2024-06

Enetic Variability and Association of Traits Among Sorghum [Sorghum Bicolor(L.) Moench] Genotypes Northeastern Ethiopia

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BAHIRDAR UNIVERSITY

COLLEGE OF AGRICULTURE AND ENVIRONMENTAL SCIENCES

GRADUATE PROGRAM

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M.Sc Thesis

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SUBMITTED IN PARTIAL FULFILLMENT OF THE REQUIREMENTS FOR THE DEGREE OF MASTER OF SCIENCE (M.SC) IN PLANT BREEDING

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Bahir Dar

THESIS APPROVAL SHEET

As member of the Board of Examiners of the Master of Sciences (M.Sc.) thesis open defense examination, we have read and evaluated this thesis prepared by Mr. Tadesse Ayalew Asmare entitled "**Genetic Variability and Association of Traits among Sorghum [***sorghum bicolor* (l.) **Moench] Genotypes Northeastern Ethiopia".** We hereby certify that, the thesis is accepted for full filling the requirements for the award of the degree of master of sciences (M.Sc.) in plant breeding.

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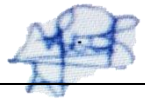
Muluken Bantayehu (M.Sc)		25/07.2024
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DECLARATION

This is to certify that this thesis entitled **"Genetic Variability and Association of Traits among Sorghum [***sorghum bicolor* **(L.) Moench] Genotypes Northeastern Ethiopia",** Submitted in partial fulfillment of the requirements for the award of the degree of Master of Science in **Plant Breeding** to the Graduate Program of College of Agriculture and Environmental Sciences, Bahir Dar University by **Mr. Tadesse Ayalew,** (ID. No. BDU 1500083) is an authentic work carried out by him under our guidance. The matter embodied in this project work has not been submitted earlier for award of any degree or diploma to the best of our knowledge and belief.

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ACKNOWLEDGMENTS

First and foremost, my deepest gratitude goes my adviser, Dr Alemu Abate for his valuable suggestions, encouragement and constructive comments in the course of my study. His continued support, insightful comments, advice, help and involvement have greatly contributed to the success of this study. I acknowledge and value all his efforts to complete this work.

I would like to express my gratitude to Sirinka Agricultural Research Center and Amhara Regional Agricultural Research Institute (ARARI) for providing me with the opportunity to pursue my MSc and funding the research. I would also like to thank the Melkassa Agricultural Research Center for providing planting materials for the experiment. I am particularly indebted to Dr. Alemu Tirfessa, the director of the Melkassa Agricultural Research Center and the integrated striga control (ISC) project coordinator for providing partial financial support for this study.

My thanks extend to the staff members of Sirinka Agricultural Research Center Mrs Yemata Bezie, Mr Eyeberu Abere, and Yibeltal Eniyih for their effort during planting and experimental field management. I am very much grateful to my wife, Muluwa Fentaw for her encouragement and support throughout my research. Finally but above all, I honor and praise God, in His word ‘I will praise thee forever.

LIST OF ABREVIATIONS AND ACRONYMS

ANOVA	Analysis of Variance
CSA	Central Statistical Agency
CV	Coefficient of Variation
EARO	Ethiopian Agricultural Research Organization
EIAR	Ethiopian Institute of Agricultural Research
ESIP	Ethiopian Sorghum Improvement Project
ETSC	Ethiopian Sorghum Crosses
FAO	Food and Agriculture Organization
GAM	Genetic Advance as a percent of the mean
GCV	Genotypic Coefficients of Variations
ICRISAT	International Crops Research Institute for the Semi-arid tropics
IDRC	International Development Research Center
IBPGR	International Board for Plant Genetic Resources
LSD	Least Significant Difference,
m a.s.l.	Meters Above Sea Level
NPS	Nitrogen, Phosphorous and Sulfur
P	Probability level
PCA	Principal Component Analysis
PCV	Phenotypic Coefficients of Variations
R^2	Coefficient of Determination
RCBD	Randomized Complete Block Design
USDA	United State Department of Agriculture

Genetic Variability and Association of Traits among Sorghum [*Sorghum bicolor* (L.) Moench] Genotypes Northeastern Ethiopia

By

Tadesse Ayalew and Alemu Abate (PhD)

ABSTRACT

Sorghum is an important food and feed crop in the semiarid regions of the world. Hence, this study was conducted to evaluate genetic variability and traits associations among 81 Sorghum genotypes Northeastern Ethiopia during the 2023 cropping season, using a 9x9 simple lattice design. Quantitative data analysis was computed by using R software. Analysis of variance revealed highly significant (P<0.001) differences among genotypes for days to 50% flowering, leaf length, leaf area index, plant height, panicle, length, head weight, biological yield, harvest index, thousand kernel weight, and grain yield. This result indicates the presence of sufficient genetic variation. The differences in PCV and GCV were small for days to 50% flowering, days to maturity, plant height, head weight, panicle length, thousand kernel weight, and grain yield, suggesting that the environment had minimal influence on the expression of these traits. High broad sense of heritability coupled with high genetic advance as a percentage of the mean were exhibited for head weight, biological yield, thousand kernel weight, and grain yield. Days to 50% flowering, days to maturity, plant height, head weight, leaf length, leaf width, leaf area index, panicle length, biological yield, thousand kernel weight, and grain yield had positive and highly significant genotypic and phenotypic correlations with grain yield. Days to 50% flowering, leaf length, leaf width, plant height, biological yield, harvest index, and thousand kernel weight had positive direct effect at genotypic level on grain yield, implying that a breeding strategy for increasing grain yield and promising genotypes could be selected based on these traits. The first four principal components accounted for 80.11% of the total variation among sorghum genotypes. The most important traits that explained the greatest variation on the PCA was grain yield, head weight, biological yield, leaf length, leaf area, plant height, harvest index, thousand kernel weight, and days to maturity. The maximum intercluster distance was found between clusters I and IV, followed by clusters I and, III and IV and clusters II and III, indicating good opportunity for hybrid crosses between clusters rather than with in clusters. The result of this

study should be needed further studies over season and location to verify the consistency of existing genotypic variability to have a better recommendation.
Keywords: Cluster analysis, Correlation, Heritability, Path analysis, Principal component

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BIOGRAPHICAL SKETCH

The author was born on 01 September, 1989 G.C. in Woyniye Kebelle, Gubalafto District, North Wello Zone, Amhara Region. He attended primary and junior secondary school in Sanka from 1995 to 2002. He then attended high school at Woldia General Secondary School from 2003 to 2004. After completing high school, he joined Alage Agricultural Technical Vocational Education and Training College in 2005 and graduated in 2007 with Diploma in Plant Science.

He was employed in the Gubalafto District Agricultural Office in the North Wello Zone from August 6, 2007 to July 28, 2011 as a development agent (DA) in the plant science. He then joined the Sirinka Agricultural Research Center Kobo Sub Center on July 29, 2011, and was employed as a cereal crop research assistant.

In 2014, he joined Woldia University to pursue his Bachelor of Science degree in plant Science and graduated on June 30, 2016 with a B.Sc. degree in Plant Sciences and served as a cereal crops research assistant until he joined the School of Graduate Studies in 2023 to pursue his study for MSc. Degree of Plant Breeding. He is married and is the father of one daughter.

Chapter 1. INTRODUCTION

1.1. Background and Justification

Sorghum (Sorghum bicolor (L) Moench) is an important cereal crop belonging to the grass family (Poaceae) with a diploid (2n = 2x = 20) C4 crop of tropical origin (House, 1985). It is a naturally self-pollinating monocotyledonous crop, and depending on the panicle type, the degree of spontaneous cross-pollination can reach 30% in some cases (Poehlman, 2013). After rice, wheat, barley, and maize, sorghum is the fifth most significant cereal crop in the world (Fontaine *et al.*, 2002). It is widely grown in arid and semiarid tropics because of its unique ability to adapt to harsh, drought-prone environments where few other crops survive and food insecurity is prevalent (Asfaw Adugna, 2007).

Ethiopia's three main agro-ecological zones—highlands over 1900 meters above sea level (masl), intermediate zones between 1600 and 1900 meters above sea level (masl), and lowland agro-ecologies below 1600 meters above sea level—are home to sorghum cultivation due to its broader agro-ecological adaption (Tesfaye Tesso *et al.*, 2008). In Africa, a major growing area runs across West Africa south of the Sahara, through Sudan, Ethiopia, and Somalia. It is grown in Egypt and Uganda, Kenya, Tanzania, Burundi, and Zambia. It is a significant crop in the drier regions of Argentina and Brazil, Venezuela, the United States, France, and Italy, as well as in India, Pakistan, Thailand, central and northern China, and Australia (Rana *et al.*, 1998). Ethiopia is the world's largest producer of sorghum, next to United States, Mexico, Nigeria, Sudan and India. Ethiopia is Africa's third largest producer of sorghum after Nigeria and Sudan, accounting for approximately 12% (Asfaw Adugna,2014).

On the global scale the 2022/2023 cropping season, sorghum production amounted to approximately 57.61 million tons, from the total harvested area of 40.64 million ha with an average yield of 1.42 ton ha-1 (FAO, 2022). In Ethiopia, the area covered by sorghum was estimated to be 1,350, 509.37 ha, with a total production of 355367.1 ton, and its productivity is 2.63ton per hectare (CSA, 2022). In the Amhara region, the area coverage, production and

productivity of sorghum was covered 576,148.05 ha, 1,529,198.1ton and 2.65 ton/ha, respectively. The North Wollo Zone also has its own contribution to sorghum production area coverage, and the production and yield of sorghum are 56,953.34 ha, 149181.26 ton and 2.62 ton/ha respectively (CSA, 2022). Sorghum is grown mainly in the lowlands of Ethiopia, which accounts for almost 66% of the country's total area coverage (Gebeyehu Geremew *et al.*, 2004).

In the United States, Australia and other developed countries, sorghum is grown primarily for animal feed. However, in Africa and Asia, grain is used for both human consumption and animal feed (Dicko *et al.*, 2006). Sorghum plant stem and foliage are used for green chop, hay, silage, and pasture. In some areas the stem is used as building material, and plant remains (after the head is harvested) may be used for fuel (House, 1985). Over the past four decades more than fifty two improved sorghum varieties have been released with various desirable traits into the four major agro ecologies by several national and regional research organizations as well as universities across the country (Werkissa Yali, 2022). Many sorghum-growing areas in Ethiopia are subject to recurring droughts due to rainfall scarcity and/or unequal distribution. Rain comes late or ends early in sorghum producing regions, resulting in a crop growing time that is too short, resulting in crop failures (Solomon Asefa, 2017).

One of the Vavilovian centers of origin, or diversity, for numerous domesticated and wild crop species, including sorghum, is recognized to exist in Ethiopia. The largest diversity of the crop germplasm provides greater opportunities for improvement regarding its environmental adaptability and acquiring better agronomic traits from the crop species(Werkissa Yali, 2020). Cultivated sorghum has a large phenotypic diversity that breeders can exploit for further improvement. Exploitation of genetic diversity requires effective characterization of the genetic pool. The genotypes can be characterized using morphological, molecular markers and analysis of nutritional quality traits (Mofokeng *et al.*, 2017). Genetic variability plays a fundamental role in any plant breeding program. Grain yield is a complex trait and is governed by other yield related traits. Therefore, it would be preferable to study the grain yield through its component traits rather than direct selection for yield (Jimmy *et al.*, 2017). Numerous studies have shown that sorghum is a very diverse crop,

with cultivated sorghum exhibiting high phenotypic variability. Many plant breeders exploit this genetic variability for crop improvement (Duy Can *et al*., 1998; Warkad *et al*., 2008; Yaqoob *et al*. 2015).

Knowledge of the genetic variability, heritability and genetic progress of the traits to be improved is essential and a prerequisite for any breeding programme to improve crop productivity and quality (Janaki *et al*., 2015). The current national average yield of sorghum in Ethiopia is still low, at approximately 2.63 t/ha compared to the global potential of 6 t/ha (CSA, 2022). In the study area, sorghum stalks are used for animal feed, construction and even as a source of cash because they are sold as fuel in towns. Overall, the value of the stalk is approximately 40% of the value of the grain produced and is highly valued in Ethiopia (Wortmann *et al.,* 2006). The limited adoption of improved early maturing sorghum varieties in the study area is mainly due to unsatisfied needs of small-holder farmers that lower biomass production of the crop. Therefore, it needs to evaluate the genetic variability and association of traits for the genotypes and identify promising genotypes for use in future breeding programs. Therefore, this research was built with the following objectives:-

1.2. Objectives of the Study

1.2.1. General objective

To assess the extent and pattern of genetic variability and association in sorghum genotypes for yield and yield components

1.2.2. Specific objectives

1. To evaluate the genetic variability among sorghum genotypes for future yield improvement;
2. To estimate the heritability and genetic advance of target traits;
3. To determine the association of sorghum genotypes for grain and biomass yield improvement;
4. To determine the relationships among genotypes and clustering based on their similarities.

Chapter 2. LITERATURE REVIEW

2.1. Genetics, Origin and Distribution of Sorghum

Sorghum is a self-pollinating, diploid (2n=2x=20) species of the Poaceae family with a genome size of 730 Mb, approximately 25% of the size of maize. Its small genome makes it an attractive model for studying the functional genomics of C4 grasses (Kumar, 2016). The geographical origin and first domestication of sorghum occurred in Africa. Ethiopia is believed to be the center of origin and cultivation of sorghum (Doggett, 1988; Vavilov, 1951). The crop is native to Ethiopia, where it has been domesticated for a long time and genetic diversity has been shown to be diverse among its concentrated domesticated and wild relatives (Werkissa Yali, 2020). Then, at least 3,000 years ago, it spread to the Middle East and India along trade and shipping routes around the African continent. It then travel along the Silk Road to China (Dicko *et al.*, 2006). The slave trade originally brought it from West Africa to North America in the 1700s and 1800s. It was then brought back to Africa for commercial cultivation in the late 19th century. From there, it spread to South America and Australia (Zigale Semahegn *et al*, 2019). Sorghum is now widespread in the dry lands of Africa, Asia (India and China), the Americas and Australia.

2.2. Botany and Taxonomy of Sorghum

Sorghum is a species of grass in the family Gramineae (Reddy *et al.*, 2002). Sorghum bicolor is an erect plant with a solid stem that can be sweet, dry or succulent. Its length can range from 0.8 to 5 meters (Chikuta, 2011).The leaf has a prominent midrib, the normal leaf blades are 50-90 cm long and 8-12 cm wide on average and are arranged in two alternating rows, and the leaf sheaths are 15-55 cm long and encircle the stem (Prasad and Staggenborg, 2009). The inflorescence of sorghum, known as the panicle, produces bisexual flowers with stamens and pistils surrounded by glumes. Because of its diverse morphophysiological characteristics and wide range of flower morphologies, sorghum is divided into a number of basic and intermediate races. Sorghum has recently been recognized as 25 species, and it is divided into five subgenera: Eu-sorghum, chaeto-sorghum, Heterosorghum, Parasorghum, and

Stiposorghum (Kumar, 2016). Eu-sorghum is composed of the wild species S. xalumParodi, S. halepense (L.) Pers., and S. propinquum, as well as the cultivated species S. bicolor (L.) Moench and its subspecies drummondii and arundinaceum (De Wet, 1978).The grain of the race bicolor is elongated, and glumes clasp the grain, which may or may not be completely covered. Most of this race's population is found in Africa's westernmost regions, as well as practically everywhere else on a smaller scale. Guinea is largely a West African country, with minor populations in Tanzania and Malawi. The grain is flattened dorso-ventrally, twisting at maturity 90 degrees between glumes that are nearly as long as or longer than the grain. The caudatum grain is asymmetrical, with glumes half the length of the grain or less. This race is most abundant in eastern Nigeria, Sudan and Uganda. Kafir is mostly a race from eastern and southern Africa. It has symmetrical grains, with glumes of variable length clasping the grains. Durra is predominant in Ethiopia and the western part of the continent, covering the driest areas near the Sahara Desert. Its grain grains are rounded, and its glumes are very wide (House, 1985).

Figure 2.1. Different panicle diversity of the sorghum accessions; A= Guinea, B= Caudatum, C= Durra, D= Kafir, E= Bicolor

Source:(Motlhaodi, 2016)

2.3. Importance of Sorghum

In the semiarid tropical regions of Africa, Asia and Latin America, sorghum is grown as a rainfed crop on more than 42 million hectares, mainly by subsistence farmers. In the semiarid areas of East Africa and South Asia, it is the most important cereal crop, while in the

developed world it is used as animal feed (Reddy *et al*., 2004). After tef and maize, sorghum is generally considered to be the most important staple food and feed crop. Cereals contribute 88.69% of the total crop production and occupy 81.97% of the total area devoted to cereals, and, sorghum contributes 12.22% of the total cereal production and 13.5% of the total area devoted to cereals nationally (CSA, 2022).

Sorghum is a C4 crop, that is mostly grown in climates with high temperatures and water scarcity (Edwards *et al.,* 2004). Around September or during the 'Meskel' season, farmers begin to harvest green heads for food. At this time, sweet stem sorghum varieties reach the middle of the grain filling stage can be chewed as important sources of nutrients (Solomon Asefa *et al*, 2018). *Injera* (flat bread), *qollo* (roasted grain), *nifro* (boiled), *chibeto* (*kitta* or chapatti combined with noug or sesame), porridge, soup, and tella (local beer) are typical foods made from sorghum grain after harvest. Stalk is used as a building material, animal feed, and even a source of income because it is traded for fuel wood in urban areas.

Sorghum provides a major source of protein, vitamins, and minerals for people (Duodu *et al.*, 2003). Starch is the primary source of stored energy in cereal grains. Starch is deposited as granules in endosperm cells and is being the main constituent of the endosperm. It is a good energy source because it is approximately 70% starch. After starch, proteins make up the majority of the sorghum grain's dry weight, or up to 12% (Ng'uni *et al*., 2012). The essential amino acid composition of sorghum protein varies (3–12% range) depending on the variety, soil, and growth environment (Labuschagne, 2018). Polyunsaturated fatty acids are abundant in the fat found in sorghum grain, which is mostly found in the germ (Glew *et al*., 1997). Sorghum fat has a fatty acid composition comparable to that of corn fat (linoleic acid 49%, oleic 31%, palmitic 14%, linolenic 2.7%, stearic 2.1%, etc.), but it is more unsaturated (Adeyeye and Ajewole, 1992). Sorghum is also rich in phosphorus, potassium, iron and zinc (Glew *et al.,* 1997). For human consumption, large, white grains with corneous endosperm are typically favored. When the endosperm is yellow from carotene and xanthophyll, the nutritional value increases (Ng'uni *et al.,* 2012). Especially in Africa, red varieties are favored for beer making, and this sorghum-derived drink is popular at traditional festivals. Tall sweet varieties are usually used to make silage and hay for livestock feed. Those with succulent,

sweet stalks and small heads and grains are preferred for chewing, as is the case for sugarcane (Motlhaodi, 2016).

2.4. Growing Environments of Sorghum in Ethiopia

Sorghum is cultivated over a wide range of elevations and rainfall conditions in Ethiopia. It grows in many of the hot, arid lowland regions, and certain varieties are also grown in cooler, wetter highland regions up to 2,700 meters above sea level. Sorghum grows in 13 of the 18 major agro ecological zones and in 41 of the 49 sub-AEZs of Ethiopia (Alemu Tirfessa, 2019). The length of the growing season, altitude and temperature are used to categorize agro-ecologies. A compromise had to be reached to reclassify the ecological zonation for research purposes on the basis of altitude, and as a result the main sorghum growing areas were divided into four primary categories. These are highlands, midlands, dry lowlands and wet lowlands. Highlands include areas above 1800 m.a.s.l., intermediate areas 1600-1800 m.a.s.l., and dry and wet lowlands include areas below 1600 m.a.s.l. (Asfaw Adugna *et al.*, 2005).

Sorghum is a short-day crop, but there is much genetic variation in its ability to adapt a wide range of photoperiod and temperature conditions (Craufurd *et al*., 1999). It requires deep, well-drained, fertile soils, fairly stable rainfall and a warm, frost-free period to grow well. A wide range of soil types can be tolerated, but growth on sandy soils is usually poor unless there is heavily textured subsoil. The suitable pH range is 5.5 to 8.5. Sorghum tolerates water logging better than maize. Warm weather crops such as sorghum need high temperatures for healthy germination and growth. Germination requires a soil temperature of 7 to 10°C, but if there is enough moisture, germination can also occur at 15°C or more. Temperatures between 27 and 30 degrees Celsius are necessary for optimum growth development after germination (Motlhaodi, 2016).

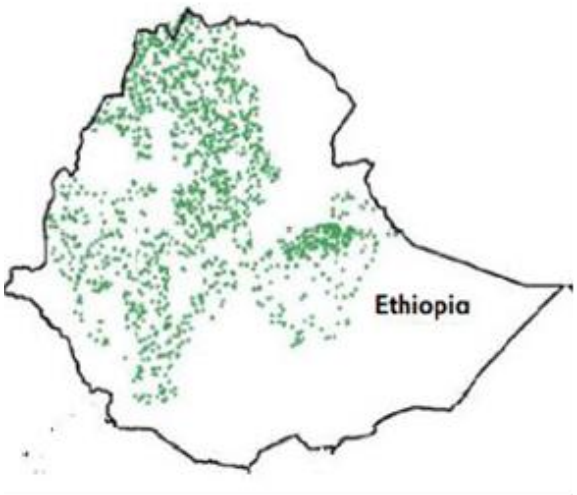

Figure 2.2. Distribution of grain sorghum production in Ethiopia; The sorghum growing areas are indicated by green dots

Source:(Wortmann *et al.*, 2006)

2.5. Production and Productivity of Sorghum

Globally, sorghum is the fifth most important cereal crop after rice, maize, wheat and barley, with an estimated production of 62.3 million tonnes on an area of 42 million hectares (Kretser *et al.*, 2017). In Ethiopia, it ranks fourth in area after teff, maize and wheat, and accounts for 12.22% of the total annual cereal production. Sorghum is grown on approximately 1,350, 509.37 hectares of agricultural land, with a total annual production of 355367.1 ton in Ethiopia (CSA, 2022). In the Amhara region, the area coverage, production and productivity of sorghum was covered 576,148.05 ha, 1,529,198.1 ton and 2.65 ton/ha, respectively.

The North Wollo Zone also has its own contribution to sorghum production with area coverage, production and yield of 56,953.34 ha, 149181.26 ton and 2.62 ton/ha respectively (CSA, 2022). Currently, the national average productivity of sorghum in Ethiopia is 2.63 ton/ha (CSA, 2022), which is far below the world average of 6 t ha^{-1}. Habru district is one of the potential area in the North Wello zone where sorghum is largely produced compared with other crops grown in the zone, sorghum contributes the greatest share (43.74%) of production (Amare Alemnew *et al*., 2015).

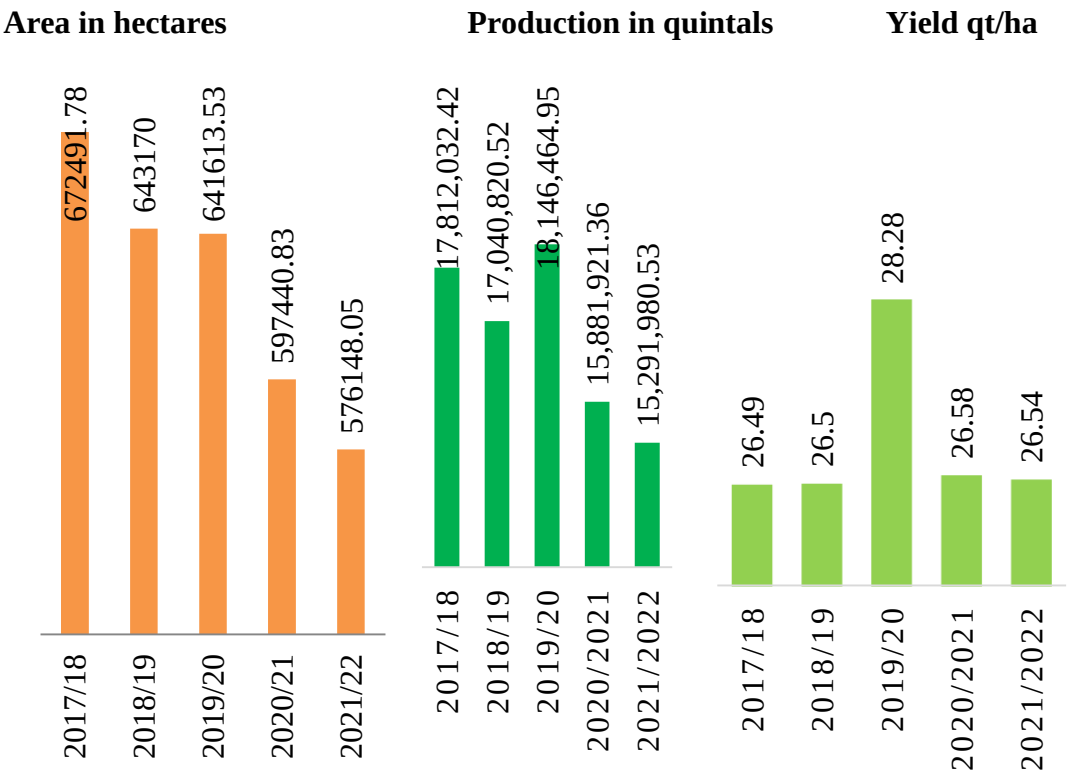

Figure 2.3. Trend of sorghum production

2.6. Production Constraints in Sorghum

Sorghum productivity in Ethiopia is relatively low, with a national average grain yield of 2.63 t h^{-1} (CSA, 2022). There are various production constraints, including abiotic conditions such as drought, low soil fertility (nutrient deficiency), lack of high yielding varieties and biotic conditions such as stem borers, shoot flies, qualia birds, striga hermonthica and other weeds, which are recognized as major production constraints in East Africa (Wortmann *et al.*, 2006) .Globally, drought is a major constraint to sorghum production and is considered to be the major cause of yield reduction in crops, especially in water-limited areas of the world, including parts of eastern and southern Africa (Yohannes Besufekad & Kassahun Bantte, 2013). In the arid and semiarid tropics, drought is more likely to occur at the beginning and end of the growing season.

Drought stress early in the growing season has a significant effect on plant establishment, while drought stress later in the growing season can lead to reduced establishment, yield or crop failure (Blum, 1996). Drought severely constrains sorghum production worldwide and is considered the major cause of yield reduction in agricultural crops, especially in water-stressed areas such as eastern and southern Africa (Hadebe *et al.*, 2017). Drought can occur at any stage of development, including at the seedling, preflowering and post flowering stages, and has the greatest impact on production. Drought stress during the seedling stage has a significant effect on plant establishment (Dhanagond *et al.*, 2019).

Ethiopian sorghum landraces have indigenous genetic variation for drought resistance that has not been used to produce sorghum varieties resistant to these critical conditions (Temesgen Begna, 2021). Because Ethiopia has a large genetic pool of drought-tolerant landraces, the breeding strategy in Ethiopia has focused mostly on screening landraces and varieties in drought-prone areas. Sorghum productivity is affected by insect pest damage. Insect pests attack seeds, seedlings, whorls, flowering structures and mature grains at different stages of growth. More than 150 insect species have been identified as pests of sorghum worldwide, of which more than 100 are found in Africa. In the last decade, entomologists have focused their attention on twenty-nine major insect families (Werkissa Yali and Temesgen Begna, 2022). Shoot flies, midges, stem borers and head bugs are serious insect pests in Africa, causing up to 85% damage in some cases (Sharma *et al.*, 2003). Major diseases limiting production include as sorghum anthracnose, powdery mildew, smut and ergot. Striga weed is believed to have originated in the Nuba Mountains of Sudan and Ethiopia, the native countries of sorghum (Gebisa Ejeta, 2007). Drought and Striga weed were identified as the major constraints in the northern and northeastern regions of Ethiopia (Rebeka Gebretsadik *et al.*, 2014). According to Haussmann *et al.* (2000), high levels of Striga infestation can result in grain production losses of up to 100% in susceptible sorghum varieties. In Africa, countries such as Ethiopia and Sudan have reported yield losses of 65% to 100% in heavily infested fields (Yousif, 2017).

2.7. Sorghum Breeding in Ethiopia

Scientific research on sorghum in Ethiopia began in 1953 at the Jimma School of Agricultural Technology (JATS), which was later transferred and formalized in 1957 at Alemaya College of Agro-Mechanical Arts (now Haramaya University) (Taye Tadesse *et al.*, 2019). The establishment of the Ethiopian Sorghum Improvement Project (ESIP) in 1972 with a large grant from the International Development Research Center (IDRC) marked a milestone for formal sorghum research in the country. In 1982, the EIAR (then the EARO) adopted the ESIP as one of its national programs and took over the initiative in sorghum research. Since that time, the Melkassa Agricultural Research Center has been organizing sorghum research across the nation.

The national sorghum research programme is now collaborating with universities and research organizations at the global, national and regional levels. For each of the four primary sorghum agro-ecologies, the breeding programme currently includes six product categories (PC1 - PC6) based on the attention of sorghum farmers, stakeholders and end-users.The allocation of resources and efforts for pipeline development has been aligned with the importance of the market segment for the outlined product types. The first three product types target dry lowland environments, which account for 72% of the total production area, while the other three product types target 8%, 11% and 9% of wet lowland, highland and midland environments, respectively (Werkissa Yali and Temesgen Begna, 2022).

2.8. Farmer's Preferences in Sorghum Breeding

The improved varieties in Ethiopia's sorghum-growing regions did not satisfy the needs of small-holder farmers. Compared with developed cultivars, local landraces generally produce more in favorable seasons and are more vulnerable to bird attack because of their high earliness and lower biomass production (Asfaw Adugna, 2007). Sorghum stover is an important product used as fuel, fodder and construction material. Overall, the value of the grain stalk is approximately 40% of the value of the grain produced and is highly valued in Ethiopia. Due to the high endosperm content, the large grain size of sorghum is also an

important qualitative characteristic. Additionally, grain color is acknowledged as a significant characteristic, with white and light yellow being strongly preferred in the study area. Although red and brown grain varieties are frequently linked to high tannin contents, they are less favored by birds and less susceptible to mold (Wortmann *et al.*, 2006).The main reason for the poor adoption rate and low impact of the improved varieties is the lack of breeders' awareness of the traits that farmers desire (McGuire, 2008).

2.9. Genetic Variability, Heritability, and Genetic Advances

2.9.1. Genetic variability

Variability is the occurrence of differences among individuals due to differences in their genetic composition and/or the environment in which they are raised (Allard, 1961; Falconer, 1996). The core of plant breeding is genetic variability, which results from genetic variations among individuals within a population. This is because diversity can be managed in a way that both improves plant performance permanently and protects it from seasonal changes (Sharma, 2006; Welsh, 1981). To satisfy the needs of the world's future food security, plant genetic resources are crucial. Sustainable sorghum production can be achieved by making greater use of such varieties in sorghum breeding projects to create cultivars with a wide genetic foundation (Karadi and Kajjidoni, 2019). Genetic variability plays a fundamental role in any plant breeding programme. The most important aspect of measuring the genetic diversity of crop species is that it serves as the basis for selecting for desirable traits. Estimation of heritability and expected genetic gain from selection also benefits from accurate estimates of genetic and environmental variability. The amount of genetic variability present in sorghum is immense (Warkad *et al*., 2008). Understanding and accurately assessing genetic diversity in germplasm collections and effectively utilizing such variability in breeding programs are essential for crop development projects.

Ethiopia is central to the genetic diversity of many domesticated crop plant species, including sorghum, barley, tef, chickpea, and coffee. These plant species are primarily represented in the nation by local landraces and wild types, which are particularly well adapted to harsh

environmental conditions due to their genetically diverse forms (Tilahun Mola and Meseret Ejeta, 2021).Using genotypes that represent particular and various sorghum-growing regions, studies of genetic diversity for both qualitative and quantitative features have also been carried out and have shown the extent of genetic variation in addition to the differentiation of panicle compactness and shape according to geographic region (Ayana Amsalu and Endashaw Bekele, 1998).

Ethiopia became the genetic resource reservoir ranking first in contributing germplasm collection worldwide in the modern sorghum breeding program due to the existence of a vast amount of sorghum variability that exhibits native genetic variation to drought, disease, and insect resistance, good grain quality, and high lysine content. The landraces of Ethiopian "zerazera" sorghum and the lineage that was created from them were utilized in the production of hybrids at ICRISAT and in other nations' current sorghum breeding programs. Sorghum plants at the Ethiopian Center of Crop Diversity are incredibly rich in genetic diversity. There is some concerted effort to adequately collect and preserve this genetic variability before it is invaded and destroyed (Tilahun Mola and Meseret Ejeta, 2021). The genetic enhancement of sorghum yield depends on genetic diversity in populations, the quality and extent of heritability and genetic progress, and the nature of the association between yield and its constituents. This enables simultaneous selection for many traits associated with yield (Chavan *et al.,* 2011). In general, sorghum possesses a wide range of genetic variability (Mlavanya and Vanjah, 2006). Appropriate variability provides options for choosing improvements and hybridization possibilities. In any crop improvement program, breeders first identify the existence of genetic variability for the trait of interest. This is due to the critical role of genetic variability in determining the amount of progress to be made by selection. Overall, comprehensive knowledge on genetic variability, heritability and genetic advance allows geneticists and breeders to design breeding strategies for improving crop productivity and quality (Johnson *et al.*, 1955).

2.9.2. Phenotypic and genotypic coefficient of variation

Phenotypic variability, which encompasses both genotypic and environmental variation, is the observable variation in a population's characteristics; as a result, its magnitude varies depending on the environment. Genotypic variation, on the other hand, is the component of variation resulting from genotypic differences between individuals within a population(Singh, 2001). To obtain elite germplasm accessions for use in subsequent breeding programmes, phenotypic selection for desirable traits with high GCV and PCV, high heritability and high genetic advance is needed. A positive or negative correlation between two traits is essential for plant breeders to develop new high-yielding varieties (Mohammed, 2006). Plant phenotype is the result of the interaction of many factors, and final yield is the sum of the effects of several constituent factors (Biradar *et al.*, 1996).

High genotypic and phenotypic variance indicates that there is wide genetic variation among genotypes. The genotypic correlation coefficient provides measures of genetic association between traits to identify the more important and less important traits to be considered in breeding programmes (Tsegau Senbetay and Tegegn Belete, 2020). According to Hamad and Dagash (2017) reported the highest genotypic coefficient of variation and phenotypic coefficient of variation values for plant height for ten advanced sorghum genotypes. According to Santhiya *et al*. (2021), high PCV and GCV for grain yield per plant and panicle length were evaluated for 102 sorghum germplasm accessions.

2.9.3. Heritability and genetic advance

In a broad sense, heritability can be defined as the proportion of genotypic variability to total variance (Allard, 1999). The heritability of a trait is important in determining its response to selection. Heritability estimates help breeders manage the resources needed to select efficiently for desirable traits and maximize genetic gain with little effort and expense (Smalley *et al.*, 2004).To have a greater chance of selecting directly for the traits of interest, high heritability is also needed. This is mainly because high heritability allows accurate genotype identification and measurement based on phenotypic values, as well as avoids errors in genotypic classification (Welsh, 1981). Heritability shows how successfully phenotypes

can be selected depending on their phenotypic performance. If heritability was 100%, then phenotypic performance would be a perfect indicator of genotypic value (Johnson *et al*., 1955).

Heritability allows a plant breeder to identify the genetic differences between strains, and variation shows a population's potential for improvement. A genotypic value that depends on three factors is genetic advance under selection (Allard, 1960). These include genetic variability, heritability and the intensity of selection applied. According to Yali Kebbede (2021), genetic advancement provides an estimate of the expected gain for a particular trait through selection. Genetic advancement aids in the selection of breeding techniques by revealing the effects of gene action on the expression of traits. Thus, heritability estimates coupled with genetic advances are more reliable and helpful in predicting gains under selection than individual considerations of parameters (Johnson *et al*., 1955).

Estimating heritability with genetic advance is more reliable and important than looking at parameters individually (Nwangburuka and Denton, 2012). Heritability and genetic advance are important selection parameters. Heritability estimates can be grouped as broad sense heritability or narrow sense heritability (Holland *et al.*, 2003). Broad sense heritability provides information on the relative magnitude of genetic and environmental variation in specific populations (Holland *et al*., 2003; Singh, 2006). The presence of additive genes is indicated by high heritability and estimated genetic advance as a percentage of the mean for most traits, suggesting reliable sorghum improvement through selection for the traits (Jimmy *et al.*, 2017). According to Jimmy *et al*. (2017), high heritability was reported for traits such as plant height, days to 50% flowering, panicle length, thousand kernel weight, and grain yield for ten sorghum cultivars. The high heritability for plant height, days to 50% flowering, days to maturity, leaf area index, thousand kernel weight and grain yield were observed (Yaqoob *et al.* 2015). Mohammed Jafar et al. (2023) indicated that high heritability for plant height, days to 50% flowering, days to maturity, leaf length, panicle length, head weight, harvest index, and grain yield for sixty-four sorghum genotypes for 17 quantitative traits at the Boko research site. Godbharle *et al.* (2010) reported high heritability coupled with high genetic advance for plant height and panicle length traits in 20 B lines and 16 R lines of

Kharif sorghum genotypes. Another study by Mohammed Jafar et al. (2023) reported high heritability coupled with high genetic advance for traits such as panicle length, head weight, harvest index and grain yield.

2.10. Correlation of Traits

Estimates of genotypic and phenotypic correlation coefficients provide a measure of genotypic relatedness between traits and provide a trait index that may serve as an index for the more important traits under consideration (Johnson *et al.*, 1955). Correlation coefficient analysis helps to determine the nature and degree of the relationship between any two measurable characters. Traits that are not easily measurable or that are greatly influenced by the environment have low heritability, so it is necessary to study the relationships between different traits. Knowing the relationships between key characters can help interpret the results already achieved and provide a basis for planning more effective programs in the future (Ermias Estifanos, 2005). Genetic correlation occurs when a single gene influences two traits. There may be many genes that influence two or more traits. A genetic correlation can be positive or negative and is indicated by a numerical value between +1 and -1. 0 indicates no genetic correlation. A correlation of +1 means that the traits always occur together and a correlation of -1, means that the presence of one trait always excludes the presence of the other. Genetic correlation refers to the relationship between one trait and the other. If the correlated trait increases with the original trait, the traits are positively correlated. The two traits are negatively correlated if the first trait increases while the second trait decreases (Aruna and Chakravarty, 2019). The correlation of phenotypic values, also known as phenotypic correlation, is the correlation between two traits that can be seen immediately (Bhasin *et al*., 2012). Phenotypic correlations involve both genetic and environmental effects. Sorghum plants differ significantly from one another in terms of their plant features, panicle and grain characteristics, physiological responses to selection, and susceptibility to environmental influences (Ezeaku and Mohammed, 2006).

The analysis of correlations between quantitative traits is crucial for determining whether joint selection of two or more qualities is feasible and, consequently, for determining how

selection for secondary traits affects genetic gain for the primary trait in question. A positive genetic correlation between two desirable traits makes it easier for breeder to improve both traits simultaneously. Even the absence of correlation helps to improve both traits together. A negative correlation between two desirable traits, on the other hand, prevents or makes it difficult to make significant improvements in both traits. However, simple correlations do not provide insight into the true biological relationships of these traits with yield (Ezeaku and Mohammed, 2006).

A study by Mulugeta Mamo and Fisseha Worede (2020), who reported significant genotypic correlations of grain yield with plant height, head weight and biological yield and phenotypic correlation with head weight, panicle length and biological yield. Approximately, forty-nine sorghum genotypes were tested for resistance and susceptibility to striga hermonthica. In addition,Ezeaku and Mohammed (2006) found significant genotypic and phenotypic correlations of the grain yield of thirty sorghum varieties with plant height, head weight and thousand kernel weight. According to Arvinth *et al*. (2021), grain yield showed strong positive genotypic and phenotypic correlations with days to 50% flowering, plant height, leaf length and leaf width in twenty-two sorghum genotypes. The eighty-one sorghum genotypes including five checks, were evaluated for trait association for yield and yield components (Deshmukh *et al.* 2021). Significant genotypic and phenotypic correlations of the grain yield of sorghum genotypes with days to 50% flowering, plant height, panicle length, days to maturity and thousand kernel weight were observed.

2.11. Path Coefficient Analysis

Path coefficient analysis is an important statistical tool that can be used to show which variables (causes) influence other variables (effects), while also allowing you to see the effects of multicollinearity (Akanda and Mundt, 1996). Path analysis is essential for a deeper comprehension of the relationships between qualities, which opens the door to understanding the specificity of the genetic material under investigation (Tsegau Senbetay and Tegegn Belete, 2020). Breeders can better understand the causes of associations between two variables by using path coefficient analysis, which quantifies the direct and indirect effects of

independent variables on dependent variables (Baranwal *et al.*, 2012). Understanding the relationship between yield and other traits are very helpful in improving any crop. The number of variables considered to increase grain yield and the direction of selection are both determined by correlation coefficients (Jimmy *et al*., 2017). Estimates of correlations alone can often be misleading due to mutual cancellation of component traits. Therefore, the study of path coefficient analysis, which considers both the degree of the relationship and the causal relationship, becomes important (Chavan *et al.*, 2011).

Path analysis is preferred because path coefficient analysis can identify the direct and indirect causes of the association and measure their relative importance to each other. This is because, in some circumstances, correlation alone does not provide an accurate picture of the direct and indirect effects of the signs on each other (Singh and Chaudhary, 1977 ; Sharma, 2006). Correlation analysis, aided by path coefficient analysis, is a powerful tool for studying traits associations. The direct effect of any component trait on grain yield indicates the reliability of indirect selection through that trait to improve grain yield. If the direct effect and the correlation are both strong and favorable, then the character selection works well because the correlation describes the true relationship between the two. In such a relationship, even if the correlation coefficient is positive, if the direct effect is negative or negligible, indirect factors must also be considered and selected (Narkhede *et al*., 2017). Adane Gebreyohannes *et al.* (2018) observed the highest positive direct effects of plant height, days to maturity, and head weight on grain yield at the genotypic level for 14 sorghum genotypes evaluated at the Bako, Jimma, and Mechara Research Centers. Sharma *et al.* (2006) also reported positive direct genotypic and phenotypic effects of one hundred and seventy-six sorghum germplasm and two checks for days to 50% flowering, panicle length and hundred kernel weight on grain yield. A study by Prakash *et al*. (2010) reported days to 50% flowering, plant height, leaf length and leaf width in both genotypic and phenotypic path coefficient analyses of 12 sorghum parents and their 35 hybrids. Therefore, during selecting material for further breeding programmes and improving genotypes for yield improvement, the traits that most influence yield should be considered.

2.12. Clustering and Genetic Diversity Analysis

Cluster analysis, or simply clustering, is the process of dividing a set of data objects (or observations) into subsets. Each subset is a cluster, so objects in one cluster are similar to each other but different from objects in other clusters. Successful classification results in individuals within clusters being closer together in a geometric representation, but different clusters being further apart (Hair *et al.*, 2006). A multivariate technique known as clustering can easily display the genetic relationship or proximity between cultivars in a way that makes each group homogeneous with regard to particular characteristics and distinct from other groups with regard to the same characteristics. Most breeding programmes use diverse parents that are genetically dissimilar to each other; cluster analysis often identifies the level of genetic diversity and combines genotypes with related parents into a cluster *(*Mohammadi *et al.*, 2015).

The average genetic divergence of cultivars or populations is measured by genetic distance (Souza and Sorrells, 1991). Genetic similarity is the inverse of genetic distance and refers to the degree of genetic similarity between cultivars (Smith, 1984). Therefore, in any breeding programme, genetic diversity must be periodically introduced into the population to provide new opportunities for recombination and selection (Welsh, 1981). Clustering using the D^2 (genetic distance) matrix is useful for analyzing the divergence of the population to identify genotypic variability. The relative contribution of each component trait to the overall divergence was calculated using the D^2 statistic, which is also used to evaluate the forces of differentiation at the intra- and intercluster levels (Sharma, 2006). The genotypes within the same clusters or groups are less divergent, whereas clusters separated by the greatest D^2 (genetic distance) exhibit the greatest degree of divergence (Singh and Chaudhary, 1977). Other significant traits, such as disease resistance, earliness, quality, or even the performance of specific characters should be taken into account when choosing genotypes from the already chosen groups. In a previous study by Mia *et al.* (2007), 20 sorghum genotypes were grouped into four clusters. About 40 yellow pericarp sorghum genotypes obtained from ICRISAT for diversity analysis were grouped into three clusters based on their similar trait performances

(Prasad and Sridhar, 2019). Deep *et al.* (2020) found that 73 diverse indigenous forage sorghum genotypes were grouped into seven different clusters.

2.13. Principal Component Analysis (PCA)

The most popular multivariate statistical method is principal component analysis (PCA), which has applications in almost all areas of science. Principal component analysis reduces the number of associated factors to a smaller set of variables, simplifying complex data. In comparison to subsequent components, the first principal component explains the most variation in the data (Leilah and Al-Khateeb, 2005). The main goal of principal component analysis (PCA) is to minimize the dimensionality of a dataset composed of many interconnected variables while preserving as much of the variance of the dataset as feasible. This is accomplished by transforming the principal components (PCs) into a new set of uncorrelated and ordered variables such that the first few retain most of the variation present in all the original variables (Jolliffe, 2002).

A study by Amelework Beyene *et al*. (2016) showed that in 262 sorghum landraces, the first four principal components (PCs) with eigenvalues greater than one explained 82% of the total variation among the landraces studied for the twelve qualitative traits. In the second PC, leaf curl and midrib color had a significant contribution. Approximately 34% of the total variation accounted for by the first PC alone was due to the contrast between panicle exsertion and the average effects of stay-green, inflorescence compactness and grain color. Similarly, the third PC accounted for approximately 16% of the total variance of the landraces, mainly due to the contrast between glume cover and the average effects of awns and glume color. The first four principal component (PC) analyses explained most of the total variation, accounting for 81.30% of the total variation among thirty-six sweet sorghum germplasms (Elenen *et al.*, 2019). In addition, Malini *et al.* (2023) reported that three principal components accounting for 81.5% of the total variation were explained by 112 sorghum lines and six quantitative traits. In previous studies on sorghum, Kavithamani *et al.* (2019) also revealed three principal components that explained approximately 66.35% of the variability in eight quantitative traits among 100 sorghum germplasm accessions. Hamidou *et al*. (2018) showed that three PCs

explained 56.22% of the total variation in two hundred and eighty-two lines evaluated at two experimental sites in Niger.

2.14. Shannon Diversity Index

The Shannon diversity index (H), also known as the information statistical index, is another index commonly used to characterize species diversity in a community. It is not diversity itself, but only an index of diversity. The use of a formula makes the definition of diversity the simplest. The Shannon- wiener diversity index H is the most widely used of the various diversity indices that have been proposed (Sarma and Dhruba Das, 2015). The Shannon diversity index is one of the indices commonly used to characterize diversity in communities. The richness and evenness of qualitative traits of different sorghum genotypes were investigated. The number of species in a community is called species richness. The relative abundance of species is also important (Sarma and Dhruba Das, 2015).

According to the Shannon diversity index, which is equal to one and is used to measure diversity, values between 0.76 and 0.99 are considered high, 0.46 and 0.75 are considered moderate, and 0.01 and 0.45 are considered low (Jamago and Rosemarie, 2012). Sorghum leaf midrib color, grain shape and plant color all showed significant variation and were polymorphic. Leaf midrib color had the highest reported phenotypic diversity index (H') of 0.95, with an overall mean phenotypic diversity index of 0.70. Substantial variation was observed in grain and glume color and grain cover. Grain color (0.80) could be an indicator of end use. A panicle compactness and shape score of 0.73 has an impact on the level of cross-pollination in sorghum. There is high variability as indicated by the diversity scores recorded; suggesting that variation in characters is the cause of diversity in populations. A high value of (H') indicates that the classes for a particular trait are diverse and evenly distributed. Conversely, a lower value indicates less diversity (Kisua *et al*., 2015). A previous study by Amelework Beyene (2015) reported that 12 qualitative traits were evaluated for 262 sorghum landraces collected from the lowlands of Wello, Ethiopia. Verma *et al.* (2017) reported that there is considerable genetic diversity among 750 sorghum germplasm lines with 4 checks for different qualitative traits.

Chapter 3. MATERIALS AND METHODS

3.1. Description of the Study Area

The experiment was conducted at Sirinka Agricultural Research Center (SARC) research station, which is located in the North Wollo zone in the 2023 cropping season under rain- fed conditions. The SARC is located approximately 507 km north of Addis Ababa and 13 km from Woldia town. It is located at a latitude of 11°45' N and longitude of 39° 36' E with an altitude of 1890 m.a.s.l. The soil type of the experimental site is Eutric Vertisol. The experimental site has an annual rainfall of 980 mm, while amount of rainfall during the growing season (July to October) was 585 mm, characterized by a bimodal rainfall pattern, and the rainfall distribution was erratic. The main rainy season called “Kiremt” that from mid-July to early September, while the short rainy season “spring”, and extends from March to mid-May. According to meteorological data from the Sirinka Agricultural Research Center, the five month mean minimum and maximum temperatures were 14.5℃ and28℃, respectively. The major crops cultivated around the study area are sorghum, tef, maize, wheat, barley, horticultural crops and legumes.

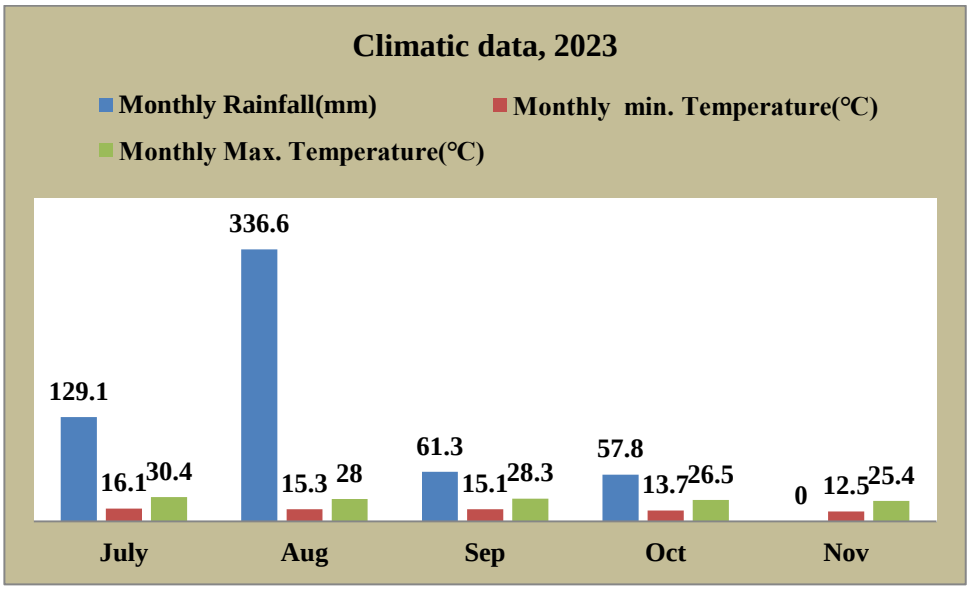

Fig 3.1. The growing season meteorological data

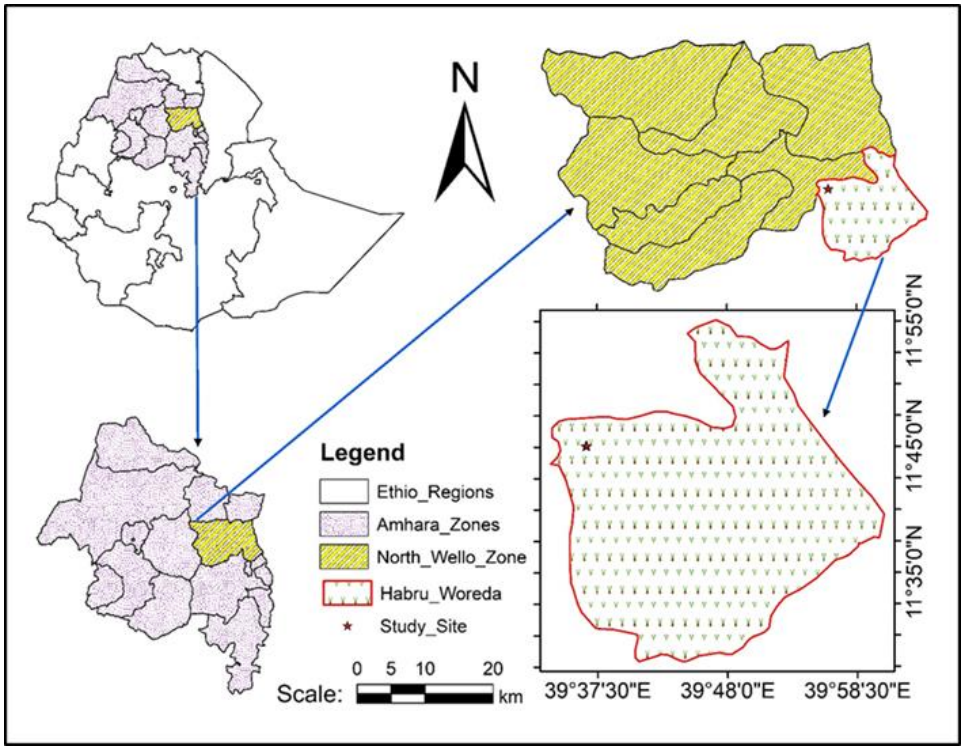

Figure 3.2. Map location of the study area, Sirinka

3.2. Experimental Materials

Eighty-one pure line sorghum genotypes including the standard checks (Melkam and Alene) were evaluated. The early maturing sorghum genotypes were obtained from the pedigree breeding of the national sorghum research programme based at the Melkassa Agricultural Research Centre (MARC). These genotypes were developed by crossing and subsequent selection of the segregating generation until they reached at the F6 generation assumed line attained homogeneity and two standard checks (Melkam and Alene) were obtained from Breeder Seeds stock of the Sirinka Agricultural Research Centre.

Table 3.1. List of sorghum genotypes used in the study

No	Genotypes	No	Genotypes	No	Genotypes
1	ETSC17296-3-1	28	ETSC18076-29-1	55	ETSC18076-13-1
2	ETSC18076-34-1	29	ETSC18034-19-1	56	ETSC15357-3-1
3	ETSC18076-6-1	30	ETSC18079-4-1	57	ETSC18025-3-1
4	ETSC17158-3-2	31	ETSC17068-3-1	58	ETSC17258-13-1
5	ETSC18076-1-1	32	ETSC16034-10-1	59	ETSC18086-35-1
6	ETSC18079-15-1	33	ETSC18086-4-1	60	ETSC17355-11-1
7	ETSC17186-2-1	34	ETSC18104-3-1	61	ETSC19051-18-7
8	ETSC18059-31-1	35	ETSC18076-21-1	62	ETSC17301-10-2
9	ETSC18059-52-5	36	ETSC17300-4-1	63	ETSC18097-38-1
10	ETSC18086-27-1	37	ETSC18012-5-1	64	ETSC18170-21-1
11	ETSC18095-14-5	38	ETSC17156-2-1	65	ETSC17121-2-1
12	ETSC14203-5-2	39	ETSC19182-7-4	66	ETSC17063-7-1
13	ETSC17201-1-2	40	ETSC17490-90-2	67	ETSC17285-5-2
14	ETSC18059-54-1	41	ETSC18074-26-7	68	ETSC18081-16-1
15	ETSC16091-10-1	42	ETSC18018-6-1	69	ETSC16034-12-1
16	ETSC17301-16-3	43	ETSC17258-5-2	70	ETSC17300-9-5
17	ETSC18015-14-1	44	ETSC17321-11-1	71	ETSC19125-7-7
18	ETSC17258-3-2	45	ETSC17300-4-2	72	ETSC15312-3-1
19	ETSC18086-3-1	46	ETSC17213-1-2	73	ETSC17113-6-1
20	ETSC18018-22-1	47	ETSC18059-47-1	74	ETSC14695-1-2
21	ETSC14225-4-2	48	ETSC18025-8-1	75	ETSC17111-3-1
22	ETSC18062-18-1	49	ETSC18018-6-1	76	ETSC17142-9-3
23	ETSC18059-47-1	50	ETSC17300-4-1	77	ETSC18025-3-1
24	ETSC18004-23-1	51	ETSC18086-27-1	78	ETSC19182-10-7
25	ETSC18073-10-1	52	ETSC17213-1-6	79	ETSC17483-233-2
26	ETSC18001-16-1	53	ETSC18076-5-1	80	Melkam
27	ETSC15363-1-2	54	ETSC17296-3-1	81	Alene

3.3. Experimental Design and procedure

The experimental design was a simple lattice (9 × 9) with two replications, and each plot consisted of two rows. The plot size and the total experimental area were 3 m × 1.5 m= 4.5 m^2 and 35 m × 43.5 m =1522.5 m^2, respectively. The inter row spacing was 0.75 m, and the intra row spacing was 0.15 m. The distances between plots, incomplete blocks and replications were 0.75 m, 1 m and 1.5 m, respectively. The experimental plots and rows were prepared accordingly. Sowing was performed on 26 July 2023 when sufficient moisture was available. Planting was performed by seeding at a rate of 12 kg/ha and thinning after emergence. Fertilizer was applied to each plot at the rate of 121 kg/ha^{-1} NPS at planting and 39 kg/ha^{-1} of urea after thinning. Weeding was carried out three times during the growing season. Weeding was performed three times during the growing period. The first round of weeding was carried out after the emergence of the plant at the 21-day or 5-leaf stage, the second round at the knee height stage, and finally at the boot stage.

3.4. Data Collected

The quantitative and qualitative data were collected from both plots and plants basis via a random sampling technique with the use of descriptors for sorghum (IBPGR/ ICRISAT, 1993).

Data to be collected on plot basis

Days to 50% flowering (days): The number of days recorded from the date of sowing until 50% of the plants in a plot have flowers.

Days to 90% physiological maturity (days): The number of days from the date of sowing to the date at which 90% of the plants in a plot reached physiological maturity was recorded. It was identified by the appearance of a dark black spot at the seed base.

Stand count at harvest (number): It was recorded by counting the total number of plants from each plot at harvest.

Number of heads per plot (number): The number of heads on each plot was counted during the harvesting period.

Head weight (kg): All panicles from harvestable plots were measured after harvest and then converted to per hectare.

Grain yield (kg /ha): The grain yield in grams obtained from the harvestable rows of each plot was measured and converted to kilograms per hectare. Grain yield (kg/ha) = 10 × grain yield (g/plot) / plot size (m^2).

Thousand kernel weight (gm): The weight of 1000 mixed grains sampled from a single plot was recorded in grams.

Aboveground biomass (ton ha^{-1}): The sun dry weight of the total aboveground plant biomass (crop + straw) was recorded per plot; and converted to ton per hectare. Aboveground biomass (ton/ha) = 10 × Aboveground biomass (kg/plot) / plot size (m^2).

Harvest index (%): The Harvest index (%) was recorded as the ratio of the dry weight of the grain to the dry weight of the total aboveground biomass and is expressed as a percentage.

$$\text{Harvest Index(HI)} = \frac{\text{grain yield(g)}}{\text{biological yield(g)}} \times 100\%$$

Data collected on plant basis

Plant height (cm): Plant height was measured from the soil surface to the top of the panicle during flowering on five randomly taken and tagged plants.

Leaf number/plant (number): The average number of leaves per plant counted from five randomly taken plants in a plot after flowering.

Leaf length (cm): The average length of the fourth leaf was recorded from the flag leaf of five randomly selected plants per plot.

Leaf width (cm): The average width of the fourth leaf from the flag leaf at the widest point on five randomly selected plants per plot was measured.

Total leaf area (cm^2): For this observation, five leaves were randomly taken from five tagged plants in each plot and the leaf area was calculated. Leaf area was expressed as length × width of the fourth leaf from the top × 0.71 following (Krishnamurthy *et al.*, 1974).

Panicle length (cm): The average length of five randomly taken plants from the base of the panicle to the tip was taken.

Qualitative traits

Observations of five qualitative traits; inflorescence compactness, seed color, glume color, inflorescence exsertion, and stay green, were recorded for each genotype on a plot basis based on visual observation. Estimates of qualitative traits diversity index had calculated by using Shannon–Wiener diversity index (H′) formula on Excel.

Seed color: Sorghum seed color that recorded from the experiment was only two and classified as 1 = white or 2 =red.

Glume color: At maturity, the sorghum glume color was recorded based on the Royal Horticultural Society (RHS) color codes (1 = white, 2 = red, 3 = yellow, 4 = grey, and, 5 = black).

Inflorescence compactness: 1= semi loose erect primary branches, 2= semi loose drooping primary branches, 3 = semi compact elliptic head, and 4 = compact elliptic head.

Panicle exsertion (cm): The length between the final (the most top) node up to the base of the panicle (1=slightly exserted (<2 cm), 2= Exserted (2-10 cm), and 3= well-exserted (>10 cm) was measured.

Stay green: The level of greenness was scored as 1-5 at maturity, where 1= very slightly senescent, 2= slightly senescent, 3= intermediate (approximately half of the leaves died), 4= mostly senescent and 5= completely senescent.

3.5. Data Analysis

3.5.1 Analysis of variance

Analysis of variance (ANOVA) for simple lattice design was computed for each measured quantitative trait using R software (R core team, 2022). Mean separation was performed using Duncan's multiple range test (DMRT) at a 5% probability level of significance to identify genotypes that were significantly different from each other. ANOVA assumptions for normality and homogeneity of variances were performed using the Shapiro-Wilk test and Bartlett's test, respectively.

The mathematical model for simple lattice design:

$Yijk = \mu + Gi + Bk(j) + Rj + Eijk.$

Where Yijk = is the phenotypic effect of the ith genotype under the jth replication and the kth incomplete block within replication j, μ = is the grand mean, Gi = is the effect of the ith genotype, Bk (j) = is the effect of the incomplete block within replication j, Rj = is the effect of the effect of replication j, and Eijk is the = the plot residual effect or effect of random error.

Table 3.2. Structure of ANOVA for simple lattice design and expected mean square

Source of Variation	Degree of freedom (DF)	Sum of square (SS)	Mean square (MS)	Calculated F value
Replication	r-1	SSR	MSR	MSR/MSE
Treatment(unadj)	K^2-1	SST (unadj.)	MST (unadj.)	MST/MSE
Treatment(adj.)	K^2-1	SST(adj.)	MST(adj.)	MST/MSE
Blocks within replication	R(k-1)	SSB(adj.)	MSB(adj.)	MSR/MSE
Intra block error	(k-1)(rk-k-1)	SSE	MSE	
Total	rk^2-1	SSTo		

Note: R = number of replications; K^2 = number of treatments; K= number of plots in a block; SS = sum square; MS = mean square; t = number of genotypes; SSR, SST, SSB, and SSE stand for sum square for replication, treatment, block and error. MSR, MST, MSB and MSE represent the mean squares for replication, treatment, block and error, respectively (Gomez and Gomez, 1984).

3.6. Estimation of Phenotypic and Genotypic Parameters

3.6.1 Estimation of variance components

The environmental, genotypic, and phenotypic variance components and their coefficients of variation for each quantitative trait were estimated based on the methods presented (Burton and De Vane, 1953).

The environmental variance ($\sigma^2 e$) = mse (error mean square).

Phenotypic variance ($\sigma^2 p$) = $\sigma^2 g + \sigma^2 e$.

$\sigma^2 g = \frac{Mg - Me}{r}$ where, $\sigma^2 g$ = genotypic variance; $\sigma^2 e$ = environmental (error) variance (error mean square); Mg= mean sum square of genotypes; Me= mean sum square of error and r=number of replications.

3.6.2. Estimation of phenotypic and genotypic coefficients of variation

The GCV and PCV were estimated by the methods of Burton and De Vane (1953).

Phenotypic coefficient of variation, $PCV = \frac{\sqrt{\sigma^2 p}}{\bar{X}} \times 100$

Genotypic coefficient of variation, $GCV = \frac{\sqrt{\sigma^2 g}}{\bar{X}} \times 100$

Where $\bar{X} = \text{population mean}$

PCV and GCV were classified as suggested by Siva subramaniam and Menon (1973).

Estimates less than 10% = Low;

10-20% = Moderate and

More than 20% = High.

3.6.3. Estimation of broad sense heritability

Heritability in the broad sense (H^2 (b)) was estimated according to the formula suggested by Allard (1961).

$H^2 = \frac{\sigma^2 g}{\sigma^2 p} \times 100$

The heritability (H^2 (b)) was categorized as suggested by Johnson *et al*. (1955).

0-30% = Low

31-60% = Medium

61% and above = High

3.6.4. Estimation of genetic advance

The genetic advance (GA) was estimated according to the formula given by Allard (1961).

GA=K×σp×H^2;

K = Selection differential at 5 percent selection intensity, which accounts for a constant value of 2.06.

σp =Phenotypic standard deviation

The genetic advance as a percentage of population mean (GAM) was calculated using the following formula and is expressed as a percentage.

$$\text{GAM} = \frac{(GA)}{\ddot{x}} \times 100\%$$

The percentage of genetic advance as percent over the mean was categorized as suggested by Johnson *et al*. (1955).

Estimates less than 10% = Low;

10-20% = Moderate and

More than 20% = High.

Where h^2 = the heritability ratio; σρ = phenotypic standard deviation; and k = constant (2.06).

The GAMs were categorized as low, moderate or high as suggested by Johnson *et al*. (1955) as follows.0 -10% = low, 10 –20 = moderate and >20 = high.

3.6.5. Correlation coefficient

Phenotypic correlation, the observable correlation between variables, which is the sum of genotypic and environmental effects was calculated from variance covariance components using the formula suggested by Miller *et al.* (1958) as follows;

Phenotypic correlation coefficients (rpxy)

$$\text{rp} = \frac{\text{pcovx.y}}{\sqrt{\sigma^2\text{px}.\,\sigma^2\text{py}}}$$

Where; rp = phenotypic correlation coefficient;

Pcovx.y = phenotypic covariance between variables x and y;

σ^2p x = phenotypic variance for variable x and σ^2py = phenotypic variance for variable y.

Genotypic correlation coefficients (rgxy)

$$\text{rg} = \frac{\text{gcovx.y}}{\sqrt{\sigma^2\text{gx}.\,\sigma^2\text{gy}}}$$

Where rg = genotypic correlation coefficient;

Gcovx.y = genotypic co-variance between variables x and y;

σ^2gx = genotypic variance for variable x and σ^2gy = genotypic variance for variable y. The significance of the phenotypic correlation coefficients was tested by the formula suggested by Singh and Chaudhary (1977). The calculated 't' value was compared with the tabulated 't' value at (n-2) the degrees of freedom at the 5% and 1% levels of significance for both genotypic and phenotypic correlation coefficients (Sharma, 2006).

$t = \frac{rp}{SE(rp)}$ where, $SE(rp) = \sqrt{\frac{(1-r^2p)}{(n-2)}}$

Where, n is the number of genotypes tested, rp is the phenotypic correlation coefficient, and SE (rp) = is the standard error of the phenotypic correlation. The coefficients of correlations at genotypic levels were tested for their significance using the formula described by Alan Robertson (1959) as indicated below:

$t = \frac{rgxy}{SErgxy}$ where, $SErgxy = \sqrt{\frac{(1-r^2gxy}{H^2x.H^2y}}$

Where: $rgxy$ is the genotypic correlation coefficient between traits x and y, $SErgxy$ is the standard error of the genotypic correlation coefficient between traits x and y, h^2x is the heritability of trait x, and h^2 is heritability of trait y.

3.6.6. Path coefficient analysis

Path coefficient analysis was performed using the formula suggested by Dewey and Lu (1959) to assess the direct and indirect effects of different variables on grain yield as follows:

$$Rij = pij + \Sigma\, rikpkj$$

Where; rij = is the mutual association between the independent trait (i) and dependent trait (j) as measured by the correlation coefficients; Pij = is the component of direct effects of the independent trait (i) on the dependent trait (j); and ΣrikPkj = is the summation of components of the indirect effect of a given independent trait (i) via all other independent character traits (k).The residual effect (U) was calculated using the formula by Dewey and Lu (1959) indicated below:

$U = \sqrt{1 - R^2}$ where $R^2 = \Sigma pij * rij$

where; Pij = direct effects of the independent character (i) and the dependent character (j) as measured by the path coefficient and rij = mutual association between the independent character (i) and dependent character (j) as measured by the correlation coefficient.

3.6.7. Cluster analysis

The data were standardized to a mean of zero and variance of one before performing the cluster analysis. Cluster analysis was performed on the Euclidean distance matrix using Ward's linkage method. Cluster analysis for genetic divergence among the genotypes was estimated by D^2 (Mahalanobis, 2018). The analysis was based on all the yield contributing traits influencing yield. The D^2 statistics were utilized to estimate the distance between and within clusters (divergence) using the R core team, software as per the following formula:

$$D^2_{ij} = (x_i - x_j)s^{-1}(x_i - x_j)$$

Where: D^2_{ij}= the distance between classes i and j;

(Xi-xj)= vector means of the traits for the i^{th} and j^{th} groups, respectively.

S^{-1}= pooled error variance and covariance matrix.

3.6.8. Principal component analysis (PCA)

The data were standardized to a mean of zero and a variance of one before principal component analysis was performed in order to identify the major traits accounting for much of the variability among the genotypes. To perform principal component analysis, the data were first standardized by using the formula used by (Stephanie, 2014):

$Z = \frac{X-\mu}{\sigma}$ where; Z is the standardized value, x is observation value, μ is the sample mean and σ is the standard deviation of the sample. Principal component analysis (PCA) was performed by using R software. The traits contributing to a large part of the total variation among the genotypes were identified by the following formula suggested by Sneath (1973).

$$PC_1 = b_{11}(x_1) + b_{12}(x_2) + \ldots\ldots b_{1p}(x_p)$$

Where: $PC1$ is the first principal component; b_{1p} is the regression coefficient (weight) for the p^{th}variable, which is the eigenvector of the covariance matrix between the variables and x_p is

the value of the p^{th} variable. A principal component with eigenvalue greater than one was taken. Principal components based on the correlation matrix were calculated using R software.

3.7. Variability of Sorghum Genotypes for Qualitative Traits

3.7.1. Shannon diversity index

Phenotypic frequencies of qualitative traits were used to calculate the frequency distribution and phenotypic diversity of the sorghum qualitative traits by employing the Shannon-Wiener diversity index (H´). In the present study, the sorghum seed color, glume color, inflorescence compactness, panicle exsertion, and stay green traits were tested for 81 sorghum genotypes and the phenotypic frequencies of these traits were used to estimate the diversity by the following formula for the Shannon diversity index (H') (Shannon, 1948). Descriptive statistics were generated using Microsoft Excel computer software.

$$H'' = -\sum_{I=1}^{N} \text{pi} \log(\text{pi})$$

Where: Pi is the relative proportion of the total number of entries (N) in the ith class, which means; Pi = S/N; Where S = is the number of individuals of one species; N = is the total number of all individuals in the sample; H = is the Shannon diversity index; and ∑ = is the sum from genotype 1 to genotype S, log = logarithm to base e.

Chapter 4. RESULTS AND DISCUSSION

4.1. Analysis of Variance

Analysis of variance (ANOVA) revealed highly significant differences (P<.001) among the 81 sorghum genotypes for days to 50% flowering, plant height, head weight, leaf length, leaf area index, panicle length, biological yield, harvest index, thousand kernel weight and grain yield (Table 4.1). In addition, there were significant differences ($p < 0.05$) among the genotypes for days to maturity and leaf width (Table 4.1). These results indicated the presence of ample genetic variation in the current population for yield and yield- related traits, which could be exploited through selection in sorghum improvement programmes in the study area or similar agro-ecologies of sorghum potential areas in Ethiopia. However, analysis of variance did not show statistically significant differences among sorghum genotypes for stand count at harvest, leaf number and head number.

The existence of high variability for different traits among sorghum genotypes has been reported by previous authors (Gebremedhn Gebregergs and Firew Mekbib, 2020;Tsegau Senbetay and Tegegn Belete, 2020;Mohammed Jafar et al., 2023). Most of the above authors reported highly significant variation among sorghum genotypes for plant height, days to 50% flowering, days to 90% maturity, biological yield, panicle length, thousand kernel weight, harvest index, head weight and grain weight. However, in contrast to the present results, highly significant differences were also reported for the number of leaves per plant among 24 sorghum genotypes (Mohammadi *et al.*, 2015). This difference may be due to differences in the genotypes used and the environmental conditions where the studies were conducted. The relative efficiency of the simple lattice design was greater than one hundred for most of the quantitative traits except stand count at harvest and thousand kernel weights, indicating that a simple lattice design had an advantage over a randomized complete block design (RCBD).

Table 4. 1. ANOVA of 15 quantitative traits of 81 sorghum genotypes

	Mean squares								
Source of variation	Replication Df=1	Block Df=16	Treatment(unadjusted and adjusted)Df=80	Error Df=64	MEAN	R^2	CV	LSD 0.5%	Efficiency Relative to RCBD
DF	6.32ns	7.21ns	17.86***	5.52	78.57	0.81	3	4.68	101.37
DM	574.23***	12.32ns	18.85*	10.96	130.07	0.76	2.5	6.59	100.27
LL (cm)	6.32ns	95.1**	82.07***	38.27	71.64	0.77	8.6	13.10	113.92
LW (cm)	7.78**	1.19ns	1.36*	0.79	7.12	0.73	12.4	1.77	103.30
LA (cm^2)	26190.5*	8441.9*	9282.2***	4065.0	365.89	0.78	17.4	133.81	108.46
LN	9.15**	1.66ns	1.08ns	0.93	8.38	0.67	11.5	2.01	106.39
PHT (cm)	46.19ns	116.37ns	574.76***	89.15	170.06	0.89	5.6	18.79	101.45
SCH	176.30***	9.71ns	9.86ns	9.75	36.34	0.64	8.6	6.21	99.91
PL(cm)	1.30ns	1.08ns	7.26***	1.01	20.03	0.90	5	2.00	100.10
HN	282.69***	20.71ns	12.96ns	13.17	34.75	0.66	10.4	7.22	103.89
HW kg ha	58898ns	313202**	3375216***	133137	6640.74	0.97	5.5	769.70	114.28
By ton/ha	139.04***	18.09***	35.07***	4.60	18.01	0.92	11.9	4.60	138.00
HI (%)	116.044***	11.81**	8.9***	4.00	17.79	0.80	11.2	4.25	122.80
TKW(gm)	3.46ns	2.86ns	65.17***	3.25	32.79	0.96	5.5	3.58	97.64
GY(kg ha)	66939ns	66665**	690315***	26814	3122.90	0.97	5.2	346.13	115.87

Note: *** significant at P<.001; ** significant difference at P<0.01; * significant difference at P<0.05; ns=not significant difference; Df= degree of freedom; CV=coefficient of variation; LSD=least significant difference; R^2=coefficient of determination; DF = days to50% flowering; DM = days to maturity; SCH=stand count at harvest; HN=head number; PHT = plant height; HW=head weight; LN=leaf number; LL=leaf length; LW=leaf width; LA =leaf area; PL= panicle length; BY= biological yield; HI = harvest index; TKW = thousand kernel weight; and GY= grain yield.

4.2. Mean Performances of Genotypes for Different Characters

In the present study, the mean performance of days to 50% flowering varied from 67.00 to 85.00 (days), with a grand mean of 78.57 (Appendix Table 2). The longest days to 50% flowering (85 days) was recorded for G76, followed by G48 (83.00 days) and G68 (82.79 days), while the shortest days to 50% flowering was obtained for G25 (67 days) (Appendix Table 2). The selection of earlier flowering and maturing genotypes is crucial for drought tolerance breeding. In the study area, sorghum production is mainly challenged by post flowering drought stress, which occurs at flowering and at the end of the growing season. According to Mohammadi *et al.* (2015), in their study on genetic variability and heritability analysis of yield and morphological traits in sorghum genotypes, 50% of the sorghum flowering period ranged from 71 to 89.67 days among twenty-four sorghum genotypes (Appendix Table 1).

The mean value of days to 90% maturity ranged from 117.00 to 138.00 days, with a grand mean of (130.07 days) among the genotypes (Appendix Table 2).The longest days to maturity (138 days) was recorded for G41, followed by G48 (134.30 days) and G66 (134.05 days), while the shortest days to maturity was obtained for G25 (117.00 days). Early maturity traits are a well-known drought escape mechanism that crop to complete their life cycle before severe post flower moisture deficits occur, but are often associated with reduced yield potential. However, late maturing hybrids are more productive (Solomon Assefa *et al.*, 2018).

The majority of farmers in the study area preferred early maturing sorghum varieties due to the presence of erratic or uneven distribution of rain fall amount. Leaf length ranged from 49.5 to 90.5 cm with an overall mean value of 71.64 cm. The highest leaf length showed G54 (90.5 cm) and smallest leaf length had G75 (49.5cm). High leaf number and leaf length genotypes may be associated with increased biomass yield output (Mohammed Jafar *et al.*, 2023). Leaf width significantly differed among the genotypes, ranging from 4.5 to 10.00 cm, with a mean value of 7.14 cm. The highest leaf width (10 cm) was recorded for genotype G39, while the lowest (4.5 cm) leaf width was recorded for genotype G75. Leaf width ranged for 6.27 to 9.28 cm (Sen *et al.*, 2019). In the present study, the leaf area ranged from 196.49 to

624.80 cm^2, with a grand mean of 365.90 cm^2. The highest leaf area (624.80 cm^2) was recorded for genotype G39 while the lowest leaf area (196.49 cm^2) was recorded for genotype G75 (Appendix Table 3). Mohammed Jafar et al. (2023) reported that the mean leaf area ranged from 224.39 to 528.39 cm^2 with a grand mean of 443.81 cm^2 among 64 sorghum genotypes. This difference values may be due to different genotypes used and environmental differences where the study tested for this two study. The variation in plant height among the genotypes ranged from 122.00 to 215.00 cm, with a grand mean of 170.06 cm. Genotype G12 (215 cm), followed by G57 (208.28 cm) and G32 (204.78 cm), was the tallest, while the standard check (Melkam) (122 cm) had the shortest variety. All sorghum genotypes included in the study were taller than the standard check (Melkam), and 74 genotypes were also taller than the second standard check (Alene, 148.85 cm). Long plant height is an important consideration in sorghum improvement programmes. In the study area, sorghum stalk is important for animal feed, building materials and fuel, and dual-purpose cultivars are the best choice.

The variation in panicle length among the genotypes ranged from 15.00-26.50 cm, with a mean of 20.03 cm. The highest difference was recorded for genotype G14 (26.5 cm), followed by G44 and G64 (24.5 cm), the lowest difference was detected for G16 and G20 (16.25 cm). Panicle length ranged from 6 cm to 45 cm with a grand mean of 19.69 cm, indicating that the presence of variation among genotypes in this trait (Bhagasara *et al.*, 2017). Panicle length is an important component because it is a place for branches containing grains (Hamad and Dagash, 2017). In the present study, the genotypes varied with respect to head weight, which ranged from 4133.33 to 9311.11 kg $ha^{-1,}$ with grand mean of 6640.741 kg ha^{-1}(Appendix Table 4). A highest head weight was obtained from G57 (9311.11 kg ha^{-1}), while the lowest was obtained from G8 (4133.33 kg ha^{-1}), with a mean value of 6640.74 kg ha^{-1}.

The mean performance of genotypes for aboveground biomass yield varied from 10.28 to 31.78 t ha-1, with a grand mean of 18.01 t ha-1. The higher above ground biomass yield was observed in G54 (31.78 t ha-1), and a lower yield was observed in G8 (10.28 t ha-1). In addition to grain yield, which is the most important trait in sorghum breeding, straw yield, is an equally important trait in sorghum, especially in drought prone areas of the North Wello

zone, where sorghum straw is the major source of fodder for animals. Therefore, there is considerable variability among the genotypes for selection aimed at improving this trait. A mean value of 14.87 ton/ha was reported by Chala lema (2019) for 36 sorghum genotypes, with a range of 12.89 to 17.37 ton/ha. The harvest index showed a highly significant difference among the sorghum genotypes, ranging from 12.09% to 28.79%, with a mean of 17.79%. The highest harvest index (28.79%) was recorded for G45, while the lowest (12.09%) was recorded for G21.The largest harvest index value represents how well sorghum genotypes convert biological yield into economic yield (Appendix Table 5). Breeders could use the harvest index as a selection criterion to increase sorghum yield. Mohammed Jafar et al. (2023) reported a mean harvest index (%) value of 12.70 and a range of 8.12-20.15 for the genetic variability, heritability and genetic advance of the quantitative traits of sorghum (Appendix Table 6).

In the present study, the mean performance of thousand kernel weight varied from 20.00 to 41.32 (gm), with the grand mean value of 32.79 (Appendix Table 7). The highest thousand kernel weight (41.32 gm) was recorded for G11, followed by G35 (40.38 gm), G12 (40.11 gm), and G57 (40.01), while the lowest thousand kernel weight was obtained for G76 (20.00 gm). They claimed that when conditions were fully irrigated as opposed to when there was drought stress, grain weight tended to increase. Grain weight is a crucial yield component that illustrates the link between the source and sink of photosynthates throughout the grain filling stage (Solomon Assefa, 2017). Grain yield, which is of primary interest in most breeding programmes, showed a wide range of variation. The grain yield ranged from 19.47 to 4208.60 kg ha-1, with a mean yield of 3122.90 kg ha-1. The highest grain yield was obtained from G12 (4208.60 kg ha-1), while G42 (19.47 kg ha-1) had a lower grain yield.

Among the sorghum genotypes tested, approximately 42 genotypes showed the highest grain yield over the grand mean, 49 and 41 genotypes also showed the highest grain yield over the standard check of Alene and Melkam, respectively. To reduce food insecurity and increase average sorghum productivity across the country, these promising genotypes are preferred for small and large-scale sorghum production. In general, there is a wide range of genetic

variability among genotypes because variations in genotype mean performance for yield and yield-related traits suggest variations in their genetic potential (Garome Shifaraw *et al.*, 2022).

4.3. Qualitative Traits in Sorghum Genotypes

The Shannon-Wiener diversity index value H′ for individual traits varied from 0.16 (seed color) to 0.98 (stay green). Stay green had the highest overall diversity (H′=0.98), followed by glume color (H′=0.87), panicle exsertion (H′=0.77), and inflorescence compactness (H′=0.70), while traits such as seed color (H′=0.16) had relatively lower H′ values, with a total mean phenotypic diversity index of 0.76. Overall, a high value of (H') represents a diverse and equally distributed classes for individual traits. Conversely, a lower value indicates less diversity (Kisua *et al.*, 2015).

The predominant seed color was white (96.3%), followed by red (3.7%) among the sorghum genotypes. These results were consistent with reports by Amelework Beyene *et al*. (2016), who investigated the proportion of sorghum seed color with white being predominant. White sorghum lacks polyphenolic chemicals that protect sorghum grains from preharvest germination in humid, intermediate and highland climates but is abundant in red and brown seeded varieties(Ayana Amsalu and Bekele Endashaw, 1998). Compared to the other two grain types, white-colored grain variety has higher quality porridge and *injera attributes*. Red and brown grain varieties are frequently linked to high tannin content, which is less preferred by birds and less affected by mold (Wortmann *et al.*, 2006).

The grain varieties with brown and red colors are mostly used to make *tella*, a homemade alcoholic beverage that is popular in the area. In addition, the market price of white- seeded sorghum is higher than that of the other two varieties (Gedifew Gebrie and Tsige Genet, 2019). Farmers preferred white- colored grain, and often they associated that color with grain quality, and it was more appreciated for selling for home consumption**.** A lack of variability in seed color means that the genes controlling this trait were already fixed, implying that only their respective gene variants were present in the populations. It may be farmers maintain the

most desirable genotypes and eliminate that less desirable traits, was the cause of the reduced or absent variation (Akatwijuka *et al.*, 2016).

Inflorescence exsertion, measured as the amount of peduncle exposed from the flag leaf to the base of the fully glume- covered spike. Approximately, 64.2% of the genotypes were well-exserted (>10 cm), followed by (32.1%) exserted (2-10 cm) and (3.70%) slightly exserted (<2 cm). Amelework Beyene *et al.* (2016) reported that panicle exsertion in phenotypic classes was observed in 48% of accessions with exserted characters, followed by those with well-exserted characters (35%). According to Gedifew Gebrie and Tsige Genet (2019), the panicles were curved (8%), long (8%), and slightly exserted (64%) or exserted (20%). Breeders always focus on panicle exsertion, also known as peduncle length, which is a crucial plant characteristic during variety development. It is particularly important on commercial farms and in seed production areas, as short panicles can reduce mechanization efficiency and result in chaffy mixtures requiring additional cleaning costs. Drought stress during panicle initiation usually interferes with peduncle elongation and results in poor emergence (Taye Tadese, 2006).

Inflorescence compactness and shape are important traits in determining grain yield and are useful for varietal identification. The inflorescence compactness was predominant (43.21%) for semi compact elliptic primary branches, followed by (33.33%) semi loose erect primary branches, compact elliptic (16.05%), and semi-loose drooping primary branches (7.41%). KU *et al*. (2015) reported that predominant inflorescence compactness was that of semi compact ellipses 53.29% and 36.2%, respectively. The open panicle, an adaptable feature of semi loose headed sorghums, helps the panicle dry quickly in humid and rainy environments, reducing grain weathering caused by fungi such as grain mold. Variation in head compactness was also reported by (Ayana Amsalu and Endashaw Bekele, 1998). According to Chaudhary (1977), in heavy rainfall and humid locations, open panicles were preferable in sorghum and pearl millet to prevent mold and ergot infections, and variations in panicles morphology also revealed the possibility of mutations and cross-pollination between cultivars growing together. The variety shown in cultivar frequencies is a result of farmers selecting these races over time based on their perception of qualitative attributes, yield, and adaptation (Akatwijuka *et al.*, 2016). The

dominant glumes were red (34.57%), followed by gray (24.69%), white (17.28%), yellow (14.81%) and black (8.64%). The present results are similar to those of KU *et al.* (2015), where black glumes were dominant in 86 lines (67.7%), while 14 lines (11%) of the accessions were white. In contrast, Akatwijuka *et al.* (2016) reported that black glumes (70.2%), followed by brown glumes (29.8%), were the most dominant. Black glumes contribute to grain mold resistance (Verma *et al*., 2017). The grain mold resistance of sorghum can be screened using the range of glumes available in this study. The genotypes produced slightly senescent (34.57%), intermediate (approximately half of the leaves died) (28.40%), very slightly senescent (20.99%), and mostly senescent (16.05%) plants. Verma *et al.* (2017) reported that the percentage of stay-green plants that experienced senescence (60.1%) was greater than that of nonsenescent plants (39.9 %) were dominant. The stalks of stay green genotypes have the capacity to transport water continuously under drought conditions. The ability to stay green could increase the value of stalks and improve their suitability as feed sources. The ability of a plant to retain its photosynthetic active leaf area after physiological maturity, a trait known as stay green or nonsenescence, is indicative of post flowering drought resistance (Amelework Beyene, 2016). Even under conditions of restricted water or moisture stress, sorghum genotypes possessing the stay-green trait allow their grains to fill normally (Batson *et al*., 1981; Rosenow and Clark, 1982; Borrell *et al*., 2000).

Table 4.2. Diversity index (H´) values explaining the genetic diversity of populations based on qualitative traits

Character States	Classification	Percentage frequency	Diversity index (H')
Inflorescence Compactness	1= semi loose erect primary branches	Genotypes 27 (33.33%)	0.70
	2= semi loose drooping primary branches	Genotypes 6 (7.41%)	
	3= semi compact elliptic	Genotypes 35 (43.21%)	
	4= compact elliptic	Genotypes 13 (16.05%)	

Diversity index (H´) values explaining the genetic diversity of populations based on qualitative traits (Continued)

Stay green	1= Very slightly senescent	Genotypes 17 (20.99%)	0.98
	2 = Slightly senescent	Genotypes 28 (34.57%)	
	3 =Intermediate (about half of the leaves dead)	Genotypes 23 (28.40%)	
	4 = Mostly senescent	Genotypes 13 (16.05%)	
	5 = completely senescent or plant leaves and stalk Dead	0	
Glume color	1=white	Genotypes 14 (17.28%)	0.87
	2=red	Genotypes 28 (34.57%)	
	3=yellow	Genotypes 12 (14.81%)	
	4=gray	Genotypes 20 (24.69%)	
	5=black	Genotypes 7 (8.64%)	
Panicle exsersion	1=slightly exserted <2 cm	Genotypes 3 (3.70%)	0.77
	2= Exserted 2-10 cm	Genotypes 26 (32.1%)	
	3= well-exserted >10cm	Genotypes 52 (64.2%)	
Seed color	1= white	Genotypes 78 (96.3%)	0.16
	2= red	Genotypes 3 (3.7%)	
Average			0.76

4.4. Estimation of Genetic Parameters

4. 4.1. Estimates of variance components

Estimates of the genotypic variance (δ^2g), phenotypic variance (δ^2p), genotypic coefficient of variation (GCV), and phenotypic coefficient of variation (PCV) are indicated in (Table 4.3). The present results on variance component showed that the phenotypic variances were small differences with genotypic variance for head weight, panicle length, thousand kernel weight, and grain yield, Indicating that the influence of environment on these traits are very low.

Therefore, the selection of these traits on a phenotypic basis may be effective for genetic improvement. Similarly, Mohammed Jafar *et al*. (2010) reported on sixty-four sorghum genotypes at the Bako research site and reported relatively slight differences between phenotypic variance and genotypic variance for days to flowering, panicle length, head weight, thousand kernel weight**.**

4.4.2. Genotypic and phenotypic coefficient of variation

The phenotypic coefficient of variance (PCV) and genotypic coefficient of variance (GCV) differences were small for days to 50% flowering, days to maturity, plant height, head weight, panicle length, thousand kernel weight, and grain yield, suggesting that the environment had a minimal influence on the expression of these traits. Similarly,Adane Gebreyohannes *et al*. (2018) reported a low degree of difference between PCV and GCV for days to 50% flowering, days to maturity, and thousand kernel weight. A high GCV value was obtained for biological yield, indication of the presence of high degree of genetic variation. This suggests that environmental influence had a low effect on trait expression. The magnitudes of GCV and PCV ranged from 1.50 (DM) to 20.69 (BY) and from 2.98 (DM) to 25.56 (BY), respectively. Higher PCV and GCV estimates were recorded for biological yield (Table 4.3). These high values of PCV and GCV revealed that the genotypes have a broad base genetic background and substantial variability to facilitate sorghum improvement through selection. Similarly, Sabiel *et al.* (2016) reported that higher PCV and GCV were associated with greater biological yield; However very high PCV (42.2) and GCV (30.7) differences by grain yield. However, in contrast to the present study, low PCV and GCV estimates of biological yield were reported by Mohammed Jafar et al. (2023). Traits with moderate GCVs were obtained for leaf area index, head weight, thousand kernel weight, and grain yield, indicating that acceptable improvement could be obtained through the selection of these traits. In line with the present results, moderate GCV was reported by Adane Gebreyohannes *et al*. (2018) for head weight.

4.4.3. Broad sense heritability

The estimated values of broad- sense heritability in the present study ranged from 21.95% for leaf width to 90.73% for thousand kernel weight (Table 4.3). High heritability estimates were recorded for thousand kernel weight (90.73%), followed by head weight (90.46%), grain yield (90.41%), panicle length (75.31%), plant height (71.69%), and biological yield (65.54%), indicating that these traits were less influenced by the environment in terms of phenotypic expression. Therefore, breeders could select promising sorghum genotypes based on the phenotypic performance of these traits (Adane Gebreyohannes *et al.,* 2018). This result is in agreement with the findings of Mohammed Jafar et al. (2023), who reported high heritability estimates for head weight, grain yield, panicle length, and plant height; Gebremedhn Gebregergs and Firew Mekbib (2020), who reported high broad sense heritability values for plant height and grain yield; Godbharle *et al.* (2010) also reported high broad sense heritability for plant height and panicle length.

4.4.4. Genetic advance as a percentage of the mean

Estimates of genetic advance as a percent of the mean (GAM) at 5% selection intensity ranged from days to maturity (1.56%) and days to maturity (37.35%) (Table 4.3). High genetic advance values as a percentage of the mean (>20%) were found for head weight (37.35%), grain yield (35.91%), biological yield (34.50%), and thousand kernel weight (33.32%), indicating the predominance of additive gene action and high potential for improving these traits under selection. Similar to the present results,Gobezayohu Haftu *et al.* (2019) reported high genetic advance as a percentage of the mean for grain yield and thousand kernel weight. Similarly, Mohammed Jafar et al. (2023) high GAMs were also found for head weight and grain yield, and high GAMs for grain yield traits were reported (Jimmy *et al.*, 2017). In the present study, high heritability coupled with high genetic advance as a percentage of the mean was exhibited by head weight, biological yield, thousand kernel weight, and grain yield. Therefore, selection based on via these traits would be more effective and reliable because these traits are predominantly controlled by additive gene action (Yaqoob *et al*., 2015).

Table 4. 3. Mean, Range, and Estimation of genetic parameters for 12 traits of 81 sorghum genotypes

Traits	Range	Mean±SE	O^2g	O^2p	GCV (%)	PCV (%)	H^2 (%)	GA (5%)	GAM (5%)
DF	67.00-85.00	78.57±1.71	6.00	11.86	3.12	4.42	50.60	3.59	4.57
DM	117.00-138.00	130.07±3.02	3.81	15.04	1.50	2.98	25.33	2.02	1.56
LL(cm)	49.5-90.5	71.64±4.94	16.21	65.85	5.62	11.33	24.62	4.12	5.74
LW(cm)	4.5-10.00	7.14±0.70	0.24	1.11	6.92	14.79	21.95	0.48	6.69
LA(cm^2)	196.49-624.80	365.89±51.25	2170.99	7111.31	12.74	23.05	30.53	53.03	14.49
PH(cm)	122.00-215.00	170.06±6.79	239.98	333.77	9.12	10.76	71.69	27.02	15.89
PL(cm)	15.00-26.50	20.03±0.72	3.12	4.14	8.82	10.16	75.31	3.16	15.77
HW($kgha^{-1}$)	4133.33-9311.11	6640.74±291.29	1603033.27	1772183.11	19.07	20.05	90.46	2480.63	37.35
BY(ton ha^{-1})	10.28-31.78	18.00±2.11	13.88	21.18	20.69	25.56	65.54	6.21	34.50
HI (%)	12.09-28.79	17.79±1.85	1.67	7.23	7.27	15.12	23.08	1.28	7.19
TKW(g)	20.00-41.32	32.79±1.26	31.00	34.17	16.99	17.83	90.73	10.92	33.32
GY(kg ha^{-1})	1947.54- 4208.60	3122.90±132.21	327765.59	362549.48	18.33	19.28	90.41	1121.36	35.91

Note: SE= standard error ; δ^2g=genotypic variance component; δ^2e =environmental variance component; δ^2p= phenotypic variance component; GCV%=genotypic coefficient of variance; PCV% =phenotypic coefficient of variance; H^2b%= broad sense heritability; GA% genetic advance; GAM% =genetic advance as percent of means; DF = days to flowering; DM = days to maturity; PHT = plant height; HW=head weight; LL=leaf length; LW=leaf width; LA = leaf area; PL= panicle length; BY= biological yield; HI= harvestindex; TKW=thousand kernel weight; and GY=grain yield

4.5. Traits Association

The estimates of the phenotypic and genotypic correlation coefficients among the 12 traits are presented in (Table 4.6). The genotypic correlation coefficient values were greater for most of the traits than were their corresponding phenotypic correlation coefficient values indicating the inherent association of the traits.

4.5.1. Correlation of grain yield with other yield-related traits

Grain yield showed a positive and highly significant ($p < 0.01$) genotypic correlation with days to 50% flowering (rg = 0.49 **), days to maturity (rg = 0.42 **), plant height (rg = 0.6**), head weight (rg = 1.00 **), leaf length (rg = 0.72 **), leaf width (rg = 0. 54 **), leaf area index (rg = 0.54 **), panicle length (rg = 0.50 **), biological yield (rg = 0.93 **), and thousand kernel weight (rg = 0.74 **). Indicating, improving either one or all of these traits could result in high grain yield. Similar results were reported by Tsegau Senbetay and Tegegn Belete (2020), who reported that grain yield had a positive and strong genotypic correlation (rg=0.92**) with head weight and (rg=0.42**) with days to 50% flowering. On the other hand, Gedifew Gebrie and Tsige Genet (2019) reported that grain yield was positively and significantly correlated with days to maturity (0.69**) and head width(0.33**). Therefore, the positive association of grain yield with these traits suggested the possibility of simultaneously improving grain yield through indirect selection of these traits. However, grain yield showed a positive but non-significant genotypic correlation with harvest index (0.03). This result indicated that harvest index is independently controlled and therefore, selection for this trait does not improve the grain yield in sorghum.

At the phenotypic level, grain yield had significant positive associations ($p <0.01$) with days to 50% flowering (rp = 0.29**), plant height (rp = 0.46**), head weight (rp = 0. 98**), leaf length (rp = 0.37**), leaf width (rp = 0.27**), leaf area (rp = 0.35 **), panicle length (rp = 0.40 **), biological yield (rp = 0.82 **) and thousand kernel weight (rp = 0.67**). On the other hand, grain yield had a positive and significant ($p <0.05$) phenotypic correlation with days to maturity (rp=0.17*). This finding is in agreement with Jimmy *et al.* (2017), who

reported that grain yield showed a positive and significant phenotypic correlation with days to 50% flowering (rp = 0.51*) and panicle length (rp = 0.35*). In contrast, Gedifew Gebrie and Tsige Genet (2019) reported negative and nonsignificant phenotypic correlations of days to 50% flowering (-0.19), days to maturity (-0.04) and plant height (-0.18) with grain yield.

4.5.2. Correlations among other yield-related traits

Correlations between traits were highly significant for most combinations in both positive and negative directions (Table 4.3). Both phenotypic and genotypic associations were positively and highly significantly correlated ($p < 0.01$) for days to 50% flowering with days to maturity (rp = 0.41**, rg = 1.02**), head weight (rp = 0.28**, rg = 0.42**) and biological yield (rp = 0.21**,rg = 0.45 **). In addition, days to 50% flowering had positive and significant correlations ($p < 0.05$) with plant height (rp = 0.16*,rg = 0.23*) and thousand kernel weight (rp = 0.16 *). This result implied that increasing the days to 50% flowering would increase the days to maturity, head weight, biological yield, plant height and thousand kernel weight. This finding is in agreement with previous findings by Girma Mengistu *et al.* (2020) who reported a genotypic correlation of 50% flowering with days to maturity (0.80**), biological yield (0.20**) and plant height (0.40**). Similarly, Tsegau Senbetay and Tegegn Belete (2020) showed a positive and highly significant correlation at both genotypic and phenotypic levels, as indicated by days to 50% flowering with days to maturity (rg=0.27**, rp=0.19*), plant height (rg=0.36**, rp=0.32**) and head weight (rg=0.46**, rp=0.36**).

The days to maturity had positive and highly significant ($p < 0.01$) genotypic correlation with head weight (rg = 0.34 **) and biological yield (rg = 0.30 **). This finding is in agreement with previous findings by Tsegau Senbetay and Tegegn Belete (2020), who reported positive and significant genotypic and phenotypic correlations of days to 90% maturity with head weight (rg=0.32**, rp=0.27**). This result also disagreed with previous study by Girma Mengistu *et al.* (2020), who reported a highly significant negative genotypic correlation of days to maturity with the harvest index (-0.21**) and a positive nonsignificant correlation with biomass (0.08 ns). Plant height ($p<0.01$) showed a positive and highly significant correlation with head weight (rp = 0.46 **, rg = 0.61 **), panicle length (rp = 0.24 **,rg =

0.33 **), and biological yield (rp = 0.54 **,rg = 0.74 **); at (p <0.05) showed a positive and significant correlation with thousand kernel weight (rp = 0.17 *). The present results are in line with the findings of Girma Mengistu *et al*. (2020) that plant height exhibited positive and highly significant genotypic correlation with panicle length (0.23**) and biological yield (0.21**). Head weight (p<0.01) showed a positive and highly significant correlation with panicle length (rp = 0.45 **, rg = 0.53 **), biological yield (rp = 0.82**, rg = 0.95**), and thousand kernel weight (rp = 0.67 **, rg = 0.75 **). These results are in accordance with the findings of Mulugeta Mamo and Fisseha Worede (2020), who reported that head weight showed positive and significant genotypic and phenotypic correlations with thousand kernel weight and biological yield at the phenotypic level.

Biological yield (p<0.01) showed a positive and highly significant correlation with thousand kernel weight (rp = 0.44**, rg = 0.60 **). This finding was in agreement with that of Mulugeta Mamo and Fisseha Worede (2020), who reported that biological yield had positive and significant genotypic and phenotypic correlations with thousand kernel weight. The harvest index showed a positive and highly significant correlation with thousand kernel weight (rg = 0.30 **). In agreement with this result, Pawar *et al.* (2017) reported a positive and highly significant genotypic correlation between the harvest index and thousand kernel weight.

Table 4. 4. Estimation of genotypic (upper diagonal) and phenotypic (lower diagonal) correlation coefficients between yield and yield related traits of 81 sorghum genotypes

	DF	DM	LL	LW	LA	PHT	PL	HW	By	HI	TKW	GY
DF	**1**	1.02**	0.32**	0.36**	0.33**	0.23*	0.07ns	0.42**	0.45**	-0.01ns	0.20ns	0.49**
DM	0.41**	**1**	0.02ns	-0.13ns	-0.09ns	0.16ns	0.01ns	0.34**	0.30**	0.17ns	0.16ns	0.42**
LL	0.25**	0.17*	**1**	0.90**	0.94**	0.42**	0.28*	0.37**	0.78**	-0.38**	0.58**	0.72**
LW	0.07ns	-0.01ns	0.53**	**1**	1.00**	0.26**	0.18ns	0.27**	0.47**	-0.23*	0.39**	0.54**
LA	0.17*	0.07ns	0.83**	0.91**	**1**	0.36**	0.22ns	0.35**	0.60**	-0.30**	0.40**	0.54**
PHT	0.16*	0.06ns	0.70**	0.48**	0.56**	**1**	0.33**	0.61**	0.74**	-0.50**	0.22ns	0.60**
PL	0.06ns	0.02ns	0.24**	0.18*	0.23**	0.24**	**1**	0.45**	0.50**	-0.03ns	0.29**	0.50**
HW	0.28**	0.14ns	0.74**	0.44**	0.57**	0.46**	0.53**	**1**	0.95**	-0.03ns	0.75**	1.00**
By	0.21**	0.04ns	0.41**	0.40**	0.43**	0.54**	0.34**	0.82**	**1**	-0.32**	0.60**	0.93**
HI	0.06ns	0.17*	-0.22**	-0.25**	-0.26**	-0.30**	-0.02ns	-0.07ns	-0.60**	**1**	0.30**	0.03ns
TKW	0.16*	0.08ns	0.27**	0.08ns	0.19*	0.17*	0.24**	0.67**	0.44**	0.15ns	**1**	0.74**
GY	0.2**	0.17*	0.37**	0.27**	0.35**	0.46**	0.40**	0.98**	0.82**	-0.05ns	0.67**	**1**

Note: DF = days to 50% flowering; DM = days to maturity; PHT = plant height; HW=head weight; LL=leaf length; LW=leaf width; LA =leaf area; PL= panicle length; BY= biological yield; HI = harvest index; TKW = thousand kernel weight; and GY= grain yield

4.6. Path Coefficient Analysis

4.6.1. Genotypic direct and indirect effects of various traits on grain yield

The results of the genotypic path analysis are presented in Table 4.5. The path coefficients were classified as suggested by Lenka and Misra (1973), where 0.00-0.09 indicates negligible association effects, 0.10-0.19 indicates low associations, 0.20-0.29 indicates moderate associations, 0.30-0.99 indicates high associations and >1.0 indicates very high associations. Direct effects of one trait on the grain yield showed that this trait directly affected the grain yield and might be helpful in selection for improving yield. At the genotypic level, very strong positive direct effects on grain yield were observed for biological yield (1.85), followed by leaf width (1.61), leaf length (0.83), harvest index (0.60), and thousand kernel weight (0.23). Similarly, high and positive genotypic direct effects of the harvest index (0.65) on grain yield were reported by Pawar *et al.* (2017) . Therefore, the positive and strong correlation values of the direct effects of traits on grain yield showed that the true relationship and indirect selection for these traits could increase grain yield. Hence, these traits should be considered as selection indices in sorghum breeding programs.

On the other hand, very high and negative direct effects on grain yield were observed for the leaf area (-2.96), head weight (-0.49), and days to maturity (-0.35). In contrast, Mulugeta Mamo and Fisseha Worede (2020) reported strong and positive genotypic direct effects of days to maturity (1.53) and head weight(1.96) on grain yield. The negative direct effects of these traits on grain yield indicate that the selection traits would not be rewarding for yield improvement. Genotypic path coefficient analysis revealed that positive and strong indirect effects of days to 50% flowering were exerted via biological yield (0.83) followed by leaf width (0.64), and leaf length (0.36). Positive genotypic indirect effects of days to maturity on grain yield were observed via biological yield (0.56) followed by days to 50% flowering (0.31). Similarly, Deshmukh *et al.* (2021a) reported a positive genotypic indirect effect of days to maturity on grain yield through days to 50% flowering. Leaf length had a strong and positive indirect effect on grain yield via biological yield (1.76) and leaf width (0.79). This result agreed with Mesut *et al*. (2020) positive indirect effects of leaf length on grain yield via

leaf width. In addition, leaf width had a strong positive indirect effect on grain yield via biological yield (1.43) and leaf length (1.12). In agreement with the present study, Arvinth *et al*. (2021) showed that leaf width had a positive indirect effect on leaf length. Strong positive indirect effects of the leaf area on grain yield were detected through leaf length (1.00), leaf width (1.79), and biological yield (0.87). The indirect effects of plant height on grain yield via biological yield (1.37), leaf width (0.85), and leaf length (0.78 were strong and positive. In line with the present study, Gedifew Gebrie and Tsige Genet (2019) reported that positive genotypic indirect effects of plant height on grain yield occurred via leaf length and leaf width. The positive indirect effects of panicle length on grain yield were via biological yield (0.89), leaf width (0.33), and leaf length (0.32). Head weight exerted strong positive indirect effects via leaf width (1.78), biological yield (1.11), and leaf length (1.06).

Biological yield also had a strong positive indirect effect on grain yield through leaf length (0.87) and leaf width (0.85). The harvest index had strong and positive indirect effect on grain yield via the leaf area index (0.86). A strong and positive indirect effect on grain yield was exerted by thousand kernel weight through biological yield (1.09), leaf length (0.66), and leaf width (0.41). Generally, important independent traits that have strong and positive direct and indirect effects on grain yield should be considered selection criteria for yield improvement in sorghum. The residual genotypic value was low (0.03), which indicated that traits included in the genotypic path analysis explained 97% of the variation in the grain yield.

Table 4.5. Genotypic path coefficient analysis of direct (bold diagonal) and indirect effects of traits on grain yield

	DF	DM	LL	LW	LA	PHT	PL	HW	BY	HI	TKW	Rg
DF	**0.31**	-0.35	0.36	0.64	-0.97	0.00	-0.00	-0.37	0.83	-0.01	0.05	0.49**
DM	0.31	**-0.35**	0.02	-0.22	0.25	0.00	-0.00	-0.30	0.56	0.10	0.04	0.42**
LL	0.13	-0.12	**0.83**	0.79	-1.67	0.01	-0.00	-0.88	1.76	-0.02	0.17	0.72**
LW	0.10	-0.01	1.12	**1.61**	-2.81	0.01	-0.00	-0.65	1.43	-0.23	0.13	0.40**
LA	0.11	0.04	1.00	1.79	**-2.96**	0.01	-0.00	-0.39	0.87	-0.14	0.05	0.54**
PHT	0.07	-0.05	0.78	0.85	-1.66	**0.02**	-0.00	-0.53	1.37	-0.30	0.05	0.60**
PL	0.02	-0.00	0.32	0.33	-0.64	0.01	**-0.01**	-0.47	0.89	-0.02	0.07	0.49**
HW	0.10	0.03	1.06	1.78	-2.98	0.01	-0.00	**-0.49**	1.11	-0.17	0.09	1.00**
BY	0.14	-0.10	0.87	0.85	-1.78	0.02	-0.00	-0.84	**1.85**	-0.19	0.13	0.93**
HI	-0.01	-0.06	-0.43	-0.42	0.86	-0.01	0.00	0.03	-0.60	**0.60**	0.07	0.03NS
TKW	0.06	-0.05	0.66	0.41	-1.17	0.00	-0.00	-0.66	1.09	0.18	**0.23**	0.74**

Note: DF = days to 50% flowering; DM = days to maturity; PHT = plant height; HW=head weight; LL=leaf length; LW=leaf width; LA =leaf area; PL= panicle length; BY= biological yield; HI = harvest index; TKW = thousand kernel weight, and rg=genotypic correlation coefficients with grain yield. Residual= 0.03

4.6.2. Phenotypic direct and indirect effects of various traits on grain yield

Phenotypic path analysis revealed that biological yield (0.47), harvest index (0.26), and head weight (0.22) had positive direct effects on grain yield (Table 4.6). These results indicated greater contribution of these traits to the maximum production of grain yield in sorghum gynotypes. Therefore, these traits can be considered as selection criteria in sorghum breeding programs. Similarly, Mulugeta Mamo and Fisseha Worede (2020) reported that head weight and biological yield had positive direct effects on grain yield. Indirect effects on grain yield indicated that such traits affected yield via other component traits. Leaf length (0.63), followed by biological yield (0.51), thousand kernel weight (0.42), plant height (0.29), panicle length (0.28), and leaf width (0.23) exerted moderate to strong positive phenotypic indirect

effects via head weight. In addition, positive indirect effects on grain yield were also exhibited by biological yield through leaf length (0.39), plant height (0.25), and thousand kernel weight (0.21). Similarly, Chala lema (2019) reported positive phenotypic indirect effects on grain yield traits such as biological yield and plant height through head weight and plant height via biological yield. Similarly, Mulugeta Mamo and Fisseha Worede (2020) reported positive phenotypic indirect effects on grain yield traits such as biological yield, thousand kernel weight, plant height, and panicle length through head weight, while plant height and thousand kernel weight also affected grain yield via biological yield. The residual phenotypic value was low (0.02), indicating that the traits included in the phenotypic path analysis explained 98% of the variation in grain yield contributed by the traits that had direct effects on grain yield (Tables 4.6). Approximately 2% of the variability in grain yield of sorghum genotypes in the present study could be due to many reasons that were not investigated, such as environmental factors and sampling errors (Sengupta, 1971).

Table 4.6. Phenotypic path coefficient analysis of direct (bold diagonal) and indirect effects of traits on grain yield

	DF	DM	LL	LW	LA	PHT	PL	HW	BY	HI	TKW	rp
DF	**-0.01**	0.01	0.01	0.00	-0.01	-0.00	-0.00	0.17	0.10	0.01	0.00	0.29**
DM	-0.00	**0.03**	0.00	-0.00	-0.00	-0.00	-0.00	0.09	0.02	0.04	0.00	0.17*
LL	-0.00	0.00	**0.01**	0.01	-0.01	-0.00	-0.01	0.63	0.39	-0.02	0.00	0.37**
LW	-0.00	0.00	0.03	**0.01**	-0.03	-0.00	-0.01	0.23	0.19	-0.06	0.00	0.27**
LA	-0.00	-0.00	0.02	0.03	**-0.04**	-0.00	-0.01	0.17	0.17	-0.07	0.00	0.35**
PHT	-0.00	0.00	0.01	0.01	-0.01	**-0.01**	-0.01	0.29	0.25	-0.07	0.00	0.46**
PL	-0.00	0.00	0.01	0.00	-0.01	-0.00	**-0.03**	0.28	0.16	-0.00	0.00	0.40**
HW	-0.00	0.00	0.02	0.02	-0.04	-0.00	-0.01	**0.22**	0.20	-0.07	0.00	0.98**
BY	-0.00	0.00	0.01	0.01	-0.02	-0.00	-0.01	0.51	**0.47**	-0.15	0.00	0.82**
HI	-0.00	0.01	-0.01	-0.01	0.01	-0.00	0.00	-0.04	-0.28	**0.26**	0.00	-0.05 NS
TKW	-0.00	0.00	0.01	0.00	-0.01	-0.00	-0.01	0.42	0.21	0.04	**0.01**	0.67**

Note: DF = days to 50% flowering; DM = days to maturity; PHT = plant height; HW=head weight; LL=leaf length; LW=leaf width; LA =leaf area; PL= panicle length; BY= biological

yield; HI = harvest index; TKW = thousand kernel weight; and rg=genotypic correlation coefficients with grain yield. Residual= 0.02

4.7. Principal Component Analysis of yield and yield related traits

The results of principal component analysis (PCA) of 12 quantitative traits are presented in (Table 4.7). In the present investigation, the first four principal components with eigenvalues greater than one (4.89, 2.11, 1.48, and 1.13 were PC1, PC2, PC3, and PC4, respectively) accounted for 80.11% of the total variation among the 81 sorghum genotypes. The percentage of variation explained by each principal component contributed 40.77%, 17.56%, 12.36% and 9.42% of the total variation in PC1, PC2, PC3 and PC4, respectively. The high positive contributing to the variation revealed by grain yield, head weight, biological yield and plant height were in accordance with the earlier findings of (Desmae *et al*., 2016; Elenen *et al*., 2019; Malini *et al*., 2023). However, Kavithamani *et al.* (2019) reported only 66.35% of the total variation among 100 sorghum germplasm accessions, PC1 explained 31.05 %, PC 2 loaded with 19.66 % and PC3 had contributed 15.64 % of the total variation for 100 seed weight, plant height and leaf width. The difference might be due to differences in sorghum genotypes, the variables considered and the environmental factors under which the genotypes were grown. Principal components analysis revealed that an eigenvalue greater than one and component loadings greater than 10% have a meaningful and significant contribution to the total variation among crop genotypes (Anderson *et al.*, 1998).

The first principal component had high positive weights for the most important traits contributing to the variation revealed by grain yield (0.40), head weight (0.40), biological yield (0.39), leaf length (0.31), leaf area (0.30) and plant height (0.30). The second principal component had high positive weights for the harvest index (0.45), thousand kernel weight (0.31) and days to maturity (0.31), but high negative weights for the leaf area (-0.41), leaf width (-0.38) and leaf length (-0.32).The third principal component had high negative weights for days to maturity (-0.55) and days to 50% flowering (-0.52). Furthermore, the fourth principal component had high positive weights for harvest index (0.56), leaf width (0.33) and thousand kernel weight (0.32), while high negative weights accounted for plant height (-0.35),

days to 50% flowering (-0.31) and days to maturity (-0.31). Similar findings were reported by Hamidou *et al*. (2018) for two-hundred and eighty-two recombinant sorghum inbred lines plus two checks among three principal components, and the first principal component had high positive weights for the most important traits contributing to the variation revealed by grain yield (0.70). Generally, principal component analysis revealed that the variation in the genotypes was due to significant contribution of a few traits rather than the smaller contribution of all traits. The positive and negative values indicated the presence of positive and negative correlation trends between the variables in the component. These results suggested that grain yield, head weight, biological yield, leaf length, leaf area, plant height, thousand kernel weight, days to maturity, leaf width, and days to 50% flowering were the important traits contributing variation among sorghum genotypes.

Table 4.7. Principal component analysis of 12 quantitative traits of 81 sorghum genotypes

Traits	PC1	PC2	PC3	PC4
Days to 50% flowering	0.18	0.22	-0.52	-0.31
Days to maturity	0.09	0.31	-0.55	-0.31
Leaf length	0.31	-0.32	-0.21	0.05
Leaf width	0.26	-0.38	-0.25	0.33
Leaf area	0.30	-0.41	-0.27	0.28
Plant height	0.30	-0.11	0.09	-0.35
Panicle, length	0.24	0.07	0.23	0.10
Head weight	0.40	0.24	0.17	0.04
Biological yield	0.39	-0.00	0.26	-0.28
Harvest index	-0.05	0.45	-0.25	0.56
Thousand kernel weight,	0.28	0.31	0.15	0.32
Grain yield	0.40	0.27	0.13	0.03
Eigenvalue	4.89	2.11	1.48	1.13
Variability (%)	40.77	17.56	12.36	9.42
Cumulative %	40.77	58.32	70.69	80.11

Note: PC1, first principal component; PC2, second principal component; PC3, third principal component; and PC4, fourth principal component

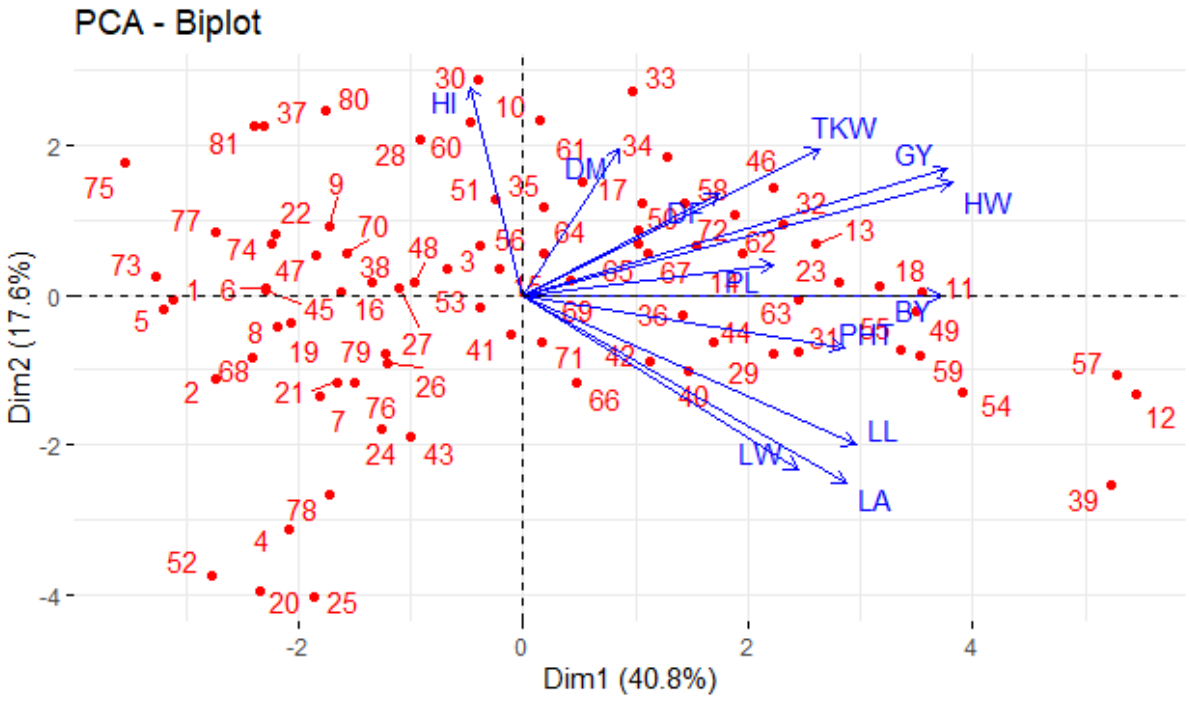

Figure 4.1. PCA- bi plot shows the contribution of sorghum traits: The red color represents genotypes (n=81) and the blue color represents the traits under study

4.8. Cluster Analysis

4.8.1. Clustering of genotypes

Cluster analysis of the 12 quantitative traits of the sorghum genotypes revealed four clusters with different numbers of genotypes in each cluster (Table 4.8). Based on the silhouette plot cut tree method the optimum number of clusters and the cluster dendrogram for 81 sorghum genotypes were classified into four clusters; cluster I consisted of 25 genotypes (30.86%), followed by cluster III with 21 genotypes (25.93%), cluster IV with 19 genotypes (23.46%), and cluster II consisting of 16 sorghum genotypes (19.75%). Similar work has been reported by Mia *et al*. (2007) who grouped 20 sorghum genotypes into four clusters; Gedifew Gebrie and Tsige Genet (2019), who observed 25 genotypes in five clusters with high contributor

traits like leaf length, leaf area, leaf width, biological yield and grain yield; Forty sorghum genotypes were grouped in three clusters and similar contributing trends of variability were observed by plant height, leaf length, 100 seed weight, days to 50% flowering and days to maturity (Prasad and Sridhar, 2019); Deep *et al.* (2020), who reported 73 sorghum genotypes in seven clusters; and Verma *et al.* (2017) , who grouped 75 genotypes in ten clusters, similar higher contributor traits were grain yield, plant height and days to maturity.

Table 4. 8. The distribution of 81 sorghum genotypes into five clusters based on D2 analysis

Cluster	Number and cluster size	Genotypes included
I	25 (30.86%)	G-12, G- 18, G- 23, G- 24, G- 11, G- 17, G- 21, G- 9, G- 20, G- 1, G- 15, G-51, G- 57, G- 2, G- 4, G- 10, G- 3, G- 8, G-19, G- 50, G- 13, G- 48, G- 49, G- 53, G- 58
II	16 (19.75%)	G- 14, G- 16, G- 60, G- 52, G- 5, G- 6, G- 22, G- 43, G- 54, G-28, G- 36, G- 41, G- 47, G-55, G- 7, G- 46
III	21 (25.93%)	G- 35, G- 39, G- 67, G- 33, G- 37, G- 27, G- 34, G- 38, G-68, G- 61, G- 79, G- 42, G- 25, G- 45, G- 29, G- 30, G- 59, G- 56, G- 26, G-31, G- 32
IV	19 (23.46%)	G- 80, G- 40, G- 44, G- 73, G- 75, G- 81, G- 71, G- 74, G-69, G- 70, G- 66, G- 72, G- 63, G- 64, G- 65, G- 77, G- 78, G- 62, G- 76

G= genotype

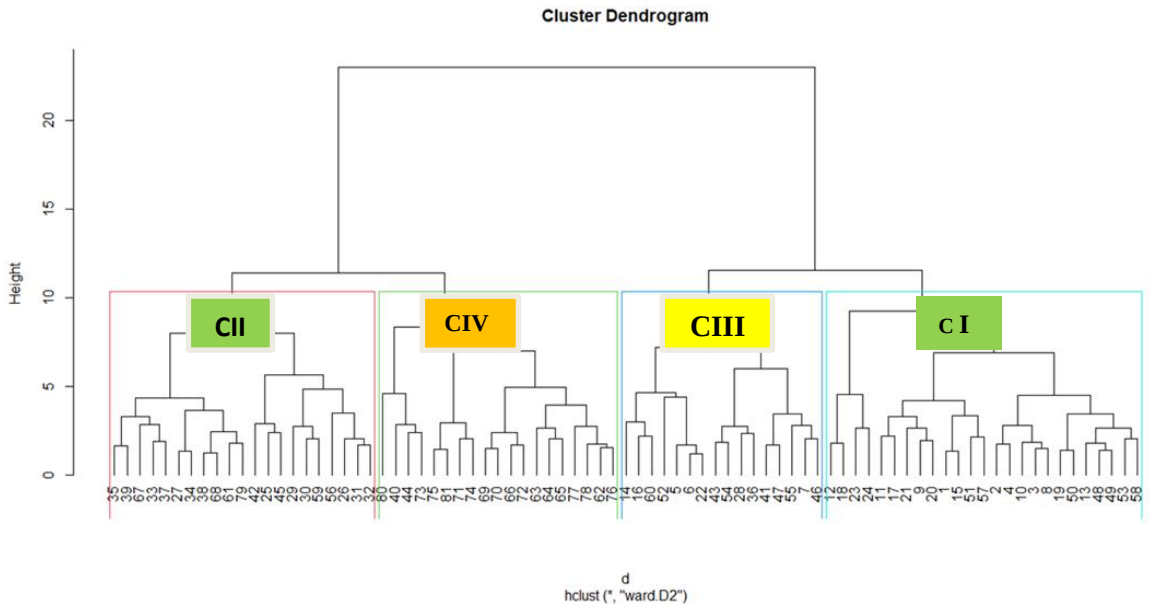

Figure 4.2. Dendrogram showing the grouping of 81 sorghum genotypes with 12 yield related traits

4.8.2. Cluster mean analysis

The mean values of four clusters across 12 traits of 81 sorghum genotypes are listed below in Table 4.9. The cluster mean values revealed considerable differences among the clusters for different traits. The sorghum genotypes in cluster I exhibited the earliest flowering, earliest maturity, shortest plant height, lowest head weight, lowest harvest index, lowest thousand kernel weight, and lowest grain yield, while the latest flowering, latest maturity, highest plant height, highest head weight, highest leaf length, highest leaf width, highest leaf area, highest panicle length, highest biological yield, highest thousand kernel weight, and highest grain yield were recorded for those in cluster II. Therefore, the genotypes in this cluster could be desirable for human consumption and animal feed due to their high grain and biomass yields resulting from the selection of parents for hybridization. The highest harvest index was recorded for cluster III. The lowest plant height, leaf length, leaf width, leaf area, panicle length and biological yield were recorded in cluster IV. In agreement with the present study, Deep *et al.* (2020) showed the earliest and latest flowering sorghum genotypes from clusters I and II, respectively.

Table 4.9. Mean values of the traits in the clustering of genotypes

Traits	I	II	III	IV	Overall mean
Days to 50% flowering	77.00	79.48	79.39	78.02	78.47
Days to maturity	128.56	130.71	130.20	130.41	129.97
Leaf length	72.53	77.96	70.45	66.17	71.78
Leaf width	7.31	7.68	7.14	6.50	7.16
Leaf area	380.82	423.27	357.95	308.22	367.57
Plant height	168.58	189.31	166.19	156.65	170.18
Panicle length	19.31	21.75	19.86	19.07	20.00
Head weight	5198.73	8087.80	7259.18	5689.76	6558.87
Biological yield	15.67	22.66	18.12	15.16	17.90
Harvest index	15.95	16.99	19.39	18.27	17.65
Thousand kernel weight	25.26	36.93	36.11	30.98	32.32
Grain yield	2448.56	3756.77	3433.23	2697.94	3084.13

4.8.3. Intra and intercluster squared distances (D^2)

The intra- and intercluster D^2 values between the four clusters are shown in Table 4.10. The intercluster distances of the genotypes ranged from 14.40 to 130.28. Chi-squared values for intercluster distances showed that there was a significant difference between clusters I and II, clusters I and IV, clusters II and III, and clusters III and IV. The maximum intercluster distance (D^2 = 130.28**) was found between clusters I and IV, followed by clusters I and II (D^2 = 65.78**), III and IV (62.73**) and clusters II and III (D^2=19.88*), indicating greater genetic divergence between these clusters. These intercluster distances indicated the presence of significant genotypic differences between the clusters tested by chi-squared (x^2) distribution. Therefore, cluster I and cluster IV are genetically very distant from each other and heterotic. The maximum amount of heterosis is expected from crosses with parents belonging to clusters I and IV. This could have implications for the genetic improvement of sorghum genotypes for the target trait. Therefore, genotypes from different clusters should be selected for crosses in sorghum hybridization programmes. The parents for hybridization

could be selected on the basis of large intercluster distances to isolate useful recombinants in the segregating generations (Arega Gashaw *et al.*, 2007). The minimum intercluster distance was also observed between cluster II and IV (D2 = 14.40 ns), followed by clusters I and III (14.56 ns). Thus, the crossing of genotypes from these clusters may not result in a high level of heterotic expression in the first generation (F1s) or a wide range of variability in the segregating second generation (F2s) populations. The intracluster distance (D^2) ranged from 3.32 to 3.51 for clusters III and cluster IV respectively, indicating that these clusters were genetically closely related. However, the chi-squared test for intracluster was not significant for all clusters. This indicates that genotypes within a cluster are less divergent than genotypes from different clusters (Garome Shifaraw *et al.*, 2022).

Table 4.10. Average intra (main diagonal) and intercluster (off- diagonal) D2 values of five clusters in 81 sorghum gynotypes

Clusters	I	II	III	IV
I	**3.34**	65.78**	14.56ns	130.28**
II		**3.44**	19.88*	14.40ns
III			**3.32**	62.73**
IV				**3.51**

Chi-square ($\chi 2$) test at 5% =19.67; at 1% = 24.72, ∗∗= highly significant, ∗ = significant, and ns = nonsignificant

Chapter 5. CONCLUSIONS AND RECOMMENDATIONS

5.1. Conclusion

Sorghum is a dual-purpose crop used for both human food and animal feed in many countries including Ethiopia. The result of the analysis of variance showed that the presence of genetic variability among sorghum genotypes for all tested traits. This result gives an opportunity to plant breeders for develop high grain and biomass yielder varieties in the study area where biomass yield and grain yield to be a critical problem for growers. Based on the results of this study, we concluded that four traits viz. Biological yield, thousand kernel weight, head weight and grain yield could be used as good selection criteria to improve both traits in one variety, thus answering the question of combining high sorghum grain yield and biological yield. Because, these traits had a high genotypic coefficient of variance, high heritability coupled with high genetic advance as a percentage of the mean, a high positive genotypic correlation coefficient, and positive direct genotypic effects on grain yield.

5.2. Recommendations

This research was conducted for one season at one location; therefore further studies should be needed over season and more locations to verify the consistency of existing genotypic variability and in order to make more reliable conclusion and recommendation. In addition, the genetic variability study of the present sorghum genotypes should be supported by molecular markers to further confirmation the outcome of this finding .

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APPENDICES

Appendix Table 1: List of sorghum genotypes used in the study and their pedigrees

No	Genotypes	Pedigree
1	ETSC17296-3-1	ETSC17296-3-1
2	ETSC18076-34-1	14MWLSDT7196/90MW5319
3	ETSC18076-6-1	14MWLSDT7196/90MW5319
4	ETSC17158-3-2	ETSC17158-3
5	ETSC18076-1-1	14MWLSDT7196/90MW5319
6	ETSC18079-15-1	14MWLSDT7196/ETSC14209-5-3
7	ETSC17186-2-1	ETSC17186-2-1
8	ETSC18059-31-1	14MWLSDT7176/2005MI5093
9	ETSC18059-52-5	14MWLSDT7176/2005MI5093
10	ETSC18086-27-1	14MWLSDT7201/ETSC14121-5-1
11	ETSC18095-14-5	14MWLSDT7234/ETSC14209-5-3
12	ETSC14203-5-2	KariMatama1/N-13
13	ETSC17201-1-2	ETSC17201-1-2
14	ETSC18059-54-1	14MWLSDT7176/2005MI5093
15	ETSC16091-10-1	235421/M204
16	ETSC17301-16-3	ETSC17301-16-3
17	ETSC18015-14-1	04MW6079/ETSC14209-5-3
18	ETSC17258-3-2	ETSC17258-3
19	ETSC18086-3-1	14MWLSDT7201/ETSC14121-5-1
20	ETSC18018-22-1	12MW6251/2005MI5057
21	ETSC14225-4-2	Gambella/S35
22	ETSC18062-18-1	14MWLSDT7176/ETSC14121-5-1
23	ETSC18059-47-1	14MWLSDT7176/2005MI5093
24	ETSC18004-23-1	ETSC300354/90MW5319
25	ETSC18073-10-1	14MWLSDT7196/13MWF66037
26	ETSC18001-16-1	ETSC300354/13MWF66037
27	ETSC15363-1-2	ETSC15363-1-2

Appendix Table 1: (Continued)

No	Genotypes	Pedigree
28	ETSC18076-29-1	14MWLSDT7196/90MW5319
29	ETSC18034-19-1	14MWLSDT7033/2005MI5057
30	ETSC18079-4-1	14MWLSDT7196/ETSC14209-5
31	ETSC17068-3-1	ETSC17068-3
32	ETSC16034-10-1	Argiti/ICSTG2372
33	ETSC18086-4-1	14MWLSDT7201/ETSC14121-5-1
34	ETSC18104-3-1	14MWLSDT7238/ETSC14219-1-1
35	ETSC18076-21-1	14MWLSDT7196/90MW5319
36	ETSC17300-4-1	ETSC17300-4
37	ETSC18012-5-1	04MW6079/90MW5319
38	ETSC17156-2-1	ETSC17156-2
39	ETSC19182-7-4	IDSG06123/ETSC14124-4-3
40	ETSC17490-90-2	ETSC17490-90-2
41	ETSC18074-26-7	14MWLSDT7196/2005MI5057
42	ETSC18018-6-1	12MW6251/2005MI5057
43	ETSC17258-5-2	ETSC17258-5
44	ETSC17321-11-1	ETSC17321-11
45	ETSC17300-4-2	ETSC17300-4-2
46	ETSC17213-1-2	ETSC17213-1
47	ETSC18059-47-1	14MWLSDT7176/2005MI5093
48	ETSC18025-8-1	14MWLSDT7325/13MWF66037
49	ETSC18018-6-1	12MW6251/2005MI5057
50	ETSC17300-4-1	ETSC17300-4
51	ETSC18086-27-1	14MWLSDT7201/ETSC14121-5-1
52	ETSC17213-1-6	ETSC17213-1
53	ETSC18076-5-1	14MWLSDT7196/90MW5319
54	ETSC17296-3-1	ETSC17296-3-1
55	ETSC18076-13-1	14MWLSDT7196/90MW5319
56	ETSC15357-3-1	ICSV700/Meko-1

Appendix Table 1: (Continued)

No	Genotypes	Pedigree
57	ETSC18025-3-1	14MWLSDT7325/13MWF66037
58	ETSC17258-13-1	ETSC17258-13
59	ETSC18086-35-1	14MWLSDT7201/ETSC14121-5-1
60	ETSC17355-11-1	ETSC17355-11
61	ETSC19051-18-7	IS38358/ETSC300386
62	ETSC17301-10-2	ETSC17301-10-2
63	ETSC18097-38-1	14MWLSDT7238/13MWF66037
64	ETSC18170-21-1	13MWF66037/ETSL100350
65	ETSC17121-2-1	ETSC17121-2
66	ETSC17063-7-1	ETSC17063-7
67	ETSC17285-5-2	ETSC17285-5-2
68	ETSC18081-16-1	14MWLSDT7201/13MWF66037
69	ETSC16034-12-1	Argiti/ICSTG2372
70	ETSC17300-9-5	ETSC17300-9
71	ETSC19125-7-7	ETSC15438-4-1/ETSC14020-1-1
72	ETSC15312-3-1	ETSL101845/ETSC17492-138-2
73	ETSC17113-6-1	ETSC17113-6
74	ETSC14695-1-2	ETSL101845/13sudanint27
75	ETSC17111-3-1	ETSC17111-3
76	ETSC17142-9-3	ETSC17142-9
77	ETSC18025-3-1	14MWLSDT7325/13MWF66037
78	ETSC19182-10-7	IDSG06123/ETSC14124-4-3
79	ETSC17483-233-2	ETSC17483-233-2
80	Melkam	Melkam
81	Alene	Alene

Appendix Table 2: Mean performances of 81 sorghum genotypes for 12 traits

Genotypes	DF(days)	DM(days)	LL(cm)	LW(cm)	LAI(cm^2)	PHT(cm)	PL(cm)
57	81.5^{a-c}	128.5^{a-d}	82.25^{a-d}	8.75^{a-c}	511.03^{a-c}	200^{ab}	22.25^{b-f}
12	83^{a}	127^{a-e}	82^{a-e}	8.25^{a-d}	480.14^{a-f}	211.75^{a}	22.5^{b-e}
49	78^{a-g}	131^{a-d}	76.25^{a-i}	8^{a-e}	433.10^{b-h}	191^{a-h}	19.75^{e-n}
18	78^{a-g}	132.5^{a-c}	77.75^{a-h}	7.75^{a-e}	395.20^{b-i}	170.25^{h-s}	21.5^{c-i}
39	81^{a-c}	130^{a-d}	87.5^{a}	9.75^{a}	605.81^{a}	163.25^{k-u}	21.25^{c-j}
11	79.5^{a-e}	127.5^{a-e}	77.25^{a-h}	6.75^{b-g}	371.69^{b-j}	199.5^{a-f}	22.25^{b-f}
13	78.5^{a-f}	133.5^{ab}	79.5^{a-g}	7.5^{a-f}	425.11^{b-i}	182.5^{c-k}	22^{c-g}
54	77.5^{a-h}	130^{a-d}	82^{a-e}	8.25^{a-d}	479.78^{a-f}	177.75^{f-m}	22.75^{b-d}
33	80^{a-e}	131.5^{a-d}	75.25^{a-i}	6.25^{d-g}	334.32^{d-j}	155.25^{m-v}	22.25^{b-f}
55	79^{a-f}	128.5^{a-d}	74.75^{a-j}	8.5^{a-d}	454.13^{a-g}	193.5^{a-g}	23.25^{a-c}
59	82.5^{ab}	131.5^{a-d}	81^{a-f}	9^{ab}	516.17^{ab}	176.5^{g-n}	20^{d-m}
62	76.5^{b-h}	133.5^{ab}	72.25^{a-j}	7.5^{a-f}	386.06^{b-i}	199.5^{a-f}	21.5^{c-i}
32	80.5^{a-d}	133.5^{ab}	78.25^{a-g}	7^{b-g}	388.10^{b-i}	205.5^{ab}	20.25^{d-m}
17	79.5^{a-e}	130^{a-d}	70.75^{a-k}	7^{b-g}	351.63^{b-j}	163.5^{k-u}	20.75^{c-k}
46	77^{a-h}	131^{a-d}	69.75^{a-k}	6.75^{b-g}	334.76^{d-j}	203.25^{a-c}	22.75^{b-d}
50	80^{a-e}	127.5^{a-e}	61.75^{g-k}	7.25^{b-g}	319.85^{f-j}	181.25^{c-l}	20^{d-m}
34	79.5^{a-e}	130.5^{a-d}	74.5^{a-j}	6.75^{b-g}	356.96^{b-j}	175.50^{g-o}	20.5^{d-l}
63	77.5^{a-h}	130^{a-d}	77^{a-i}	7.25^{b-g}	399.02^{b-i}	180.75^{d-l}	20.75^{c-k}
58	80.5^{a-d}	133.5^{ab}	80^{a-f}	7^{b-g}	401.86^{b-i}	160.50^{k-v}	19.5^{f-o}
23	78.5^{a-f}	134^{ab}	83.75^{a-c}	6.5^{c-g}	388.54^{b-i}	189.5^{b-i}	21.5^{c-i}
72	80^{a-e}	128.5^{a-d}	74.25^{a-j}	6.5^{c-g}	343.11^{b-j}	200.5^{a-e}	21.75^{c-g}
29	81.5^{a-c}	130.5^{a-d}	77.75^{a-h}	8.25^{a-d}	453.42^{a-g}	201.5^{a-d}	20.75^{c-k}
67	78.5^{a-f}	129.5^{a-d}	71.5^{a-j}	7^{b-g}	355.89^{b-j}	187^{b-j}	18.5^{k-q}
42	81^{a-c}	130.5^{a-d}	72.5^{a-j}	8^{a-e}	411.80^{b-i}	170.25^{h-s}	18.25^{k-q}
61	80.5^{a-d}	131^{a-d}	72^{a-j}	6.25^{d-g}	320.21^{f-j}	162.25^{k-v}	20.5^{d-l}
10	81^{a-c}	133.5^{ab}	64.5^{d-k}	7^{b-g}	320.56^{f-j}	170.25^{h-s}	18.75^{j-k}
31	82^{a-c}	133^{a-c}	86^{ab}	8.25^{a-d}	506.14^{a-d}	175.75^{g-o}	21.25^{c-j}
28	77.5^{a-h}	129^{a-d}	65^{d-k}	7^{b-g}	329.44^{e-j}	139.75^{s-u}	18.25^{k-q}

Appendix Table 2: (continued)

Genotypes	DF(days)	DM(days)	LL(cm)	LW(cm)	LAI(cm^2)	PHT(cm)	PL(cm)
60	78^{a-g}	133.5^{ab}	64^{f-k}	6.25^{d-g}	290.12^{g-j}	178.25^{f-m}	18.25^{k-q}
35	79.5^{a-e}	127.5^{a-e}	72.25^{a-j}	7^{b-g}	359.08^{b-j}	168.75^{h-s}	18.25^{k-q}
65	80.5^{a-d}	132^{a-c}	70.25^{a-k}	8^{a-e}	403.81^{b-i}	170.5^{h-s}	22^{c-g}
36	79.5^{a-e}	130.5^{a-d}	77.25^{a-h}	6.75^{b-g}	368.93^{b-j}	187.75^{b-j}	19^{i-p}
56	79.5^{a-e}	126^{a-e}	71.25^{a-k}	6.5^{c-g}	328.82^{e-j}	163.75^{k-u}	17.75^{m-q}
14	79.5^{a-e}	132.5^{a-c}	75 a-j	7.25^{b-g}	385.71^{b-i}	179.25^{e-l}	25.25^{a}
30	80.5^{a-d}	129.5^{a-d}	67.75^{c-j}	6.25^{d-g}	305.29^{f-j}	161.75^{k-v}	20.75^{c-k}
44	78^{a-g}	128^{a-d}	73.25^{a-j}	6.75^{b-g}	355.44^{b-j}	177.25^{f-n}	24.5^{ab}
64	74.5^{d-i}	129^{a-d}	69.25^{b-k}	7.25^{b-g}	356.60^{b-j}	148.25^{p-u}	24.5^{ab}
40	80^{a-e}	132^{a-c}	78.25^{a-g}	9^{ab}	503.29^{a-e}	168^{i-s}	17.25^{n-q}
69	79^{a-f}	129^{a-d}	75.5^{a-i}	8^{a-e}	434.16^{b-h}	158.75^{l-v}	19.5^{f-o}
15	76^{c-h}	132^{a-c}	72.75^{a-j}	7^{b-g}	360.41^{b-j}	174.25^{g-o}	20^{d-m}
80	77.5^{a-h}	130.5^{a-d}	60.25^{h-k}	6.5^{c-g}	280.45^{g-j}	128^{u}	20.75^{c-k}
51	81.5^{a-c}	131.5^{a-d}	68.75^{b-k}	7^{b-g}	341.68^{b-j}	158.72^{l-v}	22.25^{b-f}
66	80.5^{a-d}	134^{ab}	70.25^{a-k}	8^{a-e}	401.95^{b-i}	175.75^{g-o}	20^{d-m}
70	78^{a-g}	131.5^{a-d}	65^{d-k}	6.5^{c-g}	301.75^{g-j}	159.75^{k-v}	19.25^{g-o}
81	77.5^{a-h}	129^{a-d}	57.25^{j-k}	6.75^{b-g}	275.21^{h-j}	149.25^{o-u}	20.25^{d-m}
3	81^{a-c}	133.5^{ab}	65.25^{d-k}	6.5^{c-g}	296.96^{g-j}	165.75^{j-u}	19^{i-p}
37	77.5^{a-h}	130^{a-d}	67.75^{c-j}	5.25^{f-g}	254.27^{i-j}	160.75^{k-v}	19.25^{g-o}
16	80^{a-e}	133^{a-c}	70.5^{a-k}	6.5^{c-g}	325^{f-j}	174.5^{g-o}	16.25^{q}
71	81^{a-c}	127.5^{a-e}	76^{a-i}	7.25^{b-g}	387.75^{b-i}	168^{i-s}	18.75^{j-k}
47	78.5^{a-f}	127.5^{a-e}	69^{b-k}	7^{b-g}	342.93^{b-j}	133^{t-u}	19.25^{g-o}
53	78.5^{a-f}	128.5^{a-d}	71.75^{a-j}	8^{a-e}	413.40^{b-i}	171.75^{g-r}	20.5^{d-l}
9	78^{a-g}	132^{a-c}	68.5^{b-k}	6.25^{d-g}	303.35^{g-j}	177.75^{f-m}	18^{l-q}
41	80.5^{a-d}	135^{a}	74.25^{a-j}	7.5^{a-f}	400.44^{b-i}	187.25^{b-j}	22.75^{b-d}
38	78.5^{a-f}	128.5^{a-d}	70^{a-k}	7^{b-g}	347.90^{b-j}	166^{j-u}	20.5^{d-l}
27	78.5^{a-f}	129.5^{a-d}	74.25^{a-j}	6.25^{d-g}	332.01^{d-j}	159.25^{l-v}	17.25^{n-q}
1	71.5^{h-i}	124^{b-e}	53.5^{k}	6.75^{b-g}	257.11^{i-j}	173.75^{g-o}	18.75^{j-k}

Appendix Table 2: (continued)

Genotypes	DF(days)	DM(days)	LL(cm)	LW(cm)	LAI(cm^2)	PHT(cm)	PL(cm)
74	80.5^{a-d}	133^{a-c}	67.75^{c-j}	5.75^{e-g}	271.93^{h-j}	161.75^{k-v}	19.25^{g-o}
24	76.5^{b-h}	130.5^{a-d}	68.5^{b-k}	7.75^{a-e}	375.59^{b-j}	179.75^{d-l}	18.75^{j-q}
48	82.5^{ab}	134^{ab}	73^{a-j}	7.25^{b-g}	374.35^{b-j}	153^{m-u}	18.5^{k-q}
6	81^{a-c}	128.5^{a-d}	63.75^{f-k}	6.5^{c-g}	295.54^{g-j}	167.5^{i-t}	17^{pq}
75	72^{g-i}	131.5^{a-d}	59.25^{i-k}	5^{g}	209.54^{j}	150.25^{n-t}	19^{i-p}
22	76.5^{b-h}	130.5^{a-d}	66.5^{c-j}	5.75^{e-g}	271.40^{h-j}	150.50^{n-u}	21.5^{c-i}
26	80.5^{a-d}	133.5^{ab}	71^{a-k}	7.25^{b-g}	364.76^{b-j}	173^{g-q}	19.25^{g-o}
7	79^{a-f}	128.5^{a-d}	75^{a-j}	7^{b-g}	372.75^{b-j}	167^{i-t}	18.5^{k-q}
2	78^{a-g}	127^{a-e}	69^{b-k}	6.5^{c-g}	320.92^{f-j}	170.75^{g-s}	18^{l-q}
5	78.5^{a-f}	130^{a-d}	64.25^{e-k}	7.25^{b-g}	331.21^{e-j}	144.75^{q-u}	19.5^{f-o}
79	80.5^{a-d}	127^{a-e}	70.5^{a-k}	6.75^{b-g}	337.87^{c-j}	163^{k-u}	20.25^{d-m}
45	77.5^{a-h}	130^{a-d}	69.75^{a-k}	7^{b-g}	348.16^{b-j}	166.25^{j-u}	18.25^{k-q}
43	77.5^{a-h}	131.5^{a-d}	76^{a-i}	7.75^{a-e}	419.52^{b-i}	167.5^{i-t}	17^{pq}
4	70^{i}	122.5^{c-e}	75^{a-j}	7.5^{a-f}	400.62^{b-i}	167.75^{i-s}	18^{l-q}
73	74^{e-i}	129^{a-d}	63.75^{f-k}	6.5^{c-g}	293.05^{g-j}	144^{r-u}	19.25^{g-o}
77	80.5^{a-d}	131^{a-d}	63.5^{f-k}	7^{b-g}	315.80^{f-j}	139.75^{s-u}	20.5^{d-l}
21	80.5^{a-d}	134^{ab}	68.25^{b-k}	7.25^{b-g}	351.98^{b-j}	173.5^{g-p}	17.25^{n-q}
76	83^{a}	131.5^{a-d}	69.25^{b-k}	7^{b-g}	344.17^{b-j}	154.5^{m-v}	20.75^{c-k}
25	69.5^{i}	1175^{e}	69^{b-k}	7.25^{b-g}	356.07^{b-j}	168.75^{h-s}	22^{c-g}
68	82.5^{ab}	130.5^{a-d}	66^{c-j}	6.25^{d-g}	293.59^{g-j}	163.25^{k-u}	19^{i-p}
8	77.5^{a-h}	134^{ab}	74.5^{a-j}	7.25^{b-g}	382.78^{b-j}	164.75^{j-u}	17.5^{n-q}
78	73^{f-i}	129.5^{a-d}	74.25^{a-j}	8^{a-e}	428.93^{b-i}	162^{k-v}	21.25^{c-j}
52	69^{i}	121^{d-e}	69.25^{b-k}	7.25^{b-g}	356.33^{b-j}	169.25^{h-s}	20^{d-m}
19	79.5^{a-e}	128.5^{a-d}	63.25^{f-k}	6.5^{c-g}	291.90^{g-j}	156^{m-v}	20.75^{c-k}
20	71^{h-i}	123.5^{b-e}	76.75^{a-i}	8^{a-e}	441.44^{b-h}	154.25^{m-v}	16.25^{q}

Appendix 2: (continued)

Genotypes	HW(kgha-$^{1)}$	BY(ton/ha)	HI (%)	TKW(gm)	GY(kg/ha-$^{1)}$
57	9300^{a}	26.55^{a-c}	15.61^{c-h}	40.05^{a-c}	4104.3^{a}
12	8855.56^{a-d}	29.84^{a}	13.64^{g-h}	40.05^{a-c}	4054.94^{ab}
49	8711.12^{a-d}	25.55^{a-e}	15.87^{c-h}	39.56^{a-e}	4044.41^{ab}
18	9033.33^{ab}	27.61^{ab}	14.48^{f-h}	38.78^{a-g}	3994.31^{a-c}
39	8411.11^{b-h}	24.08^{a-g}	16.58^{b-h}	39.71^{a-d}	3970.3^{a-d}
11	8644.45^{a-e}	24.60^{a-f}	16.00^{c-h}	40.59^{a}	3934.55^{a-e}
13	8300^{b-i}	21.57^{b-m}	18.13^{a-h}	37.92^{a-i}	3903.37^{a-f}
54	8222.22^{b-j}	26.33^{a-d}	14.80^{f-h}	37..83^{a-i}	3884.78^{a-f}
33	8433.34^{b-g}	19.16^{e-v}	20.32^{a-f}	37.25^{a-j}	3884.39^{a-f}
55	8533.34^{a-f}	25.44^{a-e}	15.44^{d-h}	36.50^{a-m}	3878.86^{a-f}
59	8133.33^{c-k}	22.76^{b-h}	16.76^{b-h}	38.05^{a-h}	3812.16^{a-g}
62	7977.78^{d-m}	21.45^{b-n}	17.90^{a-h}	38.73^{a-g}	3781.44^{a-h}
32	8044.45^{d-m}	21.56^{b-m}	17.57^{a-h}	35.33^{d-p}	3772.87^{a-i}
17	7944.45^{d-n}	21.18^{b-o}	17.76^{a-h}	36.97^{a-k}	3751.27^{a-i}
46	8122.22^{c-k}	21.30^{b-o}	20.29^{a-f}	37.36^{a-j}	3743.85^{a-i}
50	7922.23^{d-n}	24.67^{a-f}	15.10^{e-h}	37.20^{a-j}	3726.25^{a-j}
34	8111.11^{c-k}	19.78^{d-t}	18.93^{a-h}	39.35^{a-f}	3726.16^{a-j}
63	8211.11^{b-j}	22.64^{b-i}	16.51^{b-h}	39.30^{a-f}	3689^{b-j}
58	7744.45^{e-n}	20.40^{c-r}	18.25^{a-h}	38.32^{a-h}	3678^{b-j}
23	7622.22^{f-n}	20.12^{c-r}	18.03^{a-h}	38.98^{a-f}	3623.92^{c-k}
72	7655.56^{f-n}	18.96^{e-w}	19.23^{a-h}	33.28^{j-s}	3620.45^{c-l}
29	7366.67^{i-m}	21.81^{b-k}	16.75^{b-h}	30.02^{r-w}	3588.01^{c-m}
67	7500^{g-m}	20.86^{c-p}	17.25^{a-h}	37.63^{a-j}	3584.71^{c-m}
42	7400^{h-m}	23.07^{b-g}	15.49^{d-h}	27.44^{v-B}	3572.79^{d-m}
61	7555.56^{g-n}	20.72^{c-q}	17.17^{a-h}	36.86^{a-k}	3551.4^{e-m}
10	7311.12^{i-o}	18.82^{e-w}	19.18^{a-h}	38.99^{a-f}	3536.67^{e-m}
31	7488.89^{h-m}	19.57^{e-u}	18.03^{a-h}	32.67^{k-t}	3511.85^{f-n}
28	7277.78^{j-o}	17.11^{h-x}	21.24^{a-e}	38.66^{a-g}	3494.13^{f-o}

Appendix 2: (continued)

Genotypes	HW(kgha-$^{1)}$	BY(ton/ha)	HI (%)	TKW(gm)	GY(kg ha-$^{1)}$
60	7122.23^{k-p}	17.80^{g-x}	20.56^{a-f}	35.03^{f-q}	3463.16^{g-o}
35	7122.23^{k-p}	18.46^{f-w}	18.78^{a-h}	40.39^{ab}	3461.23^{g-o}
65	7255.56^{j-o}	17.23^{h-x}	20.53^{a-f}	31.86^{n-u}	3451.49^{g-o}
36	7144.45^{k-p}	21.93^{b-j}	16.33^{b-h}	32.67^{k-t}	3426.28^{g-p}
56	7344.45^{i-o}	20.63^{c-q}	16.59^{b-h}	35.68^{c-n}	3408.65^{g-p}
14	7322.22^{i-o}	17.78^{g-x}	19.04^{a-h}	36^{b-n}	3385.28^{h-q}
30	7166.67^{k-p}	15.42^{j-x}	23.38^{a}	38.19^{a-h}	3361.5^{i-q}
44	7255.56^{j-o}	21.39^{b-n}	15.56^{c-h}	32.23^{m-u}	3329.39^{j-r}
64	7111.11^{l-p}	18.33^{f-w}	18.15^{a-h}	36.68^{a-l}	3229^{j-r}
40	6977.78^{m-q}	16.86^{h-x}	19.52^{a-h}	36.30^{a-m}	3249.17^{k-s}
69	6833.33^{m-r}	15.07^{k-x}	21.51^{a-d}	36.55^{a-m}	3233.28^{k-s}
15	6811.12^{m-s}	16.62^{h-x}	19.99^{a-f}	30.83^{q-v}	3229.37^{k-s}
80	6933.34^{m-q}	14.93^{m-x}	21.82^{a-c}	34.99^{f-q}	3208.22^{l-t}
51	6877.78^{m-q}	16.88^{h-x}	18.99^{a-h}	31.29^{p-v}	3203.62^{m-u}
66	6433.34^{o-t}	21.78^{b-l}	14.45^{f-h}	24.93^{y-E}	3108.37^{n-v}
70	6444.44^{n-t}	19.26^{e-v}	16.04^{c-h}	26.3^{w-C}	3092 o-w
81	6444.45^{n-t}	14.27^{p-x}	21.48^{a-d}	33.53^{i-s}	3044.39^{p-x}
3	6288.89^{p-u}	18.55^{f-w}	16.20^{b-h}	28.5^{t-A}	2995.13^{q-x}
37	6144.45^{q-v}	15.23^{j-x}	19.57^{a-h}	35^{c-n}	2946.61^{r-x}
16	5966.67^{r-w}	18.13^{f-w}	16.43^{b-h}	24.65^{y-E}	2907^{s-y}
71	5955.56^{s-y}	15.36^{j-x}	18.74^{a-h}	37.83^{a-i}	2858.58^{s-z}
47	5966.67^{s-x}	13.93^{q-x}	20.29^{a-f}	34.5^{g-q}	2816.2 $^{t-A}$
53	5966.67^{s-x}	13.70^{r-x}	20.63^{a-f}	35.16^{e-q}	2911.5^{t-A}
9	5922.22^{t-y}	14.53^{o-x}	19.33^{a-h}	32.32^{l-u}	2806.94^{u-A}
41	5777.78^{t-z}	14.73^{n-x}	18.89^{a-h}	21.4^{E-F}	2783.34^{u-A}
38	5955.56^{s-y}	12.54^{v-x}	22.45^{ab}	25.9^{w-D}	2757.58^{u-B}
27	5822.23^{t-y}	15.63^{j-x}	17.55^{a-h}	38.54^{a-g}	2742^{u-C}
1	5933.34^{s-y}	16.07^{i-x}	17.06^{b-h}	29.43^{s-x}	2739.34^{u-C}
74	5633.33^{t-A}	17.23^{h-x}	16.01^{c-h}	25.25^{x-E}	2726^{u-C}

Appendix 2: (continued)

Genotypes	HW(kg/ ha)	BY(ton/ha)	HI (%)	TKW(gm)	GY(kg ha-$^{1)}$
24	5533.34^{t-B}	16.55^{h-x}	16.80^{b-h}	21.15^{E-F}	2717.81^{u-C}
48	5588.89^{t-A}	16.72^{h-x}	16.25^{b-h}	34.05^{h-r}	2716.58^{u-C}
6	5777.78^{t-z}	14.14^{p-x}	19.27^{a-h}	24.27^{A-F}	2692.49^{v-C}
75	5577.78^{t-Z}	16.16^{i-x}	16.52^{b-h}	35.05^{f-q}	2859.68^{v-B}
22	5422.23^{u-C}	12.52^{v-x}	20.12^{a-f}	31.27^{p-v}	2518.17^{w-C}
26	5322.22^{v-C}	14.96^{l-x}	16.91^{b-h}	25.96^{w-D}	2506.12^{w-C}
7	5144.45^{w-D}	14.73^{n-x}	16.99^{b-h}	28.5^{t-A}	2500.77^{w-C}
2	5033.34^{w-D}	14.71^{n-x}	16.91^{b-h}	22^{D-F}	2486.95^{x-D}
5	4933.34^{y-D}	13.18^{t-x}	18.71^{a-h}	24.54^{z-F}	2454.79^{x-D}
79	5155.56^{w-D}	13.99^{q-x}	17.37^{a-h}	33.28^{j-s}	2428.16^{y-D}
45	5022.22^{x-D}	12.26^{w-x}	19.90^{a-g}	31.28^{p-v}	2425.26^{y-D}
43	5166.67^{w-D}	15.76^{j-x}	15.51^{d-h}	30.95^{q-v}	2422.83^{y-D}
4	5177.78^{w-D}	13.54^{s-x}	18.07^{a-h}	28.26^{u-B}	2422.22^{y-D}
73	5122.22^{w-D}	13.35^{s-x}	18.38^{a-h}	31.41^{o-v}	2405.42^{y-D}
77	5088.89^{w-D}	12.51^{v-x}	19.60^{a-g}	28.88^{t-y}	2394.21^{z-D}
21	5077.78^{w-D}	15.38^{j-x}	15.82^{c-h}	22.9^{C-F}	2378.2^{z-D}
76	5044.45^{w-D}	14.54^{o-x}	16.29^{b-h}	20.94^{F}	2368.48^{A-D}
25	5255.56^{v-D}	17.79^{g-x}	13.32^{h}	24.15^{B-F}	2342.15^{B-D}
68	4722.22^{A-D}	14.97^{l-x}	15.05^{e-h}	23.03^{C-F}	2185.87^{C-D}
8	4511.11^{C-D}	11.04^{x}	19.60^{a-g}	35.45^{d-p}	2151.73^{C-D}
78	4622.23^{B-D}	12.81^{u-x}	16.73^{b-h}	26.57^{w-C}	2139.68^{C-D}
52	4866.67^{z-D}	14.14^{p-x}	15.32^{d-h}	21.36^{EF}	2133.78^{C-D}
19	4622.22^{B-D}	12.57^{v-x}	16.96^{b-h}	35.55^{d-p}	2129.05^{C-D}
20	4344.45^{D}	12.87^{u-x}	16.23^{b-h}	28.75^{t-z}	2084.88^{D}

Appendix Table 3: Euclidean distances of 81 sorghum genotypes with 12 quantitative traits

	G1	G 2	G3	G4	G 5	G6	G7	G8	G9	G10	G11	G12	G13
G2	2.57												
G3	3.76	2.16											
G4	3.03	1.78	2.41										
G5	2.03	2.77	3.74	3.30									
G6	2.84	3.34	3.96	3.21	1.52								
G7	3.09	3.33	3.50	3.60	2.50	2.42							
G8	3.07	2.13	1.52	1.86	3.36	3.30	2.70						
G9	3.48	3.16	2.32	3.05	3.92	4.14	3.00	1.98					
G10	3.77	2.58	1.77	2.26	3.79	3.85	3.34	1.79	2.57				
G11	2.76	3.02	2.65	2.88	2.84	2.91	2.57	1.96	2.05	3.17			
G12	3.56	3.65	4.18	3.78	3.99	4.50	3.44	3.75	3.07	3.36	4.12		
G13	2.99	1.82	2.73	2.70	2.61	3.17	3.48	2.66	3.96	3.29	2.98	4.82	
G14	3.50	3.95	4.91	4.96	2.80	3.82	4.57	4.89	5.67	5.41	4.33	6.11	2.77
G15	1.34	2.51	3.47	2.72	2.48	3.17	2.84	2.70	2.85	3.06	2.67	2.52	3.14
G16	2.19	2.85	4.11	3.08	2.01	2.29	2.95	3.25	4.28	4.08	2.97	4.50	2.23
G17	3.53	3.77	3.46	3.99	3.58	3.49	2.09	2.70	2.55	4.01	2.20	4.33	4.09
G18	4.32	4.28	4.44	4.30	4.74	5.19	4.24	4.28	2.98	4.07	4.39	1.83	5.64
G19	3.04	1.66	2.73	2.68	2.75	3.43	2.90	2.73	3.36	2.40	3.58	2.82	2.57
G20	2.44	2.09	2.67	2.42	2.86	3.27	2.14	1.91	1.95	2.47	2.40	2.18	3.10
G21	3.11	3.19	3.38	2.25	3.80	3.48	3.26	2.36	2.68	2.74	3.12	3.05	4.31
G22	2.91	2.71	3.31	2.70	1.69	1.24	2.40	2.91	3.73	3.15	3.01	3.93	3.00
G23	4.81	5.04	6.14	5.06	5.64	6.31	6.41	5.92	5.96	5.11	6.54	3.87	6.10
G24	3.88	3.54	4.60	3.63	4.39	4.86	4.45	4.26	4.30	3.61	5.11	1.95	4.92
G25	4.86	5.66	5.73	4.84	5.58	5.27	5.19	4.54	5.28	5.03	4.56	5.93	5.30
G26	4.74	5.21	4.83	4.37	4.64	4.04	3.75	3.78	4.30	3.95	3.68	5.04	4.90
G27	4.38	5.01	4.58	5.08	3.87	4.00	3.66	4.12	4.47	4.49	3.26	5.63	4.01
G28	4.54	5.47	5.53	5.45	3.49	3.60	3.71	5.05	5.01	5.22	3.89	5.29	4.76
G29	5.37	5.36	4.59	4.74	5.82	5.74	4.85	3.95	4.12	3.50	4.50	4.83	5.41
G30	4.78	4.40	3.52	3.81	4.85	4.97	4.46	3.39	3.15	2.79	3.49	4.18	4.46

Appendix 3: (continued)

	G1	G 2	G3	G4	G 5	G6	G7	G8	G9	G10	G11	G12	G13
G31	3.68	3.74	3.51	3.42	3.57	3.44	2.64	2.55	3.24	3.01	2.54	4.20	3.29
G32	3.41	4.02	4.29	3.45	3.15	2.71	3.10	3.24	4.20	3.70	2.98	4.72	3.41
G33	4.04	4.99	4.98	5.13	3.83	4.28	3.37	4.39	4.12	4.49	3.57	4.24	4.56
G34	4.57	4.73	4.44	5.03	3.94	4.14	3.51	4.05	4.65	4.42	3.57	5.66	3.55
G35	4.57	4.44	4.09	4.34	5.08	5.48	4.55	3.65	3.67	3.67	3.76	4.52	4.21
G36	4.66	5.59	5.93	5.59	3.99	3.89	3.61	5.07	5.56	5.47	4.40	5.65	4.72
G37	3.67	4.20	4.52	4.62	3.47	4.39	3.92	4.31	4.16	4.13	3.75	3.93	3.81
G38	3.74	4.37	4.61	4.37	3.87	4.35	4.39	4.09	4.53	4.42	3.43	5.19	3.45
G39	4.44	4.86	4.50	4.92	4.65	5.09	4.09	4.03	3.92	4.01	3.70	4.56	4.42
G40	5.89	6.20	5.14	5.52	5.98	5.69	4.51	4.53	3.50	4.69	4.05	4.94	6.43
G41	4.88	5.62	5.38	5.05	4.71	4.32	3.28	4.37	3.97	4.69	3.74	4.33	5.63
G42	3.85	5.19	5.70	4.44	4.14	3.85	4.53	4.63	5.18	4.96	4.11	5.23	4.83
G43	4.16	5.10	5.59	4.95	2.92	2.71	3.97	5.01	5.56	5.37	4.01	5.82	4.19
G44	5.72	5.91	5.27	4.91	6.19	5.80	4.94	4.24	4.10	4.61	4.25	5.29	6.01
G45	4.55	5.10	5.56	4.46	5.51	5.68	5.67	4.70	5.25	4.71	4.95	5.20	5.01
G46	3.91	3.92	4.27	3.56	3.37	2.88	2.08	3.25	3.93	3.43	3.57	3.69	3.95
G47	3.96	4.84	4.75	4.40	3.97	3.55	2.39	3.62	3.60	3.92	3.43	3.70	5.02
G48	3.24	2.57	2.40	2.77	3.28	3.76	3.82	2.41	3.29	2.79	2.46	4.67	1.83
G49	3.06	2.49	2.78	2.73	2.40	2.83	3.25	2.67	3.69	2.73	2.73	4.40	1.58
G50	3.33	2.35	2.70	3.18	2.41	3.10	2.56	2.86	3.39	2.55	3.24	3.42	2.37
G51	2.70	3.37	3.72	3.96	3.05	3.93	3.01	3.29	2.82	4.02	2.30	3.62	3.29
G52	3.87	4.23	4.87	4.99	3.17	4.06	4.29	4.94	5.42	4.30	5.08	4.54	4.12
G53	3.08	2.96	3.07	3.72	2.65	3.18	2.16	2.64	3.38	3.30	2.54	4.30	2.25
G54	4.03	4.89	5.34	5.04	2.59	2.44	3.31	4.82	5.49	4.96	4.25	5.43	4.13
G55	3.10	4.11	4.71	3.97	2.30	2.33	2.51	3.95	3.87	4.39	2.95	3.71	4.06
G56	4.79	4.17	3.80	3.23	5.01	4.33	3.98	2.69	4.18	3.15	3.96	5.25	4.24
G57	3.32	4.15	4.23	4.05	3.91	4.25	2.94	3.34	2.57	3.76	2.81	2.81	4.49
G58	3.93	2.51	1.80	3.23	3.46	3.95	3.20	2.35	2.98	2.50	2.81	4.34	2.16
G59	4.29	3.61	2.50	2.74	4.62	4.50	4.30	2.23	2.89	2.02	3.02	4.57	3.79

Appendix 3: (continued)

	G1	G 2	G3	G4	G 5	G6	G7	G8	G9	G10	G11	G12	G13
G60	3.48	4.10	4.97	4.84	2.72	3.35	3.11	4.39	5.07	5.06	3.81	5.23	3.06
G61	4.72	5.49	5.41	5.33	4.69	4.83	4.27	4.64	4.89	4.89	4.04	5.43	4.71
G62	5.07	5.68	5.39	5.31	5.74	6.06	5.54	4.82	4.70	4.85	4.48	5.40	5.36
G63	5.69	5.99	5.73	5.61	6.54	6.72	5.97	4.95	5.09	5.53	4.79	6.30	5.59
G64	4.73	5.21	4.84	4.81	4.81	4.84	4.30	4.10	4.07	4.69	3.18	5.40	4.58
G65	5.48	6.00	5.55	5.35	5.93	5.78	5.21	4.63	4.87	5.00	4.35	5.98	5.52
G66	5.71	6.26	6.12	6.00	6.04	6.08	5.49	5.32	5.91	5.37	5.36	6.35	5.55
G67	4.52	5.22	5.11	5.27	4.66	5.23	5.09	4.88	5.06	4.43	4.62	5.17	4.70
G68	4.17	4.91	4.90	4.62	4.21	4.45	4.39	4.27	4.53	4.36	3.64	5.05	4.22
G69	5.58	5.67	5.05	5.47	5.93	6.03	5.08	4.44	4.83	4.58	4.56	5.94	5.08
G70	5.26	5.83	5.26	5.53	5.58	5.56	4.96	4.55	5.03	4.71	4.44	6.08	5.17
G71	6.00	6.65	6.25	5.92	6.70	6.71	6.35	5.57	5.63	5.19	5.67	5.93	6.59
G72	4.89	5.20	5.31	5.06	5.32	5.51	4.63	4.46	5.00	4.45	4.76	5.02	4.79
G73	6.30	6.77	5.88	5.93	6.79	6.67	5.98	5.27	4.67	5.19	4.94	5.79	6.81
G74	6.46	7.00	6.60	6.14	7.29	7.32	6.94	5.91	5.68	5.84	5.76	6.32	6.99
G75	7.81	8.30	7.87	7.77	8.76	9.03	8.38	7.40	7.14	7.01	7.53	7.37	8.32
G76	6.32	6.73	6.00	6.28	6.84	7.05	6.37	5.60	5.29	5.41	5.33	6.21	6.44
G77	6.19	6.80	6.80	6.55	7.05	7.45	6.79	6.16	6.17	6.10	6.10	6.31	6.51
G78	5.93	6.42	5.97	5.80	6.49	6.66	6.49	5.47	5.44	5.54	5.03	6.48	5.98
G79	5.13	5.88	6.14	5.53	4.86	4.76	4.86	5.27	5.83	5.71	4.57	6.28	4.87
G80	8.43	8.95	8.22	7.88	9.14	8.97	8.42	7.60	6.78	7.52	7.29	7.54	9.25
G81	7.70	8.22	7.61	7.57	8.49	8.58	7.87	7.04	6.75	6.70	7.10	7.18	8.20

Appendix 3: (continued)

	G14	G15	G 16	G17	G18	G19	G20	G21	G22	G23	G24	G25	G26
G15	4.18												
G16	3.00	2.47											
G17	5.26	3.57	3.89										
G18	6.93	3.57	5.52	4.44									
G19	4.27	2.55	3.24	4.05	3.85								
G20	4.82	1.73	3.04	2.67	2.94	1.97							
G21	6.07	2.64	3.89	3.44	3.44	3.48	2.29						
G22	4.14	3.06	2.80	3.48	4.53	2.62	2.77	3.09					
G23	6.96	4.19	5.86	7.41	4.84	4.60	4.99	5.02	5.80				
G24	6.34	3.09	4.73	5.48	3.10	2.81	3.03	3.33	4.13	2.65			
G25	6.47	4.37	4.36	5.67	7.01	5.94	5.06	4.69	5.76	6.82	6.34		
G26	6.17	4.09	4.14	4.61	6.02	5.07	4.28	4.02	4.46	6.91	5.82	2.62	
G27	4.23	4.15	3.80	4.38	6.52	4.88	4.52	5.38	4.52	7.54	6.63	4.27	3.14
G28	4.53	4.28	3.90	4.89	6.08	5.05	4.75	5.59	4.23	7.31	6.38	5.31	3.75
G29	7.03	4.38	5.41	5.45	5.80	5.12	4.48	4.44	5.68	6.27	5.53	3.32	2.77
G30	6.10	3.80	4.83	5.02	4.76	4.25	3.79	4.17	4.77	5.84	5.04	4.37	3.31
G31	4.82	3.00	2.95	3.56	5.25	3.63	2.95	3.67	3.67	6.37	5.04	3.17	1.97
G32	4.48	3.08	2.33	4.19	5.82	4.06	3.57	3.74	3.31	6.24	5.20	2.84	1.96
G33	4.83	3.37	3.87	4.45	5.29	4.45	3.87	5.01	4.62	6.40	5.52	4.41	3.31
G34	4.01	4.29	3.61	4.43	6.69	4.50	4.41	5.61	4.55	7.66	6.55	4.61	3.56
G35	5.69	3.62	4.43	5.04	5.46	4.40	3.83	4.79	5.48	6.06	5.37	3.73	3.69
G36	4.73	4.39	3.43	4.98	6.86	5.18	4.85	5.68	4.66	7.54	6.50	4.33	3.28
G37	4.05	2.98	3.64	5.05	5.01	3.65	3.68	5.11	4.45	5.35	4.83	5.03	4.33
G38	3.91	3.35	3.11	5.13	6.22	4.52	4.22	5.14	4.76	6.24	5.84	3.53	3.61
G39	5.26	3.60	4.33	4.83	5.61	4.52	4.01	5.06	5.24	6.34	5.64	3.86	3.28
G40	7.78	5.07	6.12	4.42	4.97	6.00	4.66	4.61	5.75	7.85	6.46	5.16	3.52
G41	6.65	4.12	4.58	4.04	5.02	5.22	4.01	4.21	4.67	7.16	5.70	4.23	2.42
G42	5.37	3.56	3.32	5.43	6.29	5.30	4.62	4.34	4.54	5.99	5.61	2.51	2.74

G43	3.78	4.29	3.01	5.16	6.68	5.01	4.93	5.45	3.65	7.24	6.40	5.15	4.04

Appendix 3: (continued)

	G14	G15	G 16	G17	G18	G19	G20	G21	G22	G23	G24	G25	G26
G44	7.74	4.84	5.51	5.02	5.83	6.00	4.68	4.32	5.97	7.43	6.28	3.19	2.67
G45	6.22	3.81	4.39	6.38	6.38	5.30	4.80	4.76	5.88	5.09	5.25	2.43	3.92
G46	5.38	3.26	3.04	3.76	4.89	3.34	2.91	3.38	2.99	6.11	4.30	4.33	2.79
G47	6.07	3.32	3.96	3.41	4.65	4.39	3.25	3.25	3.81	6.38	4.82	3.98	2.36
G48	3.60	2.98	2.99	4.21	5.38	3.19	3.19	4.14	3.68	5.93	5.09	4.49	4.13
G49	3.12	2.84	2.40	4.25	5.32	2.61	3.08	4.07	2.75	5.68	4.69	4.69	3.88
G50	3.73	2.89	3.14	3.90	4.37	1.41	2.48	4.04	2.54	5.46	3.89	5.84	4.61
G51	3.92	2.32	3.06	3.23	4.20	3.44	2.53	4.24	4.02	6.00	4.84	5.07	4.56
G52	3.81	3.80	4.24	5.77	5.73	3.34	4.44	5.37	3.80	4.95	4.51	6.55	5.65
G53	3.31	2.93	2.61	3.02	5.27	2.82	2.71	4.27	3.23	6.53	5.08	4.89	4.00
G54	3.69	4.17	3.19	4.87	6.49	4.43	4.65	5.27	3.16	6.96	5.94	5.51	4.14
G55	4.49	2.85	2.76	3.67	4.39	3.82	3.11	3.85	2.79	6.07	4.70	5.09	3.79
G56	6.42	4.34	4.23	4.40	6.13	4.47	3.91	3.31	4.28	6.88	5.38	3.61	3.10
G57	5.57	2.33	3.76	3.39	3.60	3.90	2.45	3.41	4.32	5.60	4.31	4.15	3.44
G58	4.11	3.54	3.68	3.70	4.95	2.51	2.86	4.38	3.51	6.46	4.98	5.72	4.69
G59	5.85	3.65	4.43	4.47	5.08	4.02	3.51	3.29	4.24	5.96	5.01	4.02	3.39
G60	2.68	3.64	2.21	4.27	6.35	3.91	3.97	5.45	3.87	7.01	5.85	5.35	4.77
G61	5.23	4.11	4.01	5.19	6.58	5.25	4.70	5.47	5.35	7.06	6.37	3.16	2.68
G62	6.28	4.26	5.09	5.98	6.29	5.72	5.00	5.45	6.29	6.37	6.24	3.20	3.69
G63	6.88	5.01	5.38	5.97	7.10	6.35	5.38	5.87	7.00	7.59	7.09	3.14	4.32
G64	5.56	4.13	4.12	4.60	6.10	5.35	4.39	5.07	5.28	7.43	6.52	3.35	2.83
G65	6.71	4.77	5.02	5.56	6.88	6.11	5.16	5.30	6.18	7.49	6.85	2.12	2.52
G66	6.34	5.06	5.07	6.35	7.67	6.08	5.69	6.12	6.49	7.33	6.95	2.76	3.30
G67	4.92	3.94	4.64	6.09	6.31	4.87	4.92	5.61	5.39	5.65	5.75	4.36	4.07
G68	4.81	3.56	3.68	5.27	6.10	4.83	4.39	5.01	4.87	6.23	5.82	3.14	2.80
G69	6.33	4.85	5.15	5.55	6.99	5.61	5.05	5.67	6.24	7.48	6.76	3.26	3.29
G70	6.03	4.72	4.95	5.50	7.16	5.78	5.21	5.52	5.93	7.42	6.86	2.80	2.80
G71	7.67	5.14	6.18	6.96	6.91	6.54	5.89	5.59	6.88	6.32	6.45	3.15	3.67

G72	5.94	4.03	4.34	5.65	6.46	4.86	4.49	5.19	5.72	6.21	5.58	2.89	3.20

Appendix 3: (continued)

	G14	G15	G 16	G17	G18	G19	G20	G21	G22	G23	G24	G25	G26
G73	8.09	5.40	6.51	6.11	6.19	6.74	5.63	5.40	6.82	7.45	6.91	4.07	3.56
G74	8.23	5.57	6.58	7.19	6.97	7.14	6.20	5.95	7.51	6.95	7.02	3.58	4.39
G75	9.37	6.88	8.15	8.77	8.18	8.22	7.58	7.57	9.11	7.39	7.93	5.22	6.13
G76	7.44	5.45	6.40	6.71	6.95	6.66	5.95	6.28	7.22	7.32	7.17	4.10	4.18
G77	7.34	5.34	6.14	7.37	7.43	6.73	6.15	6.65	7.67	6.69	6.91	3.78	4.93
G78	6.94	5.26	5.83	6.76	7.18	6.66	5.94	6.12	6.93	7.19	7.21	3.56	4.19
G79	5.25	4.75	3.79	5.84	7.41	5.83	5.38	5.98	5.49	7.62	6.97	3.30	3.13
G80	10.58	7.51	8.77	8.35	7.57	9.03	7.78	7.16	9.09	8.75	8.54	6.03	6.03
G81	9.32	6.75	7.94	8.25	7.97	8.09	7.31	7.17	8.71	7.72	7.90	4.72	5.29

	G27	G28	G29	G30	G31	G32	G33	G34	G35	G36	G37	G38	G39
G28	2.49												
G29	4.18	5.39											
G30	3.81	4.47	2.46										
G31	2.43	3.43	2.93	2.81									
G32	2.75	3.17	3.84	3.70	1.69								
G33	2.24	2.24	3.97	3.56	2.57	3.09							
G34	1.37	3.03	4.40	4.10	2.32	2.96	2.62						
G35	3.61	4.80	2.56	2.29	2.55	3.72	3.20	3.51					
G36	2.66	2.37	5.11	5.10	2.94	2.59	2.55	2.57	4.63				
G37	3.06	3.01	4.43	3.36	3.16	3.55	1.93	3.15	3.02	3.66			
G38	2.46	3.36	4.10	3.42	2.61	2.62	2.65	2.69	2.62	3.34	2.27		
G39	2.47	3.68	2.77	2.69	2.34	3.37	1.84	2.64	1.68	3.63	2.27	2.30	
G40	4.63	4.91	3.70	3.47	3.83	4.77	4.13	5.16	4.34	5.47	5.22	5.36	4.08
G41	3.81	3.40	3.97	3.95	2.82	3.23	2.88	4.19	4.28	3.39	4.30	4.43	3.66
G42	3.87	3.78	4.40	4.42	3.25	2.00	3.66	4.44	4.40	3.39	4.10	3.06	4.05
G43	3.21	2.00	6.06	5.20	3.76	2.71	3.61	3.57	5.48	2.65	3.86	3.50	4.71
G44	4.80	5.52	2.74	3.39	3.22	3.96	4.50	5.11	3.52	5.23	5.38	4.69	3.91
G45	4.98	5.69	3.50	3.93	3.75	3.61	4.54	5.16	3.12	5.12	4.28	3.21	3.74

Appendix 3: (continued)

	G27	G28	G29	G30	G31	G32	G33	G34	G35	G36	G37	G38	G39
G46	3.98	3.81	4.23	4.15	2.23	2.36	3.51	3.72	4.31	3.13	4.07	4.25	4.05
G47	3.76	3.76	3.74	4.12	2.56	2.81	3.03	4.08	4.35	3.40	4.25	4.44	3.71
G48	3.25	4.39	4.18	3.00	2.67	3.12	3.87	3.17	2.91	4.68	3.12	2.46	3.26
G49	3.05	3.67	4.47	3.34	2.52	2.56	3.56	2.88	3.55	3.98	2.83	2.62	3.48
G50	3.88	4.03	4.92	3.83	3.12	3.63	3.69	3.46	4.11	4.41	2.99	3.94	3.90
G51	3.43	3.71	4.88	3.86	3.03	3.70	2.70	3.46	3.25	4.12	2.45	2.95	3.02
G52	4.63	4.55	5.92	5.34	4.78	4.60	4.34	4.62	5.55	4.96	3.52	4.68	4.83
G53	2.66	3.72	4.57	4.10	2.27	2.99	3.04	2.14	3.59	3.46	3.06	3.16	3.15
G54	3.22	2.49	5.92	5.43	3.75	2.95	3.56	3.38	5.68	2.63	3.91	4.09	4.71
G55	3.77	2.47	5.42	4.45	3.21	2.83	2.98	4.05	4.82	3.21	3.34	3.82	4.26
G56	4.86	5.96	3.59	4.26	2.91	3.22	5.35	4.69	4.38	5.19	5.72	4.92	4.82
G57	3.79	3.90	3.64	3.28	2.59	3.38	2.41	4.03	2.94	4.01	3.03	3.50	2.70
G58	3.70	4.65	4.62	3.43	2.97	3.96	4.10	3.20	3.51	4.97	3.52	3.81	3.69
G59	4.16	5.31	2.77	2.06	2.86	3.50	4.58	4.38	3.04	5.57	4.41	3.86	3.67
G60	3.26	3.37	5.98	5.50	3.38	3.27	3.33	2.71	4.76	2.65	3.36	3.34	4.12
G61	2.09	3.07	3.49	3.66	2.30	2.63	1.93	2.39	2.84	2.40	2.92	2.06	1.80
G62	3.78	4.82	2.83	2.92	3.41	3.96	3.35	4.23	1.97	4.80	3.46	2.60	2.10
G63	4.63	6.02	3.61	4.11	3.78	4.55	4.57	4.70	2.46	5.41	4.88	3.52	3.30
G64	2.59	3.47	3.61	3.08	2.28	2.93	2.69	2.98	2.57	3.50	3.43	2.32	2.34
G65	3.52	4.81	2.61	3.44	2.82	3.34	3.65	3.92	2.72	4.24	4.48	3.17	2.72
G66	3.57	5.01	3.09	4.37	3.29	3.64	3.71	3.58	3.16	3.82	4.35	3.26	2.77
G67	3.07	3.94	3.65	3.37	3.61	3.75	2.87	3.57	3.15	4.27	2.39	2.45	2.30
G68	2.31	3.00	3.41	2.95	2.40	2.39	2.20	2.86	2.60	3.10	2.38	1.25	1.94
G69	3.28	5.11	2.36	3.42	2.77	3.83	3.62	3.22	2.14	4.41	4.19	3.24	2.11
G70	2.73	4.64	2.57	3.72	2.83	3.35	3.41	3.14	2.99	3.99	4.20	3.09	2.35
G71	4.95	5.89	2.39	3.64	4.33	4.55	4.58	5.53	3.57	5.70	4.93	4.28	3.58
G72	3.73	4.84	2.71	3.77	2.61	3.27	3.22	3.49	2.36	3.71	3.59	3.02	2.28
G73	4.82	5.54	2.74	3.04	4.19	4.86	4.43	5.50	3.60	5.88	5.16	4.72	3.64

G74	5.64	6.40	3.32	3.80	4.83	5.19	5.17	6.18	3.60	6.39	5.43	4.58	4.14

Appendix 3: (continued)

	G27	G28	G29	G30	G31	G32	G33	G34	G35	G36	G37	G38	G39
G75	6.91	7.91	4.21	5.19	6.37	6.91	6.30	7.31	4.58	7.74	6.36	5.90	4.99
G76	4.37	5.54	2.79	3.15	4.23	4.98	4.11	4.88	2.74	5.68	4.43	3.85	2.75
G77	5.20	6.22	3.70	4.47	4.70	5.19	4.53	5.39	3.00	5.69	4.55	3.82	3.30
G78	4.41	5.45	3.57	3.38	4.23	4.53	4.45	5.00	3.02	5.62	4.49	3.25	3.35
G79	2.97	3.24	4.73	4.63	3.02	2.53	3.18	3.11	4.01	2.27	3.83	2.46	3.46
G80	7.66	7.94	5.28	5.44	6.84	7.30	6.99	8.34	6.01	8.35	7.57	7.16	6.37
G81	6.35	7.36	3.54	4.79	5.83	6.40	5.84	6.85	4.45	7.20	6.25	5.75	4.63

	G40	G41	G42	G43	G44	G45	G46	G47	G48	G49	G50	G51	G52
G41	2.60												
G42	5.33	3.74											
G43	6.07	4.36	3.28										
G44	2.71	3.04	4.29	6.10									
G45	5.90	5.12	3.07	5.59	4.15								
G46	4.59	2.81	3.73	3.85	4.25	4.80							
G47	3.37	1.71	3.52	4.33	3.56	4.87	2.15						
G48	5.36	5.06	4.31	4.28	4.95	4.10	4.15	4.70					
G49	5.56	4.76	3.96	3.35	5.31	4.39	3.38	4.28	1.42				
G50	5.55	4.77	5.09	4.20	5.84	5.45	3.14	4.15	2.77	1.94			
G51	4.74	4.06	4.47	4.29	4.98	4.79	3.97	3.93	2.89	3.11	3.10		
G52	7.15	6.08	5.34	4.54	7.46	5.95	4.69	5.14	4.38	3.44	2.98	4.65	
G53	5.21	4.30	4.59	3.93	5.24	5.10	3.13	3.65	2.49	2.19	2.12	2.44	3.83
G54	6.23	4.49	3.92	1.86	6.46	5.98	3.43	3.90	4.49	3.33	3.61	4.48	3.41
G55	4.74	3.00	3.41	2.59	5.09	5.27	2.74	2.93	4.13	3.40	3.40	2.98	4.49
G56	5.06	4.57	4.52	5.67	3.72	4.51	3.25	3.80	4.04	4.04	4.58	5.28	6.19
G57	3.32	2.54	3.82	4.74	3.45	4.11	3.22	2.48	3.82	3.91	3.79	2.18	5.18
G58	5.27	5.09	5.56	4.92	5.43	5.49	3.91	4.70	2.00	2.11	1.85	3.06	4.37
G59	4.19	4.64	4.46	5.44	3.59	3.95	4.18	4.26	2.50	3.09	3.91	4.24	5.48
G60	6.49	4.82	4.43	3.10	6.32	5.54	3.61	4.38	3.79	3.11	3.29	3.11	4.12

Appendix 3: (continued)

G40	G41	G42	G43	G44	G45	G46	G47	G48	G49	G50	G51	G52
G61	4.54	3.33	3.13	3.82	3.94	3.72	3.83	3.58	3.84	3.75	4.55	3.67	5.27
G62	4.53	4.45	3.83	5.52	3.58	2.69	5.18	4.69	3.88	4.45	5.37	4.08	6.09
G63	5.10	5.06	4.71	6.46	3.40	3.28	5.62	5.34	4.38	5.22	6.17	4.57	7.48
G64	3.67	3.14	3.51	4.17	3.07	3.97	4.10	3.82	3.44	3.78	4.71	3.26	6.18
G65	4.01	3.70	3.52	5.33	2.42	3.24	4.60	4.05	4.29	4.70	5.70	4.64	6.78
G66	5.55	4.69	3.92	5.43	4.26	3.35	4.74	4.56	4.65	4.76	5.63	5.16	6.06
G67	5.55	5.00	3.91	4.56	5.36	3.70	4.96	4.73	3.54	3.49	4.29	4.11	3.89
G68	4.63	3.69	2.60	3.49	4.04	3.08	3.98	3.86	3.10	3.07	4.20	3.42	4.80
G69	4.59	4.46	4.62	5.78	3.52	3.77	4.70	4.46	3.91	4.38	5.12	4.53	6.21
G70	4.66	4.30	3.90	5.18	3.80	3.77	4.67	4.09	4.02	4.30	5.24	4.69	5.79
G71	4.91	4.92	4.07	6.44	3.72	2.93	5.62	4.87	5.21	5.52	6.36	5.79	6.59
G72	5.18	4.17	3.79	5.29	3.88	2.82	3.81	3.92	4.07	4.11	4.64	4.28	5.40
G73	2.79	3.91	4.78	6.50	2.42	4.45	5.58	4.53	5.29	5.76	6.38	5.35	7.44
G74	4.81	5.18	4.59	6.98	3.34	3.19	6.26	5.58	5.49	6.09	7.02	5.83	7.81
G75	6.44	6.92	6.39	8.67	5.32	4.36	7.78	7.08	6.82	7.44	8.14	7.15	8.45
G76	4.38	4.93	4.97	6.50	3.75	3.91	6.02	5.33	4.82	5.42	6.20	5.15	6.94
G77	6.00	5.68	4.81	6.84	4.64	2.85	6.20	5.82	5.27	5.78	6.57	5.35	6.99
G78	5.03	5.21	4.24	5.96	3.92	3.25	6.06	5.62	4.37	5.05	6.28	5.06	7.04
G79	5.57	3.93	2.77	3.21	4.59	4.02	4.06	4.33	4.36	4.05	5.18	4.45	5.93
G80	4.75	5.99	6.71	8.80	4.24	6.10	7.86	6.80	7.77	8.30	8.89	7.61	9.95
G81	5.50	6.09	5.97	8.22	4.45	4.47	7.23	6.34	6.69	7.22	7.90	6.98	8.32

	G53	G54	G55	G56	G57	G58	G59	G60	G61	G62	G63	G64	G65
G54	3.41												
G55	3.45	2.92											
G56	4.12	5.44	5.15										
G57	3.34	4.81	2.93	4.58									
G58	2.06	4.67	4.30	4.28	4.00								
G59	3.91	5.53	4.85	2.96	3.88	3.21							

Appendix 3: (continued)

	G53	G54	G55	G56	G57	G58	G59	G60	G61	G62	G63	G64	G65
G60	2.22	2.83	3.25	5.41	4.19	3.85	5.58						
G61	3.51	4.09	3.98	4.82	3.31	4.55	4.40	3.72					
G62	4.73	5.97	5.20	5.24	3.49	5.02	3.79	5.50	2.59				
G63	5.07	6.99	6.05	4.98	4.13	5.39	4.31	5.84	3.46	2.32			
G64	3.72	4.90	3.89	4.63	3.00	4.22	3.76	4.31	1.95	2.54	2.84		
G65	4.68	5.77	5.16	4.23	3.73	5.24	3.79	5.44	2.29	2.09	2.16	2.04	
G66	4.60	5.42	5.71	4.71	4.54	5.48	4.69	5.04	2.21	2.84	3.25	3.44	2.33
G67	4.06	4.48	4.79	5.64	4.12	4.51	4.14	4.67	2.84	2.74	4.64	3.80	3.90
G68	3.59	4.02	3.69	4.78	3.26	4.24	3.72	3.93	1.44	2.13	3.55	2.00	2.54
G69	4.03	5.79	5.67	4.24	4.03	4.46	3.73	5.15	2.45	2.47	2.50	2.80	1.95
G70	4.06	5.12	5.38	4.28	4.14	4.84	3.82	5.00	2.19	2.63	3.24	2.94	1.95
G71	5.97	6.60	6.16	5.21	4.58	6.28	4.15	6.87	3.81	2.37	3.80	4.19	2.79
G72	3.87	5.17	4.98	4.15	3.54	4.64	4.20	4.44	2.28	2.76	3.13	3.31	2.64
G73	5.95	6.91	5.76	5.36	3.99	5.98	3.95	7.10	4.06	2.81	3.76	3.37	2.71
G74	6.59	7.57	6.46	5.78	4.68	6.66	4.46	7.43	4.39	2.33	3.11	3.95	2.85
G75	7.76	8.93	8.22	7.28	6.11	7.81	5.93	8.67	5.62	3.47	4.33	5.77	4.50
G76	5.63	6.86	6.21	5.84	4.38	5.69	4.21	6.65	3.41	1.56	2.99	3.27	2.51
G77	5.90	7.16	6.55	6.19	4.66	6.33	5.24	6.41	3.60	1.96	2.69	4.07	3.12
G78	5.67	6.68	5.94	5.72	4.62	5.74	4.06	6.41	3.47	1.58	2.74	2.97	2.45
G79	4.24	4.05	4.03	5.13	4.33	5.28	5.15	3.73	1.84	3.71	4.17	2.55	3.08
G80	8.67	9.46	7.84	7.53	6.11	8.54	6.25	9.64	6.67	5.07	5.59	5.81	5.13
G81	7.43	8.44	7.77	6.72	5.72	7.58	5.56	8.42	5.08	3.26	4.18	5.21	3.78

	G66	G67	G68	G69	G70	G71	G72	G73	G74	G75	G76	G77	G78
G67	3.32												
G68	2.82	2.11											
G69	1.90	3.51	2.94										
G70	1.70	3.03	2.58	1.51									
G71	3.16	3.48	3.44	3.37	3.01								

G72 1.71 3.29 2.73 2.07 2.48 3.39

Appendix 3: (continued)

	G66	G67	G68	G69	G70	G71	G72	G73	G74	G75	G76	G77	G78
G73	4.41	4.58	3.84	3.67	3.69	2.73	4.42						
G74	4.14	4.58	3.92	3.93	4.04	2.09	4.20	2.29					
G75	4.71	5.08	5.34	4.65	4.89	2.76	4.88	3.98	2.61				
G76	3.35	3.40	3.18	2.66	2.90	2.33	3.60	2.23	2.28	2.92			
G77	2.91	3.71	3.53	3.15	3.52	2.77	2.86	4.08	2.80	2.70	2.54		
G78	3.62	3.56	2.80	3.27	3.27	2.70	3.93	2.90	2.08	3.61	1.87	2.77	
G79	3.14	3.99	2.19	3.76	3.47	4.81	3.30	5.11	5.11	6.69	4.68	4.56	4.12
G80	6.85	7.12	6.36	6.34	6.47	4.62	6.82	3.02	3.28	4.67	4.51	5.72	4.78
G81	4.30	4.97	4.98	4.14	4.26	2.17	4.59	3.01	2.28	1.48	2.40	2.98	3.39

	G79	G80
G80	7.36	
G81	6.21	3.98