogeneous, adapted to diverse growing conditions and are potential sources of desirable traits for crop improvement (Habyarimana et al., 2016; Ochieng et al., 2021). Given its center of origin and diversity (De Wet and Harlan, 1971; Dillon et al., 2007) and tremendous variation in agro-ecologies, Ethiopia is harbored with extremely rich genetic diversity of sorghum farmers’ varieties (Adugna, 2014; Girma et al., 2020; Mamo et al., 2023; Shegro et al., 2012) which serves as sources of various important traits. For instance, drought tolerance (Adugna, 2014; Enyew et al., 2022; Reddy et al., 2009), nutritional quality traits (Gerrano et al., 2016; Rhodes et al., 2017; Shegro et al., 2012), resistance to grain mold (Nida et al., 2019) and resistant to ergot and green bug (Wu et al., 2006). Ethiopia is also among the top nations that have made significant contributions to the sorghum germplasm collections in the world (Doggett, 1965). Moreover, there is still unexplored high genetic variability in Ethiopian sorghum farmers’ varieties (Enyew et al., 2022; Girma et al., 2020).

Selecting genotypes farmers’ varieties with improved yield and nutritional quality, especially with respect to mineral content would have a significant contribution to intervening the high prevalence of food shortage and malnutrition, especially in arid and semi-arid areas where sorghum is the stable food (Andiku et al., 2022; Badigannavar et al., 2016). Nonetheless, selecting in one trait may result in the reduced level of the other one or more target traits (Yan et al., 2007) which hinders the progress of crop improvement. To address the challenges of unfavorable association of key traits, Yan and Frégeau-Reid (2018) introduced the genotype by trait by yield (GYT) analysis approach. The GYT approach is a new novel tool to identify superior genotypes based on multiple traits such that grain yield is the main trait that determines the usefulness of the genotypes while the other target traits are valued based on their merit in combining with grain yield (Yan and Frégeau-Reid, 2018). The average tester coordinator (ATC) graph of the biplot in GYT analysis meaningfully and effectively rank genotypes based on multiple yield by trait combinations and shows the strengths and weaknesses of the genotypes (Yan and Frégeau-Reid, 2018). GYT analysis has been widely applied to identify superior genotypes in various crops such as oat (Yan et al., 2019), wheat (Merrick et al., 2020), cotton (Peixoto et al., 2022) and sorghum (Welderufael et al., 2023).

Although numerous publications are available regarding the high genetic diversity of sorghum in Ethiopia, most of the studies are concentrated on yield and other agronomic traits with less emphasis on the genetic variability of nutritional quality traits, and the genetic variation of local farmers' varieties in Tigray has not been studied adequately using agronomic and nutritional quality traits. Moreover, there is no research conducted so far to evaluate sorghum genotypes based on the genotype by yield by trait (GYT) approach using grain yield and nutritional quality traits. In this study we have examined two-year data from three locations for grain yield and nutritional quality traits of sorghum genotypes to evaluate genetic diversity and association in grain yield, starch, protein, ash, zinc (Zn); iron (Fe), calcium (Ca) and magnesium (Mg) contents, and to identify superior genotypes for grain yield and nutritional quality.

4.2. Materials and Methods

4.2.1. Planting materials and study locations

The study used 108 sorghum farmers' varieties collected from Tigray, northern Ethiopia along with two improved varieties (Melkam and Dekeba) obtained from Tigray Agricultural Research

Institute (TARI). The field trials were conducted at three locations (Tahtay Adyabo, Tselemti, and Mereb Leke) of Tigray in the 2018 and 2019 main growing seasons.

4.2.2. Experimental design and field evaluation

The experimental layout was an alpha lattice design with two replications at each experimental site. On each plot, the seeds were sown in a single 5 meters long row. The spacing between rows and between plants within rows were 0.75 and 0.25 meters, respectively. The land was tilled twice-using traditional oxen-drawn plows and seedbeds were prepared using human power, and planting and harvesting were done manually. All other agronomic practices were applied as per the recommendations for the area. After harvesting at physiological maturity, panicles were sun-dried for 15 days. Thereafter, panicles from each plot were threshed, winnowed and seeds packed.

4.2.3 Data collection

Data on grain yield was obtained on a plot basis and converted to quintal per hectare (q ha^{-1}). A composite seed sample of one kg from each accession was tagged and packed in cloth bags. Thereafter, the samples were taken to Mekelle University, Ethiopia, for grain nutritional quality analysis using Near Infra-Red Spectrophotometers (DA 7250 Perkin) method. Each sample were placed in a sample cup for scanning of the whole seeds. The samples were scanned twice, and average values of protein and starch were recorded. This method is a time and cost-effective method to analyze grain quality (Caporaso et al., 2018). The traits such as protein, ash and starch content of the sorghum seeds were expressed in terms of percentages, whereas Fe, Zn, Ca and Mg concentrations were expressed in terms of parts per million (ppm).

4.2.4. Data analysis

4.2.4.1. Mean performance, trait association and broad-sense heritability estimations

The data collected on grain yield and nutritional traits of one hundred and eight sorghum Farmers' varieties along with two improved varieties planted at three different locations of Tigray in the 2018 and 2019 growing seasons were analyzed using linear mixed models in META-R software (Alvarado et al., 2015ence the mean performance, association among the traits, variances and heritability in individual environment (Tahtay Adyabo 2018, Mereb-Leke 2018, Tselemti 2018, Tahtay Adyabo 2019; Mereb-Leke 2019, and Tselemti 2019, hereafter referred as En1, En2, En3, En4, En5 and En). Each location and year were treated as an independent environment. H 6, respectively), and combined across the testing environments using the models implemented in lmer from package lme4 of R. The formula and models used for this study are according to the description made by (Alvarado et al., 2020).

The model for the analysis of variance in individual environments the model is given as

$$Y_{ijkl} = \mu + rep_i + block_k(rep_j) + gen_j + \varepsilon_{ijk}$$

Where Y_{ijk} = the trait of interest, μ = the mean effect, rep_i = the effect of the ith replicate, $block_j$ (rep_i) = the effect of the jth incomplete block within the ith replicate, gen^k = the effect of the kth genotype, ijk = the error associated with the ith replication, jth incomplete block and the kth genotype.

For the combined analysis, new terms are added to the model for the individual environment as:

$$Y_{ijkl} = \mu + env_i + rep_j + rep_j(env_i) + block_k(env_i \times rep_j) + gen_j + env_j \times gen_j + \varepsilon_{ijkl}$$

Where env_i and $gnv_i \times gen_l$ = the effects of the ith environment and the environment by genotype interaction, respectively.

Broad-sense heritability (H^2) in individual and overall environments were estimated using the formula:

$$H^2 = \frac{\sigma_g^2}{\sigma_g^2 + \sigma_e^2 / nr}, \text{ and}$$

$$H^2 = \frac{\sigma_g^2}{\sigma_g^2 + \sigma_{ge}^2 / nEnvs + \sigma_e^2 / (nEnvs \times nr)}$$

Where $\sigma^2{}_g$, $\sigma^2{}_e$, $\sigma^2{}_{ge,}$ nr and $nEnvs$ = the genotype variance, error variance, genotype by environment interaction variance, number of replication and number of environments, respectively.

The least of significance differences (LSD) at 5% of significance was calculated as:

$$LSD = t(0.05, dfErr) \times ASED$$

Where t = the cumulative Student's t distribution, 0.05 = the selected α level (5%), dfErr = the degrees of freedom for error in the linear mixed model, and ASED = the average standard error of the differences of the means**.**

The coefficient of variation was calculated using the formula:

$$CV(\%) = (\frac{\sqrt{MSE}}{Grandmean}) \times 100,$$ where MSE = the mean squared error.

4.2.4.2. Genotype by Yield by Trait (GYT) analysis

GYT analysis was done following the steps described by Yan and Frégeau-Reid (2018). First, the Genotype by trait (GT) two-way table was converted to GYT two-way table. This was done by multiplying grain yield by each trait (grain*starch, grain yield*protein, grain*ash content, grain yield*zinc, grain yield*iron, grain yield*calcium and grain yield*magnesium, hereafter, referred to as gy*sta, gy*pro, gy*ash, gy*Zn, gy *Fe, gy*Ca and gy*Mg, respectively. Then after, the GYT table was standardized to mean zero and unity variance to minimize biases due to differences using the formula:

$$P_{ij} = \frac{T_{ij} - Tj}{S_j}$$

Where: P_{ij} = the standardized value of genotype i for a trait or yield-trait combination j in the standardized table, T_{ij} = the original value of genotype i for yield-trait combination j in the GY*T table, T_j = the mean across genotypes for yield-trait combination j, and S_j = the standard deviation for yield-trait combination j.

The standardized GYT tables for each trait were used to generate biplots using GGEBiplotGUI package in R-software version 4.0.1 (Team, 2021). The biplots were based on singular value decomposition of trait-standardized data (scaled by standard deviation, centered by tester-centered G+E and trait-focused symmetrical singular value partition). For clarity purposes, we use only the numbers of the genotype with the prefix +. For example, LR1, was replaced to +1; LR80 was replaced to +80; LR100 was replaced to +100 and so on for GYT biplot constructions.

The following equation was used to construct the GYT biplot:

$$P_{ij} = (\alpha\lambda_1^{\alpha}\varsigma_{i1})*(\lambda_1^{1-\alpha}\Gamma_{1j} / d) + (d\lambda_2^{\alpha}\varsigma_{i2})*(\lambda_1^{2-\alpha}\Gamma_{2j} / d) + \varepsilon_{ij}$$

Where ς_{i1} and ς_{i2} = eigenvalues for PC1 and PC2, respectively, for genotype Γ_{1j}; Γ_{2j} = eigenvalues for PC1 and PC2, respectively for yield-trait combination (or trait) j, and ε_{ij} = residual from fitting the PC1 and PC2 for genotype i on yield-trait combination j; λ_1^{α} and λ_2^{α} = singular values for PC1 and PC2, respectively, and α = singular value partitioning factor. When α = 1 (i.e., SVP=1), the biplot is said to be genotype-focused and is suitable for comparing genotypes. When α = 0 (i.e., SVP=2), the biplot is said to be environment-focused and is suitable for visualizing correlations among environments. The scalar d is chosen such that the length of the longest vector among genotypes equals to that among environments; this is important for generating a functional biplot (Yan, 2014).

4.3. Results

4.3.1. Mean performance and range of traits

The mean performance, range, standard deviation and significant test of the sorghum genotypes in the individual environments are illustrated in Table 4.1. Accordingly, all the genotypes showed highly significant variation ($p < 0.001$) in mean performance overall testing environments. Higher grain yield (31q ha-^{1}), starch (67.6%), protein (11.2%), ash (2.2%), zinc (38.4 ppm), iron (41.9 ppm), calcium (251.7 ppm), and magnesium (1133.5 ppm) content were recorded in En4, En3, En4, En3, En2, En5, En3, and En6, respectively. On the other hand, lower mean of genotype performance for starch (60.8%), protein (9.5%) ash (1.6%), zinc (33 ppm), iron (32.1 ppm), and magnesium concentrations (1043.3 ppm) were attained in En1. The lower mean of grain yield (25q ha^{-1}) and calcium contents (223.3 ppm) was attained in En2. The maximum grain yield (49.8 q ha^{-1}) and protein content (14.6%) were attained in En4 whereas, the maximum amount of ash (3.8 ppm), zinc (63.2 ppm), iron (84.2 ppm), calcium (415 ppm) and magnesium (1981 ppm) were attained in En1. The highest starch content (77.2%) was recorded in En3. On the other hand, minimum grain yield (8.5 q ha^{-1}), starch (33.7%), protein (4.3%), iron (11.2 ppm) calcium (125 ppm) and magnesium (652.3 ppm) contents were recorded in En1, and minimum ash (0.4%) and zinc (12.7 ppm) were recorded in En6 and En3, respectively.

The average performance of the genotypes for all the traits across the testing enlivenments (three locations and two years) is presented in Table 4.2 and Appendix 3. The result showed that highly significant mean variation ($p < 0.001$) in all traits studied. The average grain yield was 28.6q ha^{-1} with the highest score of 40.1q ha-^{1} attained from LR106. The average starch, protein, ash, zinc, iron, calcium and magnesium contents were 65.1%, 10.3%, 1.9%, 35.3 ppm, 36.8 ppm, 243 ppm, and 1096.8 ppm, respectively. The highest starch, protein, ash, zinc, iron, calcium and magnesium contents were recorded from LR14 (69.4%), LR65 (11.2%), LR10 (2.3%), LR23 (43.7 ppm), LR38 (47.8 ppm), LR16 (289 ppm) and LR4 (1345.6 ppm), respectively. The next four best-ranked genotypes for each trait are also presented in Table 4.2. The minimum values were 13.8q ha^{-1}, 59.1%, 9.5%, 1.5%, 29.7 ppm, 26.5 ppm, 210.2 ppm and 932 ppm for grain yield, starch, protein, ash, zinc iron, calcium and magnesium, respectively (Table 4.2).

Table 4.1. Mean performance (BLUPs), range, standard deviation and significant tests of grain yield and nutritional quality traits

Traits	En1			En2			En3		
	Mean	Range	SD	Mean	Range	SD	Mean	Range	SD
GY q/ha	29.8***	8.5-43.2	7.0	25.0***	12.1-48.3	8.1	30.0***	13.2-46.9	8.2
Starch %	63.7***	33.7-76.7	6.2	65.8***	49.9-74.2	5.3	67.6***	53.2-77.2	5.5
Protein %	9.5***	4.3-14	1.9	10.9***	7.8-13.5	1.2	9.9***	5.6-13.0	2.0
Ash %	1.6***	0.5-3.8	0.7	1.7***	1-2.8	0.4	2.2***	1.3-3	0.3
Zn (ppm)	33.0***	19-63.2	11.0	36.9***	20.3-56.8	7.5	34.4***	12.7-57.6	10.1
Fe (ppm)	32.1***	11.2-84.2	14.4	44.2***	13.2-67.5	13.3	34.0***	14.6-67.5	11.6
Ca (ppm)	244.2***	125-415	48.9	223.3***	136-346	39.9	251.7***	161-376	44.5
Mg (ppm)	1043.3***	652-1981	182.4	1096***	745-1604	172.4	1125.9***	783-1479	158.0
		En4			En5			En6	
GY q/ha	31.3***	11.3-49.9	12.6	26.8***	11.5-45.7	8.1	27.3***	12.1-45.1	7.1
Starch %	60.8***	46.9-76.1	5.3	67.2***	49.9-74.2	5.3	65.3***	51.8-74	5.0
Protein %	11.2***	7.2-14.6	1.5	10.4***	7.8-13.5	1.3	10.0***	6.1-12.2	1.5
Ash (ppm)	1.8***	0.8-3.3	0.5	1.91***	0.91-2.9	0.4	2.0***	0.4-2.9	0.4
Zn (ppm)	33.9***	19.3-55.8	7.7	38.4***	19.7-56.7	7.5	34.8***	12.8-57.2	8.7
Fe (ppm)	35.4***	12.5-79.3	12.0	41.9***	13.2-67.5	13.3	33.7***	15.6-66.2	9.0
Ca (ppm)	247.5***	126-366	48.0	247.5***	137-345	39.7	246.0***	172.0-322.0	32.0
Mg (ppm)	1112.3***	672-1678	207.1	1074.8***	714-1612	188.4	1133.5***	801-1496	135.2

GY= grain yield expressed in quintal t ha^{-1}, SD = standard deviation, *** = significant at P<0.001, Zn, Fe, Ca, Mg, = zinc, iron, calcium and magnesium, respectively.

Table 4.2. Combine mean, range, standard deviation and five best sorghum farmers' varieties evaluated in six test environments of Tigray

Traits	Mean	Range	SD	Top five genotypes for each trait
GY (q ha^{-1})	28.6^{***}	13.8-41.3	5.6	LR106 >LR102 > LR25 > LR75 > LR23
Starch (%)	65.1^{***}	59.1-69.4	2.3	LR14 > LR27 > LR25 > LR16 > LR > LR4
Protein (%)	10.3^{***}	9.5-11.2	0.3	LR 65 > LR 57 > LR 107 > LR 95 > LR 98
Ash (%)	1.9^{***}	1.5-2.3	0.2	LR10 > LR 84 > LR 12 > LR 81 > LR 110
Zn (ppm)	35.3^{***}	29.7-43.7	2.4	LR 23 > LR 45 > LR 12 > LR 27 > LR 98
Fe (ppm)	36.8^{***}	26.5-47.8	4.9	LR 38 > LR 12 > LR 87 > LR 10> LR 69
Ca (ppm))	243.4^{***}	210.2-289	16.7	LR 16 > LR 26 > LR 15 > LR 39 > LR 74
Mg (ppm)	1096.8^{***}	932-1345.6	71.5	LR 4 > LR 41 > LR 27 > LR 99 > LR 86

LR = farmers' varieties, SD = standard deviation, *** = significant at P<0.001, Zn, Fe, Ca, Mg, = zinc, iron, calcium and magnesium, respectively.

4.3.2. Variance and broad-sense heritability (H^2) of traits

Table 4.3 demonstrates the genotype variance and heritability for grain yield and nutritional quality traits of the sorghum genotypes in each testing environment. All traits showed highly significant genotypic variances ($p < 0.001$) over all the environments except in En2 which was significant ($p < 0.05$) for ash and magnesium concentrations. All the traits showed the highest genotype variance in En1 except grain yield, which showed the highest genotype variance in En4. On the contrary, the lowest genotype variance due to starch, ash, zinc and magnesium content was attained in E3 while, the lowest genotype variance due to grain yield, protein and calcium was recorded in En4, En2 and En6, respectively (Table 4.3)

The combined analysis of variance (pooled over six testing environments) displayed in Table 4.4 showed highly significant variance ($p < 0.001$) due to genotypes (σ^2g) and genotype by environment interaction (σ^2g x e) effects for all the traits. The same trend was shown for σ^2e except for calcium, which was significant ($p < 0.05$). The variance due to genotype by environment interaction effect was higher for all the studied traits except for grain yield in which the variance due to genotype was relatively higher than the σ^2g x e and σ^2e.

In the present study, all traits were highly heritable ($H^2 > 0.9$) as per the scale of Robinson (1966) in all individual environments (Table 4.3) However, a partitioned genotype by environment interaction component reduced the broad-sense heritability across environments (pooled analysis) to the range from $H^2 = 0.41$ (protein content) to $H^2 = 0.82$ (grain yield) (Table 4.4).

Table 4.3. Heritability, genotypic variance, standard error, LSD and coefficient of variation for grain yield and nutritional quality traits

	En1					En2					En3				
Statistics	H^2	σ^2g	SE	LSD	CV	H^2	σ^2g	SE	LSD	CV	H^2	σ^2g	SE	LSD	CV
Starch (%)	0.98	38.6***	0.2	0.95	0.75	0.97	28.4***	0.05	0.5	0.4	0.97	30.7***	0.1	0.5	0.36
Protein(%)	0.99	3.6***	0.0	0.29	1.52	0.97	1.6***	0.03	0.3	1.6	0.98	3.9***	0.0	0.2	0.78
Ash (%)	0.98	0.5***	0.0	0.13	3.81	0.98	0.2***	0.0	0.1	3.5	0.96	0.1***	0.0	0.2	4.86
Zn (ppm)	0.97	122.0***	0.2	0.93	1.38	0.96	56.4***	0.07	0.6	0.7	0.97	103.2***	0.1	0.7	0.99
Fe (ppm)	0.96	211.3***	1.3	2.24	3.49	0.96	179.4***	0.03	0.4	0.4	0.98	135.6***	0.2	0.8	1.18
Ca (ppm)	0.97	2412.8***	3.4	3.64	0.75	9.94	1604.1***	1.95	2.8	0.6	0.96	2015.6***	38.6	12.3	2.49
Mg(ppm)	9.91	33640.7***	158	24.87	1.2	0.91	33005.5***	6612	153.8	7.5	0.98	25202.6***	17	8.2	0.37
GY q ha^{-1}	0.9	51.9***	6.5	4.9	9.3	0.98	60.1***	5.2	4.4	9.3	0.99	68.9	4.1	4.0	6.7
	En4					En5					En6				
Starch (%)	0.96	28.2***	0.2	0.9	0.7	0.99	28.1***	0.05	0.4	0.3	0.94	25.4***	0.38	1.2	0.94
Protein(%)	0.99	2.4***	0.1	0.4	1.9	0.98	1.7***	0.03	0.3	1.6	0.98	2.4***	0.02	0.3	1.52
Ash (%)	0.92	0.3***	0.0	0.2	5.3	0.96	0.2***	0.0	0.1	3.7	0.91	0.2***	0.01	0.2	4.9
Zn (ppm)	0.94	60.9***	1.1	2.1	3.1	0.99	56.7***	0.02	0.3	0.4	0.98	77.5***	0.24	0.8	1.4
Fe (ppm)	0.95	146.7***	0.9	1.9	2.7	0.99	178.7***	0.09	0.6	0.7	0.97	81.5***	0.26	1.0	1.51
Ca (ppm)	0.96	2333.0***	15.6	7.8	1.6	0.96	1594.4***	12.4	7.0	1.5	0.95	1035.5***	2.52	3.2	0.64
Mg(ppm)	0.93	43299.5***	47.1	13.7	0.6	0.99	36134.0***	611.0	48.9	2.3	0.96	18530.7***	143	23.7	1.06
GY q ha^{-1}	0.98	69.5***	3.6	3.7	6.3	0.97	67.7***	2.8	3.4	6.4	0.96	52.1***	3.0	3.4	6.4

Abbreviations: *** = significant variation at $p < 0.001$, CV =coefficient of variations, σ^2g = genotype variance, H^2 = broad sense heritability, LSD =least of significant difference, SE= standard error

Table 4.4. Heritability, variance components, standard error, list of significant differences and coefficient of variations of grain yield and nutritional quality traits

Statistic	Starch (%)	Protein (%)	Ash (%)	Zn (ppm)	Fe (ppm)	Ca (ppm)	Mg (ppm)	GY q ha^{-1}
H^2	0.7	0.4	0.6	0.5	0.6	0.6	0.7	0.82
σ^2g	8.1***	0.3***	0.1***	11.7***	36.7***	432.3***	7839.6***	25.4***
σ^2g x e	21.8***	2.3***	0.3***	67.7***	118.8***	1400***	23797.2***	25.2***
σ^2e	5.9***	0.4***	0.1***	3.4***	21.9***	27.1*	917.8***	5.3***
SE	0.2	0.0	0.0	0.3	0.5	12.4	1263.9	15.2
LSD	4.4	1.1	0.4	6.7	10.0	34.4	144.5	6.0
CV (%)	0.6	1.5	4.5	1.5	1.8	1.4	3.2	14.2

Where *** = significant variation at $p < 0.001$, * = significant variation at $p < 0.05$, CV = coefficient of variations, σ^2_g = genotype variance, H^2 = broad sense heritability, LSD =least of significant difference, SE = standard error,

4.3.4. Correlation between traits

Pearson's correlations among the traits were computed for each individual and across environments using the best linear unbiased prediction (blup) mean (Table 4.5). Some of the traits were significantly ($p < 0.001$; 0.01; 05) correlated while many of them had weak correlations ($p > 0.05$). Protein content had highly significant positive association with starch (En1, $p < 0.01$), calcium (En2, $p < 0.001$ and En3, $p < 0.001$), magnesium (En3, $p < 0.001$) contents, and grain yield (En4, $p < 0.05$; En5, $p < 0.05$ and En6, $p < 0.01$). On the other hand, protein showed a significant negative association with traits such as ash (En1, $p < 0.001$ and En2, $p <0.05$), iron (En1, $p < 0.01$ and En2, $p < 0.001$), and zinc (En1, $p < 0.01$; En2, $p < 0.001$ and En4, En2, $p <0.05$). Ash content showed significant positive association with zinc (En1, En2, $p < 0.001$; En4, $p < 0.001$ and En5, $p < 0.05$) and iron concentrations (En1, $p < 0.001$; En2, $p < 0.001$; En4, $p < 0.001$ and En5, $p < 0.05$). Similar to protein content, ash content had also a significant negative association with some traits such as calcium and zinc concentration (En3, $p < 0.01$). Zinc content exhibits a significant ($p < 0.001$) positive correlation with iron in En1, En2, En4 and En5, and significant negative ($p < 0.05$) associations in En3 and En6. A significant negative ($p < 0.05$) association was attained between calcium and iron contents in En2 and En6, whereas a significant positive (($p < 0.05$) association was found between calcium and grain yield in En4 and En6. Grain yield and magnesium showed a significant positive ($p < 0.05$) association in En6 only.

The correlation of the traits pooled over the six environments is presented in Table 4.6. Ash showed a highly significant positive ($p < 0.001$) correlation with zinc and iron contents. Besides, zinc and iron, starch and protein, and zinc and grain yield showed highly significant positive correlations while, calcium and iron had positive significant ($p < 0.05$) correlation with grain yield and starch, respectively (Table 4.6). On the other hand, protein had a highly significant ($p < 0.001$) negative association with iron concentration and significant ($p < 0.05$) association with ash and zinc contents. The rest traits had no significant association ($p > 0.05$) (Table 4.6).

Table 4. 5. Correlations among grain yield and nutritional quality traits of sorghum

			En1				
Traits	Starch	Protein	Ash	Zn	Fe	Ca	Mg
Protein	0.25^{**}						
Ash	-0.04^{ns}	-0.32^{***}					
Zn	-0.10^{ns}	-0.30^{**}	0.72^{***}				
Fe	-0.13^{ns}	-0.28^{**}	0.64^{***}	0.68^{***}			
Ca	0.05^{ns}	-0.16^{ns}	0.11^{ns}	0.13^{ns}	0.03^{ns}		
Mg	0.11^{ns}	0.02^{ns}	0.10^{ns}	0.00^{ns}	-0.05^{ns}	-0.02^{ns}	
GY	0.11^{ns}	-0.16^{ns}	0.18^{ns}	0.11^{ns}	0.13^{ns}	0.00^{ns}	-0.14^{ns}
			En2				
Protein	-0.06^{ns}						
Ash	0.00^{ns}	-0.23^{*}					
Zn	0.01^{ns}	-0.34^{***}	0.17^{ns}				
Fe	0.21^{*}	-0.48^{***}	0.33^{***}	0.38^{***}			
Ca	-0.08^{ns}	0.35^{***}	-0.15^{ns}	-0.15^{ns}	-0.19^{*}		
Mg	0.04^{ns}	0.15^{ns}	-0.0^{ns}	0.06^{ns}	-0.12^{ns}	-0.13^{ns}	
GY	0.15^{ns}	-0.19^{*}	0.13^{ns}	0.16^{ns}	0.00^{ns}	0.08^{ns}	0.05^{ns}
			En3				
Protein	0.00^{ns}						
Ash	0.05^{ns}	-0.12^{ns}					
Zn	-0.05^{ns}	0.17^{ns}	-0.25^{**}				
Fe	0.31^{***}	-0.10^{ns}	0.04^{ns}	-0.20^{*}			
Ca	-0.06^{ns}	0.37^{***}	-0.20^{*}	0.17^{ns}	-0.08^{ns}		
Mg	0.07^{ns}	0.36^{***}	0.05^{ns}	0.08^{ns}	-0.07^{ns}	0.18^{ns}	
GY	0.12^{ns}	-0.01^{ns}	-0.05^{ns}	0.02^{ns}	0.10^{ns}	0.08^{ns}	0.01^{ns}

				En4			
Pro	0.15^{ns}						
Ash	0.12 ^{ns}	-0.15^{ns}					
Zn	0.00 ^{ns}	-0.20*	0.48***				
Fe	-0.09 ^{ns}	-0.04^{ns}	0.42***	0.52***			
Ca	0.15 ^{ns}	-0.03^{ns}	0.00^{ns}	0.06^{ns}	0.02^{ns}		
Mg	0.10 ^{ns}	0.08^{ns}	0.04^{ns}	0.00^{ns}	-0.08^{ns}	-0.13^{ns}	
GY	0.23*	0.21*	0.09^{ns}	0.09ns	-0.05^{ns}	0.24*	-0.10^{ns}
				En5			
Pro	0.16^{ns}						
Ash	-0.03^{ns}	-0.04 ^{ns}					
Zn	0.16^{ns}	-0.16 ^{ns}	0.27**				
Fe	0.23*	-0.02 ^{ns}	0.23*	0.38***			
Ca	-0.19*	0.11 ^{ns}	-0.04^{ns}	-0.15^{ns}	-0.21*		
Mg	0.08^{ns}	-0.00 ^{ns}	-0.04^{ns}	-0.13^{ns}	0.05^{ns}	-0.05^{ns}	
GY	-0.10^{ns}	0.24*	0.14^{ns}	0.17^{ns}	0.18^{ns}	-0.03^{ns}	0.07^{ns}
				En6			
Pro	0.15^{ns}						
Ash	-0.08 ^{ns}	0.02 ^{ns}					
Zn	-0.05 ^{ns}	0.13 ^{ns}	-0.14 ^{ns}				
Fe	0.05 ^{ns}	-0.05 ^{ns}	0.12 ^{ns}	-0.22*			
Ca	0.00 ^{ns}	0.20*	-0.12 ^{ns}	0.17^{ns}	-0.13^{ns}		
Mg	0.01 ^{ns}	0.08 ^{ns}	-0.02 ^{ns}	0.05^{ns}	-0.10^{ns}	0.12^{ns}	
GY	-0.05 ^{ns}	0.28**	0.06 ^{ns}	0.08^{ns}	-0.03^{ns}	0.23*	0.21*

Table 4.6. Pearson correlation of grain yield and nutritional quality traits pooled over six environments

	Starch	Protein	Ash	Zn	Fe	Ca	Mg
Protein	0.03^{ns}						
Ash (ppm)	0.01^{ns}	-0.23*					
Zn (ppm)	0.06^{ns}	-0.21*	0.35***				
Fe(ppm)	0.20*	-0.34***	0.49***	0.32***			
Ca(ppm)	0.00^{ns}	0.13^{ns}	-0.01^{ns}	0.04^{ns}	-0.10^{ns}		
Mg(ppm)	0.06^{ns}	-0.03^{ns}	0.21*	0.09^{ns}	0.08^{ns}	0.03^{ns}	
GYqha^{-1}	0.30**	0.18 ^{ns}	0.02 ^{ns}	0.26**	0.04^{ns}	0.22*	0.07^{ns}

GY = grain yield qha^{-1}, ppm = parts per million, ***= significant at p<0.001, ** significant at P<0.01, * = significant at P<0.05, ns = not significant (P>0.05)

4.3.5. Genotype by yield by trait (GYT) analysis of traits

In this study, we determine how the grain yield of sorghum is combined with other important nutritional traits using the Pearson correlations coefficient (Table 4.7) and GYT biplots (Figure 4.2 A-C) using the pooled over mean. Highly significant positive correlations ($p < 0.001$) were detected for all the trait combinations with correlation coefficients ranging from 0.53-0.89. The strongest multi-trait correlation was manifested between grain yield*starch and grain yield*protein (r = 0.89), grain yield*starch and grain yield*calcium (r = 0.87) and grain yield*starch and grain yield * magnesium (r = 0.86). The strong positive correlation between the trait combinations is also indicated by the acute angles between the vectors of the traits on the scatter plot generated from genotype by yield by trait data (Figure 4.2A). The GYT biplot (Figure 4.2 A-C) explores about 87.5% (PC1= 78.34%, PC2= 9.2%) of the total variation. The polygon of which won where/what (Figure 4.1B) divided the biplot into six sectors and the yield trait combinations are located in three sectors only. The ATC view of the GYT biplot (Figure 4.2 C) shows the weakness and strengths of the genotypes and graphically ranks the genotypes based on their overall superiority.

Table 4.7. Correlation of GYT traits of sorghum genotypes analyzed over three locations and two years in Tigray

GYT traits	gy*Sta	gy*Pro	gy*ash	gy*Zn	gy*Fe	gy*Ca
GY*Pro	0.89^{***}					
GY*Ash	0.75^{***}	0.66^{***}				
GY*Zn	0.83^{***}	0.74^{***}	0.78^{***}			
GY*Fe	0.69^{***}	0.53^{***}	0.76^{***}	0.71^{***}		
GY*Ca	0.86^{***}	0.84^{***}	0.66^{***}	0.75^{***}	0.57^{***}	
GY*Mg	0.87^{***}	0.81^{***}	0.74^{***}	0.77^{***}	0.63^{***}	0.79^{***}

***= significant at p < 0.001,

4.4. Discussions

Sorghum is one of the most import multipurpose crops worldwide mainly in arid and semi-arid areas. Sorghum genotypes that combine high yield with enhanced nutritional value are essential in achieving food and nutrition security in the area where sorghum is the stable food crop, which in turn, needs the knowledge of genetic nutritional diversity. The present study was accordingly conducted to evaluate the diversity of grain yield and nutritional quality traits of sorghum Farmers' varieties in Tigray, thereby exploring its worth for effective breeding and conservation programs, and to identify superior genotypes based on their ability to combine grain yield and other important nutritional traits.

In the present study, we found farmers' varieties that showed highly significantly higher grain yield and nutritional traits in each test environment and combined analysis. The higher performance of farmers' varieties could be due to their greater dry root-to-shoot ratio (Ali et al., 2009). As shown in Table 6.2, the five top genotypes were not in the same trend for all the traits such that different genotypes perform better for different traits. This suggests that the highest-performing genotypes for a particular trait could serve as parental sources for further breeding programs. Genotypes that contain iron and zinc better than the acceptable level which is >60 ppm for iron and >32 ppm for zinc (Chapke and Tonapi, 2016) can be used for bio-fortification programs (Andiku et al., 2022) to alleviate acute malnutrition deeply rooted in underdeveloped countries such as Ethiopia. From the present study, LR106, LR102, LR25 and LR16 can be selected for higher grain yield and starch zinc and calcium, LR23, LR45, LR38 and LR12 can be selected for higher zinc and iron content, and LR14, LR27, LR65 and LR57 can be selected for higher protein and starch contents. Nonetheless, selection in one trait may result in the reduction of the level of the other target trait (Yan et al., 2007), suggesting that the need to evaluate the genotypes based on their ability to combine grain yield with other important traits such as nutritional quality traits used in this study as suggested by (Yan and Frégeau-Reid, 2018). Interestingly, all traits studied showed a wide array of variability. In individual environment, the range of grain yield, protein, starch, ash, iron, zinc, calcium and magnesium were 8.5 (E1)-49.8q ha^{-1} (En4), 33.7% (En1)-77.2% (En3), 4.3% (En1) -14.6% (En4), 0.4% (En6)-3.8% (En1), 11.2 ppm (En1)-84.2 ppm (En1), 12.7 ppm (En3)- 63.2 ppm (En1), 125 ppm (En1)-415 ppm (En1) and

652.3 ppm (En1)- 1981 ppm (En1), respectively. Likewise, the combined environment data showed a range of 13.8-41.3q ha^{-1} (grain yield), 59.1-69.4% (starch), 9.5-11.2% (protein), 1.5-2.3% (ash), 29.7 - 43.7 ppm, (iron) 26.5-47.8 ppm (zinc), 210.2-289 ppm (calcium) and 932-1345.6 ppm (magnesium). The wide range showed in the value of the traits revealed that it is possible to distinguish among the genotypes for effective breeding activities. Similar to the present finding, earlier studies detected wide range of values for grain yield (Girma et al., 2020; Phuke et al., 2017), ash (Chung et al., 2011; Moharram and Youssef, 1995), starch and protein (Ng'uni et al., 2012; Shegro et al., 2012), iron and zinc (Gerrano et al., 2016; Makebe and Shimelis, 2023), calcium (Gerrano et al., 2016; Osman et al., 2022) and magnesium (Badigannavar et al., 2016; Ragaee et al., 2006) in sorghum genotypes.

The test genotypes showed highly significant variations ($p < 0.001$) for all studied traits in all individual environments. Likewise, the combined analysis showed strong significant variance (P<0.001) for all studied traits due to genotype (σ^2g), genotype by environment interaction (σ^2 g x e) and environments (σ^2e) with the exception that variance due to environment (σ^2e) had significant variation (<0.05) for calcium content. This indicates that sorghum Farmers' varieties collected from Tigray harbor high genetic variation useful for the development and deployment of nutritionally enhanced and high-yielding sorghum varieties. This agrees with the report by Hummer and Hancock (2015) who noted that enormous variations are available in Farmers' varieties that are evolved in Vavilov centers of crop origin and diversity such as Ethiopia. The large genotype by environment interaction (σ^2 g x e) variance relative to the genotype variance indicates the need to select for trait stability in the target environment. The high level of genetic variation for various quantitative traits identified in the present study could be attributed to the genetic constitution of the genotypes, varied agro-ecologies and environmental conditions that could affect mineral uptake translocation and distribution. Gene flow between wild and cultivated relatives could be also a likely reason for the high genetic diversity in sorghum Farmers' varieties (Tesso et al., 2008). The present results support the high genetic diversity of various sorghum traits reported earlier (Badigannavar et al., 2016; Makebe and Shimelis, 2023; Phuke et al., 2017 and Shegro et al., 2012).

The genetic variance (σ^2g) component is also helpful to estimate heritability such that high σ^2g implies minimal environmental effect on the trait and vice versa. According to the classification made by Robinson (1966), the magnitude of broad-sense heritability was higher ($H^2 > 0.9$) in each environment for all the studied traits indicating that the minimal environmental effect, and thus any of the traits can be used for selection (Bashir et al., 2014; Phuke et al., 2017)). The broad-sense heritability of the pooled over traits was medium ($H^2 > 30 < 60$) for protein ($H^2 = 0.4$) and zinc ($H^2 = 0.5$), and high ($H^2 > 0.6$) for the other studied traits. The medium to high broad sense heritability over environments indicates the possibility of effective selection among the genotypes for further breeding activities. The high broad sense heritability recorded in the present study also indicates these traits are controlled by the additive gene action, which could be improved through selection. As in this study, high to medium heritability in sorghum germplasm has been also reported for various agronomic and nutritional traits of sorghum by (Andiku et al., 2022; Phuke et al., 2017). As compared to the individual environment, the heritability of the pooled over analysis was reduced to the range from 0.4 (protein content) to 0.82 (grain yield). This is due to the strong effect of genotype by environment interaction (σ^2g x e) effect. This calls for the need to conduct the genotype by environment interaction analysis of the traits to identify high-yielding and stable genotypes.

Determinations of the association between grain yield and other nutritional quality traits of sorghum could play a pivotal role in reducing the widespread food and nutrition deficiencies, especially in the community deeply dependent on sorghum for their staple crop (Phuke et al., 2017). In the present study, both negative and positive significant associations between some of the traits were detected in the individual environments as well as in combined environments. However, the correlations were not in the same trend though out the individual environments. For instance, zinc content had a significant positive correlation with iron in En1, En2, En4 and En5 while significant negative associations of zinc and iron were recorded in En3 and En6. Besides, ash content had a significant positive association with zinc in En1, En4 and En5 whereas; zinc content had a significant negative association with iron concentration in En3. The variation in the association of traits in different environments might be due to variations in the nutrient content of the soil and genotype by environment interaction that may affect mineral adsorption and translocation of crops (Sankaran et al., 2009). In the pooled analysis, significant positive associations were detected in traits such as ash content with zinc, iron and magnesium contents, zinc with iron and grain yield, and calcium with grain yield. On the other hand, protein showed a significant negative association with iron, with ash, iron and zinc contents (Figure 4.1).

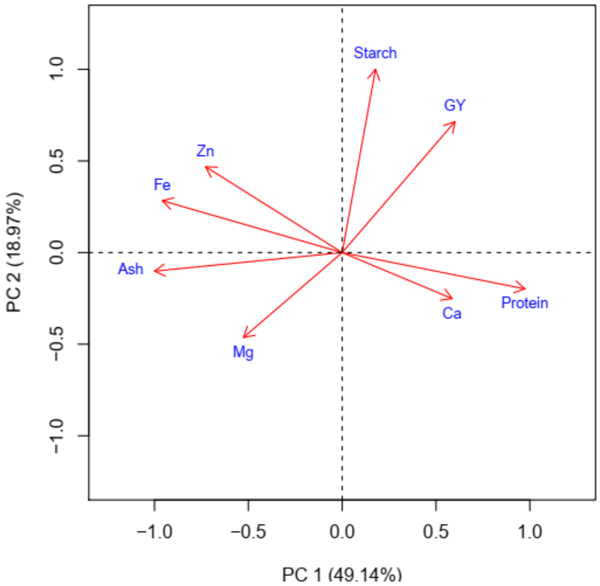

Figure 4.1. Scatter plot showing the association among grain yield and nutritional quality traits of sorghum genotypes evaluated in six testing environments of Tigray

The strong positive associations between traits might be due to common and overlapping quantitative trait loci (Kumar et al., 2016) suggesting that the traits can be improved concurrently through direct selection. In this case, the application of marker-assisted selection would be helpful for the selective introgression of targeted genes and genomic regions into the parental lines with high-yielding backgrounds to facilitate breeding activities. In line with the present study, earlier researchers noted a significant positive association between iron and zinc (Andiku et al., 2022; Shegro et al., 2012), and zinc and protein contents (Badigannavar et al., 2016; Gerrano et al., 2016; Ng'uni et al., 2012). Whereas negative associations were reported for grain yield with zinc and iron content (Andiku et al., 2022; Ashok Kumar et al., 2012), and calcium content with iron and magnesium content (Badigannavar et al., 2016). Growing and selection among large segregating populations could break the negative association of grain yield with other key traits reported in the present study as well as in another earlier research (Ambekar et al., 2011; Diatta et al., 2019).

One of the key challenges that hinder progress in the identification of superior varieties out of a population of genotypes is the unfavorable associations of key traits (Yan et al., 2007). To overcome this inconvenience, (Yan and Frégeau-Reid, 2018) introduced a new novel approach known as genotype by yield by trait (GYT) analysis. The GYT analysis is based on the concept that yield is the main objective and the other target traits are evaluated based on their value to combine with grain yield. In the present study, the GYT biplot (Figure 4.2) explores about 87.5% of the total variation indicating the suitability of the biplot to graphically display the data for further interpretation. The positive association between the traits as revealed by the acute angle (Figure 4.2A) and Pearson correlation coefficient (Table 4.7) is because all the yield by trait combinations have yield as a component that is the special feature of genotype by yield by trait (GYT) (Yan and Frégeau-Reid, 2018). The highly significant ($p < 0.001$) positive associations between the traits identified in the present study (Table 4.7) indicates that there is possibility of selection among the genotype based on their yield performance and nutritional quality. The finding of the present study agrees with the previous finding by Kendal (2019), Peixoto et al., (2022), Welderufael et al. (2023) and Yan and Frégeau-Reid, (2018) who reported strong positive association of various traits in oat, durum wheat, cotton and sorghum genotypes, respectively.

The ‘which-won-where’ view of the GYT biplot (Figure 4.2 B) was useful to demonstrate the trait profile of the genotypes. The genotypes located in the same sector are closely related, and different genotypes are associated with different traits in each sector. The polygon peak contains the most effective genotypes (vertex genotypes) associated with the trait/s profile in each sector (Yan and Tinker, 2006). In this case, genotypes such as LR12, LR25, LR23 and LR 106 were the best genotypes in combining grain yield with zinc, ash and iron contents, while LR102, LR103, LR107 were the best genotypes in combining grain yield with protein and calcium, and genotype LR75 and LR28 were best genotypes in combining grain yield with starch and magnesium.

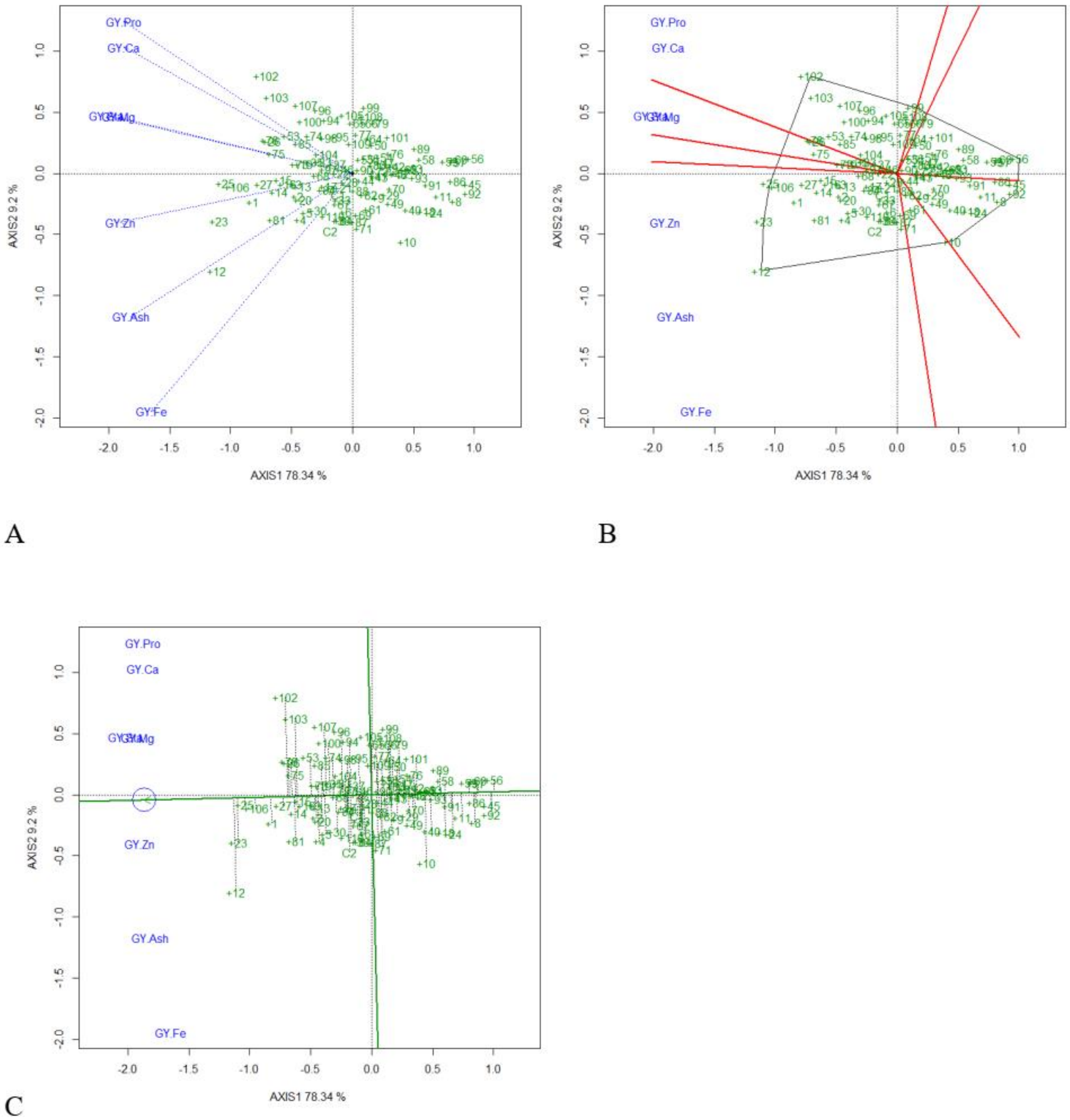

Figure 4.2. GYT biplot of grain yield and nutritional traits of sorghum genotypes evaluated in six environments of Tigray.

A = correlation between traits, B = ‘which-won where’ view of the traits, and C = the average tester coordinator (ATC) of the traits

The line perpendicular to the average tester axis (ATA) (Figure 4.2C) separates genotypes with below-average means (example: LR56, LR45, LR11, LR92, LR60 and LR57) from those with above-average means (example: LR12, LR23, LR25, LR106, and LR1). Genotypes far from the ideal center are not desirable, whereas genotypes displayed near/at the ideal center are superior genotypes (Yan and Rajcan, 2002). Therefore, farmers' varieties such as LR12, LR23, LR25, LR106, and LR1 are superior genotypes whereas, LR56, LR45, LR57, LR92, LR60 are less performed farmers' varieties. Genotypes holding higher mineral content with high-yielding backgrounds can improve the nutritional value of the crop (Badigannavar et al., 2016). In the present study, ten promising and five bottom farmers' varieties were identified based on the overall superiority index (Table 4.8) and average tester coordinator (ATC) view of the GYT biplot. These genotypes could contribute significantly to overcoming malnutrition in arid and semi-arid areas including Tigray. As in this study, Merrick et al. (2020), Peixoto et al. (2022), Welderufael et al. (2023) and Yan and Frégeau-Reid (2018) also stated the ATC view of the GYT biplot is an instrumental to rank based on overall superiority and to show their overall superiority and their strengths and weaknesses. They can be also sources of parental lines for further breeding activities. Our finding confirms that the Ethiopian sorghum farmers' varieties often harbored various important traits explained by earlier researchers (Enyew et al., 2022; Girma et al., 2020; Mamo et al., 2023; Shegro et al., 2013).

Table 4.8. Top ten promising sorghum farmers' varieties identified using GYT index

	Genotype	gy*sta	gy*pro	gy*ash	gy*Zn	gy*Fe	gy*Ca	gy*Mg	(Av.SI)
Top ten genotype									
1	LR12	1.69	1.30	3.14	2.64	3.14	0.80	2.05	2.11
2	LR23	1.59	1.18	1.87	3.58	2.40	1.91	1.84	2.05
3	LR25	2.37	0.76	1.75	2.48	1.60	2.28	2.34	1.94
4	LR106	1.98	2.16	1.63	2.30	1.91	1.49	1.01	1.78
5	LR1	1.58	1.92	2.26	1.52	1.54	0.52	1.42	1.54
6	LR27	1.47	0.91	0.96	1.83	1.35	1.03	1.94	1.36
7	LR102	2.20	2.33	0.35	0.38	-0.09	2.37	1.49	1.29
8	LR78	1.54	2.07	1.00	0.92	0.64	1.01	1.63	1.26
9	LR26	1.52	0.70	0.70	1.55	0.43	2.16	1.46	1.22
10	LR81	0.36	1.15	2.35	1.48	1.38	0.96	0.64	1.19
Bottom five genotypes									
1	LR57	-1.41	-1.31	-1.62	-1.64	-1.65	-1.76	-1.88	-1.61
2	LR60	-1.59	-1.40	-1.69	-1.68	-1.61	-1.31	-2.13	-1.63
3	LR92	-1.97	-2.01	-1.78	-1.31	-1.35	-2.02	-2.36	-1.83
4	LR45	-2.33	-2.20	-1.47	-1.02	-2.00	-1.98	-1.85	-1.83
5	LR56	-1.87	-1.68	-1.84	-1.69	-2.11	-1.97	-1.98	-1.88

Av.SI = average superiority index

4.5. Conclusions

Identification and selection of superior sorghum genotypes for grain yield and nutritional traits is essential to tackle the challenges of acute food shortage and malnutrition in arid and semi-arid areas like Tigray. This study identified sorghum farmers' varieties with higher mean performance, large and useful genetic variations for grain yield and nutritional quality traits. Accordingly, various Farmers' varieties were selected as breeding parents for each of the traits studied. All the traits studied were highly heritable in each environment ($H^2 > 0.9$) and moderate to highly heritable in the pooled environments implying the possibility of effective selection among the genotypes for further breeding activities. The study further found strong significant positive and negative associations between some of the traits in each environment as well as in combined environments. Nonetheless, highly significant positive ($p < 0.001$) associations were detected in the genotype by yield by trait combinations. The significant positive association between traits suggests that the traits can be improved concurrently through direct selection. Whereas, the strong negative association between traits implies the need for growing and selection among large segregating populations to break the unfavorable association. Using average tester coordination (ATC) view of GYT biplot and overall superiority index (Mean SI) of the GYT analysis, ten promising sorghum Farmers' varieties were selected for direct use or breeding programs in arid and semi-arid areas in general and in Tigray in particular.

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CHAPTER FIVE

Analysis of Sorghum Social Seed Network in Tigray, NorthEthiopia

Abstract

Proper understanding of the nature of seed exchange among farming communities is fundamental to achieving a sustainable seed system and maintaining crop genetic resources. The objective of this study was to investigate sorghum (*Sorghum bicolor*) seed sources and analyze their network flow among farmers in Tigray in northern Ethiopia. A survey was conducted using a semi-structured questionnaire, involving 153 sorghum household farmers selected randomly from six villages: namely Gezaadara, Medabe, Gezameker, Waekel, Munira and Gandostela. Farmers who played major roles in the sorghum seed exchange network were identified using social seed network analysis. Results showed the major means for the acquisition of sorghum seeds in Tigray by farmers were through exchanging seeds of different varieties, bartering, as gifts, purchasing from local markets using cash, and seed loans which indicates that sorghum farmers in Tigray are over-reliant on the informal seed exchange system. Bartering and own-saved seeds were the dominant sources of sorghum seed for farmers throughout the study area and seed exchange network in Tigray is active and hyper-localized as the majority of exchanges took place within their villages than beyond. Moreover, farmers who were identified as nodal and bridging farmers in the seed network conserved more local sorghum farmers' varieties and had better access to quality and quantity of sorghum seeds than the non-nodal farmers. Social capital such as cultural norms, trust, and farmers' desire to increase sorghum production in the community were the fundamental drivers for farmer sorghum seed exchange. Households distinguished as nodal farmers who had high bridging roles could also act as entry points for improved sorghum seed exchange interventions in Tigray.

Keywords: Seed exchange, social capital, seed availability, seed network

5.1. Introduction

Seeds are genetic resources that carry plant genetic diversity that is vital for breeding and crop improvement (McGuire and Sperling, 2016). Seeds are valuable assets not only for farmers but for the global society as a whole due to interdependence on genetic resources. Seed is considered as the most important element of the sorghum value chain in Eastern Africa (McGuire and Sperling, 2016). Seed availability, access, affordability, adaptability of quality, and farmer-preferred crop varieties are determinants of the efficiency and productivity of associated technologies in increasing crop production. Better farmer access to quality seed is key, not only to increased crop productivity but also to conserving crop genetic resources (Coomes et al., 2015; Okry et al., 2011). There are three types of seed systems through which farmers acquire seeds and other planting materials namely, the formal, the informal and the integrated seed exchange system. The formal seed exchange system is distinguished by its clear-cut activities, starting with formal plant breeding, varieties release and regulations to maintain varietal identity and purity; as well as guarantee physical, physiological and sanitary quality (Atilaw et al., 2016). Seed marketing under this system takes place through officially recognized seed outlets and by way of national agricultural research systems (Kansiime and Mastenbroek, 2016).

The informal type of seed system is also called a local seed system. Through this system, the seeds are managed by farmers using their indigenous knowledge and capacity (Almekinders and Louwaars, 2002). Seed transactions are usually through barter, local markets, exchange, farmer's own-saved seeds, gifts and loans often in kind (McGuire, 2007). The informal seed system accounts for the largest share (>80%) of seed sources throughout the world, mainly in developing countries (Louwaars and De Boef, 2012). In Ethiopia, about 95% of farmers' sorghum seed requirements are fulfilled mainly through the informal seed system (Adugna, 2014).

The integrated seed system is characterized by entrepreneurial farmers and farmer groups that produce and market crops that are not covered by the formal seed system (Sperling et al., 2014). The integrated seed system is an inclusion of both formal and informal seed systems and receives high technical support from research, non-government organizations (NGOs) and seed projects, and some regulatory oversight from bureaus of agriculture (Sperling et al., 2014).

In the case of the informal seed system, farmers build unique social seed networks to access seed and related information, and thus, ensure the availability of sufficient planting materials (Abay et al., 2011; Subedi et al., 2003). A social seed network refers to the interconnection of farmers to exchange seeds and share seed-related experiences (Subedi *et al*., 2005). The process of analyzing the features and mechanisms involved in the networks is known as social seed network analysis (SSNA) (Subedi et al., 2005). It is a mathematical and graphical illustration of farmers' role in which the actors who play what and the links from where and to where can be easily justified (Poudel et al., 2015; Ricciardi, 2015). Using SSNA, it is possible to identify farmers who plaid major roles in the seed exchange network (Abay et al., 2011). Unfortunately, information pertinent to the social sorghum seed network and the assets that might sustain local exchanges of sorghum seed is generally limited in Ethiopia. The objective of this study were to investigate sorghum (Sorghum bicolor) seed sources and their flow network among farmers and factors that determine the seed exchange in Tigray, in northern Ethiopia.

5.2. Methodology

5.2.1. Study sites

This study was carried out in two districts of Tigray, north Ethiopia, namely, Raya Azebo and Tahtay Adyabo. Raya Azebo is located in the southern Zone of Tigray, while Tahtay Adyabo is found in the northwestern Zone of Tigray (Figure 1.4). The characteristic features of the two study areas are indicated in Table 5.1. The districts were selected purposely based on their status of high sorghum production and their possession of local seed flow and its social seed networks. Three villages were subsequently selected from each district for the survey. From Raya Azebo, the villages included Waekel, Gandostela and Munira; while from Tahtay Adyabo district, they included Gezameker, Medabe, and Gezaadre. A village is the smallest administrative unit in Ethiopia.

Table 5. 1. Characteristic features of the study sites used for sorghum social seed network analysis in Tigray, North Ethiopia

Characteristics	Raya Azebo	Tahtay Adyabo
Major crop grown	sorghum, teff	sorghum, sesame, millet,
Major farmers' varieties of sorghum grown (local name)	abaaro, kodem, zeriehadis, gano, dengle, gedalit, chibrak jamuye	zeriegebru, dagnew, merowey, wediaker, chimroy, getsharas, coden, shilquit, ganseber,
Altitude (m.a.s.l.)	1000-1660	700-1400
Mean temperature (^{O}C)	25-35	26.5-37
Mean annual rainfall (mm)	400-900	350-850
Main farming system	Subsistent farming	Subsistent farming

5.2.2. Survey process:

This study was carried out from October 2018 to November 2019. A total of 153 household heads selected through a snowball sampling method, were interviewed using a semi-structured questionnaire, supplemented by focus group discussions (FGDs). The snowball sampling method has been applauded as an effective approach to social network analysis (Subedi *et al*., 2003). The questionnaire was originally prepared in English and translated into Tigrigna (the main local language in Northern Ethiopia). Oral translators were also engaged to translate from Tigrigna to Kunama for the Kunama Ethnic group located in the Tahtay Adyabo district. Five individuals who spoke both languages fluently were used to ensure the correctness of the translations.

The survey followed three main steps; the first step was a reconnaissance survey coupled with a discussion with eight agricultural experts, six community leaders, and ten elders. Discussion with these groups was done to gain background insights about sorghum cultivation in the study areas. In the second step, 36 sorghum farmers (50% females) were selected purposely. Based on the information obtained during the baseline survey, these farmers were technology adopters and expected to command a good sorghum production experience. Since these were the first participants to be engaged in the study, they acted as 'entry points' for the social network analysis for sorghum in Tigray; thus they were designated as first-batch farmers. Following the group discussion, an in-depth interview was done at the household level with the first-batch farmers, using the following criteria: (i) their source of sorghum seed used in the previous growing season, (ii) persons shared sorghum seed within the previous season, (iii) main seed sources for sharing seed, (iv), sorghum varieties exchanged, (v) the quality and quantity of sorghum seed the exchanged (vi) factors affecting the sorghum seed exchange process. These first-batch farmers listed at least 151 farmers as their seed exchange partners. Subsequently, we termed these 151 farmers as the “second-batch farmers”, and subjected them to interviews using the same semi-structured questionnaire.

In the third step, 117 of the second-batch farmers were asked to name their seed exchange partners. The number of second-batch farmers was reduced from 151 to 117 because 20 farmers were already interviewed during the first step and the rest (14 farmers) were not available due to various reasons. The second-batch farmers, in turn, listed 309 (third-batch) farmers as their seed exchange partners. The third batch of farmers were not interviewed due to resource limitations. However, they were included in the seed networks, seed sources and flow analysis based on the information obtained from the first and second-batch farmers, as they were seed exchange partners. For the data on the socioeconomics of farmers in the sorghum seed networks and factors that influenced farmers to participate in the sorghum seed exchange sorghum, only the first and second-batch farmers’ (a total of 153 farmers) were interviewed. Likert scales were used to explore the level of seed quality (1 = excellent quality, 2 = very good quality; 3 = Good quality, 4 = fair quality, 5 = poor quality), and seed quantity of sorghum farmers access (1= excess, 2 = sufficient, 3 = moderate, 4 = less than required, and 5= acute shortage).

5.2.3. Socioeconomic characteristics of respondents

Land size per household ranged from 0.2 to 4.5 ha while mean age of the respondents was 54 years, with a minimum and maximum age of 31 and 89 years. Among the 153 households interviewed, 37 (11.1%) household heads were females. The majority of the respondents (76.5%) were illiterate as they did not have formal school; 19.6% attended elementary school; and 3.9% attended high school (Table 5.2).

Table 5.2. Socioeconomic characteristics of the households involved in the study of sorghum seed exchange networks in Tigray, North Ethiopia

Characteristics	Level	N	%	*P-value*
Sex	Male	97	63.0	
	Female	56	37.0	0.001
Education status	Illiterate	117	76.5	
	Elementary	30	19.6	0.001
	≥High school	6	3.9	
Land size (ha)	<0.5	68	44.4	
	0.5-1	44	28.8	0.001
	1-2	28	18.3	
	>2	13	8.5	
Age (years)	< 45	43	28.1	
	45-60	75	49.0	0.001
	>60	35	22.9	

5.2.4. Data analysis

Data obtained were triangulated and checked for consistency before analysis. The primary data collected were coded and entered into Microsoft Office Excel; before analysis using UCINET and Net draw software package (Borgatti et al., 2002). While coding the data, farmers were considered as node data, whereas the seed exchange modes and the varieties under exchanged were used as tie data. The role of the farmers in the network was computed using degree and betweenness centrality measures as described by (Abay et al., 2011). A farmer with more direct connections with other persons in the network is called a nodal farmer (Abay et al., 2011) but there are no clear-cut standards for such a category (Poudel et al., 2015). Bridging farmers refers to those who can exchange seeds and information through their direct and indirect connections (Abay et al., 2011)

Descriptive statistics about the respondents’ socioeconomic characteristics, seed exchange means, seed flow, sorghum varieties maintained per household, and motivations and discouragement to exchange sorghum seed were analyzed using the Statistical Package for Social Scientists version 20.0 (SPSS) software. Significant treatment mean differences were separated using the T-test and Chi-square test for the numerical data and categorical data, respectively.

5.3. Results

5.3.1. Sorghum seed flow and seed sources

Seed exchange with non-relatives was the most dominant seed source (47%) among sorghum farmers in Tigray, followed by their own-saved seed (Table 7.3). Nevertheless, seed exchange with relatives and friends, gifts, local grain markets and seed loans played a pivotal role in the seed flow of sorghum seeds throughout the villages (Table 7.3).

5.3.2. Farmers’ access to quantity and quality seeds

Farmers were asked if they have access to sufficient quantities of sorghum seed at appropriate time. More than half (51%) of the respondents stated that the sorghum seeds were easily available in sufficient quantity whereas 18% of the farmers stated that sorghum seeds were moderately available and just sufficient (Figure 5.1). Furthermore, excess sorghum seed access was reported by 9% of the respondents. On the other hand, 14% and 8% of the respondents claimed that they had access to less than required and acute shortage of sorghum seeds, respectively (Figure 5.1).

Table 5.3. Modes of sorghum farmers' seed sources in Tigray

Nature of seed sources	Tahtay Adyabo district					Raya Azebo district			
	GM	Me	GA	Un	Total (%)	WA	Gn	Mn	Total (%)
Own saved	3	9	8	0	20	10	13	11	34
Bartering with non-relatives	10	17	19	1	47	18	9	10	37
Bartering with relatives	2	6	3	0	11	3	2	1	6
Gift/friend	1	4	4	0	9	5	6	1	12
Local grain market	2	3	4	0	9	4	1	2	7
Seed loan	1	2	2	0	5	2	1	1	4
P value					0.00				0.00
Mode of exchanges seed exchanges within villages									
Bartering with non-relatives	12	20	25	0	57	28	13	12	53
Bartering with relatives	2	7	5	0	14	3	3	3	9
Gift/friend	2	6	7	0	15	8	10	2	20
Local market	2	2	4	0	8	6	2	3	11
Seed loan	1	2	3	0	6	3	2	2	7
P-value					0.00				0.00
Mode of exchanges seed exchanges outside villages									
Bartering with non-relatives	15	24	17	4	60	28	13	12	52
Bartering with relatives	5	7	1	0	13	3	3	2	8
Gift/friend	1	2	1	0	4	8	10	2	21
Local market	4	7	5	0	16	6	2	3	12
Seed loan	1	5	1	0	7	3	2	2	7
P-value					00				00

GM = Gezameker, Me = Medabe, GA = Gezaadra, WA = Waekel, Gn = Gandostela, Mn = Munira, uk = unknown village,

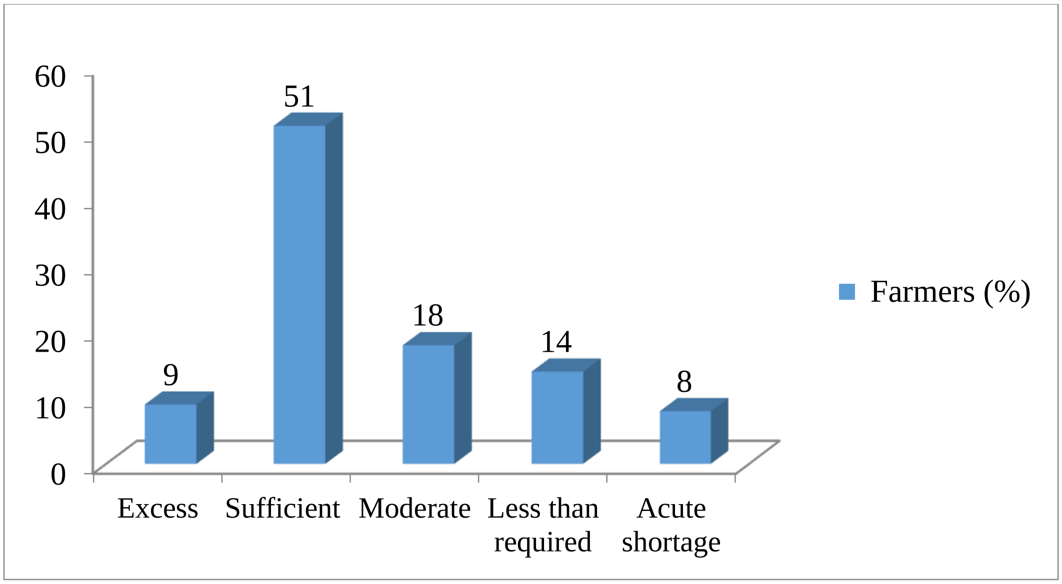

Figure 5.1. Farmers' access to sorghum seed quantity in Tigray

Concerning the quality of the seeds they access (Figure 5.2), 19%, 34%, and 16% of the respondents mentioned that they access excellent, very good, and good quality sorghum seed from their seed network, respectively. On the other hand, fair-quality seeds, and poor-quality seeds were mentioned by 15% and 16% of the respondents, respectively.

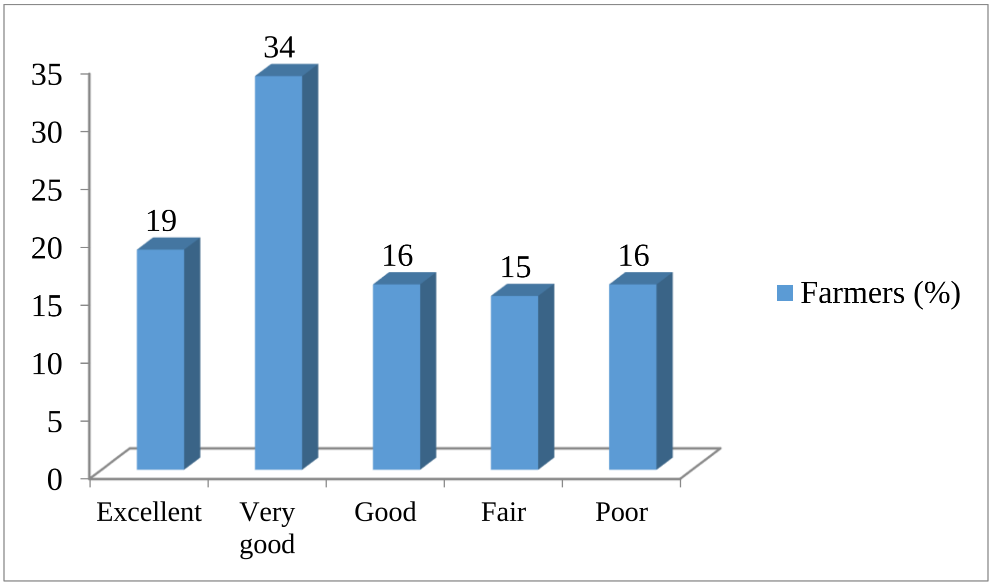

Figure 5.2. Farmers' access to sorghum seed quality in Tigray

5.3.3. Seed exchange events

A total of 384 seed exchange events were recorded in the present study. Most (79%) of the seed exchange were within villages, whereas dismal (21%) were executed outside villages (Table 5.4).

Table 5.4. Sorghum seed exchange events (N) within and outside study villages in Tigray

Villages	Within village	Outside village	Total N	*P value*
Waekel	64 (85%)	11(15%)	75	
Gandestela	56(84%)	11(16%)	67	
Munira	44(86%)	7(14%)	51	
Gezameker	28(74%)	10 (26%)	38	0.00
Medabe	48(71%)	20(29%)	68	
Gezaadra	63(74%)	22(26%)	85	
Total	303 (79%)	81(21%)	384	

5.3.4. Flow of sorghum varieties:

The distribution of farmer grown-varieties sorghum varied significantly across the villages under study (Table 7.5). Ten varieties were the most frequently exchanged of all the sorghum varieties presented by the respondents. In Raya Azebo district, the most popular varieties were abaaro, codem, zerihadis, dengle and jamuye; while in Tahtay Adyabo district, they included wediaker, zerigebru, dagnew, merowey and chimroy. In addition, there were significant variations ($p < 0.05$) in the farmers' varieties among villages in each particular district. For instance, abaaro was the dominant variety in all the villages in Raya Azebo; while merowey and zeriegebru were the more popular varieties in Gezameker, Medabe and Gezaadre (Table 5.5).

Table 5.5. Flow of sorghum varieties in Tigray

Village	Tahtay Adyabo					
Villages	Sorghum varieties (Local varieties)					
	Wediaker	Zerie Gebru	Dagnew	Merowey	Chimroy	Others
Gezameker	1	4	2	7	3	1
Medabe	2	13	8	7	9	2
Gezaadre	2	16	7	10	4	1
Total (%)	5	33	17	25	16	4
P value			<0.001			
District	Raya Azebo					
	Abaaro	Codem	Zerihadis	Dengle	Meshala	others
Waekel	17	6	8	8	2	1
Gandestola	19	4	5	4	2	0
Munira	9	6	2	3	1	0
Total (%)	45	17	15	16	6	1
P value			<0.001			

5.3.6. Centrality measures

The degree of centrality and betweenness centrality of farmers who played active nodal, bridging and/or a combination of the roles are presented in Table 5.6. The average degree centrality and betweenness centrality in Tahatay Adyabo district were 3.3 and 5.0, respectively, with a network centralisation of 1.2%. In Raya Azebo district, the average degree centrality and betweenness centrality were 2.6 and 3.5, respectively, with a network centralization of 2.2%. There were 37 households, of whom 14 had both nodal and bridging roles, 12 had nodal roles, and 11 had bridging roles across the study districts (Table 5.6). A farmer was considered nodal when he/she had direct connections with more than five farmers in the seed network. There were only eight females (23%) among the 37 nodal and/or bridging farmers (Table 5.6).

Table 5.6. Nodal and bridging farmers present among sorghum seed networks across villages of Tigray

		Centrality measures				
Farmer (node)	Villages	Degree centralities	Out degree	In degree	Betweenness centralities	Position hold in the network
8	Gandostela				23	B
10	Gandostela	9	9	0		N
15	Gandostela	6	6	5		N
14	Gandostela	8	7	1		N
20	Gandostela	6	9	0		N
42	Gandostela	8	6	2	65	NB
152	Gandostela				38	B
29	Munira	8	7	1		N
30	Munira	8			38	B
24	Munira	9	7	2		N
1	Waekel	8	5	3	90	NB
2	Waekel	6	5	1	30	NB
3	Waekel	7	6	1	36	NB
33	Waekel	10	8	2	52	NB
35	Waekel				24	B
43	Waekel	7	6	1	24	B
47	Waekel	21	21	0		N
191	Medabe				28	NB
193	Medabe	6	5	1	20	NB
192	Medabe				21	B
195	Medabe	8	8	0		N
198	Medabe	9	8	1		N
211	Medabe	8	4	4	63	NB
224	Medabe				30	B
229	Medabe	6	3	3	39	NB
236	Medabe	6	5	1		N
184	Gezameker	6	3	3	51	NB
192	Gezameker				21	B
210	Gezameker				28	B
207	Gezameker				40	B
358	Gezameker	6	4	2	20	NB
359	Gezaadre	10	10	0		N
360	Gezaadre	7	4	3	30	NB
370	Gezaadre	9	8	1	34	NB
390	Gezaadre	13	12	1	23	NB
204	Gezaadre				36	B
385	Gezaadre	7	1	6		N

N = a farmer with a nodal role; B = a farmer with a bridging role; NB = a farmer with both a nodal and bridging role in the seed network

5.3.7. Seed exchange network maps

The maps generated for the degree centralities for sorghum seed flow networks across villages in the districts are presented in Figure 5.3 and 5.4, respectively. According to the network maps, in addition to the main network of seed flow, there were sub-networks connected by nodal and bridging farmers. Isolated farmers were not part of the seed networks. Many farmer-grown varieties were exchanged within the farmers' seed network.

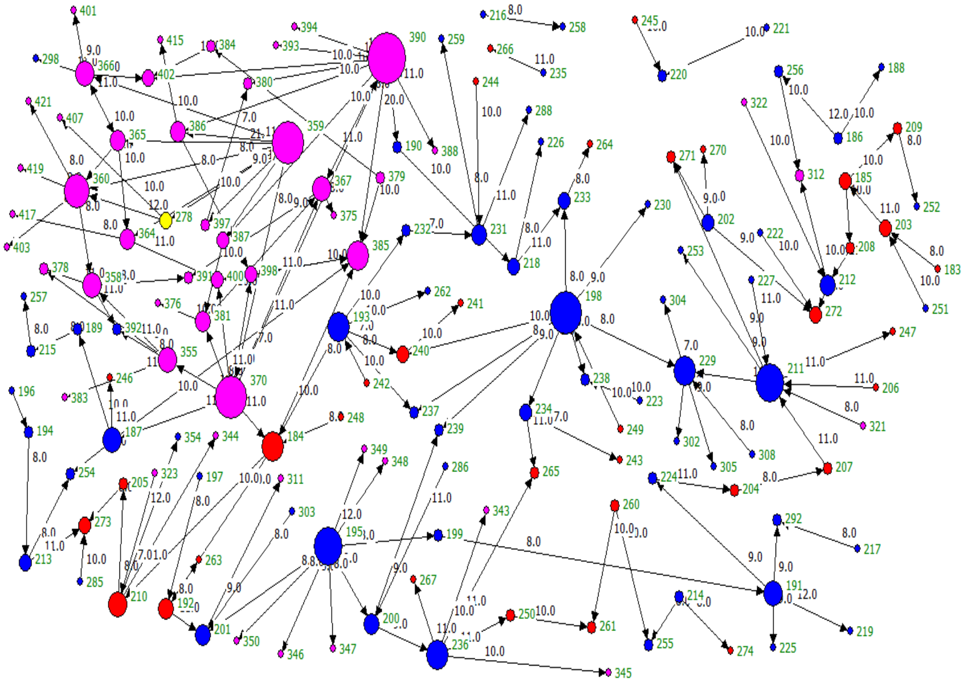

Figure 5.3. Famers' seed networks map for Tahtay Adyabo district in Tigray in North Ethiopia.

Node size (dots) is an indication of the degree of centrality of the households such that the larger the size of the node, the higher the centrality and the greater the number of direct connections with other households in the network. Arrows indicate the direction of the seed flow; while node color indicates the location of the households (red = Medabe; blue = Gezaadra; pink = Gezameker; yellow = unknown village), the green numbers indicate the codes for the households and the black numbers indicates the variety type exchanged (7.0 = Wediaker; 8.0 = Zeriegebru; 9.0 = Dangew; 10.0 = Merowey; 11.0 = Chimroy; 12.0 = Other Varieties)

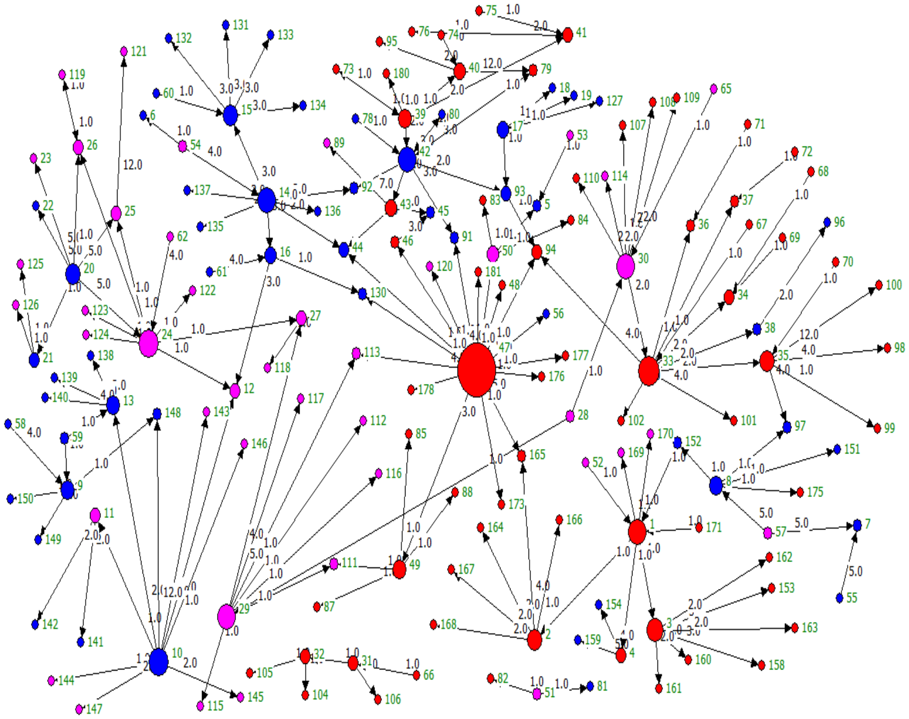

Figure 5.4. Farmers' sorghum seed network map for Raya Azebo district in Tigray in North Ethiopia.

Node size is an indication of the degree of centrality of the households such that the larger the size of the node, the higher the centrality and the greater the number of direct connections with other households in the network. The node colour shows the villages of the households (red = Waekel; blue = Gandestola; pink = Munira). The arrows show the direction of the seed flow from one household to the other. The green numbers indicate the code for the households and the black colors show the type of sorghum varieties transacted (1.0 = abaaro; 2.0 = kodem; 3.0 = zeriehadis; 4.0 = meshalla; 5.0 = dengle; 12 = others)

5.3.8. Sorghum varieties maintained per households

Farmers were asked to list the number of sorghum varieties they maintain. The varieties maintained per household varied from zero (households with no varieties conserved) to seven (one household retains seven sorghum varieties) with a mean of 1.91 varieties per household (Table 5.7). The nodal farmer maintains more sorghum varieties (an average of 3.08 per household) as compared to the none nodal farmers (an average of 1.53 per household). Sixty-seven (44%), 42 (27%), and 25 (16 %) households retain one, two, and three varieties, respectively which occupies 87% of the total farmers interviewed. Moreover, two households had maintained six varieties. Furthermore, households identified as nodal and/or bridging farmers have also been found to conserve a greater number of sorghum varieties (mean = 3.08) as compared to other farmers (mean = 1.53) (Table 5.7).

Table 5.7. Frequency sorghum varieties retained per household in six villages of Tigray

Number of Sorghum varieties per HH	Total HH N=153	HH holds a specific position, N = 37	Nonnodal HH N = 116
0	5 (3%)	0(0%)	5(4%)
1	67(44%)	6(16%)	61(53%)
2	42(27%)	7(19%)	35(30%)
3	25(16%)	13(35%)	12(10%)
4	6(4%)	4(11%)	2(2%)
5	5(3%)	4(11%)	1(1%)
6	2(1%)	2(5%)	0(0%)
7	1(1%)	1(3%)	0(0%)
Mean	1.91	3.08	1.53

HH, households

5.3.9. Nodal farmers versus non-nodal farmers' access to sorghum seeds

For statistical and discussion purposes we grouped the nodal and connector farmers under the term 'nodal farmers' whereas the farmers other than the nodal farmers were treated as non-nodal farmers. The response of nodal farmers and non-nodal farmers concerning the quantity and quality of sorghum seeds usually accessed through their networks were compared using a 1-5 Likert scale. Accordingly, 8(22%), 17(46%), and 12(32%) of the nodal farmer's access to excess, sufficient, and moderate amounts of sorghum seeds, respectively, (Table 5.8) revealing that nodal farmers have no problem with the quantity of sorghum seeds for sowing season after season. On the other hand, 6(5%), 61(53%), and 16(14%) of the non-nodal farmers cited that they access excess, sufficient, and moderate amounts of sorghum seeds, respectively (Table 5.8). Moreover, more proportion of the nodal farmers’ access higher-grade seed quality as compared to the non-nodal farmers (Table 5.8). To some proportion, poor quality seed, and seed shortages were claimed by the non-nodal farmers.

Table 5.8. Nodal vs non-nodal farmers’ access to sorghum seed quantity and quality in Tigray

Access	Scale	Nodal farmers, N = 37	Non-nodal HH N = 116
Access to seed quantity	Excess	8 (22%)	6 (5%)
	Sufficient	17 (46%)	61 (53%)
	Moderate	12 (32%)	16 (14%)
	< required	0	21 (18%)
	Acute shortage	0	12(10%)
Seed quality grade	Excellent	16 (43%)	14 (12%)
	Very good	11 (30%)	41 (35%)
	Good	10 (27%)	14 (12%)
	Fair	0	23 (20%)
	Poor	0	24(21%)

5.3.10. Factors influencing sorghum seeds exchange

Several factors significantly ($P < 0.001$) motivated farmers to exchange sorghum seeds with other farmers. The major ones included (i) long-standing culture of seed exchange (87%), (ii) trust in the quality of farmer-saved seed (69), and (iii) a desire to increase productivity at the household and community level (65%) (Table 5.9). Other factors such as ease of mutual farmer-farmer assistance (44%), replacement of non-performing varieties (23%), previous natural and manmade factors leading to loss of varieties (44%), ability to create and maintain friendship (33%), adoption of new varieties (22%), for diverse culinary use (21%), and ease of information access from farmers (23%) also motivate farmers to exchange sorghum seeds in Tigray (Table 5.9).

Table 5.9. Reasons for motivation of farmers to exchange sorghum seeds in Tigray

Motivating reasons	Frequency	Percentages	*P-value*
To replace existing varieties	35	23	
To trace back lost varieties	67	44	
To increase productivity in the community	99	65	
Culture to exchange seed	133	87	<0.001
Helping each other	68	44	
Friendship	51	33	
To adopt new varieties	34	22	
Trusting farmers’ seed	105	69	
For diverse culinary purposes	32	21	
Ease of information access	35	23	

The main challenges presented by respondents related to sorghum seed exchange in Tigray included (i) inferior quality seed in return (51%), (ii) increased farmer dependence on others for seed (46%), (iii) time required for seed exchange (39%), (iv) unwillingness of some farmers to share seeds (27%), (v) increased workload due to the seed exchange process (46%), (vi) lack of guarantee for seed quality (25%), and (vii) discrimination of some farmers during sharing seeds (6%) (Table 5.10).

Table 5.10. Factors that influenced sorghum seed exchange in Tigray

Challenges	Frequency	Percentages	*P-value*
Time-consuming	59	39	<0.001
Inferior quality seed in return	78	51	
Farmers' dependency	71	46	
Unwilling farmers to exchange seed	42	27	
Increase workload	46	30	
Lack of guarantee	39	25	
Discriminations	9	6	

5.4. Discussion

5.4.1. Characteristics of sorghum seed sources and flows

It is clear from this study that the major means for the acquisition of sorghum seeds in Tigray by farmers were through exchanging seeds of different varieties, barter-trade, as gifts, purchasing from local markets using cash, and seed loans (borrowing seeds for reimbursement after the next harvesting). All these characteristics could be due to the social and cultural customs of sharing seeds and the long history of cultivations of farmer-preferred local sorghum varieties, which in turn, implies that sorghum farmers in Tigray are over-reliant on the informal seed exchange system. The low adoption rate of improved varieties of sorghum in Ethiopia, which is only 1-2 % (Adugna, 2014) may also indicate the failure of the formal seed system to deliver farmer-preferred varieties. Besides, cases of better yields by Farmers' varieties have been reported compared to improved varieties (Welderufael et al., 2023). This emphasizes the need for careful attention to different seed intervention strategies in Tigray including the promotion of farmer-preferred sorghum varieties through quality-declared seed systems and integrating the local seed systems with the formal seed systems. Other researchers have also underscored the significance of integrated seed systems in fulfilling the seed requirement of farmers (Sperling et al., 2014).

Bartering of sorghum seeds accounted for the largest share of sorghum seed sources for the farmers in both the study districts (Table 3). Moreover, more respondents tended to barter sorghum seed with non-relatives (47%), particularly in Tahray Adyabo; compared to bartering seed with relatives. Similar reports exist elsewhere for seed exchange of a range of crops. For instance, Otieno et al. (2021) reported that East African farmers use informal seed systems as primary seed sources for crops such as sorghum, finger millet and beans.

Own saved seed was the second most important source of sorghum seeds for network exchange. in both districts; accounting for 20 and 37% in Tahtay Adyabo and Raya Azebo, respectively Earlier finding similarly noted that Ethiopian farmers often saved their seeds for the next and other seasons (Thijssen et al. 2008). Farmers accessed sorghum seed from these sources because it was easily available in their stock and they were familiar with agronomic traits, cultivation and culinary purposes. It also saved their time spent accessing seeds from neighbors or local markets. However, farmers isolated from other seed and information sources may resort to planting seeds of low-quality grades. It is, therefore, important to capacitate farmers on seed selection, cleaning and storage as highlighted by (Abay et al., 2011). The barely important sources of sorghum seeds in the form of gifts, from the local market and as seed loans in Tigray could be attributed to the over-reliance of Tigray sorghum farmers on the informal seed systems. This emphasizes the need for the establishment of local seed businesses to support the local market to fulfill the sorghum seed requirements of farmers in Tigray

5.4.2. Farmers’ seed access

Farmers' seed access to sufficient and farmer-preferred varieties is a precursor to achieving food security and sustainable livelihood for smallholders. Investigating seed access at the household level in the local seed sources is crucial to design effective seed intervention strategies (McGuire, 2007). This study revealed that most of the farmers in Tigray access locally adapted sorghum varieties at sufficient quantity and quality levels through the local seed system. However, considerable proportions of the farmers have encountered lower quality and shortage of seeds at the required quantity in their seed network. In line with this study, (McGuire, 2007) found variation among households to seed access in Harerghe, Ethiopia. To overcome such seed shortfalls, interventions like strengthening the social seed networks through training on seed saving and seed management practices, promoting farmers with the decisive role to share their experience on seed saving, storage and other agronomic activities with other farmers, and establishing local seed banks which could serve as a reservoir of diversity of crops and varieties are necessary (Abay et al., 2011; Louwaars and De Boef, 2012; Poudel et al., 2015). Integrating the local seed system with the formal seed sector is also crucial to enhance subsistence farmers' access to seed at the appropriate time, required quality and quantity (Kansiime and Mastenbroek, 2016; Louwaars and De Boef, 2012; Sperling et al., 2014).

5.4.3. Livelihood assets as drivers for sorghum seeds exchange

The main reason for sorghum seed exchange in Tigray was embedded in the culture. This was evidenced by the belief that “seed belongs to the earth and thus should not be denied to any farmer” (Rodier and Struik, 2018). The authors contented that cultural norms were important social capital in sustaining seed exchange among farmers in Ethiopia. In the present study, respondents exchanged sorghum seeds with other farmers because they trusted the quality of their seeds. Information on why farmers exchange sorghum seeds is crucial to uplifting the role of farmers in sustainable seed exchanges. This is also rooted in the strong belief that telling a lie about sorghum seed exchange is an act of disobedience to God. Cultural norms and trustworthiness are important motivating factors for sorghum seed exchange practices in Ethiopia. Social assets such as creating new and/or maintaining old friendships; the desire to help each other and increase production at the household and community also reportedly inspired many farmers to exchange sorghum seeds.

The farmers’ awareness that seed exchange is important to boost sorghum production at the community level is a form of altruism, described as “the spirit of sharing (Kiptot and Franzel, 2014). Respondents stated that beyond cultural norms and altruistic purposes, they were motivated to share seeds to help others as a risk-sharing mechanism that implied reciprocity. In line to this result, (Rodier and Struik, 2018) reported that a mix of personal and community interests that are deeply rooted in cultural norms motivate farmers to exchange sorghum seeds in northwestern Ethiopia. Investments in human, social, and financial capital are crucial to continuing farmers motivated (Kiptot and Franzel, 2014). Respondents on the contrary noted that in the process of seed exchange, they were often disadvantaged, because the seeds they in return got were of inferior quality to their seeds in terms of market value. To avoid the farmers’ dependence on other farmers, they were unwilling to share their seeds with farmers who regularly asked them to barter seeds every year. Another important issue mentioned by the respondents was selective seed donations by some farmers which was interpreted as discrimination.

5.4.4. Nodal vs non-nodal farmers in the seed network

Most of the farmers (nodal and non-nodal farmers) stated that they access sufficient amounts of seeds having very good quality. Better farmers' access to quality seeds is a key factor to increase crop productivity, improving the livelihood of smallholder farmers, and promising farmers to maintain crop diversity on-farm (Okry et al., 2011). As compared to the other farmers, nodal farmers have more land, grow more varieties, are wealthy, and have better access to seeds and information than that of non-nodal farmers. The relatively better access to quality seed and information of the nodal farmers might be partly due to the reason that they are more educated and are elder than the non-nodal farmers. In line with our findings, (Poudel et al., 2015) found that nodal farmers were wealthy and more educated in their study on social seed network analysis in Nepal. Our result agrees with the findings of (Wencélius et al., 2016) who noted wealthy farmers could be in a better position to have a prominent role in the seed network.

5.4.5. Farmers' seed network for promoting seed dissemination and genetic diversity conservation

In the last few decades, the importance of local seed exchange and biodiversity conservation for sustainable food security becomes at the forefront of research and policy priorities. Seed exchange among farmers through bartering and purchasing from local markets has a direct link to sustainable food security and livelihood strategies (Abay et al., 2011). It is evident that the sorghum seed network in Tigray was fairly active and hyper-localized as the majority (79%) of the exchanges took place between farmers living in the same village. Specific roles of farmers in the seed network are important for sustainable seed transactions at the local level. Nodal farmers are important hotspots for effective seed provision and maintenance of crop genetic diversity in their environment; and have better experience and exposure to information (Pautasso et al., 2013; Subedi et al., 2003). In the present study, bridging farmers who linked two or more sub-networks were important mediators of the sorghum seed network to continue functioning within and beyond the villages. Their role has been underscored as seed flow publicists in the informal seed system and more targeted for effective quality seed and information dissemination (Calvet-Mir et al., 2012). Therefore, one way of contributing to seed network efficiency is to stabilize the seed flows or support key farmers in the network. Such support could be given by providing training on seed production and management, by increasing access to genetic materials, or by providing information (Abay et al., 2011). Other measures could include awareness creation on the importance of local seed exchange among the key farmers and providing incentives in seed supply could significantly support to enhancing seed network efficiency (De Boef et al., 2010). We also found farmers with a higher degree and betweenness centralities to conserve a greater number of sorghum varieties. Similar results were also reported on the seed flow of Tartary buckwheat in southeast China (Song et al., 2019). Strong connections between central farmers and biodiversity conservations have been also reported by (Calvet-Mir et al., 2012). On the contrary, Rodier and Struik (2018), conclude that seed interevention through nodal and/or brignig farmers could limit introduction of new sorghum improved varietes, however they did not explain how these farmers are supposed to confine the transactions improved seeds.

In contrast, farmers occupying the central position can be a point of disruption and affect the seed exchange network in case of their absence or turnover (Poudel et al., 2015). Thus, as stated by Abay et al. (2011) to be most effective in disseminating quality seed and in meeting the demand for improved and local varieties, social seed network analysis needs to find the right balance in identifying nodal and connector farmers. Identifying farmers in key positions and designing a conducive approach to capacitate these farmers through training and feeding information, and awareness creation on the importance of local varieties (De Boef et al., 2010). Similar interventions were also advocated by several researchers (Abay et al., 2011; McGuire, 2007; Otieno et al., 2018) as robust strategies to strengthen informal seed exchanges.

5.5. Conclusion

Our study shows that farmers in Tigray predominantly access sorghum seeds through informal seed systems to fulfill their seed requirements. Bartering and own saved seeds are the main seed sources for farmers. This study underscores the significance of social network analysis in describing the complexity of farmers' seed systems on-farm. Some farmers play a major role as nodal, bridging farmers, or a combination of activities within their seed network. The analysis is useful for designing interventions related to seed exchanges that is a leap to enhance the effectiveness of the informal seed network. The sorghum seed exchange network in Tigray is active and hyper-localized, as the majority of exchanges took place within their villages than beyond. Social, cultural, natural, human, and physical assets of the community are the most important driving assets for farmers to share seeds. Farmers in Tigray maintain large diversity of sorghum varieties and seeds to deal with food insecurities due to environmental changes and pest and disease outbreaks, and to sustain crop production in their community. Efforts such as training farmers on seed selection, promoting nodal and bridging farmers to share their seed management and seed sharing experience, and awareness creation on the significance of seed exchange to farmers and extension workers could have a significant positive impact to smooth the informal seed system of sorghum in Tigray. Moreover, establishing local seed banks which could serve as a reservoir of the diversity of crops and varieties and designing effective approaches to familiarize new and improved crop varieties could be helpful for sustainable seed intervention and conservation of plant genetic resources strategies.

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APPEDIX

Appendix 1 Local name, altitudes, districts and geographical zones collections and codes given for the landrace used for the study.

Sn	Local name	alt^a	ds^b	zn^c	LR^d	Sn	Local name	alt^a	ds^b	zn^c	LR^d
1	Merowey 1	890	ATS	NW	LR 27	29	Wedihdar	1270	KH	W	LR 37
2	Tewzale1	1130	ATS	NW	LR 15	30	Koden 1	1500	MR	C	LR 74
3	Hareiekli	950	ATS	NW	LR 18	31	Dagnew	1445	MR	C	LR 77
4	Merowey 2	1050	ATS	NW	LR 106	32	Kumbilu 1	1420	MR	C	LR 73
5	Gahateni	1100	ATS	NW	LR 25	33	Zeriseytan	1510	MR	C	LR 11
6	Feterit	1110	ATS	NW	LR 14	34	Kumbilu 2	1900	MR	C	LR 3
7	Adar	1005	ATS	NW	LR 24	35	Shilquit 1	1850	MR	C	LR 4
8	Wediaker	920	ATS	NW	LR 17	36	Wedi Geremedhn	1900	MR	C	LR 72
9	Meshela	980	ATS	NW	LR 16	37	Koden 2	1700	MR	C	LR 1
10	Wedisbuh	980	ATS	NW	LR 26	38	Tewzale	1795	MR	C	LR 5
11	Kemkem	918	ATS	NW	LR 21	39	Safadin	1800	MR	C	LR 9
12	Tewzale 2	900	ATS	NW	LR 20	40	Shilquit 2	1800	MR	C	LR 2
13	Dagnew	900	ATS	NW	LR 23	41	Wedihdar 1	1390	MR	C	LR 7
14	Coden	1100	ATS	NW	LR 13	42	Wedihdar 2	1400	MR	C	LR 6
15	Coden	1000	KH	W	LR 53	43	Zeriseytan	1410	MR	C	LR 8
16	Wediaker	650	KH	W	LR 41	44	Merowey	1430	MR	C	LR 75
17	Deber 1	1105	KH	W	LR 39	45	Lequa	1700	MR	C	LR 71
18	Deber 2	700	KH	W	LR 51	46	Arogosh	1710	MR	C	LR 10
19	Ganseber	1005	KH	W	LR 98	47	Wedigere	1350	MR	C	LR 76
20	Getsharas	1110	KH	W	LR 38	48	Abaaro	1705	RA	S	LR 59
21	Korekora	710	KH	W	LR 52	49	Kodem	1670	RA	S	LR 63
22	Dagnew 3	1130	KH	W	LR 34	50	Chibrak 1	1650	RA	S	LR 58

23	Kinjiga	1180	KH	W	LR 29	51	Dangle	1710	RA	S	LR 56
24	Chimroy	1070	KH	W	LR 33	52	ZeriHadush	1620	RA	S	LR 55
25	Safra	670	KH	W	LR 40	53	Jugurte	1685	RA	S	LR 62
26	Amal	680	KH	W	LR 42	54	Chibrak 2	1700	RA	S	LR 54
27	Shilquit	1050	KH	W	LR 35	55	Meshala	1710	RA	S	LR 61
28	Dagnew 2	1135	KH	W	LR 36	56	Jamiyu	1750	RA	S	LR 57
57	America	1690	RA	S	LR 60	84	Melkam	–	TARI		LR 31
58	Wedihidar	1100	TA	NW	LR 88	85	Dekeba	–	TARI	–	LR 30
59	Hriray	1035	TA	NW	LR 91	86	Hugurtay	700	TSE	W	LR 45
60	Zerieseytan	940	TA	NW	LR 92	87	Deber	715	TSE	W	LR 47
61	Zerie Tsegay	1005	TA	NW	LR 87	88	Tekemche	690	TSE	W	LR 32
62	Meretatfi	1150	TA	NW	LR 86	89	Wediaker	650	TSE	W	LR 49
63	Wediaker	1070	TA	NW	LR 46	90	Korekora	650	TSE	W	LR 48
64	Wanze	1070	TA	NW	LR 89	91	Merawi	1255	TSL	NW	LR 104
65	Tewzale	1080	TA	NW	LR 84	92	Tewzale	1310	TSL	NW	LR 102
66	Dagnew 1	1100	TA	NW	LR 83	93	Gedelabay	1420	TSL	NW	LR 105
67	wediferej	1000	TA	NW	LR 94	94	Wedihdar	1370	TSL	NW	LR 107
68	Dagnew Deqala	1015	TA	NW	LR 90	95	Kemkem	1475	TSL	NW	LR 108
69	Merowey	1075	TA	NW	LR 81	96	Zeriadis 1	1315	TSL	NW	LR 103
70	Tewzale dekala	1110	TA	N W	LR100	97	Zeriadis 2	1295	TSL	NW	LR 12
71	Dagnew 2	1110	TA	NW	LR 96	98	Wediaker	1305	TSL	NW	LR 50
72	Ganseber 1	1090	TA	NW	LR 28	99	Wedisbuh	1400	TSL	NW	LR 19
73	Chimroy 1	1100	TA	NW	LR 79	100	Achire	1300	TSL	NW	LR109
74	Kinjiga	1005	TA	NW	LR 93	101	Kemkem1	815	WL	W	LR 44

75	Shilquit	1030	TA	NW	LR 85	102	Wedihdar	900	WL	W	LR 68
76	Wedisubuh	1030	TA	NW	LR 22	103	Beyan	870	WL	W	LR 43
77	Kimbiba	1060	TA	NW	LR 82	104	Gule	915	WL	W	LR 66
78	Zerigebru	1055	TA	NW	LR 78	105	Tuemay	1010	WL	W	LR 69
79	Chimroy 2	1070	TA	NW	LR 99	106	Dagnew	995	WL	W	LR 67
80	Ganseber 2	1100	TA	NW	LR 97	107	Bayush	1005	WL	W	LR 70
81	Getsharas 2	995	TA	NW	LR 95	108	Wareta	1035	WL	W	LR 101
82	Chimroy 3	1120	TA	NW	LR 80	109	Kemkem2	1045	WL	W	LR 64
83	Chramutsu	715	TSE	W	LR 32	110	Getsharas	1100	WL	W	LR 65

alt[a], altitude classes; ds[b], districts; ATS, Asgede Tsimbla; KH, Kafta Humera; MR, Mereb Leke; RA, Raya Azebo; TA, Tahyat Adyabo; TARI, Tigray agricultural research institute; TSE, Tsegede; TSL, Tselemti; WL, Welkait; zn[c], Geographical Zones, C, central; NW, north western; S, Sothern; W, western; LR[d], landrace.

Appendix 2. Mean perfromance of agromorphological traits of sorghum genotypes in six environments of Tigray

Genotype	DH	DF	DM	LN	LL	Lwd	PH	Pnht	Pnwd	Pnwt	Pnwt	TGWT	GY
LR1	69.6	74	109.4	11	71.3	7.1	2.3	24.4	8.2	72.5	74	36.4	35.7
LR2	69.7	74.4	108.7	11.3	70.6	7.5	2.4	24.5	8.7	71.9	73.4	35.6	33.5
LR3	72.6	76.9	110.6	11	71.1	7.3	2.5	25.4	9	69.7	70.9	31.8	32.8
LR4	70.7	75.1	109.7	11.1	73.4	7.5	2.4	24.9	9	68.9	70	35.5	30
LR5	68.1	72.5	107.7	9.9	71.4	7	2.3	23.4	7.6	74.2	76	35.8	32.3
LR6	67.5	71.4	105.9	10.5	69.2	7	2.2	29.8	9.3	53.8	53	26.6	27.3
LR7	67.8	71.8	108.9	10.7	71.6	7.7	2.1	27.4	8.9	54.8	54.1	26.5	29.1
LR8	66.4	70.7	105.3	8.9	67.7	7.6	2.3	20.8	6.7	36.5	33.5	14.4	17.6
LR9	71.6	76.1	109.2	11.7	67	7.3	2.2	20.9	8.5	49.3	47.9	24.1	24.3
LR10	69.4	75.5	110.3	11.1	65.1	7.6	2.4	23.7	8.3	41	38.6	22.4	20.2
LR11	67.1	71	105.2	10.3	66.8	6.5	2.4	23.8	8	45.7	43.9	20.2	18.4
LR12	69.7	73.4	108.8	10.8	73.2	7.2	2.4	27.1	9.3	76.1	78.1	37.8	37.3
LR13	73	77.3	112.6	10.8	71.4	6.9	2.4	25.3	9.7	61.5	61.7	32.9	32.2
LR14	69.7	74.5	112.7	10.3	69.9	7.9	2.3	26.9	9.3	69.7	70.9	31.8	32.3
LR15	65.6	69.7	104.3	10.4	65.4	7.3	2.1	25.6	8.1	68.8	69.9	32.4	34.1
LR16	73.9	78.2	113	12	71	6.5	2.3	22.5	9	68.8	69.8	32.4	31.6
LR17	69.7	73.7	106.1	11.8	70.7	6.8	2.3	22	7.8	49.7	48.3	23	28.9
LR18	73.4	77.8	115.7	12.7	70.6	6.8	2.5	17.1	8.4	35.1	32	14.7	19.7
LR19	72.6	76.5	115	10.6	71.1	7.5	2.4	23.7	9.6	73.9	75.6	32.8	33.7
LR20	70.6	74.6	114	9.7	69.5	7.9	2.5	22.7	7.9	56.5	56	27.2	33
LR21	73.4	78	115.1	11.4	73.2	7.4	2.5	22.8	8.3	54	53.2	29.3	29.9
LR22	72	76	111.7	12.1	70.9	7.5	2.4	21.3	8.6	66.1	66.8	34.6	30.5
LR23	69.4	73.7	111	11.4	67.9	7.4	2.4	25.3	9.3	72.8	74.4	34	37.7
LR24	70.4	74.6	110.7	11.5	63.9	6.9	2.2	17.4	7.1	39.9	37.3	17.1	17.9
LR25	73.6	77.9	113.1	11.6	68.8	7.5	2.3	26.1	9.1	96.6	101.1	44.5	39
LR26	73.9	78.4	111.7	12.7	66.2	7.4	2.3	24.4	8	65.4	66	37.8	35.4
LR27	73.1	77.5	111.3	11.3	65.2	7.3	2.1	22.1	9.3	70.3	71.5	38.5	33.6
LR28	69.3	73.3	108.2	10.9	63.7	7.3	2.3	20.6	8.3	53.8	53	29.2	29.4

LR29	71.8	76.4	110.3	10.7	68.7	6.5	2.4	22.3	8.3	44.2	42.1	21.9	23.1
Melkam	68.2	72.3	105.2	10.4	67.1	7.5	2	22.8	8.4	63.2	63.6	25.8	31.1
Dekeba	68.1	72.4	109.9	10.1	65.7	7.1	2	22.3	8	66.6	67.4	28.3	28.8
LR32	67.7	72.1	107.3	11.1	67.8	7.1	2.1	20.7	8.2	67.9	68.9	27.7	30.7
LR33	70.1	74.2	107.9	11	67.5	6.8	2.3	22.4	8.6	61.7	61.8	26.8	28.2
LR34	66.4	70.6	103.8	11	67	7.9	2.4	24.6	8.8	53.2	52.3	27	28.5
LR35	69.8	74	109.9	11.4	65.3	7	2.4	24.8	8.9	62.6	62.9	36.9	32.5
LR36	66.4	70.8	103.4	10.2	69.5	7.3	2.1	24.4	8.7	56.9	56.4	27.5	27.1
LR37	65.5	69.6	104.9	9.6	68.9	6.8	2.3	21.8	8.2	58.1	57.8	25.8	29.4
LR38	65.3	69.3	103.7	8.7	65.6	6.2	2.3	18.8	8.7	57	56.6	23.7	26.9
LR39	70.7	74.4	107.6	11.8	75.1	6.9	2.2	20.6	8.5	48.9	47.4	24.2	24.2
LR40	64.7	68.9	102.6	9.8	66.1	6.9	2.4	18	7.7	49.1	47.7	19.8	21.1
LR41	68.4	72.5	106.5	10.2	67.9	7.6	2.1	19.8	7.9	53.1	52.2	22.9	25.3
LR42	68.7	73.1	104.2	11.1	69.1	8	2.2	18.4	7.7	55.8	55.2	24	24.9
LR43	69.3	73.8	112	10.6	66.7	7.7	2.2	23.4	8.9	61.2	61.3	27.2	23.6
LR44	68.8	72.7	108.7	12	68.9	7.6	2.4	21.9	7.4	64.6	65.2	30.2	27
LR45	70.7	75.1	110.6	11.6	70.8	7.2	2.3	17.7	7	39.4	36.7	14.1	14.3
LR46	67.2	71.5	105.5	9.6	66.8	7.6	1.7	20.5	8.5	52	51	25	28.5
LR47	66.9	71	104.3	9.9	67.4	7.9	1.9	20.3	7.6	51.4	50.2	20.6	24.2
LR48	70.3	75.4	108.3	11.4	70.6	7.1	2.2	19.6	7.7	53.4	52.5	20.8	22.7
LR49	65.5	70.8	105.2	10.6	68.4	7	2.2	18.7	7.6	53.2	52.3	22.9	24.3
LR50	65.5	69.6	104.6	11.8	68.5	7.5	2.2	17.4	7.7	57	56.6	20	26.2
LR51	68.3	72.3	108.2	9.7	71.4	7.3	2	21.1	7.8	51.9	50.8	22.9	20.9
LR52	65.8	69.4	104.3	10.1	67.4	7.4	1.9	19.3	7.6	49.7	48.4	25	22.5
LR53	66.5	70.7	104.6	10.5	67.2	6.9	2	20.9	8.8	69.1	70.2	29.1	33.2
LR54	70.9	75.3	112.2	10.2	68.8	7.5	2.5	22.5	9	64.2	64.7	26.8	24
LR55	67.1	71.6	108.4	10.6	66.2	6.8	2.3	22.1	7.9	58.4	58.1	26.9	25.8
LR56	75.7	80	119.5	11.3	67.8	6.6	2.4	15.1	8.8	54.7	54	35.3	16.4
LR57	73.3	77.8	111.7	10.4	67.8	6.8	2.4	17.2	9.3	51.8	50.7	27.5	18.3
LR58	74.5	78.9	119	11.2	72.2	7.3	2.4	23.3	9.9	58.6	58.4	31.4	21.3
LR59	73.2	77.4	117.8	11.1	63.6	7.6	2.5	13.7	8.9	57.1	56.7	34.9	18.7

LR60	72.9	77.2	112.8	11.2	70.2	6.9	2.6	14.5	8.6	51	49.8	26.5	17.2
LR61	73.6	77.9	118.3	10.3	68	7.9	2.1	23.9	8.5	57.9	57.6	28.7	24.8
LR62	74.7	79.4	114.7	11.6	70.4	8.6	2.2	24	8.2	58.9	58.7	31.7	22.4
LR63	72.9	77.2	114.4	10.6	69.1	7.4	2.3	22.2	9.2	62.1	62.4	35.4	22.6
LR64	72.3	76.5	113	11.6	75	7	2.4	22.2	8.3	65.3	65.9	31.1	29
LR65	67.5	72.1	109.6	10.2	70.1	7.3	2.3	19.6	8.6	74.4	76.2	25.6	28.3
LR66	66.8	70.6	105.5	10.5	65.2	7.4	2.1	18.6	8.8	73.8	75.5	28.5	28.3
LR67	67.7	71.9	108.1	10.9	68.6	6.9	2.4	20.5	8.4	73.5	75.2	31.7	30.3
LR68	70.3	74.7	113.3	11	72.4	7.3	2.3	25	8.9	74.2	76	28.1	31.3
LR69	70.6	75.1	113.9	10.6	74.1	7.4	2.4	21.7	8.1	57.4	57	27.7	25.3
LR70	68.6	73.1	107.7	9.8	70.1	7.5	2.3	19.1	7.6	56	55.4	29.8	22.8
LR71	71.8	76	111.3	10.6	69	6.8	2	22.3	8.3	49.3	47.9	23.6	25.9
LR72	70.4	74.7	110.7	11.3	70.4	8.1	2.3	25.7	8.3	49.2	47.8	22.6	23.5
LR73	71.2	75.6	108.4	11.6	69.1	7.9	2.3	27.1	8.9	70.2	71.5	29	31.4
LR74	70.3	74.6	112.4	10.7	72.1	7.4	2.3	28.6	9.2	78.3	80.5	37.5	33.2
LR75	72.6	77.3	115.1	11.4	69.7	8	2.2	25.3	8.7	72.8	74.4	38.6	38.8
LR76	68.8	72.9	107.3	10.5	69.6	7.8	2.1	23.9	8.6	56.3	55.8	25.2	24.5
LR77	71.6	76	112	11.3	67.9	6.8	2.4	23.1	9	72.7	74.2	33.8	28.4
LR78	67.4	71.7	108.3	10.5	65.3	7.1	2.2	21.4	8.2	64.6	65.2	34.7	37.2
LR79	73.2	77.9	115.4	11.7	70.5	6.8	2.4	19.6	8.6	61.9	62.1	28.1	26.2
LR80	67.9	72.1	106.8	10.1	68.8	7.1	2.4	19	8.3	59.8	59.7	26.1	24.5
LR81	72.8	77.4	112.3	11.2	71.8	7.2	2.4	22.6	8.5	71.7	73.2	34.2	33.6
LR82	71.2	75.8	110.6	11	69.3	6.3	2.1	20	7.7	46.4	44.7	25.3	27
LR83	66.5	70.8	107.4	9.6	68.9	6.6	2.4	21.5	9.1	68.7	69.8	28.7	31.5
LR84	69.4	73.7	106.7	11.2	72.5	7.2	2.8	29	7.5	59.4	59.3	27.2	26.3
LR85	70.8	75	110.2	10.5	69.9	6.9	2.5	25.4	8.6	65	65.5	34.4	34.8
LR86	67.7	71.9	106	9.8	68	7.3	2.1	17.4	7.7	38.2	35.5	17.2	16
LR87	68.1	72.1	108.7	10.5	66.5	7.2	2.2	21.6	9.1	55.5	54.9	24	24.3
LR88	71.7	76	113.4	11.6	66.3	7	2.3	23.1	8.7	64.2	64.7	29.5	27.4
LR89	72	76.3	110.6	11.8	69.3	7.6	2.2	20.5	7.4	40.8	38.3	15.5	20.8
LR90	66.8	71.1	106.8	10.8	69.2	6.8	2.3	22.6	8.1	59.8	59.7	21.1	26.6

LR91	71.6	75.9	112.3	10.7	71	7.1	2.3	22.3	7.4	38.9	36.2	16	21.1
LR92	70.3	74.6	111.8	9.6	66.5	7	2.1	21.5	7.4	36.6	33.6	17.1	15.9
LR93	73.6	78.7	113.1	10.8	67.8	6.5	2.2	20.9	7.5	49.5	48.1	24.4	22.5
LR94	69.2	73.6	109.6	10.7	70.8	7.2	2.6	24.9	7.8	68.7	69.8	28	30.5
LR95	66.8	70.8	105.2	9.9	69.6	6.8	2.4	22.7	8.7	70.6	71.9	28	28.5
LR96	68.6	72.8	108.2	10.5	73.5	7	2.5	22.6	8.6	68.3	69.3	28.6	32.5
LR97	69.2	73.7	108.9	11.5	69.5	6.8	2.4	19.2	8.7	60.6	60.7	29.3	30
LR98	67.8	71.6	105.9	11.2	70.4	6.3	2.4	24	8.3	61.7	61.8	29.6	28.8
LR99	67.9	72.2	109.2	10.8	69.6	7.3	2.2	20.4	8.9	58.3	58.1	25.3	26.7
LR100	66.9	71.1	107.2	10.7	73	6.6	2.4	28.5	7.8	67.9	68.8	31.9	33.6
LR101	69.7	74.1	109.3	11.5	70.8	7.3	2.5	25.8	7.8	56.8	56.3	23.3	24.7
LR102	69.2	73.9	109.9	11.2	68.1	6.9	2.5	28.2	8.2	72.1	73.6	33.4	40.9
LR103	72.4	76.5	115.2	10.9	68.3	6.8	2.4	23.1	8.8	86.2	89.5	36.5	35.5
LR104	71.7	75.8	114.3	10.5	71	7.2	2.4	26.8	9.3	61	61.1	31.9	31.9
LR105	71.1	75.4	111.8	11.7	70.9	7.2	2.3	20.4	7.9	67.5	68.5	32.9	30.6
LR106	69.2	73.5	108.4	11.2	68	7.3	2.4	23.8	8.6	79.7	82.2	36.2	30.9
LR107	69.5	73.6	112	10.9	68.4	7.9	2.4	27	8.8	68.9	69.9	33.1	32.7
LR108	70.5	74.8	114.7	11.2	70.2	7.2	2.2	25	8.9	65.2	65.8	30.8	27
LR109	69.7	73.6	114.1	10.8	68.6	7.2	2.4	21.4	8.4	58.9	58.8	24.5	27.2
LR110	74.3	78.6	119.3	10.6	71.7	7.3	2.3	20.6	8.4	64.3	64.8	25.5	27.8
Mean	69.9	74.2	109.9	10.8	69.1	7.2	2.3	22.3	8.4	60.3	60.3	28.1	27.6
Max	64.7	68.9	102.6	8.7	63.6	6.2	1.7	13.7	6.7	35.1	32	14.1	14.3
Min	75.7	80	119.5	12.7	75.1	8.6	2.8	29.8	9.9	96.6	101.1	44.5	40.9
STD	2.5	2.6	3.8	0.7	2.4	0.4	0.2	3.1	0.6	11.1	12.5	6.0	5.6

DH = days to 50%, DF = days to 50% flowering; DH = 50% days to heading; DM = days to 50% maturity; GY, grain yield; Pnl; panicle lenght; Pwd, panicle width; Pwt, panicle weight; TGWT, thousand seed weight.

Appendix 3. Mean perfromance of grain yield and nutritional qaulity traits of sorghum in six environments of Tigray

Genotype	gy (q/ha	Sta (%	Protein (%	Ash (%)	Zinc (ppm)	Iron (ppm)	Calcium (ppm)	Magnesium (ppm)
LR1	36.1	67.6	10.8	2.1	37.4	40.2	226.2	1121.2
LR2	34.1	66.5	10.2	2	34.4	39.7	235.2	1092.3
LR3	33.4	67.3	10.5	2	35.4	38.4	243.7	1071.3
LR4	30.8	68.9	9.9	2.1	38.1	42	226.3	1335.4
LR5	33	68.1	10	2.1	33.2	40.4	232.3	1091.1
LR6	28.3	68.5	10.2	2.1	36.4	40.2	219.6	1113.3
LR7	30	65.4	10.7	2	34.9	40.2	239.8	1104
LR8	19.2	65	10	1.8	34.3	39.4	210.9	1018.7
LR9	25.5	66	10.2	1.9	34.4	40.6	225.8	1189.9
LR10	21.7	66.1	9.9	2.3	34.7	45.7	212.7	1158
LR11	19.9	61.9	10.1	1.8	34.5	40.8	224.1	1152
LR12	37.7	66.4	10.2	2.3	40.6	47.3	228.4	1165.5
LR13	32.8	66.8	10.4	1.9	33.9	40.4	234.4	1178.6
LR14	33	69.5	10.6	2.1	37.6	40.9	254.6	1117.6
LR15	34.6	66.7	10.3	1.7	33.4	45.5	275.1	1085.3
LR16	32.3	68.9	10.5	2	33.1	43.5	289	1097.6
LR17	29.7	65.9	10.3	1.9	34	41.2	260.6	1135.8
LR18	21.2	65.8	10.2	1.7	37.7	44.6	212.6	1064.9
LR19	34.3	67.1	10.5	1.8	34.6	37.4	242.8	1006.6
LR20	33.6	64.6	10.2	2.1	35.3	38.3	238.9	1040.9
LR21	30.7	64	10.4	1.7	35.6	39.6	221.1	1047.8
LR22	31.3	66.3	10.3	1.7	36.4	37.5	227.8	1019.7
LR23	38	65.3	10.1	2	43.8	43.2	257.4	1132.9
LR24	19.5	62.5	9.5	2	39.4	41.6	245.8	1176.6
LR25	39.2	69.3	9.7	1.9	39.2	38.3	262.5	1166.5
LR26	35.8	67.5	10	1.8	37.7	34.4	275.8	1132.5
LR27	34.1	69.5	10.3	1.9	39.8	40.7	250	1232.9
LR28	30.2	66.2	10.2	1.5	36.5	40.7	226.9	1044.5
LR29	24.4	65.1	9.9	1.9	37.5	39.2	243.3	1127.1
Melkam	31.8	67.7	9.9	1.9	39.2	38.6	217.4	1088.9
Dekeba	29.7	65.6	10.4	2	36.4	38.3	233.5	1024.7
LR32	31.4	65.2	9.8	2	37	41.4	210.1	1046.4
LR33	29.1	67.6	9.9	1.8	34.7	42.8	248.1	1115.5
LR34	29.4	68.3	9.9	1.9	37.5	41.2	270.9	1140.2
LR35	33.1	66.6	10.5	1.5	38.3	39	226.7	1087.4
LR36	28.1	66.3	10.1	1.7	36	33.7	225.8	1123.1
LR37	30.3	67.2	10.1	1.8	34.7	36.2	243.9	1157
LR38	27.9	67.4	10.4	1.9	35.8	47.8	243.1	1093.9

LR39	25.4	63.9	9.7	1.9	34.3	34.2	274.9	1077.7
LR40	22.5	63.5	10	2	35.4	41.7	244.4	1024
LR41	26.4	60.6	10.2	1.9	33.5	35.7	230.7	1236.3
LR42	26.1	63.9	10.2	1.6	32.8	36.1	225.9	1114.6
LR43	24.8	68.5	10.7	2	32.4	39.1	239.9	1190
LR44	28	65.7	10.7	1.8	33.7	40	232.2	1005.3
LR45	16.1	61.5	10.1	2	40.8	31.4	238.2	1152.8
LR46	29.4	61.8	10.5	2	38.3	32.6	243.8	1038.8
LR47	25.4	63.3	10.4	1.7	35.6	37.8	270	1063.3
LR48	23.9	62.7	10.6	1.9	34.2	36.8	243.4	1121.7
LR49	25.4	59.5	10.3	1.9	35.8	39.4	239.2	932
LR50	27.3	65.2	10.3	1.6	35.1	32.9	249.3	1069.3
LR51	22.2	65.6	10.3	1.9	34.8	35.8	268.9	1021.1
LR52	23.8	66.4	10.4	2	32.6	34.9	248.2	1089.8
LR53	33.8	66.4	10.6	2	36.8	31.7	266.7	1088.2
LR54	25.2	63.4	11.1	1.8	34.6	35.6	244.2	1092.5
LR55	26.9	62.6	10.5	1.9	33.6	35.7	262.6	1163.4
LR56	18.1	63.6	10.4	1.7	33.1	28.1	221.7	1031.3
LR57	19.9	66	10.5	1.7	32	31.3	220.5	996.6
LR58	22.7	64.9	10.5	1.8	31.7	32.5	232.4	1048
LR59	20.3	65.8	10.3	1.7	31.7	32.9	240.3	1040.6
LR60	18.8	65.9	10.6	1.7	32.6	32.7	253.1	972.5
LR61	26	62.9	9.7	2.1	35.4	39.8	252.9	1129
LR62	23.7	59	10.5	1.7	33.3	38.2	262.9	1060.7
LR63	23.9	62.1	10.1	1.9	31.9	33.8	250.8	1037.6
LR64	29.9	60	10	1.7	32.3	29.8	233.4	1116.8
LR65	29.2	63.4	11.2	1.7	35.5	28.9	215.9	1161.1
LR66	29.2	61	10.6	1.8	31.5	26.5	224.8	1197.4
LR67	31.1	63.1	9.7	1.9	34.7	39.1	229.4	1092.2
LR68	32	62.7	10.5	1.6	35.3	42.2	243.6	1112.8
LR69	26.4	67	10.2	1.9	35.1	45.5	242.9	1087.1
LR70	24	66.6	10.5	1.8	35.3	40.4	238.6	1040.4
LR71	27	60.4	9.8	2.0	38	44.2	248.1	1053.2
LR72	24.8	65.3	10.3	2.0	35.4	36	264.2	1170.2
LR73	32.2	60.2	10.6	2.0	39.2	35.8	265.7	1158.4
LR74	33.8	63.9	10.6	1.7	33.8	35	273.1	954.6
LR75	39	64.3	10.1	1.7	34.1	35.1	251	960.8
LR76	25.7	67.9	10.3	1.8	34.5	31.7	244.4	995.9
LR77	29.3	65.1	10.4	1.7	35.9	29.6	253.3	970.5
LR78	37.5	65.6	10.7	1.8	34.5	34.5	235	1118.9
LR79	27.3	65.9	10.4	1.5	33.9	31.4	258.9	1118.4
LR80	25.7	66.3	10.2	1.8	36	35.6	251.4	1181.8
LR81	34.2	60.7	10.5	2.2	38.4	40.9	247.9	1063.8

LR82	28	63.8	9.7	1.9	35.1	38	243.1	1061.5
LR83	32.2	65.6	10.3	2	36.7	31.9	241.6	1016.2
LR84	27.4	68	10.4	2.3	37.7	41.4	247.5	999
LR85	35.3	67.4	10.1	1.7	37.7	31.1	233.4	1066.5
LR86	17.7	64.8	10.4	1.9	34.5	37.2	232.9	1218.4
LR87	25.5	66	10.5	2.1	36.6	46	236.3	1160.8
LR88	28.3	63	10.4	2	30.9	39.9	232.5	1140.6
LR89	22.2	63.7	10.3	1.7	33	33.4	270.1	1140.6
LR90	27.6	62.1	10.4	2	33.1	36.4	259.2	1087.4
LR91	22.5	64.5	10.2	1.7	31.9	38.9	220.8	1006.6
LR92	17.6	63.3	10	1.8	36.5	36.9	222	955.1
LR93	23.8	64.4	9.6	1.9	35.2	31.2	230.9	1039.7
LR94	31.2	65	10.6	1.8	33.7	30.3	256.4	1170.9
LR95	29.4	67.2	10.9	1.9	31.8	33.8	254.1	1180.5
LR96	33.1	66.1	10.8	1.6	29.7	34	254.6	1146.4
LR97	30.8	62.3	10	2	36.9	33.5	246.3	1197.4
LR98	29.7	59.5	10.9	2	39.5	30.2	264.6	1167.6
LR99	27.7	66	10.8	1.6	32.8	28.3	245.6	1223.2
LR100	34.1	65.1	10.4	1.8	32.7	30.9	246.5	1172.6
LR101	25.9	67.4	10.4	1.7	31	29.3	229.8	1145.2
LR102	41	66	10.5	1.6	31.2	29.2	257.1	1040.4
LR103	36	65.3	10.8	1.6	37.3	32.1	266.2	1167.9
LR104	32.6	64.3	10.6	2	34.1	31.3	223.4	1075.8
LR105	31.4	64.9	10.5	1.7	34.6	26.8	230	1082.3
LR106	39.2	66.6	10.6	1.9	38.5	39.9	241	1016.2
LR107	33.3	68.1	11	1.7	38.2	29.5	265.8	991.3
LR108	28.3	65.3	10.7	1.6	35.2	30.7	268.8	1026.1
LR109	28.2	65.3	10.6	1.8	34.9	32.6	246.7	1145
LR110	28.8	62.6	9.9	2.1	36.8	42.3	260.4	1158.3