Pre-Breeding of Sorghum [*Sorghum bicolor* (L.) Moench] for Drought Tolerance in the Semi-arid Zones of Nigeria

By

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Thesis Abstract

Sorghum [*Sorghum bicolor* (L.) Moench] is a staple food crop serving millions of people in Africa and Asia's arid and semi-arid agro-ecologies. Sorghum is widely cultivated in Northern Nigeria, serving diverse value chains, including the food and feed sectors and the brewery industry. However, the potential production and productivity of sorghum in Africa, including Northern Nigeria, is constrained by severe drought stress associated with climate change. Furthermore, smallholder farmers in Nigeria still cultivate low-yielding and drought-susceptible unimproved sorghum landraces. Developing drought-tolerant sorghum cultivars adapted to semi-arid regions would enhance yield gains and stability with desirable product profiles according to the needs of the farmers and the marketplace. Therefore, the overall objective of this study was to improve sorghum productivity in Nigeria by developing new generation, locally adapted and drought-tolerant varieties. The specific objectives of this study were to: (1) present the current opportunities and constraints to sorghum production in Nigeria and make recommendations as a guide to new variety design and sustainable production, (2) determine drought tolerance and genotype-by-environment interaction (GEI) effect on grain yield of a population of African sorghum genotypes to identify high-yielding and drought-adapted genotypes for production and breeding, (3) assess the genetic diversity and deduce the population structure among 200 sorghum accessions to guide the selection of contrasting parents for pre-breeding and breeding of drought-tolerant sorghum cultivars and (4) determine the combining ability, heterosis and gene action conditioning agronomic traits and grain yield among sorghum genotypes to select genetically superior and contrasting parental genotypes and new families for drought tolerance breeding, cultivar release and commercialization.

In the first chapter, a participatory rural appraisal (PRA) study was conducted in three selected sorghum growing zones in Northern Nigeria involving 250 farmers. Socio-economic data were collected through surveys and focus group discussions. Results showed that sorghum was cultivated mainly by males (80%) who had grade 6-12 level of education (31.3%), with a productive age of 21-45 years (75.7%) and a household family size of below five members (52.3%). Low-yielding landrace varieties such as Kaura (37.4%) and Fara-fara (29.3%) were the most widely cultivated types across the study zones due to their good grain quality. The major farmers' preferred traits from a sorghum variety were high yield, drought tolerance and *Striga* resistance. The study recommends integrated sorghum technology development incorporating the described preferences of the farmers for sustainable production and economic gains of the crop.

The second chapter examined 225 sorghum genotypes assembled from diverse origins to determine drought tolerance and GEI effects on grain yield. The collections were evaluated under non-stressed (NS), pre-anthesis drought stress (PreADS), and post-anthesis drought stress (PoADS) conditions under field and greenhouse environments. The additive main effect and multiplicative interaction (AMMI) analysis revealed that genotype (G), environment (E), and GEI were significant ($p<0.05$) and accounted for 38.7, 44.6, and 16.6% of the total explained variation in grain yield, in that order. AMMI 4 was the best-fitting model for genotype selection with better

grain yield. Based on AMMI 4 and the Best Linear Unbiased Predictors (BLUPs) analyses, genotypes Yar Lazau and Dangama Wulchichi, with a grain yield of 5.6 t/ha and 6.3 t/ha, were selected as being suitable for non-stressed conditions, respectively. Genotypes ICNSL2014-022-4 and Takumbo with BLUPs of 2.5 t/ha and 2.6 t/ha were best-suited for pre-anthesis drought stress conditions, whereas genotypes Danyar Bana and Gagarau - 4 with BLUPs of 4.2 t/ha and 4.3 t/ha are recommended for post-anthesis drought-prone environments, respectively. The identified sorghum genotypes are valuable genetic resources to develop novel drought tolerance cultivars or for production in dry agro-ecologies of sub-Saharan Africa characterized by pre-and-post anthesis drought stress.

In the third chapter, diversity arrays technology (DArT) –derived single nucleotide polymorphism (SNP) markers were used to assess the genetic diversity and discern the population structure of 200 sorghum accessions to select complementary lines for breeding. The markers have moderate discriminatory power, with the polymorphism information content ranging between 0.09 to 0.38. The average gene diversity value (0.32) was high, while the average observed heterozygosity (0.15) was relatively low, a typical value for autogamous crop species like sorghum. The population structure and cluster analyses revealed four main clusters with a high level of genetic diversity among the accessions studied. The variation within populations (41.5%) was significantly higher than that among populations (30.8%) and between samples within a structure (27.7%). The high genetic variation within the population could be attributed to the preservation of sorghum landraces by farmers and differences in the genetic constitution, adaptation and parentage. The study identified distantly related sorghum accessions such as Samsorg 48, Kaura Red Glume (from Cluster 1); Gadam, AS 152 (Cluster 2); CSRO1, ICNSL2014−062 (Cluster 3); and Yalai, Kafi Mori (Cluster 4) useful in developing new gene pools and novel genotypes for the West and Central Africa (WCA) sorghum breeding programs. Based on the phenotypic and genotypic data, 12 contrasting parents were selected for breeding population development with high yield and drought tolerance.

In the last chapter, 12 contrasting sorghum parents were selected from a diverse set of 225 genotypes exhibiting variable agronomic traits, including high grain and drought tolerance and farmer-preferred attributes. The 12 parents were crossed using a half-diallel mating design to create 66 F_1 progenies. The F_1 progenies, the parents, and two check varieties were evaluated under three environments in Nigeria. The results revealed the presence of significant variations amongst test genotypes allowing the selection of suitable parents and hybrids for traits of interest. The contribution of the specific combining ability (SCA) variance to total variance was higher than that of the general combining ability (GCA) for most of the studied traits, indicating that non-additive gene action was more dominant in conditioning trait inheritance. GCA x environment and SCA x environment interaction effects were significant ($p<0.05$) for days to anthesis, above-ground biomass and grain yield. Parental genotypes Samsorg 7, Masakwa, and SSV2008091, recorded significant and positive GCA effects for grain yield and are useful germplasm resources for breeding high-yielding cultivars. Crosses AS 152 x SSV2008091, Samsorg 7 x Kurumbasau, AS 152 x ICNSL2014-022-8, and Masakwa x Hindatu exhibited high and positive SCA effects

and were the top performers recording above-ground biomass yield of 29.3, 23.4, 27.2 and 16.5 t/ha and grain yield of 6.4, 6.6, 6.6 and 6.5 t/ha, in that order. The crosses exhibited high parent heterosis for grain yield and other agronomic traits, revealing that hybrid breeding is an effective strategy for boosting sorghum production. The newly selected F_1 progenies had higher yields than the local checks and are recommended for hybrid or pure line breeding and variety release in Nigeria's drought-prone areas and similar sub-Saharan Africa (SSA) agro-ecologies after continuous selection and multi-environment testing.

Overall, the study identified drought stress as the most critical sorghum production constraint in Northern Nigeria. Also, the study highlighted significant genetic diversity among the test genotypes. Best performing genotypes Yar Lazau, ICNSL2014-022-4 and Danyar Bana were selected as suitable for non-stressed, pre-anthesis and post-anthesis drought stress conditions, respectively. The selected genotypes are recommended for production or breeding in drought-prone areas. In addition, the study identified drought-tolerant and early-maturing genotypes (e.g., Samsorg 7, Masakwa, and SSV2008091) with good general combining ability effects for breeding population development and heterosis breeding in the semi-arid region of Northern Nigeria.

Declaration

I, Muhammad Ahmad Yahaya, declare that:

1. The research reported in this thesis, except where otherwise indicated, is my original research.

2. This thesis has not been submitted for any degree or examination at any other university.

3. This thesis does not contain other persons' data, pictures, graphs or other information, unless specifically acknowledged as being sourced from other persons.

4. This thesis does not contain other persons' writing, unless specifically acknowledged as being sourced from other researchers. Where other written sources have been quoted, then:

    a. Their words have been re-written, but the general information attributed to them has been referenced.

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5. This thesis does not contain text, graphics or tables copied and pasted from the Internet, unless specifically acknowledged, and the source being detailed in the thesis and in the references sections.

Signed

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Muhammad Ahmad Yahaya

As the candidate's supervisors, we agree to the submission of this thesis:

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Prof. Shimelis Hussein (Supervisor)

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Dedication

This thesis work is dedicated to my dad, Alhaji Ahmadu Danladi Yahaya; my mum, Hajiya Hauwa'u Ibrahim (Hajiya Asabe); my beloved wife, Aisha Baffa Bello and my wonderful kids, Rayyan and Ayoosh.

I love you all, dearest.

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Introduction to Thesis

Background

Sorghum (*Sorghum bicolor* L. Moench, 2n = 2x = 20) is one of the top five world cereal crops widely cultivated in the dry regions of Africa and Asia. It is predominantly self-fertilizing hardy crop and indigenous to sub-Saharan Africa (SSA), primarily serving food and feed and for developing value-added products (Ejeta and Knoll, 2007; Thilakarathna et al., 2022). Continental Africa is the largest sorghum producer, with an estimated annual grain yield of 26.3 million tons on 28.1 million hectares of land (FAOSTAT 2022). The leading sorghum producers in Africa are Nigeria (6.7 million tons per annum), Ethiopia (4.5 million tons), Sudan (3.5 million tons) and Burkina Faso (1.6 million tons) (FAOSTAT 2022). The mean grain yield of sorghum in Africa is approximately 0.9 t/ha, much lower compared to 4.1 t/ha recorded in Europe, 3.7 t/ha in the Americas, and 1.6 t/ha in Asia (FAOSTAT 2022). In SSA, sorghum is an important staple crop where it is the primary source of carbohydrates and proteins (Proietti et al., 2015; Hadebe et al., 2020). The grain contains vitamins, including niacin, riboflavin, and thiamin, and essential minerals, such as magnesium, potassium, phosphorus, iron, and zinc (Ejeta and Knoll, 2007; Thilakarathna et al., 2022). Gluten-free sorghum grains provide an alternative option for gluten-sensitive consumers (Thilakarathna et al., 2022).

Due to several production and productivity constraints, sorghum's economic potential has not yet been fully realized in Nigeria andSSA countries. Lack of high-yielding sorghum varieties, drought stress, declining soil fertility, *Striga* infestation, limited access to production inputs, lack of credit systems, and low-income farmers are among the factors accounting for the low sorghum production and value-added product development (Sani et al., 2013). Sorghum research programs in Nigeria have pioneered developing and releasing introduced varieties suited to some specific agroecological zones for industrial purposes (Ajeigbe et al., 2018). However, small-scale farmers, who account for over 90% of sorghum production, prefer to use their farm-saved seed of local unimproved varieties due to their intrinsic qualities such as good eating quality, adaptation, low insect pest attack, and minimum production input requirements. The local landraces have low yield potential, long maturity, tall plant height and are respond poorly to improved agronomic management practices (Ajeigbe et al., 2018). Ndjeunga et al., (2015) reported that only about 20% of the total sorghum production area is planted with improved cultivars in Nigeria. Climate change

models show a high probability (>90%) of an increase in water scarcity and extreme temperatures, which will be detrimental to crop production in many tropical areas, especially in West Africa (Battisti and Naylor, 2009). Breeding drought-tolerant and climate-resilient sorghum varieties have the potential to offset the yield gap presented by climate change (Fedoroff et al., 2010).

Progress and gap in sorghum breeding in Nigeria

International research and development projects and African national breeding programs are striving to develop new, well adapted sorghum cultivars with high yield potential and tolerance to major biotic and abiotic stresses (Ojiewo and Gekanana, 2018). There are notable international collaborative sorghum projects, including the pearl millet and sorghum improvement (PROMISO), harnessing opportunities for productivity enhancement (HOPE I and II) for sorghum and millets in SSA and accelerated varietal improvement and seed delivery of legumes and cereals in Africa (AVISA). The international projects are led by the International Crops Research Institute for the Semi-arid Tropics (ICRISAT). For instance, the research collaboration of ICRISAT with the Institute for Agricultural Research/Nigeria strengthened sorghum breeding and capacity development. The collaboration enabled the development and release of sorghum varieties such as Samsorg 47 (*Zauna-Inuwa*), Samsorg 48 (*Kaura Bornu*), and Samsorg 49 (CF35:5). The released varieties are suitable for cultivation under semi-arid conditions in SSA (Ndjeunga et al., 2015; Ajeigbe et al., 2018; Mundia et al., 2019). Both Samsorg 47 and Samsorg 48 were developed by mass selection from landraces, while Samsorg 49 (CF35:5) was an introduction from ICRISAT/Mali. Farmers highly prefer Samsorg 49 for its earliness, medium-sized grain, and ability to stay green (Ojiewo and Gekanana, 2018).

Due to recurrent drought stress on sorghum production and productivity, the International Sorghum and Millet Program (INTSORMIL ICRISAT) and various National Agricultural Research Systems (NARS) in SSA have forged research collaboration on drought tolerance breeding. Thus far, few improved sorghum cultivars were developed with drought adaptation and enhanced yield gains. Global yields had increased by about 1,500 kg/ha (300% yield advantage) in non-stressed production environments using improved cultivars developed by sorghum breeding programs (Kumar et al., 2013). However, the yield level of genetically unimproved sorghum

landraces in Africa is approximately 500 kg/ha. Sorghum genetic resources exhibiting diverse responses to drought stress at seedling, pre-flowering and post-flowering have been identified based on improved yield under drought stress (Rosenow and Dahlberg, 2000). The breeding programs have primarily utilized plant introductions and pure line selection (mainly from landraces) in natural environments to assess some form of tolerance, primarily to terminal drought tolerance. Hence, modern sorghum breeding methods and technologies such as marker assisted selection, double haploid technology, speed breeding and high throughput phenotyping can substantially enhance the current yield gaps in Africa by developing drought-tolerant and locally adapted genetic resources. This will deliver climate-smart and resilient varieties that tolerate abiotic and biotic stresses under the dryland farming systems. There is need for concerted breeding to develop drought-tolerant cultivars to mitigate the effects of drought stress and improve sorghum production in SSA, including Nigeria.

Drought as a challenge to sorghum production in Nigeria

Breeding drought-tolerant and climate-resilient sorghum varieties is the most economical approach to narrow the yield gap exacerbated by climate change (Fedoroff et al., 2010). Ndjeunga et al., (2015) reported that only about 20% of the total sorghum production area is planted with improved cultivars in Nigeria. Mundia et al., (2019) opined that small-scale farmers in the region use landraces because of poor access to seeds of improved cultivars and production technologies (Mundia et al., 2019) and a lack of financial support (Ajeigbe et al., 2018). Assessing the current sorghum production challenges in the country helps prioritize crop production and breeding goals. Participatory rural appraisal (PRA) is a multidisciplinary research tool and a form of market research to document the needs and requirements of farmers and their marketplace. The PRA method engages farmers and stakeholders to seek their insights and production challenges, which could help develop fit-for-purpose new technologies. The ultimate aim of a plant breeder and agronomist is to develop a cultivar preferred by farmers and needed by the value chains.

Genetic variations exist among grain sorghum genotypes regarding grain yield and drought tolerance (Rosenow et al., 1996). Complementary agro-morphological and physiological proxy traits are essential to select drought-tolerant genotypes through greenhouse and field screening experiments (Harris et al., 2007; Kumar et al., 2008; Mutava et al., 2011). Two different drought stress responses in sorghum, pre-flowering and post-flowering, have been distinguished. Drought

stress responses can be identified through genotype screening employing agronomic, biochemical and physiological traits and molecular markers (Rosenow and Clark, 1981). Pre-flowering drought response is observed when there is water stress before flowering, namely during panicle initiation and differentiation. In pre-flowering drought stress, sorghum plants present leaf curl, floral abortion and sterility, reduced plant height, delayed flowering, discolouration and reduced grain yield by more than 40% (Rosenow et al., 1983; de Souza et al., 2021). Post-flowering drought stress occurring during anthesis, and seed set is the most detrimental to sorghum production and productivity (Tsago et al., 2014). Post-flowering drought stress leads to premature plant death, stalk lodging, stalk rot, accelerated leaf and plant senescence or death and reduced yield or complete crop failure (de Souza et al., 2021; Tesso et al., 2012).

Sorghum was first domesticated around 5000 years ago in northeastern Africa, with Sudan, Ethiopia, and West Africa serving as the centre of genetic diversity and the origin of sorghum (Venkateswaran et al., 2019). Phenotypic and genetic analysis of African sorghum genetic resources revealed wide diversity for multiple breeding utilities, including drought tolerance (Tesso et al., 2012; Mofokeng et al., 2017; Angarawai et al., 2021). Genetic diversity in germplasm collections is routinely assessed using different phenotypic and molecular markers. Molecular markers have been extensively used in genetic diversity studies because they are not affected by changes in environmental factors. The extensive diversity in the cultivated sorghum germplasm will aid the selection of contrasting genotypes for specific and broad adaptation. However, the lack of comprehensive and integrated information on the drought response of African sorghum genotypes, especially their adaptation to the adverse growing conditions in semi-arid regions of SSA, has limited the recommendation of improved varieties with desirable product profiles and drought-resilience. Pre-breeding and breeding programs were initiated to develop and recommend drought-tolerant sorghum varieties (Rosenow and Dahlberg, 2000; Kumar et al., 2013). As a result, valuable sorghum genetic resources, including historic accessions, wild relatives, landraces, and improved breeding lines, were collected, and conserved in national gene banks (Rosenow and Dahlberg, 2000; Angarawai et al., 2021). These collections are yet to be exhaustively characterized to identify germplasm exhibiting various essential and winning traits. Furthermore, there is a need for a rigorous evaluation of African sorghum germplasm in drought-stricken environments to aid in recommending drought-adapted genotypes for cultivation and breeding in the target arid and semi-arid production environments of SSA.

Research objectives

The overall objective of this study was to improve sorghum grain yield by developing varieties with farmer and market-preferred traits that are adapted to drought stress in the semi-arid regions of Nigeria.

The specific objectives of the study were as follows:

1. To present the current opportunities and constraints to sorghum production in Northern Nigeria and make recommendations as a guide to a new variety design and sustainable production.
2. To determine drought tolerance and genotype-by-environment interaction (GEI) effect on grain yield of a population of African sorghum genotypes to identify high-yielding and drought-adapted genotypes for production and breeding.
3. To assess the genetic diversity and deduce the population structure among 200 sorghum accessions to guide the selection of contrasting parents for pre-breeding and breeding of drought-tolerant sorghum cultivars and;
4. To determine the combining ability effects, heterosis and gene action conditioning agronomic traits and grain yield among sorghum genotypes to select genetically superior and contrasting parental genotypes and new families for drought tolerance breeding, cultivar release and commercialization.

Research hypotheses

1. In sorghum growing areas of Nigeria, farmers' preferences, and perceptions of sorghum traits, especially for drought tolerance, are different due to different social, cultural, and economic conditions.
2. There exists genetic variability among locally adapted and African sorghum genotypes for drought tolerance breeding.
3. Sorghum lines and new families show good combining ability, heterosis, and higher trait heritability to select promising parents and families, which can be exploited by population or hybrid breeding programs.

Outline of this thesis

This thesis comprises five chapters, developed according to the objectives set above. Chapter 1 is written as a separate review paper, while Chapters 2 to 5 are written as discrete research papers, each following a stand-alone research paper format, followed by a general overview of the research and its implications. The literature review and four experimental chapters of the study made the thesis chapters that were condensed into discrete but inter-dependant papers according to the University of KwaZulu-Natal's dominant thesis format. Chapter 1 was published in the Journal of Crop Improvement [2020, 34(2): 268-289. https://doi.org/10.1080/15427528.2019.1698483] and Journal of Agronomy and Crop Science [2022, 208 (2): 127-142. https://doi.org/10.1111/jac.12573]; Chapter 2 in Acta Agriculturae Scandinavica, Section B — Soil & Plant Science [2022, 72(1): 660-672. https://doi.org/10.1080/09064710.2022.2047771]; Chapter 3 in Agronomy [2023, 13(2): 557. https://doi.org/10.3390/agronomy13020557]; Chapter 4 in Genes [2023, 14(7), 1480; https://doi.org/10.3390/genes14071480]. There may be some overlap and unintentional repetition across the chapters and references.

The outline of the thesis is, therefore, as follows:

Chapters	Titles
-	Introduction to Thesis
1	A Review of the Literature
2	Sorghum production in Nigeria: opportunities, constraints, and recommendations
3	Drought tolerance response of African sorghum [*Sorghum bicolor* (L.) Moench] genotypes under variable environments
4	Genetic diversity and population structure of African sorghum [*Sorghum Bicolor* (L.) Moench] accessions assessed through single nucleotide polymorphism markers.
5	Genetic analysis of agronomic traits and grain yield performance among African sorghum [*Sorghum bicolor* (L.) Moench] genotypes.
6	An overview of the research findings

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CHAPTER 1 : Review of the Literature

Abstract

Agriculture accounts for 70% of the global use of available freshwater. Projections show that demand for water will increase significantly due to climate change, population growth and the development of agricultural enterprises globally. There is a need to develop drought-adapted and water-use-efficient crop cultivars for sustainable agricultural production. Sorghum [*Sorghum bicolor* (L.) Moench.] is a powerhouse crop in drier regions supporting more than 500 million people. It is a relatively drought-tolerant crop adapted to grow and yield in marginal environments where other dominant crops, such as maize and wheat, fail to survive. However, the mean yield of sorghum in the semi-arid regions has stagnated at around 1.0 ton/ha compared with the global average of 2.5 ton/ha, mainly due to recurrent droughts and heat stress. Breeding for drought-tolerant cultivars is an economical and sustainable mitigation strategy against the current and projected drought stress. Therefore, the objective of this review were to document the impact of drought stress and the key mitigation strategies under drought-prone sorghum production systems. The review chapter is divided into four sections. The first section highlighted the importance of sorghum in the food systems of small-holder farmers in sub-Saharan Africa (SSA). This is followed by the impact of drought and its mitigation strategies emphasizing on the use of drought-tolerant cultivars as a climate-smart adaptation strategy. A perspective on drought response mechanisms, breeding methods and complementary technologies for drought tolerance is discussed in subsequent sections. The last section highlights exploitation of heterosis breeding to increase sorghum's production and productivity in SSA's semi-arid regions. Information presented in this review will guide the development and deployment of drought-tolerant sorghum cultivars targeting production in the semi-arid regions.

Keywords: climate change, drought tolerance, marker-assisted selection, sorghum production constraints, post-flowering drought stress, pre-flowering drought tolerance, stay green

1.1 Introduction

Sorghum [*Sorghum bicolor* (L.) Moench] (2n = 2x = 20) is an important grain crop that belongs to the family Poaceae (Gramineae) (Menz et al., 2002). In 1753, Linnaeus identified sorghum as Holcus, but later Moench distinguished it from Holcus and grouped all sorghums under *Sorghum bicolor* (Reddy et al., 2008). Sorghum has various agronomic forms, including grain sorghum, sweet stem sorghum, Sudan grass, and broomcorn, which are categorized as *S. bicolor* subsp. *bicolor* (Berenji and Dahlberg, 2004). Currently, there are five cultivated races of sorghum, including bicolor, guinea, kafir, caudatum, and durra based on five fundamental spikelet kinds (Figure 1.1), (Harlan and de Wet, 1972; Reddy et al., 2008).

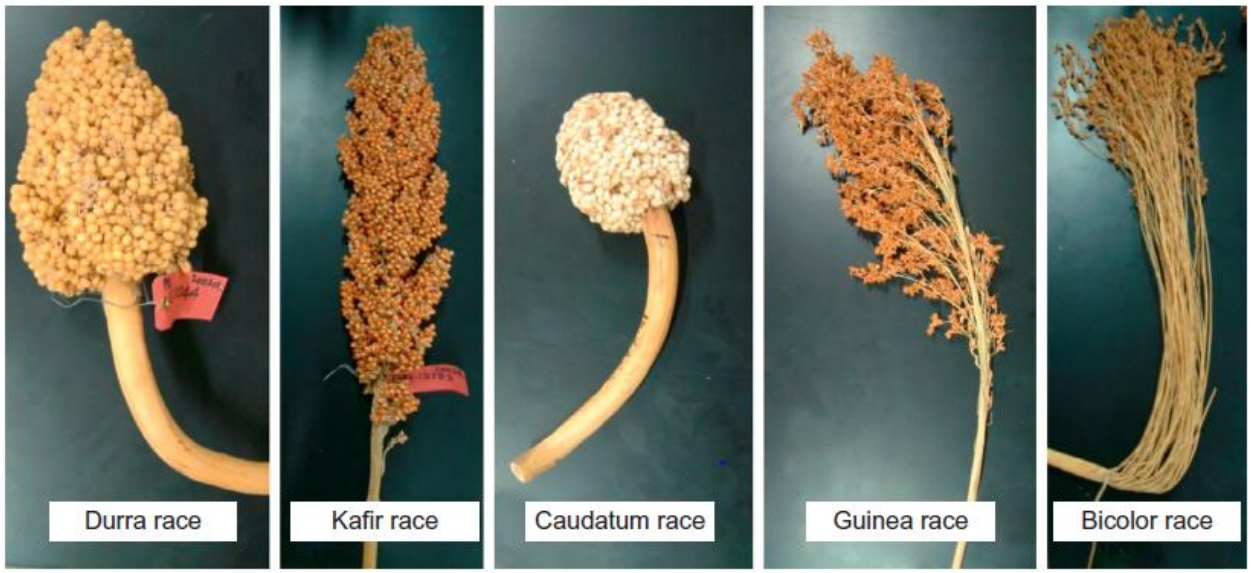

Figure 1.1: Panicle architecture of the five races of *S. bicolor* at maturity (Source: Reddy et al., 2008).

1.2 Origin and distribution

Archeological evidence indicates that sorghum originated from Africa and was first domesticated around 5000 years ago, with Sudan, Ethiopia, and West Africa being centres of origin (House, 1995; Kimber et al., 2013). The diversity of *S. bicolor* is attributable to the disruptive selection, isolation, and recombination in the ecosystems of Northeast Africa and human migration that

dispersed the crop across the continent (House, 1995; Kimber et al., 2013). The Indian subcontinent is regarded as the secondary centre of origin of sorghum (Kimber et al., 2013).

The bicolor race is believed to be the most primitive and diverse race of sorghum, with various ecotypes found throughout Africa, India, Indonesia, and China (de Wet et al., 1976). It is thought to have crossed with wild forms to produce the caudatum, kafir, guinea, and durra races (Dahlberg, 1995). The caudatum race is dominantly grown in most parts of Africa, while the kafir race is widely grown in Nigeria and Ghana (Kimber et al., 2013). The durra race originated in Ethiopia and adapted to drier conditions. The guinea race originated in the West African savannah and is the dominant race grown in South Asia (Rooney and Smith, 2000). The guinea race covers over 70% of sorghum cultivation in West and Central Africa and 50% in other parts of Africa (Folkertsma et al., 2005).

1.3 Agriculture in Nigeria

Agriculture is a crucial sector in Nigeria's economy, contributing 22% of the Gross domestic product (GDP) directly and 30% indirectly through linkages with other sectors (Olomola, 2007). Most Nigerians (64%) live in rural areas and rely on agriculture for their livelihoods (Nwahia et al., 2021). Small-scale farmers make up 80% of the farmers in Nigeria, and food supply comes from domestic production, imports, and food aid (Nwahia et al., 2021). Subsistence crop production includes maize, rice, soybean, wheat, and traditional crops such as sorghum, finger millet, groundnut, cassava, green leafy vegetables, and fruits. Small-scale farmers play a significant role in the agricultural sector.

1.4 Sorghum production and breeding in West and Central Africa

Nigeria is the largest and most important producer of sorghum in West and Central Africa (WCA), accounting for about 71% of the total regional sorghum output. The largest world’s producers of sorghum are Nigeria, with annual total grain production of 7.7 million tons on 5.8 million hectares, USA (6.6 million tons on 2.5 million hectares), Sudan (5.5 million tons on 9.2 million hectares) and India (4.1 million tons on 5.7 million hectares) (FAOSTAT, 2021; USDA, 2023). Sorghum is

the 3rd cereal in quantity of production in Nigeria (FAOSTAT, 2021). Sorghum is grown mostly in the country's Northwest and Northeast regions (Figure 1.2).

Sorghum breeding in WCA began in the 1950s through landrace selections in Burkina Faso, Cameroon, Mali, Niger, and Nigeria. Nigerian sorghum landraces were classified into four main types, namely: guinea, kaura (mostly yellow endosperm types of durra-caudatum hybrid race), fara-fara (white grain type of the race durra), and caudatum types (Curtis, 1967).

Genetic improvement of sorghum started in Nigeria in 1956 at the Institute for Agricultural Research (IAR). Attempts to improve sorghum productivity using hybrid seeds from the USA and India prior to the 1970s were unsuccessful due to poor adaptation (Reddy et al., 2008). As a result, breeders started crossing introduced parents with local breeding lines to create male-sterile lines in the 1970s. The International Crops Research Institute for the Semi-Arid Tropics (ICRISAT) started its collaboration in sorghum breeding in WCA in 1979 (Reddy et al., 2008). The IAR's program for evaluating sorghum identified germplasm lines with desirable traits. The development of cultivars in Nigeria was primarily achieved through the use of pure line, pedigree, or mass selection techniques from local sorghum germplasms and introduced varieties. Large-scale testing of hybrids involving three locally developed male-sterile lines (RCFA, ISNIA, and Kurgi A) and improved varieties was intensified from the late '70s onwards. Among them, five hybrids (SSH 1, SSH 2, SSH 3, SSH 4, and SSH 5) were promising (Obilana, 2004). The collaboration with IAR and ICRISAT has resulted in the development and release of over 50 improved sorghum varieties suited to specific ecological zones with farmer-preferred traits in Nigeria (Ojiewo and Gekanana, 2018). Significant efforts have been made to support research and development of improved sorghum varieties and production practices by both the public and private sector. However, there is still a shortage of improved varieties and hybrids in Nigeria due to drought stress associated with climate change.

Figure 1.2: Sorghum yield and harvested area in Nigeria from 2011-2023 (Source: USDA, 2023).

1.5 Adoption of improved cultivars in Nigeria

The adoption of improved sorghum varieties remains low in Nigeria (Ajani and Igbokwe, 2014). In a study conducted in eight African countries, only 28% of the harvested area was planted with improved sorghum varieties (Sheahan et al., 2014) due to a lack of high-yielding varieties (Reddy et al., 2008). Another reason for low adoption rates is farmers' tendency to stick with local accessions that have proven to be resilient to prevalent biotic and abiotic stress, reducing the risk for total crop failure. Numerous policy and structural constraints, including a slow transition from entirely state-managed seed supply channels, limited access to production inputs and credit facilities, and a lack of extension and program services, have also hindered adoption of sorghum varieties in Nigeria (Yahaya et al., 2022).

1.6 Participatory rural appraisal (PRA)

The participatory rural appraisal (PRA) is a multidisciplinary research tool and a form of market research to guide future crop production and breeding (Chambers, 1994). The PRA method engages farmers and stakeholders to seek their insights and production challenges, which could help develop new technologies that will meet their needs and requirements. The ultimate aim of a breeder is to develop a cultivar that will be used by farmers. According to Rose et al., (2016), a complex and highly variable set of factors influences farm-level decisions to adopt a sorghum cultivar. These include demographic characteristics of the household, expected profitability of the technology, farmer consumption preferences and availability and cost of seeds.

Several studies have identified farmers' preferences and constraints in many crops such as maize, Bambara groundnut, and sorghum in countries such as Kenya, Nigeria, Ethiopia, and Niger Republic (Odendo et al., 2002; Amelework et al., 2016; Ousseini et al., 2022; Yahaya et al., 2022). Farmers have varied criteria for selecting varieties and face production constraints such as low soil fertility, limited access to credit, insect pests, and water scarcity. In maize and sorghum, farmers prefer varieties with high yield, early maturity, and tolerance to *Striga*, whereas Bambara groundnut farmers prefer varieties with oval-shape, large, and pure seeds (Odendo et al., 2002; Amelework et al., 2016; Ousseini et al., 2022). Incorporating farmers' opinions in the breeding process is crucial for developing varieties that farmers and markets prefer.

1.7 Drought as the major constraint to sorghum production

Sorghum is mainly produced under rainfed conditions in the semi-arid regions (Mundia et al., 2019). In these regions, drought associated with climate change presented environmental and economic catastrophe, which had affected the social wellbeing of millions of smallholder farmers (Traore et al., 2014). For instance, extreme droughts in the 1980s substantially impacted on the socioeconomic developments in West Africa, where over half a million people died as a result of food shortages (Traore et al., 2014). Carrão et al., (2016) reported that severe droughts that occurred between 2000 and 2010 resulted in extreme poverty affecting some 2 to 3 million people in North Africa. Further, demand for water will increase significantly due to climate change, population growth and development of agricultural enterprises globally. Reports indicated that a

30% reduction in annual precipitation and a rise in temperature by up to 4°C could lead to a decrease in groundwater level by 50-70% (Evans, 2014; Carrão et al., 2016). Also, global warming is associated with increased aridity, shortened growing seasons, and declined crop production and yield gains (Evans, 2014).

Various approaches are recommended to mitigate drought stress such as the use of irrigation water (Solh and van Ginkel, 2014), agronomic management (fertilization, soil cultivation and irrigation), cultural practices (e.g., mulching, fallowing, and use of ground cover) and breeding and deployment of drought-tolerant crop cultivars (Mofokeng et al., 2017). Farmers in the semi-arid regions of SSA, where sorghum is the main staple food crop, do not have access to irrigation water for crop production. This approach is expensive, unsustainable, and unaffordable by smallholder farmers. Moreover, most SSA countries are water scarce, and the availability of clean water for irrigation is strictly regulated because of population growth and climate change. Use of drought-adapted sorghum cultivars remains the most economic and feasible approach to mitigate drought stress (Mofokeng et al., 2017). Development and deployment of new sorghum varieties with drought tolerance, high water use efficiency (WUE) and enhanced agronomic traits is a novel strategy to support and integrate into alternative drought stress management approaches.

1.8 The impact of drought stress on sorghum production and productivity

Drought stress remains the most common cause of yield gap and food insecurity in many countries of the semi-arid regions (Mundia et al., 2019). It affects crop production and productivity, especially under dryland or rainfed agro-ecologies. About 80% of the 45 million hectares of world sorghum production area is situated in the semi-arid regions of Africa and India (FAOSTAT 2021). These regions are heavily dependent on dryland sorghum production which is prone to recurrent droughts. Drought reduces grain yield potential by up to 70% in crop species globally (Kukal and Irmak, 2018). It is projected that sorghum production will decline by 10-15% in the next 50 years and average yield will likely decrease by 10% for each degree Celsius rise in temperature due to climate change (Tack et al., 2017). Total monetary losses of crop enterprises due to drought stress exceed over $29 billion based on the 2005 to 2015 estimations (Conforti et al., 2018). Average yield losses exceeding 20 million tons or 20% of rainfed sorghum production are incurred in the

semi-arid regions every year (Kukal and Irmak, 2018). The amount of yield loss due to drought can vary depending on the genotype, drought severity and duration, soil nutrition, plant health and their interactions (Mofokeng et al., 2017).

Furthermore, drought stress exacerbates the impact of plant diseases and insect pests and reduces soil biome and soil nutrients. Drought reduces transpiration rates, impairs active transport of nutrients, and reduces membrane permeability (Assefa et al., 2010). Under drought conditions sorghum plants will have low turgor pressure leading to stem lodging and predisposing them to stalk rot and ergot diseases (Tesso et al., 2012). Drought-stressed plants exhibit leaf rolling, leaf chlorosis, aborted flowering, panicle blasting, and produce small panicles, which all contribute to a significant reduction in yield gains or crop failure (Assefa et al., 2010). Two types of drought stress are distinguished, pre-flowering and post-flowering. In pre-flowering drought stress, sorghum plants present leaf curl, discoloration and reduced grain yield by more than 40% (de Souza et al., 2021). Post-flowering drought stress occurring during anthesis, and seed set is the most detrimental to sorghum production and productivity (Tsago et al., 2014). Post-flowering drought stress leads to premature plant death, stalk lodging, stalk rot, and reduced yield or complete crop failure (Tesso et al., 2012; de Souza et al., 2021).

1.9 Mitigation of drought stress in sorghum production

There are several mechanisms of drought response in plants, broadly categorized as drought escape, avoidance, and tolerance. These mechanisms enable drought adaptation and relative yield advantage that can be explored in sorghum improvement programs. The following section presents mitigation strategies to alleviate the effects of drought.

1.9.1 Use of early maturing varieties

Drought escape is the most common adaptive trait to drought in sorghum. Breeding for drought escape genotypes is a focus of many sorghum improvement programs. Early maturity is a key mechanism of drought escape since these genotypes can complete their growth cycle before the onset of severe moisture deficit (Chaves et al., 2003). Early maturing varieties with suitable planting dates are valued to manage terminal drought stress in low rainfall environments (Reddy

et al., 2009). Key attributes of early maturing genotypes include early flowering, a shorter vegetative phase characterized by high metabolic rate, reduced total seasonal evapotranspiration, and high gas exchange rates which facilitates effective photosynthesis with low WUE (Chantereau et al., 2001). However, early maturing varieties have a yield penalty as they have shorter vegetative and reproductive stages, leading to reduced photosynthesis and yield expression. Studies have found negative correlations between grain yield and earliness (Blum, 2005; Assefa et al., 2010). Early maturation allows plants to escape drought but limits their ability to take advantage of favorable growing conditions as they may not be in the field long enough. An example is the S-35 sorghum cultivar, which was selected from ICRISAT's germplasm collection in Northern Nigeria and tested in regional trials in Cameroon. S-35 produced twice the yield compared to new and local cultivars in a severe drought year but did not provide the same yield advantage in subsequent years with normal or good rainfall due to early flowering (Ahmed et al., 2000). Reduced yield expression in early maturing varieties is attributable to insufficient development of vegetative growth for maximum photosynthesis and inadequate source-sink mobilization due to accelerated growth (Subudhi et al., 2000). Drought stress imposed during booting and anthesis stages can cause up to an 87% reduction in grain yield in early maturing genotypes, and an increase in the duration of pre-flowering and post-flowering drought stress can reduce grain yield by 50–60% (Craufurd and Peacock, 1993). However, some studies suggest that early maturing sorghum cultivars have a 20% higher yield potential in non-stressed conditions and are well adapted under moderate and severe drought stress conditions compared to late maturing cultivars (Reddy et al., 2009).

The reduced yields observed in early maturing sorghum cultivars imply a lack of inherent genetic mechanisms for drought tolerance. While drought escape is effective in regions with terminal drought stress, it might curtail yields in late-maturing genotypes when rainfall is ample. There is a need for a breeding initiative to pinpoint early maturing cultivars that exhibit strong yields under both pre- and post-flowering drought conditions. Early maturing varieties are suitable for environments with prolonged drought stress or accurate weather predictions (Blum, 2005).

1.9.2 Use of drought avoidance varieties

Sorghum genotypes can avoid drought by slowing down metabolic processes and minimizing transpirational water loss (Blum, 2005; Assefa et al., 2010). This is achieved through a prolific and profuse root system, ability to maintain stomatal opening at low leaf water potential, high osmotic

adjustment, and reduced evapotranspiration associated with higher WUE. Sorghum plants can penetrate undifferentiated soils at a rate of 3.4 cm per day and extract water from as deep as 2.5 m, which is associated with drought tolerance and higher yield under drought stress conditions (Robertson et al., 1993; Cabelguenne and Debaeke, 1998). Selection of sorghum genotypes with higher stomatal conductance, cool canopy temperature, and higher osmotic adjustment by solute accumulation have been used as proxy traits for selection of sorghum genotypes with drought avoidance mechanism (Tuberosa, 2012). Prolonged drought stress can lead to complete crop failure, hence early onset of drought may trigger the induction of drought avoidance if test genotypes cannot complete their life cycle before the onset of drought.

1.9.3 Use of drought-tolerant varieties

Drought tolerance is the ability to sustain physiological activity and attain reasonable economic yield despite exposure to prolonged drought stress conditions (Schaffert et al., 2011). Blum (2005) posited that drought resistance is often used to refer to mechanisms such as drought avoidance and drought tolerance. Drought resistant genotypes can survive under limited and irregular water supply conditions to produce reasonable yield where non-resistant genotypes would otherwise fail. Several physiological traits (e.g., WUE, stay-green, osmotic adjustment, transpiration efficiency, and stomatal conductance) have been associated with drought tolerance. So far only few characteristics (e.g., stay-green) were demonstrated to be reliable in predicting the expression of drought tolerance under field conditions. Typically, in most sorghum breeding programs drought tolerance is regarded as a secondary objective. Hence there has been limited attempt at combining drought tolerance and other characteristics such as yield, insect pest and disease resistance and yield stability (Rosenow et al., 2000). Also, the polygenic inheritance of drought tolerance and the confounding effects of genotype-by-environment interaction (GEI) on selection has limited the progress in drought tolerance breeding. Currently, plant breeding research efforts have focused on pre-breeding geared towards parent-line development and genetic improvement of existing germplasm to incorporate drought tolerance and other important agronomic traits into adapted and high-yielding lines.

1.9.4 Exploiting stay-green character

The stay-green trait in sorghum is an adaptive mechanism that helps maintain photosynthetically active leaves during post-flowering drought, leading to longer grain-filling periods (Borrell et al., 2000). This trait is primarily due to a balance between water supply and demand and high WUE (Jordan et al., 2012). Several sorghum genotypes have been identified with this trait, including BTx642 (B35), ET36-1, M35, SC56, and K19, which have demonstrated increased resistance to diseases, lodging tolerance, and good grain-filling under drought stress (Xu et al., 2000). Breeding programs have successfully incorporated the stay-green trait into early senescent genetic backgrounds to improve drought tolerance (Subudhi et al., 2000; Vadez et al., 2011). The trait is controlled by dominant and recessive epistatic genes and a third locus with modifying effects (Rosenow et al., 1983). The stay-green trait has high broad-sense heritability (0.80) and narrow-sense heritability (0.60) (Walulu et al., 1994; Subudhi et al., 2000). Selection for stay-green under drought stress is associated with better grain yield performance under environments with sustainable water availability, and heterosis breeding can enhance genetic gain.

1.9.5 Use of sorghum varieties with high harvest indices

Breeding for yield improvement in sorghum requires genotypes with a high conversion efficiency of assimilates into yield components. Harvest index (HI) is a measure of the economic yield (grain) of sorghum expressed as a fraction of the above-ground biomass. Genotypes differed in their response to water deficit and HI, which can be attributed to a reduced biomass allocation under drought (Hammer and Broad, 2003). Thus, higher HI can be utilized as a vital drought-tolerant trait which is the result of optimum allocation of assimilates to the grain. Vadez et al., (2011) reported that stay-green genotypes had higher harvest indices compared with non-stay-green genotypes. The genotypes with stay-green traits will continue to grow when there is moisture deficit which will affect the assimilates partitioned to the yield component. Tall growing sorghum genotypes produce higher total biomass accumulation with a small source to sink biomass partitioning, which results in lower HI under water-limiting conditions (Mutava et al., 2011). Hence there is a limitation in the use of HI approach in yield prediction in drought tolerance breeding programs. Compared with other cereal crops (e.g., wheat, barley and maize), the HI in sorghum is relatively better under water stress owing to relatively low total biomass, taller plant height and effective remobilization of reserves from the source to sink (Menezes et al., 2015). This

suggests that sorghum allocates a smaller proportion of its resources to non-grain parts of the plant, allowing for a higher proportion of resources to be channelled into grain production, even in water-limited conditions. The positive correlation between plant height and grain yield in sorghum is an important insight (George-Jaeggli et al., 2011). This suggests that taller sorghum plants tend to have higher grain yields, potentially due to increased access to soil moisture and efficient resource allocation. This correlation could provide plant breeders with valuable information for selecting traits that enhance grain yield in sorghum varieties, especially in water-limited environments. Interestingly, i''s worth recalling the history of the“"Combine Kafir-6”" which is a testament to the intentional development of dwarf or semi-dwarf grain sorghum varieties (Smith and Frederiksen 2000). These varieties were created to enhance crop management and harvest efficiency. While these types may deviate from the natural tall stature of sorghum, they still retain the advantageous attributes related to resource allocation and effective remobilization.

Reportedly HI has moderate broad-sense heritability (Blum, 1996). Therefore, selection of genotypes that partition more assimilates to yield components can improve grain yield under drought. There existed a positive correlation between HI and stay-green (Blum, 1996). This suggests a possibility of developing sorghum cultivars with dual-purpose traits, i.e., improved grain and stover yields along with genotypes resilient to drought stress. Hence, it is prudent to characterize genetically diverse sorghum germplasm to select genotypes with better agronomic values, stay-green and higher HI to deploy cultivars adapted to both optimum and water-limiting conditions.

1.10 Breeding sorghum for drought tolerance: Methods

1.10.1 Phenotyping for drought tolerance

Several genotype screening techniques are reported primarily based on morpho-physiological traits. These techniques have allowed cultivar design by identifying best parents for population development or hybrid breeding. A successful screening technique depends on highly heritable traits that are strongly associated with grain yield. Phenotyping for drought tolerance can be conducted under greenhouse, field, and laboratory conditions.

1.10.2 Phenotyping for drought tolerance in the laboratory

The laboratory is an ideal place to screen for drought tolerance due to its simplicity, rapidity, and low cost. Polyethylene glycol (PEG)-induced drought stress is the most widely used screening method in the laboratory, and it enables negative selection against susceptible genotypes in an early screening stage (Tuberosa, 2012). The use of PEG to induce drought stress has reportedly discriminated genotypes with variable tolerance to drought stress during the early growth stage (Tsago et al., 2014). However, due to several factors, PEG-induced drought stress may not represent the field environment. Rapid stress development in PEG-induced drought stress may affect several mechanisms that plants use to tolerate drought stress, and the use of PEG with a low molecular weight can alter the hydraulic properties of the leaf (Tuberosa, 2012).

1.10.3 Phenotyping for drought tolerance under greenhouse condition

The screenhouse is a structure that allows crops to be grown under controlled environmental conditions. It enables the control of ecological parameters such as water, temperature, air humidity, and light, which is important for screening secondary traits (Shamshiri et al., 2018). The screenhouse can be equipped with state-of-the-art imaging systems that enable quick and accurate trait assessment for the analysis of drought tolerance. Controlling the environmental parameters is crucial for screening secondary traits (e.g., stay-green, chlorophyll fluorescence, canopy temperature and transpiration efficiency) because fluctuation in environmental conditions can affect the expression of the traits under stress conditions. Sorghum genotypes have been evaluated in the screenhouse for drought tolerance, but the use of a controlled environment facility to investigate the response of agronomic traits under drought stress is variable compared with *in situ* evaluation (Burke et al., 2015). The small pot space, volume of soil available for the plant, and growing media used can result in the roots facing fewer mechanical difficulties during exploration for nutrients. Furthermore, there are construction and operation costs associated with a screenhouse that limit the size of the facility and experimental plot.

1.10.4 Phenotyping for drought tolerance under field conditions

Drought tolerance can be assessed in controlled field environments or in drought-affected production areas to select desirable genotypes for economic traits. However, spatial and temporal variabilities and other factors can limit selection response for drought tolerance (Schaffert et al.,

2011). Custom-made plastic mulch and rain-out shelters can improve selection gains, but target field production areas with long dry spells and low rainfall conditions are ideal sites to select terminal drought-tolerant genotypes. Selection for drought tolerance and yield stability should be conducted across a broad range of the target production environments to account for GEI and enhance response to selection. GEI can reduce the expected degree of correlation between genotype and phenotype values, affecting the accuracy of field phenotyping and slowing breeding progress (Schaffert et al., 2011).

1.11 Constitutive and responsive traits in phenotyping sorghum for drought tolerance

Traits that are involved in drought response have been categorized as constitutive or responsive (Blum, 2005). Constitutive traits are expressed under optimum conditions, while responsive traits are expressed under severe drought stress. Marked progress in drought tolerance breeding in sorghum has been achieved through exploiting constitutive traits compared to responsive traits (Tuberosa, 2012). The variable expression of responsive traits under drought stress conditions confounds genotype selection. This has led breeders to focus more on selection for constitutive than responsive traits (Blum, 2005). The following constitutive traits are widely used in phenotyping sorghum for drought tolerance: transpiration efficiency, stay-green characteristics, root architecture and stomatal conductance (Table 1.1). The various morphological, physiological, and biochemical markers reported in phenotyping for drought tolerance in sorghum are briefly outlined below.

Table 1.1: Traits associated with drought tolerance in sorghum.

Traits/markers	Description	Reference(s)
Morphological	High grain-yield; root architecture; above-ground biomass production; High harvest index (HI); small leaf area; delayed flowering	Mace et al., (2012); Blum (2005)
Phenological	Earliness; delayed flowering; high germination rate; early seedling vigour; photosensitivity	Tsago et al., (2014)
Physiological	High osmotic adjustment (OA); high stomatal conductance; transpiration efficiency; reduced evapotranspiration; leaf cuticular wax; stay-green	Geetika et al., (2019)
Biochemical	High production of abscisic acid (ABA); auxin	Blum, (2011)
Oxidative stress	Heat shock proteins; leaf water potential; water use efficiency (WUE); dehydrins, increased proline accumulation	Goche et al., (2020)

1.11.1 Germination and seedling vigour

Genotypes with high germination rate and early seedling vigour are linked with early drought tolerance. Genotypes mobilise metabolites during the early growth stage and develop extensive root systems (Tsago et al., 2014). Early seedling vigour can result in increased root biomass and a high root to shoot ratio, which are drought-responsive traits (Tsago et al., 2014). Germination rates and seedling vigour indices such as shoot length and root dry weight have been integrated into breeding programs for early generation selection for drought tolerance improvement (Quieroz et al., 2019). However, trait performance at early vegetative growth stages may not be translated into reproductive stage including drought tolerance. Takele (2000) and Tsago et al., (2014) reported that the growth environment affects germination rates and seedling vigour. A high germination rates and seedling vigour *per se* not indicators of drought tolerance but they are vital to establish a good crop stand to escape early onset of drought stress. There are reports that substantiated the genetic control of seed germination and seedling establishment of sorghum under drought stress conditions (Takele, 2000; Tsago et al., 2014; Queiroz et al., 2019). Further studies are needed to

elucidate the precise genetic mechanism underlying drought tolerance during germination and seedling establishment stage.

1.11.2 Root architecture

Root traits such as fine roots, specific root length and area, root angle, root length density, and root weight are critical components in response to drought tolerance and determine the amount of soil area that a plant can explore for water and nutrient extraction from the soil as well as anchor the plant system (Bucksch et al., 2014). Root system architecture (RSA) is directly linked to the depth of the soil horizon that is explored by the root system. Genotypic variation for root architecture and their relevance for pursuing water and increasing yield under drought condition have been reported in sorghum (Mace et al., 2012). Root architecture such as fine roots, and root angle (Singh et al., 2011) influence yield under drought stress conditions. Reportedly, sorghum genotypes with a more acute root angle expressed higher drought tolerance and stay–green properties (Mace et al., 2012). Nodal root angle in sorghum influences horizontal and vertical root distribution in the soil profile enabling positive association with stay-green and grain yield productivity (Mace et al., 2012). Thus, nodal root angle is a vital selection criterion in sorghum breeding programs for improving drought adaptation. However, root traits have been neglected in most cereal breeding programs due to the destructive nature of root sampling and difficulties associated with root phenotyping. Non-destructive methods such as the “clear pot” method and optical imaging systems like mini-rhizotron and RadiMax have been developed to study genotypic differences (Hickey et al., 2017; Svane et al., 2019). Incorporating RSA as a breeding strategy for crop improvement holds excellent prospects for accelerating genetic gain for yield in the semi-arid regions.

1.11.3 Physiological traits

Physiological traits like stomatal conductance, photosynthesis, transpiration efficiency, and osmotic adjustment (OA) are used to study drought tolerance in crops (Goche et al., 2020). Sorghum has a highly efficient C_4 photosynthetic pathway that maintains photosynthesis and transpiration efficiency with reduced stomatal conductance, but severe drought stress affects these traits (Endris et al., 2021). Genotypes that activate a swift and robust stomatal shutdown and maintain favourable leaf water status in the event of water deficit are likely to tolerate drought stress. Sorghum’s ability to deposit epicuticular leaf wax at the peak of reproductive activity

improves terminal drought stress resistance by minimizing cuticular transpiration and sustaining WUE (Geetika et al., 2019). OA, which maintains cell turgor at low water potential, helps sorghum cope with drought stress. Goche et al., (2020) reported that genotypes with high OA produced a larger leaf area and had better leaf retention during grain-filling compared to genotypes with low OA. This suggests that osmotic adjustments in the leaves maintain high relative water content at low water potential under drought stress. The reduction in leaf water potential strengthens the plant to meet its transpiration demand. Identifying and utilizing sorghum hybrids with high OA values can be a useful approach in reducing the adverse effects of drought stress.

1.11.4 Biochemical markers

Biochemical markers have become valuable tools in sorghum breeding programs for assessing and enhancing drought tolerance (Table 1.1). These markers provide insights into sorghum plants' physiological and biochemical responses to water stress, aiding breeders in selecting and developing drought-resistant varieties. The use of biochemical markers in sorghum breeding has significantly advanced our understanding of drought tolerance mechanisms and improved the efficiency of breeding processes. Phytohormones such as abscisic acid (ABA) and auxin are crucial regulators of plant responses to drought stress (Blum, 2011). A higher accumulation of ABA is associated with water stress, as it promotes stomatal closure and reduces water loss through transpiration (Table 1.1). Therefore, leaf ABA content can be adopted as a robust parameter for distinguishing cultivar response to drought stress in sorghum. Auxins, on the other hand, play a role in root development and water uptake. Differential expression of auxin levels in sorghum roots and leaves indicates a complex role played by auxin in drought stress response (Wang et al., 2010). Monitoring the levels of these phytohormones provides breeders with insights into the stress response and the potential for improved drought tolerance (Blum, 2011). Proline is another important biochemical marker used in assessing drought tolerance in sorghum. Proline accumulation in drought-tolerant sorghum cultivars increases their capacity for OA, scavenging harmful reactive oxygen compounds and enhancing photosynthetic capacity under drought stress (Goche et al., 2020). Varieties that exhibit higher proline levels under drought conditions are often considered more drought-tolerant, as this indicates their ability to manage cellular stress.

Antioxidant responses are also employed as markers in sorghum breeding for drought tolerance. Higher antioxidant capacity in tolerant sorghum genotypes, up-regulation of protective proteins,

and higher levels of peroxidases protect against oxidative damage to cellular components (Goche et al., 2020). When plants experience drought stress, reactive oxygen species (ROS) accumulate, leading to oxidative stress and cellular damage. Antioxidant enzymes such as superoxide dismutase (SOD), catalase (CAT), and peroxidase (POD) counteract ROS and mitigate oxidative damage (Goche et al., 2020). The protective mechanism activated by the tolerant genotypes ensures normal leaf function under severe moisture stress. Varieties that demonstrate a higher capacity to scavenge ROS through enhanced antioxidant activity are regarded as more resilient to drought stress. Thus, the differential pattern of the biochemical markers could be used to predict plant performance and grain yield under different water stress.

The extent to which biochemical markers are used in sorghum breeding varies. These markers are employed in both early screening of potential drought-tolerant genotypes and in later stages of variety development. Molecular techniques such as quantitative polymerase chain reaction (qPCR) and enzyme assays are used to measure phytohormones, proline, and antioxidant enzyme levels. Although biochemical markers provide valuable insights into the genetics of drought tolerance, they are often used in conjunction with other phenotypic and agronomic traits to ensure a comprehensive assessment of drought tolerance.

1.12 Breeding sorghum for drought tolerance

1.12.1 Genomic-assisted breeding (GAB) for drought tolerance in sorghum

Genome-assisted breeding refers to using genomic tools to complement conventional breeding in developing superior cultivars with enhanced tolerance to biotic and abiotic stresses and improved yield. The integration of GAB in breeding programs reduces costs associated with phenotyping by selecting a subset from a large population that has been genotypically characterized (Xu et al., 2000). The goal of GAB is to find the best combinations of alleles (or haplotypes), optimal gene networks, and specific genomic regions to facilitate crop improvement.

1.12.2 Quantitative trait loci (QTL) analysis

Trait-specific genes linked to drought tolerance in sorghum have been detected using mapping population that have been validated across a range of diverse environments. Genes that control quantitative traits are located within the genomic region of the DNA referred to as quantitative trait loci (QTL) (Xu et al., 2000). QTL are identified using a combination of phenotypic and molecular data of a reasonably large mapping population (Tuberosa and Salvi, 2007). Several drought-tolerant QTL and their effects in different environments in sorghum have been identified (Subudhi et al., 2000; Sanchez et al., 2002). More than 15 unique QTL associated with the stay-green trait have been identified using bi-parental populations (Subudhi et al., 2000; Xu et al., 2000; Sanchez et al., 2002). Xu et al., (2000) used a restriction fragment length polymorphism (RFLP) map, developed from a recombinant inbred line (RIL) population and identified four stay-green QTL located on three linkage groups and three QTL for chlorophyll content. Similarly, Harris et al., (2007) identified four QTL associated with stay-green characteristics and were able to correlate stay-green with drought tolerance. Sanchez et al., (2002) identified several QTL associated with resistance to pre-flowering and post-flowering drought stress. These results showed that more than one chromosomal region controls the expression of traits related to drought tolerance under water-limited conditions.

The reported QTL have provided candidate gene-based markers, which show a very close association with the trait of interest, such as those related to drought stress, but there is a need to unravel the key role of genes in encoding critical regulatory proteins in response to drought in sorghum.

1.12.3 Marker-assisted selection (MAS) for drought tolerance

The identification of markers and genes controlling constitutive and adaptive traits will facilitate the use of marker-assisted selection in drought tolerance breeding. Marker-assisted selection (MAS) can also be deployed in increasing the frequency of beneficial additive alleles with independent effects. Single nucleotide polymorphisms (SNP) or QTL discovery is still limited by the need to phenotype a large number of polymorphic populations. The development of bi-parental, nested association mapping (NAM) and multiparent advanced generation intercross (MAGIC)

populations has been used to identify and develop genetic markers for quantitative traits. However, results from bi-parental populations may not be inferred to other populations, while developing a MAGIC population is challenging due to several intermating generations required with multiple parental lines in a crossing scheme. Also, use of large and heterogeneous populations may lead to false discoveries. The use of MAS has advanced through the advent of molecular technologies and statistical prowess; its application in breeding is still limited by interdependence with phenotyping requirements at some stage of breeding. MAS has been routinely used for traits conditioned by few genes, such as disease resistance and nutritional quality. MAS has limited application for quantitatively inherited traits such as drought tolerance and grain yield that are conditioned by polygenes and QTL each with a smaller genetic effect. The success of MAS relies on an effective genotyping platform and the accuracy of the QTL mapping studies. However, the high costs of genotyping associated with a more significant number of samples, and the use of high-density markers have limited the use of MAS to commercial breeding programs in developed countries (Schuster 2011). Currently, few sorghum breeding programs utilize molecular markers for selecting drought-resistant genotypes (Sanchez et al., 2002; Mace et al., 2012). Increasing marker availability and utility will facilitate the development and deployment of high-yielding cultivars that are drought-resistant and adapted to the semi-arid regions.

1.13 Heterosis breeding in sorghum

Heterosis or hybrid vigour, is the basis for developing high-performing hybrids, compared to their parental genotypes. Sorghum hybrids have been reported to have a 30–40% heterosis in grain yield compared to the best pure line varieties (Ashok Kumar et al., 2011). For example, the first sorghum hybrid variety in Africa, named Hageen Dura – 1 was released for commercial production in Sudan. This variety outperformed other local varieties with a yield gain of 4.9 t/ha under rainfed conditions (Maunder, 1990). Since then, sorghum hybrids suitable for production in SSA were developed by crossing introduced elite breeding lines with locally adapted varieties (Weltzien et al., 2018). Combining ability analysis, which provides information on the nature and extent of gene action conditioning trait inheritance, allows for selecting suitable parents and families. The diallel mating design proposed by Griffing (1956) is widely used technique used to determine the

general combining ability (GCA) of parents and the specific combining ability (SCA) effects of crosses. The GCA measures a parent's average performance in a hybrid combination, whereas the SCA refers to cases where the hybrid's performance is relatively better or worse than would be expected based on the average performance of the parents involved. The GCA/SCA variance ratio is a measure of gene action conditioning traits, such that a high ratio indicates the importance of additive gene effects, whereas a low ratio indicates the presence of non-additive gene effects (Baker, 1978). Both GCA and SCA effects are significant in the parental selection and the development of breeding populations.

1.14 Conclusion and future outlook

Agriculture currently accounts for 70% of global freshwater demand, which is expected to increase. Breeding and deploying drought-tolerant sorghum cultivars have been identified as the most economical and reliable approach to mitigate present and future drought events for farmers in semi-arid regions. This involves targeting several agronomic, physiological, and molecular traits in sorghum to ensure effective water use with high heritability. Sorghum cultivars with specific secondary traits such as increased stomatal conductance, rapid OA, improved root architecture, and stay green have been identified in various instances. However, these traits were not systematically targeted through active selection in most sorghum breeding programs in developing countries, apart from stay-green to some extent. Regarding the stay-green attribute, there have indeed been instances of successful and practical incorporation of stay-green loci into senescent backgrounds, contributing to advancements in cultivar enhancement under water-limited conditions. This approach has been successful in developing and releasing sorghum cultivars with improved yields in marginal areas of the semi-arid region. Molecular markers associated with traits that confer resistance to drought in sorghum can be used to select superior lines through marker-assisted breeding. The review highlighted the need to combine data from different studies and integrate conventional and biotechnology approaches to produce high-performing drought-tolerant sorghum cultivars for the semi-arid regions to offset the effects of climate change.

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CHAPTER 2 : Sorghum production in Nigeria: opportunities, constraints, and recommendations

Abstract

Sorghum production has considerable socio-economic values in sub-Saharan Africa for food security and to serve the increased industrial demands due to high population pressure and climate change. However, the production and productivity of the crop are yet to be expounded in Nigeria for economic gains. Therefore, the objective of this study was to present the current opportunities and constraints to sorghum production in Nigeria. A participatory rural appraisal (PRA) study was conducted in three selected sorghum growing zones in Northern Nigeria involving 250 farmers. Socio-economic data were collected through surveys and focus group discussions. Sorghum was cultivated mainly by males (80%) who had grade 6-12 level of education (31.3%), with the productive age of 21–45 years (75.7%) and a household family size of below five members (52.3%). Low-yielding landrace varieties such as Kaura (37.4%) and Fara-fara (29.3%) were the most widely cultivated types across the study zones due to their good grain quality. The major farmers' preferred traits from a sorghum variety were: high yield, drought tolerance and *Striga* resistance. The study recommends integrated sorghum technology development incorporating the described preferences of the farmers for sustainable production and economic gains of the crop.

Keywords: crop management, drought tolerance, farmer-preferred traits, focus group discussion, Northern Nigeria, participatory rural appraisal, sorghum production, *Striga* infestation

2.1 Introduction

Sorghum (*Sorghum bicolor* [L.] Moench) is the 5th most important world cereal crop after maize (*Zea mays* L.), wheat (*Triticum aestivum* L.), rice (*Oryza sativa* L.), and barley (*Hordeum vulgare* L.) (FAO, 2019). It is a staple food crop in the drier parts of Africa, China, and India (Ajeigbe et al., 2018; Mrema et al., 2020). The largest world's sorghum producers are the USA with total annual grain production of 8.7 million tons from 2.0 million hectares, Nigeria (6.9 million tons on 5.4 million hectares), Ethiopia (5.3 million tons on 1.9 million hectares), and Sudan (3.7 million tons on 6.8 million hectares) (FAO, 2019). Nigeria is the leading sorghum producer, followed by Ethiopia in Africa in terms of total production. Sorghum is the largest staple cereal crop accounting for 50% of the total output and occupying about 45% of the total land area devoted to cereal crops production in Nigeria (FAO, 2019). The sorghum productivity in the country is 1.23 t/ha, which is relatively low compared with the world average of 1.45 t/ha and the USA with 4.58 t ha^{-1} (FAO, 2019). Sorghum is relatively tolerant to drought and waterlogging (Curtis, 1967; Mrema et al., 2017) and has a wide adaptation to varied soil conditions (Ajeigbe et al., 2018). These characteristics make sorghum the staple crop of choice in Africa's most drier regions to pursue food and income security. However, sorghum productivity in the region is low (≤1.0 t/ha) due to several production constraints.

Nigeria's bulk of sorghum production is derived from the Northern Guinea and Sudan/Sahel ecologies of Northern Nigeria. Sorghum is regarded as a traditional food crop in this agro-ecologies. In Northern Nigeria, sorghum is consumed in various forms, including as a *Tuwo* (a thick porridge made from dry-milled, non-fermented grain flour eaten with soup), *Kumu* or *Ogi* (flour paste made by wet-milling after fermentation and cooked like a thin porridge), fermented pancakes and snack as roasted grain (Ega et al., 1992; NRC, 1996). Occasionally, sorghum grain is fermented for malting and used in preparing local brewing products. Industrially, sorghum is predominantly used by companies producing beverages, breakfast cereals, and confectionery and a small percentage of the grain is also used as animal feed. The stalks are used to build shelters or fences and as livestock feed. Other future sorghum values are recognized in the country, including as raw materials for the biofuel industries (GAIN, 2020).

The crop's economic potential has not been fully realized in Nigeria and sub-Saharan African (SSA) countries due to a number of production and productivity constraints. Lack of high-yielding

sorghum varieties, declining soil fertility, drought stress, *Striga* infestation, limited access to production inputs and credit facility and finance are among the factors accounting for the low sorghum production and product development (Sani et al., 2013). Sorghum research programs in Nigeria have pioneered the development and release of varieties suited to some specific agro-ecological zones for industrial purposes (Ajeigbe et al., 2018). However, small-scale farmers, who account for over 90% of sorghum production, prefer to use their farm-saved seed of local unimproved varieties due to their intrinsic quality attributes such as good eating quality, adaptation, low insect pest attack and minimum production input requirements. However, the local landraces have low yield potential, long maturity, tall plant height, and respond poorly to improved agronomic management practices (Ajeigbe et al., 2018). Climate change models show a high probability (>90%) of an increased in water scarcity and temperature, which will be detrimental to food production in many tropical areas, especially in West Africa (Battisti and Naylor 2009). Breeding drought-tolerant and climate-resilient sorghum varieties have the potential to offset the yield gap presented by climate change (Fedoroff et al., 2010). Ndjeunga et al., (2015) reported that only about 20% of the total sorghum production area is planted with improved cultivars in Nigeria. Mundia et al., (2019) opined that small-scale farmers in the region use landraces because of poor access to seed of improved cultivars and production technologies (Mundia et al., 2019) and a lack of financial support (Ajeigbe et al., 2018)**.**

The participatory rural appraisal (PRA) is a multidisciplinary research tool and a form of market research to guide future crop production and breeding. The PRA method engages farmers and stakeholders to seek their insights and production challenges, which could help develop new technologies that will meet their needs and requirements. The ultimate aim of a plant breeder and agronomist is to develop a cultivar adopted by farmers and needed by the value chains. According to Morris (2002), farm-level decision to adopt a modern variety is influenced by a complex and highly variable set of factors such as the household's demographic characteristics, expected profitability, consumption preferences, availability, and cost of the seed of the improved variety, among others. Langyintuo and Mekuria (2008) argued that farmers might not adopt an appropriate technology because of inadequate information and limited access. Farmer positive perception of a new technology is vital if it is to be adopted. Understanding farmer perceptions of the appropriateness of production technology characteristics can strengthen the focus of plant breeding and guide appropriate technology development and deployment strategies. PRA studies have been

conducted in sorghum production areas in the eastern and central part of the northern region of Nigeria to assess farmers' perceptions of modern technologies and production constraints (Baiyegunhi and Fraser, 2009; Okoro and Ujah, 2009; Gourichon, 2013; Sani et al., 2013; Ajeigbe et al., 2018). However, the production and productivity of the crop is yet to be expounded in Nigeria for economic gains. Therefore, the objective of this study was to present the current opportunities and constraints to sorghum production in Nigeria and make recommendations as a guide to new variety design and sustainable production.

2.2 Materials and methods

2.2.1 Description of the study area

The study was conducted in the northern region of Nigeria in three agro-ecological zones, namely, the Sub-humid Southern Guinea Savannah, the Northern Guinea Savannah and the Sahel Savannah. The zones are known for their sorghum production and are characterized by semi-arid to arid agro-ecologies. The geographical positions of the study zones are shown in Figure 2.1, and their typical agro-ecological characteristics are summarized in Table 2.1. Northern Nigeria has two distinct meteorological seasons: the rainy season from May to September and the dry season from October to early May. The mean annual rainfall varies from 500 to 1,500 mm and temperatures between 17^{o}C to 40^{o}C. The maximum humidity may increase drastically during the middle of the rainy season to about 96% in August and drop sharply to about 10% during harmattan around December. Agriculture is the primary sector of the economy in the region. Crop production and livestock rearing are the key activities for about 80% of the total population (NBS, 2019).

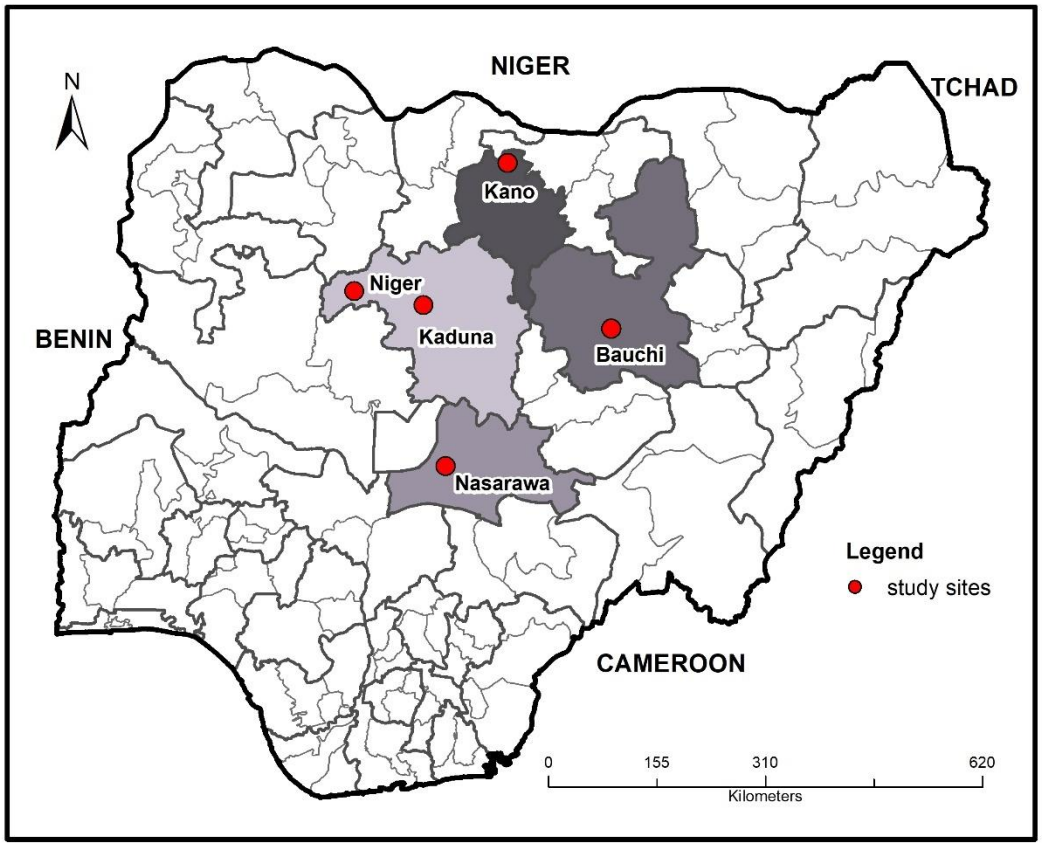

Figure 2.1: Map of Nigeria showing the study zones (adapted from NBS, 2019).

Table 2.1: Description of the study locations for the participatory rural appraisal conducted in Northern Nigeria in 2018/2019

Zone	State	Agro-ecology	Latitude	Longitude	Altitude (masl)
North-West	Kano	Sahel Savannah	12^0 26' N	8^0 30' E	488
	Kaduna	Sub-humid Southern Guinea Savannah	10^0 36' N	07^0 25' E	250
North-Central	Nasarawa	Southern Guinea Savannah	8^0 32' N	07^0 42' E	600
	Niger	Southern Guinea Savannah	10^0 47' N	06^0 32' E	243
North-East	Bauchi	Sahel Savannah	10^0 18' N	09^0 50' E	616

masl = meters above sea level
Source: adapted from NBS, 2019

2.2.2 Sampling procedure

A multi-stage purposive sampling was used for the study based on the dominance of sorghum production and the occurrence of drought. The study was conducted in three agro-ecological zones in Northern Nigeria (North-West, North-Central and North-East) selected based on the importance of sorghum production. A total of six states were sampled, with two states selected from each zone. Within each state, a total of twelve (12) local government areas (LGAs) were sub-sampled, encompassing two LGAs from each state. From each LGA five wards were selected. A ward is the smallest administrative unit in Nigeria. From each ward, one village known for experiencing recurrent droughs was purposely selected, and 25 farmers with the experience of sorghum production were selected in each village. The target wards and villages were chosen based on sorghum area coverage, production, consumption and prior information on the occurrences and severity of drought and S*triga* infestation with the assistance of the agriculture development project (ADP) officers. Owing to security challenges in the North-East, the survey was conducted in 10 LGAs selected from five states. A total of 250 farmers that cultivated sorghum during the 2018/19 cropping season participated in the study with ADP officers and two researchers (Socio-Economist and Plant Breeder) drawn from the Institute for Agricultural Research (IAR) Samaru, Nigeria. A further five focus groups were established with 145 farmers for focus group discussions (FGDs). Each focus group had between 20 and 30 farmers selected by local leaders and ADP officers. Participants for FGDs were sampled based on their experience in sorghum production and gender balance.

2.2.3 Data collection

Primary data were collected through a semi-structured questionnaire interview and FGDs. Demography, socio-economic characteristics, sorghum production constraints, sorghum production inputs, types of crops grown, attributes of farmers' most preferred sorghum variety and trait preferences were recorded.

2.2.4 Data analysis

The data collected were subjected to statistical analysis using the cross-tabulation procedure to determine the relationships among study zones and assessed variables. Descriptive statistics, percentages, Chi-square ($\chi 2$) values and Kruskal–Wallis test (H-test) were carried out to ascertain the existence of significant differences in the socio-economic characteristics of sampled sorghum farmers. Farmers perceived production constraints to sorghum production were subjected to rank analysis using Kendall's coefficient of concordance (*W*). Kendall's coefficient of concordance (*W*) was adopted to measure agreement among several (*m*) quantitative or semiquantitative variables after assessing a set of *n* objects of interest. In this study, the variables are farmers, assessing the perceived sorghum production constraints. The individual respondent was also entitled to give their constraint ranking, from less important to the most important constraint. The Kendall's concordance coefficient (*W*) is given as:

$$W = 12\left|\frac{\sum T^2 - (\sum T)^2}{m^2(n^2 - 1)}\right| \quad (1)$$

Where: *T* = sum of ranks for each variable,
m = number of ranks and,
n = number of constraints (variables) being ranked.

The value of the *W* ranges between 0 and 1, 1 representing perfect concordance between the farmers and 0 illustrating strong disagreement among the farmers in ranking the perceived production constraints. Data were subjected to analyses using IBM Statistical Package for Social Sciences (SPSS)-20 (SPSS, 2020).

2.3 Results

2.3.1 Socio-economic description of sampled households

The Kruskal-Wallis test for socio-economic characteristics of sampled sorghum farmers in the study areas is shown in Table 2.2. The results revealed a significant difference ($p<0.05$) among zones for all variables assessed except for the level of education. Results from the interviewed

respondents showed that 80.0% of the interviewed farmers ($p<0.0001$, $\chi2 = 17.294$) were males and 20.0% were females in the three surveyed zones, which implied that men still play dominant roles in sorghum production and related enterprises in the study area. Few female farmers participated in this survey except in the North-West, which had 35.0% female respondent farmers. In comparison, the North-East zone had the lowest percentage (6.0%) of interviewed female farmers (Table 2.2). Among the respondent farmers, 75.7% were between 21 and 45 years of age ($p<0.0001$, $\chi2 = 54.982$), indicating that middle-aged adults dominated sorghum production. Sorghum producing farmers' mean age was 34, 37, and 38 years for North-Central, North-West, and North-East zones, in that order. About 17.0% of respondents aged over 45 years accessed their long-term knowledge of sorghum diversity and sorghum cultivation trends in Northern Nigeria. About 7.3% of the respondents aged between 12-20 years old were categorized as young adults. In the surveyed areas, it is customary for young adults and children to help with sorghum farming.

The focus group discussion revealed that children aged 12-15 years engage in farm work such as land preparation for sorghum planting (May), sowing of sorghum seeds (early June), and helping to deliver cooked food to the farm for the family members and or laborers engaged in farming activities. A high proportion (73.3%) of the respondents had formal education among the surveyed zones, and secondary (Grade 6–12) level of education had the highest proportion of literate farmers with 31.3%. Most of the respondent farmers (26.3%) attended primary school (Grade 1 to 6 education), and 31.3% attended secondary education (Grade 6-12). In comparison, the least proportion was recorded for tertiary level of education (above Grade 12) at 15.5%. Only about 26.3% of respondents had no formal education (Table 2.2). Most respondent farmers in North-Central and North-West zones had education levels ranging from Grade 1-12. North-West recorded the highest proportion of individuals completing primary (30.0%) and secondary (40.0%) level of education while North-East recorded the highest proportion of farmers who had no formal education (34.0%). Education is vital to the improvement of agricultural management and productivity and the creation of rural prosperity. Farmers with formal education can easily make decisions about their farms and adopt innovative agricultural production methods.

The focus group discussion revealed that farmers with formal education have a better understanding and knowledge, while non-formal education gives the farmer hands-on training and better farming methods. In all the surveyed zones, most of the interviewed sorghum growers had

family sizes of less than 10. In North-West, 83.0% of the interviewed farmers had a family size of ≤5 individuals, whereas, in the North-Central, 49.0% of the respondents had a family size of 5-10 individuals. Only a few interviewees had a family size greater than 10, with the most (23.0%) being in the North-Central zone. Focus group discussions revealed that family size has a vital role in farm labour in the three surveyed zones' rural farming systems. The household heads are primarily senior citizens and weak. Therefore, they may not have the energy to meet the labour-intensive requirements of sorghum production, and in most cases, they do not have the finance to hire workers. The young males in the household often help with field activities. The female members are majorly responsible for housework, including nurturing the children.

The focus group discussion further revealed that women actively participate in sorghum planting and harvesting activities. There was a significant difference ($p<0.0001$, $\chi2 = 47.418$) in the farm sizes of sorghum farmers among the three zones (Table 2.2). About 52.3% of respondents owned a farm of <5 hectares, whereas 36.7% owned a farm ranging from 5 to 10 hectares, and 11.0% owned a farm of >10 hectares. The respondents' farm size was skewed mainly to the small-scale landholding (0.1-5 hectares) in the study area, which implies that sorghum production in the study area falls within a small-scale (1.0–5.9 ha) farm holding enterprise. The PRA further revealed a statistically significant difference ($p<0.0001$, $\chi2 = 13.636$) for means of livelihood for respondents. From the results, most of the respondents are engaged in farming as a means of livelihood across the study regions, with an average of 68.7%. Apart from agriculture, about 20.3% of the respondents reported were self-employed, owning a business in their community, such as buying and selling farm inputs and foodstuffs. A smaller proportion of the respondents (10.7%) work on bigger farms in their community and the neighbouring areas.

Table 2.2: Kruskal-Wallis test for socioeconomic characteristics of sampled sorghum farmers in the study zones of Northern Nigeria

Variables	North-Central		North-East		North-West		DF	χ2 value	P-value	%Mean
	Freq.	%	Freq.	%	Freq.	%				
Sex of the respondent										
Male	81.0	81.0	47.0	94.0	65.0	65.0	2	17.294	0.0001	80.0
Female	19.0	19.0	3.0	6.0	35.0	35.0				20.0
Age of farmer (years)										
12-20	0.0	0.0	0.0	0.0	22.0	22.0				7.3
21-45	67.0	67.0	45.0	90.0	70.0	70.0	4	54.982	0.0001	75.7
>45	33.0	33.0	5.0	10.0	8.0	8.0				17.0
Level of education										
Non-formal	30.0	30.0	17.0	34.0	16.0	16.0				26.7
Primary (Grade 1-6)	23.0	23.0	13.0	26.0	30.0	30.0	6	11.893	0.0640	26.3
Secondary (Grade 6-12)	34.0	34.0	10.0	20.0	40.0	40.0				31.3
Tertiary (>Grade 12)	13.0	13.0	10.0	20.0	14.0	14.0				15.7
Household size (persons)										
1-5	28.0	28.0	23.0	46.0	83.0	83.0				52.3
6-10	49.0	49.0	22.0	44.0	17.0	17.0	4	68.509	0.0001	36.7
>10	23.0	23.0	5.0	10.0	0.0	0.0				11.0
Land size (hectares)										
1.0-5	68.0	68.0	45.0	90.0	93.0	93.0				83.7
5.1-10	32.0	32.0	1.0	2.0	7.0	7.0	4	47.418	0.0001	13.7
>10	0.0	0.0	4.0	8.0	0.0	0.0				2.7
Farmer means of livelihood										
Crop and livestock farming	63.0	63.0	31.0	62.0	81.0	81.0				68.7
Self-employed (artisans)	27.0	27.0	11.0	22.0	12.0	12.0	6	13.636	0.0340	20.3
Employee (laborers)	10.0	10.0	8.0	16.0	6.0	6.0				10.7
Unemployed	0.0	0.0	0.0	0.0	1.0	1.0				0.3

DF = degrees of freedom, χ^2 = Chi-square value, Freq. = Frequency, % = Percent

2.3.2 Sorghum production inputs

Production inputs such as seed, inorganic fertilizers and crop protection chemicals are imperative for increasing agricultural productivity. Results revealed a non-significant difference ($p>0.05$, $\chi2= 4.442$) difference among zones for the type of sorghum seed use by respondents (Table 2.3). The majority of the farmers (74.4%) reported using low-yielding local landraces that have been developed through mass selection and saved from the previous harvest. The farmers have been using farm-saved seeds for several generations, often inheriting from their parents or sourced from neighbours or family members. Only 28.0%, 34.0%, 19.0% of the respondents in North-Central, North-East, and North-West, respectively, used seeds of improved varieties bought from seed companies or received from research institutes. Results on the type of fertilizers used by respondents revealed a significant difference ($p=0.0001$; $\chi2 = 38.716$). Use of inorganic fertilizer (e.g., compound fertilizer such as NPK 20:10:10) was the highest (44.3%) among the farmers, followed by the combination of inorganic and organic fertilizer (e.g., NPK 20:10:10 and farmyard manure) (35.3%) among respondents. Farmers apply farmyard manure during land preparation, while a combination of NPK and urea fertilizers are applied before or at flowering. Only about 11.3% of the respondents reported not applying fertilizers for sorghum production. Factors such as the high cost of inorganic fertilizers, lack or low yield response of landraces to fertilizer application and lack of knowledge on the recommended fertilizer rate have limited the use of inorganic fertilizers in the study areas. The use of crop protection chemicals for the control of weeds (e.g., glyphosate, a non-selective systemic herbicide), insect pests (Karate 5EC; a broad-spectrum insecticide), and diseases (Mancozeb, a broad-spectrum fungicide) was higher among the respondents (70.7%) across the study areas during the sorghum production season (Table 2.3).

Table 2.3: Sorghum production inputs used by respondent farmers in three selected zones in Northern Nigeria (percentage)

Variables	North-Central	North-East	North-West	DF	χ2 value	P-value	%Mean
Seed use							
Modern cultivar	28.0	34.0	19.0	2	4.442	0.109	27.0
Farm-saved	72.0	66.0	81.0				73.0
Type of fertilizer							
None	18.0	4.0	12.0	6	38.716	0.0001	11.3
Organic (farmyard manure)	3.0	16.0	8.0				9.0
Inorganic (NPK, urea)	51.0	22.0	60.0				44.3
Combination	28.0	58.0	20.0				35.3
Use of crop protection chemical							
No	37.0	22.0	29.0	2	3.772	0.152	29.3
Yes	63.0	78.0	71.0				70.7

DF = degrees of freedom, χ^2 = Chi-square value

2.3.3 Types of crops cultivated in the study areas

Table 2.4 summarizes other crops grown in the surveyed zones. The crops listed by the respondents included maize, soybean, rice, cowpea, and millet in decreasing order of importance. The *Chi-square* test revealed a significant difference (χ^2=8.716; P=0.0001) in the proportions of crops grown among the respondents in the three study areas. More respondent farmers across the study regions cultivate maize (20.7%) and soybean (16.3%). The cultivation of cereals (such as maize) and legumes (cowpea) affords the farmers opportunity to diversify the family's dietary intake and sell excess produce in the local markets to earn cash. Focus group discussions revealed that extra produce is sold at the end of the farming season, usually around December–February, to buy clothes, settle debts, conduct house maintenance, and purchase farming implements such as hoes and cutlass. Other crops reportedly grown by the respondents included groundnut, yam, and sesame. The cultivation of sorghum and other cereals and pulses have been known since time immemorial in the study area.

The results from Table 2.4 further elucidated the degree of crop diversification among the respondents. The livelihood strategies in the study area tend to combine various ways of earning a living in addition to the primary production of crops. Such diversification serves a dual purpose of alternative income and job opportunities for smallholder farmers in rural areas.

Table 2.4: Other crops grown by sorghum farmers in a cropping season in Northern Nigeria

Crop	*North-Central*		*North-East*		*North-West*		*DF*	*χ^2 value*	*P-value*	*%Mean*
	Freq.	**%**	**Freq.**	**%**	**Freq.**	**%**				
Cowpea	18.0	14.8	14.0	16.1	30.0	12.7				14.5
Maize	25.0	20.5	14.0	16.1	60.0	25.4				20.7
Rice	17.0	13.9	14.0	16.1	38.0	16.1				15.4
Soybean	16.0	13.1	13.0	14.9	49.0	20.8	12	22.945	0.028	16.3
Millet	23.0	18.9	16.0	18.4	19.0	8.1				15.1
Pepper	15.0	12.3	7.0	8.0	13.0	5.5				8.6
Others	8.0	6.6	9.0	10.3	27.0	11.4				9.4

DF = degrees of freedom, χ^2 = Chi-square value, Freq. = Frequency, % = Percent

2.3.4 Farmer-preferred sorghum varieties in Northern Nigeria

The study also investigated farmers' preferred variety in Northern Nigeria using the local names, and the results are shown in Table 2.5. The Kruskal-Wallis test revealed a significant difference (χ^2 =77.774; p=0.0001) for farmer-preferred sorghum variety among the study zones in Northern Nigeria. Farmers grow several sorghum varieties in any cropping season that match the growing conditions and their food preferences. Other factors that made the local landraces preferable to the respondents include low input requirement, drought resistance, *Striga* tolerance, low bird damage, and seed availability.

The majority of the farmers across the region preferred Kaura (37.4%) and Fara-fara (29.3%) varieties compared to all other varieties owing to compact panicles, bulging grains and adapted to the dry Sudan Savanna zone. The next farmer-preferred variety is guinea corn (7.0%) due to its wide food and feed grain utilization. The respondents reportedly cultivate different sorghum varieties such as Bagaje, Buhu arha and others in both mono- and inter-cropping farming systems (Table 2.5). The most preferred sorghum varieties in Northern Nigeria have been Kaura and Fara-fara, which are well-adapted to the region and cultivated for food.

Table 2.5: List of and proportion (%) of farmer-preferred varieties of sorghum across the study zones in Northern Nigeria

Variety	North-Central		North-East		North-West		*DF*	*χ^2 value*	*P-value*	*% Mean*
	Freq.	**%**	**Freq.**	**%**	**Freq.**	**%**				
Kaura	75.0	43.9	23.0	19.7	77.0	48.7				37.4
Fara-fara	46.0	26.9	39.0	33.3	44.0	27.8				29.3
Guinea corn	9.0	5.3.0	8.0	6.8	14.0	8.9				7.0
Bagaje	1.0	0.6	10.0	8.5	4.0	2.5				3.9
Buhu arha	0.0	0.0	10.0	8.5	8.0	5.1	18	77.774	0.0001***	4.5
Gajera	7.0	4.1	4.0	3.4	0.0	0.0				2.5
Doguwa	8.0	4.7	7.0	6	0.0	0.0				3.6
Yalel	11.0	6.4	3.0	2.6	0.0	0.0				3.0
Mori	5.0	2.9	1.0	0.9	5.0	3.2				2.3
Others	9.0	5.3	12.0	10.3	6.0	3.8				6.5

DF = degrees of freedom, χ^2 = Chi-square value, Freq. = Frequency, % = Percent

2.3.5 Farmer-preferred traits in a sorghum variety

Table 2.6 presents farmers' preferred traits in a sorghum variety in Northern Nigeria. The results showed significant differences (χ^2 =34.116; p=0.0001) among farmers' traits preferences across the three study zones. High yield was the most preferred trait (34.3%), followed by drought tolerance (28.3%), *Striga* resistance (13.5%) and grain quality/taste (11.8%). In the North-West, about 54 respondents preferred high-yield variety followed by tolerance to drought (53 respondents) and good taste (24 respondents). *Striga* resistance was the second most preferred sorghum trait among respondents in North-Central after high yield. *Striga hermonthica* (also referred to as witchweed), a parasitic weed that attacks and significantly reduces sorghum yields, is the most predominant species in Northern Nigeria. The results show that different regions have different trait preferences, suggesting the need to develop a specific variety to meet the farmers' needs across the zones.

Table 2.6: Farmers preferred traits in a sorghum variety across the study zones in Northern Nigeria

Traits	*North-Central*		*North- East*		*North-West*		*DF*	χ^2 **value**	*P-value*	*%Mean*
	Freq.	**%**	**Freq.**	**%**	**Freq.**	**%**				
High yield	46	31.7	27	35.1	54	36.2				34.3
Grain quality/taste	15	10.3	7	9.1	24	16.1				11.8
Early maturity	4	2.8	4	5.2	4	2.7				3.5
Drought tolerance	34	23.4	20	26.0	53	35.6	10	34.116[a]	0.0001	28.3
Striga resistance	35	24.1	10	13.0	5	3.4				13.5
Insect pest and disease resistance	11	7.6	9	11.7	9	6.0				8.4

DF = degrees of freedom, χ^2 = Chi-square value, Freq. = Frequency, % = Percent

2.3.6 Farmer-perceived constraints to sorghum production

Farmer-perceived sorghum production constraints in Northern Nigeria are presented in Table 2.7. About 34.6% of the North-Central farmers indicated that lack of access to production inputs was the overriding constraint for sorghum production in the area, followed by *Striga* infestation (20.7%). Drought stress was the primary production constraint in the North-East (22.4%), followed by a lack of access to production inputs (21.1%). The main constraint to sorghum production in the North-West includes lack of access to production inputs (33.6%), drought stress (23.5%) and limited agricultural lands (13.4%). The least important constraint from the pooled sample was land availability (6.9%), suggesting that the farmers are yet contending with the land allocated for the sorghum production.

Respondent farmers were asked to rank the constraints listed in Tables 2.7 and 2.8 in order of importance. The ranked data were subjected to Kendall's coefficient of concordance analysis to draw an overall rank on the farmer constraints to sorghum production, and the results are presented

in Table 2.8. This was necessary to ascertain the level of agreement in the ranking of the perceived constraints.

The Kendall's coefficient of concordance (*W*) computed from the analysis were 0.203, 0.226, 0.163 and 0.309 for the pooled sample, North-Central, North-East North-West, respectively. The estimated value of *W* indicates about 22, 16, and 31% level of agreements among respondents from North-Central, North-East, and North-West, respectively, on the ranking of productions constraints. Thus, there was a relatively low level of agreement among the respondents. When pooled samples were considered, the agreement level was about 20%, reflecting a low level of agreement. This is depicted in the ranked constraints, which differs slightly from the percentage distribution of farmer-perceived constraints. The most ranked constraint across all surveyed zones was confirmed to be a lack of production inputs. In addition, the pooled sample suggested drought stress was the second pressing constraint. The zone-specific concordance values showed that *Striga* infestation was the second most pressing constraint perceived by sorghum farmers across the study regions. Kendall's coefficient of concordance revealed limited agricultural lands was the least perceived constraint to sorghum production in the study zones.

Table 2.7: Farmer-perceived constraints to sorghum production across the study zones in Northern Nigeria (%)

Constraints	North-Central		North-East		North-West		DF	χ^2 value	P-value	%Mean
	Frequency	Percent	Frequency	Percent	Frequency	Percent				
Lack of access to production inputs	72	34.6	32	21.1	80	33.6				29.8
Drought stress	29	13.9	34	22.4	56	23.5				19.9
Striga infestation	43	20.7	30	19.7	15	6.3				15.6
Bird damage	25	12.0	26	17.1	17	7.1	12	61.294	0.0001	12.1
Lack of access to credit	19	9.1	10	6.6	19	8.0				7.9
Stem borer pest	16	7.7	12	7.9	19	8.0				7.9
Limited agricultural lands	4	1.9	8	5.3	32	13.4				6.9

DF = degrees of freedom, χ^2 = Chi-square value

Table 2.8: Farmers perceived constraints to sorghum production and summary Kendall's coefficient of concordance across the study zones in Northern Nigeria

	Pooled sample		**North-Central**		**North-East**		**North-West**	
Constraints	**Mean rank**	**Position**	**Mean rank**	**Position**	**Mean rank**	**Position**	**Mean rank**	**Position**
Lack of access to production Inputs	7.51	1st	5.14	1st	6.07	1st	6.10	1st
Drought stress	4.21	2nd	3.74	4th	4.38	3rd	4.38	3rd
Striga infestation	4.09	3rd	4.71	2nd	4.52	2nd	4.52	2nd
Bird damage	3.67	4th	3.74	3rd	3.70	4th	3.71	4th
Lack of access to credit facilities	3.55	5th	3.53	5th	3.42	5th	3.42	7th
Stem borer pest	3.44	6th	3.40	6th	3.41	6th	3.42	5th
Limited agricultural lands	3.41	7th	3.36	7th	3.40	7th	3.42	6th
Kendall's W[a]	0.203		0.226		0.163		0.309	
DF	6		6		6		6	
P-Value	0.0001		0.0001		0.0001		0.0001	

DF = degrees of freedom, *Kendall's W*[a] = Kendall's coefficient of concordance

2.4 Discussion

2.4.1 Socio-economic description of sampled households

Sorghum cultivation is predominant in Northern Nigeria, where it is a traditional crop supporting the dietary needs of rural farmers for time immemorial. Sorghum provides food, fodder, raw material, and a source of cash income to rural farmers. However, farmers in the region realize low sorghum yields due to numerous biotic, abiotic, and socio-economic constraints that limit productivity. Hence, a PRA was conducted to decipher the critical sorghum production constraints and farmer-preferred traits in Northern Nigeria.

The Kruskal-Wallis test revealed a significant difference among the North-Central, North-East and the North-West zones in most assessed socio-economic characteristics (Table 2.2). The search and adoption of modern farming technologies are relatively easy for educated farmers. The study revealed that most of the respondents had attained some level of formal education (Table 2.2), with 31.3% of the respondents having a grade 6-12 level of education. This is contrary to Fidelugwuowo (2021) findings, who reported that only 13.0% of respondents farmers had grade 6-12 levels of education. Other respondents with no formal education obtain extension service or farm information through the Hausa language, the predominant language in the Northern region of Nigeria. Education helps farmers reduce transaction costs for accessing and interpreting data regarding alternative income-generating activities (Mrema et al., 2017) and agricultural subsidies (Okoro and Ujah, 2009). Adewuyi and Okunmadewa, (2001) pinpointed that education significantly impacts farmers' managerial and technical skills. The respondents' significant literacy level showed that farmers in the Northern region could adopt modern and innovative technologies for productive farming to ensure food security.

Gender (male and female household head) had significant impact on access to technical information, extension services, training, and farm inputs. The majority of the respondents in the study have a male household head (Table 2.2). This can be attributed to the land tenure system in Nigeria, which favours male ownership of land. The reason could also be attributed to the dominant role of patriarchy in West Africa which prompts the male to assume a leadership role in both men and women. However, in some parts of the North-West and North-Central region, female farmers play a significant role in sorghum farming activities on a par with male farmers. In almost all

cases and zones, the female farmers are not the owners of the farm plot. They are allowed to run the farm because either their husbands are engaged in non-farm labour, or the women are allocated the poorest part of the land where valuable crops like maize cannot thrive (Curran and Cook, 2009; Jirgi et al., 2019). The result of restricted access to better land and other farm inputs is lower productivity on land farmed by women. The gender difference (20.0%) between male and female farmers present in the study agrees with the reported average gender difference (20 to 30%) across SSA countries (Kilic et al., 2015; Mukasa and Salami, 2015; Gebre et al., 2019). Age significantly influences farmers' decision-making process to adopt improved farming technologies and other production-related decisions. The significant difference (Table 2.2) among zones for household members' age among the respondents revealed that different age groups practice sorghum cultivation. The study further revealed that more than two-thirds (75.7%) of the sorghum farmers in Northern Nigeria were still within their productive age of 21-45 years (Table 2.2). This agrees with Jirgi et al., (2019) findings that the majority of sorghum farmers are within an active age group (20-45 years). The participation of young farmers in sorghum cultivation suggested a better future for crop production enterprise in Nigeria. The younger farmers will be more flexible to new ideas and risks; hence, they are expected to adopt innovations more readily than older farmers. This finding agrees to that of Adenegan et al., (2013), who reported that age significantly impacts farm and farmer productivity. However, Eboh et al., (2004) and Oyediran et al., (2017) reported an aged population among sorghum farmers due to the youth reluctance in crop farming. The gradual inflow of the younger entrepreneurial labour force into sorghum production may be attributed to the increased price and demand of sorghum and the government's renewed vigour to promote local production in recent times (FEWS NET, 2020).

The study revealed that small farm holdings (0.1–5.0 hectares) dominate sorghum production in Northern Nigeria (83.7% respondents). The present finding agrees with Shaib et al., (1997) and Sabo et al., (2017), who reported that small farm holdings dominate Nigeria's agriculture accounting for about 81% of the total farm area and 95% of the agricultural output. The significant differences in farm sizes and the preponderance of small farm sizes in the study area implied that smallholder farmlands are highly fragmented. In the rural areas of Northern Nigeria, the majority of the farmers obtain their farmland through inheritance. The larger the household size, the more fragmented the land at the household head's demise. Small farms hinder large-scale agricultural activity such as farm mechanization and access to credit necessary to expand cultivation and invest

in facilities such as irrigation. Therefore, it is imperative to implement land protection and consolidation policies that decrease the current fragmentation trend. Previous studies by Baiyegunhi and Fraser (2009) in Kaduna state, Sani et al., (2013) in Bauchi state and Oyediran et al., (2017) in Katsina state showed a similar preponderance of small-scale producers of sorghum in the respective states. Adama et al., (2016) reported that small-scale farmers are the backbone of Nigerian agriculture, implying that Nigeria's agricultural policy thrust should be centred around the smallholder farmers.

The household size enhances labour availability which can be used for different agricultural activities (Oyewole, 2012). The average household size across the study region was about five persons (52.3%) implying a reasonable number of family labour to accomplish various farm operations. Sorghum in Nigeria is often produced by extended family members who are vertically (unmarried sons, married sons and their families) or horizontally (brothers and multiple wives) related to the family's patriarch. The older patriarch ensures the cultivation of large plots of land with the sole aim of meeting the staple food needs of the overall extended family (Thériault et al., 2017). The significance of household size in agriculture hinges on the availability of labour for farm production, the total area cultivated to different crop enterprises, the amount of farm produce retained for domestic consumption, and the surplus for the marketplace (Olusayo et al., 2019). The primary occupation of the majority (68.7%) of the respondents is farming. This suggests that farming is the mainstay of the economy in the region. However, some respondents engage in non-farming activities such as retail marketing, artisanship, and transportation.

2.4.2 Sorghum production inputs

Although sorghum requires little improved technologies to be a profitable crop, the effects of climate change and declining soil fertility in Northern Nigeria are changing that perception. The study revealed a significant difference among respondents on fertilizer use for sorghum production (Table 2.3). The majority of the respondents reportedly use organic (9.0%) and inorganic (44.3%) fertilizers and their combinations (35.3%) for sorghum production. These results agree with Omonona et al., (2019), who reported that over 50% of sorghum farmers in Nigeria use fertilizers during the cropping season. Inorganic fertilizers are officially subsidized in Nigeria for crop

production. However, unlike maize and rice farmers, the subsidized fertilizers are not readily accessible by sorghum farmers, resulting in farmers across the regions augmenting the application of inorganic fertilizer with an organic type of fertilizer such as farmyard manure or compost. In addition, the farmers reported applying fertilizer below the recommended rate. Although sorghum seeds of imported variety are available in Nigeria, the respondents reportedly cultivate local landraces due to their intrinsic quality attributes such as eating quality, local adaptation, low pest attack and reduced production input demand. However, the currently introduced varieties lack the attributes needed by farmers. Also, poor extension services limit their availability in rural communities. This limited access to quality seeds of improved varieties, hindering the adoption of the available varieties. In addition, there is a lack of interest by seed companies in marketing the seeds of sorghum. Also, sorghum is excluded in the government's low-interest Anchor Borrowers Program (ABP), limiting farmers access to inputs. These combined negatively affected sorghum production and productivity in Nigeria (Gourichon, 2013; Mundia et al., 2019; GAIN, 2020).

2.4.3 Crops cultivated by the respondents

Farming is the economic mainstay of the Sudan savanna, Northern Guinea savanna, Southern Guinea savanna, and the Jos Plateau of Northern Nigeria. In 2019, sorghum was grown on an estimated 6 million hectares of land (Shahbandeh, 2020). Sorghum is produced as a mixed crop with maize, millet, and other leguminous crops such as cowpea, groundnut, and soybean (Shahbandeh, 2020). The low input requirement allows sorghum to fit in new and emerging farming systems as farmers grow more profitable crops like maize and soybean. Farmers in the North-West intercrop sorghum late in the season with vegetables such as tomatoes and onions, while North-Central farmers intercrop with tuber crops such as yam. Intercropping is rewarding to the farmers to maximize output from their small land holdings and utilize legumes' biological nitrogen fixation attributes to improve soil fertility or the high yield of cereals such as maize for the market.

2.4.4 Farmer-preferred sorghum varieties and traits

The majority of sorghum-growing areas in Nigeria are occupied by traditional landrace varieties such as Kaura, Fara-fara and Guinea corn. The landraces are indigenous to the localities and are

grown extensively as rainfed crops in Northern Nigeria (Mundia et al., 2019). Farmers grow more than one variety of sorghum in a field; for instance, in Zaria, Nigeria, more than 100 local landraces have been identified to be cultivated by local farmers (NRC, 1996). Selected varieties were mainly derived from local landraces through mass selection (such as Fara-fara and Kaura). Sometimes, the landraces are improved by introgressions from exotic lines obtained from international organizations such as the International Crops Research Institute for the Semi-Arid Tropics (ICRISAT). Sorghum genetic improvement is conducted by National Agricultural Research Systems (NARS) in Nigeria, such as the Institute for Agricultural Research (IAR) Samaru. The Kruskal-Wallis test revealed a significant difference for most preferred sorghum varieties among the respondents (Table 2.5). Kaura (37.4%) and Fara-fara (29.3%) were the dominant varieties preferred across all zones, followed by Guinea corn (7.0%). The Kaura varieties have large grains with yellow endosperm that are derived from durra-caudatum races. The Fara-fara variety is an early-maturing, large-seeded, white-grained sorghum derived from guinea-caudatum races (Curtis 1967). In addition, the Kaura and Fara-fara sorghums varieties possess higher grain quality, produce acceptable *kamu* and *kunu* traditional foods in Nigeria, and high market demand in Nigeria. These characteristics have made the local landraces the most preferred varieties over the modern and introduced types.

The traits of interest to farmers are an important attribute that forms breeding and socio-economics research premises. The results from the study revealed high yield as the most essential farmer-preferred trait across all regions (Table 2.6). The findings revealed farmers' openness to accepting high yielding and improved cultivars with other traits of interest. Tolerance to drought and *Striga* are traits of interest to sorghum farmers in Northern Nigeria (Table 2.6). Sorghum is cultivated under rainfed conditions in Northern Nigeria, where drought and *Striga* infestation cause severe economic damage to sorghum production (Reddy et al., 2009). High-yielding cultivars that mature early and with drought and S*triga* tolerance attributes can be developed through breeding to release novel varieties for production in low/erratic rainfall environments like Northern Nigeria.

2.4.5 Farmer-perceived constraints to sorghum production

The results revealed that limited access to production inputs such as improved seed, fertilizers, and crop protection chemicals are the most important sorghum production problems perceived by the farmers in the study area (Table 2.7). This is followed by drought stress, *Striga* infestation and bird

damage. Kendall's coefficient of concordance revealed a low agreement between respondents who ranked the perceived production constraints in sorghum production. The farmers ranked production inputs as key perceived constraints to sorghum production. Limited access to production inputs ranked the highest among the perceived constraints because smallholder farmers seldom have access to quality seeds of improved varieties, fertilizers, and crop protection chemicals. Limited access to production inputs contributed significantly to sorghum's low production and productivity in Nigeria (Philip et al., 2009; Mundia et al., 2019). These findings agree with reports from Reddy et al., (2009) on sorghum production constraints in Africa.

Contrary to results from this study, a study conducted by Mengistu et al., (2019) in Ethiopia ranked anthracnose disease and birds attack as the most important sorghum production constraints. Nigeria launched the Agricultural Transformation Agenda (ATA) program in 2009, which had played an important role in improving farmers' access to sorghum production input in selected farming communities in Northern Nigeria (Ajeigbe et al., 2017). An appraisal of the ATA program revealed that improved production technologies in farmers' fields increased yield on average by 46% across the study areas. However, the program's success is yet to be upscaled to reach all sorghum farmers in Nigeria. Therefore, the present findings underscore the need for a systematic approach to improving farmers' adoption of new production technologies.

Sorghum production is an essential component of food security and economic empowerment for smallholder farmers in Nigeria. The study assessed farmer preferences and identified key production constraints that farmers encounter in sorghum farming in three agro-ecological zones of Nigeria. The results indicated that sorghum farmers in the study zones are primarily male, educated, young and possess small landholdings. Farmers in the study area grow a wide array of local landraces to meet different purposes, and the most important landrace varieties are Kaura and Fara-fara. The different varieties grown serve many purposes, such as food, feed, and raw material for malting and brewing. The most farmer-preferred traits of sorghum across the three study zones are high yield, tolerance to drought and *Striga*. Farmers will likely adopt improved cultivars with attributes such as early maturity, tolerance to drought, and *Striga* and good taste to ensure reliable and stable yield under erratic rainfall prevalent in the region. Sorghum production in the study area is constrained by several factors whose importance varies across the regions. The most critical constraints are limited production inputs, drought stress, *Striga* infestation, and bird damage. Bird

damage, particularly due to the quelea bird menace, poses a significant challenge to sorghum production in the study. These birds can cause extensive losses by consuming and damaging sorghum crops, impacting food security and livelihoods. Effective bird control strategies are essential to mitigate these losses and ensure sustainable sorghum cultivation. In regions where farmers tend to have limited land holdings, like the study area, diverse methods are employed to counter the quelea bird challenge. One common approach involves scare tactics, wherein farmers utilize visual and auditory deterrents such as reflective tape, bright objects, and loud sounds to dissuade quelea birds from their fields. Therefore, to sustain sorghum production, there is a need to breed and release high yielding, early maturing, drought and *Striga*-tolerant cultivars with good food quality traits for production in semi-arid regions of Northern Nigeria.

2.4.6 Conclusion

The study highlighted the challenges smallholder farmers encounter in sorghum production in Nigeria. Therefore, based on the survey findings, it is recommended that the sorghum seed business be supported by incentives and subsidies to rural farmers in remote areas. Nigerian policymakers can address the identified production constraints of limited access to production inputs by making sorghum a focus crop in the anchor borrowers' program (ABP), which provides farmers with a low-interest loan for purchasing production inputs. Sorghum outreach programs that disseminate information on improved varieties and new technologies need to be supported at the grassroots levels to ensure the adoption of high-yielding and improved cultivars. Production constraints such as lack of high yielding cultivars, drought stress and *Striga* infestation can be addressed by breeding programs. Therefore, it is recommended that the sorghum breeding program consider integrating the farmer-preferred traits and the highlighted constraints during the development of improved sorghum varieties suitable for production in the semi-arid regions.

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CHAPTER 3 : Drought tolerance response of African sorghum [*Sorghum bicolor* (L.) Moench] genotypes under variable environments

Abstract

Sorghum is the main food staple for millions of people in sub-Saharan Africa (SSA) and Asia. Sorghum is relatively drought-tolerant and cultivated in arid and semi-arid regions under rainfed production. However, severe drought stress often leads to crop loss and declined productivity. The development and deployment of high-yielding and drought-adapted genotypes is a cost-effective strategy for sustainable sorghum production globally. The objective of this study was to determine drought tolerance and genotype-by-environment interaction (GEI) effects on grain yields of a population of African sorghum genotypes to identify high-yielding and drought-adapted genotypes for direct production and also for use in breeding programs. Two hundred and twenty-five sorghum genotypes were evaluated under non-stressed (NS), pre-anthesis drought stress (PreADS), and post-anthesis drought stress (PoADS) conditions under field and greenhouse environments using a 15 × 15 alpha lattice design in two replicates. The three water regimes and two environments resulted in six testing environments. Data were collected on grain yield and drought tolerance parameters, and additive main effect and multiplicative interaction (AMMI) analysis were computed. The mean grain yield under NS, PreADS, and PoADS were 3.70, 1.76, and 2.58 t/ha, in that order. The best genotypes adapted to non-stressed environments were G09, and G109, whereas G114 and G56 were suitable for non-stressed and stressed conditions. G72 and G75 displayed the best performance in PreADS conditions only, whereas genotypes G210 and G12 were identified as high performers under PoADS only. The AMMI analysis revealed that genotype (G), environment (E), and GEI were significant (p<0.05), which accounted for 38.7, 44.6, and 16.6% of the total explained variation in grain yield. AMMI 4 was the best-fitting model for grain yield. Based on AMMI 4 and the best linear unbiased predictors (BLUPs) calculations, genotypes G119 and G127 with a grain yield of 5.6 t/ha and 6.3 t/ha were selected as being suitable for non-stressed conditions. Genotypes G8 and G71 with BLUPs of 2.5 t/ha and 2.6 t/ha were best suited for pre-anthesis drought stress conditions, whereas genotypes G115 and G120 with BLUPs of 4.2 t/ha and 4.3 t/ha are recommended for post-anthesis drought-prone environments, respectively. The identified sorghum genotypes are recommended for production in dry agro-ecologies of SSA characterized by pre- and post-anthesis drought stress. In addition, the identified genotypes are valuable genetic resources to develop novel drought-tolerant material.

Keywords: abiotic stress; AMMI, BLUEs, BLUPs, drought tolerance indices, sorghum

3.1 Introduction

Sorghum [*Sorghum bicolor* (L.) Moench] is a highly valued cereal crop native to sub-Saharan Africa (SSA) and has been cultivated for centuries (Ejeta and Knoll, 2007). Globally, sorghum is the fifth most important and widely cultivated cereal crop after maize, wheat, rice, and barley. It is a staple food in the drier parts of Africa, China, and India (FAOSTAT, 2021). Sorghum is Africa's second most important cereal in terms of area harvested (28.1 million hectares) preceded by maize with 42.5 million hectares and followed by rice with 15.8 million hectares (FAOSTAT, 2021). In terms of yield, sorghum is the third most important cereal crop in Africa with 26.3 million metric tons after maize (96.6 million metric tons) and rice (37.2 million metric tons) (FAOSTAT, 2021). The grains are an important food source that is processed into a variety of traditional cuisines such as couscous, porridge, and semi-leavened bread (Teferra and Awika, 2019; Yahaya et al., 2022). Sorghum is a major component in the flour blend that is used to produce gluten-free flour with a low glycemic index that is rich in iron and zinc, vitamin B6, vitamin B3 (niacin), magnesium, phosphorus, fiber, unsaturated fats, and protein (Ejeta and Knoll, 2007; Thilakarathna et al., 2022).

Sorghum's nutrient profile makes it appealing to the food industry and a food of choice among health-concerned consumers due to its gluten- and allergen-free nature. Furthermore, the crop is used to develop various feed products for livestock, including pigs, poultry, and cattle (Rad et al., 2020). In addition, grains are widely used to prepare local beers and beverages (Teferra and Awika, 2019). According to Tenywa et al., (2018) there is an increased consumption of sorghum and sorghum-derived products in SSA and Asia, which has rendered the crop a staple food contributing to about 70% of the daily calorie requirements.

The world's largest sorghum producers are the USA, with an annual grain production of 8.7 million tons, Nigeria (6.9 million tons), Ethiopia (5.3 million tons), and Sudan (3.7 million tons) (FAOSTAT, 2021). In 2021, continental Africa produced about 26.2 million tons from 28.1 million hectares of land, resulting to an average yield of 0.93 t/ha, which is lower than the world average of 1.45 t/ha and the 4.58 t/ha achieved in the USA (FAOSTAT, 2021). The lower yields in SSA are attributed to abiotic stresses (e.g., drought stress and poor soil fertility) (Ejeta and Knoll, 2007) and biotic factors e.g., anthracnose caused by *Colletotrichum graminicola* (Ces.) Wilson (Marley et al., 2005), stem borer [*Chilo partellus* (Swinhoe)], leaf blight [*Exserohilum*

turcicum (Pass.) Leo and Suggs.] (Beshir et al., 2015), and the parasitic weed [*Striga hermonthica* (Del.) Benth] (Odeny et al., 2021). The cultivation of susceptible varieties to various biotic and abiotic stresses exacerbates yield losses and poor yield gains of the crop in the region.

Sorghum is a relatively drought-tolerant crop, making it an ideal candidate to mitigate against the risks of crop loss posed by climate change (Jordan et al., 2012; Sabadin et al., 2012; Ouedraogo et al., 2017; Abreha et al., 2022). Drought stress is the most yield-limiting factor for sorghum production in SSA (Sabadin et al., 2012; Abreha et al., 2022). For example, drought caused yield losses of 36% and 55% during vegetative and reproductive growth stages, respectively (Assefa et al., 2010). Pre-flowering drought stress reduced grain yield of sorghum by more than 40% (de Souza et al., 2021), whereas post-flowering drought stress caused grain yield losses by 50 to 90% (Harris et al., 2007). Yield-component traits such as the number of grains per panicle and seed size are reduced by drought stress (Burke et al., 2018; Abreha et al., 2022). Drought stress occurring during the critical growth stages of the crop, including pre- and post anthesis, has a detrimental effect on grain quality (Kebede et al., 2001; de Souza et al., 2021). Surveys in Ethiopia, Burkina Faso, and Nigeria indicated that severe drought during the pre- and post-flowering growth stage is a major sorghum production constraint (Ouedraogo et al., 2017; Derese et al., 2018, Yahaya et al., 2022). As a result, concerted breeding efforts are required to develop drought-tolerant cultivars to urgently mitigate the effects of drought stress and improve sorghum production in SSA.

Phenotypic and genetic analysis of African sorghum genetic resources revealed wide diversity for multiple breeding utilities, including drought tolerance (Tesso et al., 2008; Amelework et al., 2016; Mofokeng et al., 2017; Olatoye et al., 2018; Angarawai et al., 2021). The extensive diversity in the cultivated sorghum germplasm will aid the selection of contrasting genotypes for specific and broad adaptation. However, the lack of information on the drought response of African sorghum genotypes, especially their adaptation to the adverse growing conditions in semi-arid regions of SSA, has limited the recommendation of improved varieties with desirable profiles and drought-resilience.

Genotype-by-environment interaction (GEI) is the differential response in the performance of genotypes grown in multiple environments (Yan et al., 2000). Its analysis is an essential step for cultivar recommendation. To quantify the effects of genotype, environment, and GEI, several statistical methods are used, including the additive main effects and multiplicative interaction

(AMMI) and genotype, genotype-by-environment (GGE) biplots (Zobel et al., 1988; Yan et al., 2000). Of the two methods, AMMI analysis is recommended as the most effective due to its ability to illustrate the complex interaction between genotypes and environments accurately and graphically (Zobel et al., 1988). AMMI has been applied successfully to understand genotype-by-environment reactions in sorghum which allowed the identification of suitable genotypes for a wide range of environments (Gebeyehu et al., 2019; Al-Naggar et al., 2020; de Souza et al., 2021). The GEI of African sorghum genotypes under drought stress environments can aid the efficient selection and recommendation of the best-suited genotypes for multiple purposes.

Drought stress under rainfed agricultural systems has been hampering sorghum productivity in SSA and Asia. This has prompted research collaboration by the International Crops Research Institute for the Semi-Arid Tropics (ICRISAT) and various National Agricultural Research Systems (NARS) under different projects such as the International Sorghum and Millet Program (INTSORMIL). Pre-breeding and breeding programs were initiated to develop and recommend drought-tolerant sorghum varieties (Rosenow and Dahlberg, 2000; Reddy et al., 2009; Kumar et al., 2013). As a result, valuable sorghum genetic resources, including historic accessions, wild relatives, landraces, and improved breeding lines, were collected, and conserved in national gene banks (Rosenow and Dahlberg, 2000; Reddy et al., 2009; Angarawai et al., 2021). These collections are yet to be exhaustively characterized to identify germplasm exhibiting various essential and winning traits. Furthermore, there is a need for a rigorous evaluation of African sorghum germplasm in drought-stricken environments to aid in recommending drought-adapted genotypes for cultivation and breeding in arid and semi-arid environments of SSA. Therefore, the objective of this study was to determine drought tolerance and GEI effects on the grain yield of a population of African sorghum genotypes to identify high-yielding and drought-adapted genotypes for production and breeding.

3.2 Materials and methods

3.2.1 Plant materials

Two hundred and twenty-five (225) sorghum genotypes assembled from diverse origins were used for the study. These comprised 225 landraces and 52 elite lines from the International Crops Research Institute for the Semi-arid Tropics-Kano (ICRISAT-KN); 15 registered cultivars, 22 elite

lines, and 83 landraces from the Institute for Agricultural Research (IAR), Samaru, Nigeria; nine elite lines from the African Centre for Crop Improvement (ACCI) in South Africa; and 21 genotypes from the United States Department of Agriculture, Agricultural Research Service, National Plant Germplasm System (USDA-ARS, NPGS). The names, codes, pedigree information, and genotype sources of origin are presented in Table 3.1.

Table 3.1: Code, pedigree, and origin of 225 sorghum genotypes.

Code	Genotype	Source	Code	Genotype	Source	Code	Genotype	Source
G1	S7-LATA/RIB/BC1-3-1-1-V	ICRISAT-KN	G76	AS 66	ACCI-SA	G151	Danjiba	IAR-NG
G2	ICNSL2014-024-2	ICRISAT-KN	G77	E 41	ACCI-SA	G152	Bog Farwa	IAR-NG
G3	Gadam	ICRISAT-KN	G78	E 29	ACCI-SA	G153	Ginzo-2 Yellow	IAR-NG
G4	ICNSL2014-062	ICRISAT-KN	G79	E 11	ACCI-SA	G154	SSV20064	IAR-NG
G5	CAPARLKSG20150308	ICRISAT-KN	G80	AS 71	ACCI-SA	G155	Yar Koma	IAR-NG
G6	CAPARLGSG2015-0078	ICRISAT-KN	G81	E 119	ACCI-SA	G156	Kaura Short Panicle- 2	IAR-NG
G7	ICNSL2014-025-8	ICRISAT-KN	G82	AS 13	ACCI-SA	G157	Kaura Mai Baki Kona	IAR-NG
G8	ICNSL2014-022-4	ICRISAT-KN	G83	AS 152	ACCI-SA	G158	Kaura Red Glume	IAR-NG
G9	Yar Gumel	ICRISAT-KN	G84	AS 1	ACCI-SA	G159	Gagaran Mai Baka Kona	IAR-NG
G10	CF35:5	ICRISAT-KN	G85	Samsorg 44	IAR-NG	G160	Kitse Kaza	IAR-NG
G11	ICSV111	ICRISAT-KN	G86	Samsorg 9	IAR-NG	G161	CAPARLGSG20150124.1	IAR-NG
G12	Yarwasha	ICRISAT-KN	G87	Samsorg 14	IAR-NG	G162	Fara Dawa	IAR-NG
G13	ICSV 400	ICRISAT-KN	G88	Samsorg 38	IAR-NG	G163	Hipusini	IAR-NG
G14	ICNSL2014-065	ICRISAT-KN	G89	Samsorg 39	IAR-NG	G164	Chakallari	IAR-NG
G15	ICNSL2014-034	ICRISAT-KN	G90	Samsorg 40	IAR-NG	G165	ICNSL2014-026-11	IAR-NG
G16	CAPARLGSG2015-0035	ICRISAT-KN	G91	Samsorg 41	IAR-NG	G166	SSV20071012	IAR-NG
G17	S7-LATA/RIB/BC1-1-17-1-V	ICRISAT-KN	G92	Samsorg 42	IAR-NG	G167	Magara	IAR-NG
G18	Aguasasin Jan'dawa	ICRISAT-KN	G93	Samsorg 47	IAR-NG	G168	Kwar Biyu	IAR-NG
G19	Mai-Ruwan Zuma	ICRISAT-KN	G94	Samsorg 45	IAR-NG	G169	Kaura Mai Jan Kono	IAR-NG
G20	Wago Sane Red Sorghum	ICRISAT-KN	G95	Samsorg 46	IAR-NG	G170	Kaura Koma	IAR-NG
G21	Gagarawa - 3	ICRISAT-KN	G96	Samsorg 17	IAR-NG	G171	Yar Agaji	IAR-NG
G22	Yar'getso	ICRISAT-KN	G97	Samsorg 7	IAR-NG	G172	Kurum Basau	IAR-NG
G23	Yar'fargore	ICRISAT-KN	G98	Samsorg 43	IAR-NG	G173	CAPARLKSG20150285	IAR-NG
G24	Adamawa - 2	ICRISAT-KN	G99	Samsorg 6	IAR-NG	G174	Farmer Local	IAR-NG
G25	Wild Sorghum	ICRISAT-KN	G100	AS 97	IAR-NG	G175	Hindatu	IAR-NG
G26	Mai-Goje	ICRISAT-KN	G101	Mori Masaba	IAR-NG	G176	ICNSL2014-027-4	IAR-NG
G27	12KNICSV-297-3	ICRISAT-KN	G102	E 119	IAR-NG	G177	SSV2008113	IAR-NG
G28	12KNICSV-297-1	ICRISAT-KN	G103	Kirbati	IAR-NG	G178	Yar Magogo	IAR-NG

Table 3.1: Continued.

Code	Genotype	Source	Code	Genotype	Source	Code	Genotype	Source
G29	12KNICSV-293	ICRISAT-KN	G104	Dan Yara	IAR-NG	G179	Kaura - 1	IAR-NG
G30	12KNICSV-297-2	ICRISAT-KN	G105	Jarwa	IAR-NG	G180	Kaura Yellow Glume	IAR-NG
G31	12KNICSV-107-3	ICRISAT-KN	G106	ICNSL2014-021-1	IAR-NG	G181	Kaura Kaduna I	IAR-NG
G32	12KNICSV-295	ICRISAT-KN	G107	Village Ofumpo Mkt	IAR-NG	G182	Gwaza Banji Borno	IAR-NG
G33	12KNICSV-176	ICRISAT-KN	G108	Takanbo	IAR-NG	G183	Jibrin Agaiy Awala	IAR-NG
G34	12KNICSV-297-4	ICRISAT-KN	G109	Yalai	IAR-NG	G184	CAPARLKSG20150291	IAR-NG
G35	12KNICSV-93	ICRISAT-KN	G110	Kaura - 3	IAR-NG	G185	Farafara Kaduna	IAR-NG
G36	12KNICSV-260	ICRISAT-KN	G111	Kafi Mori	IAR-NG	G186	Harjiu	IAR-NG
G37	12KNICSV-107-2	ICRISAT-KN	G112	Fara Dogon Dawa	IAR-NG	G187	ICNSL2014-042-1	IAR-NG
G38	12KNICSV-418	ICRISAT-KN	G113	Jar Balakwama	IAR-NG	G188	SSV2008091	IAR-NG
G39	12KNICSV-179	ICRISAT-KN	G114	Jar Lau	IAR-NG	G189	Yar Kai Kabayat	IAR-NG
G40	CAPARLKSG20150293	ICRISAT-KN	G115	Danyar Bana	IAR-NG	G190	Kaura - 2	IAR-NG
G41	12KNICSV-252	ICRISAT-KN	G116	Jar Kaura	IAR-NG	G191	Kaura Borno	IAR-NG
G42	12KNICSV-107-1	ICRISAT-KN	G117	ICNSL2014-022-8	IAR-NG	G192	Fara Bauchi	IAR-NG
G43	CAPARLKSG20150280	ICRISAT-KN	G118	ICNSL2014-044-1	IAR-NG	G193	Mai Bako Kono	IAR-NG
G44	CAPARLGSG2015-0058	ICRISAT-KN	G119	Yar Lazau	IAR-NG	G194	Kadil	IAR-NG
G45	12KNICSV-296-1	ICRISAT-KN	G120	Gagarau - 4	IAR-NG	G195	Bahausa	IAR-NG
G46	CAPARLGSG2015-0055	ICRISAT-KN	G121	Kaura Awangala	IAR-NG	G196	Baba Diya 1	IAR-NG
G47	CAPARLGSG20150206	ICRISAT-KN	G122	Kaura Black Glume-1	IAR-NG	G197	Shinkawa	IAR-NG
G48	ICNSL2014-027-2	ICRISAT-KN	G123	Masakwa	IAR-NG	G198	Buk Wakana	IAR-NG
G49	Macia	ICRISAT-KN	G124	Makari	IAR-NG	G199	Yar Burunduzu	IAR-NG
G50	KAT 487	ICRISAT-KN	G125	CAPARLGSG2015-0057	IAR-NG	G200	Buhu Banza 1	IAR-NG
G51	KL-1	ICRISAT-KN	G126	Jan Kaura 1	IAR-NG	G201	Ako Variety	IAR-NG
G52	Samsorg 45a	ICRISAT-KN	G127	Dangama Wulchichi	IAR-NG	G202	Buhu Banza 2	IAR-NG
G53	CAPARLGSG20150124	ICRISAT-KN	G128	Bassa Dawa	IAR-NG	G203	Basharanbiya	IAR-NG
G54	NR 71151	ICRISAT-KN	G129	ICNSL2014-023-5	IAR-NG	G204	Tsawan Zakara	IAR-NG
G55	ICNSL2014-026-9	ICRISAT-KN	G130	S7-LATA/RIB/BC1-1-7-V	IAR-NG	G205	Pato	USDA-ARS, NPGS
G56	CSRO1	ICRISAT-KN	G131	Yar Labe	IAR-NG	G206	Jawar	USDA-ARS, NPGS

Table 3.1: Continued.

Code	Genotype	Source	Code	Genotype	Source	Code	Genotype	Source
G57	CSRO2	ICRISAT-KN	G132	Kurkura	IAR-NG	G207	Juar	USDA-ARS, NPGS
G58	Samsorg 49	ICRISAT-KN	G133	Kaura Massaba	IAR-NG	G208	GTPP7R(H)C5	USDA-ARS, NPGS
G59	Samsorg 48	ICRISAT-KN	G134	Kaura Black Glume-2	IAR-NG	G209	GPP5BR(M/H/F)C3	USDA-ARS, NPGS
G60	Samsorg 3	ICRISAT-KN	G135	Ndu Vari	IAR-NG	G210	4569	USDA-ARS, NPGS
G61	Samsorg 1	ICRISAT-KN	G136	Tunkura	IAR-NG	G211	GP11BR	USDA-ARS, NPGS
G62	Zago Red Glume - 2	ICRISAT-KN	G137	CAPARLGSG20150111-1	IAR-NG	G212	Radar	USDA-ARS, NPGS
G63	Tun Buman Maiduguri	ICRISAT-KN	G138	Fara Fara - 3	IAR-NG	G213	Zaer	USDA-ARS, NPGS
G64	ICNL2014 026-8	ICRISAT-KN	G139	Dunkurau	IAR-NG	G214	GPP4BR(H)C5	USDA-ARS, NPGS
G65	Mace Da Kunya	ICRISAT-KN	G140	Bantako Mai Baiki Kono	IAR-NG	G215	ICSV 145	USDA-ARS, NPGS
G66	Agu Akunu	ICRISAT-KN	G141	ICNSL2014-024-7	IAR-NG	G216	P9401	USDA-ARS, NPGS
G67	Yulu Shinkafa	ICRISAT-KN	G142	Mori Shabal	IAR-NG	G217	P9402	USDA-ARS, NPGS
G68	Pam Para - 2	ICRISAT-KN	G143	Yar Jargada	IAR-NG	G218	IS 8264	USDA-ARS, NPGS
G69	Lisha Lisha	ICRISAT-KN	G144	Kaura Short Panicle- 1	IAR-NG	G219	IS 8265	USDA-ARS, NPGS
G70	Fara Fara Mai-Shaho	ICRISAT-KN	G145	Keres	IAR-NG	G220	IS 8266	USDA-ARS, NPGS
G71	Takumbo	ICRISAT-KN	G146	Kaura Black Glume-3	IAR-NG	G221	IS 8267	USDA-ARS, NPGS
G72	Sambulmu- 3	ICRISAT-KN	G147	Geddawaki Panguga	IAR-NG	G222	IS 8268	USDA-ARS, NPGS
G73	Zago Black Glume	ICRISAT-KN	G148	Koma	IAR-NG	G223	Wiley	USDA-ARS, NPGS
G74	Farin Illo	ICRISAT-KN	G149	CAPARLGSG20150114-1	IAR-NG	G224	Deer	USDA-ARS, NPGS
G75	Fara Fara Kyal-Kyal	ICRISAT-KN	G150	Fate Fate	IAR-NG	G225	RTX432	USDA-ARS, NPGS

ACCI = African Centre for Crop Improvement South Africa; IAR = The Institute for Agricultural Research, Samaru Nigeria; ICRISAT-KN = The International Crops Research Institute for the Semi-arid Tropics; USDA-ARS, NPGS = United States of America Department of Agriculture, Agricultural Research Service, National Plant Germplasm System

3.2.2 Experimental sites

The experiments were conducted at the University of KwaZulu-Natal's Ukulinga Research and Training Farm (29°24′E, 30°24′S, altitude 845 m.a.s.l.) and Controlled Environment Facility (CEF) in Pietermaritzburg, South Africa (29°62′62″S; 30°40′34″E). Pietermaritzburg is characterized by warm to hot summers with a mean monthly maximum temperature of 26.4 °C in February, whereas winters are mild with occasional frost and a mean monthly minimum temperature of 8.8 °C in July (Fynn and O'Connor 2005). The greenhouse experiment was designed to resemble those of a warm subtropical climate; therefore, the meteorological conditions in the CEF were semi-controlled and the temperatures were set at ~18/33°C, day/night, and the relative humidity ranging between 60 and 80%.

3.2.3 Experimental design and cultural practices

The two hundred and twenty-five (225) sorghum genotypes were evaluated under non-stressed (NS), pre-anthesis drought stress (PreADS), and post-anthesis drought stress (PoADS) conditions under field and greenhouse environments using a 15 × 15 alpha lattice design with two replicates. The three water regimes and two environments resulted in six testing environments, namely: greenhouse and non-stressed (E1); greenhouse and pre-anthesis drought stress (E2); greenhouse and post- anthesis drought stress (E3); field and non-stressed (E4); field and pre-anthesis drought stress (E5); field and post-anthesis drought stress (E6). Planting was carried out during the summer cropping season (October to March) in 2019/2020.

Under the greenhouse environment, four seeds of each variety were sown in 5 L capacity plastic pots (upper diameter: 30 cm, lower diameter: 20 cm, depth: 28 cm) filled with 4 kg of Gromor potting media. Plants were thinned out to two plants per pot two weeks after emergence. The plants were fertilized with Agchem hydroponic water-soluble fertilizer with the following nutrient compositions: 2:1:2 (nitrogen 175 g/kg, phosphorus 85 g/kg and potassium 174 g/kg). The plants received optimum fertigation four times a day for 3 min.

Under the field environment at Ukulinga, a tunnel was constructed using a steel frame covered by a 0.1 mm thick transparent polyethene bird net to prevent bird damage. It had a centre height of 3.00 m and was 0.8 m high at the open sides (40 m long and 10 m wide). Sorghum plants were

planted in ridges on a two-row of 3 m plot, with 30 cm intra-row and 70 cm inter-row spacing. Each ridge was covered with polyethene mulch, and a surface drip irrigation system was installed down the center. Two seeds were planted and thinned to one plant two weeks after emergence. Osmocote® slow-release fertilizer (Dynatrade, Johannesburg South Africa) was directly applied in the field before sowing. The fertilizer was applied at the following rates: 120 kg/ha of urea (18% N), 60 kg/ha superphosphate (6%, P_2O_5), and 60 kg/ha potassium chloride (12% K_2O). To monitor soil moisture content under field conditions two tensiometer sensors (Decagon Ech10HS, Pullman WA USA) were inserted at two depth zones: above, at the active root zone, and below the root zone at depths of 250 mm and 500 mm, respectively. The sensors recorded field capacity and permanent wilting point values at 22% and 8% volumetric moisture content, respectively.

Under both field and greenhouse environments, pre- and post-anthesis drought stress were imposed, according to Reddy et al., (2009). PreADS was imposed at growth stage 3 (when about one-third of the total leaf area has fully developed) and continued to stage 6 (half bloom stage), at which half of the plants in the plot have flowered (Vanderlip, 1993). PoADS was imposed by withdrawing irrigation during the booting stage approximately 45 days after sowing (Vanderlip, 1993). In our case, PoADS was imposed between 90 and 100 days after sowing in the greenhouse and between 95 and 105 days in the field. Weed control was performed manually, whereas sugarcane aphid [*Melanaphis sacchari* (Zehntner)] was controlled by spraying chlorpyrifos (Avima SA) at a recommended rate of 1 mL per 100 litres of water.

3.2.4 Data collection

The grain yield per plot (GY), measured in kilograms per plot, was gathered within an environmental plot. This data was collected by selecting a random sample of 10–15 plants from the inner-middle rows of each plot. The yield data, represented in kilograms per plot, was then extrapolated to estimate the potential yield per hectare. This estimation was achieved through the following formula: Grain Yield (in kg/ha) = (Yield per plot in kilograms × 10,000) / Plot size in square meters and converted to metric tons per hectare (t/ha). Under greenhouse conditions, GY was determined by harvesting all sorghum panicles within each plot. The size of the plot was defined using the formula for the area of a circle: $A = \pi r^2$. This plot size calculation served as the foundation for determining the grain yield per individual plot. Subsequently, the data was corrected

to account for a moisture content of 12.5%. The outcome was initially expressed in plot/kg and subsequently converted to t/ha.

3.2.5 Data analysis

3.2.5.1 BLUP and BLUE estimates for grain yield

Best linear unbiased estimates (BLUEs) and best linear unbiased predictors (BLUPs) for grain yield were calculated using META-R software version 6.0 (Alvarado et al., 2020).

The following linear model was used for combined analysis based on the alpha lattice design procedure:

$$\bar{Y}_{ijk} = \mu + Env_i + Rep_j(Env_i) + Block_k(Env_i Rep_j) + Gen_l + Env_i \times Gen_l + \varepsilon_{ijkl} \quad (1)$$

Where: $\bar{Y}_{ijk}$ = the yield of the *i*th genotype in the *j*th environment, μ is the overall mean, Env_i = the effects of the *i*th environment, Rep_j = the effect of the *j*th replication, $Rep_j\ (Env)_I$ = the effect of the *jth* replicate within *i*th environment, $Block_k$ ($Env_i Rep_j$) is the effect of the *k*th incomplete block within the *i*th environment and *j*th replicate, Gen_l = the effect of the *k*th genotype, and ε_{ijk} = the residual/error terms associated with *i*th environment, *j*th replications, and *k*th genotype.

The replications and blocks were treated as fixed factors, whereas genotypes, environment, and interactions were treated as random (Sabadin et al., 2012; Alvarado et al., 2020).

3.2.6 Drought tolerance/susceptibility indices

Based on the BLUPs data summary, the following10 selection indices of drought tolerance were computed (Table 3.2): tolerance index (TOL), mean productivity (MP), harmonic mean (HM), stress susceptibility index (SSI), geometric mean productivity (GMP), stress tolerance index (STI), yield index (YI), yield stability index (YSI), modified stress tolerance index I (K_1STI), and modified stress tolerance index II (K_2STI).

Table 3.2: Drought tolerance/susceptibility indices used to evaluate 225 African sorghum genotypes.

S/No	Drought Tolerance Index	Abbreviation	Equation [1]	References
1	Tolerance index	TOL	$Y_p - Y_s$	Rosielle and Hamblin, 1981
2	Mean productivity	MP	$(Y_s + Y_p)/2$	Rosielle and Hamblin, 1981
3	Harmonic mean	HM	$\frac{2(Y_P \times Y_s)}{(Y_p - Y_s)}$	Jafari et al., 2009
4	Stress susceptibility index	SSI	$\frac{1-\left(Y_s/Y_p\right)}{1-\left(\overline{Y}_s/\overline{Y}_p\right)}$	Fisher and Maurer, 1978
5	Geometric mean productivity	GMP	$\sqrt{(Y_p \times Y_s)}$	Schneider et al., 1997
6	Stress tolerance index	STI	$\frac{(Y_p - Y_s)}{(\overline{Y}_p)^2}$	Schneider et al., 1997
7	Yield index	YI	$\frac{Y_s}{\overline{Y}_s}$	Gavuzzi et al., 1997
8	Yield stability index	YSI	$\frac{Y_s}{Y_p}$	Bouslama and Schapaugh, 1984
9	Modified stress tolerance index	MSTI/ K_1STI	$\left(\frac{{Y_p}^2}{\overline{Y}_p{}^2}\right) \times \left[(Y_p + Y_S)/\overline{Y}_p^2\right]$	Farshadfar and Sutka, 2003
10	Modified stress tolerance index	MSTI/ K_2STI	$\left(\frac{{Y_s}^2}{\overline{Y}_s{}^2}\right) \times \left[(Y_p + Y_S)/\overline{Y}_p^2\right]$	Farshadfar and Sutka, 2003

Y_s and Y_p = stress and optimal (potential) grain yield of a given genotype, respectively. $\overline{Y}_s$ and $\overline{Y}_p$ =average grain yield of all genotypes under stress and nonstressed conditions, respectively. [1] Mathematical formula of drought tolerance/susceptibility indices.

3.2.7 Scatterplots and regression of grain yield under non-stressed and drought-stressed conditions

Biplots were constructed based on BLUPs for grain yield under NS vs PreADS and NS vs PoADS for field and greenhouse environments and across each drought condition and environment. This allowed grouping the sorghum genotypes for different levels of drought tolerance using the ggplot2 package in R version 4.1.0 (R Core Team 2021). According to Fernandez (1992), the scatterplots

present intersecting lines through mean values for grain yield under non-stress condition vs grain yield under drought-stress condition to aid the identification of genotypes possessing four groups of drought tolerance, namely: Group A, which comprises genotypes expressing high grain yield under both non-stress and drought-stress conditions; Group B genotypes which comprises genotypes which perform favourably only in non-stress conditions; Group C genotypes which are relatively higher performers under drought stress conditions; and Group D genotypes which are low yielders under both non-stress and drought-stress conditions.

Simple linear regression models were fitted using the ggplot2 package in R to determine the relationship between grain yield among the tested sorghum genotypes under NS, PreADS, and PoADS conditions in greenhouse and field environments. Regression model diagnosis (e.g., fitted vs residual and quantile-quantile (QQ) plots) was performed in R using the ggfortify package (Horikoshi and Tang, 2016; Tang et al., 2016).

3.2.8 Ranking genotypes for drought tolerance

To determine the most desirable drought-tolerant genotype based on drought tolerance indices, the mean rank and standard deviation of ranks were calculated according to Farshadfar et al., (2011) using the following relationship formula:

Rank Sum (RS) = Rank Mean ($\bar{R}$) + Standard Deviation of Rank (SDR) (2)

Standard deviation of rank (SDR) was measured as:

$$SDR = \sqrt{S_i^2} = \frac{\sum_{i=1}^{m} \left(R_{ij} - \bar{R}_i\right)^2}{n-1} \quad (3)$$

Where: S = sample standard deviation, n = number of observations, R_{ij} =the rank of X_{ij} within the jth environment, $\bar{R}_i$ = mean rank across all environments for the ith genotype.

3.2.9 AMMI analysis

AMMI analysis was carried out using Genstat 20th edition (Payne et al., 2017). The AMMI analysis fits additive effects due to genotypes (G) and environments (E) by the usual additive analysis of variance procedure and then fits multiplicative effects for GEI by principal components analysis (PCA). According to Gauch (2013), model diagnosis is useful to determine the best

AMMI model family for a given data set. It is recommended to use the F_R test (Cornelius, 1993) to evaluate model diagnostics and identify significant interaction principal components (IPCs) in the AMMI model with AMMISOFT software for yield trial data analysis. The AMMI model is as follows:

$$\bar{Y}_{ijk} = \mu + G_i + E_j + \sum_{k=1}^{m} \lambda_k \sigma_{ik} \gamma_{jk} + \rho_{ij} \quad (4)$$

Where: $\bar{Y}_{ijk}$ = the yield of the *i*th genotype in the jth environment, μ = the grand mean, G_i = the mean of the *i*th genotype minus the grand mean, E_j = the mean of the *j*th environment minus the grand mean, λ_k = the square root of the eigenvalue of the *k*th IPCA axis, σ_{ik} and γ_{jk} = the principal component scores for IPCA axis *k* of the *i*th genotypes and the j[th] environment, and ρ_{ij} = the deviation from the model.

3.2.10 AMMI stability value analysis

AMMI stability value (ASV) was calculated to quantify and rank genotypes in terms of yield stability using the formula suggested by Purchase et al., (2000) as follows:

$$AMMI\ Stabilty\ Value\ (ASV) = \sqrt{\left[\frac{SSIPCA1}{SSIPCA2}(IPCA1score)\right]^2 + [IPCA2score]^2} \quad (5)$$

Where: *SS* = Sum of squares; *IPCA*1 = interaction principal component analysis axis 1; *IPCA*2 = interaction principal component analysis axis 2.

The larger the IPCA score, either in negative or positive direction, the more specifically adapted a genotype is to specific environments. Smaller ASV scores indicate a more stable genotype across environments, whereas larger ASV values indicate unstable performance (Purchase, 1997). AMMI-1 biplot was constructed based on the genotype and environment mean yields and their IPCA1 scores to characterize the GEI.

3.3 Results

3.3.1 BLUPs and BLUEs for grain yield among sorghum genotypes evaluated under non-stressed and drought-stressed conditions

BLUPs and BLUEs for the grain yield of the sorghum genotypes under six test environments are presented in Table 3.3. Under test environment E1 (greenhouse environment, NS condition), 52.9% (119 genotypes) of the test genotypes recorded yields greater than the mean grain yield (3.34 t/ha). The grain yield ranged from 1.31 t/ha for G179 (Kaura– 1) to 5.41 t/ha for G9 (Yar Gumel). Under environment E1, 32 genotypes recorded a grain yield >4.50 t/ha, and the top yielders included G9 (5.41 t/ha), G144 (5.15 t/ha), G123 (4.99 t/ha), G180 (4.93 t/ha), G119 (4.93 t/ha), and G15 (4.87 t/ha). Under a greenhouse environment and a PreADS condition (Environment E2), 48.9% (110 genotypes) of the genotypes recorded values greater than the mean (1.76 t/ha), which varied from 0.70 t/ha for G30 (12KNICSV-297-2) to 2.66 t/ha for G56 (CSRO1). Genotypes G56, G106, G102, G63, G129, G158, and G120 were top yielders under E2 recording grain yields of >2.40 t/ha. Under test environment E2, six genotypes recorded a grain yield <1.0 t/ha, whereas 151 genotypes recorded a grain yield ranging from 1.00 to 1.99 t/ha, and 68 genotypes had a grain yield of >2.0 t/ha. Under test environment E3 (greenhouse and PoADS), 49% (112 genotypes) of the test genotypes recorded grain yields greater than the mean grain yield of 2.46 t/ha. Top yielders with grain yield values of >3.50 t/ha under E3 included the following genotypes: G144, G115, G157, G152, G78, and G120. The worst yielders under E3 were G29, G3, and G190, which recorded grain yield of <1.00 t/ha.

The grain yield under test environment E4 (field and NS condition) varied from 1.35 t/ha for G3 (Gadam) to 6.71 t/ha for G109 (Yalai). The grand mean yield was 4.05 t/ha across the test genotypes. Of the test genotypes, 52.4% (118 genotypes) recorded grain yields greater than the mean (4.05 t/ha). Genotypes G109, G131, G104, G144, G105, G127, and G114 were the top yielders with >4.05 t/ha. The lowest yielder under E4 was G3, which recorded grain yield of <1.50 t/ha. Under test environment E5 (field and PreADS), 53.3% (120 genotypes) of the genotypes recorded a grain yield of >1.75 t/ha, such as G56, G152, G182, G157, G63, G194, and G71. Furthermore, 10 genotypes recorded a grain yield <1.0 t/ha, whereas 144 genotypes recorded grain yields ranging from 1 to 1.99 t/ha, and 71 genotypes recorded grain yields >2.0 t/ha. Under environment E6 (field and PoADS), 52.0% (117 genotypes) of the test genotypes recorded a mean

grain yield of 2.68 t/ha. Genotype G29 (12KNICSV-293) recorded the lowest grain yield (0.78 t/ha), whereas G126 (Jan Kaura 1) recorded the highest grain yield of 4.49 t/ha. Only three genotypes recorded a grain yield <1.0 t/ha, 44 genotypes recorded a grain yield ranging from 1 to 1.99 t/ha, and 178 genotypes recorded a grain yield >2.0 t/ha. Across testing environments, 52.9% (119 genotypes) recorded a grain yield greater than the grand mean (2.68 t/ha). The highest grain yield recorded was at 3.91 t/ha for G144 (Kaura Short Panicle-1) and 3.86 t/ha for G56 (CSRO1) which were above the mean grain yield (2.68 t/ha). The lowest grain yield across environments were recorded for genotype G3 (Gadam) at 1.01 t/ha and G100 (AS 97) at 1.10 t/ha.

Overall, drought stress (PreADS and PoADS) reduced grain yields to varying degrees in all sorghum genotypes. PreADS caused a severe yield reduction of 75% for G30 (12KNICSV-297-2) followed by G80 (AS 71) with 74.3%. Under the PoADS, G81 (E 119) and G200 (Buhu Banza 1) recorded yield reductions of 64.9 and 60.1%, respectively, across test environments. The extent of grain yield reduction differed under greenhouse and field environments. Yield loss were more detrimental under PreADS than PoADS compared with the NS condition in a greenhouse environment. PreADS (E2) led to reduced grain yield by 47.5% and PoADS (E3) by 26.3%. PreADS (E5) and PoADS (E6) reduced grain yields by 56.8 and 33.4% in the field environment, respectively.

Table 3.3: Best linear and unbiased predictions (BLUPs) and best linear and unbiased estimates (BLUEs) of 225 grain sorghum genotypes grown under non-stressed conditions and with stress at pre- and post-anthesis among six test environments

Genotype	E1		E2		E3		E4		E5		E6		OVERALL	
	BLUPs	BLUEs	BLUPs	BLUEs	BLUPs	BLUEs	BLUPs	BLUEs	BLUPs	BLUEs	BLUPs	BLUEs	BLUPs	BLUEs
G1	3.45	3.47	2.16	2.27	2.80	2.83	3.85	3.85	2.22	2.30	2.85	2.86	2.90	2.93
G2	4.39	4.53	1.49	1.42	3.02	3.07	5.10	5.15	1.53	1.50	3.19	3.22	3.11	3.15
G3	1.41	1.16	0.85	0.60	0.89	0.77	1.35	1.23	0.76	0.60	0.88	0.77	1.01	0.85
G4	2.56	2.46	1.29	1.16	1.85	1.80	2.73	2.67	1.25	1.17	1.87	1.82	1.92	1.85
G5	4.21	4.32	1.46	1.37	2.21	2.19	4.82	4.86	1.45	1.40	2.26	2.23	2.72	2.73
G6	4.28	4.40	2.21	2.34	2.38	2.38	4.86	4.90	2.28	2.36	2.41	2.40	3.09	3.13
G7	4.07	4.17	1.93	1.98	2.40	2.39	4.70	4.74	2.03	2.08	2.53	2.52	2.95	2.98
G8	4.66	4.84	2.45	2.65	3.69	3.79	5.04	5.09	2.53	2.66	3.75	3.81	3.71	3.81
G9	5.41	5.69	1.96	2.02	2.43	2.43	6.09	6.18	2.00	2.04	2.46	2.45	3.40	3.47
G10	4.68	4.86	1.65	1.62	2.66	2.68	5.39	5.46	1.67	1.66	2.73	2.73	3.12	3.17
G11	4.06	4.15	2.01	2.09	2.30	2.29	4.59	4.61	2.06	2.11	2.33	2.31	2.91	2.93
G12	2.59	2.49	1.32	1.20	1.39	1.31	2.88	2.83	1.33	1.26	1.45	1.38	1.82	1.74
G13	4.55	4.71	1.91	1.96	2.70	2.72	4.91	4.95	1.94	1.97	2.73	2.73	3.13	3.17
G14	3.59	3.62	1.60	1.55	2.41	2.41	3.94	3.94	1.59	1.56	2.44	2.43	2.59	2.58
G15	4.87	5.07	1.83	1.85	3.22	3.28	5.62	5.69	1.87	1.89	3.31	3.35	3.45	3.52
G16	4.45	4.59	1.52	1.45	2.74	2.77	5.05	5.10	1.51	1.47	2.79	2.80	3.00	3.03
G17	3.08	3.05	1.46	1.38	1.75	1.70	3.49	3.46	1.49	1.45	1.84	1.79	2.18	2.14
G18	4.71	4.89	1.83	1.86	2.03	2.00	5.10	5.15	1.85	1.87	2.04	2.01	2.93	2.96
G19	2.79	2.72	1.48	1.40	1.26	1.17	3.00	2.95	1.46	1.41	1.26	1.18	1.88	1.80
G20	3.65	3.69	1.64	1.61	2.12	2.10	4.13	4.14	1.65	1.64	2.17	2.14	2.56	2.55
G21	2.45	2.34	1.31	1.19	1.12	1.02	2.65	2.59	1.27	1.20	1.12	1.03	1.65	1.56
G22	2.46	2.35	1.38	1.28	1.89	1.84	2.73	2.67	1.40	1.35	1.98	1.94	1.97	1.90
G23	3.92	4.00	1.42	1.33	2.07	2.04	4.20	4.21	1.39	1.34	2.09	2.05	2.51	2.49
G24	2.26	2.13	1.36	1.25	1.13	1.03	2.39	2.32	1.33	1.27	1.13	1.04	1.61	1.50

Table 3.3: Continued

Genotype	E1		E2		E3		E4		E5		E6		OVERALL	
	BLUPs	**BLUEs**	**BLUPs**	**BLUEs**	**BLUPs**	**BLUEs**	**BLUPs**	**BLUEs**	**BLUPs**	**BLUEs**	**BLUPs**	**BLUEs**	**BLUPs**	**BLUEs**
G25	3.06	3.02	2.24	2.37	2.58	2.59	3.42	3.40	2.33	2.42	2.65	2.65	2.73	2.74
G26	2.72	2.64	1.12	0.94	1.51	1.44	2.98	2.93	1.06	0.95	1.52	1.46	1.81	1.72
G27	3.47	3.49	1.05	0.86	2.20	2.18	3.97	3.97	1.02	0.90	2.32	2.30	2.31	2.28
G28	4.86	5.06	1.36	1.25	2.50	2.50	5.27	5.33	1.32	1.26	2.53	2.52	2.96	2.98
G29	1.69	1.48	0.89	0.65	0.79	0.66	1.71	1.61	0.80	0.65	0.78	0.67	1.10	0.95
G30	2.48	2.36	0.70	0.40	1.09	0.99	2.72	2.66	0.60	0.41	1.10	1.01	1.42	1.30
G31	3.30	3.29	1.32	1.20	2.29	2.28	3.67	3.65	1.29	1.21	2.32	2.30	2.35	2.32
G32	3.75	3.81	1.71	1.70	2.45	2.45	4.32	4.34	1.78	1.79	2.59	2.58	2.77	2.78
G33	1.72	1.51	1.02	0.82	1.07	0.96	1.70	1.60	0.95	0.83	1.06	0.97	1.25	1.11
G34	1.62	1.39	1.08	0.89	1.04	0.93	1.63	1.52	1.01	0.90	1.03	0.94	1.23	1.09
G35	3.15	3.13	1.19	1.03	1.38	1.30	3.53	3.51	1.15	1.05	1.41	1.33	1.96	1.89
G36	2.43	2.31	1.63	1.60	1.82	1.78	2.63	2.57	1.63	1.62	1.84	1.79	2.01	1.94
G37	3.30	3.29	1.73	1.73	1.92	1.88	3.75	3.74	1.81	1.82	2.02	1.99	2.43	2.41
G38	3.91	3.99	1.76	1.77	2.68	2.70	4.19	4.20	1.77	1.78	2.71	2.72	2.84	2.86
G39	4.62	4.79	1.87	1.91	2.75	2.77	5.15	5.21	1.90	1.93	2.79	2.80	3.18	3.23
G40	4.19	4.30	1.99	2.05	2.70	2.72	4.80	4.83	2.04	2.09	2.77	2.78	3.09	3.13
G41	2.73	2.66	1.97	2.04	1.97	1.93	3.00	2.95	2.02	2.06	1.99	1.95	2.30	2.26
G42	3.73	3.78	1.97	2.03	2.93	2.97	4.29	4.30	2.08	2.14	3.10	3.12	3.02	3.05
G43	2.53	2.43	1.88	1.91	2.38	2.37	2.62	2.56	1.90	1.92	2.40	2.39	2.30	2.26
G44	2.92	2.87	1.87	1.90	2.59	2.61	3.16	3.12	1.90	1.92	2.63	2.63	2.52	2.51
G45	4.56	4.72	1.91	1.95	3.21	3.27	5.25	5.31	1.96	1.99	3.30	3.34	3.36	3.43
G46	3.51	3.54	1.47	1.39	2.59	2.60	3.94	3.93	1.45	1.41	2.63	2.63	2.59	2.58
G47	3.67	3.71	2.32	2.48	3.19	3.25	4.21	4.22	2.49	2.61	3.38	3.42	3.23	3.28
G48	3.20	3.18	1.84	1.87	2.19	2.17	3.38	3.35	1.86	1.88	2.21	2.18	2.46	2.44
G49	3.08	3.04	1.61	1.57	2.51	2.52	3.34	3.31	1.60	1.58	2.55	2.54	2.45	2.43

Table 3.3: Continued

Genotype	E1		E2		E3		E4		E5		E6		OVERALL	
	BLUPs	**BLUEs**	**BLUPs**	**BLUEs**	**BLUPs**	**BLUEs**	**BLUPs**	**BLUEs**	**BLUPs**	**BLUEs**	**BLUPs**	**BLUEs**	**BLUPs**	**BLUEs**
G50	2.77	2.69	1.91	1.95	2.24	2.23	3.07	3.02	1.96	1.99	2.29	2.27	2.38	2.36
G51	2.82	2.76	2.11	2.21	2.55	2.56	3.10	3.06	2.17	2.24	2.59	2.59	2.58	2.57
G52	2.61	2.51	2.05	2.14	2.10	2.07	2.91	2.86	2.18	2.25	2.21	2.18	2.36	2.33
G53	4.55	4.72	2.39	2.58	3.10	3.15	4.92	4.96	2.47	2.59	3.13	3.16	3.45	3.53
G54	4.59	4.76	1.73	1.73	2.23	2.21	5.13	5.18	1.75	1.75	2.26	2.23	2.95	2.98
G55	3.31	3.31	2.40	2.58	2.54	2.55	3.73	3.72	2.51	2.63	2.61	2.61	2.88	2.90
G56	4.87	5.07	2.66	2.92	3.53	3.62	5.56	5.63	2.78	2.95	3.60	3.65	3.86	3.97
G57	3.03	2.99	1.52	1.45	2.85	2.88	3.42	3.39	1.56	1.53	3.00	3.02	2.55	2.54
G58	2.48	2.37	1.59	1.54	1.54	1.47	2.56	2.50	1.57	1.54	1.54	1.48	1.89	1.81
G59	3.39	3.40	2.22	2.35	2.40	2.40	3.71	3.69	2.28	2.37	2.44	2.43	2.76	2.77
G60	1.94	1.76	1.53	1.47	1.82	1.77	2.06	1.97	1.53	1.50	1.85	1.80	1.79	1.71
G61	3.12	3.10	2.04	2.12	2.44	2.44	3.47	3.44	2.09	2.15	2.47	2.46	2.62	2.62
G62	3.66	3.70	1.87	1.90	2.33	2.32	4.20	4.21	1.97	2.00	2.46	2.45	2.75	2.76
G63	3.50	3.52	2.57	2.80	3.48	3.56	3.72	3.71	2.66	2.81	3.53	3.58	3.27	3.33
G64	2.36	2.23	1.41	1.32	2.04	2.01	2.50	2.43	1.39	1.33	2.07	2.03	1.96	1.89
G65	2.44	2.32	1.84	1.87	2.42	2.42	2.67	2.61	1.88	1.91	2.48	2.47	2.30	2.26
G66	4.64	4.81	2.05	2.13	3.10	3.16	5.28	5.34	2.10	2.16	3.16	3.19	3.39	3.46
G67	2.64	2.55	1.69	1.68	2.60	2.61	2.95	2.90	1.76	1.77	2.74	2.75	2.40	2.37
G68	4.63	4.81	2.11	2.22	3.75	3.85	5.02	5.06	2.17	2.24	3.81	3.87	3.59	3.67
G69	4.82	5.02	2.12	2.23	3.46	3.54	5.39	5.46	2.18	2.25	3.52	3.57	3.59	3.68
G70	4.54	4.70	2.24	2.38	3.40	3.47	5.22	5.28	2.33	2.43	3.49	3.54	3.55	3.63
G71	4.00	4.09	2.46	2.66	2.66	2.68	4.52	4.54	2.55	2.69	2.70	2.71	3.18	3.23
G72	2.65	2.56	1.06	0.86	1.60	1.53	2.96	2.91	1.02	0.91	1.67	1.62	1.81	1.73
G73	2.32	2.19	1.24	1.10	1.79	1.74	2.38	2.30	1.19	1.10	1.80	1.75	1.78	1.69

Table 3.3: Continued

Genotype	E1		E2		E3		E4		E5		E6		OVERALL	
	BLUPs	BLUEs	BLUPs	BLUEs	BLUPs	BLUEs	BLUPs	BLUEs	BLUPs	BLUEs	BLUPs	BLUEs	BLUPs	BLUEs
G74	3.76	3.82	1.73	1.72	2.88	2.91	4.14	4.15	1.73	1.73	2.93	2.94	2.86	2.88
G75	2.19	2.04	1.42	1.33	1.64	1.58	2.37	2.29	1.41	1.36	1.57	1.50	1.77	1.68
G76	4.04	4.13	1.69	1.67	3.23	3.29	4.56	4.59	1.69	1.69	3.28	3.32	3.07	3.11
G77	4.23	4.35	1.60	1.56	3.35	3.42	4.90	4.94	1.66	1.65	3.54	3.59	3.20	3.25
G78	4.46	4.61	1.89	1.93	3.82	3.93	4.81	4.85	1.91	1.94	3.88	3.95	3.46	3.53
G79	4.12	4.22	1.61	1.57	2.72	2.74	4.56	4.58	1.60	1.58	2.76	2.77	2.89	2.91
G80	4.21	4.33	1.18	1.02	2.08	2.05	4.82	4.86	1.14	1.04	2.12	2.09	2.57	2.56
G81	3.76	3.82	1.12	0.94	1.40	1.32	4.23	4.24	1.06	0.95	1.41	1.33	2.15	2.10
G82	2.63	2.54	2.04	2.12	2.39	2.39	2.94	2.89	2.17	2.24	2.52	2.51	2.47	2.45
G83	4.37	4.51	1.91	1.97	3.72	3.82	4.71	4.75	1.94	1.98	3.78	3.84	3.41	3.48
G84	2.26	2.13	1.69	1.68	1.70	1.64	2.39	2.32	1.70	1.70	1.71	1.65	1.92	1.85
G85	2.59	2.49	1.65	1.62	2.40	2.39	2.85	2.80	1.67	1.66	2.45	2.44	2.27	2.23
G86	3.46	3.48	2.16	2.28	3.78	3.88	3.88	3.87	2.23	2.31	3.85	3.92	3.24	3.29
G87	4.23	4.35	1.96	2.02	3.31	3.38	4.90	4.94	2.07	2.13	3.51	3.56	3.33	3.39
G88	4.85	5.05	1.50	1.43	3.52	3.60	5.26	5.32	1.48	1.44	3.56	3.62	3.34	3.41
G89	3.08	3.05	1.44	1.36	2.67	2.69	3.35	3.32	1.42	1.37	2.71	2.72	2.44	2.41
G90	3.06	3.03	1.50	1.43	2.35	2.35	3.42	3.40	1.50	1.47	2.41	2.40	2.37	2.34
G91	3.25	3.24	1.90	1.95	2.64	2.66	3.62	3.60	1.94	1.97	2.69	2.69	2.68	2.68
G92	2.36	2.24	1.06	0.87	1.82	1.77	2.61	2.54	1.03	0.91	1.91	1.87	1.78	1.70
G93	2.56	2.46	1.72	1.71	1.99	1.95	2.64	2.58	1.72	1.72	2.00	1.96	2.12	2.06
G94	2.38	2.26	1.54	1.48	1.97	1.94	2.53	2.46	1.53	1.49	2.00	1.96	1.99	1.93
G95	2.37	2.25	1.89	1.92	2.14	2.11	2.59	2.52	1.93	1.96	2.18	2.16	2.20	2.15
G96	2.15	1.99	1.58	1.53	2.00	1.96	2.29	2.21	1.57	1.54	2.02	1.98	1.94	1.87
G97	2.62	2.53	1.23	1.08	1.10	0.99	2.93	2.88	1.22	1.14	1.14	1.05	1.70	1.61
G98	2.66	2.58	1.54	1.49	1.84	1.80	2.77	2.71	1.53	1.50	1.85	1.81	2.04	1.98

Table 3.3: Continued

Genotype	E1		E2		E3		E4		E5		E6		OVERALL	
	BLUPs	**BLUEs**	**BLUPs**	**BLUEs**	**BLUPs**	**BLUEs**	**BLUPs**	**BLUEs**	**BLUPs**	**BLUEs**	**BLUPs**	**BLUEs**	**BLUPs**	**BLUEs**
G99	2.00	1.83	1.73	1.73	1.72	1.66	2.08	1.99	1.75	1.75	1.73	1.68	1.85	1.77
G100	1.75	1.54	0.71	0.42	1.01	0.90	1.61	1.50	0.61	0.43	1.01	0.92	1.10	0.95
G101	3.66	3.70	2.26	2.40	2.89	2.92	4.70	4.73	1.28	1.21	2.84	2.85	2.94	2.97
G102	4.06	4.16	2.58	2.81	3.41	3.49	5.06	5.11	1.88	1.91	3.24	3.28	3.39	3.46
G103	3.41	3.42	2.13	2.23	3.04	3.09	6.10	6.20	2.25	2.33	3.39	3.43	3.38	3.45
G104	4.61	4.78	2.09	2.18	3.74	3.84	6.54	6.66	1.86	1.88	3.84	3.91	3.77	3.87
G105	4.54	4.70	2.01	2.08	3.22	3.28	6.35	6.46	2.22	2.30	3.64	3.70	3.66	3.75
G106	4.17	4.28	2.65	2.91	2.08	2.05	5.67	5.75	2.38	2.48	2.66	2.66	3.29	3.35
G107	3.88	3.95	2.04	2.12	2.89	2.93	5.15	5.20	1.40	1.34	3.16	3.19	3.08	3.12
G108	1.64	1.42	1.86	1.89	1.73	1.68	1.61	1.50	1.61	1.59	1.79	1.74	1.73	1.64
G109	4.22	4.34	1.87	1.90	2.55	2.56	6.71	6.83	1.35	1.29	2.75	2.76	3.23	3.28
G110	4.21	4.33	2.41	2.60	2.22	2.20	5.65	5.73	1.75	1.75	2.60	2.60	3.15	3.20
G111	4.62	4.79	1.82	1.84	3.39	3.47	5.02	5.07	1.41	1.36	3.46	3.50	3.28	3.34
G112	3.63	3.67	2.16	2.28	2.32	2.31	4.56	4.59	2.03	2.08	2.36	2.34	2.86	2.87
G113	1.54	1.31	1.17	1.01	1.25	1.16	1.61	1.50	1.01	0.89	1.31	1.23	1.31	1.18
G114	4.31	4.44	2.32	2.48	3.29	3.35	6.25	6.35	2.34	2.44	3.76	3.82	3.71	3.81
G115	4.32	4.45	2.01	2.08	3.97	4.09	6.15	6.25	2.15	2.22	4.24	4.33	3.80	3.90
G116	4.54	4.70	2.17	2.29	3.44	3.52	5.50	5.57	2.43	2.54	3.34	3.38	3.58	3.66
G117	4.42	4.56	1.88	1.92	3.33	3.40	5.15	5.20	1.78	1.79	3.62	3.67	3.36	3.42
G118	3.99	4.08	2.23	2.37	2.43	2.43	4.51	4.54	1.13	1.03	3.23	3.26	2.92	2.95
G119	4.93	5.14	1.67	1.64	3.64	3.73	5.63	5.70	2.10	2.16	3.72	3.79	3.60	3.69
G120	4.44	4.59	2.50	2.71	3.81	3.92	4.94	4.99	1.98	2.02	4.30	4.39	3.67	3.77
G121	3.61	3.65	1.94	2.00	2.55	2.56	3.62	3.60	1.55	1.52	2.53	2.52	2.64	2.64
G122	4.67	4.85	1.87	1.90	2.57	2.58	5.38	5.45	1.98	2.02	2.33	2.31	3.14	3.18
G123	4.99	5.21	2.16	2.28	3.52	3.61	5.80	5.88	2.21	2.28	3.26	3.30	3.66	3.76

Table 3.3: Continued

Genotype	E1		E2		E3		E4		E5		E6		OVERALL	
	BLUPs	BLUEs	BLUPs	BLUEs	BLUPs	BLUEs	BLUPs	BLUEs	BLUPs	BLUEs	BLUPs	BLUEs	BLUPs	BLUEs
G124	3.98	4.06	2.35	2.52	3.05	3.10	5.35	5.41	2.07	2.12	3.53	3.58	3.40	3.46
G125	4.17	4.28	2.07	2.16	2.89	2.92	5.63	5.71	2.33	2.43	3.50	3.55	3.43	3.51
G126	3.96	4.05	2.09	2.19	3.18	3.24	5.12	5.17	2.25	2.33	4.49	4.60	3.51	3.59
G127	4.31	4.44	1.64	1.61	3.12	3.18	6.27	6.37	1.67	1.66	4.33	4.43	3.53	3.61
G128	4.20	4.31	2.32	2.49	3.72	3.82	5.20	5.25	2.53	2.66	3.65	3.71	3.62	3.70
G129	4.77	4.97	2.51	2.73	3.32	3.39	6.21	6.31	2.00	2.04	4.17	4.26	3.84	3.95
G130	3.61	3.65	1.77	1.77	3.30	3.37	5.15	5.21	1.90	1.93	4.33	4.43	3.33	3.39
G131	3.45	3.46	1.93	1.98	2.45	2.45	6.68	6.81	1.37	1.31	4.13	4.21	3.31	3.37
G132	4.07	4.17	1.95	2.00	3.50	3.58	5.65	5.73	2.03	2.07	3.61	3.67	3.46	3.53
G133	2.72	2.64	1.52	1.45	2.31	2.30	4.73	4.76	1.84	1.86	3.05	3.08	2.68	2.68
G134	3.41	3.42	1.72	1.71	3.16	3.22	4.87	4.91	1.30	1.23	3.47	3.51	2.97	3.00
G135	1.47	1.22	1.34	1.22	1.19	1.10	1.65	1.54	0.79	0.63	1.02	0.92	1.24	1.10
G136	4.30	4.43	2.37	2.54	3.10	3.15	5.33	5.39	2.30	2.39	4.00	4.08	3.58	3.66
G137	3.55	3.58	1.98	2.05	2.53	2.54	4.27	4.28	1.40	1.35	3.47	3.51	2.86	2.88
G138	3.70	3.75	2.00	2.07	2.55	2.56	4.96	5.00	1.97	2.01	3.77	3.83	3.16	3.20
G139	4.05	4.14	1.87	1.90	3.36	3.43	5.45	5.52	1.84	1.86	3.27	3.30	3.30	3.36
G140	3.73	3.78	2.01	2.09	2.65	2.66	4.33	4.35	1.79	1.80	2.81	2.82	2.89	2.91
G141	4.25	4.37	2.37	2.55	3.63	3.73	5.02	5.06	1.84	1.85	4.12	4.20	3.54	3.63
G142	3.95	4.03	1.79	1.80	2.35	2.34	5.17	5.22	1.45	1.41	2.72	2.73	2.90	2.92
G143	4.51	4.66	2.15	2.26	3.41	3.48	5.67	5.75	1.86	1.88	3.78	3.84	3.56	3.64
G144	5.15	5.39	1.91	1.96	3.98	4.10	6.37	6.48	2.11	2.17	3.99	4.07	3.91	4.03
G145	3.07	3.04	2.10	2.20	2.80	2.83	4.93	4.98	2.21	2.28	3.48	3.53	3.10	3.14
G146	3.45	3.46	2.15	2.27	2.76	2.78	4.81	4.84	1.94	1.97	3.33	3.37	3.08	3.12
G147	3.49	3.52	2.14	2.25	2.74	2.76	4.61	4.64	2.05	2.10	3.03	3.05	3.02	3.05
G148	1.53	1.29	1.15	0.97	1.21	1.12	1.61	1.50	0.68	0.51	1.10	1.01	1.20	1.07

Table 3.3: Continued

Genotype	E1		E2		E3		E4		E5		E6		OVERALL	
	BLUPs	**BLUEs**	**BLUPs**	**BLUEs**	**BLUPs**	**BLUEs**	**BLUPs**	**BLUEs**	**BLUPs**	**BLUEs**	**BLUPs**	**BLUEs**	**BLUPs**	**BLUEs**
G149	4.80	4.99	2.14	2.24	3.34	3.41	5.55	5.62	1.78	1.79	3.88	3.95	3.58	3.67
G150	3.86	3.93	2.24	2.38	3.13	3.18	5.34	5.40	2.04	2.09	3.35	3.39	3.33	3.39
G151	1.90	1.72	1.15	0.98	1.31	1.22	3.59	3.57	1.57	1.54	2.74	2.74	2.02	1.96
G152	4.18	4.29	2.18	2.30	3.83	3.94	5.54	5.61	2.72	2.88	3.79	3.86	3.71	3.81
G153	3.39	3.40	2.11	2.21	2.68	2.70	4.50	4.53	1.43	1.38	3.55	3.60	2.94	2.97
G154	2.76	2.69	1.46	1.38	2.78	2.81	4.54	4.56	1.34	1.28	2.87	2.88	2.60	2.60
G155	1.35	1.09	1.16	0.99	1.23	1.14	1.61	1.50	1.20	1.11	1.14	1.05	1.28	1.15
G156	3.25	3.24	2.08	2.17	3.01	3.05	3.51	3.49	1.88	1.91	2.67	2.67	2.75	2.75
G157	4.50	4.66	2.25	2.39	3.86	3.97	5.67	5.75	2.70	2.86	3.93	4.01	3.83	3.94
G158	4.07	4.17	2.50	2.72	3.27	3.34	6.08	6.18	1.79	1.80	3.64	3.70	3.57	3.65
G159	3.41	3.43	2.13	2.25	3.01	3.06	3.57	3.55	2.14	2.21	2.53	2.52	2.82	2.83
G160	2.04	1.87	1.40	1.30	1.64	1.58	3.75	3.74	2.15	2.22	2.71	2.72	2.27	2.23
G161	2.54	2.44	1.42	1.34	2.18	2.16	4.70	4.73	1.81	1.82	3.24	3.28	2.63	2.63
G162	4.74	4.93	1.92	1.97	3.20	3.26	5.50	5.57	1.87	1.90	3.55	3.60	3.46	3.53
G163	1.53	1.29	0.94	0.71	1.92	1.88	3.38	3.35	1.39	1.34	2.23	2.21	1.87	1.79
G164	2.92	2.86	1.84	1.87	2.77	2.79	4.62	4.65	1.91	1.93	3.07	3.10	2.85	2.86
G165	2.97	2.92	1.77	1.78	2.67	2.69	4.47	4.49	2.37	2.47	3.72	3.79	2.99	3.02
G166	3.72	3.77	1.53	1.47	3.27	3.33	5.10	5.15	1.97	2.00	3.33	3.37	3.14	3.18
G167	4.26	4.39	2.35	2.52	3.07	3.12	5.60	5.68	2.20	2.27	4.23	4.32	3.62	3.71
G168	3.45	3.47	1.53	1.47	2.16	2.14	3.13	3.09	1.20	1.12	2.59	2.58	2.34	2.31
G169	2.45	2.33	1.52	1.45	2.06	2.03	5.41	5.47	2.26	2.34	3.72	3.78	2.88	2.90
G170	1.36	1.10	1.10	0.91	1.78	1.73	1.61	1.50	1.10	0.99	1.41	1.33	1.38	1.26
G171	2.55	2.45	1.44	1.35	2.65	2.67	5.38	5.45	2.37	2.47	4.02	4.10	3.04	3.08
G172	4.32	4.45	1.99	2.06	3.11	3.16	5.67	5.74	1.78	1.78	3.38	3.43	3.37	3.43
G173	4.26	4.39	1.96	2.02	3.07	3.12	3.39	3.36	1.84	1.85	2.43	2.42	2.84	2.86

Table 3.3: Continued

Genotype	E1		E2		E3		E4		E5		E6		OVERALL	
	BLUPs	**BLUEs**	**BLUPs**	**BLUEs**	**BLUPs**	**BLUEs**	**BLUPs**	**BLUEs**	**BLUPs**	**BLUEs**	**BLUPs**	**BLUEs**	**BLUPs**	**BLUEs**
G174	3.92	4.00	1.71	1.70	2.71	2.73	4.58	4.61	1.29	1.22	3.15	3.18	2.88	2.90
G175	4.04	4.13	1.75	1.75	2.37	2.36	4.97	5.01	2.04	2.09	3.00	3.02	3.03	3.06
G176	4.20	4.32	1.62	1.59	3.14	3.19	5.41	5.47	2.08	2.14	3.59	3.65	3.33	3.39
G177	3.57	3.61	1.72	1.71	2.30	2.29	3.48	3.45	1.34	1.28	2.92	2.93	2.55	2.54
G178	4.59	4.76	2.09	2.18	3.79	3.89	5.39	5.46	2.54	2.67	3.61	3.67	3.67	3.77
G179	1.31	1.05	1.18	1.02	1.26	1.17	1.61	1.50	1.34	1.27	1.25	1.17	1.32	1.19
G180	4.93	5.14	1.76	1.76	2.36	2.35	3.73	3.71	1.72	1.71	2.55	2.54	2.85	2.87
G181	3.65	3.69	2.18	2.31	2.80	2.83	4.75	4.79	2.23	2.31	3.52	3.57	3.20	3.25
G182	4.26	4.39	2.32	2.48	3.00	3.04	4.37	4.39	2.72	2.88	2.89	2.91	3.29	3.35
G183	3.38	3.38	2.09	2.19	2.66	2.68	4.85	4.89	1.60	1.57	3.08	3.10	2.94	2.97
G184	4.22	4.33	2.42	2.60	3.15	3.21	5.59	5.67	2.28	2.37	3.97	4.04	3.61	3.70
G185	4.57	4.73	2.21	2.34	3.42	3.50	5.35	5.42	2.17	2.24	4.07	4.15	3.63	3.73
G186	3.35	3.36	1.90	1.94	2.40	2.39	3.62	3.61	1.23	1.14	2.87	2.88	2.56	2.55
G187	3.31	3.31	2.18	2.30	2.79	2.82	4.24	4.25	2.34	2.43	3.69	3.75	3.10	3.14
G188	3.51	3.53	2.05	2.14	2.15	2.13	3.50	3.48	1.96	2.00	2.44	2.42	2.62	2.61
G189	3.68	3.73	2.13	2.24	2.73	2.76	5.30	5.36	2.51	2.64	3.03	3.05	3.24	3.29
G190	1.36	1.10	0.92	0.69	0.91	0.79	1.61	1.50	1.69	1.68	1.54	1.48	1.33	1.21
G191	2.48	2.37	1.34	1.23	2.13	2.10	2.74	2.68	1.10	1.00	1.34	1.27	1.85	1.77
G192	3.26	3.25	1.45	1.37	2.32	2.31	3.94	3.94	1.79	1.80	2.32	2.30	2.51	2.49
G193	2.29	2.15	1.31	1.19	1.54	1.47	2.23	2.15	1.44	1.40	1.80	1.75	1.77	1.68
G194	3.73	3.79	2.12	2.22	3.41	3.49	4.76	4.80	2.57	2.70	3.51	3.56	3.36	3.42
G195	1.86	1.66	1.63	1.59	1.42	1.34	4.27	4.29	1.96	2.00	2.51	2.50	2.27	2.23
G196	2.66	2.57	1.75	1.75	1.99	1.95	3.71	3.69	1.85	1.87	2.30	2.28	2.38	2.35
G197	3.54	3.57	1.52	1.46	2.44	2.44	3.43	3.41	1.12	1.02	2.17	2.14	2.37	2.34
G198	3.05	3.01	1.93	1.98	2.89	2.93	3.95	3.95	1.88	1.91	3.11	3.13	2.80	2.82

Table 3.3: Continued

Genotype	E1		E2		E3		E4		E5		E6		OVERALL	
	BLUPs	BLUEs	BLUPs	BLUEs	BLUPs	BLUEs	BLUPs	BLUEs	BLUPs	BLUEs	BLUPs	BLUEs	BLUPs	BLUEs
G199	1.36	1.10	1.12	0.94	1.17	1.07	1.61	1.50	1.18	1.09	1.22	1.13	1.27	1.14
G200	3.24	3.23	1.71	1.69	1.67	1.61	4.70	4.73	1.67	1.66	1.50	1.44	2.42	2.39
G201	1.45	1.20	1.05	0.85	1.25	1.16	1.78	1.68	0.64	0.46	1.03	0.94	1.19	1.05
G202	2.63	2.54	1.47	1.40	1.65	1.59	3.50	3.48	1.65	1.64	1.79	1.74	2.11	2.06
G203	2.63	2.54	1.71	1.71	2.12	2.09	2.83	2.77	1.23	1.15	2.01	1.97	2.09	2.04
G204	2.28	2.15	1.35	1.25	1.93	1.89	3.64	3.63	1.17	1.08	2.66	2.66	2.16	2.11
G205	2.63	2.54	1.68	1.66	2.07	2.04	3.08	3.04	2.12	2.18	2.14	2.11	2.29	2.26
G206	3.02	2.98	1.66	1.64	2.07	2.04	3.98	3.98	1.72	1.72	2.30	2.28	2.46	2.44
G207	2.77	2.70	1.54	1.48	1.89	1.84	4.67	4.70	2.23	2.31	3.14	3.17	2.70	2.70
G208	2.67	2.59	1.50	1.42	1.82	1.77	4.24	4.25	2.35	2.45	3.12	3.15	2.61	2.60
G209	2.66	2.57	1.49	1.42	1.80	1.75	3.12	3.08	1.72	1.72	2.95	2.97	2.29	2.25
G210	2.15	2.00	1.41	1.31	1.63	1.57	1.61	1.50	1.22	1.14	1.43	1.36	1.58	1.48
G211	2.10	1.94	1.32	1.20	1.51	1.44	1.61	1.50	0.98	0.86	0.99	0.89	1.42	1.30
G212	2.97	2.93	1.64	1.61	2.49	2.50	2.99	2.94	1.90	1.92	3.51	3.56	2.58	2.57
G213	3.16	3.14	1.73	1.73	2.63	2.64	2.82	2.77	2.01	2.05	3.01	3.03	2.57	2.56
G214	2.18	2.02	1.25	1.11	1.45	1.38	2.73	2.67	1.30	1.23	1.58	1.51	1.74	1.65
G215	1.38	1.13	1.25	1.11	1.36	1.28	1.61	1.50	0.96	0.83	1.07	0.97	1.27	1.14
G216	2.42	2.30	1.52	1.46	1.77	1.72	3.40	3.37	2.08	2.13	2.47	2.46	2.28	2.24
G217	2.75	2.67	1.45	1.37	2.62	2.63	4.66	4.69	2.07	2.13	3.47	3.52	2.82	2.83
G218	2.79	2.72	1.81	1.83	3.18	3.24	3.73	3.72	1.32	1.26	3.39	3.44	2.70	2.70
G219	2.66	2.57	1.70	1.69	2.57	2.58	2.67	2.61	1.84	1.85	2.71	2.72	2.36	2.34
G220	2.56	2.46	1.44	1.36	1.74	1.68	4.78	4.81	1.76	1.76	2.74	2.74	2.49	2.47
G221	2.55	2.45	1.44	1.35	2.01	1.97	3.00	2.95	1.50	1.46	3.13	3.15	2.26	2.22
G222	2.06	1.90	1.35	1.24	1.26	1.17	2.77	2.72	1.04	0.92	1.24	1.16	1.62	1.52
G223	2.48	2.36	1.40	1.30	1.90	1.86	2.76	2.71	1.12	1.02	2.26	2.24	1.98	1.91

Table 3.3: Continued

Genotype	E1		E2		E3		E4		E5		E6		OVERALL	
	BLUPs	**BLUEs**	**BLUPs**	**BLUEs**	**BLUPs**	**BLUEs**	**BLUPs**	**BLUEs**	**BLUPs**	**BLUEs**	**BLUPs**	**BLUEs**	**BLUPs**	**BLUEs**
G224	2.01	1.83	1.17	1.01	1.99	1.95	2.63	2.56	1.41	1.36	2.40	2.38	1.92	1.85
G225	2.50	2.39	1.58	1.53	2.38	2.38	3.48	3.45	1.75	1.76	3.20	3.23	2.47	2.45
H^2	0.88		0.78		0.93		0.96		0.86		0.94		0.91	
$\hat{\sigma}_g^2$	1.08		0.21		0.60		1.75		0.24		0.80		0.54	
$\hat{\sigma}_{g\times e}^2$													0.24	
$\hat{\sigma}_e^2$	0.28		0.12		0.09		0.16		0.08		0.09		0.14	
Grand Mean (t/ha)	3.34		1.76		2.46		4.05		1.75		2.7		2.68	
CV (%)	29.13		23.00		30.11		31.88		26.11		32.05		13.90	
Significance (G)	**		**		**		**		**		**		***	
Significance GEI													***	

CV= coefficient of variation, G = Genotype, GEI = genotype x environment, E1=greenhouse and non-stressed, E2 = greenhouse and pre-anthesis drought stress, E3 = greenhouse and post- anthesis drought stress, E4 = Field and non-stressed, E5 = Field and pre- anthesis drought stress, E6 = Field and post-anthesis drought stress, **, *** = Significant at the 1% and 0.1% probability level respectively, H^2 = broad-sense heritability, $\hat{\sigma}_g^2$ = genotypic variance, $\hat{\sigma}_{g\times e}^2$ = GEI variance, $\hat{\sigma}_e^2$ = environmental variance. See codes of genotypes in Table 3.1.

3.3.2 Drought tolerance indices

The drought tolerance/susceptibility indices of evaluated sorghum genotypes are presented in Table 3.4. TOL under PreADS varied from 0.22 (G108) to 3.52 (G109), and 48.0% of the evaluated sorghum genotypes (108) recorded TOL values less than the grand mean (1.94) and were identified as less sensitive to PreADS. Under PoADS, G108 and G170 recorded the lowest TOL values of 0.06 and 0.07 and were identified as tolerant, whereas a high TOL value of 2.96 indicated high drought sensitivity.

Mean productivity (MP) under PreADS varied from 0.89 for G3 to 4.11 for G56. High MP values of >4 were recorded for G56 and G144, whereas genotypes G100 and G3 recorded MP values <1.00. Under PoADS, MP values varied from 4.89 (G144) to 1.06 (G3), and 49 genotypes recorded MP values >4.00 whereas 28 genotypes recorded values <2.00. Genotypes G100 (0.83) and G30 (0.96) recorded the lowest HM values under PreADS, whereas the highest values were recorded for G108 (23.89) and G63 (19.32). Under PoADS, the lowest HM values were recorded for genotypes G29 (2.48) and G3 (3.57), whereas the highest HM values were recorded for G86 (369.22) and G218 (135.93). Genotypes G108 (0.24) and G99 (0.51) recorded the lowest SSI values under PreADS compared with G30 and G100 with an SSI of >1.5. Under PoADS, the genotypes with the lowest stress sensitivity were G86 with an SSI value of 0.07 and G108 with an SSI value of 0.11, whereas G81 (2.03) and G97 (1.92) recorded the SSI highest values and were identified as drought-susceptible.

Values for GMP, under PreADS were high for G109 (1.88) and G28 (1.87), whereas genotypes G108 (0.47), G190 (0.72), and G179 (0.73) recorded the lowest values. Under PoADS, lower GMP values were recorded for G108 (0.24) and G170 (0.26) compared with higher values recorded for G9 (1.72) and G18 (1.61). Values for STI under PreADS were low for genotypes G108 (0.02), G190 (0.04), G179 (0.04), and G99 (0.04), whereas high values were recorded for genotypes G109 (0.26), G28 (0.26), G9 (0.25), G144 (0.25), and G127 (0.25). STI values under PoADS identified genotypes G108 and G170 as susceptible, recording values <0.01, and G9 as a tolerant genotype with STI values >0.20.

Under PreADS, lower YI values ≤0.30 were recorded for G201, G29, G3, G30, and G100 whereas YI values ≥1.50 were recorded for G182, G106, G152, G8, G157, G63, and G56. Under PoADS,

lower YI values ≤0.30 were recorded for G3 and G29 compared with YI values ≥1.50 for G141, G157, G120, G144, and G115.

Under PreADS, lower YSI values ≤0.30 were recorded for G28, G27, G80, G81, G100, and G30 whereas higher YSI values ≥0.70 were recorded for G95, G82, G52, G63, G99, and G108. Under PoADS, genotypes G81 (0.39), G97 (0.42), and G30 (0.42) recorded the lowest YSI values whereas genotypes G86 (0.98) and G108 (0.97) recorded the highest YSI values.

Indices such as K_1STI and K_2STI are a modification to improve the efficiency of the STI. The two indices are based on correction coefficients (K_1 and K_2) which correct the STI as a weight. As a result, K_1STI and K_2STI represent the ideal selection indices for conditions of stress and non-stress, respectively. Under PreADS, G144 (Kaura Short Panicle-1) and G9 (Yar Gumel) recorded high K_1STI values of 1.42 and 1.31, whereas G3 (Gadam) and G100 (AS 97) recorded the lowest K_1STI values of 0.02 and 0.03. Consequently, the genotypes G3 and G100, characterized by low K_1STI values, were identified as being susceptible to drought conditions. Under PoADS, high K_1STI values were recorded for G144 (1.73), G104 (1.54), and G129 (1.50), whereas genotypes with low values included G3 (0.02) and G155 (0.03). High K_2STI values were recorded to genotypes G56 (CSRO1) at 1.71 and G157 (Kaura Mai Baki Kona) at 1.37 compared with genotypes G3 (Gadam) and G100 (AS 97), which recorded the lowest K_2STI of 0.01 and 0.01, respectively, under PreADS. Under PoADS, the G3 (Gadam) genotype recorded the lowest K_2STI value of 0.12 followed by G29 (12KNICSV-293) (0.13), while high values were recorded by G144 (Kaura Short Panicle-1) (14.83), followed by G115 (Danyar Bana) (14.13) and G104 (Dan Yara) (12.95).

Table 3.4: Values of tolerance, susceptibility indices, and grain yield of the assessed sorghum genotypes under stress and non-stress conditions in greenhouse and field environments.

Code	TOL		MP		HM		SSI		GMP		STI		YI		YSI		MSTI/ K_1STI		MSTI/ K_2STI	
	PreADS	PoADS	PreADS	PoADS	PreADS	PoADS	PreADS	PoADS	PreADS	PoADS	PreADS	PoADS	PreADS	PoADS	PreADS	PoADS	PreADS	PoADS	PreADS	PoADS
G1	1.50	0.88	2.97	3.28	11.02	23.92	0.77	0.79	1.22	0.94	0.11	0.06	1 27	1.10	0.60	0.76	0.44	0.49	0.70	4.74
G2	3.06	1.57	3.16	3.90	5.01	18.68	1.24	1.11	1.75	1.25	0.22	0 11	0 93	1.21	0.35	0.67	0.75	0.92	0.40	7.19
G3	0.90	0.58	0.89	1.06	1.33	3.57	1.27	1.42	0.95	0.76	0.07	0.04	0 25	0.30	0.33	0.57	0.02	0.02	0.01	0.12
G4	1.52	0.83	1.87	2.21	3.84	11.35	1.10	1.05	1.23	0.91	0.11	0.06	0.63	0.70	0.42	0.68	0.14	0.16	0.11	1.34
G5	2.92	2.10	2.94	3.35	4.46	9.66	1.26	1.58	1.71	1.45	0.21	0 15	0.84	0.89	0.34	0.52	0.61	0.69	0.31	3.63
G6	2.22	2.00	3.42	3.53	9.47	11.46	0.93	1.46	1.49	1.41	0.16	0 15	1 32	0.98	0.51	0.56	0.75	0.78	0.87	4.54
G7	2.31	1.80	3.19	3.45	7.64	12.33	1.01	1.37	1.52	1.34	0.17	0 13	1 16	0.99	0.47	0.59	0.65	0.70	0.63	4.42
G8	2.23	1.15	3.82	4.35	11.98	32.26	0.86	0.78	1.49	1.07	0.16	0.08	1 54	1.46	0.55	0.77	1.00	1.14	1.33	11.15
G9	3.46	2.96	3.87	4.13	6.95	10.03	1.17	1.75	1.86	1.72	0.25	0 22	1 22	1.03	0.38	0.47	1.31	1.39	0.85	6.10
G10	3.16	2.15	3.36	3.86	5.54	12.77	1.22	1.45	1.78	1.47	0.23	0 16	1.01	1.08	0.36	0.56	0.88	1.01	0.50	5.98
G11	2.20	1.86	3.18	3.35	8.10	11.14	0.98	1.44	1.48	1.36	0.16	0 14	1 19	0.94	0.49	0.57	0.63	0.66	0.66	3.92
G12	1.54	1.27	1.91	2.05	3.95	5.99	1.10	1.57	1.24	1.13	0.11	0.09	0.65	0.55	0.42	0.53	0.15	0.16	0.12	0.84
G13	2.66	1.88	3.35	3.74	7.13	13.94	1.08	1.33	1.63	1.37	0.19	0 14	1 15	1.09	0.43	0.60	0.79	0.88	0.65	5.75
G14	2.16	1.31	2.66	3.08	5.47	13.89	1.10	1.16	1.47	1.14	0.16	0 10	0 90	0.94	0.42	0.65	0.40	0.46	0.32	3.47
G15	3.16	1.85	3.61	4.26	6.67	18.72	1.16	1.18	1.78	1.36	0.23	0 14	1 16	1.29	0.39	0.64	1.04	1.23	0.71	9.09
G16	3.06	1.85	3.14	3.74	4.91	14.19	1.25	1.32	1.75	1.36	0.22	0 14	0 92	1.09	0.34	0.60	0.73	0.87	0.39	5.79
G17	1.86	1.42	2.30	2.52	4.76	8.24	1.10	1.46	1.36	1.19	0.14	0 10	0.78	0.70	0.42	0.56	0.26	0.28	0.21	1.65
G18	2.88	2.59	3.34	3.49	6.30	8.12	1.15	1.79	1.70	1.61	0.21	0 19	1.08	0.85	0.40	0.46	0.82	0.86	0.57	3.58
G19	1.54	1.53	2.06	2.06	4.72	4.77	1.04	1.80	1.24	1.24	0.11	0 11	0.73	0.50	0.45	0.46	0.18	0.18	0.16	0.73
G20	2.21	1.64	2.73	3.01	5.62	10.24	1.10	1.42	1.49	1.28	0.16	0 12	0 92	0.85	0.42	0.57	0.43	0.47	0.34	2.88
G21	1.42	1.37	1.77	1.80	3.72	4.08	1.09	1.82	1.19	1.17	0.10	0 10	0.61	0.43	0.43	0.45	0.12	0.12	0.10	0.48
G22	1.36	0.73	1.92	2.23	4.72	13.33	1.00	0.93	1.17	0.85	0.10	0.05	0.70	0.72	0.48	0.72	0.14	0.16	0.14	1.44
G23	2.58	1.85	2.68	3.05	4.26	9.12	1.24	1.54	1.61	1.36	0.19	0 14	0.79	0.82	0.35	0.53	0.45	0.51	0.24	2.79
G24	1.18	1.17	1.70	1.70	4.28	4.38	0.98	1.69	1.09	1.08	0.09	0.09	0.63	0.43	0.48	0.49	0.10	0.10	0.10	0.44
G25	1.07	0.71	2.80	2.98	14.16	24.71	0.61	0.70	1.03	0.84	0.08	0.05	1 29	1.02	0.68	0.79	0.33	0.35	0.68	3.64
G26	1.86	1.29	1.84	2.13	2.73	6.41	1.28	1.54	1.36	1.13	0.14	0.09	0 52	0.58	0.33	0.54	0.15	0.18	0.07	0.96

Table 3.4: Continued

Code	TOL		MP		HM		SSI		GMP		STI		YI		YSI		MSTI/ K_1STI		MSTI/ K_2STI	
	PreADS	PoADS	PreADS	PoADS	PreADS	PoADS	PreADS	PoADS	PreADS	PoADS	PreADS	PoADS	PreADS	PoADS	PreADS	PoADS	PreADS	PoADS	PreADS	PoADS
G27	2.64	1.41	2.31	2.93	2.71	11.48	1.39	1.28	1.63	1.19	0.19	0 10	0 56	0.86	0.27	0.61	0.33	0.41	0.11	2.81
G28	3.49	2.33	3.18	3.76	4.05	10.95	1.35	1.57	1.87	1.53	0.26	0 17	0.82	1.00	0.29	0.53	0.83	0.98	0.31	5.16
G29	1.13	0.93	1.07	1.17	1.47	2.48	1.31	1.89	1.06	0.96	0.08	0.07	0 29	0.27	0.31	0.43	0.03	0.03	0.01	0.13
G30	2.07	1.43	1.43	1.75	0.96	3.61	1.59	1.92	1.44	1.19	0.15	0 10	0 23	0.40	0.16	0.42	0.09	0.11	0.01	0.41
G31	2.19	1.17	2.35	2.86	3.93	13.39	1.21	1.13	1.48	1.08	0.16	0.09	0.71	0.88	0.36	0.66	0.30	0.36	0.17	2.80
G32	2.24	1.46	2.89	3.28	6.34	14.05	1.06	1.20	1.50	1.21	0.16	0 11	1.01	0.99	0.44	0.64	0.50	0.57	0.43	4.10
G33	1.00	0.71	1.18	1.33	2.29	4.64	1.13	1.39	1.00	0.84	0.07	0.05	0 39	0.38	0.41	0.58	0.04	0.04	0.03	0.25
G34	0.87	0.65	1.16	1.27	2.69	4.62	1.03	1.36	0.93	0.81	0.06	0.05	0.42	0.37	0.46	0.59	0.03	0.03	0.03	0.22
G35	2.20	1.80	2.13	2.33	3.00	5.10	1.30	1.85	1.48	1.34	0.16	0 13	0 58	0.55	0.32	0.44	0.24	0.26	0.11	1.01
G36	1.08	0.76	2.01	2.18	6.97	12.11	0.80	0.98	1.04	0.87	0.08	0.06	0.84	0.70	0.58	0.70	0.14	0.15	0.21	1.30
G37	1.79	1.48	2.60	2.76	6.69	9.55	0.97	1.40	1.34	1.22	0.13	0 11	0 97	0.78	0.49	0.58	0.34	0.36	0.36	2.23
G38	2.23	1.32	2.92	3.38	6.53	16.59	1.05	1.09	1.49	1.15	0.16	0 10	1.03	1.05	0.45	0.67	0.51	0.59	0.45	4.70
G39	2.82	1.96	3.41	3.85	6.85	14.10	1.11	1.35	1.68	1.40	0.21	0 14	1 14	1.11	0.42	0.59	0.85	0.96	0.65	6.20
G40	2.37	1.66	3.29	3.64	7.93	15.15	1.01	1.23	1.54	1.29	0.17	0 12	1 20	1.09	0.47	0.63	0.70	0.78	0.69	5.55
G41	1.02	0.92	2.40	2.45	10.79	12.62	0.67	1.05	1.01	0.96	0.07	0.07	1.08	0.77	0.65	0.68	0.22	0.22	0.41	1.82
G42	1.95	1.02	3.07	3.53	8.66	23.90	0.92	0.84	1.40	1.01	0.14	0.07	1 19	1.17	0.52	0.75	0.54	0.62	0.64	5.85
G43	0.88	0.34	2.22	2.50	10.77	36.66	0.63	0.42	0.94	0.58	0.06	0.02	1.02	0.90	0.67	0.87	0.17	0.19	0.34	2.31
G44	1.27	0.54	2.47	2.84	8.99	29.68	0.78	0.57	1.13	0.73	0.09	0.04	1.05	1.00	0.59	0.83	0.26	0.29	0.40	3.27
G45	2.79	1.58	3.49	4.10	7.32	20.51	1.09	1.07	1.67	1.26	0.20	0 12	1 19	1.28	0.43	0.68	0.89	1.05	0.73	8.43
G46	2.24	1.12	2.58	3.14	4.81	17.11	1.15	1.00	1.50	1.06	0.16	0.08	0.83	1.00	0.39	0.70	0.38	0.46	0.26	3.90
G47	1.54	0.74	3.27	3.67	13.13	35.97	0.72	0.61	1.24	0.86	0.11	0.05	1.43	1.28	0.62	0.82	0.57	0.64	0.97	6.98
G48	1.51	1.10	2.55	2.76	7.81	13.33	0.87	1.10	1.23	1.05	0.11	0.08	1.02	0.86	0.54	0.67	0.30	0.32	0.39	2.54
G49	1.67	0.75	2.39	2.86	6.01	21.42	0.99	0.77	1.29	0.87	0.12	0.05	0.89	0.96	0.48	0.77	0.27	0.32	0.28	3.16
G50	1.12	0.72	2.41	2.61	9.81	18.48	0.72	0.81	1.06	0.85	0.08	0.05	1.06	0.87	0.62	0.76	0.23	0.25	0.39	2.38
G51	0.97	0.51	2.57	2.80	13.23	30.59	0.60	0.55	0.98	0.71	0.07	0.04	1 19	0.99	0.68	0.83	0.26	0.28	0.54	3.16
G52	0.81	0.68	2.42	2.49	14.04	17.83	0.55	0.80	0.90	0.83	0.06	0.05	1 15	0.83	0.71	0.76	0.21	0.21	0.47	2.07
G53	2.18	1.55	3.68	3.99	11.33	19.73	0.87	1.08	1.48	1.25	0.16	0 11	1.48	1.25	0.54	0.67	0.90	0.97	1.17	7.76

Table 3.4: Continued

Code	TOL		MP		HM		SSI		GMP		STI		YI		YSI		MSTI/ K_1STI		MSTI/ K_2STI	
	PreADS	PoADS	PreADS	PoADS	PreADS	PoADS	PreADS	PoADS	PreADS	PoADS	PreADS	PoADS	PreADS	PoADS	PreADS	PoADS	PreADS	PoADS	PreADS	PoADS
G54	2.93	2.38	3.28	3.56	5.85	9.47	1.18	1.66	1.71	1.54	0.21	0 17	1.03	0.92	0.38	0.50	0.79	0.86	0.51	4.15
G55	1.14	0.98	3.03	3.12	15.58	19.41	0.60	0.90	1.07	0.99	0.08	0.07	1.40	1.02	0.68	0.73	0.42	0.43	0.88	3.94
G56	2.31	1.58	4.11	4.48	13.48	24.57	0.84	1.00	1.52	1.26	0.17	0 12	1.69	1.43	0.56	0.70	1.22	1.33	1.71	11.30
G57	1.75	0.44	2.39	3.05	5.66	42.42	1.02	0.44	1.32	0.66	0.13	0.03	0.87	1.10	0.46	0.87	0.27	0.35	0.26	4.19
G58	1.13	0.99	1.95	2.02	6.22	7.72	0.85	1.31	1.06	1.00	0.08	0.07	0.79	0.59	0.55	0.61	0.13	0.14	0.18	0.92
G59	1.35	1.12	2.92	3.03	11.95	15.81	0.71	1.04	1.16	1.06	0.10	0.08	1 28	0.96	0.62	0.69	0.40	0.42	0.70	3.46
G60	0.73	0.31	1.69	1.90	7.50	22.88	0.67	0.51	0.85	0.56	0.05	0.02	0.76	0.68	0.65	0.85	0.08	0.09	0.14	1.00
G61	1.31	0.89	2.69	2.91	10.37	18.63	0.75	0.88	1.15	0.94	0.10	0.06	1 16	0.95	0.61	0.74	0.32	0.35	0.53	3.21
G62	1.98	1.46	2.92	3.18	7.59	13.07	0.97	1.24	1.41	1.21	0.15	0 11	1 10	0.95	0.49	0.63	0.48	0.52	0.52	3.67
G63	1.06	0.28	3.25	3.64	19.32	94.33	0.53	0.25	1.03	0.53	0.08	0.02	1 55	1.35	0.72	0.93	0.50	0.56	1.14	7.40
G64	1.22	0.49	1.85	2.21	5.03	19.77	0.94	0.66	1.10	0.70	0.09	0.04	0.71	0.76	0.51	0.80	0.12	0.14	0.14	1.51
G65	0.88	0.27	2.20	2.51	10.56	47.28	0.64	0.33	0.94	0.52	0.06	0.02	1.01	0.92	0.67	0.90	0.17	0.19	0.33	2.40
G66	2.70	1.72	3.58	4.07	8.15	18.43	1.04	1.16	1.64	1.31	0.20	0 13	1 27	1.25	0.45	0.65	0.94	1.06	0.85	8.01
G67	1.21	0.28	2.27	2.73	7.88	52.23	0.80	0.33	1.10	0.53	0.09	0.02	0 95	1.00	0.58	0.90	0.20	0.24	0.30	3.08
G68	2.53	1.08	3.61	4.34	9.03	34.27	0.99	0.73	1.59	1.04	0.19	0.08	1 34	1.47	0.48	0.78	0.92	1.11	0.94	11.14
G69	2.76	1.56	3.74	4.34	8.74	23.41	1.03	1.01	1.66	1.25	0.20	0 11	1 34	1.38	0.46	0.70	1.05	1.22	0.99	10.23
G70	2.44	1.40	3.69	4.21	9.93	24.65	0.95	0.94	1.56	1.18	0.18	0 10	1.41	1.36	0.50	0.72	0.95	1.09	1.07	9.54
G71	1.71	1.51	3.44	3.54	13.02	15.90	0.76	1.16	1.31	1.23	0.13	0 11	1.48	1.08	0.60	0.65	0.68	0.70	1.10	5.26
G72	1.87	1.15	1.80	2.16	2.54	7.56	1.30	1.39	1.37	1.07	0.14	0.08	0.49	0.61	0.32	0.58	0.14	0.17	0.06	1.08
G73	1.33	0.64	1.68	2.03	3.62	12.54	1.08	0.90	1.15	0.80	0.10	0.05	0 58	0.66	0.44	0.73	0.10	0.12	0.08	1.08
G74	2.19	1.07	2.87	3.43	6.43	21.50	1.05	0.89	1.48	1.03	0.16	0.08	1.01	1.12	0.45	0.73	0.48	0.58	0.43	5.24
G75	1.07	0.74	1.75	1.92	5.15	9.61	0.90	1.07	1.04	0.86	0.08	0.05	0.69	0.60	0.53	0.68	0.10	0.11	0.12	0.86
G76	2.51	1.07	3.05	3.77	6.14	26.05	1.11	0.82	1.58	1.03	0.18	0.08	1.02	1.25	0.42	0.75	0.61	0.75	0.47	7.13
G77	2.79	1.14	3.16	3.99	5.77	27.46	1.17	0.83	1.67	1.07	0.20	0.08	1.01	1.33	0.39	0.75	0.71	0.89	0.47	8.46
G78	2.60	0.87	3.39	4.26	7.54	41.43	1.05	0.61	1.61	0.93	0.19	0.06	1 19	1.48	0.45	0.82	0.80	1.00	0.70	10.90
G79	2.63	1.52	2.98	3.53	5.43	15.60	1.17	1.18	1.62	1.23	0.19	0 11	0 95	1.07	0.39	0.65	0.59	0.70	0.39	5.16
G80	3.20	2.21	2.77	3.26	3.19	8.54	1.39	1.68	1.79	1.48	0.23	0 16	0.67	0.84	0.27	0.49	0.56	0.67	0.18	3.16

Table 3.4: Continued

Code	TOL		MP		HM		SSI		GMP		STI		YI		YSI		MSTI/ K_1STI		MSTI/ K_2STI	
	PreADS	PoADS	PreADS	PoADS	PreADS	PoADS	PreADS	PoADS	PreADS	PoADS	PreADS	PoADS	PreADS	PoADS	PreADS	PoADS	PreADS	PoADS	PreADS	PoADS
G81	2.82	2.34	2.41	2.65	2.70	4.81	1.41	2.03	1.68	1.53	0.21	0 17	0 57	0.57	0.26	0.39	0.38	0.41	0.11	1.28
G82	0.86	0.46	2.46	2.66	13.69	30.49	0.56	0.53	0.93	0.68	0.06	0.03	1 16	0.94	0.70	0.84	0.22	0.24	0.48	2.71
G83	2.49	0.87	3.35	4.16	7.74	39.50	1.03	0.63	1.58	0.93	0.18	0.06	1 20	1.44	0.46	0.81	0.76	0.94	0.70	10.15
G84	0.85	0.70	1.94	2.02	8.45	11.31	0.68	0.98	0.92	0.84	0.06	0.05	0.86	0.65	0.64	0.71	0.12	0.12	0.21	1.04
G85	1.21	0.43	2.17	2.56	7.18	30.57	0.83	0.51	1.10	0.65	0.09	0.03	0.89	0.91	0.56	0.85	0.18	0.21	0.25	2.44
G86	1.51	0.08	3.06	3.78	11.69	369.22	0.75	0.07	1.23	0.28	0.11	0.01	1 32	1.45	0.60	0.98	0.48	0.59	0.78	8.59
G87	2.43	1.16	3.37	4.01	8.16	27.06	1.01	0.84	1.56	1.08	0.18	0.09	1 23	1.33	0.47	0.75	0.76	0.90	0.75	8.53
G88	3.34	1.47	3.34	4.28	5.00	24.10	1.27	0.97	1.83	1.21	0.24	0 11	0 95	1.37	0.33	0.71	0.90	1.15	0.44	9.92
G89	1.85	0.63	2.31	2.93	4.87	27.04	1.09	0.64	1.36	0.79	0.14	0.05	0.79	1.01	0.43	0.81	0.26	0.33	0.21	3.51
G90	1.80	0.90	2.34	2.79	5.20	16.93	1.06	0.92	1.34	0.95	0.13	0.07	0.82	0.91	0.45	0.72	0.26	0.31	0.23	2.81
G91	1.57	0.83	2.70	3.07	8.48	22.20	0.86	0.79	1.25	0.91	0.11	0.06	1.09	1.03	0.55	0.76	0.35	0.40	0.47	3.88
G92	1.60	0.69	1.66	2.12	2.67	12.61	1.23	0.93	1.26	0.83	0.12	0.05	0.49	0.69	0.35	0.72	0.11	0.14	0.06	1.22
G93	1.06	0.68	2.11	2.30	7.93	15.12	0.76	0.86	1.03	0.83	0.08	0.05	0 90	0.76	0.60	0.74	0.16	0.17	0.25	1.60
G94	1.11	0.57	1.93	2.20	6.14	16.80	0.85	0.76	1.06	0.75	0.08	0.04	0.78	0.74	0.55	0.77	0.13	0.15	0.17	1.45
G95	0.78	0.44	2.17	2.34	11.69	24.38	0.58	0.58	0.88	0.67	0.06	0.03	1.01	0.82	0.70	0.83	0.15	0.16	0.33	1.82
G96	0.88	0.35	1.84	2.10	7.28	25.04	0.73	0.51	0.94	0.59	0.06	0.03	0.80	0.75	0.62	0.85	0.10	0.12	0.17	1.34
G97	1.67	1.56	1.85	1.91	3.25	3.90	1.19	1.92	1.29	1.25	0.12	0 11	0 58	0.44	0.38	0.42	0.14	0.15	0.09	0.53
G98	1.33	0.90	2.05	2.27	5.68	10.95	0.93	1.10	1.15	0.95	0.10	0.07	0.79	0.70	0.51	0.67	0.16	0.18	0.19	1.42
G99	0.56	0.43	1.82	1.89	11.55	16.21	0.51	0.68	0.75	0.66	0.04	0.03	0.88	0.65	0.73	0.79	0.09	0.09	0.21	0.93
G100	1.29	0.73	0.98	1.26	0.83	3.99	1.51	1.49	1.14	0.85	0.09	0.05	0 19	0.35	0.20	0.55	0.03	0.04	0.01	0.20
G101	2.30	1.28	3.01	3.52	6.71	18.68	1.05	1.02	1.52	1.13	0.17	0.09	1.06	1.12	0.45	0.69	0.56	0.65	0.49	5.44
G102	2.20	1.22	3.50	3.99	10.02	25.44	0.91	0.88	1.48	1.10	0.16	0.09	1 37	1.31	0.52	0.73	0.79	0.90	0.96	8.28
G103	2.40	1.45	3.53	4.00	9.22	21.37	0.96	1.02	1.55	1.20	0.18	0 11	1 33	1.27	0.49	0.69	0.85	0.96	0.92	8.02
G104	3.29	1.68	3.88	4.69	7.52	25.41	1.13	1.01	1.81	1.29	0.24	0 12	1 28	1.49	0.40	0.70	1.27	1.54	0.93	12.95
G105	3.06	1.87	3.86	4.46	8.22	20.34	1.08	1.15	1.75	1.37	0.22	0 14	1 33	1.37	0.43	0.65	1.20	1.39	1.00	10.53
G106	2.23	2.31	3.75	3.71	11.46	10.77	0.87	1.57	1.49	1.52	0.16	0 17	1 50	0.99	0.54	0.53	0.95	0.94	1.24	4.96
G107	2.64	1.43	3.16	3.76	6.22	19.14	1.12	1.06	1.63	1.19	0.19	0 10	1.05	1.18	0.41	0.68	0.68	0.81	0.51	6.56

Table 3.4: Continued

Code	TOL		MP		HM		SSI		GMP		STI		YI		YSI		MSTI/ K_1STI		MSTI/ K_2STI	
	PreADS	PoADS	PreADS	PoADS	PreADS	PoADS	PreADS	PoADS	PreADS	PoADS	PreADS	PoADS	PreADS	PoADS	PreADS	PoADS	PreADS	PoADS	PreADS	PoADS
G108	0.22	0.06	1.62	1.70	23.89	102.67	0.24	0.11	0.47	0.24	0.02	0.00	0.86	0.65	0.87	0.97	0.05	0.05	0.18	0.78
G109	3.52	2.52	3.53	4.03	5.31	11.66	1.27	1.58	1.88	1.59	0.26	0 18	1.01	1.07	0.33	0.52	1.06	1.21	0.53	6.35
G110	2.65	2.29	3.52	3.70	8.01	10.82	1.04	1.57	1.63	1.51	0.19	0 17	1 25	0.99	0.45	0.53	0.88	0.93	0.80	4.92
G111	3.02	1.37	3.29	4.11	5.66	24.00	1.20	0.95	1.74	1.17	0.22	0 10	1.01	1.33	0.37	0.71	0.81	1.01	0.50	8.90
G112	1.94	1.65	3.10	3.25	8.93	11.96	0.91	1.34	1.39	1.28	0.14	0 12	1 21	0.94	0.52	0.59	0.55	0.58	0.67	3.74
G113	0.79	0.42	1.19	1.37	3.17	8.85	0.95	0.87	0.89	0.65	0.06	0.03	0.45	0.45	0.50	0.74	0.03	0.04	0.04	0.34
G114	2.71	1.65	3.91	4.44	9.93	23.07	0.98	1.04	1.65	1.28	0.20	0 12	1.46	1.40	0.49	0.69	1.16	1.32	1.22	10.85
G115	2.91	1.13	3.79	4.68	8.43	38.21	1.06	0.71	1.71	1.06	0.21	0.08	1 33	1.60	0.45	0.78	1.12	1.38	0.99	14.13
G116	2.54	1.55	3.76	4.25	9.82	22.45	0.96	1.03	1.59	1.25	0.19	0 11	1.42	1.35	0.49	0.69	1.02	1.15	1.10	9.56
G117	2.78	1.29	3.39	4.13	6.86	25.75	1.11	0.90	1.67	1.14	0.20	0.09	1 14	1.35	0.42	0.73	0.83	1.01	0.64	9.19
G118	2.46	1.38	3.00	3.54	6.10	17.40	1.11	1.08	1.57	1.18	0.18	0 10	1.01	1.10	0.42	0.67	0.57	0.68	0.45	5.39
G119	3.16	1.54	3.68	4.49	6.97	25.50	1.14	0.97	1.78	1.24	0.23	0 11	1 19	1.44	0.40	0.71	1.09	1.33	0.77	11.51
G120	2.31	0.74	3.63	4.41	10.22	52.43	0.92	0.51	1.52	0.86	0.17	0.05	1.41	1.57	0.52	0.85	0.89	1.08	1.05	12.47
G121	1.88	1.09	2.69	3.08	6.76	16.84	0.99	1.00	1.37	1.05	0.14	0.08	1.00	0.98	0.48	0.70	0.38	0.44	0.39	3.68
G122	2.91	2.35	3.48	3.76	6.88	10.88	1.12	1.58	1.70	1.53	0.21	0 17	1 16	1.00	0.41	0.52	0.91	0.98	0.68	5.15
G123	2.97	1.87	3.89	4.43	8.71	20.03	1.05	1.16	1.72	1.37	0.22	0 14	1 37	1.35	0.45	0.65	1.20	1.37	1.07	10.32
G124	2.31	1.33	3.52	4.01	9.61	23.49	0.94	0.94	1.52	1.15	0.17	0 10	1 35	1.30	0.51	0.72	0.83	0.94	0.94	8.26
G125	2.53	1.61	3.62	4.08	9.10	19.87	0.99	1.09	1.59	1.27	0.19	0 12	1 34	1.27	0.48	0.67	0.93	1.04	0.96	8.25
G126	2.26	0.79	3.48	4.22	9.60	44.74	0.93	0.57	1.50	0.89	0.17	0.06	1 34	1.48	0.51	0.83	0.79	0.96	0.92	10.72
G127	3.36	1.49	3.55	4.48	5.82	26.17	1.22	0.95	1.83	1.22	0.25	0 11	1.07	1.45	0.36	0.71	1.04	1.31	0.59	11.52
G128	2.15	1.04	3.69	4.25	11.61	34.26	0.86	0.72	1.47	1.02	0.16	0.08	1.49	1.44	0.55	0.78	0.90	1.03	1.20	10.51
G129	2.95	1.65	4.00	4.65	9.38	25.41	1.03	1.00	1.72	1.29	0.22	0 12	1.44	1.48	0.46	0.70	1.29	1.50	1.22	12.68
G130	2.43	0.66	3.20	4.09	7.22	50.33	1.05	0.50	1.56	0.81	0.18	0.05	1 13	1.46	0.45	0.85	0.67	0.86	0.60	9.97
G131	3.14	1.65	3.39	4.14	5.77	20.00	1.20	1.10	1.77	1.28	0.23	0 12	1.04	1.29	0.37	0.67	0.90	1.09	0.54	8.59
G132	2.69	1.27	3.51	4.22	7.81	27.32	1.05	0.87	1.64	1.13	0.20	0.09	1 23	1.39	0.45	0.74	0.89	1.07	0.78	9.85
G133	2.02	1.03	2.69	3.18	6.15	19.08	1.04	0.93	1.42	1.02	0.15	0.08	0 96	1.03	0.45	0.72	0.39	0.47	0.36	4.15
G134	2.52	0.87	2.87	3.69	5.27	31.02	1.16	0.70	1.59	0.93	0.18	0.06	0 92	1.26	0.39	0.79	0.52	0.67	0.35	6.96

Table 3.4: Continued

Code	TOL		MP		HM		SSI		GMP		STI		YI		YSI		MSTI/ K_1STI		MSTI/ K_2STI	
	PreADS	PoADS	PreADS	PoADS	PreADS	PoADS	PreADS	PoADS	PreADS	PoADS	PreADS	PoADS	PreADS	PoADS	PreADS	PoADS	PreADS	PoADS	PreADS	PoADS
G135	0.79	0.54	1.15	1.28	2.96	5.80	0.97	1.15	0.89	0.73	0.06	0.04	0.43	0.39	0.49	0.65	0.03	0.03	0.03	0.25
G136	2.33	1.25	3.69	4.23	10.53	27.89	0.91	0.86	1.53	1.12	0.17	0.09	1.44	1.40	0.52	0.74	0.93	1.07	1.12	9.97
G137	2.16	0.95	2.84	3.44	6.37	24.44	1.05	0.81	1.47	0.98	0.16	0.07	1.00	1.15	0.45	0.76	0.47	0.57	0.42	5.48
G138	2.25	1.16	3.21	3.76	8.07	23.65	0.99	0.89	1.50	1.08	0.16	0.09	1 19	1.23	0.48	0.73	0.65	0.76	0.67	6.91
G139	2.72	1.38	3.36	4.03	6.97	22.87	1.09	0.97	1.65	1.17	0.20	0 10	1 14	1.29	0.42	0.71	0.80	0.96	0.64	8.33
G140	2.08	1.28	2.99	3.39	7.56	17.40	0.98	1.05	1.44	1.13	0.15	0.09	1 11	1.07	0.48	0.68	0.52	0.59	0.54	4.83
G141	2.39	0.83	3.51	4.28	9.10	43.57	0.97	0.59	1.54	0.91	0.17	0.06	1 32	1.50	0.49	0.82	0.83	1.01	0.89	11.17
G142	2.78	1.87	3.08	3.53	5.43	12.39	1.18	1.39	1.67	1.37	0.20	0 14	0 96	1.01	0.38	0.58	0.66	0.76	0.42	4.71
G143	2.86	1.44	3.65	4.36	7.85	25.59	1.07	0.94	1.69	1.20	0.21	0 11	1 26	1.41	0.44	0.72	1.01	1.20	0.85	10.60
G144	3.44	1.69	4.01	4.89	7.66	27.52	1.14	0.98	1.85	1.30	0.25	0 12	1 31	1.57	0.40	0.71	1.42	1.73	1.01	14.83
G145	1.80	0.89	3.14	3.59	10.00	28.50	0.85	0.73	1.34	0.94	0.13	0.07	1 27	1.22	0.55	0.78	0.55	0.63	0.74	6.34
G146	2.01	1.08	3.14	3.60	8.81	23.54	0.92	0.86	1.42	1.04	0.15	0.08	1 22	1.19	0.52	0.74	0.58	0.66	0.68	6.16
G147	1.91	1.16	3.12	3.50	9.23	20.51	0.89	0.94	1.38	1.08	0.14	0.08	1 23	1.13	0.53	0.72	0.56	0.62	0.70	5.48
G148	0.94	0.51	1.08	1.30	2.00	6.37	1.16	1.09	0.97	0.71	0.07	0.04	0 35	0.40	0.39	0.67	0.03	0.03	0.02	0.27
G149	2.98	1.51	3.67	4.41	7.55	24.99	1.10	0.97	1.73	1.23	0.22	0 11	1 24	1.42	0.42	0.71	1.05	1.26	0.83	10.87
G150	2.32	1.32	3.44	3.94	9.07	22.95	0.96	0.95	1.52	1.15	0.17	0 10	1 30	1.27	0.50	0.71	0.78	0.90	0.86	7.85
G151	1.51	0.76	1.96	2.33	4.35	13.85	1.06	0.93	1.23	0.87	0.11	0.06	0.69	0.76	0.44	0.72	0.16	0.18	0.14	1.63
G152	2.26	1.07	3.79	4.39	11.55	35.57	0.88	0.72	1.50	1.03	0.17	0.08	1 51	1.49	0.54	0.78	0.98	1.14	1.27	11.61
G153	2.12	0.88	2.91	3.53	6.90	27.75	1.02	0.74	1.46	0.94	0.16	0.06	1.05	1.20	0.47	0.78	0.49	0.60	0.47	5.99
G154	2.22	0.85	2.51	3.19	4.58	23.51	1.17	0.78	1.49	0.92	0.16	0.06	0.80	1.07	0.39	0.76	0.35	0.45	0.24	4.39
G155	0.63	0.41	1.18	1.29	4.11	7.89	0.80	0.91	0.79	0.64	0.05	0.03	0.49	0.42	0.58	0.73	0.03	0.03	0.04	0.28
G156	1.46	0.64	2.72	3.13	9.37	30.54	0.81	0.61	1.21	0.80	0.11	0.05	1 13	1.09	0.58	0.82	0.35	0.40	0.51	4.35
G157	2.44	1.19	3.93	4.55	11.42	34.26	0.90	0.77	1.56	1.09	0.18	0.09	1 54	1.53	0.53	0.77	1.11	1.29	1.37	12.77
G158	2.69	1.53	3.71	4.29	8.88	23.28	1.01	1.00	1.64	1.24	0.20	0 11	1 35	1.37	0.47	0.70	1.02	1.18	0.99	9.92
G159	1.42	0.79	2.86	3.17	10.86	24.95	0.76	0.74	1.19	0.89	0.10	0.06	1 23	1.08	0.60	0.78	0.39	0.43	0.63	4.37
G160	1.25	0.76	2.28	2.52	7.69	16.43	0.82	0.87	1.12	0.87	0.09	0.06	0 94	0.83	0.57	0.74	0.21	0.23	0.30	2.12
G161	1.99	0.92	2.60	3.13	5.80	20.94	1.05	0.85	1.41	0.96	0.15	0.07	0 92	1.04	0.45	0.74	0.36	0.43	0.32	4.07

Table 3.4: Continued

Code	TOL		MP		HM		SSI		GMP		STI		YI		YSI		MSTI/ K_1STI		MSTI/ K_2STI	
	PreADS	PoADS	PreADS	PoADS	PreADS	PoADS	PreADS	PoADS	PreADS	PoADS	PreADS	PoADS	PreADS	PoADS	PreADS	PoADS	PreADS	PoADS	PreADS	PoADS
G162	3.00	1.66	3.59	4.26	7.06	21.00	1.12	1.08	1.73	1.29	0.22	0 12	1 19	1.33	0.41	0.67	1.00	1.18	0.74	9.41
G163	1.44	0.47	1.71	2.20	3.33	20.52	1.13	0.63	1.20	0.68	0.11	0.03	0 56	0.76	0.41	0.81	0.11	0.14	0.08	1.49
G164	1.87	0.88	2.84	3.34	7.71	25.03	0.94	0.77	1.37	0.94	0.14	0.06	1.09	1.13	0.50	0.77	0.44	0.51	0.49	5.06
G165	1.66	0.61	2.95	3.47	9.64	39.08	0.84	0.54	1.29	0.78	0.12	0.04	1 21	1.23	0.56	0.84	0.45	0.53	0.63	6.03
G166	2.54	1.11	3.12	3.84	6.42	26.08	1.10	0.84	1.59	1.05	0.19	0.08	1.06	1.27	0.42	0.75	0.65	0.80	0.51	7.52
G167	2.48	1.27	3.72	4.33	9.96	28.88	0.95	0.85	1.57	1.13	0.18	0.09	1.42	1.43	0.50	0.74	0.98	1.14	1.10	10.71
G168	1.97	0.96	2.30	2.80	4.36	15.88	1.14	0.97	1.40	0.98	0.14	0.07	0.75	0.90	0.40	0.71	0.27	0.32	0.19	2.80
G169	1.99	1.02	2.91	3.39	7.51	22.02	0.97	0.87	1.41	1.01	0.15	0.07	1.09	1.12	0.49	0.74	0.47	0.55	0.51	5.13
G170	0.71	0.07	1.16	1.48	3.49	64.77	0.89	0.15	0.84	0.26	0.05	0.00	0.46	0.56	0.53	0.96	0.03	0.04	0.04	0.51
G171	2.01	0.69	2.97	3.63	7.75	38.10	0.96	0.57	1.42	0.83	0.15	0.05	1 12	1.27	0.49	0.83	0.50	0.62	0.54	6.85
G172	2.89	1.64	3.50	4.12	7.01	19.89	1.11	1.10	1.70	1.28	0.21	0 12	1 17	1.28	0.41	0.67	0.92	1.08	0.70	8.49
G173	1.94	1.11	2.90	3.32	7.73	19.34	0.95	0.95	1.39	1.05	0.14	0.08	1 10	1.07	0.50	0.71	0.47	0.53	0.52	4.68
G174	2.64	1.30	2.89	3.57	5.03	19.00	1.19	1.02	1.62	1.14	0.19	0.09	0 90	1.13	0.37	0.69	0.55	0.68	0.34	5.67
G175	2.49	1.71	3.21	3.61	7.05	14.39	1.06	1.27	1.58	1.31	0.18	0 12	1 12	1.07	0.44	0.62	0.68	0.77	0.59	5.30
G176	2.78	1.39	3.39	4.09	6.87	23.31	1.11	0.96	1.67	1.18	0.20	0 10	1 14	1.31	0.42	0.71	0.83	1.00	0.65	8.68
G177	2.01	0.96	2.53	3.05	5.33	18.90	1.09	0.90	1.42	0.98	0.15	0.07	0.87	1.00	0.43	0.73	0.34	0.41	0.28	3.69
G178	2.51	1.28	3.77	4.39	10.08	29.56	0.95	0.84	1.59	1.13	0.18	0.09	1.44	1.45	0.50	0.75	1.02	1.19	1.14	11.22
G179	0.54	0.33	1.22	1.32	5.24	10.38	0.69	0.74	0.73	0.57	0.04	0.02	0 54	0.45	0.64	0.78	0.03	0.03	0.05	0.31
G180	2.52	1.78	3.04	3.41	6.09	12.15	1.11	1.37	1.59	1.33	0.18	0 13	1.02	0.98	0.41	0.59	0.60	0.68	0.46	4.27
G181	1.93	1.05	3.28	3.72	10.14	25.67	0.87	0.82	1.39	1.03	0.14	0.08	1 32	1.24	0.54	0.75	0.63	0.72	0.83	6.83
G182	1.76	1.35	3.50	3.71	13.06	19.77	0.76	1.02	1.33	1.16	0.13	0 10	1 50	1.18	0.60	0.69	0.72	0.76	1.15	6.37
G183	2.19	1.21	3.01	3.49	7.19	19.50	1.01	0.98	1.48	1.10	0.16	0.09	1.09	1.12	0.47	0.70	0.54	0.63	0.53	5.39
G184	2.38	1.31	3.74	4.28	10.55	27.19	0.92	0.88	1.54	1.15	0.17	0 10	1.45	1.40	0.52	0.73	0.98	1.12	1.16	10.23
G185	2.59	1.22	3.70	4.39	9.26	30.95	0.99	0.81	1.61	1.10	0.19	0.09	1 37	1.46	0.48	0.76	0.99	1.17	1.02	11.29
G186	1.94	0.91	2.53	3.05	5.61	19.98	1.06	0.86	1.39	0.95	0.14	0.07	0.89	1.00	0.44	0.74	0.33	0.40	0.29	3.72
G187	1.53	0.63	3.10	3.54	11.81	39.29	0.75	0.54	1.24	0.80	0.11	0.05	1 33	1.25	0.60	0.84	0.50	0.57	0.80	6.41
G188	1.55	1.20	2.75	2.93	9.03	13.71	0.83	1.13	1.24	1.10	0.11	0.09	1 13	0.90	0.56	0.66	0.37	0.39	0.51	3.01

Table 3.4: Continued

Code	TOL		MP		HM		SSI		GMP		STI		YI		YSI		MSTI/ K_1STI		MSTI/ K_2STI	
	PreADS	PoADS	PreADS	PoADS	PreADS	PoADS	PreADS	PoADS	PreADS	PoADS	PreADS	PoADS	PreADS	PoADS	PreADS	PoADS	PreADS	PoADS	PreADS	PoADS
G189	2.06	1.52	3.45	3.73	10.52	17.54	0.88	1.12	1.44	1.23	0.15	0 11	1 38	1.15	0.54	0.66	0.74	0.80	0.96	6.21
G190	0.52	0.38	1.24	1.32	5.65	9.02	0.66	0.83	0.72	0.61	0.04	0.03	0 56	0.44	0.65	0.75	0.03	0.03	0.06	0.30
G191	1.53	0.90	1.82	2.13	3.56	9.64	1.13	1.16	1.24	0.95	0.11	0.07	0.60	0.65	0.41	0.65	0.13	0.15	0.10	1.15
G192	1.99	1.25	2.58	2.95	5.67	13.30	1.06	1.16	1.41	1.12	0.15	0.09	0 90	0.90	0.44	0.65	0.35	0.40	0.31	3.04
G193	1.10	0.67	1.72	1.94	4.82	10.89	0.92	0.98	1.05	0.82	0.08	0.05	0.67	0.62	0.51	0.71	0.10	0.11	0.11	0.92
G194	1.86	0.84	3.39	3.90	11.50	35.64	0.82	0.65	1.36	0.92	0.14	0.06	1.41	1.35	0.57	0.80	0.68	0.78	0.98	8.32
G195	1.35	1.06	2.36	2.50	7.57	11.22	0.85	1.16	1.16	1.03	0.10	0.08	0 96	0.76	0.56	0.65	0.23	0.25	0.32	1.84
G196	1.46	1.03	2.45	2.66	7.49	13.19	0.87	1.08	1.21	1.02	0.11	0.08	0 98	0.83	0.54	0.67	0.27	0.29	0.34	2.30
G197	2.18	1.18	2.37	2.86	4.06	13.32	1.20	1.13	1.48	1.09	0.16	0.09	0.73	0.88	0.37	0.66	0.30	0.37	0.18	2.81
G198	1.63	0.60	2.74	3.26	8.45	35.09	0.87	0.56	1.28	0.77	0.12	0.04	1 10	1.15	0.54	0.83	0.37	0.44	0.49	4.96
G199	0.66	0.40	1.16	1.29	3.76	8.04	0.84	0.90	0.81	0.63	0.05	0.03	0.47	0.42	0.56	0.73	0.03	0.03	0.04	0.28
G200	2.22	2.15	2.74	2.77	5.63	6.05	1.10	1.86	1.49	1.47	0.16	0 16	0 93	0.66	0.42	0.44	0.43	0.44	0.34	1.71
G201	1.04	0.56	1.06	1.30	1.62	5.78	1.26	1.17	1.02	0.75	0.08	0.04	0 30	0.40	0.34	0.65	0.03	0.03	0.01	0.26
G202	1.59	1.29	2.23	2.38	5.45	8.11	1.00	1.42	1.26	1.14	0.12	0.09	0.82	0.67	0.47	0.57	0.22	0.23	0.22	1.42
G203	1.38	0.73	2.05	2.37	5.37	14.98	0.96	0.89	1.18	0.86	0.10	0.05	0.77	0.78	0.49	0.73	0.17	0.19	0.18	1.75
G204	1.77	0.72	2.05	2.57	3.87	18.02	1.15	0.81	1.33	0.85	0.13	0.05	0.67	0.86	0.40	0.75	0.19	0.24	0.13	2.28
G205	1.11	0.80	2.34	2.49	9.34	15.05	0.73	0.92	1.05	0.90	0.08	0.06	1.02	0.81	0.62	0.72	0.21	0.22	0.36	1.99
G206	1.83	1.28	2.56	2.83	6.21	11.92	1.00	1.22	1.35	1.13	0.13	0.09	0 93	0.85	0.47	0.63	0.33	0.37	0.33	2.62
G207	1.83	1.18	2.78	3.11	7.55	15.88	0.94	1.05	1.35	1.08	0.13	0.09	1.07	0.98	0.50	0.68	0.41	0.46	0.46	3.71
G208	1.58	1.00	2.67	2.96	8.22	17.13	0.87	0.95	1.26	1.00	0.12	0.07	1.07	0.96	0.54	0.71	0.34	0.38	0.45	3.32
G209	1.41	0.61	2.21	2.62	6.25	22.24	0.92	0.69	1.19	0.78	0.10	0.04	0.86	0.90	0.52	0.79	0.20	0.24	0.24	2.48
G210	0.85	0.47	1.49	1.68	4.84	11.69	0.84	0.82	0.92	0.69	0.06	0.03	0.61	0.56	0.56	0.75	0.06	0.07	0.08	0.63
G211	0.97	0.68	1.37	1.51	3.36	6.36	1.00	1.22	0.99	0.83	0.07	0.05	0 50	0.45	0.48	0.63	0.05	0.06	0.05	0.40
G212	1.34	0.18	2.41	2.99	7.99	100.13	0.83	0.19	1.16	0.42	0.10	0.01	0 99	1.12	0.56	0.94	0.25	0.30	0.35	4.17
G213	1.26	0.34	2.46	2.92	8.99	49.83	0.78	0.37	1.12	0.58	0.09	0.02	1.04	1.07	0.59	0.89	0.25	0.30	0.39	3.73
G214	1.34	0.94	1.74	1.94	3.84	7.50	1.06	1.30	1.16	0.97	0.10	0.07	0.61	0.57	0.44	0.61	0.11	0.12	0.09	0.82
G215	0.70	0.40	1.15	1.30	3.43	8.34	0.89	0.88	0.84	0.63	0.05	0.03	0.46	0.43	0.53	0.74	0.03	0.03	0.04	0.29

Table 3.4: Continued

Code	TOL		MP		HM		SSI		GMP		STI		YI		YSI		MSTI/ K_1STI		MSTI/ K_2STI	
	PreADS	PoADS	PreADS	PoADS	PreADS	PoADS	PreADS	PoADS	PreADS	PoADS	PreADS	PoADS	PreADS	PoADS	PreADS	PoADS	PreADS	PoADS	PreADS	PoADS
G216	1.24	0.82	2.31	2.51	7.98	14.96	0.81	0.93	1.11	0.91	0.09	0.06	0.96	0.81	0.58	0.72	0.21	0.23	0 31	2.04
G217	1.93	0.72	2.75	3.36	6.87	31.02	0.99	0.64	1.39	0.85	0 14	0.05	1.02	1 16	0.48	0.81	0.41	0.50	0.42	5.31
G218	1.73	0.16	2.46	3.25	6.13	135.93	0.99	0.15	1.32	0.39	0 13	0.01	0.91	1 23	0.48	0.95	0.29	0.39	0 30	5.37
G219	1.07	0.21	2.23	2.66	8.71	67.84	0.74	0.25	1.03	0.46	0.08	0.02	0.96	0 99	0.61	0.92	0.18	0.22	0 30	2.88
G220	2.04	1.35	2.58	2.92	5.48	11.93	1.08	1.25	1.43	1.16	0 15	0.10	0.89	0.87	0.43	0.62	0.36	0.41	0 30	2.85
G221	1.44	0.36	2.10	2.64	5.41	38.64	0.97	0.42	1.20	0.60	0 11	0.03	0.79	0 95	0.49	0.87	0.18	0.23	0 19	2.73
G222	1.38	1.13	1.66	1.79	3.30	5.08	1.12	1.59	1.18	1.06	0 10	0.08	0.55	0.47	0.41	0.52	0.10	0.11	0.07	0.55
G223	1.50	0.63	1.87	2.31	3.92	16.66	1.09	0.79	1.23	0.79	0 11	0.05	0.64	0.77	0.43	0.76	0.14	0.17	0 11	1.65
G224	1.22	0.27	1.73	2.21	4.32	35.40	0.99	0.39	1.10	0.52	0.09	0.02	0.64	0.80	0.48	0.88	0.10	0.13	0 10	1.61
G225	1.42	0.34	2.33	2.87	6.89	48.53	0.89	0.37	1.19	0.58	0 10	0.02	0.92	1.05	0.53	0.89	0.23	0.28	0 29	3.54
Mean	1.94	1.11	2.72	3.14	7.22	23.24	0.99	0.99	1.37	1.02	0 14	0.08	1.00	1.00	0.48	0.70	0.49	0.57	0.49	4.86
Minimum	0.22	0.06	0.89	1.06	0.83	2.48	0.24	0.07	0.47	0.24	0.02	0.00	0.19	0 27	0.16	0.39	0.02	0.02	0.01	0.12
Maximum	3.52	2.96	4.11	4.89	23.89	369.22	1.59	2.03	1.88	1.72	0 26	0.22	1.69	1.60	0.87	0.98	1.42	1.73	1.71	14.83

PreADS and PoADS = pre-anthesis drought stress and post-anthesis drought stress, respectively; TOL = tolerance index; MP = mean productivity, HM = harmonic mean; STI = stress susceptibility index; GMP = geometric mean productivity; STI = stress tolerance index; YI = yield index; YSI = yield stability index; K_1STI = modified stress tolerance index I; K_2STI = modified stress tolerance index II

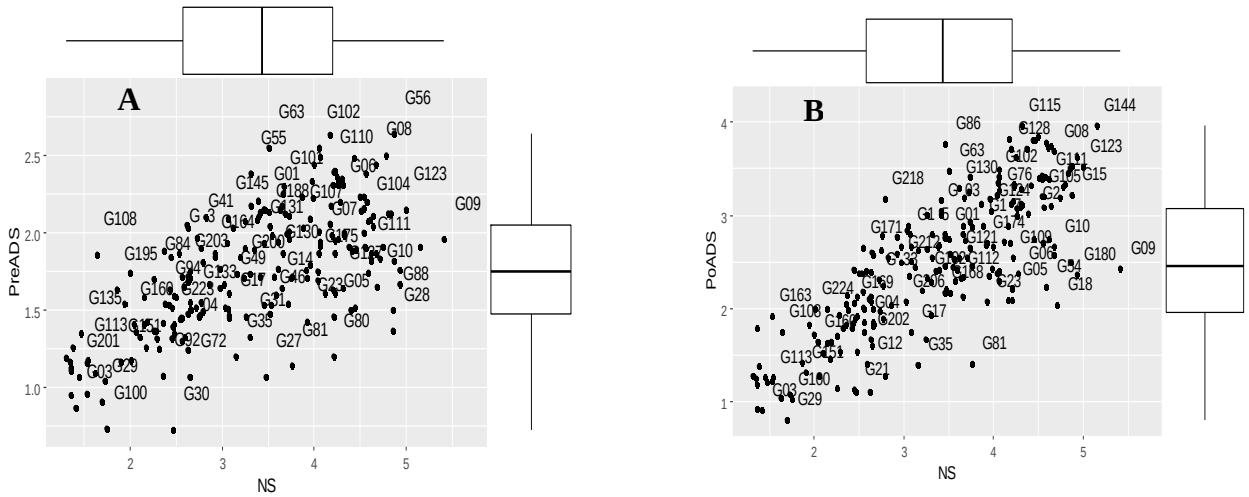
3.3.3 Genotype and trait correlations under non-stressed and drought-stressed conditions

Biplots showing the groupings of 225 sorghum genotypes based on grain yield under NS, PreADS, and PoADS in greenhouse and field environments are shown in Figure 3.1. Grain yield performance under PreADS versus NS conditions in a greenhouse environment (Figure 3.1A) revealed genotypes G56 as being more suitable for both stressed and non-stressed environments (Group A), while G09 is more desirable for non-stress conditions (Group B). Similarly, genotypes G145 and G01 recorded relatively higher grain yield only under PreADS in a greenhouse environment (Group C), whereas genotypes G100 and G03 were sensitive to drought due to poor yield performance in both PreADS and non-stress conditions (Group D). Biplots showing grain yield performance under PoADS versus NS conditions in a greenhouse environment (Figure 3.1B) revealed genotypes G08 and G144 as drought-tolerant with high performance in both conditions (Group A), while genotypes G09 and G10 were more suitable for a non-stress environment (Group B) and recorded a high grain yield of ~2.40 t/ha (Figure 3.1B). Genotypes G81 and G35 are more desirable for stressed conditions (Group C). Genotypes G29 and G100 are drought-susceptible and recorded low grain yields under PoADS and NS conditions in a greenhouse environment (Group D).

Under the field environment (Figure 3.1C), sorghum genotypes G152, G08, and G106 were allocated to Group A and recorded high grain yield values under PreADS and NS conditions. The second group (Group B) comprised G109, which is semi-tolerant and recorded a grain yield below the mean value (1.76 t/ha) under PreADS condition, whereas G55 and G63 were highly tolerant to PreADS, recording a grain yield >2.5 t/ha. Similarly, genotypes including G27, G81, G80, and G28 were clustered in the third group (Group C). In this group, the genotype had a more desirable yield under stressed conditions and comprised G22, G04, and G191. Finally, Group D consisted of genotypes G03, G29, and G100 with a low yield performance under both stressed and non-stressed conditions. The genotypes in group D were susceptible to PreADS conditions (<1.00 t/ha) under a greenhouse environment (Figure 3.1C). Under PoADS in a greenhouse environment (Figure 3.1D), G131, G115, and G104 were identified as high performers under PoADS and NS conditions (Group A), whereas genotype G109 belonged to Group B (high-yielding only under NS condition) and recorded a grain yield of 2.75 t/ha. Genotypes G81 and G18 belong to Group C with a high grain yield only under PoADS condition and Group D comprises G03 and G29 with a low yield (<1.00 t/ha) under both PoADS and NS conditions.

Across greenhouse and field environments, genotypes G114 and 56 were identified as drought-tolerant with high performances in both stress conditions under NS and PreADS conditions (Group A), while genotypes G09 and G109 were more suitable for non-stress environments (Group B). Genotype G72 and G75 were more desirable for stressed conditions recording 2.65 t/ha and 2.19 t/ha (Group C). Genotypes G03, G29, and G100 were drought susceptible and recorded low grain yields under PreADS and NS conditions across both greenhouse and field environments (Group D) (Figure 3.1E). Genotypes G144, G115, and G104 were identified as high performers under PoADS and NS condition (Group A), whereas genotypes G109 and G09 belonged to Group B (high-yielding only under NS conditions) (Figure 3.IF). Genotypes G210 and G12 belong to Group C with high grain yield only under PoADS conditions and Group D comprises G03, G135, and G29 with low yields (<1.00 t/ha) under both PoADS and NS conditions across test environments.

Simple linear regression models showing the relationships between grain yield under drought stress (e.g., PreADS and PoADS) and NS conditions in greenhouse and field environments are shown in Figure 3.2. For grain yield under PreADS vs NS conditions and PoADS vs NS conditions in a greenhouse environment, the model was highly significant (p<0.001) and explained 42% (R^2 = 0.42) and 63% (R^2 = 0.63) of the total explained variations in grain yield, respectively (Figure 3.2A,B). Under PreADS vs NS conditions and PoADS vs NS conditions in the field environment, the model was highly significant (p<0.001) and explained 32% (R^2 = 0.32) and 78% (R^2 = 0.78) of the total explained variation in grain yield, respectively (Figure 3.2C,D). Across greenhouse and field environments (Figure 3.2E,F), the model was highly significant (p<0.001) for grain yield under PreADS vs. NS conditions, and PoADS vs NS conditions and was explained by 42% (R^2 = 0.42) and 73% (R^2 = 0.73) of the total variation in grain yield of the tested sorghum genotypes.



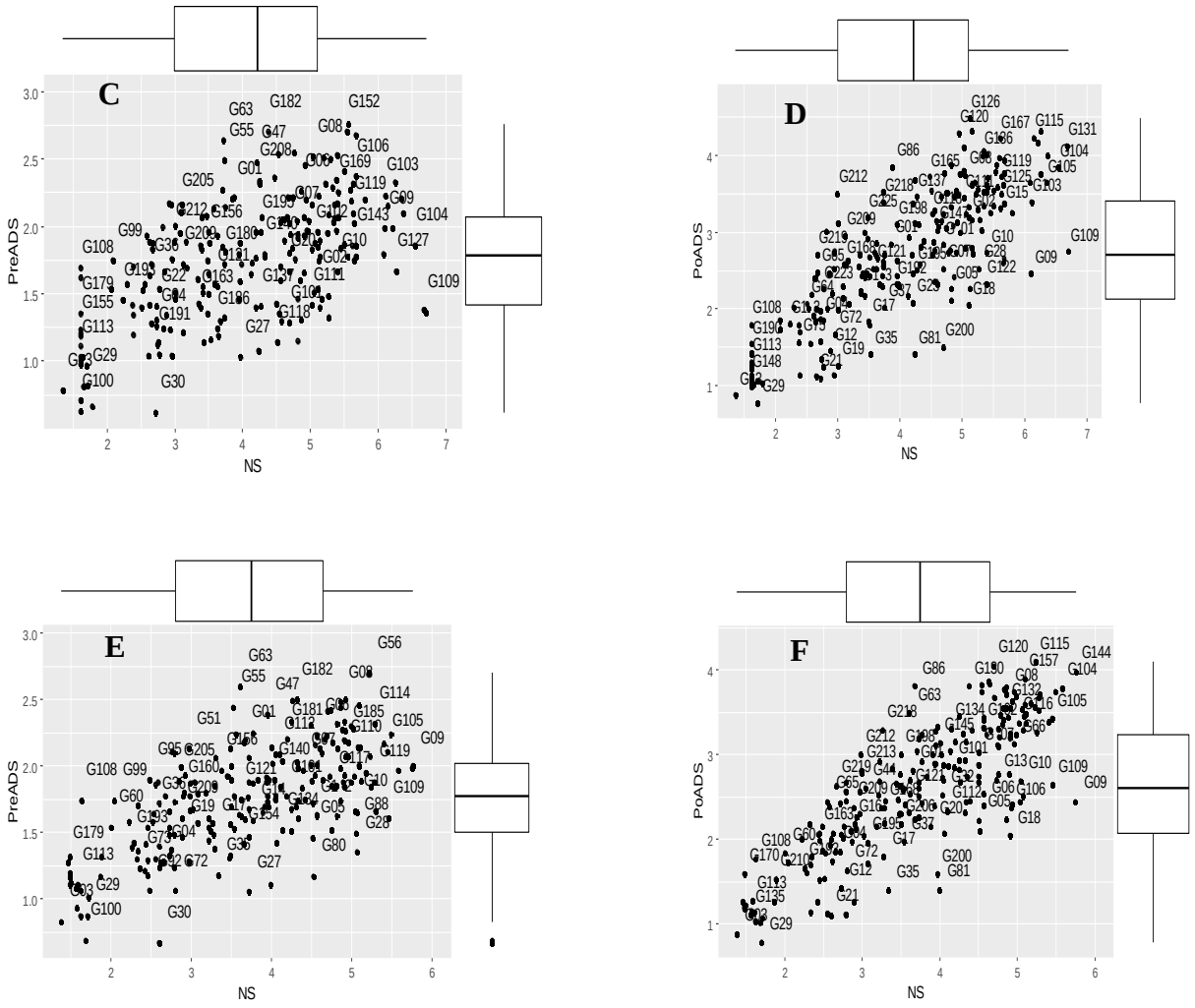
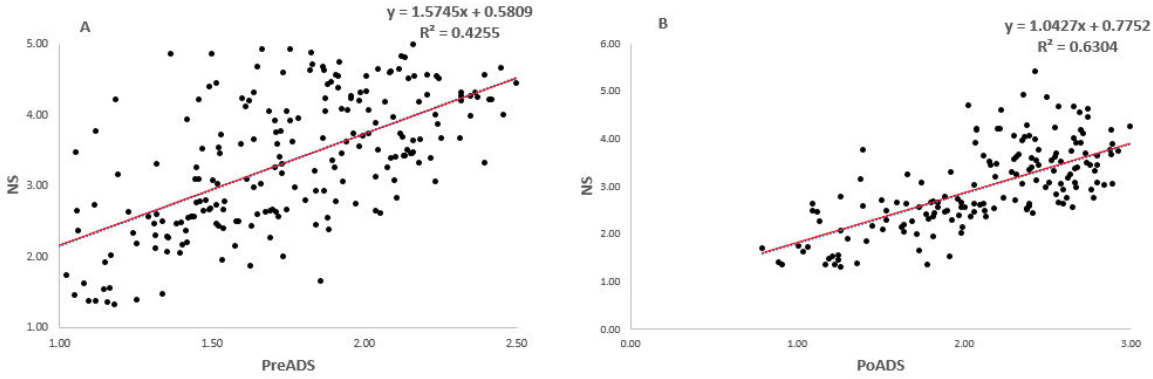


Figure 3.1:. Scheme showing grouping of 225 sorghum genotypes for mean grain yield (t/ha) when evaluated under non-stressed (NS), pre-anthesis drought stress (PreADS), and post-anthesis drought stress (PoADS) conditions in the greenhouse (**A**, **B**) and field (**C**, **D**) environments, and across both greenhouse and field (**E**, **F**) environments. The box plots summarise the five data summaries (minimum, first quartile, median, third quartile, and maximum) of grain yields under NS, PreADS, and PoADS conditions.



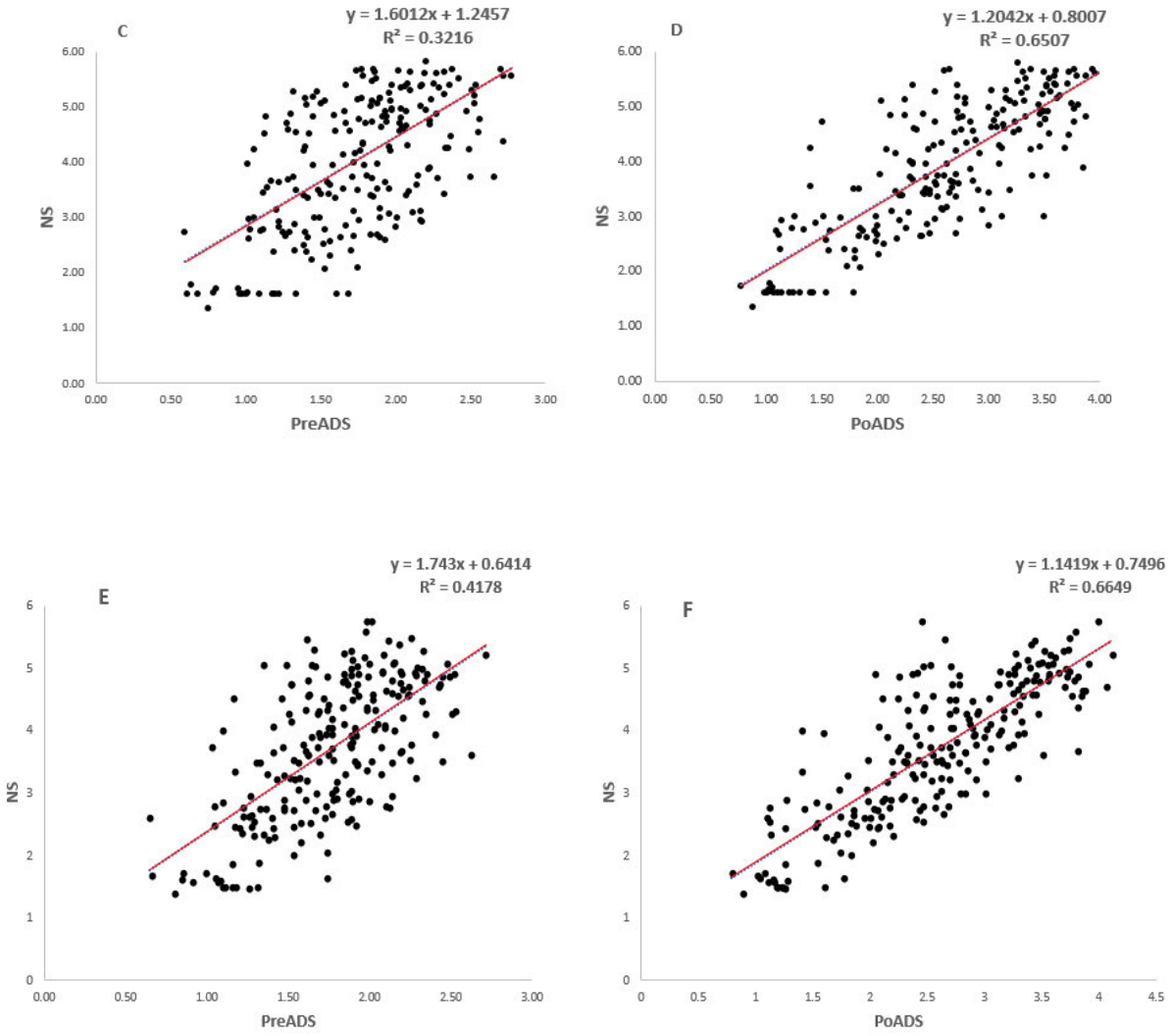


Figure 3.2: Simple linear regression model fitting grain yield (t/ha) performance of 225 sorghum genotypes evaluated under non-stressed (NS), pre-anthesis drought stress (PreADS), and post-anthesis drought stress (PoADS) in the greenhouse (**A**,**B**) and field (**C**,**D**) environments, and across both greenhouse and field (**E**,**F**) environments.

3.3.4 Genotype ranking for drought tolerance

The drought tolerance/susceptibility presented in Table 3.4 highlighted some challenges in the identification of drought-tolerant genotypes. For example, different indices identified drought-tolerant and susceptible genotypes. To determine the most desirable drought-tolerant genotypes according to all indices, the mean rank and the standard deviation of ranks of all drought tolerance criteria were calculated and presented in Tables 3.5 and 3.6. On the basis on these two criteria, the most desirable drought-tolerant cultivars were identified. For PreADS, genotypes G56 (CSRO1), G157 (Kaura Mai Baki Kona), G8 (ICNSL2014-022-4), and G152 (Bog Farwa) exhibited the best

mean rank and low standard deviation of rank. Hence, they were identified as the most drought-tolerant genotypes, while G3 (Gadam) and G100 (AS 97) were identified as the most drought-susceptible genotypes (Table 3.5).

Under PoADS condition, genotypes G115 (Danyar Bana), followed by G157 (Kaura Mai Baki Kona), G120 (Gagarau–4), and G144 (Kaura Short Panicle-1) recorded high rank mean and were identified (Table 3.6) as the most drought-tolerant. The genotypes G115 (Danyar Bana), G157 (Kaura Mai Baki Kona), G120 (Gagarau–4), G144 (Kaura Short Panicle-1), and G152 (Bog Farwa) were identified as the most desirable drought-tolerant genotypes. In contrast, genotypes G3 (Gadam), G29 (12KNICSV-293), and G100 (AS 97) exhibited the worst mean rank and high standard deviation of rank and are considered as the most susceptible to drought stress (Table 3.6).

Table 3.5: Rank, rank mean ($\bar{R}$) and standard deviation of ranks (SDR) of drought tolerance indices of the sorghum genotypes in PreADS

Code	Yp	Ys	TOL	MP	HM	SSI	GMP	STI	YI	YSI	K_1STI	K_2STI	$\bar{R}$	SDR
G1	116	48	69	98	24	30	157	157	48	30	111	60	79.00	45.76
G2	55	140	211	77	173	209	15	15	140	209	63	120	118.92	70.17
G3	225	223	21	225	223	215	205	205	223	215	225	224	202.42	55.16
G4	184	193	74	188	197	167	152	152	193	167	187	193	170.58	32.92
G5	72	162	204	100	184	212	22	22	162	212	80	147	131.58	67.23
G6	65	37	140	50	46	78	86	86	37	78	62	39	67.00	28.34
G7	76	72	154	73	92	120	72	72	72	120	77	77	89.75	25.85
G8	31	4	142	10	12	53	84	84	4	53	21	3	41.75	41.50
G9	2	56	223	8	115	196	3	3	56	196	2	43	75.25	81.67
G10	27	118	216	59	157	205	10	10	118	205	43	97	105.42	73.89
G11	83	69	136	74	75	101	90	90	69	101	79	68	86.25	18.72
G12	180	190	79	186	193	162	147	147	190	162	182	189	167.25	31.05
G13	56	76	185	60	108	153	41	41	76	153	58	69	89.67	46.55
G14	115	150	128	129	159	164	98	98	150	164	119	143	134.75	22.82
G15	13	73	215	30	126	191	11	11	73	191	15	55	83.67	74.32
G16	58	145	212	80	175	210	14	14	145	210	65	127	121.25	70.66
G17	150	176	101	162	180	161	125	125	176	161	152	170	153.25	23.39
G18	44	95	200	63	132	188	26	26	95	188	51	81	99.08	61.08
G19	170	180	78	176	182	129	148	148	180	129	173	182	156.25	30.36
G20	109	142	138	121	155	163	88	88	142	163	114	136	129.92	24.99
G21	192	197	63	196	200	158	163	163	197	158	193	199	173.25	37.19
G22	186	184	58	185	181	114	168	168	184	114	186	184	159.33	39.69
G23	100	173	177	127	189	208	49	49	173	208	109	161	143.58	53.83
G24	202	194	41	202	188	104	185	185	194	104	204	197	166.67	50.89
G25	142	43	30	114	4	9	196	196	43	9	136	63	82.08	68.54
G26	173	208	102	191	213	216	124	124	208	216	180	206	180.08	39.21
G27	122	204	183	160	214	221	43	43	204	221	139	194	162.33	61.31

Table 3.5: Continued

Code	Yp	Ys	TOL	MP	HM	SSI	GMP	STI	YI	YSI	K_1STI	K_2STI	$\bar{R}$	SDR
G28	32	166	224	75	192	220	2	2	166	220	49	145	124.42	83.31
G29	212	222	39	222	222	219	187	187	222	219	214	222	198.92	49.77
G30	193	224	124	209	224	225	102	102	224	225	205	223	190.00	47.82
G31	140	182	134	155	194	204	92	92	182	204	143	179	158.42	37.60
G32	98	121	145	108	131	148	81	81	121	148	99	114	116.25	22.90
G33	211	219	25	214	219	182	201	201	219	182	211	219	191.92	51.94
G34	214	218	17	216	216	128	209	209	218	128	212	218	183.58	59.59
G35	151	199	137	173	211	217	89	89	199	217	156	195	169.42	43.95
G36	189	163	33	180	112	35	193	193	163	35	185	168	137.42	63.04
G37	134	129	94	130	125	100	132	132	129	100	134	128	122.25	14.28
G38	94	109	143	101	127	137	83	83	109	137	97	110	110.83	19.99
G39	42	79	198	51	122	173	28	28	79	173	44	70	90.58	58.26
G40	68	60	157	65	81	119	69	69	60	119	68	62	83.08	29.91
G41	164	96	26	150	26	13	200	200	96	13	162	119	105.42	68.66
G42	93	64	112	87	66	73	114	114	64	73	94	74	85.67	18.72
G43	181	114	19	168	27	10	207	207	114	10	174	137	114.00	74.75
G44	153	104	49	141	58	32	177	177	104	32	153	121	108.42	51.96
G45	35	63	196	44	103	157	30	30	63	157	39	54	80.92	55.59
G46	118	164	146	132	179	189	80	80	164	189	123	158	143.50	36.20
G47	95	16	77	68	9	19	149	149	16	19	86	28	60.92	49.11
G48	144	111	73	137	84	58	153	153	111	58	142	126	112.50	34.45
G49	149	153	88	151	143	107	138	138	153	107	146	156	135.75	21.44
G50	160	102	37	147	42	18	189	189	102	18	159	123	107.17	61.80
G51	156	65	23	135	8	7	203	203	65	7	151	85	92.33	71.79
G52	169	77	13	146	5	4	213	213	77	4	165	105	99.25	77.86
G53	48	9	131	24	23	55	95	95	9	55	37	9	49.17	37.94
G54	50	108	205	66	144	197	21	21	108	197	57	93	105.58	64.27

Table 3.5: Continued

Code	Yp	Ys	TOL	MP	HM	SSI	GMP	STI	YI	YSI	K_1STI	K_2STI	$\bar{R}$	SDR
G55	124	22	40	91	3	8	186	186	22	8	115	38	70.25	65.19
G56	8	1	152	1	7	43	74	74	1	43	5	1	34.17	44.62
G57	146	158	91	152	152	124	135	135	158	124	145	157	139.75	18.82
G58	190	170	38	182	135	49	188	188	170	49	189	175	143.58	58.55
G59	126	44	57	102	13	17	169	169	44	17	118	59	77.92	54.64
G60	207	178	9	203	101	14	217	217	178	14	207	183	144.00	81.54
G61	141	71	51	124	32	23	175	175	71	23	140	86	92.67	54.18
G62	104	90	114	103	93	95	112	112	90	95	105	90	100.25	8.81
G63	114	2	29	69	2	3	197	197	2	3	100	12	60.83	71.87
G64	195	183	44	189	172	82	182	182	183	82	192	186	156.00	51.13
G65	182	124	20	170	28	11	206	206	124	11	175	140	116.42	74.53
G66	28	47	188	33	74	132	38	38	47	132	29	42	69.00	50.27
G67	168	137	43	165	82	34	183	183	137	34	168	149	123.58	56.27
G68	37	32	174	31	57	110	52	52	32	110	32	32	62.58	43.36
G69	16	29	191	17	63	126	35	35	29	126	14	25	58.83	54.90
G70	34	20	164	23	39	85	62	62	20	85	28	19	53.42	40.77
G71	81	10	89	49	11	27	137	137	10	27	70	16	55.33	45.29
G72	176	210	103	195	218	218	123	123	210	218	183	207	182.00	40.30
G73	200	200	52	204	201	151	174	174	200	151	200	202	175.75	41.86
G74	102	119	133	110	128	135	93	93	119	135	103	115	115.42	14.80
G75	203	185	32	197	170	67	194	194	185	67	202	188	157.00	59.86
G76	79	110	169	89	138	172	57	57	110	172	81	107	111.75	40.61
G77	64	123	195	76	147	194	31	31	123	194	67	104	112.42	58.18
G78	54	67	179	56	98	141	47	47	67	141	54	56	83.92	43.21
G79	82	136	180	96	162	195	46	46	136	195	83	125	123.50	51.11
G80	75	188	218	116	209	222	8	8	188	222	87	176	143.08	77.75
G81	110	202	197	149	215	223	29	29	202	223	124	190	157.75	67.66

Table 3.5: Continued

Code	Yp	Ys	TOL	MP	HM	SSI	GMP	STI	YI	YSI	K_1STI	K_2STI	$\bar{R}$	SDR
G82	167	74	16	144	6	5	210	210	74	5	160	102	97.75	76.08
G83	62	61	168	61	87	127	58	58	61	127	61	57	82.33	35.84
G84	198	159	15	183	69	15	211	211	159	15	194	167	133.00	76.91
G85	172	152	42	171	107	41	184	184	152	41	171	159	131.33	55.42
G86	111	40	72	88	16	24	154	154	40	24	104	49	73.00	47.04
G87	63	54	161	57	73	118	65	65	54	118	60	51	78.25	33.32
G88	22	135	220	62	174	214	6	6	135	214	35	113	111.33	79.78
G89	148	171	99	159	176	156	127	127	171	156	150	166	150.50	21.65
G90	147	165	95	156	169	143	131	131	165	143	149	164	146.50	19.90
G91	135	93	81	123	67	52	145	145	93	52	131	106	101.92	32.80
G92	194	211	84	205	217	207	142	142	211	207	197	208	185.42	39.15
G93	183	148	28	174	80	28	198	198	148	28	178	160	129.25	65.54
G94	191	175	36	184	139	50	190	190	175	50	191	180	145.92	59.71
G95	188	117	10	172	15	6	216	216	117	6	181	139	115.25	80.99
G96	204	169	18	192	104	21	208	208	169	21	199	181	141.17	74.93
G97	179	201	87	190	208	199	139	139	201	199	184	201	177.25	35.20
G98	177	172	53	177	149	79	173	173	172	79	177	172	146.08	44.73
G99	206	156	4	193	18	2	222	222	156	2	206	169	129.67	89.68
G100	213	225	50	224	225	224	176	176	225	224	224	225	200.92	48.83
G101	87	100	150	92	124	139	76	76	100	139	88	99	105.83	24.56
G102	61	26	135	43	36	70	91	91	26	70	56	31	61.33	31.31
G103	51	35	160	35	52	93	66	66	35	93	45	35	63.83	35.29
G104	3	45	219	7	99	183	7	7	45	183	4	34	69.67	77.39
G105	5	36	213	9	71	152	13	13	36	152	6	23	60.75	68.27
G106	38	6	144	15	21	60	82	82	6	60	27	5	45.50	40.29
G107	67	105	182	78	134	178	44	44	105	178	72	96	106.92	48.45
G108	210	161	1	207	1	1	225	225	161	1	209	178	131.67	94.59

Table 3.5: Continued

Code	Yp	Ys	TOL	MP	HM	SSI	GMP	STI	YI	YSI	K_1STI	K_2STI	$\bar{R}$	SDR
G109	7	122	225	36	166	213	1	1	122	213	12	88	100.50	85.01
G110	41	50	184	38	77	131	42	42	50	131	42	46	72.83	46.53
G111	43	116	210	64	151	201	16	16	116	201	52	98	107.00	68.31
G112	92	58	110	84	60	69	116	116	58	69	91	66	82.42	21.43
G113	215	216	12	213	210	87	214	214	216	87	213	215	176.00	68.17
G114	9	11	189	5	40	102	37	37	11	102	8	7	46.50	54.30
G115	11	33	203	11	70	142	23	23	33	142	9	24	60.33	62.51
G116	21	18	176	14	41	92	50	50	18	92	19	15	50.50	46.42
G117	46	81	194	55	121	171	32	32	81	171	47	73	92.00	55.56
G118	85	120	165	94	141	169	61	61	120	169	85	112	115.17	37.79
G119	10	62	217	25	114	186	9	9	62	186	11	50	78.42	74.54
G120	45	19	153	28	33	75	73	73	19	75	40	20	54.42	36.97
G121	121	126	105	125	123	106	121	121	126	106	122	124	118.83	7.80
G122	30	75	202	45	118	177	24	24	75	177	34	65	87.17	62.53
G123	6	24	207	6	65	136	19	19	24	136	7	18	55.58	64.10
G124	57	27	151	37	44	81	75	75	27	81	50	33	61.50	33.40
G125	36	30	173	29	54	105	53	53	30	105	31	30	60.75	42.84
G126	59	31	148	46	45	80	78	78	31	80	55	36	63.92	31.24
G127	12	98	221	34	145	206	5	5	98	206	16	80	93.83	79.74
G128	49	8	127	21	17	51	99	99	8	51	36	8	47.83	38.83
G129	4	13	206	3	47	125	20	20	13	125	3	6	48.75	63.63
G130	71	82	162	72	105	133	64	64	82	133	73	78	93.25	31.06
G131	24	107	214	53	148	203	12	12	107	203	38	84	100.42	73.14
G132	40	52	186	39	85	140	40	40	52	140	41	48	75.25	48.98
G133	120	134	121	126	137	130	105	105	134	130	120	129	124.25	10.13
G134	89	144	172	109	167	192	54	54	144	192	95	131	128.58	46.63
G135	218	217	11	220	212	98	215	215	217	98	216	217	179.50	67.04

Table 3.5: Continued

Code	Yp	Ys	TOL	MP	HM	SSI	GMP	STI	YI	YSI	K_1STI	K_2STI	$\bar{R}$	SDR
G136	39	14	156	22	30	71	70	70	14	71	30	14	50.08	39.28
G137	103	125	129	113	130	134	97	97	125	134	107	117	117.58	13.31
G138	77	66	147	70	76	108	79	79	66	108	75	67	84.83	23.26
G139	52	78	190	58	113	160	36	36	78	160	53	72	90.50	50.50
G140	97	87	125	95	95	103	101	101	87	103	96	83	97.75	10.35
G141	53	38	159	40	53	96	67	67	38	96	48	37	66.00	34.40
G142	69	131	192	86	161	198	34	34	131	198	74	116	118.67	57.69
G143	18	49	199	27	83	150	27	27	49	150	20	41	70.00	59.22
G144	1	41	222	2	91	184	4	4	41	184	1	22	66.42	79.70
G145	96	46	96	81	37	48	130	130	46	48	92	52	75.17	32.11
G146	88	57	118	79	62	76	108	108	57	76	84	64	81.42	19.87
G147	91	53	106	83	51	66	120	120	53	66	89	61	79.92	24.39
G148	217	220	22	221	220	190	204	204	220	190	222	220	195.83	53.64
G149	14	51	208	26	96	165	18	18	51	165	13	45	72.50	66.31
G150	60	42	155	48	55	90	71	71	42	90	59	40	68.58	30.82
G151	178	186	71	181	186	145	155	155	186	145	179	185	162.67	31.77
G152	33	5	149	12	19	61	77	77	5	61	24	4	43.92	41.43
G153	101	103	126	105	116	123	100	100	103	123	102	103	108.75	9.70
G154	123	168	139	140	183	193	87	87	168	193	129	163	147.75	35.20
G155	222	212	5	215	190	33	221	221	212	33	220	212	166.33	83.03
G156	139	83	68	122	48	37	158	158	83	37	132	94	96.58	42.72
G157	15	3	163	4	22	68	63	63	3	68	10	2	40.33	45.72
G158	19	28	187	19	61	121	39	39	28	121	18	26	58.83	52.26
G159	129	55	62	111	25	26	164	164	55	26	121	75	84.42	49.48
G160	165	138	47	164	90	39	179	179	138	39	166	151	124.58	53.03
G161	127	146	115	131	146	138	111	111	146	138	127	141	131.42	12.78
G162	17	68	209	32	109	179	17	17	68	179	22	53	80.83	68.11

Table 3.5: Continued

Code	Yp	Ys	TOL	MP	HM	SSI	GMP	STI	YI	YSI	K_1STI	K_2STI	$\bar{R}$	SDR
G163	196	203	66	201	206	181	160	160	203	181	196	204	179.75	37.71
G164	112	94	104	112	89	84	122	122	94	84	112	100	102.42	13.07
G165	113	59	86	99	43	44	140	140	59	44	110	76	84.42	34.41
G166	73	101	175	82	129	168	51	51	101	168	76	92	105.58	42.66
G167	25	17	166	18	38	86	60	60	17	86	25	17	51.25	42.73
G168	145	179	113	163	185	185	113	113	179	185	147	173	156.67	28.38
G169	105	92	116	104	100	97	110	110	92	97	106	95	102.00	7.39
G170	219	214	8	217	203	63	218	218	214	63	217	214	172.33	74.94
G171	99	86	120	97	86	94	106	106	86	94	98	82	96.17	10.38
G172	26	70	201	42	111	174	25	25	70	174	33	58	84.08	62.17
G173	106	88	109	106	88	89	117	117	88	89	108	89	99.50	11.50
G174	86	151	181	107	171	200	45	45	151	200	90	135	130.17	52.84
G175	70	85	167	71	110	149	59	59	85	149	69	79	96.00	36.69
G176	47	80	193	54	119	170	33	33	80	170	46	71	91.33	55.05
G177	131	157	119	139	165	155	107	107	157	155	135	155	140.17	19.59
G178	20	15	170	13	35	88	56	56	15	88	17	13	48.83	45.41
G179	224	207	3	212	168	16	223	223	207	16	218	210	160.58	87.18
G180	80	115	171	90	142	175	55	55	115	175	82	109	113.67	42.05
G181	84	39	108	67	34	54	118	118	39	54	78	44	69.75	29.90
G182	74	7	92	41	10	29	134	134	7	29	66	11	52.83	45.09
G183	90	91	132	93	106	122	94	94	91	122	93	87	101.25	14.75
G184	29	12	158	16	29	74	68	68	12	74	26	10	48.00	41.35
G185	23	25	178	20	50	109	48	48	25	109	23	21	56.58	47.68
G186	133	154	111	138	156	144	115	115	154	144	137	153	137.83	15.67
G187	107	34	75	85	14	25	151	151	34	25	101	47	70.75	46.55
G188	132	84	80	117	56	42	146	146	84	42	126	91	95.50	36.10
G189	66	23	123	47	31	62	103	103	23	62	64	29	61.33	32.16

Table 3.5: Continued

Code	Yp	Ys	TOL	MP	HM	SSI	GMP	STI	YI	YSI	K_1STI	K_2STI	$\bar{R}$	SDR
G190	220	205	2	211	153	12	224	224	205	12	215	209	157.67	87.86
G191	187	198	76	194	202	180	150	150	198	180	190	198	175.25	34.33
G192	128	149	117	134	150	147	109	109	149	147	130	146	134.58	15.21
G193	205	187	34	200	178	77	192	192	187	77	203	191	160.25	57.68
G194	78	21	100	52	20	38	126	126	21	38	71	27	59.83	38.21
G195	158	133	56	154	94	47	170	170	133	47	157	142	121.75	45.81
G196	152	128	67	145	102	59	159	159	128	59	148	133	119.92	36.91
G197	138	181	130	153	191	202	96	96	181	202	141	174	157.08	35.88
G198	130	89	85	119	68	56	141	141	89	56	125	101	100.00	29.74
G199	223	213	6	218	199	46	220	220	213	46	223	213	170.00	80.08
G200	108	141	141	120	154	166	85	85	141	166	113	134	129.50	26.56
G201	216	221	27	223	221	211	199	199	221	211	219	221	199.08	52.50
G202	159	167	83	166	160	116	143	143	167	116	161	165	145.50	25.85
G203	175	177	60	179	164	91	166	166	177	91	176	177	149.92	40.93
G204	161	189	93	178	196	187	133	133	189	187	169	187	166.83	30.22
G205	166	112	35	157	49	20	191	191	112	20	164	130	112.25	62.77
G206	136	139	98	136	136	117	128	128	139	117	138	138	129.17	12.11
G207	119	99	97	115	97	83	129	129	99	83	116	108	106.17	15.08
G208	137	97	82	128	72	57	144	144	97	57	133	111	104.92	31.32
G209	163	160	61	169	133	72	165	165	160	72	167	162	137.42	40.92
G210	208	195	14	208	177	45	212	212	195	45	208	203	160.17	73.41
G211	209	209	24	210	205	115	202	202	209	115	210	211	176.75	57.40
G212	155	127	54	148	78	40	172	172	127	40	155	132	116.67	48.02
G213	154	106	48	142	59	31	178	178	106	31	154	122	109.08	52.63
G214	197	196	55	198	198	146	171	171	196	146	195	200	172.42	40.29
G215	221	215	7	219	204	64	219	219	215	64	221	216	173.67	75.61
G216	162	132	46	161	79	36	180	180	132	36	163	144	120.92	53.71

Table 3.5: Continued

Code	Yp	Ys	TOL	MP	HM	SSI	GMP	STI	YI	YSI	K_1STI	K_2STI	$\bar{R}$	SDR
G217	117	113	107	118	120	111	119	119	113	111	117	118	115.25	3.94
G218	143	147	90	143	140	112	136	136	147	112	144	150	133.33	17.79
G219	174	130	31	167	64	22	195	195	130	22	170	148	120.67	64.63
G220	125	155	122	133	158	154	104	104	155	154	128	152	137.00	19.44
G221	171	174	65	175	163	99	161	161	174	99	172	171	148.75	36.47
G222	199	206	59	206	207	176	167	167	206	176	201	205	181.25	39.98
G223	185	192	70	187	195	159	156	156	192	159	188	192	169.25	33.59
G224	201	191	45	199	187	113	181	181	191	113	198	196	166.33	47.11
G225	157	143	64	158	117	65	162	162	143	65	158	154	129.00	38.97

Y_p = grain yield under no-stressed condition; Y_s = grain yield under drought-stress condition; $(\bar{R})$ = Rank mean, SDR = Standard deviation of rank. See codes of genotypes in Table 3.1 and codes of drought tolerance indices in Table 3.4.

Table 3.6: Rank, rank mean ($\bar{R}$), and standard deviation of ranks (SDR) of drought resistance/tolerance indices of the sorghum genotypes (PoADS).

Code	Yp	Ys	TOL	MP	HM	SSI	GMP	STI	YI	YSI	K_1STI	K_2STI	$\bar{R}$	SDR
G1	116	87	83	109	74	58	143	143	87	58	113	100	97.58	27.33
G2	55	67	184	55	116	157	42	42	67	157	56	57	87.92	48.99
G3	225	224	37	225	224	197	189	189	224	197	225	225	198.42	50.85
G4	184	183	75	183	175	140	151	151	183	140	183	185	161.08	31.24
G5	72	149	213	105	188	211	13	13	149	211	81	128	127.75	69.41
G6	65	127	212	87	174	201	14	14	127	201	71	104	116.42	66.89
G7	76	124	201	96	165	189	25	25	124	189	79	105	116.50	58.07
G8	31	13	123	18	33	56	103	103	13	56	26	14	49.08	37.96
G9	2	108	225	38	187	216	1	1	108	216	5	72	98.25	88.06
G10	27	94	214	57	160	199	12	12	94	199	42	75	98.75	72.40
G11	83	139	206	104	178	198	20	20	139	198	88	117	124.17	61.98
G12	180	204	138	194	210	206	88	88	204	206	186	200	175.33	43.27
G13	56	92	210	66	149	185	16	16	92	185	61	78	100.50	63.43
G14	115	136	149	123	150	168	77	77	136	168	116	132	128.92	28.58
G15	13	47	205	26	115	173	21	21	47	173	14	37	74.33	68.62
G16	58	90	204	67	146	184	22	22	90	184	62	77	100.50	60.71
G17	150	182	163	165	198	200	63	63	182	200	155	173	157.83	45.37
G18	44	157	224	94	199	217	2	2	157	217	65	129	125.58	79.40
G19	170	205	178	193	216	218	48	48	205	218	178	203	173.33	58.13
G20	109	159	188	131	186	196	38	38	159	196	114	144	138.17	53.16
G21	192	212	156	204	220	219	70	70	212	219	199	208	181.75	52.67
G22	186	180	61	181	155	101	165	165	180	101	185	181	153.42	40.10
G23	100	164	203	129	193	204	23	23	164	204	110	151	139.00	62.07
G24	202	213	128	207	219	215	98	98	213	215	205	209	185.17	45.33
G25	142	110	56	133	67	43	170	170	110	43	142	127	109.42	44.54
G26	173	198	145	190	206	203	81	81	198	203	179	195	171.00	43.41
G27	122	154	162	137	173	181	64	64	154	181	128	148	139.00	38.09

Table 3.6: Continued

Code	Yp	Ys	TOL	MP	HM	SSI	GMP	STI	YI	YSI	K_1STI	K_2STI	$\bar{R}$	SDR
G28	32	113	219	64	179	207	7	7	113	207	46	92	107.17	75.95
G29	212	225	93	224	225	222	133	133	225	222	217	224	196.25	45.36
G30	193	218	164	206	223	223	62	62	218	223	201	210	183.58	56.69
G31	140	151	127	145	153	159	99	99	151	159	140	149	139.33	19.93
G32	98	123	168	108	148	174	58	58	123	174	104	114	120.83	38.23
G33	211	221	55	213	217	193	171	171	221	193	211	220	191.42	44.63
G34	214	222	46	222	218	188	180	180	222	188	215	222	193.08	47.36
G35	151	203	202	177	213	220	24	24	203	220	157	193	165.58	66.81
G36	189	184	67	187	167	124	159	159	184	124	188	186	159.83	35.91
G37	134	169	171	153	191	194	55	55	169	194	141	163	149.08	45.89
G38	94	103	152	102	132	150	74	74	103	150	98	102	111.17	26.85
G39	42	85	211	58	147	187	15	15	85	187	50	70	96.00	66.40
G40	68	91	194	75	140	177	32	32	91	177	70	80	102.25	53.69
G41	164	172	91	172	161	139	135	135	172	139	169	170	151.58	23.58
G42	93	72	102	86	75	72	124	124	72	72	94	76	88.50	18.68
G43	181	145	14	169	24	13	212	212	145	13	174	160	121.83	77.53
G44	153	119	34	146	41	28	192	192	119	28	152	135	111.58	59.93
G45	35	49	185	41	97	145	41	41	49	145	36	45	75.75	51.01
G46	118	117	117	118	127	128	109	109	117	128	117	118	118.58	6.08
G47	95	51	65	74	25	31	161	161	51	31	90	59	74.50	44.06
G48	144	156	114	152	154	153	112	112	156	153	147	155	142.33	17.46
G49	149	130	66	144	92	54	160	160	130	54	148	139	118.83	39.11
G50	160	152	59	161	119	63	167	167	152	63	158	159	131.67	42.13
G51	156	125	32	148	37	24	194	194	125	24	156	137	112.67	62.64
G52	169	161	49	170	122	61	177	177	161	61	171	165	137.00	48.24
G53	48	60	180	51	107	147	46	46	60	147	47	54	82.75	46.87
G54	50	141	222	82	192	213	4	4	141	213	63	113	119.83	76.55
G55	124	109	98	121	109	94	128	128	109	94	124	116	112.83	12.11

Table 3.6: Continued

Code	Yp	Ys	TOL	MP	HM	SSI	GMP	STI	YI	YSI	K_1STI	K_2STI	$\bar{R}$	SDR
G56	8	22	186	8	69	125	40	40	22	125	8	10	55.25	56.60
G57	146	88	25	127	16	15	201	201	88	15	143	110	97.92	66.18
G58	190	197	99	196	203	183	127	127	197	183	194	198	174.50	33.93
G59	126	131	118	130	138	137	108	108	131	137	126	133	126.92	10.01
G60	207	186	11	202	85	17	215	215	186	17	207	194	145.17	82.07
G61	141	133	85	141	118	85	141	141	133	85	144	136	123.58	23.20
G62	104	135	169	116	159	178	57	57	135	178	109	126	126.92	39.68
G63	114	35	9	76	5	6	217	217	35	6	105	56	73.42	73.63
G64	195	173	30	182	105	39	196	196	173	39	191	178	141.42	65.18
G65	182	140	7	166	13	9	219	219	140	9	175	158	119.75	81.49
G66	28	61	199	45	120	164	27	27	61	164	35	52	81.92	59.80
G67	168	115	10	154	9	8	216	216	115	8	160	140	109.92	77.58
G68	37	11	112	20	30	48	114	114	11	48	28	15	49.00	39.00
G69	16	29	182	19	80	131	44	44	29	131	15	26	62.17	53.65
G70	34	33	161	34	68	107	65	65	33	107	30	34	64.25	39.69
G71	81	93	173	84	135	170	53	53	93	170	78	89	106.00	42.49
G72	176	195	122	188	204	192	104	104	195	192	180	191	170.25	35.70
G73	200	188	45	195	163	96	181	181	188	96	198	190	160.08	49.20
G74	102	81	108	98	91	91	118	118	81	91	101	90	97.50	11.94
G75	203	196	63	200	190	144	163	163	196	144	202	199	171.92	39.22
G76	79	58	110	61	55	67	116	116	58	67	76	58	76.75	22.65
G77	64	42	121	52	48	69	105	105	42	69	60	44	68.42	26.16
G78	54	9	79	28	17	33	147	147	9	33	43	16	51.25	46.88
G79	82	98	176	89	139	172	50	50	98	172	80	91	108.08	43.60
G80	75	160	216	110	196	214	10	10	160	214	86	138	132.42	71.77
G81	110	199	220	158	215	225	6	6	199	225	127	187	156.42	76.22
G82	167	137	27	157	40	21	199	199	137	21	163	153	118.42	67.20
G83	62	19	80	35	18	34	146	146	19	34	53	27	56.08	44.02

Table 3.6: Continued

Code	Yp	Ys	TOL	MP	HM	SSI	GMP	STI	YI	YSI	K_1STI	K_2STI	$\bar{R}$	SDR
G84	198	193	54	197	176	122	172	172	193	122	197	192	165.67	42.49
G85	172	142	23	163	38	18	203	203	142	18	172	157	120.92	70.89
G86	111	16	3	60	1	1	223	223	16	1	99	41	66.25	78.91
G87	63	41	125	49	51	73	101	101	41	73	57	42	68.08	26.47
G88	22	30	170	24	72	119	56	56	30	119	22	30	62.50	46.59
G89	148	111	41	138	52	36	185	185	111	36	145	131	109.92	53.40
G90	147	143	87	150	128	98	139	139	143	98	149	146	130.58	21.80
G91	135	107	74	125	89	59	152	152	107	59	134	119	109.33	31.61
G92	194	185	53	191	162	102	173	173	185	102	193	188	158.42	44.47
G93	183	176	51	179	141	78	175	175	176	78	181	177	147.50	46.90
G94	191	179	36	185	130	52	190	190	179	52	190	180	146.17	59.66
G95	188	165	26	175	71	29	200	200	165	29	184	169	133.42	68.70
G96	204	178	16	192	63	19	210	210	178	19	200	184	139.42	79.38
G97	179	210	183	201	222	224	43	43	210	224	189	206	177.83	62.00
G98	177	181	89	180	180	155	137	137	181	155	177	183	161.00	27.27
G99	206	192	24	203	134	40	202	202	192	40	206	196	153.08	70.92
G100	213	223	60	223	221	202	166	166	223	202	214	223	194.67	45.19
G101	87	84	144	91	117	135	82	82	84	135	89	83	101.08	23.24
G102	61	44	134	53	60	87	92	92	44	87	58	48	71.67	25.91
G103	51	55	167	50	93	132	59	59	55	132	49	51	79.42	39.60
G104	3	7	196	2	61	130	30	30	7	130	2	3	50.08	63.09
G105	5	32	207	9	99	162	19	19	32	162	4	22	64.33	70.03
G106	38	120	218	70	184	208	8	8	120	208	52	96	110.83	75.11
G107	67	70	165	62	111	143	61	61	70	143	66	64	90.25	37.34
G108	210	191	1	208	3	2	225	225	191	2	210	202	139.17	97.51
G109	7	96	223	46	172	210	3	3	96	210	16	67	95.75	83.09
G110	41	121	217	72	183	205	9	9	121	205	55	98	111.33	73.50
G111	43	39	157	40	73	110	69	69	39	110	39	38	68.83	36.86

Table 3.6: Continued

Code	Yp	Ys	TOL	MP	HM	SSI	GMP	STI	YI	YSI	K_1STI	K_2STI	$\bar{R}$	SDR
G112	92	138	191	113	168	186	35	35	138	186	100	120	125.17	51.69
G113	215	208	22	212	195	84	204	204	208	84	212	212	171.67	64.42
G114	9	26	192	10	83	138	34	34	26	138	10	18	59.83	59.97
G115	11	1	119	3	22	44	107	107	1	44	6	2	38.92	44.17
G116	21	38	181	29	87	136	45	45	38	136	23	33	67.67	51.81
G117	46	36	147	37	56	93	79	79	36	93	41	36	64.92	32.93
G118	85	86	159	85	125	149	67	67	86	149	83	85	102.17	32.13
G119	10	20	179	6	59	115	47	47	20	115	9	9	53.00	53.06
G120	45	3	64	12	8	20	162	162	3	20	31	6	44.67	55.30
G121	121	126	113	124	129	126	113	113	126	126	122	125	122.00	5.55
G122	30	116	221	63	182	209	5	5	116	209	45	93	107.83	77.62
G123	6	34	209	11	100	166	17	17	34	166	7	24	65.92	70.90
G124	57	45	153	48	79	108	73	73	45	108	54	49	74.33	31.95
G125	36	56	187	44	104	152	39	39	56	152	37	50	79.33	52.35
G126	59	10	70	33	14	26	156	156	10	26	51	19	52.50	49.81
G127	12	17	172	7	53	109	54	54	17	109	11	8	51.92	50.50
G128	49	18	105	30	31	46	121	121	18	46	38	23	53.83	37.24
G129	4	8	193	4	62	127	33	33	8	127	3	5	50.58	61.25
G130	71	14	47	42	10	16	179	179	14	16	64	28	56.67	58.06
G131	24	48	190	36	101	154	36	36	48	154	29	40	74.67	56.53
G132	40	28	140	32	49	83	86	86	28	83	34	32	60.08	33.69
G133	120	106	103	115	112	100	123	123	106	100	115	112	111.25	7.95
G134	89	57	81	73	35	42	145	145	57	42	85	60	75.92	35.09
G135	218	220	33	221	211	163	193	193	220	163	219	221	189.58	51.57
G136	39	27	137	31	45	77	89	89	27	77	33	29	58.33	33.58
G137	103	74	95	97	70	62	131	131	74	62	102	82	90.25	22.90
G138	77	63	126	65	76	90	100	100	63	90	74	61	82.08	18.91
G139	52	46	158	47	86	116	68	68	46	116	48	46	74.75	35.40

Table 3.6: Continued

Code	Yp	Ys	TOL	MP	HM	SSI	GMP	STI	YI	YSI	K_1STI	K_2STI	$\bar{R}$	SDR
G140	97	100	142	100	124	141	84	84	100	141	97	99	109.08	20.90
G141	53	5	76	23	15	30	150	150	5	30	40	13	49.17	49.12
G142	69	112	208	88	164	191	18	18	112	191	75	101	112.25	61.91
G143	18	24	166	17	58	105	60	60	24	105	17	21	56.25	45.37
G144	1	2	197	1	47	120	29	29	2	120	1	1	45.83	62.12
G145	96	66	86	80	44	47	140	140	66	47	92	68	81.00	31.14
G146	88	69	111	79	77	80	115	115	69	80	87	71	86.75	16.61
G147	91	78	124	92	98	106	102	102	78	106	93	81	95.92	12.85
G148	217	217	31	218	207	151	195	195	217	151	218	218	186.25	52.47
G149	14	23	174	13	65	117	52	52	23	117	13	17	56.67	50.53
G150	60	54	151	54	84	112	75	75	54	112	59	53	78.58	29.90
G151	178	177	69	176	151	104	157	157	177	104	176	175	150.08	35.49
G152	33	6	109	15	27	45	117	117	6	45	25	7	46.00	41.54
G153	101	68	84	90	46	50	142	142	68	50	96	74	84.25	31.04
G154	123	97	78	114	78	57	148	148	97	57	119	106	101.83	29.40
G155	222	216	21	220	202	97	205	205	216	97	224	217	178.50	64.57
G156	139	89	44	120	39	32	182	182	89	32	133	108	99.08	52.33
G157	15	4	131	5	32	53	95	95	4	53	12	4	41.92	42.04
G158	19	31	177	22	82	129	49	49	31	129	20	31	64.08	50.81
G159	129	95	71	117	66	51	155	155	95	51	123	107	101.25	34.87
G160	165	162	68	164	133	81	158	158	162	81	166	164	138.50	36.78
G161	127	105	92	119	95	75	134	134	105	75	125	115	108.42	19.98
G162	17	40	195	27	94	148	31	31	40	148	19	35	68.75	58.93
G163	196	175	28	186	96	35	198	198	175	35	192	179	141.08	67.81
G164	112	79	82	106	64	55	144	144	79	55	111	95	93.83	29.29
G165	113	65	40	95	20	22	186	186	65	22	108	73	82.92	55.45
G166	73	53	115	59	54	71	111	111	53	71	68	55	74.50	22.98
G167	25	21	139	21	43	76	87	87	21	76	24	20	53.33	37.25

Table 3.6: Continued

Code	Yp	Ys	TOL	MP	HM	SSI	GMP	STI	YI	YSI	K_1STI	K_2STI	$\bar{R}$	SDR
G168	145	147	96	149	137	118	130	130	147	118	146	150	134.42	16.02
G169	105	83	101	101	90	82	125	125	83	82	106	94	98.08	14.81
G170	219	201	2	211	7	3	224	224	201	3	213	207	142.92	98.67
G171	99	52	52	77	23	27	174	174	52	27	95	62	76.17	49.69
G172	26	50	189	39	103	156	37	37	50	156	32	43	76.50	55.96
G173	106	99	116	107	110	111	110	110	99	111	107	103	107.42	4.86
G174	86	77	148	81	113	134	78	78	77	134	82	79	97.25	25.89
G175	70	101	198	78	145	180	28	28	101	180	72	88	105.75	55.31
G176	47	43	160	43	81	114	66	66	43	114	44	39	71.67	37.02
G177	131	118	97	126	114	95	129	129	118	95	129	124	117.08	13.34
G178	20	15	141	14	42	74	85	85	15	74	18	12	49.58	39.85
G179	224	209	12	214	185	49	214	214	209	49	222	213	167.83	76.78
G180	80	129	200	99	166	190	26	26	129	190	84	109	119.00	57.44
G181	84	62	106	69	57	68	120	120	62	68	77	63	79.67	21.94
G182	74	71	154	71	106	133	72	72	71	133	73	66	91.33	30.11
G183	90	82	133	93	108	123	93	93	82	123	91	84	99.58	16.93
G184	29	25	150	25	50	88	76	76	25	88	27	25	57.00	37.77
G185	23	12	135	16	36	64	91	91	12	64	21	11	48.00	39.01
G186	133	114	90	128	102	79	136	136	114	79	132	122	113.75	20.58
G187	107	59	43	83	19	23	183	183	59	23	103	65	79.17	54.14
G188	132	144	132	136	152	160	94	94	144	160	135	142	135.42	20.67
G189	66	75	175	68	123	158	51	51	75	158	67	69	94.67	43.61
G190	220	211	18	215	194	70	208	208	211	70	220	214	171.58	70.04
G191	187	190	88	189	189	165	138	138	190	165	187	189	167.92	30.59
G192	128	146	136	135	157	167	90	90	146	167	131	141	136.17	24.00
G193	205	194	48	199	181	121	178	178	194	121	203	197	168.25	45.58
G194	78	37	77	56	26	38	149	149	37	38	69	47	66.75	40.16
G195	158	174	107	168	177	169	119	119	174	169	159	168	155.08	23.90

Table 3.6: Continued

Code	Yp	Ys	TOL	MP	HM	SSI	GMP	STI	YI	YSI	K_1STI	K_2STI	$\bar{R}$	SDR
G196	152	163	104	155	158	146	122	122	163	146	153	161	145.42	18.31
G197	138	150	130	143	156	161	96	96	150	161	138	147	138.83	21.13
G198	130	76	38	111	29	25	188	188	76	25	120	97	91.92	55.84
G199	223	215	20	219	201	92	206	206	215	92	223	216	177.33	65.68
G200	108	189	215	151	209	221	11	11	189	221	121	172	151.50	72.19
G201	216	219	35	217	212	171	191	191	219	171	216	219	189.75	49.86
G202	159	187	146	173	200	195	80	80	187	195	164	182	162.33	39.90
G203	175	170	62	174	143	89	164	164	170	89	173	171	145.33	39.09
G204	161	155	58	162	121	65	168	168	155	65	162	162	133.50	42.56
G205	166	167	72	171	142	99	154	154	167	99	168	167	143.83	32.68
G206	136	158	143	147	170	175	83	83	158	175	139	154	143.42	29.76
G207	119	128	129	122	136	142	97	97	128	142	118	123	123.42	14.05
G208	137	132	100	134	126	113	126	126	132	113	137	134	125.83	11.01
G209	163	148	39	160	88	41	187	187	148	41	161	156	126.58	55.17
G210	208	202	29	209	171	66	197	197	202	66	208	204	163.25	64.57
G211	209	207	50	210	208	176	176	176	207	176	209	211	184.58	43.30
G212	155	80	5	132	4	5	221	221	80	5	150	111	97.42	77.98
G213	154	102	15	140	11	10	211	211	102	10	151	121	103.17	72.71
G214	197	200	94	198	205	182	132	132	200	182	196	201	176.58	34.89
G215	221	214	19	216	197	86	207	207	214	86	221	215	175.25	66.62
G216	162	166	73	167	144	103	153	153	166	103	165	166	143.42	30.70
G217	117	73	57	103	34	37	169	169	73	37	112	87	89.00	44.98
G218	143	64	4	112	2	4	222	222	64	4	136	86	88.58	77.21
G219	174	122	6	156	6	7	220	220	122	7	170	143	112.75	80.70
G220	125	153	155	139	169	179	71	71	153	179	130	145	139.08	34.53
G221	171	134	17	159	21	14	209	209	134	14	167	152	116.75	74.36
G222	199	206	120	205	214	212	106	106	206	212	204	205	182.92	42.02
G223	185	171	42	178	131	60	184	184	171	60	182	174	143.50	53.64

Table 3.6: Continued

Code	Yp	Ys	TOL	MP	HM	SSI	GMP	STI	YI	YSI	K_1STI	K_2STI	$\bar{R}$	SDR
G224	201	168	8	184	28	12	218	218	168	12	195	176	132.33	84.53
G225	157	104	13	142	12	11	213	213	104	11	154	130	105.33	73.72

Y_p = grain yield under non-stressed condition; Y_s = grain yield under drought stress condition; ($\bar{R}$) = Rank mean; SDR = Standard deviation of rank. See codes of genotypes in Table 3.1 and codes of drought tolerance indices in Table 3.3

3.3.5 AMMI analysis of the GEI

AMMI analysis of variance for sorghum grain yield showed that 44.6% of the total sum of squares was attributed to environmental effects, 38.7% to genotypic effects, and 16.7% to GEI effects (Table 3.7). Three interactive principal components axes (IPCA), including IPCA1, IPCA 2, and IPCA 3 were significant in the AMMI model (Table 3.7). IPCA1, IPCA2, and IPCA3 explained 61.4%, 19.4%, and 12.8% of the GEI variation, respectively. The three IPCAs cumulatively explained 93.6% of the variation to GEI, indicating that the AMMI model was a good fit for the grain yield data. The F_R statistic is considered under the null hypothesis that no more than *n* terms determine the interaction. Thus, a significant result by the test suggests that at least one multiplicative term should be added to the already adjusted *n*. In the present study, three significant IPCAs were detected, indicating the need for adding a multiplicative term. As a result, AMMI model 4 is the best-fitting model for the yield dataset based on the F_R-test.

Table 3.7: Additive main effects and multiplicative interaction analysis of variance for grain yield of 225 sorghum accessions tested in six environments.

Source of variation	Degree of freedom	Sum of square	†TV (%)	F_R-test MS
Total	2699	4305.32		1.60
Treatments	1349	4117.54		3.05
Genotype (G)	224	1593.18	38.7	7.11 **
Environment (E)	5	1837.03	44.6	367.30 **
GEI	1120	687.22	16.7	0.61 **
Error	1344	186.71		0.14
Block/E	6	2.25		0.40
IPCA1	228	421.81	61.4	1.85 **
IPCA2	226	133.14	19.4	0.59 **
IPCA3	224	88.10	12.8	0.39 **
Residuals	442	44.11		0.10

** Highly significant at $p<0.01$ probability level; †TV = total variance; GEI = genotype-by-environment interaction; IPCA1 = The first interaction principal components axes; IPCA2 = The second interaction principal components axes; IPCA3 = The third interaction principal components axes; F_R-test MS = The mean sum of squares and test of significance.

The AMMI model family showing the best-performing sorghum genotypes in the test environments under NS, PreADS, and PoADS for grain yield are displayed in Table 3.8. Each model identifies the best-performing genotypes to guide selection. The mean comparison of environments showed that drought stress conditions significantly decreased sorghum grain yield

compared with non-stressed environmental conditions. Four genotypes, G9 (Yar Gumel), G144 (Kaura Short Panicle-1), G123 (Masakwa), and G119 (Yar Lazau) were best-performers under test environment E1 (greenhouse and NS) based on AMMI model families 1, 2, 3, and 4 in that order. Under test environment E2, the genotypes G56 (CSRO1), G63 (Tun Buman Maiduguri), G182 (Gwaza Banji Borno), and G8 (ICNSL2014-022-4) were selected as the top-performing genotypes based on AMMI models 1, 2, 3, and 4, respectively. The genotypes G131 (Yar Labe), G109 (Yalai), G104 (Dan Yara), and G127 (Dangama Wulchichi) were the best performers under environment E4 based on AMMI model families 1, 2, 3, and 4 model families. Under E5 (field and PreADS), genotypes G56 (CSRO1), G63 (Tun Buman Maiduguri), G106 (ICNSL2014-021-1), and G71 (Takumbo) were selected for high yield performance based on AMMI model families 1, 2, 3, and 4. The top four genotypes in E6 (field and PoADS) were G115 (Danyar Bana), G130 (S7-Lata/RIB/BC1-1-7-V), G126 (Jan Kaura 1), and G120 (Gagarau-4). AMMI 4 was the best-fitting model allowing genotypes to be selected for specific environments.

Table 3.8: Winning sorghum genotypes for grain yield based on additive main effects and multiplicative interaction (AMMI) model families.

Test environment designation	Environment Designations	Mean	Score	AMMI model family #			
				1	2	3	4
E1	GH-NS	3.344	1.382	G9	G144	G123	G119
E2	GH-PR	1.755	−1.598	G56	G63	G182	G8
E3	GH-PO	2.464	−0.432	G120	G144	G78	G115
E4	FL-NS	4.049	2.565	G131	G109	G104	G127
E5	FL-PR	1.750	−1.809	G56	G63	G106	G71
E6	FL-PO	2.698	−0.109	G115	G130	G126	G120

Genotype (G) codes are presented in Table 3.1. E1 = greenhouse and non-stressed ; E2 = greenhouse and pre-anthesis drought stress; E3 = greenhouse and post-anthesis drought stress; E4 = Field and non-stressed; E5 = Field and pre-anthesis; E6 = Field and post-anthesis.

3.3.6 AMMI stability value

The AMMI model does not provide for a quantitative measure of stability. However, such a measure is essential to quantify and rank genotypes according to their yield stability. The AMMI stability value (ASV) measure was proposed by Purchase et al., (2000) to address this problem. The ASV of the top- and poor-performing genotypes in yield stability are shown in Table 3.9. An

ideal genotype should have a high mean grain yield and small ASV. In this study, genotypes G42 (12KNICSV-107-1), G206 (Jawar), G186 (Harjiu), G147 (Geddawaki Panguga), and G177 (SSV2008113) showed the lowest ASV with a yield >2.5 t/ha and above the total average. The genotypes G109 (YALAI), G9 (YAR GUMEL), G131 (Yar Labe), and G127 (Dangama Wulchichi) had the highest ASV and were identified as the most unstable genotype recording ASV values >1.5.

Table 3.9: Mean grain yield value, IPCA-1 and IPCA-2 scores, and AMMI stability values (ASV) of 225 sorghum genotypes for grain yield.

Genotype code	Means (t/ha)	IPCA1	IPCA2	ASV
Top 10 most stable				
G42	3.05	−0.01	0.00	0.03
G206	2.44	−0.01	0.02	0.05
G186	2.55	−0.02	0.00	0.06
G147	3.05	0.01	−0.05	0.06
G177	2.54	−0.01	0.05	0.06
G192	2.49	0.02	0.05	0.07
G181	3.25	0.02	−0.13	0.14
G72	1.73	−0.04	0.09	0.15
G168	2.31	−0.04	0.11	0.16
G194	3.42	−0.03	−0.13	0.16
Top 10 least stable				
G109	3.28	0.62	0.00	1.97
G108	1.64	−0.6	−0.01	1.89
G9	3.47	0.54	0.48	1.77
G131	3.37	0.52	−0.53	1.72
G127	3.61	0.51	−0.35	1.65
G28	2.98	0.51	0.3	1.63
G144	4.03	0.49	−0.04	1.56
G104	3.87	0.48	−0.15	1.54
G190	1.21	−0.48	−0.09	1.52
G179	1.19	−0.48	−0.03	1.51

See genotype (G) codes in Table 3.1; IPCA1 = The first interaction principal components axes; IPCA2 = The second interaction principal components axes.

3.4 Discussion

Sorghum is an important cereal crop in the dry regions of Africa, mainly grown under dry conditions. The crop often experiences severe drought stress leading to significant yield losses and reduced yield gains. There is a lack of information on the response of African sorghum genotypes to drought, particularly their adaptation to adverse growing conditions in the semi-arid regions of SSA. Breeding efforts have been made to develop and upscale abiotic stress-tolerant and high-yielding sorghum varieties. However, the developed varieties were not readily adopted by farmers due to a lack of farmer-preferred traits and poor adaptation to local conditions (Camara et al., 2014; Yahaya et. Al., 2022). The present study examined the response of African sorghum genetic resources (Table 3.3) under variable environments to select unique germplasm for production and breeding. The results revealed a wide genetic diversity for yield gains and drought tolerance. The diversity recorded in the presently assessed sorghum germplasm will facilitate the selection of contrasting and promising genotypes with specific and broad adaptations.

The significance of the environment effects shows that there are trends and variations in how genotypes respond to variable environments. The higher environment effect relative to the genotype effect suggests a differential expression of phenotypes across the test environments (Table 3.7). Hence, the testing environments were distinct and discriminative of the genotypes for selection (Kapanigowda et al., 2013; Emendack et al., 2018; de Souza et al., 2021). Grain yield response was significantly ($p<0.01$) affected by the test environments, which accounts for 44.6% of the model's sum of square (SS) (Table 3.7). This agrees with the mean yield varying from 1.75 t/ha at environment E5 to 4.05 t/ha at environment E4 (Table 3.3), indicating a significant variance in yield productivity of the 225 sorghum genotypes in the six selected environments. Several studies have also reported that grain yield in multi-environment trials is highly affected by environmental influence (Amelework et al., 2016; Gebeyehu et al., 2019; Al-Naggar et al., 2020; de Souza et al., 2021). Therefore, the selection of genotypes suited for specific environments is critical to improving grain production. In the current study, considerable yield improvements were recorded in environments without stress (NS) compared with stress conditions (e.g., PreADS and PoADS) (Table 3.3). However, under both non-stressed and stressed conditions, the landraces and breeding lines from IAR-NG and ICRISAT-KN demonstrated a high superiority for grain yield than the collections from the USDA-ARS, NPGS, and to a lesser extent, ACCI-SA collections

(Table 3.3). The high yield response of the collections from IAR-NG and ICRISAT-KN under stressed and non-stressed conditions suggested that evaluating the genotypes in drought-prone locations was worthwhile. The yield variability could be attributed to the inherent differences in the genetic composition of the test materials and the long agricultural and selection history by farmers in regions that are prone to drought.

The genotypic variation was the second largest contributor to grain yield differences. Hence, the genetic composition of the test lines was diverse, allowing for the selection of desirable genotypes for current and future sorghum improvement programs (Table 3.7). The present results agree with previous studies that reported extensive variation in sorghum genetic resources for grain yield in east African, Indian, and Brazil (Amelework et al., 2016; Rosenow and Dahlberg, 2000; Kumar et al., 2013; de Souza et al., 2021).

The GEI effect was significant but accounted for the lowest contribution to variation for grain yield relative to environmental and genotypic components. In agreement with the present findings, other studies in sorghum (Rakshit et al., 2017), wheat (Koutis et al., 2012) and rice (Samonte et al., 2005), reported lower variation in grain yield due to GEI. These indicated that highly stable genotypes for grain yield could be selected for multiple growing conditions, particularly drought-stressed environments. The current results showed that the genotypes, e.g., G42, G206, G186, were adapted to both low- and high-yielding environments, while G56 and G106 were adapted to high-yielding environments (Table 3.8). Based on stability analysis, the average stable performers for grain yield were G42, G206, and G186, with mean grain yield ranging between 2.4 and 3.0 t/ha (Table 3.9). The selected genetic resources are useful for cultivation or breeding. Different drought tolerance traits can be pyramided through recurrent selection in novel varieties to buffer the effects of drought stress in water-limited growing conditions.

Drought imposed during pre- and post-anthesis stages markedly decreased grain yield (Table 3.3). Pre-anthesis drought stress reduced grain yield significantly compared with post-anthesis drought stress (Table 3.3), suggesting that the studied sorghum genotypes were more prone to pre-anthesis drought stress and less susceptible to post-anthesis drought stress. Several studies on sorghum have shown that drought stress at both pre- and post-anthesis growth stages significantly reduced grain quantity and quality (Kapanigowda et al., 2013; Emendack et al., 2018; de Souza et al., 2021). Emendack et al., (2018) reported 55% and 52% sorghum yield reduction under pre-and post-

flowering irrigation treatments, respectively. Rosenow et al., (1996) pointed out that drought stress during the pre-flowering growth stage may significantly impact grain yield, as this is the most prolonged crop growth and development stage. Drought stress at this stage resulted in delayed flowering, poor panicle emergence, panicle blasting and ovary abortion, and a reduction in panicle size and grain number, which are economic traits directly contributing to grain yield (Rosenow et al., 1996; Kapanigowda et al., 2013; Emendack et al., 2018; de Souza et al., 2021). Sorghum is relatively better adapted to drought stress and has genetic variability for pre-and post-anthesis drought tolerance and related traits when compared with major crops such as maize and wheat (Rosenow et al., 1996; Burke et al., 2018; Kapanigowda et al., 2013; Emendack et al., 2018).

Genotypes respond to drought stress in various ways (Farshadfar and Sutka, 2003; Jafari et al., 2009; de Souza et al., 2021). Regarding this, several criteria have been put forth to select genotypes based on their performance in an environment under stressed or non-stressed conditions (Farshadfar and Sutka, 2003). Tolerant genotypes exhibit the lowest SSI, and TOL values while greater values were found for MP, HM, GMP, STI, YI, and YSI (Rosielle and Hamblin 1981; Farshadfar and Sutka, 2003; Jafari et al., 2009). Based on mean rank and the high standard deviation of the rank, it can be inferred that genotypes G56, G157, G8, and G152 were the most drought-tolerant selections to pre-anthesis drought stress conditions, while genotypes G115, G157, G120, and G144 were the most tolerant to post-anthesis drought stress conditions (Table 3.6). This was supported by the biplot summary presented in Figure 3.1. The linear regression models (Figure 3.2) fitted the observed grain yield under non-stressed conditions and post-anthesis under greenhouse and field environments and across both environments. The model was a good predictor of post-anthesis grain yield response and allowed for the selection of post-anthesis drought-tolerant genotypes. Based on the biplot analyses for grain yield performance under non-stressed and post-anthesis drought conditions across environments, the following genotypes were selected as being highly tolerant to post-anthesis drought stress, namely: G144 (3.91 t/ha), G115 (3.80 t/ha), G105 (3.66 t/ha), G157 (3.83 t/ha), G08 (3.81 t/ha), and G120 (3.67 t/ha). A relatively low correlation was recorded for grain yield under non-stressed and pre-anthesis drought stress conditions (R^2 = 41.677%). This indicated that the grain yield recorded under non-stressed conditions provides information about the pre-anthesis drought-stress yield performance response. Further, the results inferred that the non-stress grain yield response might not discern the pre-anthesis grain yield response. Nevertheless, genotypes such as G72 and G75 were highly tolerant to pre-anthesis

drought stress. These genotypes recorded a grain yield of >2.30 t/ha under non-stress conditions and >1.50 t/ha under pre-anthesis drought stress. Emendack et al., (2018) reported that grain yield under well-watered treatment was a strong predictor for grain yield under both pre-flowering and post-flowering drought treatments.

The genotypes such as G144 (Kaura Short Panicle-1) and G157 (Kaura Mai Baki Kona) were selected due to their high grain yield performance under drought stress environments. These genotypes have yellow endosperm and are derived as hybrid selections from the durra and caudatum sorghum races. Furthermore, the selections have farmer-preferred traits, and drought tolerance attributes that are popular with local farmers in West Africa (Curtis, 1967; Smith and Frederiksen, 2000; Reddy and Reddy, 2019; Angarawai et al., 2021). In addition, G08 (ICNSL2014-022-4) is an elite and high-yielding breeding line developed at ICRISAT-Kenya with a drought tolerance (Reddy and Reddy, 2019; Angarawai et al., 2021). Genotypes G144, G157, and G08 outperformed some registered cultivated varieties in West Africa, such as G59 (Samsorg 48) with a grain yield of 2.76 t/ha and G94 (Samsorg 45) with 1.99 t/ha. The genotypes have superior grain quality and a wider adaptability compared with the currently registered cultivars and can thus be valuable parents in sorghum breeding programs to exploit heterosis (Angarawai et al., 2021).

3.5 Conclusions

The present study evaluated the drought tolerance and GEI effects on grain yield involving a genetically diverse population of African sorghum genotypes to identify high-yielding and drought-tolerant sorghum genotypes for production and breeding programs. Results from our study have shown the existence of significant and intricate GEI, which suggests that genotype performance varied among the test conditions. This information can be used to enhance selection, evaluation which can pave the way for more informed decisions in optimizing genotypic choices to suit specific environmental contexts. The environment, which accounted for more than 44.6% of all variation, was the main cause of variation in grain yield. According to AMMI, appropriate genotypes for all locations or for specific locations were identified, with the following genotypes, G119 and G127, with grain yields of 5.6 t/ha and 6.3 t/ha, respectively, chosen as suitable for non-stressed conditions due to their stability and high yield. The genotypes G56, G157, G8, and G152 were highly tolerant to pre-anthesis drought stress based on yield performance and drought

tolerance ranking, while the genotypes G144, G115, G157, and G08 were selected with tolerance to post-anthesis drought stress. The identified sorghum genotypes are recommended for production in the dry agro-ecologies of SSA characterized by pre-and-post anthesis drought stress and as valuable genetic material for pre- and/or post-drought tolerance, contributing to enhancing farmers' resilience. To strengthen these findings and ensure their relevance in semi-arid and arid environments, it is prudent to undertake additional trials under field conditions. This step will further authenticate the suitability of these genotypes and their adaptive qualities in semi-arid environments.

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CHAPTER 4 : Genetic diversity and population structure of African sorghum [*Sorghum bicolor* (L.) Moench] accessions assessed through single nucleotide polymorphism markers

Abstract

Assessing genetic diversity and population structure of cultivated sorghum is important for heterotic grouping, breeding population development, marker-assisted cultivar development, and release. The objective of the present study was to assess the genetic diversity and deduce the population structure of 200 sorghum accessions using diversity arrays technology–derived single nucleotide polymorphism (SNP) markers. The observed heterozygosity values ranged from 0.10 to 0.50 with an average of 0.32 while the average observed heterozygosity (0.15) was relatively low, which is a typical value for autogamous crop species like sorghum. Moderate polymorphic information content values were identified with a mean of 0.26, which indicates the informativeness of the chosen SNP markers. The population structure and cluster analyses revealed four main clusters with a high level of genetic diversity among the accessions studied. The variation within populations (41.5%) was significantly higher than that among populations (30.8%) and between samples within structure (27.7%). The study identified distantly related sorghum accessions such as Samsorg 48, Kaura red glume (Cluster 1); Gadam, AS 152 (Cluster 2); CSRO1, ICNSL2014−062 (Cluster 3); and Yalai, Kafi mori (Cluster 4). The accessions exhibited wide genetic diversity that will be useful in developing new gene pools and novel genotypes for the West and Central Africa sorghum breeding programs.

Keywords: accessions, population structure, gene flow, single nucleotide polymorphism, *Sorghum bicolor*

4.1 Introduction

Sorghum [*Sorghum bicolor* (L.) Moench, 2n=2x=20] is the fifth most important cereal crop in the world after maize (*Zea mays* L.), wheat (*Triticum aestivum* L.), rice (*Oryza sativa* L.) and barley (*Hordeum vulgare* L.). The global production area of sorghum is close to 50 million hectares, with production levels exceeding 60 million tons per annum (FAOSTAT, 2021). Sorghum is relatively more tolerant to biotic and abiotic stresses than other cereals, resulting in its wide adaptation, leading to production in marginal conditions across the globe. In these agro-ecologies, sorghum production is more dependable than other cereal crops such as wheat, rice, and maize (Dillon et al., 2007). These characteristics have contributed to sorghum being the staple food crop for more than 500 million resource-poor people in more than 98 countries in the semi-arid and arid regions of Africa and Asia (Pennisi, 2009). Nigeria grows approximately 40% of sorghum production in Africa (6.9 million tons) and is the second largest global producer after the USA (9.24 million tons). However, the area planted to sorghum in Nigeria (5.82 million ha) is more than double the sorghum production area in the USA (2.04 million ha) (FAOSTAT, 2021). However, productivity in the USA is at 4.5 t/ha, while the productivity of sorghum in Nigeria is trailing at 1.2 t/ha. A similar trend has been existing for the past three decades in West Africa, where the area planted to sorghum has increased by 50% but yields average <1 t/ha (Atokple, 2003). The farmers in Nigeria and West Africa mainly cultivate unimproved landraces that are low yielding but are adapted to thrive under the region's harsh environmental conditions, generating reliable harvests (Atokple, 2003).

Several constraints, including drought, low soil fertility, witchweed [*Striga hermonthica* (Delile) Benth.] and stem borer disease are limiting sorghum productivity in Africa. Fortunately, there is a broad diversity of landraces mainly grown by farmers and also used for sorghum improvement in the region in response to these different constraints. The Landraces are adapted to harsh conditions which make them vital genetic resources, possessing stress tolerance genes that can be exploited in sorghum breeding programs. The Institute for Agricultural Research (IAR) Samaru, Nigeria, maintains the most extensive *ex situ* sorghum germplasm collection (about 2,500 germplasms) among the National Agricultural Research Systems (NARS) in West Africa. The germplasm collection is a priceless genetic resource for various breeding programs, nationally and internationally. To fully utilize these genetic resources in genebanks, breeders should explore the

genetic variation within and among the collections and accessions. This is necessary for efficient use of genetic resources and resource allocation to breeding projects, and to minimize handling of duplicated accessions or closely related accessions. At present, the genetic diversity and genetic structure of IAR's conserved sorghum germplasm have not been fully documented. Thus, there is a need to assess the underlying genetic diversity and structure in the germplasm to devise optimal breeding strategies for sorghum at IAR.

Genetic diversity in germplasm collections is routinely assessed using different phenotypic and molecular markers. Molecular markers have been extensively used in genetic diversity studies because they are not affected by changes in environmental factors. Several molecular marker technologies have been developed and used in genetic diversity analysis studies, including proteins (Ayana et al., 2001), random amplified polymorphic DNA (RAPD) (Prakash et al., 2006), restriction fragment length polymorphism (RFLP) (Gerrano et al., 2014), inter-simple sequence repeat (ISSR) (Tadesse and Feyissa, 2013), amplified fragment length polymorphism (AFLP) (Ritter et al., 2007), simple sequence repeat (SSR) (Cuevas et al., 2018), expressed sequence tag-simple sequence repeat (EST-SSR) (Ramu et al., 2013) and single nucleotide polymorphism (SNP) (Morris et al., 2013; Afolayan et al., 2019). Each of these markers has its own advantages and limitations, which include low marker density, inadequate genome coverage, or cost per sample.

Diversity array technology (DArT) was developed in early 2000 to minimize a bottleneck inherent to other marker platforms. The DArT platform utilizes a microarray hybridization method to produce thousands of polymorphic loci in a single assay. The platform is fast becoming a marker of choice because it provides a cost-effective sequencing that is independent of prior sequence information with ultra-high-throughput marker systems. DArT markers have been used successfully in population genetic studies of sorghum (Mace et al., 2008); but also in other crops such as barley (Matthies et al., 2012); wheat (Laidò et al., 2013); macadamia (Alam et al., 2018) and maize (Adu et al., 2019). Cuevas et al., (2018) and Girma et al., (2019) assessed genetic diversity in sorghum using SNPs and found high levels of differentiation among the Ethiopian accessions they studied. Conversely, Lasky et al., (2015) reported less genomic variation among sorghum accessions from East Africa when assessed using SNPs. The differences in genomic variations can be attributed to genotype differences, the autogamous nature of sorghum, the accumulation of local diversity over time and more recombination events that break linkages

between adaptive and neighbouring loci. Information is lacking on population genetic structures and familial relatedness among sorghum accessions in West Africa based on reliable marker systems such as SNPs. Therefore, the objective of this study was to assess the genetic diversity and deduce the population structure among 200 sorghum accessions. The accessions form part of a core collection of germplasm used as parental lines in several sorghum breeding programs in Nigeria and neighbouring countries. The information generated will be valuable for sorghum pre-breeding by identifying diverse parental germplasm for core breeding.

4.2 Materials and methods

4.2.1 Germplasm

Seeds of 200 sorghum accessions from an existing collection (Table 4.1) were obtained from national and international research institutes; 130 landraces from Institute for Agricultural Research (IAR) Samaru, Nigeria, 60 elite breeding lines and landraces from the International Crops Research Institute for the Semi-Arid Tropics (ICRISAT) Kano Station Nigeria, and 10 lines from the African Centre for Crop Improvement (ACCI) South Africa used in this study. The selected accessions from IAR and ICRISAT were collected in farmers' fields in 2018 from sorghum growing regions and agro-ecological zones in Nigeria and are landraces that are well adapted to the environmental conditions and agricultural practices under which they are grown. In addition, the ACCI collections are accessions adapted to the growing agro-ecologies in South Africa.

Table 4.1: Source populations of 200 sorghum accessions used in the present study.

S/No.	Genotype	Source	Race	S/No.	Genotype	Source	Race	S/No.	Genotype	Source	Race
1	12KNICSV-293	ICRISAT	Bicolor	68	CAPARLKSG20150308	ICRISAT	Guinea	135	ICNSL2014-024-7	ICRISAT	Caudatum
2	Mai-Ruwan Zuma	IAR	Bicolor	69	CSRO2	IAR	Caudatum	136	Mori Shabal	IAR	Caudatum
3	Mori Masaba	IAR	Durum	70	Samsorg 46	IAR	Caudatum	137	Yar Jargada	IAR	Guinea
4	Tun Buman Maiduguri	IAR	Caudatum	71	Samsorg 7	IAR	Caudatum	138	Kaura Short Panicle- 1	IAR	Durum
5	12KNICSV-260	ICRISAT	Caudatum	72	Yar'fargore	IAR	Guinea	139	Keres	IAR	Guinea
6	ICNSL2014-027-2	ICRISAT	Guinea	73	12KNICSV-176	ICRISAT	Guinea	140	Kaura Black Glume-3	IAR	Durum
7	Gadam	ICRISAT	Guinea	74	Mai-Goje	IAR	Guinea	141	Geddawaki Panguga	IAR	Guinea
8	CAPARLGSG20150206	ICRISAT	Caudatum	75	Pam Para - 2	IAR	Guinea	142	Koma	IAR	Guinea
9	CAPARLGSG2015-0058	ICRISAT	Bicolor	76	12KNICSV-252	ICRISAT	Guinea	143	CAPARLGSG20150114-1	ICRISAT	Guinea
10	Samsorg 48	IAR	Caudatum	77	ICNSL2014-026-9	ICRISAT	Bicolor	144	Fate Fate	IAR	Bicolor
11	Samsorg 39	IAR	Bicolor	78	KAT 487	ICRISAT	Guinea	145	Danjiba	IAR	Bicolor
12	AS 152	ACCI	Guinea	79	Yarwasha	IAR	Bicolor	146	Bog Farwa	IAR	Guinea
13	12KNICSV-297-1	ICRISAT	Guinea	80	CSRO1	IAR	Caudatum	147	Ginzo-2 Yellow	IAR	Bicolor
14	AS 1	ACCI	Caudatum	81	Samsorg 41	IAR	Bicolor	148	SSV20064	IAR	Bicolor
15	Fara Fara Kyal-Kyal	IAR	Caudatum	83	Wago Sane Red Sorghum	ICRISAT	Bicolor	149	Yar Koma	IAR	Bicolor
16	AS 66	ACCI	Guinea	83	Samsorg 3	IAR	Bicolor	150	Kaura Short Panicle- 2	IAR	Durum
17	12KNICSV-93	ICRISAT	Caudatum	84	12KNICSV-295	ICRISAT	Guinea	151	Kaura Mai Baki Kona	IAR	Guinea
18	NR 71151	ICRISAT	Bicolor	85	Mace Da Kunya	IAR	Guinea	152	Kaura Red Glume	IAR	Guinea
19	ICSV111	ICRISAT	Caudatum	86	Zago Red Glume - 2	IAR	Guinea	153	Gagaran Mai Baka Kona	IAR	Guinea
20	S7-LATA/RIB/BC1-3-1-1-V	ICRISAT	Bicolor	87	12KNICSV-296-1	ICRISAT	Guinea	154	Kitse Kaza	IAR	Guinea
21	ICNSL2014-024-2	ICRISAT	Caudatum	88	ICNSL2014-062	ICRISAT	Caudatum	155	CAPARLGSG20150124.1	ICRISAT	Durum
22	Samsorg 42	IAR	Guinea	89	CAPARLGSG2015-0055	ICRISAT	Guinea	156	Fara Dawa	IAR	Guinea
23	Samsorg 38	IAR	Bicolor	90	CAPARLKSG20150280	ICRISAT	Guinea	157	Hipusini	IAR	Guinea
24	Samsorg 1	IAR	Guinea	91	Samsorg 49	IAR	Caudatum	158	Chakallari	IAR	Guinea
25	12KNICSV-297-3	ICRISAT	Guinea	92	Samsorg 40	IAR	Guinea	159	ICNSL2014-026-11	ICRISAT	Bicolor
26	Adamawa - 2	IAR	Durum	94	Wild Sorghum	IAR	Guinea	160	SSV20071012	ICRISAT	Guinea
27	Agu Akunu	IAR	Guinea	95	E 119	IAR	Guinea	161	Magara	IAR	Durum
28	E 41	ACCI	Guinea	95	E 119	ACCI	Guinea	162	Kwar Biyu	IAR	Durum
29	12KNICSV-179	ICRISAT	Guinea	96	Kirbati	IAR	Guinea	163	Kaura Mai Jan Kono	IAR	Durum
30	ICSV 400	ICRISAT	Caudatum	97	Dan Yara	IAR	Guinea	164	Kaura Koma	IAR	Durum
31	ICNSL2014-065	ICRISAT	Durum	98	Jarwa	IAR	Bicolor	165	Yar Agaji	IAR	Bicolor
32	CAPARLGSG20150124	ICRISAT	Guinea	99	ICNSL2014-021-1	ICRISAT	Guinea	166	Kurum Basau	IAR	Durum
33	CAPARLKSG20150293	ICRISAT	Guinea	100	Village Ofumpo Mkt	IAR	Guinea	167	CAPARLKSG20150285	ICRISAT	Durum

Table 4.1: Continued

S/No.	Genotype	Source	Race	S/No.	Genotype	Source	Race	S/No.	Genotype	Source	Race
34	Samsorg 43	IAR	Caudatum	101	Takanbo	IAR	Bicolor	168	Farmer Local	IAR	Guinea
35	Samsorg 17	IAR	Durum	102	Yalai	IAR	Bicolor	169	Hindatu	IAR	Guinea
36	Aguasasin Jan'dawa	IAR	Caudatum	103	Kaura - 3	IAR	Bicolor	170	ICNSL2014-027-4	ICRISAT	Caudatum
37	12KNICSV-107-3	ICRISAT	Guinea	104	Kafi Mori	IAR	Guinea	171	SSV2008113	IAR	Durum
38	Zago Black Glume	IAR	Guinea	105	Fara Dogon Dawa	IAR	Bicolor	172	Yar Magogo	IAR	Durum
39	Farin Illo	IAR	Durum	106	Jar Balakwama	IAR	Caudatum	173	Kaura - 1	IAR	Guinea
40	E 29	ACCI	Guinea	107	AS 13	ACCI	Caudatum	174	Kaura Yellow Glume	IAR	Durum
41	12KNICSV-418	ICRISAT	Guinea	108	Jar Lau	IAR	Guinea	175	Kaura Kaduna I	IAR	Guinea
42	Yar Gumel	IAR	Guinea	109	Danyar Bana	IAR	Guinea	176	Gwaza Banji Borno	IAR	Kafir
43	ICNSL2014-034	ICRISAT	Durum	110	Jar Kaura	IAR	Bicolor	177	Jibrin Agaiy Awala	IAR	Guinea
44	KL-1	ACCI	Guinea	111	ICNSL2014-022-8	ICRISAT	Durum	178	CAPARLKSG20150291	ICRISAT	Kafir
45	CF35:5	ICRISAT	Bicolor	112	ICNSL2014-044-1	ICRISAT	Durum	179	Farafara Kaduna	IAR	Bicolor
46	Samsorg 44	IAR	Guinea	113	Yar Lazau	IAR	Guinea	180	Harjiu	IAR	Bicolor
47	AS 97	ACCI	Kafir	114	Gagarau - 4	IAR	Bicolor	181	ICNSL2014-042-1	ICRISAT	Durum
48	Yar'getso	IAR	Guinea	115	Kaura Awangala	IAR	Caudatum	182	SSV2008091	IAR	Guinea
49	12KNICSV-297-2	ICRISAT	Caudatum	116	Kaura Black Glume-1	IAR	Guinea	183	Yar Kai Kabayat	IAR	Guinea
50	Takumbo	IAR	Guinea	117	Masakwa	IAR	Bicolor	184	Kaura - 2	IAR	Durum
51	Fara Fara Mai-Shaho	IAR	Bicolor	118	Makari	IAR	Kafir	185	Kaura Borno	IAR	Guinea
52	E 11	ACCI	Bicolor	119	CAPARLGSG2015-0057	ICRISAT	Guinea	186	Fara Bauchi	IAR	Guinea
53	12KNICSV-107-2	ICRISAT	Bicolor	120	Jan Kaura 1	IAR	Kafir	187	Mai Bako Kono	IAR	Guinea
54	ICNSL2014-022-4	ICRISAT	Bicolor	121	Dangama Wulchichi	IAR	Guinea	188	Kadil	IAR	Guinea
55	CAPARLGSG2015-0035	ICRISAT	Caudatum	122	Bassa Dawa	IAR	Guinea	189	Bahausa	IAR	Guinea
56	S7-LATA/RIB/BC1-1-17-1-V	ICRISAT	Guinea	123	ICNSL2014-023-5	ICRISAT	Kafir	190	Samsorg 14	IAR	Durum
57	CAPARLGSG2015-0078	ICRISAT	Caudatum	124	S7-LATA/RIB/BC1-1-7-V	ICRISAT	Guinea	191	Baba Diya 1	IAR	Durum
58	Samsorg 45	IAR	Guinea	125	Yar Labe	IAR	Guinea	192	Shinkawa	IAR	Durum
59	Samsorg 9	IAR	Bicolor	126	Kurkura	IAR	Guinea	193	Buk Wakana	IAR	Bicolor
60	Gagarawa - 3	IAR	Guinea	127	Kaura Massaba	IAR	Guinea	194	Yar Burunduzu	IAR	Guinea
61	12KNICSV-297-4	ICRISAT	Bicolor	128	Kaura Black Glume-2	IAR	Guinea	195	Buhu Banza 1	IAR	Durum
62	Sambulmu- 3	IAR	Guinea	129	Ndu Vari	IAR	Bicolor	196	Ako Variety	IAR	Guinea
63	Lisha Lisha	IAR	Bicolor	130	Tunkura	IAR	Durum	197	Buhu Banza 2	IAR	Guinea
64	AS 71	ACCI	Kafir	131	CAPARLGSG20150111-1	ICRISAT	Guinea	198	Basharanbiya	IAR	Guinea
65	12KNICSV-107-1	ICRISAT	Caudatum	132	Fara Fara - 3	IAR	Bicolor	199	Tsawan Zakara	IAR	Guinea
66	ICNSL2014-025-8	ICRISAT	Caudatum	133	Dunkurau	IAR	Bicolor	200	Pato	IAR	Guinea
67	Macia	ICRISAT	Caudatum	134	Bantako Mai Baiki Kono	IAR	Bicolor				

4.2.2 DNA extraction and genotyping-by-sequencing (GBS)

The genotypes were grown in a plant growth chamber (Conviron, Canada) at the Biosciences eastern and central Africa-International Livestock Research Institute (BecA-ILRI) hub using cell trays. Three seeds of each genotype were sown per tray. Three-week-old leaf sample was collected from the three seedlings and the pooled leaf samples were frozen in liquid nitrogen and stored at −80 °C for later use (IGSS, 2019). Genomic DNA (gDNA) was extracted from the frozen tissue according to the CTAB protocol, with some modifications (IGSS, 2019). The quantity of extracted DNA in each sample was determined using a Thermo Scientific NanoDrop Spectrophotometer 2000 c. The quality of the extracted DNA was checked on 0.8% agarose gel run in 1% TAE buffer at 70 V for 45 min. After the quality had been checked, 40 µL of a 50 ng/µL gDNA of each sample of the 200 sorghum lines was sent for whole genome scanning using Genotyping by sequencing (GBS) technology as described by Elshire et al., (2011), using DArTseqTM technology [https://www.diversityarrays.com/ (accessed on 22 February 2022)] of the Integrated Genotype Service and Support (IGSS) platform in Nairobi, Kenya. The GBS was performed by using a combination of DArT complexity reduction methods and next generation sequencing following protocols described in (Elshire et al., 2011; IGSS, 2019). Marker development was based on the protocol of Elshire et al., (2019) using the ApeKI restriction enzyme (recognition site, G| CWCG). Reads and tags found in each sequencing result were aligned to the sorghum reference genome v2.1 (available via https://phytozome.jgi.doe.gov/pz/portal.html#!info?alias=Org_SbicolorRio_er (accessed on 5 April 2022). Each allele was scored in a binary fashion ("1" = Presence, "0" = Absence and '-'for failure to score) while heterozygotes were scored as 1/1 (presence for both alleles/both rows).

4.2.3 Data analysis

The raw genotypic data consists of 15114 SNPs and 200 sorghum accessions. SNP markers were filtered for minor allele frequency (MAF ≥ 0.05), maximum missing sites per SNP <20% resulting in 7516 (49.7%) SNP's and 200 accessions for further analysis. Genetic diversity parameters: polymorphic information content (PIC), minor allele frequency (MAF), major allele frequency (MaF), observed heterozygosity (Ho), and expected heterozygosity or gene diversity (GD) were estimated for each defined group with R software (R Core Team, 2020). Bayesian-based clustering was performed using STRUCTURE software v.2.3.4 (Pritchard et al., 2000) with four independent runs with K from

2 to 10, each run with a burn-in period of 10,000 iterations and 50,000 Monte Carlo Markov iterations, assuming the admixture model. The output was subsequently visualized by STRUCTURE HARVESTER v.06.94 (Earl and von Holdt, 2012), and the number of clusters was inferred according to Evanno method (Evanno et al., 2005). Phylogenetic relationships between the lines were inferred using the unweighted neighbour-joining method (Saitou and Nei, 1987) and plotted using R software (R Core Team, 2020) based on Rogers' dissimilarity (Rogers, 1972). Heatmap of the genetic distance value among lines was generated using gplots R package. The adegenet R package (Jombart, 2008) was used to extract and plot pairwise distances between different groups identified from structure analysis. The Eigenstrat method (Price et al., 2006) based on principal components analysis was used to study population relationships further, and two-dimension principal component analysis (PCA) plot was generated using ggplot2.

The number of subpopulations determined with STRUCTURE was used for Analysis of molecular variance (AMOVA) and the calculation of Nei's genetic distance in R software (R Core Team, 2020). From AMOVA, the fixation index (F_{ST}) and Nm (haploid number of migrants) within the population were obtained. F_{ST} measures the amount of genetic variance that can be explained by population structure based on Wright's F-statistics (Wright, 1965), while gene flow was estimated using an indirect method based on the number of migrants per generation (Nm) as $(1- F_{ST})/4 F_{ST}$.

4.3 Results

4.3.1 Genetic parameters

The summary statistics of the 7,516 SNP markers are presented in Table 4.2. The collection exhibited important diversityvalues ranging from 0.10 to 0.50 with an average value of 0.32. The heterozygosity (He) value ranged from 0.01 to 0.79 with an average value of 0.15. In connection, the average inbreeding coefficient (F_{IS}) of 0.53 was moderate. From the DArT SNP markers, Table 4.2 showed 30.7% of the SNP markers had a PIC $\leqslant$ 0.20, 27.6% had a PIC $\leqslant$0.29, approximately 41.6% of the markers had a PIC $\leqslant$0.37. Measures of MAF ranged from 0.05 to 0.50, with a mean of 0.23. The MaF was 0.50 for minimum and 0.95 for maximum, with an average of 0.77 (Table 4.2).

Table 4.2: Summary statistics of diversity indices for 200 sorghum accessions based on 7,516 single nucleotide polymorphisms (SNP) markers

	Genetic parameters				
Statistics	**GD**	**Ho**	**PIC**	**MAF**	**MaF**
mean	0.32	0.15	0.26	0.23	0.77
lower	0.10	0.01	0.09	0.05	0.50
upper	0.50	0.79	0.38	0.50	0.95

GD = Gene diversity, Ho = Observed heterozygosity, PIC = Polymorphic information content, MAF = Minor allele frequency, MaF = Major allele frequency

4.3.2 Population structure and genetic relationships

The population structure of the 200 sorghum accessions revealed four distinct subpopulations (Figure 4.1A and 4.1B). The number of clusters (K) was plotted against ΔK which revealed the highest peak to occur at K=4 (Figure 4.1A) and each genotype was assigned to a cluster (represented by different colours in Figure 4.1B). The list of genotypes and the overall representation of membership of the sample in each of the four clusters are presented in Table 4.3. The optimal K value suggests that four groups (G1, G2, G3, and G4) revealed the highest probability for population clustering which consisted of 50, 49, 48, and 53 accessions, respectively (Figure 4.1B). The group, G1 which comprised of 25% (50 accessions) of the collection included drought-tolerant accessions from ICRISAT and landrace collections from IAR obtained from local farmers in Nigeria. The G2 group consisted of 24.5% of the population (49 accessions) that of local landraces and elite breeding lines from ACCI, ICRISAT and IAR. The diverse membership from different sources of collections containing local landraces and improved cultivars suggested a shared ancestry. In addition, Groups G3 and G4 consisted of 24% (48 accessions) and 26.5% (53 accessions) of the total population, respectively, and comprised of landraces from IAR and ICRISAT obtained from local farmers in Nigeria and improved sorghum cultivar (improvement of local landraces by introgression with introductions obtained from ICRISAT by IAR). The pairwise genetic distances of the four subpopulations identified in STRUCTURE revealed members from the same group were closer than those from different groups (Figure 4.2).

Table 4.3: Proportion of membership of each pre-defined population in each of the 4 clusters

Clusters	No	Genotypes	% membership Expected	Average distances (expected heterozygosity)	Mean fxation index (Fst)
1	50	Mai−Ruwan Zuma, Mori Masaba, Caparlgsg2015−0058, Samsorg 48, Icnsl2014−024−2, Agu Akunu, Caparlgsg20150124−1, Samsorg 17, Aguasasin, Jan'dawa, Zago Black Glume, Kl−1 Caparlgsg2015−0078, Icnsl2014−025−8, Caparlksg20150308, Mace Da Kunya, Zago Red Glume − 2, Caparlksg20150280, Icnsl2014−021−1, Kaura − 3, Jar Lau, Icnsl2014−044−1, Kaura Awangala, Kaura Black Glume−1, Kaura Massaba, Caparlgsg20150111−1, Kaura Short Panicle− 1, Kaura Black Glume−3, Koma, Caparlgsg20150114−1, Ginzo−2 Yellow, Yar Koma, Kaura Short Panicle− 2, Kaura Mai Baki Kona, Kaura Red Glume, Caparlgsg20150124−2, Kaura Mai Jan Kono, Kaura Koma, Caparlksg20150285, Farmer Local, Icnsl2014−027−4, Kaura − 1, Kaura Yellow Glume, Kaura Kaduna I, Icnsl2014−042−1, Kaura Borno, Kadil, Bahausa, Shinkawa, Ako Variety, Basharanbiya	0.224	2.137	0.557
2	49	12knicsv−293, Gadam, Samsorg 39, As 152, 12knicsv−297−1, As 1, As 66, 12knicsv−93, Nr 71151, Icsv111 S7−Lata/Rib/Bc1−3−1−1−V, Samsorg 38, Samsorg 1, 12knicsv−297−3, E 41, Icsv 400, E 29, 12knicsv−418, Cf35:5, As 97, 12knicsv−297−2, E 11, Caparlgsg2015−0035, Samsorg 9, 12knicsv−297−4, As 71, Macia, Samsorg 7, 12knicsv−176, Kat 487, Samsorg 41, 12knicsv−295, 12knicsv−296−1, Caparlgsg2015−0055, Samsorg 49, Samsorg 40, Samsorg 3, Wild Sorghum, E 119, As 13, Caparlgsg2015−0057, Icnsl2014−023−5, S7−Lata/Rib/Bc1−1−7−V, Mori Shabal, Chakallari Jibrin, Agaiy Awala, Caparlksg20150291, Baba Diya 1, Pato	0.279	2.131	0.489
3	48	12knicsv−260, Icnsl2014−027−2, Samsorg 42, 12knicsv−179, Icnsl2014−065, Caparlksg20150293, Samsorg 43, 12knicsv−107−3, Yar Gumel, Icnsl2014−034, Samsorg 44, Fara Fara Mai−Shaho, 12knicsv−107−2, Icnsl2014−022−4, S7−Lata/Rib/Bc1−1−17−1−V, Samsorg 45, 12knicsv−107−1, Csro2, Samsorg 46, Mai−Goje, 12knicsv−252, Icnsl2014−026−9, Yarwasha, Csro1, Caparlasg2015002, Icnsl2014−062, Jar Balakwama, Danyar Bana, Icnsl2014−022−8, Yar Lazau, Jan Kaura 1, Yar Labe, Kurkura, Kaura Black Glume−2, Tunkura, Fara Fara − 3, Dunkurau, Icnsl2014−024−7, Icnsl2014−026−11, Kwar Biyu, Kurum Basau, Hindatu, Farafara Kaduna, Ssv2008091 ,Yar Kai Kabayat, Fara Bauchi, Samsorg 14, Buhu Banza 2	0.274	2.138	0.501
4	53	Tun Buman Maiduguri, Caparlgsg20150206, Fara Fara Kyal−Kyal ,Adamawa − 2, Farin Illo, Yar'getso, Takumbo, Gagarawa − 3, Sambulmu−3, Lisha Lisha, Yar'fargore, Pam Para − 2, Wago Sane Red Sorghum, Kirbati, Dan Yara, Jarwa, Village Ofumpo Mkt, Takanbo, Yalai, Kafi Mori, Fara Dogon Dawa, Jar Kaura, Gagarau − 4, Masakwa, Makari, Dangama Wulchichi, Bassa Dawa, Ndu Vari, Bantako Mai Baiki Kono, Yar Jargada, Keres, Geddawaki Panguga Fate Fate, Danjiba, Bog Farwa, Ssv20064, Gagaran Mai Baka Kona, Kitse Kaza, Fara Dawa, Hipusini ,Ssv20071012, Magara, Yar Agaji, Ssv2008113, Yar Magogo, Gwaza Banji Borno, Harjiu, Kaura − 2, Mai Bako Kono, Buk Wakana, Yar Burunduzu, Buhu Banza 1, Tsawan Zakara	0.223	2.205	0.684

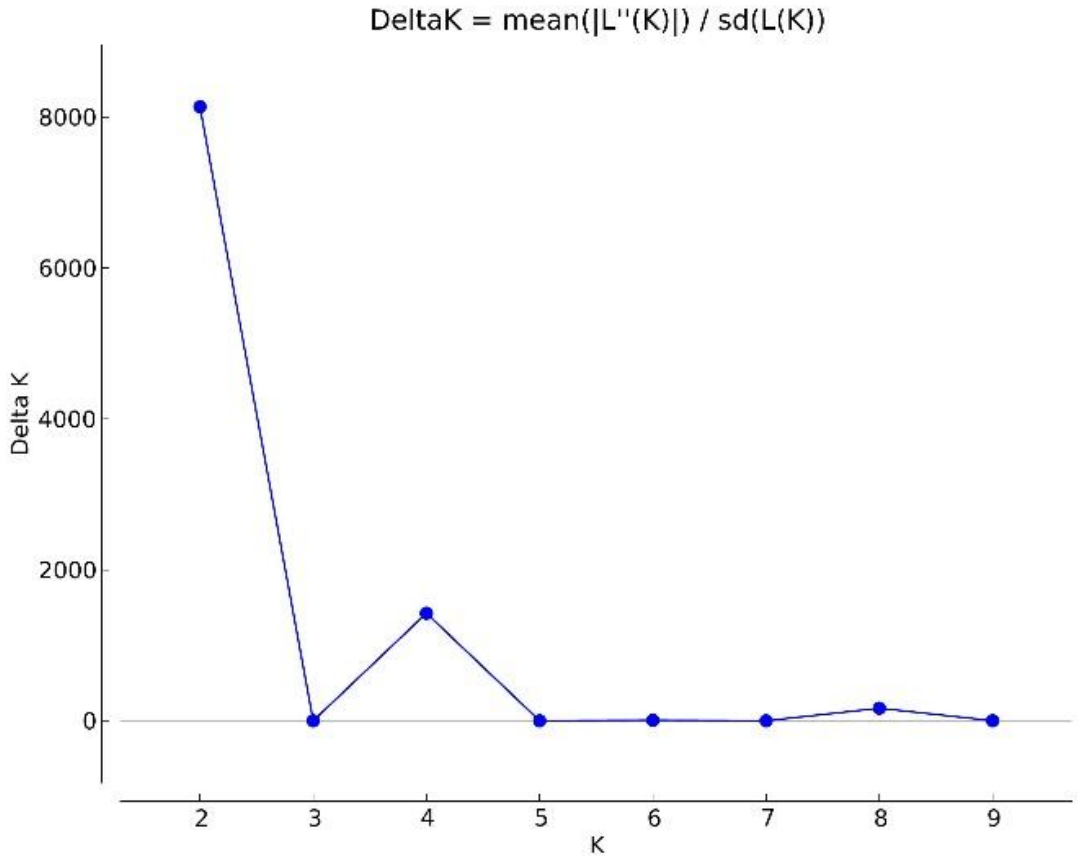

Figure 4.1A: Graph of estimated membership fraction based on Structure Analysis. The maximum of adhoc measure ΔK determined by structure harvester was found to be K = 4, which indicated that the entire population could be grouped into four clusters.

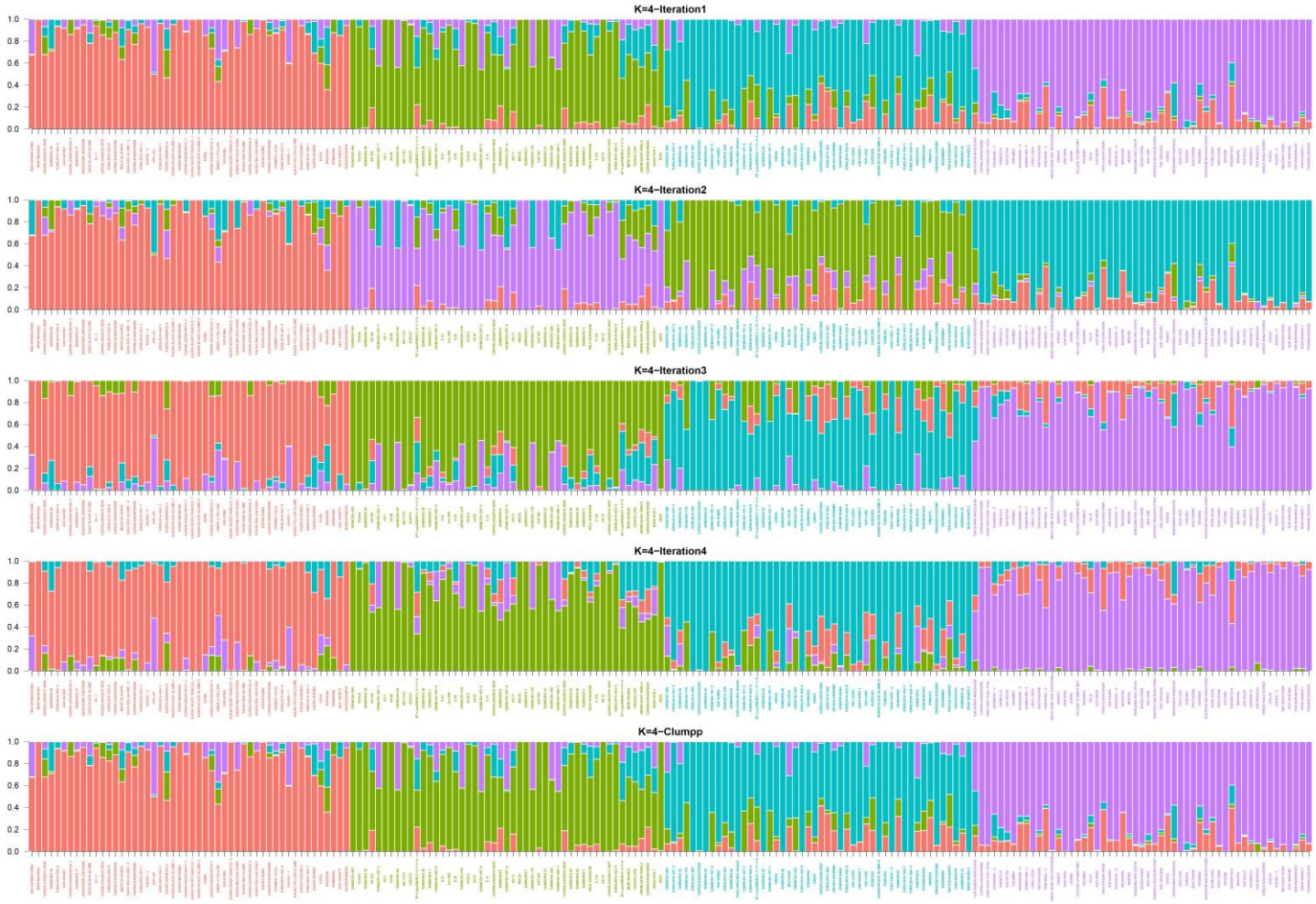

Figure 4.1B: The Structure Plot for K=4 at individual and across iteration of 200 sorghum accessions based on 7,516 DArT SNP markers. Values in the y-axis show coefficient of membership/assignment. Each coloured segment per genotype estimates the membership fraction to each of the four sub-populations (G1 = pink, G2 = turquoise blue, G3 = green, G4 = purple).

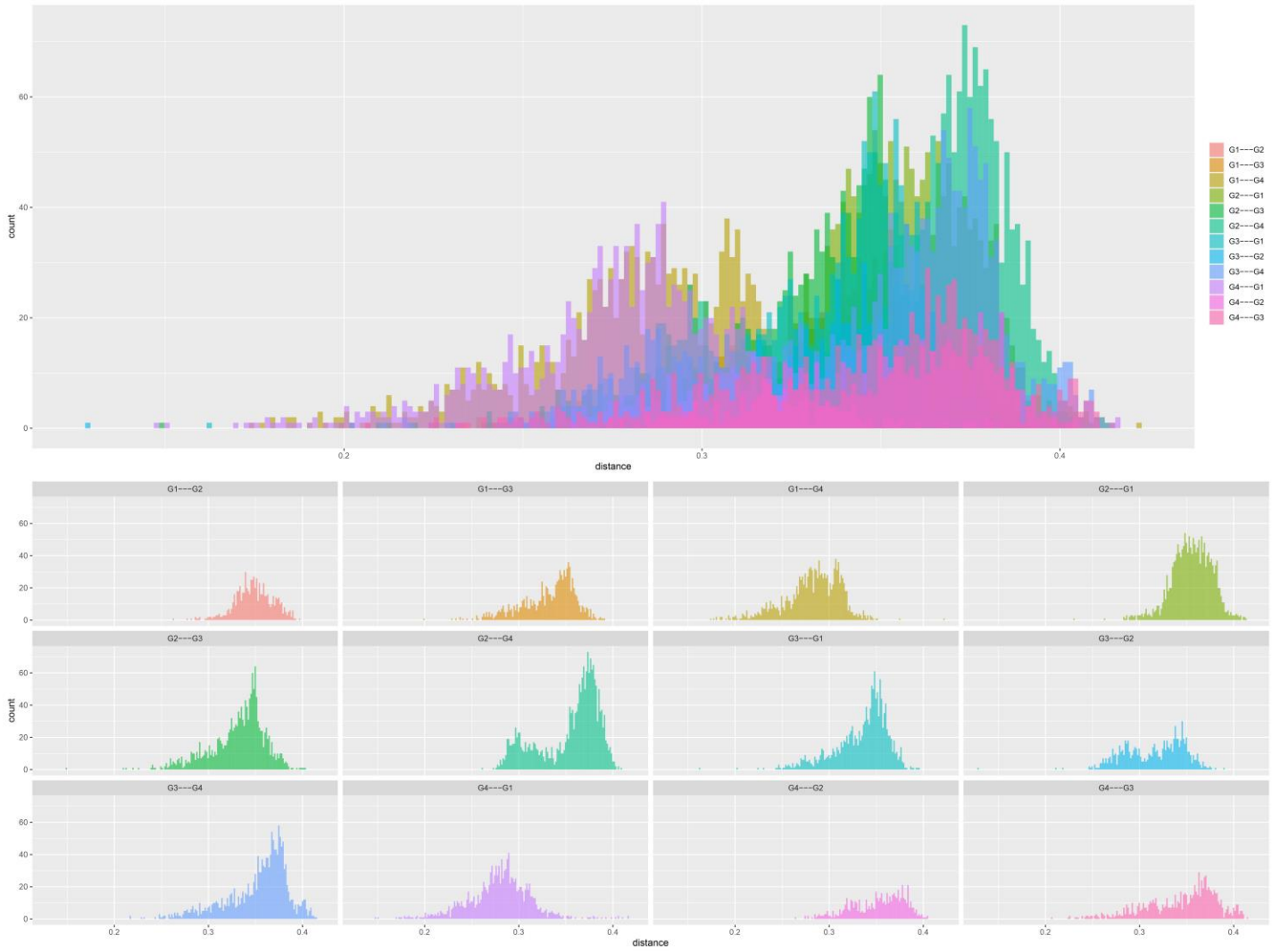

Figure 4.2: Distribution of genetic distances (GD) obtained using DArT SNP markers based on structure group for 200 sorghum accessions (G1 = pink, G2 = turquoise blue, G3 = green, G4 = purple).

Based on the pairwise genetic distance matrix among all the 200 accessions, the principal coordinate analysis (PCoA) revealed four clustered groups in accordance with the STRUCTURE results (Figure 4.3). The total amount of genetic variation explained by the first two principal coordinates was 25.1%. The PCoA clearly separated Groups G1 and G4 by PC2, which showed a higher degree of admixture between ICRISAT and IAR collections. The other two Groups, G2 and G3 were distributed along PC1, including 2 members from G1. Although some degree of overlap among G1 and G4 gene pools appeared at the center of PC2 quadrant, there was no apparent overlap in PC1 with G2 members located at the upper extreme of PC1 while G3 members were

distributed along the lower extreme of PC1. From the results of the PCoA, the groups G1 and G3 distributed along the lower and upper extremes of PC1 were the most distant of the four groups and comprised of all the collections in ACCI in G2 and the majority of the collections from ICRISAT and IAR in G3. Overall, there was a high level of overlap between the ACCI, IAR and ICRISAT sorghum accessions.

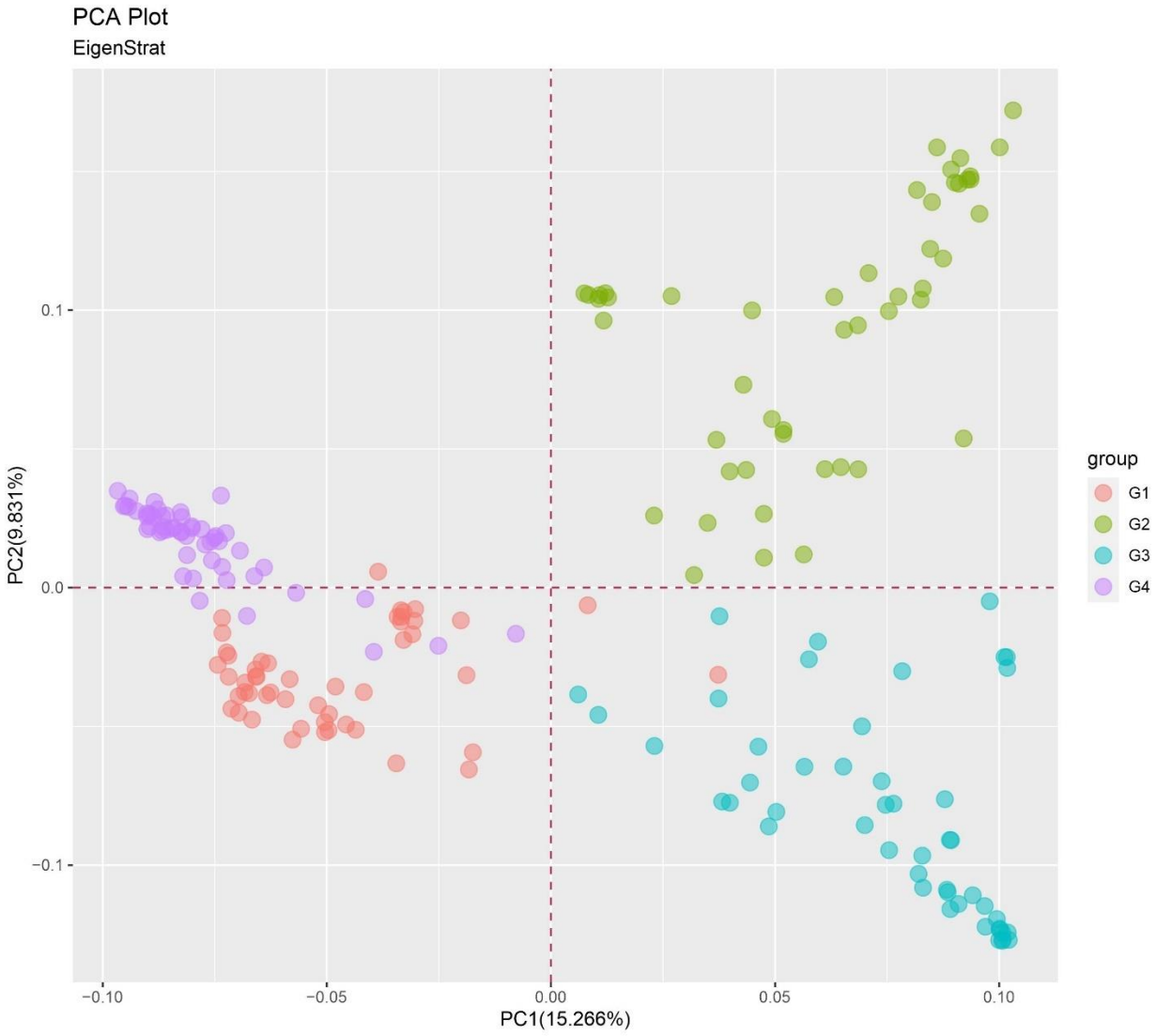

Figure 4.3: Principal coordinate analysis (PCoA) plot of the 200 sorghum accessions based on the 7,516 DArT SNP markers. PC1 and PC2 are the first and second principal coordinate, respectively, and number in parentheses refer to the proportion of variance explained by the principal coordinates. (G1 = pink, G2 = turquoise blue, G3 = green, G4 = purple).

The GD among the population is represented by the neighbor-joining phylogenetic tree (Figure 4.4A). The neighbor-joining phylogenetic tree grouped the 200 accessions into four significant clusters in concordance with the STRUCTURE (Figure 4.1B) and PCoA (Figure 4.3) results with high degrees of admixture among the sources of collection. When the neighbor-joining tree was performed for the accessions according to their biological race (Figure 4.4B), there was no clustering in accordance with race. However, collections from IAR (especially the improved and released cultivars such Samsorg 43) were found to be interspersed with all the collections from ACCI. Finally, other materials from IAR and ICRISAT seem to have been obtained from the common landraces grown in Nigeria i.e., Kaura and Fara-fara varieties and they form different clusters from those introductions used in breeding programs. The Kaura variety is derived from mostly durra-caudatum races while the Fara-fara variety is derived mostly from guinea-caudatum races. As expected, they form the same clusters with their derivatives and different clusters from the other groups. From the results, the phylogenetic tree revealed the branching history of common ancestry of the accessions under study.

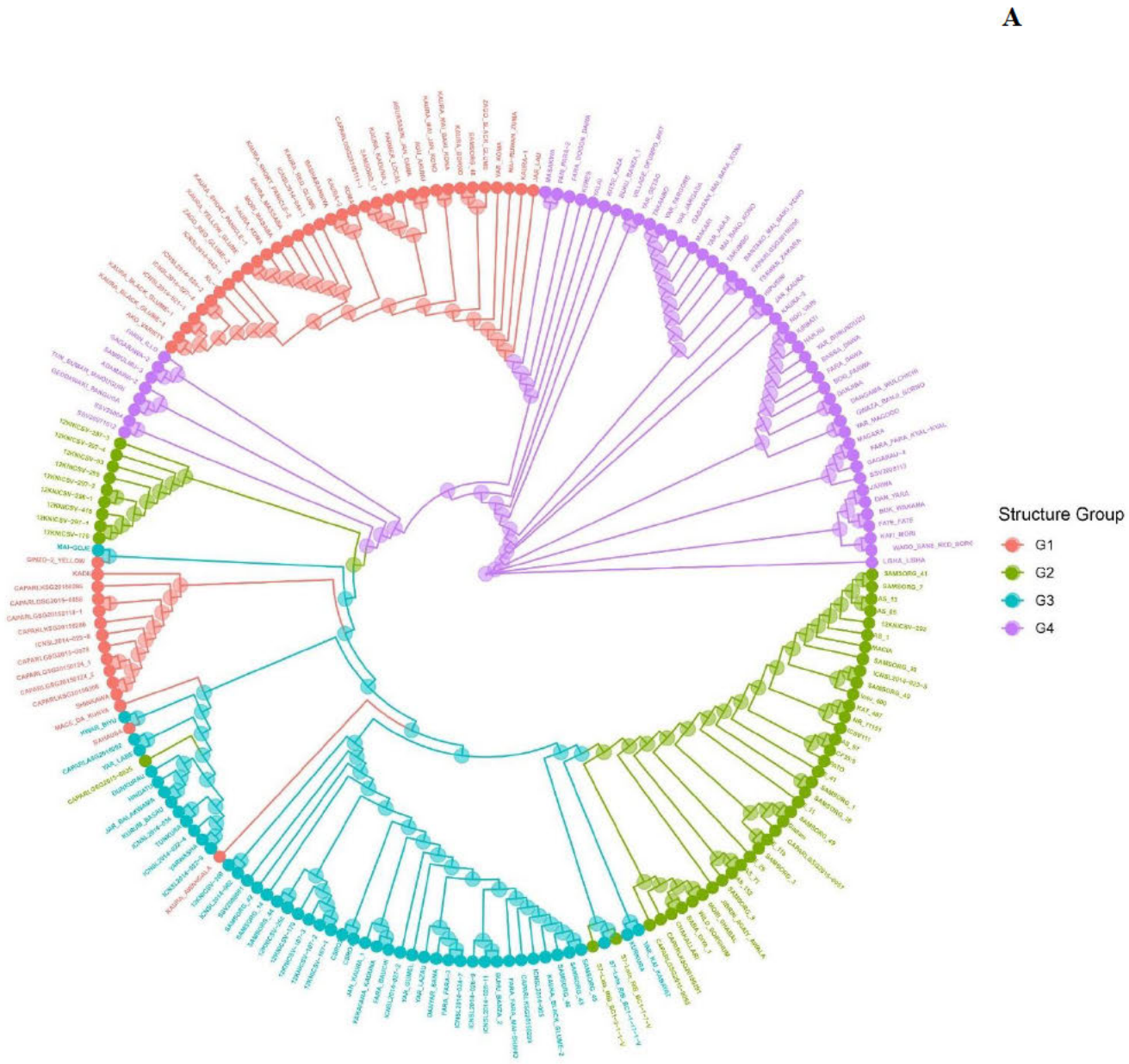

Figure 4.4A: Neighbor joining clustering based on Roger's distance (cladogram view) for 200 sorghum accessions. Colors are assigned based on population structure (G1 = red, G2 = green, G3 = blue, G4 = purple)

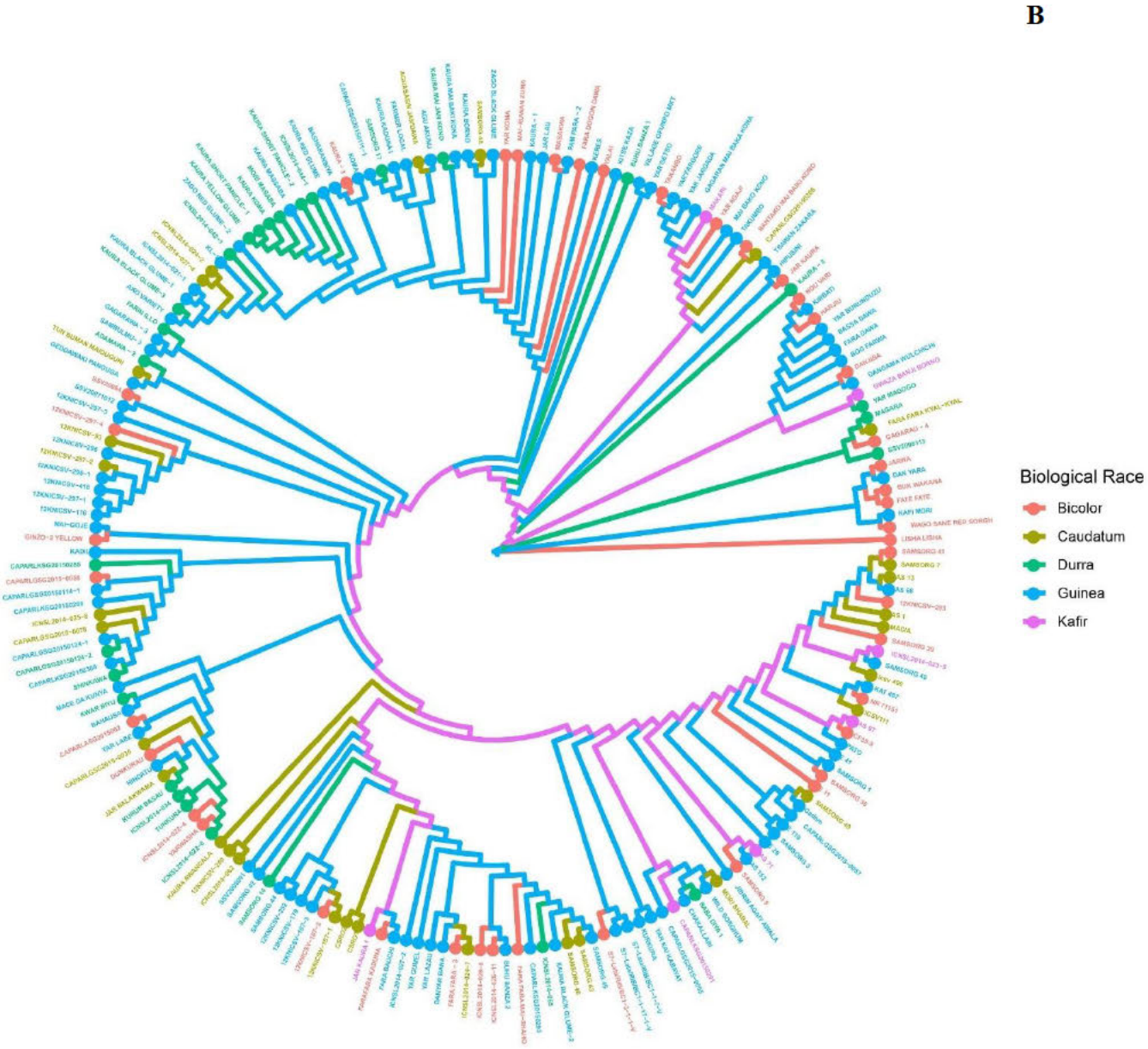

Figure 4.4B: Neighbor joining clustering based on Roger's distance (cladogram view) for 200 sorghum accessions. Colors are assigned based on race (bicolor = red, caudatum = yellow, durra = green, guinea = blue, kafir = purple)

4.3.3 Analysis of molecular variance (AMOVA)

The four subpopulations identified in STRUCTURE were applied in R software to calculate the AMOVA, fixation index (F_{ST}) and the number of migrants per generation (Nm) (Table 4.4). The AMOVA indicated that 30.8% of the variance was due to the differences between structure groups, while 27.7% of the variance was between samples within structure groups. The majority of the variation was found within individuals (41.5%).

Pairwise population F_{ST} values between different groups of accessions, sources of collection and biological races are presented in Table 4.5. From the results in Table 4.5, the structure groups had the highest F_{ST} value G3 and G4 (0.23), and G1 and G4 had the lowest (0.13). For the sources of collection F_{ST} values, the highest was recorded between IAR and ACCI (0.11) and the lowest between ACCI and ICRISAT (0.07). The highest F_{ST} values ranged from 0.04 for caudatum and durra and 0.01 for guinea and bicolor. Overall, the F_{ST} estimates, averaged 0.18, 0.09 and 0.02 for structure groups, sources of collection and races respectively which indicated that there is moderate genetic differentiation. The average F_{ST} value (0.18) among the structure group was less than 0.25 which revealed the possibility of migration among the accessions. The result was confirmed by the Nm average value of 1.14 which revealed that there was enough gene flow and no clear partitioning of levels of genetic exchange according to structure group. Similar results were obtained for groupings among the sources of collections (F_{ST} = 0.09 and Nm = 2.60) and the biological race (F_{ST} = 0.02 and Nm = 16.58).

Table 4.4: Analysis of molecular variance among and within four subpopulations of 200 sorghum accessions evaluated based on 7,516 SNP markers.

Source of variation	Degree of freedom	Sum Square	Mean Square	Components of covariance	Proportion of variance (%)	P-value
Between structure groups	3	247342.6	82447.5	799.7	30.8	0.0010
Between samples within structure groups	196	493070.7	2515.7	719.9	27.7	0.0010
Within samples	200	215176.0	1075.9	1075.9	41.5	0.0010
Total	399	955589.3	2395.0	2595.5	100.0	

Table 4.5: Pairwise F_{ST} matrix among four subpopulations of 200 sorghum accessions evaluated based on 7,516 SNP markers [Note: values in top diagonal shows gene flow (Nm), while bottom diagonal values are genetic differentiation (F_{ST})]

Gene flow (Nm)

	G1	G2	G3	G4
G1	0.000	1.026	1.026	1.616
G2	0.196	0.000	1.342	0.994
G3	0.196	0.157	0.000	0.861
G4	0.134	0.201	0.225	0.000

	ACCI	IAR	ICRISAT
ACCI	0.000	2.044	3.321
IAR	0.109	0.000	2.438
ICRISAT	0.07	0.093	0.000

	Kafir	Bicolor	Caudatum	Durra	Guinea
Kafir	0.000	14.036	11.166	5.024	26.066
Bicolor	0.018	0.000	11.542	9.790	40.734
Caudatum	0.022	0.021	0.000	5.619	22.686
Durra	0.047	0.025	0.043	0.000	19.130
Guinea	0.010	0.006	0.011	0.013	0.000

Genetic differentiation (F_{ST})

4.4 Discussion

Crop improvement depends on access to new sources of genetic variation. The most notable sources of genetic variation are landraces, wild or semi-wild relatives of cultivated crop species. In Africa, smallholder farmers produce the bulk of sorghum crops, mostly using unimproved landrace varieties and this enhance their resilience to climate variability. Landraces are valued for their beneficial genetic traits as they have been favored by local farmers for their ability to adapt to various environmental challenges (Afolayan et al., 2019). To effectively harness these genetic resources, it is essential to understand and characterize the local germplasms. Assessing the genetic diversity and population structure of sorghum landraces is important for heterotic grouping, breeding population development, cultivar development and release (Reddy et al., 2008).

The current study examined the genetic diversity present among 200 sorghum accessions, including landraces obtained from Nigeria using DArT-SNP markers. The PIC provides an estimate of the information content of a marker. In this study, the highest PIC value observed was 0.38, indicating the presence of alleles in approximately 14.1% of the population. The average PIC value of 0.26 is similar to the findings of Afolayan et al., (2019) and Enyew et al., (2022) who used SNP markers to analyze sorghum germplasm collections. The findings of this study suggest that the SNP markers employed were sufficient in providing valuable information for assessing the extent of genetic diversity within the 200 examined sorghum accessions. The average Ho value of 0.15 obtained in this study aligns with the findings of Afolayan et al., (2019), who used SNP markers for sorghum analysis (Ho = 0.22). However, it significantly surpasses the results from previous studies conducted by Enyew et al., (2022) using SNP markers and Ng'uni et al., (2011) using SSR markers (Ho = 0.04). The Ho value recorded was expected since sorghum is predominantly a self-pollinating crop, as noted by Sleper and Poehlman (2006).

Heterozygosity is a fundamental measure of genetic variation in a population. The GD of a locus, also known as its expected heterozygosity (He) describes the expected proportion of heterozygous genotypes under Hardy-Weinberg equilibrium (Nei, 1972). In this study, the GD of the SNP markers exhibited a range of 0.1 to 0.50 across all accessions, with an average of 0.32, indicating a high level of diversity. These informative markers can be effectively utilized for genotyping populations in genetic diversity studies, as suggested by Salem and Sallam (2016). In addition, the noticeable disparity between the observed heterozygosity (0.15) and the expected heterozygosity

(0.32) values, and the relatively higher number of pairwise individuals with low genetic distance observed in this study indicates a limited genetic variation among the sorghum accessions. Another possible explanation may be that small-scale farmers frequently rotate the relevant landrace each year, employing rigorous selection criteria such as rainfall duration, panicle size, and plant aspects (Yahaya et al., 2022). However, similar findings indicating a deficiency in heterozygosity have been reported in previous studies conducted by Motlhaodi et al., (2017) and Enyew et al., (2022).

The population structure analysis provides insights into the genetic diversity among sorghum genotypes and is useful in controlling false-positive associations between marker loci and traits of interest (Eltaher et al., 2018). The results of STRUCTURE and PCoA analyses indicated a genetic structure comprised of four sub-populations of the sorghum accessions under study. The structure analysis did not display any pattern reflecting geographic adaptation. Clusters 1 and 3 were dominated by landraces grown by farmers in West Africa that were mostly tall, late maturing, adaptable and relatively high yielding. All the accessions from ACCI and some improved cultivars from ICRISAT and IAR were distinctly placed in Clusters 2 based on their relatedness in terms of early maturity, dwarf height and tolerance or susceptibility to drought. The grouping in cluster 2 suggested that they shared a common ancestry. The collections from ACCI were obtained from ICRISAT, while most of the breeding lines from IAR are a mixture of indigenous landraces and elite breeding lines obtained from ICRISAT. An intrinsic genetic subpopulation was visible for cluster 4, which included accessions from Nigeria obtained from IAR. The accessions are generally landraces grown by local farmers, and the cluster had the highest F_{ST} value (0.68). The SNP data showed that the test accessions had high ancestry membership coefficients of more than 0.60. The grouping of accessions from various collection areas together, despite their diverse origins, indicates a strong genetic association. These findings suggest that sorghum landrace genotypes are likely exchanged among regions by farmers, possibly through multiple routes. This aligns with the hypothesis of seed mixing, exchanging, and trade among small-scale farmers, highlighting the dynamic nature of genetic interactions and seed movement in agricultural communities.

Sorghum breeding efforts in West Africa were initiated in 1966 through the introduction of exotic lines. Subsequent pedigree breeding programs utilized local and exotic crosses, resulting in the release of improved pure line varieties and hybrids in the region (Reddy et al., 2008). Analysis using heatmap/dendrogram revealed four clusters that were consistent with the population

structure analysis, indicating broad genetic variation among the 200 sorghum accessions studied. In contrast to the population structure analysis, the clusters identified through the neighbor-joining dendrogram analysis exhibited partial alignment with geographical localization such as those from ACCI (AS 152, AS 1, and AS 66) and recent improved cultivars obtained from IAR (Samsorg 44, 45, 46, and 49). The ACCI and IAR collections originated from introduced landraces from Sudan and shared early maturing and relatively drought-tolerant characteristics. Furthermore, nine elite breeding lines from ICRISAT formed a distinct cluster, indicating their high differentiation from other accessions, which is important for crop improvement purposes. In contrast, previous studies successfully clustered accessions based on geographic origins and racial groups (Wang et al., 2013; Morris et al., 2013). Geographically isolated locations with limited interaction may become genetically distinct over time due to inbreeding. However, tracing such distinctiveness becomes challenging as germplasm movement frequently occurs across regions, facilitated by organizations like ICRISAT and ACCI.

Analysis of molecular variance in this study indicated that the genetic variation within populations (41.5%) was higher than that of among populations (30.8%) and between samples within the structure (27.7%). In self-pollinating species like sorghum, the usual pattern is to maintain genetic variation within populations, while genetic variation tends to be lower among populations. This observation is consistent with previous studies that investigated genetic diversity using SNP markers (Afolayan et al., 2019; Sejake et al., 2021) and SSR markers (Adugna, 2014). These studies also found higher genetic variation within sorghum accessions compared to the variation observed among the accessions, indicating that the accessions are not experiencing significant selection pressures. Nevertheless, a recent genetic diversity study utilizing SNP markers on sorghum accessions from Ethiopia revealed that 64.5% of the total variation was attributed to the variation among accessions, while 35.5% was attributed to the variation within accessions (Enyew et al., 2022). Similarly, in a study by Motlhaodi et al., (2014) involving 22 sorghum accessions, a substantial genetic variation of 66.9% was observed among the accessions, with within-accession variation accounting for 23.6% of the total variation. The low genetic variation within the accessions is anticipated in self-pollinating crops, such as sorghum, as noted by Hamrick (1983). Furthermore, the high genetic variation within the population could be attributed to the preservation of sorghum landraces by farmers in Africa and suggested differences in adaptation and parentage. Genetic differentiation (F_{ST}) quantifies the extent of genetic diversity resulting from

allele frequency variations among populations, thereby reflecting population structure (Wright, 1943). Values above 0.15 are considered significant in distinguishing populations, while values below 0.05 indicate a lack of substantial genetic structuring (Frankham et al., 2002). In the current study, the highest F_{ST} value (0.23) was observed between subpopulations 3 and 4 (Table 4.5), indicating a notable genetic differentiation between these two subpopulations.

Additionally, a substantial F index was identified within the groups derived from the three collection sources (ACCI, IAR, and ICRISAT), particularly between IAR and ACCI (0.11), indicating a pronounced genetic differentiation between these two groups. Furthermore, the F value for ACCI and ICRISAT (0.07) suggests a lower genetic variability. Although, overall, the F values among the three regions exhibit a continuous pattern, the observed degree of differentiation suggests a moderate gene flow between populations. This could potentially be attributed to seed exchange practices among neighboring farmers, as it is well-known that local farmers exchange seeds to enhance crop productivity. The Gene flow (Nm) value between subpopulation 2 and 4 (Nm=0.994) was low suggesting that a low genetic exchange might occur which led to a high genetic differentiation (0.201) between the subpopulations (Table 4.5). Accessions in subpopulation 2 were mostly comprised of materials collected from ACCI and ICRISAT while subpopulation 4 comprised of local landraces adapted to Nigeria and obtained from IAR. There is a possibility that low gene flow between the subpopulations can be because of isolation from gene exchange by distance or due to small population size in the study. High Nm value of 1.616 was shown by subpopulation 1 and 4, revealing a possibility of high genetic exchange. This suggests subpopulation 1 and 4, which are landraces and elite breeding lines from Nigeria collected from IAR and ICRISAT may have had common ancestry. According to Wright (1965), an Nm value less than one indicate limited gene exchange among subpopulations. The result of the study reveals sufficient genetic variability in the sorghum accessions, which could be useful in sorghum breeding programs. The germplasm collections were composed mainly of landraces, which are known to be highly heterogeneous. Previous studies from Nigeria (Afolayan et al., 2019), Ethiopia (Adugna, 2014), South Africa (Mofokeng et al., 2014; Sejake et al., 2021), Burkina Faso (Barro-Kondombo et al., 2010) and Cameroon (Barnaud et al., 2007) have documented the existence of large genetic variation within landrace collections of sorghum in Africa.

4.5 Conclusions

The present study reports genetic diversity studies and population structure analysis on a panel of 200 sorghum collections of West African origin, using DArT-SNP markers, as a basis for future breeding. The SNP markers employed in this study exhibited a considerable degree of polymorphism, effectively revealing the genetic differences between and within the sorghum populations. Approximately half of the SNP markers were highly informative, making them valuable candidates for future genetics studies. Interestingly, a notable proportion of loci displayed an excess of heterozygosity. Exploring these loci further by studying genotypes with different alleles could provide insights into their relevance and importance in terms of desirable traits. The significant genetic differentiation observed among the sorghum accessions stemming from diverse germplasm collections across Africa will be valuable for sorghum breeders in identifying and selecting desirable parent plants for effective hybrid breeding strategies. Therefore, future sorghum improvement should focus on genetic improvement using the landraces. The formation of four distinct clusters among the sorghum accessions highlights the potential for crossbreeding genotypes from different clusters to assess their progenies for desirable traits. The study identified distantly related sorghum accessions such as Samsorg 48, ICNSL2014−024−2, Kaura red glume (cluster 1); Gadam, AS 152, AS 1, macia (cluster 2); CSRO1, CAPARLASG2015002, ICNSL2014−062 (cluster 3); and Yalai, kafi mori, Fara dogon dawa (cluster 4). The distantly related sorghum accessions will be used in creating new gene pools and novel genotypes for sorghum breeding programs in Nigeria and similar agro-ecologies in Africa. Although the SNP markers used in this study adequately discriminated between the accessions, it is important to conduct phenotypic evaluations to fully elucidate the genetic basis of phenotypic variation for crop improvement.

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CHAPTER 5 : Genetic analysis of agronomic traits and grain yield performance among African sorghum [*Sorghum bicolor* (L.) Moench] genotypes

Abstract

Sorghum is a major staple cereal crop in the world's dry regions. In Sub-Saharan Africa (SSA), there is a yield gap of 3.0 t/ha of sorghum due to several production and socio-economic constraints. The development and deployment of high-yielding sorghum genotypes and modern production technologies would narrow the yield gap. Therefore, this study aimed to determine the combining ability, heterosis and gene action conditioning agronomic traits and grain yield among sorghum genotypes to select genetically superior and contrasting parental genotypes and new progenies for breeding, cultivar release and commercialization. Twelve agronomically complementary and drought-tolerant preliminarily selected sorghum parents were crossed using a half-diallel mating design, and 66 F_1 progenies were developed. The F_1 progenies, the parents, and two check varieties were evaluated under three environments in Nigeria. Parental genotypes Samsorg 7, Masakwa, and SSV2008091 recorded significant and positive general combining ability effects for grain yield (GY) and are useful germplasm resources for breeding. Crosses AS 152 x SSV2008091, Samsorg 7 x Kurumbasau, AS 152 x ICNSL2014-022-8, and Masakwa x Hindatu exhibited high and positive specific combining ability effects and were the top performers recording stover yield of 29.3, 23.4, 27.2 and 16.5 t/ha and GY of 6.4, 6.6, 6.6 and 6.5 t/ha. The newly selected F_1 progenies had high yields compared with the local check (CSR-O4H) and are recommended for hybrid or pure line breeding and variety release in drought-prone areas of Nigeria and similar agro-ecologies of SSA after continuous selection and multi-environment testing.

Keywords: climate change, combining ability, drought stress, diallel mating design, sorghum, sub-Saharan Africa

5.1 Introduction

Sorghum [*Sorghum bicolor* (L.) Moench] ranks in the top five world cereal crops widely cultivated in the dry regions of Africa and Asia. It is indigenous to sub-Saharan Africa (SSA) and primarily serves for food, feed, and some value-added products (Yahaya et al., 2022). Continental Africa is the largest sorghum producer, with an estimated annual grain yield of 26.3 million tons on 28.1 million hectares of land (FAOSTAT 2022). The leading sorghum producers in Africa are Nigeria (6.7 million tons per annum), Ethiopia (4.5 million tons), Sudan (3.5 million tons) and Burkina Faso (1.6 million tons) (FAOSTAT 2022). The mean grain yield of sorghum in Africa is approximately 0.9 t/ha, much lower compared to 4.1 t/ha recorded in Europe, 3.7 t/ha in the Americas, and 1.6 t/ha in Asia (FAOSTAT 2022). In SSA, sorghum is an important and staple cereal crop where it is the primary source of carbohydrates and proteins (Proietti et al., 2015; Hadebe et al., 2020). The grain is rich in vitamins, including niacin, riboflavin, and thiamin, and essential minerals such as magnesium, potassium, phosphorus, iron, and zinc (Ejeta and Knoll, 2007; Thilakarathna et al., 2022). The gluten-free sorghum grains provide an alternative option for gluten-sensitive consumers (Thilakarathna et al., 2022)

In Nigeria, sorghum is predominantly cultivated in the Sudan savanna, Northern Guinea savanna, Southern Guinea savanna, and Jos Plateau. Also, sorghum grows in southern Nigeria, including in the Southern Guinea savanna, derived savannas, and rain forests. In the last decades, sorghum production has increased in Nigeria under low-input systems due to the use of locally adapted varieties (Yahaya et al., 2022). Despite the diverse economic value of sorghum, several production constraints, including biotic and abiotic stress factors, hampers sorghum's production and productivity in Africa, including Nigeria. The most critical abiotic constraints include drought, heat stress, and low soil fertility, while the biotic factors are stalk rot and foliar diseases, and insect pests, among others (Tesso et al., 2012; Mohemed et al., 2016; Mbuvi et al., 2017). Improved and climate-smart sorghum varieties would bolster production and productivity globally (Yahaya and Shimelis 2022).

In SSA sorghum is largely produced by small-scale farmers using farm-saved seed derived from low-yielding open-pollinated landrace varieties (Kante et al., 2019). The average grain yield in farmers' fields varies between 0.8 - 2.5 t/ha, far below the potential yield gains ranging from 3.5 -

5.0 t/ha using improved varieties. In the region, there is a yield gap of 3.0 t/ha of sorghum due to a multitude of production constraints.

Heterosis or hybrid vigour is an effective breeding method for developing high-yielding hybrid sorghum varieties. Heterosis or hybrid vigor is a phenomenon where hybrid progeny has superior performance compared to both parents. Sorghum hybrids have been reported to have a 30–40% heterosis in grain yield compared to the best varieties (Ashok Kumar et al., 2011). For example, the first sorghum hybrid variety in Africa, named Hageen Dura – 1 was released for commercial production in Sudan. This variety out-performed other local varieties with a yield gain of 4.9 t/ha under rainfed conditions (Maunder, 1990). Since then, sorghum hybrids suitable for production in SSA were developed by crossing introduced elite breeding lines with locally adapted varieties (Weltzien et al., 2018). Combining ability analysis provides information on the nature and extent of gene action conditioning trait inheritance, allowing breeders to select suitable parents and families. The diallel technique was proposed by Griffing (1956) and used to determine the general combining ability (GCA) of parents and the specific combining ability (SCA) effects of the F_1 progenies. The GCA measures a parent's average performance in a hybrid combination, whereas the SCA refers to cases where the hybrid's performance is relatively better or worse than would be expected based on the average performance of the parents involved. A high GCA/SCA variance ratio indicates the importance of additive gene effects, whereas a low ratio indicates the presence of dominant and/or epistatic gene effects (Mangena et al., 2022). Consequently, both GCA and SCA effects are significant in breeding population development or selection.

International research and development projects and African national breeding programs are actively developing new, well adapted sorghum cultivars with high yield potential and tolerance to major biotic and abiotic stresses (Ojiewo and Gekanana, 2018; Yahaya et al., 2022a). The international projects include the pearl millet and sorghum improvement (PROMISO), harnessing opportunities for productivity enhancement (HOPE I and II) for sorghum and millets in sub-Saharan Africa and accelerated varietal improvement and seed delivery of legumes and cereals in Africa (AVISA) led by the International Crops Research Institute for the Semi-Arid Tropics (ICRISAT). For instance, the research collaboration of ICRISAT with the Institute for Agricultural Research/Nigeria strengthened sorghum breeding and capacity development. The collaboration

enabled the development and release of sorghum varieties such as Samsorg 47 (*Zauna-Inuwa*), Samsorg 48 (*Kaura Bornu*), and Samsorg 49 (CF35:5). The released varieties are suitable for cultivation under semi-arid conditions in SSA (Ndjeunga et al., 2015; Ajeigbe et al., 2018). Both Samsorg 47 and Samsorg 48 were developed from landraces, while Samsorg 49 (CF35:5) was an introduction from ICRISAT/Mali. Farmers highly prefer Samsorg 49 for its earliness, medium-sized grain, and ability to stay green (Ojiewo and Gekanana, 2018).

In an attempt to develop climate-smart sorghum genotypes, Yahaya et al., (2023) identified drought-tolerant sorghum varieties with high yield potential (>4.0 t/ha). The lines were selected among 225 sorghum genotypes sourced from diverse origins and evaluated for pre-and-post anthesis drought tolerance based on grain yield potential. Furthermore, the study identified genotypes with variable agronomic traits and yield stability suitable for multi-location or targeted production environments and breeding. The identified germplasm has complementary traits that are useful for new variety design and development with improved yield gains and agronomic characteristics. This will enable variety replacement in drought-prone areas of Nigeria and similar agro-ecologies of SSA. Therefore, this study aimed to determine the combining ability, heterosis and gene action conditioning agronomic traits and grain yield among sorghum genotypes to select genetically superior and contrasting parental genotypes and new families for breeding, cultivar release and commercialization.

5.2 Materials and methods

5.2.1 Plant materials

The study used 12 selected sorghum genotypes. The parents were initially selected from a diverse set of 225 genotypes exhibiting variable agronomic traits, including high grain and above-ground biomass yields and drought tolerance (Yahaya et al., 2023). The names and agronomic attributes of the 12 parental genotypes used in the current study are presented in Table 5.1. The check varieties CSR-03H and CSR-04H were included in the study as comparative controls and selected for being extra-early maturing, high yielding, and adapted to the semi-arid agro-ecologies of West Africa.

Table 5.1: Names, sources of origin and agronomic description of 12 selected parental sorghum genotypes used in the study.

Parent code	Name or designation	Source	Principal agronomic characteristics
P1	AS 13	ACCI-SA	Early maturity, short plant stature
P2	Samsorg 7 (aka KSV 13)	IAR-NG	Photoperiod sensitive, semi-dwarf, semi-compact panicle, early maturing
P3	Masakwa	Landrace	Suitability for post-rainy cultivation
P4	Samsorg 40 (aka ICSV 400)	IAR-NG/ICRISAT-KN	Drought-tolerant grains with good food and malting quality.
P5	CSR-02 (aka Farafara ExKatsina)	Landrace	Excellent grain quality for the malting and brewing industry
P6	ICSV111	ICRISAT-KN	Hard grains with good food quality, drought-tolerant
P7	AS 152	ACCI-SA	Early maturity, short plant stature
P8	Samsorg 9 (aka L.2281/79)	IAR-NG	Early maturity
P9	Hindatu	IAR-NG/ICRISAT-KN	Hard grains with good food quality, drought-tolerant
P10	ICNSL2014-022-8	ICRISAT-KN	Hard grains with good food quality, drought-tolerant
P11	SSV2008091	ICRISAT-KN	Short plant height
P12	Kurumbasau	IAR-NG/ICRISAT-KN	Drought-tolerant, grains have good food quality.

ACCI-SA = African Centre for Crop Improvement, South Africa; IAR-NG = Institute for Agricultural Research (IAR), Samaru Nigeria;
ICRISAT-KN = International Crops Research Institute for the Semi-Arid Tropics – Kano station
aka = also known as

5.2.2 Mating design and crosses

The 12 parental lines were planted in a half-diallel mating design under field conditions at the Institute for Agricultural Research (IAR) Samaru breeding nursery (11° 10' 41.45" N, 7° 36' 50.31" E), Nigeria. The parents' seeds were planted on three different dates (7th, 14th and 21st December 2020) to synchronize the flowering times for emasculation and pollination. The seeds of each genotype were sown in 5-row plots, with an intra-row spacing of 0.5m and inter-row spacing of 0.75m. At the booting stage, when the flag leaf emerged approximately 50-60 days after sowing, at least four panicles per parent of the genotypes were covered to avoid uncontrolled pollination. Hand emasculation was done between 4 and 6 PM before anthers dehiscence. The corolla of the selected spikelets was opened, and the anthers were carefully removed using forceps. Only spikelets from the middle section of the panicle were kept, and the remaining part of the panicle was removed. Some15-30 florets were emasculated per panicle. The emasculated panicle was covered with a see-through plastic bag creating high relative humidity inside the bag, making the stigma open and ready for pollination. Immediately after emasculation, the panicles were covered with brown paper bags to prevent random cross-pollination. Selected male parent panicles were covered with brown paper bags the previous day before the dehiscence of anthers. The next day between 6 and 7 AM, the pollen was collected by tapping the bag. The collected pollen was carefully dusted onto the emasculated panicle of the female parents and then the pollinated panicle was covered with a properly labelled brown paper bag. Pollination was done for two to three days continuously to ensure successful crosses. Successful crosses were harvested manually at physiological maturity, and the seed was stored in labelled paper bags.

5.2.3 Test locations, experimental design, and trial management

The 66 hybrids, their 12 parents, and two commercial check hybrids were evaluated under field conditions during the 2021 growing season at three locations in Nigeria, namely: Samaru (Kaduna state), Birnin-Kudu (Jigawa state), and Minjibir (Kano state) providing three testing environments. A map showing the study sites is shown in Figure 5.1. The rainfall duration, temperature, elevation and the global positioning system (GPS) coordinates of the sites are provided in Table 5.2. All the locations are in the major sorghum production agroecological zones which experience recurrent

droughts (Yahaya et al., 2022). The experiment was laid out as an 8 x 10 α- lattice design with three replications. Each experimental unit consisted of two 5m long rows with similar spacing described above and giving a population density of 53,333 plants ha^{-1} at all sites. Standard agronomic and cultural practices were performed as recommended for each location. The trials were planted under optimal management in all locations and were entirely rainfed.

Table 5.2: The global positioning system (GPS) coordinates, fertilizer application rates and weather conditions at the three study locations in Nigeria.

Location	State	Latitude	Longitude	Elevation	Fertilizer application rate (kg/ha)	Rainfall (mm)	Temperature (°C)	
							min	max
Birnin-Kudu	Jigawa	11° 27' 58.18" N	9° 28' 34.29" E	1461 ft	60 P, 60 K, 120 N	595	19.6	35.8
Minjibir	Kano	12° 11' 32.77" N	8° 37' 42.52" E	1464 ft	60 P, 60 K, 120 N	1000	19.7	33.3
Samaru	Kaduna	11° 10' 41.45" N	7° 36' 50.31" E	2285 ft	60 P, 60 K, 120 N	1159.9	21.9	33.5

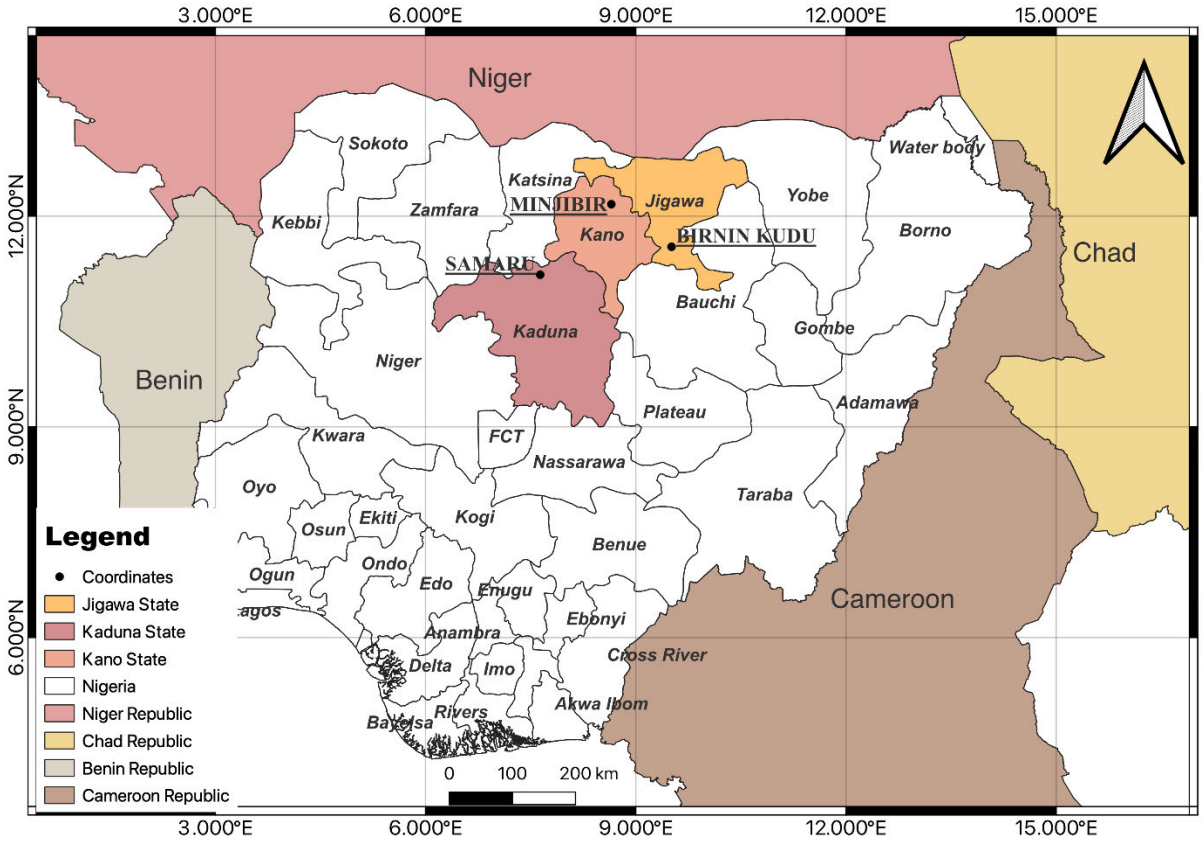

Figure 5.1: Map of Nigeria showing the study locations and neighboring countries.

5.2.4 Data collection

Ten plants for each parent and 25-30 plants for each cross were randomly sampled and tagged per replication and utilized for data collection. For each test location data were recorded on the following agronomic traits, namely: days to anthesis (DTA), recorded as days from planting to when 50% of the plants in a plot started to shed pollen, plant height (PH), measured in centimeters as the distance from the base of the plant to the tip of the panicle, panicle length (PL), measured in centimeters as the length from the base to the tip of the ear), thousand kernel weight (TKW), measured in grams as the weight of 1000 kernels at moisture content of 12%, foliage stay-green (SG), assessed by visual scoring of the leaf using a scale of 1-5 scale (1 = 0 to 10% leaves dried and 5 = >75% leaves dried) at maturity, above-ground biomass yield (ABY), measured in t/ha as the dried weight of the above-ground plant parts (including the grain, leaves and stem), and harvest

index (HI), as the ratio of dried grain yield to the dried above-ground biomass yield. Grain yield (GY) was determined from a 7.50 m^2 area in the middle of each plot by calculating the weight of threshed grains at a shelling percentage of 80% and adjusted to a moisture content of 12.0% using an LDS-1H portable grain moisture (LDS-1H/1S, Zhejiang TOP Cloud-agri Technology Co, Ltd).

5.2.5 Data analyses

5.2.5.1 Analysis of variance

A separate analysis of variance was conducted across each location to verify the homogeneity of variances before conducting a combined analysis of variance for significance tests. A combined analysis of variance was performed using PROC MIXED of R studio (R Core Team, 2022). Entries were considered fixed effects, whereas locations, replications and blocks were considered as random effects. The following linear model was used for combined analysis across locations as proposed by Barreto and Barnett (1999):

$$Y_{ijkl} = \mu + G_i + E_j + GE_{ij} + E(R)_{jk} + E[R(B)]_{jkl} + \varepsilon_{ijkl}$$

Where: Y_{ijkl} = observed performance of the *i*th genotype in the *l*th incomplete block within the *k*th replication of the *j*th environment; μ = grand mean, G_i is the effect of the *i*th genotype, E_j the effect of the *j*th environment; GE_{ij} = effect of the interactions of the *i*th genotype with the *j*th environment; $E(R)_{jk}$ = effect of the *k*th replication in the *j*th environment; $E[R(B)]_{jkl}$ = effect of the *l*th block within the *k*th replication in the *j*th environment; ε_{ijkl} = residual effect associated with each Y_{ijkl}.

5.2.5.2 Diallel analysis

The collected data, excluding that of the checks, were subjected to analysis of variance for a half-diallel mating design using Griffing's Method II, Model II (Griffing, 1956) according to the linear model:

$$X_{ij} = \mu + g_i + g_j + s_{ij} + E_k + E_k g_i + E_k g_j + ES_{ij} + e_{ijk}$$

Where; X_{ij} = mean of i × j[th] genotype (g) over kth Environments (E); μ = population mean, g_i and g_j are the GCA effects; s_{ij} = SCA effects such that $s_{ij} = s_{ji}$ (thus, assuming the absence of reciprocal effects); e_{ijk} = random error term. $E_k g_i$, $E_k g_j$, and ES_{ij} = GCA × Environment and SCA × Environment interaction effects, respectively.

Diallel analysis was performed using Plant Breeding Tools Version: 1.4 (PBTools 2020). The significance effects of the GCA and SCA sources of variation were determined using the corresponding interactions with the environment as error terms. Mean squares for the GCA x environment and SCA x environment interactions were tested using the pooled error variance as proposed by Griffing (1956). Test of significance for GCA and SCA effects were determined by t-test using their respective standard errors (Singh and Chaudhary, 1985).

The additive genetic variance $(\hat{\sigma}_A^2)$, dominance genetic variance $(\hat{\sigma}_D^2)$, additive by environment interaction variance $(\hat{\sigma}_{AE}^2)$, dominance by environment interaction variance $(\hat{\sigma}_{DE}^2)$, broad-sense (H^2) heritability, and narrow-sense (h^2) heritability were estimated considering the three test environments in a joint analysis using the following equations (Griffing 1956; Hallauer et al., 2010).

$\hat{\sigma}_A^2 = 4\hat{\sigma}_g^2$,

$\hat{\sigma}_D^2 = 4\hat{\sigma}_s^2$, and

$$H^2 = \frac{\frac{\hat{\sigma}_A^2}{2} + \frac{\hat{\sigma}_D^2}{4}}{\frac{\hat{\sigma}_A^2}{2} + \frac{\hat{\sigma}_D^2}{4} + \hat{\sigma}_{AE}^2 + \hat{\sigma}_{DE}^2 + \hat{\sigma}_R^2}$$

$$h^2 = \frac{\frac{\hat{\sigma}_A^2}{2}}{\frac{\hat{\sigma}_A^2}{2} + \hat{\sigma}_{AE}^2 + \hat{\sigma}_R^2}$$

Where: $\hat{\sigma}_g^2$ and $\hat{\sigma}_s^2$ = estimates of the general and specific combining ability variances, respectively; $\hat{\sigma}_R^2$ = error of the variance component; R = residual variance matrix.

Heritability was categorized as low (0-30%), moderate (30-60%), and high (>60%), according to Robinson et al., (1949).

5.2.5.3 The magnitude of heterosis

High-parent heterosis (HPH) was calculated and expressed as percentages according to Hallauer et al., (2010) as given below.

High-parent heterosis (%) = $\frac{F_1 - HP}{HP} \times 100$

Where, F_1 = Mean value of cross; HP = Mean value of the high parent.

The significance of heterosis was tested using the critical difference (CD) procedure according to Kumar et al., (2011).

5.3 Results

5.3.1 Analysis of variance and genetic effects

A combined analysis of variance involving data collected from the parents, crosses, and the checks, showing mean square values and level of significance of traits assessed across environments, is presented in Table 5.3. The environment effect was highly significant ($P<0.001$) for all traits except harvest index (HI) which recorded significance at $P<0.05$ and PL which recorded a non-significant difference ($P>0.05$). The genotypic effect was highly significant ($P<0.001$) for all measured traits. Significant differences ($P<0.001$) due to genotype × environment interaction effect were observed for days to anthesis (DTA), above-ground biomass (ABY), HI and grain yield (GY). Coefficient of variation (CV) were high (15.0 to 25.0%) for PL, SG, ABY, HI and GY, and moderate (5.0 to 15.0%) for DTA, PH and TKW (Table 5.3).

A combining ability analysis of variance is presented in Table 5.4, showing mean squares, significant tests and variance components for assessed traits and estimates across the three testing environments. The effect of the environment was significant ($P<0.05$) for all studied traits except DTA, panicle length (PL), stay-green (SG) and HI. The mean squares of the crosses were significant ($P\leq0.05$) for all the traits. Similarly, the crosses by environment interaction revealed significant ($P<0.05$) differences for all traits except SG (Table 5.4). GCA and SCA effects were

significant (P<0.05) for all measured traits. GCA × environment interaction effects were significant (P<0.05) for all traits except PL, whereas SCA × environment interaction effect was non-significant (P>0.05) for PL, weight of 1000 kernel (TKW) and SG. The GCA mean squares values were higher than the SCA mean squares except for ABY (Table 5.4).

The estimates of variance components attributable to the GCA and SCA effects are presented in Table 5.4. The analysis of variance components indicated that the magnitude of $\hat{\sigma}_s^2$ values were greater than $\hat{\sigma}_g^2$ values for all traits. The variances of the combining ability effects with the different environments (i.e., $\hat{\sigma}_{g\times e}^2$ and $\hat{\sigma}_{s\times e}^2$) revealed higher interaction with SCA for all assessed traits except for panicle length (PL) and SG. The combined analyses revealed higher dominance genetic variances than additive genetic variances for all measured traits (Table 5.4). In addition, there was higher dominance by environment interaction ($\hat{\sigma}_{DE}^2$) compared to additive by environment interaction ($\hat{\sigma}_{AE}^2$) variances for most traits except for PL and SG.

The broad-sense heritability (H^2) for all measured traits ranged from 54.3% (DTA) to 92.0% (PH), whereas narrow-sense heritability varied from 0.002% (ABY) to 15.1% (TKW) (Table 5.4). High H^2 values were recorded for all measured traits except for DTA, which recorded a moderate value (54.3%). Traits such as ABY, PL, DTA, GY and HI had low h^2 estimates between 0.002 and 15.3% (Table 5.4). The magnitude of the difference between H^2 and h^2 ranged between 50.9 (DTA) and 84.3% (SG).

Table 5.3: Analysis of variance showing mean squares for agronomic traits assessed among sorghum parental genotypes and their hybrids evaluated under field conditions across three environments in Nigeria.

Source of variation	df	Days to anthesis (DTA)	Plant height (cm) (PH)	Panicle length (cm) (PL)	Weight of 1000 kernel (g) (TKW)	Stay-green (SG)	Biomass yield (t/ha) (ABY)	Harvest index (HI)	Grain yield (t/ha) (GY)
Env:Rep	6	3611.200	345.000	53.211	78.671	10.252	46.570	0.017	0.565
Env:Rep:Block	42	36.000	638.000	10.964	19.880	0.324	15.540	0.002	0.329
Environment (E)	2	292.900***	8776.400***	17.944ns	963.031***	3.048***	1721.211***	0.011*	78.537***
Genotype (G)	79	585.901***	24914.201***	313.198***	280.710***	4.256***	288.020***	0.039***	14.183***
G x E	158	141.001***	749.700ns	8.821ns	18.201ns	0.293ns	53.601***	0.015***	1.712***
Error	432	38.101	712.300	23.627	19.550	0.326	22.530	0.003	0.396
Trial statistics	Means	113.14	244.24	30.55	34.32	2.64	20.68	0.21	4.13
	CV(%)	5.46	10.93	15.91	12.88	21.63	22.95	26.10	15.24

*, **, *** Significant at 0.05 and 0.01 and 0.001 probability levels, respectively, ns = non-significant, df = degrees of freedom, Env = environment., Rep = replication; CV = coefficient of variation

Table 5.4: Analysis of variances for general combining ability (GCA) and specific combining ability (SCA) effects for agronomic traits assessed among sorghum parental genotypes and their hybrids evaluated under field conditions across three environments in Nigeria.

Source of variation	df	Days to anthesis	Plant height (cm)	Panicle length (cm)	Weight of 1000 kernel (g)	Stay-green	Biomass yield (t/ha)	Harvest index	Grain yield (t/ha)
Env	2	238.767ns	9056.181**	18.286ns	899.128*	3.067	1717.853***	0.014ns	80.751***
Env:Rep	6	3434.295	396.432	55.447	83.116	9.909	39.79	0.015	0.538
Env:Rep:Blk	63	61.993	2684.335	39.583	75.819	0.696	73.537	0.007	1.4697
Crosses	77	597.162***	25436.51***	313.436***	275.711***	4.309***	290.806***	0.031***	14.458***
Crosses x Env	154	142.539***	764.2617***	9.027***	18.281***	0.300ns	53.723***	0.005***	1.712***
Residuals	399	34.1776	362.176	20.2597	9.5271	0.272	13.799	0.0023	0.221
GCA	11	1086.266**	58729.160***	418.880***	761.765***	5.215***	275.819***	0.063***	22.830***
SCA	66	515.644***	19887.740***	295.862***	194.701***	4.159***	293.304***	0.025***	13.063***
GCA x E	22	312.275***	1021.480***	17.959ns	26.595***	0.520*	38.654***	0.004*	1.637***
SCA x E	132	114.250***	721.392***	7.538ns	16.894***	0.264ns	56.234***	0.006***	1.725***
Residuals	399	34.1776	362.176	20.2597	9.5271	0.272	13.799	0.0023	0.2212
$\hat{\sigma}_g^2$		2.957	305.884	0.894	4.424	0.006	0.001	0.000	0.078
$\hat{\sigma}_s^2$		44.599	2129.594	32.036	19.756	0.433	26.341	0.002	1.260
$\hat{\sigma}_{g\times e}^2$		4.715	7.145	0.248	0.231	0.006	0.000	0.000	0.000
$\hat{\sigma}_{s\times e}^2$		26.691	119.739	0.000	2.456	0.000	14.145	0.001	0.501
$\hat{\sigma}_E^2$		34.178	362.176	20.260	9.527	0.272	13.799	0.002	0.221
$\hat{\sigma}_A^2$		11.828	1223.535	3.575	17.694	0.025	0.003	0.001	0.313
$\hat{\sigma}_{AE}^2$		18.860	28.580	0.992	0.924	0.024	0.000	0.000	0.000
$\hat{\sigma}_D^2$		178.397	8518.375	128.144	79.025	1.731	105.364	0.009	5.039
$\hat{\sigma}_{DE}^2$		106.763	478.955	0.000	9.823	0.000	6.581	0.004	2.005
h^2 (%)		3.379	11.530	2.337	15.124	1.236	0.002	7.456	4.129
H^2 (%)		54.346	91.804	86.107	82.671	85.575	59.954	60.203	70.624

GCA = general combining ability; SCA = specific combining ability; df.= degrees of freedom; Rep = replication, Env = environment; Blk = block; *, **, *** Significant at 0.05 and 0.01 and 0.001 probability levels, respectively, $\hat{\sigma}_g^2$ = GCA variance, $\hat{\sigma}_s^2$= SCA variance, $\hat{\sigma}_{g\times e}^2$ = GCA × Environment interaction variance, $\hat{\sigma}_{s\times e}^2$ = SCA × Environment interaction variance, $\hat{\sigma}_A^2$ = additive variance, $\hat{\sigma}_{AE}^2$= additive × Environment interaction variance, $\hat{\sigma}_{DE}^2$= dominance × Environment interaction variance, $\hat{\sigma}_D^2$= dominance variance, $\hat{\sigma}_E^2$= environmental variance, h^2= narrow-sense heritability, H^2 = broad-sense heritability

5.3.2 Mean performance

The mean performance of parents and their derived crosses for assessed agronomic traits across environments is presented in Table 5.5. DTA of parents varied from 100 days for Samsorg 9 to 117 days for Kurumbasau, with a mean of 109 days. DTA among the crosses varied from 82 days for AS 13 x AS 152 to 130 days for Samsorg 40 x CSR-02, with a grand mean of 113 days. Except crosses between parental genotypes from South Africa (i.e., AS 13 and AS 152) and released cultivars from Nigeria (i.e., Samsorg 40 and Samsorg 9), most crosses were late maturing (>100 days to anthesis). Cross AS 13 x AS 152 was early-flowering (82 days to anthesis). Crosses Samsorg 40 x CSR-02 and Masakwa x SSV2008091 derived from late-maturing parental genotypes Masakwa, Samsorg 40 and CSR-02 tended to be late flowering (131 and 130 days to anthesis).

PH of parental genotypes varied from 131.5 cm for AS 152 to 336.4 cm for ICSV111, with a mean of 218.8 cm. The crosses were tall compared to the parents, with mean PH of 249.4 cm. PH varied from 141.9 cm for CSR-02 x AS 152 to 373.4 cm for ICSV111 x ICNSL2014-022-8. Fifty-eight percent (38 crosses) recorded intermediate PH (≤ 250cm) and 42% (28 crosses) had taller plants (>250 cm). Taller plants were recorded for ICSV111 x ICNSL2014-022-8 (373.4 cm), Samsorg 40 x ICSV111 (356.7 cm), Masakwa x ICSV111 (346.9 cm) and ICNSL2014-022-8 x SSV2008091 (342.0 cm), whereas short plants were recorded for CSR-02 x AS 152 (141.9 cm), AS 13 x AS 152 (142.7 cm) and Samsorg 7 x Samsorg 40 (156.9 cm). The check varieties CSR-03H and CSR-04H recorded medium plant height of 212.7 and 243.8 cm, respectively.

The highest PL was expressed by the parent Hindatu (34.5 cm) compared to the short PL of 21.1 cm recorded for AS 152. Among the crosses, the highest PL was recorded for ICSV111 x ICNSL2014-022-8 (51.1 cm), Samsorg 7 x ICNSL2014-022-8 (48.3 cm) and AS 13 x Samsorg 40 (44.4 cm). The lowest PL was recorded for Samsorg 7 x Kurumbasau (22.0 cm), AS 13 x Masakwa (22.6 cm) and Samsorg 7 x Samsorg 40 (23.1 cm). Twenty-two of the 66 crosses out-performed the standard check variety CSR-03H for PL.

TKW varied from 16.7 g for Samsorg 9 to 46.2 g for ICSV111, with a mean of 33.3 g recorded across the parents. Among the crosses, TKW varied from 23.8g for AS 13 x Samsorg 9 to 49.9 g for Samsorg 40 x ICSV111, with a mean of 34.7 g. The highest TKW was recorded for crosses

Samsorg 40 x ICSV111 (49.9 g), Samsorg 7 x ICSV111 (47.5 g) and Masakwa x ICSV111 (45. 5 g), whereas the lowest TKW was recorded for AS 13 x Samsorg 9 (23.8 g), Hindatu x Kurumbasau (25.9 g) and Samsorg 40 x Samsorg 9 (26.5 g). Fifty-eight crosses recorded TKW >28.0 g.

SG of the parents varied from 2 for AS 152 to 3 for CSR-02, with a mean of 3. SG varied from 1 for cross CSR-02 x Kurumbasau to 5 for AS 152 x Hindatu with a mean of 3. The following crosses recorded SG of 1 namely: CSR-02 x Kurumbasau and Hindatu x SSV2008091, whereas crosses Samsorg 9 x ICNSL2014-022-8, Samsorg 9 x ICNSL2014-022-8 and AS 152 x Hindatu recorded a score of 4. Crosses involving parental genotype Samsorg 9 tended to be more stay-green, whereas crosses derived from AS 13 had the most senesced leaves.

ABY varied from 11.9 for ICSV111 to 19.3 t/ha for Masakwa, with a mean of 14.9 t/ha across parental genotypes. For crosses, ABY varied from 11.5 for SAMSORG 40 x Samsorg 9 to 34.4 t/ha for ICSV111 x Hindatu with a mean of 21.9 t/ha. Higher ABY was recorded for crosses ICSV111 x Hindatu (21.9 t/ha), Samsorg 40 x CSR-02 (32.3 t/ha), and Samsorg 40 x ICSV111 (31.6 t/ha). A total of 66 crosses out-performed the standard check variety CSR-03H (16.0 t/ha), recording ABY >16.0 t/ha.

HI varied from 0.14 for Kurumbasau to 0.25 for ICSV111 with a mean of 0.19 across the parental genotypes. For crosses, HI varied from 0.11 for CSR-02 x ICSV111 to 0.41 for Masakwa x Hindatu with a mean of 0.22. Of these crosses, Masakwa x Hindatu, AS 152 x Samsorg 9, and Samsorg 40 x Samsorg 9 had the highest HI (~4.0). The lowest HI was recorded for CSR-02 x ICSV111 (0.11), CSR-02 x AS 152 (0.12) and CSR-02 x Hindatu (0.13), Samsorg 7 x ICSV111 (0.13) and Masakwa x ICSV111 (0.13). Twenty-five crosses recorded high HI (>0.24) which was higher than the standard check, CSR-04H (0.24) (Table 5.5).

GY was low for parental genotype Kurumbasau (2.1 t/ha) and high for SSV2008091 (2.9 t/ha), with a mean of 2.7 t/ha recorded across parental genotypes. GY of crosses varied from 2.0 t/ha for CSR-02 x AS 152 to 6.6 t/ha for AS 152 x ICNSL2014-022-8, with a mean of 4.4 t/ha. The highest GY was recorded for crosses AS 152 x ICNSL2014-022-8 (6.6 t/ha), Samsorg 7 x Kurumbasau (6.6 t/ha), and Masakwa x Hindatu (6.5 t/ha). The lowest yielders among the crosses were CSR-02 x AS 152 (2.0 t/ha) and CSR-02 x ICSV111 (2.1 t/ha). Among the 66 experimental hybrids, 53 out-performed the standard check CSR-04H.

Table 5.5: Mean performance for parental genotypes and crosses for assessed agronomic traits when evaluating combining ability of sorghum under field conditions across three environments in Nigeria.

Means	Days to anthesis	Plant height (cm)	Panicle length (cm)	Weight of 1000 kernel (g)	Stay-green	Biomass yield (t/ha)	Harvest index	Grain yield (t/ha)
Parents								
AS 13	108.7	168.2	28.4	34.2	1.9	17.1	0.2	2.5
AS 152	112.7	131.5	21.1	33.0	1.6	15.1	0.2	2.5
CSR-02	117.3	220.5	27.5	32.8	3.4	14.3	0.2	2.8
Hindatu	111.8	269.9	34.5	38.5	2.7	14.5	0.2	2.8
Kurumbasau	117.3	205.4	23.9	39.3	2.3	16.5	0.1	2.1
Samsorg 40	105.5	193.0	32.8	29.5	2.7	12.3	0.2	2.4
Samsorg 7	110.1	183.4	24.5	27.8	2.1	13.3	0.2	2.9
ICSV111	103.1	336.4	29.7	46.2	2.7	11.9	0.3	2.9
Samsorg 9	100.6	173.7	26.9	16.7	3.3	13.9	0.2	2.6
SSV2008091	106.7	209.4	33.1	34.3	1.9	15.7	0.2	2.9
Masakwa	107.9	247.4	27.7	35.6	2.4	19.3	0.2	2.9
ICNSL2014-022-8	110.2	286.5	32.4	31.9	2.6	15.4	0.2	2.5
Parents mean	109.3	218.8	28.5	33.3	2.5	14.9	0.2	2.7
Crosses								
AS 13 x AS 152	82.1	142.7	28.5	27.2	4.0	14.2	0.3	3.9
AS 13 x CSR-02	114.4	208.7	28.0	27.4	2.9	18.9	0.2	2.6
AS 13 x Hindatu	103.5	283.6	29.0	42.9	2.8	19.5	0.3	4.8
AS 13 x ICNSL2014-022-8	110.9	237.9	32.7	34.9	2.0	25.4	0.3	6.1
AS 13 x ICSV111	109.3	248.0	32.2	35.5	3.1	18.8	0.2	2.7
AS 13 x Kurumbasau	103.6	212.6	27.0	34.9	2.0	25.0	0.2	4.3
AS 13 x Samsorg 40	109.3	298.9	44.4	42.9	2.2	20.4	0.3	5.2
AS 13 x Samsorg 7	102.9	226.6	28.6	35.1	2.6	15.0	0.3	4.2
AS 13 x Samsorg 9	108.9	213.4	34.0	23.8	2.9	22.3	0.2	5.0
AS 13 x SSV2008091	126.0	183.3	25.4	35.0	2.2	19.9	0.3	4.8

Table 5.5: Continued

Means	Days to anthesis	Plant height (cm)	Panicle length (cm)	Weight of 1000 kernel (g)	Stay-green	Biomass yield (t/ha)	Harvest index	Grain yield (t/ha)
Crosses								
AS 13 x Masakwa	107.8	229.7	22.6	32.4	2.4	24.4	0.3	6.4
AS 152 x Hindatu	118.8	222.3	33.0	32.8	4.5	19.8	0.3	4.5
AS 152 x ICNSL2014-022-8	107.9	267.9	36.2	32.7	3.4	27.2	0.3	6.6
AS 152 x Kurumbasau	115.9	285.9	32.8	42.8	3.0	19.3	0.2	3.5
AS 152 x Samsorg 9	125.0	293.3	33.6	27.3	2.8	12.0	0.4	4.7
AS 152 x SSV2008091	114.0	248.0	38.2	34.2	2.5	29.3	0.2	6.4
CSR-02 x AS 152	114.4	141.9	23.3	32.8	2.9	16.5	0.1	2.0
CSR-02 x Hindatu	114.5	315.0	38.9	38.2	1.5	24.3	0.1	3.2
CSR-02 x ICNSL2014-022-8	125.4	313.1	32.5	29.1	1.8	15.2	0.2	2.6
CSR-02 x ICSV111	117.8	225.6	31.5	28.5	3.5	18.3	0.1	2.1
CSR-02 x Kurumbasau	122.7	306.5	32.1	30.4	1.3	11.7	0.2	2.1
CSR-02 x Samsorg 9	127.6	243.6	34.4	34.3	3.0	14.3	0.2	2.5
CSR-02 x SSV2008091	114.5	246.0	28.0	34.2	2.2	24.1	0.2	3.8
Hindatu x ICNSL2014-022-8	111.3	262.8	23.2	35.1	2.8	17.1	0.3	4.3
Hindatu x Kurumbasau	115.1	226.9	25.3	25.9	2.2	26.8	0.2	4.9
Hindatu x SSV2008091	110.4	266.6	29.9	39.2	1.4	22.0	0.3	5.4
ICNSL2014-022-8 x SSV2008091	113.7	342.0	43.4	30.7	2.1	17.7	0.3	4.3
ICSV111 x AS 152	126.3	309.1	25.2	37.7	2.7	25.4	0.2	3.8
ICSV111 x Hindatu	127.9	242.7	37.9	39.2	2.6	34.4	0.1	4.7
ICSV111 x ICNSL2014-022-8	124.4	373.4	51.1	38.1	2.2	31.6	0.2	6.2
ICSV111 x Kurumbasau	129.4	261.0	32.3	35.1	1.7	16.5	0.2	3.3
ICSV111 x Samsorg 9	117.1	316.3	29.0	31.5	3.4	27.6	0.1	3.8
ICSV111 x SSV2008091	114.1	214.8	32.6	35.3	2.1	23.3	0.2	3.8
Kurumbasau x ICNSL2014-022-8	108.0	269.9	23.7	33.0	3.4	21.0	0.2	4.8

Table 5.5: Continued

Means	Days to anthesis	Plant height (cm)	Panicle length (cm)	Weight of 1000 kernel (g)	Stay-green	Biomass yield (t/ha)	Harvest index	Grain yield (t/ha)
Crosses								
Kurumbasau x SSV2008091	109.4	327.7	24.9	40.9	3.6	20.6	0.2	3.7
Samsorg 40 x AS 152	111.1	215.8	23.2	42.4	2.0	31.1	0.2	5.8
Samsorg 40 x CSR-02	131.0	244.2	33.8	33.3	3.5	32.3	0.1	4.5
Samsorg 40 x Hindatu	106.7	204.2	26.4	37.7	3.1	23.7	0.2	4.9
Samsorg 40 x ICNSL2014-022-8	111.4	280.8	37.7	32.6	2.1	23.2	0.2	4.7
Samsorg 40 x ICSV111	119.4	356.7	32.2	50.0	1.9	31.6	0.2	4.6
Samsorg 40 x Kurumbasau	112.3	223.1	23.3	32.8	2.8	25.4	0.2	5.7
Samsorg 40 x Samsorg 9	100.0	168.5	28.6	26.5	4.0	11.5	0.3	4.0
Samsorg 40 x SSV2008091	112.8	181.8	24.4	40.2	1.9	20.1	0.3	4.7
Samsorg 7 x AS 152	114.2	273.4	26.5	34.5	2.7	26.7	0.2	5.2
Samsorg 7 x CSR-02	112.8	239.9	27.4	34.9	3.5	17.7	0.2	3.6
Samsorg 7 x Hindatu	126.0	331.1	36.6	39.6	1.7	29.3	0.2	4.8
Samsorg 7 x ICNSL2014-022-8	112.6	202.0	48.3	32.4	2.3	21.6	0.3	4.7
Samsorg 7 x ICSV111	118.2	253.4	33.7	47.5	2.5	31.3	0.1	4.1
Samsorg 7 x Kurumbasau	111.0	198.0	22.0	33.3	2.3	23.4	0.3	6.6
Samsorg 7 x Samsorg 40	106.7	156.9	23.1	27.8	2.6	20.2	0.3	5.3
Samsorg 7 x Samsorg 9	103.0	256.6	33.2	33.7	2.6	17.5	0.3	5.0
Samsorg 7 x SSV2008091	122.2	260.6	34.9	34.0	3.1	31.1	0.2	4.7
Samsorg 7 x Masakwa	106.4	244.1	26.1	31.9	2.7	22.6	0.3	5.5
Samsorg 9 x Hindatu	109.8	225.2	24.6	27.2	4.4	16.9	0.2	4.1
Samsorg 9 x ICNSL2014-022-8	108.1	223.3	28.7	32.5	4.1	21.6	0.3	5.2
Samsorg 9 x Kurumbasau	110.6	174.6	27.6	36.9	2.7	13.2	0.2	2.6
Samsorg 9 x SSV2008091	106.9	260.8	30.7	28.7	3.6	20.0	0.3	5.1
Masakwa x AS 152	112.6	239.6	32.7	35.3	2.7	13.6	0.2	2.2

Table 5.5: Continued

Means	Days to anthesis	Plant height (cm)	Panicle length (cm)	Weight of 1000 kernel (g)	Stay-green	Biomass yield (t/ha)	Harvest index	Grain yield (t/ha)
Crosses								
Masakwa x CSR-02	120.6	209.1	27.3	35.5	3.7	24.0	0.2	4.0
Masakwa x Hindatu	110.7	322.4	26.5	36.8	2.7	16.5	0.4	6.5
Masakwa x ICNSL2014-022-8	110.4	225.4	27.6	34.3	2.3	20.8	0.3	5.6
Masakwa x ICSV111	127.3	346.9	39.4	45.5	3.0	23.7	0.1	3.1
Masakwa x Kurumbasau	110.4	243.1	35.9	37.3	2.0	25.2	0.2	5.8
Masakwa x Samsorg 40	106.7	248.4	31.2	32.2	2.9	18.4	0.2	3.3
Masakwa x Samsorg 9	113.9	186.0	32.4	36.0	1.7	22.0	0.3	5.2
Masakwa x Ssv2008091	129.5	255.9	35.3	37.4	2.5	27.5	0.2	4.1
CSR-03H (Check 1)	106.9	212.7	32.8	27.1	2.4	16.0	0.2	3.3
CSR-04H (Check 2)	112.2	243.8	22.7	28.4	2.1	15.4	0.2	3.4
Cross mean	113.9	249.4	31.0	34.7	2.7	21.9	0.2	4.4
Check mean	109.5	228.2	27.8	27.7	2.3	15.7	0.2	3.4
Overall mean	113.1	244.2	30.6	34.3	2.6	20.7	0.2	4.1
LSD (5%)	6.5	24.6	4.4	4.1	0.6	4.3	0.1	0.6

LSD = least significant difference

5.3.3 General combining ability effects of the parents for agronomic traits

Estimates of GCA effects for parental genotypes for the studied traits of parental genotypes across environments are presented in Table 5.6. AS 13 and Samsorg 9 recorded the highest and negative GCA effects of -5.244 and -2.734 for DTA, respectively, in a desirable direction. The parental genotypes, AS 13 and Samsorg 9 with significant negative GCA effects were good combiners for earliness.

For PH, ICSV111 had the highest positive and significant ($p<0.001$) GCA effect of (45.696) followed by SSV2008091 (27.869), whereas negative GCA effects were recorded for AS 13 (-25.639) and Samsorg 9 (-20.079) (Table 5.6).

For PL, positive and significant ($p<0.001$) GCA effects were recorded for SSV2008091 (3.699), ICSV111 (2.809) and Kurumbasau (1.092). Negative and significant GCA effects for PL were recorded for the following parental genotypes namely: ICNSL2014-022-8 (-3.083), AS 152 (-1.595), and AS 13 (-0.717).

Estimates of GCA effects for TKW ranged from -5.629 for Samsorg 9 to 4.759 for ICSV111. Positive and significant ($p<0.001$) GCA effects for TKW were recorded for parents ICSV111 (4.759), Hindatu (1.672) and Masakwa (1.338), in a desirable direction. Negative GCA effects were recorded for Samsorg 9 (-5.629), CSR-02 (-1.729), and SSV2008091 (-1.309).

GCA effects for SG ranged from -0.242 for Kurumbasau to 0.526 for Samsorg 9. Positive and significant GCA effects were recorded for genotypes Samsorg 9 (0.526) and AS 152 (0.144), whereas negative GCA effects were recorded for Kurumbasau (-0.242), ICNSL2014-022-8 (-0.193), Samsorg 7 (-0.126) and AS 13 (-0.125).

The GCA effects for ABY varied from -2.972 for Samsorg 9 to 2.673 for ICSV111. Significant and positive GCA effects for ABY were recorded for ICSV111 (2.673), Kurumbasau (1.123), and Samsorg 7 (0.853). Contrastingly, negative GCA effects were recorded for genotypes Samsorg 9 (-2.972), CSR-02 (-1.897), and AS 13 (-0.734).

For HI, GCA effects varied from -0.043 for ICSV111 to 0.031 for Samsorg 9. Parental genotypes Samsorg 9 (0.031), SSV2008091 (0.016), and Samsorg 7 (0.013) recorded positive and significant

($p<0.01$) GCA effects of 0.036, 0.019 and 0.016, respectively, while negative and significant effects were recorded for genotypes ICSV111 (-0.043) and CSR-02 (-0.042).

The GCA effects for GY varied from -1.098 for CSR-02 to 0.437 for SSV2008091. Among the parents, the genotypes SSV2008091 (0.437), Samsorg 7 (0.373) and Hindatu (0.296) recorded the highest positive and significant ($p<0.01$) GCA effects. Negative GCA effects were recorded for genotypes CSR-02 (-1.098), ICSV111 (-0.412), and ICNSL2014-022-8 (0.172)

Table 5.6: Estimates of general combining ability (GCA) effects and standard errors (SE) for agronomic traits assessed among sorghum parental genotypes evaluated under field conditions across three environments in Nigeria.

Code	Parent	Days to Anthesis	Plant height (cm)	Panicle length (cm)	Weight of 1000 kernel (g)	Stay-green	Biomass yield (t/ha)	Harvest index	Grain yield (t/ha)
P1	AS 13	-5.244**	-25.639**	-0.717*	-0.663**	-0.125**	-0.734**	0.010**	0.068*
P2	Samsorg 7	-1.114**	-12.522**	-0.597*	-0.569**	-0.126**	0.853**	0.013**	0.373**
P3	Masakwa	-0.036ns	4.917**	-0.429*	1.338**	-0.064*	0.413*	0.005*	0.235**
P4	Samsorg 40	-2.400**	-15.342**	-0.306ns	0.715**	0.001ns	0.791**	0.010**	0.254**
P5	CSR-02	5.279**	-2.896*	-0.443*	-1.729**	0.133**	-1.897**	-0.042**	-1.098**
P6	ICSV111	4.750**	45.696**	2.809**	4.759**	-0.038ns	2.673**	-0.043**	-0.412*
P7	AS 152	-0.273ns	-19.865**	-1.595**	-0.294*	0.144**	-0.388*	0.001ns	-0.044*
P8	Samsorg 9	-2.734**	-20.080**	-0.614*	-5.629**	0.526**	-2.972**	0.031**	-0.116**
P9	Hindatu	0.520*	19.261**	0.183ns	1.672**	0.052*	0.676**	0.013**	0.296**
P10	ICNSL2014-022-8	0.760*	-2.991*	-3.083**	1.028**	-0.193**	-0.731**	-0.012**	-0.172**
P11	SSV2008091	-0.584*	27.869**	3.699**	-1.309**	-0.068**	0.194ns	0.016**	0.437**
P12	Kurumbasau	1.076**	1.591ns	1.092**	0.682**	-0.242**	1.123**	-0.003ns	0.178**
	SE	0.499	1.623	0.384	0.263	0.045	0.317	0.004	0.040

*, **,and Significant at 0.05, 0.01 and 0.001 probability levels, respectively, SE = standard error.

5.3.4 Specific combining ability of the crosses

The SCA effects of the 66 sorghum crosses for the studied agronomic traits are presented in Table 5.7. Negative and significant SCA effects for DTA were recorded for AS 13 x Kurumbasau (-24.934), Kurumbasau x ICNSL2014-022-8 (-8.055) and CSR-02 x AS 152 (-6.174). The highest positive and significant SCA effect of 17.202, 15.346 and 14.930 for DTA was displayed for AS 13 x Masakwa, ICSV111 x ICNSL2014-022-8 and Samsorg 7 x SSV2008091 respectively.

Estimates of the SCA effects for PH varied from -80.461 for Samsorg 40 x ICSV111 to 93.648 for AS 13 x Hindatu. Out of the 66 crosses, 26 had negative and significant SCA effects ($p< 0.05$) for PH, while 32 had positive and significant SCA effects. The crosses with negative SCA effects for PH were Samsorg 40 x ICSV111 (-80.461), Samsorg 7 x Samsorg 9 (-79.439), and Samsorg 7 x ICSV111 (-67.582). The following crosses exhibited positive higher SCA effects for PH, namely: AS 13 x Hindatu (93.648), Samsorg 7 x SSV2008091 (87.035) and Masakwa x Samsorg 9 (84.161)

For PL, SCA effects varied from -11.591 for Masakwa x ICSV111 to 14.450 for AS 13 x Hindatu. The following crosses recorded the highest positive and significant SCA effects for PL, namely AS 13 x Hindatu (14.450), CSR-02 x ICSV111 (14.24) and Samsorg 7 x Samsorg 40 (13.878). Negative and significant SCA effects were recorded for Masakwa x ICSV111 (-11.591), Masakwa x Samsorg 40 (-7.674) and Samsorg 40 x Hindatu (-7.424).

For TKW, significantly ($p < 0.01$) high and positive SCA effects were recorded for ICSV111 x Samsorg 9 (10.786), whereas the lowest and negative SCA effects was recorded by Masakwa x ICNSL2014-022-8 (-11.37). Twenty-one crosses, including ICSV111 x Samsorg 9 (10.786), AS 152 x Samsorg 9 (9.035), AS 13 x Hindatu (8.414) and Masakwa x AS 152 (7.551) exhibited positive and significant SCA effects for TKW.

SCA effects for SG varied from -1.337 for Hindatu x SSV2008091 to 1.664 for Samsorg 7 x Masakwa. Out of the 66 crosses, 27 recorded negative and significant SCA effects, including Hindatu x SSV2008091 (-1.337), Samsorg 40 x Samsorg 9 (-1.334) and Samsorg 40 x SSV2008091 (-1.311).

For ABY, the SCA effects ranged from -7.222 (Hindatu x Kurumbasau) to 12.70 (ICSV111 x Kurumbasau). Twenty-seven crosses recorded significant and positive SCA effects, including ICSV111 x Kurumbasau (12.70), Samsorg 7 x ICSV111 (10.288), ICSV111 x SSV2008091 (10.154) and CSR-02 x Kurumbasau (8.053).

The SCA estimates for HI ranged from -0.069 for ICSV111 x ICNSL2014-022-8 to 0.181 for ICNSL2014-022-8 x SSV2008091. Twenty-seven crosses recorded positive and significant effects, including ICNSL2014-022-8 x SSV2008091 (0.181), Samsorg 7 x SSV2008091 (0.129), Kurumbasau x ICNSL2014-022-8 (0.082) and AS 13 x AS 152 (0.078) (Table 5.7).

SCA effects for GY ranged from -2.131 for Hindatu x Kurumbasau to 2.229 for CSR-02 x ICNSL2014-022-8. Positive and significant SCA effects ($p<0.05$) for GY were recorded for 37 crosses, including CSR-02 x ICNSL2014-022-8 (2.229), Samsorg 9 x Kurumbasau (2.122), Samsorg 9 x ICNSL2014-022-8 (2.091) and Samsorg 7 x Samsorg 40 (2.025).

Table 5.7: Estimates of specific combining ability (SCA) effects for agronomic traits assessed among sorghum crosses evaluated under field conditions across three environments in Nigeria.

Crosses	Days to anthesis	Plant height (cm)	Panicle length (cm)	Weight of 1000 kernel (g)	Stay-green	Biomass yield (t/ha)	Harvest index	Grain yield (t/ha)
AS 13 x AS 152	-3.719**	20.595**	-0.926ns	1.655*	0.265*	-5.703**	0.078**	-0.425**
AS 13 x CSR-02	0.091ns	6.224*	-6.886**	-2.832**	-0.130ns	3.976**	0.053**	1.926**
AS 13 x Hindatu	4.256**	93.648**	14.450**	8.414**	-0.321**	-0.569ns	0.040**	0.711**
AS 13 x ICNSL2014-022-8	0.292ns	-6.430*	-1.462*	-4.578**	0.170*	0.606ns	-0.035**	-0.555**
AS 13 x ICSV111	-3.003*	-15.480**	-0.634ns	-3.072**	0.619**	-3.549**	-0.031**	-1.115**
AS 13 x Kurumbasau	-24.934**	-56.965**	-0.099ns	-6.553**	1.333**	-5.304**	0.051**	-0.352**
AS 13 x Samsorg 40	3.812**	12.164**	4.989**	-5.112**	-0.199*	5.791**	-0.015*	0.898**
AS 13 x Samsorg 7	-5.109**	45.720**	-1.187ns	7.521**	0.235*	-1.175*	0.021*	0.315**
AS 13 x Samsorg 9	-4.815**	-4.048ns	0.449ns	0.199ns	-0.348**	6.127**	-0.039**	0.288**
AS 13 x SSV2008091	3.328**	-9.474*	-0.703ns	2.557**	-0.476**	5.131**	0.008ns	1.450**
AS 13 x Masakwa	17.202**	-36.776**	-5.695**	0.111ns	-0.120ns	-0.975ns	0.030**	0.430**
AS 152 x Hindatu	-5.373**	5.606*	-3.695**	-3.068**	0.297**	0.538ns	0.016*	0.676**
AS 152 x ICNSL2014-022-8	-3.041*	-60.307**	-6.549**	-6.683**	0.091ns	-2.693**	0.033**	0.513**
AS 152 x Kurumbasau	-5.256**	11.967**	-2.019*	2.711**	0.789**	-2.248**	0.022*	0.185*
AS 152 x Samsorg 9	2.051*	-24.782**	0.639ns	9.035**	0.082ns	7.085**	-0.051**	0.024ns
AS 152 x SSV2008091	1.976*	61.701**	-1.751*	0.915*	-0.018ns	5.253**	-0.024*	0.780**
CSR-02 x AS 152	-6.174**	43.243**	3.536**	5.139**	-0.431**	-1.068*	0.020*	0.547**
CSR-02 x Hindatu	13.602**	78.846**	6.305**	4.065**	-0.975**	7.004**	-0.068**	0.014ns
CSR-02 x ICNSL2014-022-8	-2.168*	-29.809**	-4.522**	-1.607*	-0.029ns	2.389**	0.073**	2.229*
CSR-02 x ICSV111	0.920ns	-59.733**	14.240**	-0.248ns	-0.228*	-0.079ns	0.000ns	-0.347**
CSR-02 x Kurumbasau	9.104**	24.477**	3.830**	-1.079*	0.766**	8.053**	-0.065**	-0.012ns
CSR-02 x Samsorg 9	-3.975**	14.083**	1.010ns	-4.077**	0.355**	-3.624**	-0.043**	-1.380**
CSR-02 x SSV2008091	2.284*	-36.556**	-2.479*	1.691*	1.005**	4.586**	-0.009ns	0.725**
Hindatu x ICNSL2014-022-8	8.939**	52.294**	6.283**	5.032**	0.457**	-0.467ns	-0.042**	-0.854**

Table 5.7: Continued

Crosses	Days to anthesis	Plant height (cm)	Panicle length (cm)	Weight of 1000 kernel (g)	Stay-green	Biomass yield (t/ha)	Harvest index	Grain yield (t/ha)
Hindatu x Kurumbasau	-0.522ns	10.900**	4.308**	0.031ns	0.012ns	-7.222**	-0.045**	-2.131**
Hindatu x SSV2008091	3.581**	-42.063**	2.753**	5.834**	-1.337**	3.539**	0.001ns	0.950**
ICNSL2014-022-8 x SSV2008091	-3.318**	56.067**	-3.677**	-0.714ns	0.113ns	-5.597**	0.181**	1.870**
ICSV111 x AS 152	-3.246**	-4.915ns	8.563**	0.064ns	-0.399**	4.681**	0.027*	1.584**
ICSV111 x Hindatu	-2.236*	-51.585**	-6.717**	-0.268ns	-0.200*	-0.563ns	0.057**	0.761**
ICSV111 x ICNSL2014-022-8	15.346**	3.617ns	4.195**	0.757ns	0.098ns	5.429**	-0.069**	-0.522**
ICSV111 x Kurumbasau	14.881**	17.688**	4.012**	-0.672ns	0.711**	12.700**	-0.041**	1.203**
ICSV111 x Samsorg 9	3.909**	83.651**	-0.650ns	10.786**	-0.667**	7.187**	-0.028**	0.677**
ICSV111 x SSV2008091	0.706ns	7.830*	-5.515**	7.364**	-0.742**	10.154**	-0.028**	1.431**
Kurumbasau x ICNSL2014-022-8	-8.055**	-40.145**	-0.940ns	-3.599**	0.765**	-6.579**	0.082**	-0.298**
Kurumbasau x SSV2008091	-5.087**	-41.819**	-3.912**	0.998*	0.363**	1.082*	-0.018*	0.231*
Samsorg 40 x AS 152	0.674ns	-1.640ns	-3.915**	-3.000**	0.317**	4.310**	0.024*	1.479**
Samsorg 40 x CSR-02	0.706ns	23.818**	3.885**	-1.063*	-0.461**	1.132*	-0.022*	-0.215*
Samsorg 40 x Hindatu	1.136ns	-50.049**	-7.424**	4.333**	-0.380**	-2.554**	0.025*	0.070ns
Samsorg 40 x ICNSL2014-022-8	-5.659**	-60.703**	-1.694*	-9.185**	0.756**	-3.583**	-0.010ns	-0.529**
Samsorg 40 x ICSV111	-4.586**	-80.461**	-5.147**	0.173ns	-0.037ns	-2.304**	-0.047**	-1.011**
Samsorg 40 x Kurumbasau	11.266**	22.926**	4.645**	7.102**	-0.308**	-1.580*	-0.025*	-0.482**
Samsorg 40 x Samsorg 9	-4.005**	53.590**	8.184**	3.692**	-1.334**	4.599**	-0.049**	-0.187*
Samsorg 40 x SSV2008091	3.652**	65.920**	4.546**	-3.349**	-1.311**	-6.445**	0.030**	-0.772**
Samsorg 7 x AS 152	6.884**	44.297**	-1.141ns	-2.415**	-0.936**	-3.672**	-0.010ns	-0.831**
Samsorg 7 x CSR-02	-5.591**	3.315ns	-3.368**	0.855ns	-0.322**	3.633**	-0.004ns	0.514**
Samsorg 7 x Hindatu	8.648**	37.464**	-7.098**	-1.627*	-0.080ns	2.514**	-0.020*	0.109ns
Samsorg 7 x ICNSL2014-022-8	1.496ns	45.885**	-3.615**	-2.319**	0.197*	6.905**	-0.058**	0.178*
Samsorg 7 x ICSV111	9.743**	-67.582**	4.447**	-1.680*	-0.052ns	10.288**	-0.046**	0.653**
Samsorg 7 x Kurumbasau	10.362**	-26.001**	2.470*	-5.691**	-0.751**	-5.824**	0.039**	-0.213*

Table 5.7: Continued

Crosses	Days to anthesis	Plant height (cm)	Panicle length (cm)	Weight of 1000 kernel (g)	Stay-green	Biomass yield (t/ha)	Harvest index	Grain yield (t/ha)
Samsorg 7 x Samsorg 40	6.727**	56.406**	13.878**	0.122ns	-0.383**	7.733**	0.011ns	2.025**
Samsorg 7 x Samsorg 9	-4.546**	-79.439**	-1.612*	-4.899**	-0.209*	-1.350*	0.000ns	-0.162*
Samsorg 7 x SSV2008091	14.930**	87.035**	5.185**	-1.635*	-0.558**	-4.910**	0.129ns	0.661**
Samsorg 7 x Masakwa	5.230**	-18.318**	4.007**	-3.056**	1.664**	-1.242*	0.037**	0.155*
Samsorg 9 x Hindatu	2.098*	65.066**	7.084**	7.435**	0.419**	-0.446ns	-0.013ns	-0.418**
Samsorg 9 x ICNSL2014-022-8	-4.199**	13.591**	3.368**	-0.512ns	0.666**	6.928**	0.035**	2.091**
Samsorg 9 x Kurumbasau	-0.103ns	24.566**	8.395**	-0.681ns	-0.096ns	7.453**	0.023*	2.122**
Samsorg 9 x SSV2008091	-0.619ns	-18.927**	-5.507**	-3.634**	1.176**	-1.014ns	-0.016*	-0.208*
Masakwa x AS 152	-0.348ns	-46.406**	0.521ns	7.551**	-0.264*	-3.973**	-0.018*	-1.170**
Masakwa x CSR-02	-1.738*	-31.601**	-5.057**	4.745**	0.995**	3.444**	0.011ns	0.686**
Masakwa x Hindatu	-4.753**	32.161**	-0.910ns	-0.779ns	0.707**	0.832ns	0.031**	0.836**
Masakwa x ICNSL2014-022-8	0.865ns	-36.308**	-2.727**	-11.370**	-0.290*	6.197**	-0.027*	0.596**
Masakwa x ICSV111	-1.770*	-28.009**	-11.591**	0.477ns	0.159*	-4.496**	0.021*	-0.525**
Masakwa x Kurumbasau	-4.452**	1.762ns	-1.913*	2.264**	-0.989**	-0.679ns	0.032**	0.822**
Masakwa x Samsorg 40	-5.476**	-1.137ns	-7.674**	-0.734ns	0.997**	0.536ns	0.014*	0.282**
Masakwa x Samsorg 9	-5.558**	84.161**	-3.709**	5.176**	1.393**	-0.921ns	-0.012ns	-0.464**
Masakwa x SSV2008091	-0.437ns	69.886**	8.429**	-2.721**	-0.287*	-4.564**	0.022*	-0.457**
$SE \pm$	1.660	5.402	1.278	0.876	0.148	1.055	0.014	0.134

*, **, Significant at 0.05 and 0.01, and 0.001 probability levels, respectively; ns = non-significant; SE = standard error.

5.3.5 Heterosis for agronomic traits

Estimates of high-parent heterosis (HPH) for the crosses across testing environments and agronomic traits are presented in Table 5.8. HPH for DTA varied from -27.2% for AS 13 x AS 152 to 20.0% for Masakwa x SSV2008091. Four crosses displayed negative and significant ($p<0.05$) HPH for DTA in the desirable direction, including AS 13 x AS 152 (-27.2%), AS 13 x Kurumbasau (-11.7%), and Kurumbasau x ICNSL2014-022-8 (-7.9 %). For PH, HPH varied from -36.1% for ICSV111 x SSV2008091 to 68.8% for AS 152 x Samsorg 9. Twenty-five crosses expressed negative and significant ($p<0.05$) values for PH , including ICSV111 x SSV2008091 (-36.1%), CSR-02 x AS 152 (-35.6%), and CSR-02 x ICSV111 (-32.9%). The HPH for PL varied from -32.88 for Hindatu x ICNSL2014-022-8 to 57.68% for ICSV111 x ICNSL2014-022-8. Twenty-four crosses expressed positive and significant ($p<0.05$) HPH for PL, including ICSV111 x ICNSL2014-022-8 (57.7%), Samsorg 7 x ICNSL2014-022-8 (48.8%) and AS 152 x Kurumbasau (37.5%). For TKW, HPH varied from -38.3 for CSR-02 x ICSV111 to 28.4% for Samsorg 40 x AS 152, and eight crosses expressed positive and significant ($p<0.05$) HPH, including SAMSORG 40 x AS 152 (28.4%), AS 13 x Samsorg 40 (25.5%), and Samsorg 7 x Samsorg 9 (21.2%). HPH for ABY varied from -29.72 for Masakwa x AS 152 to 156.3% for Samsorg 40 x ICSV111, and 54 crosses displayed positive and significant ($P<0.05$) values, including Samsorg 40 x ICSV111 (156.3%), ICSV111 x Hindatu (136.9%) and Samsorg 7 x ICSV111 (135.7%). Crosses with negative and significant ($p<0.05$) HPH values for ABY were Masakwa x AS 152 (-29.7%) and CSR-02 x Kurumbasau (-28.8%). HPH for GY varied from -28.2 for CSR-02 x AS 152 to 163.9% for AS 152 x ICNSL2014-022-8. Fifty-seven crosses displayed positive and statistically significant ($p<0.05$) values for GY, including AS 152 x ICNSL2014-022-8 (163.9%), Samsorg 40 x AS 152 (134.8%), Samsorg 40 x Kurumbasau (133.7%), Samsorg 7 x Kurumbasau (129.8%), and Masakwa x Hindatu (125.6%).

Table 5.8: Magnitude of high-parent heterosis (%) for sorghum crosses evaluated for agronomic traits evaluated under field conditions across three environments in Nigeria.

Crosses	Days to anthesis	Plant height (cm)	Panicle length (cm)	Weight of 1000 kernel (g)	Stay-green	Biomass yield (t/ha)	Harvest index	Grain yield (t/ha)
AS 13 x AS 152	-27.18**	-15.15ns	0.16ns	-20.55**	112.56**	-16.96**	66.72**	55.26**
AS 13 x CSR-02	-2.44ns	-5.35ns	-1.42ns	-19.88**	-15.90**	10.53**	-29.08**	-7.63**
AS 13 x Hindatu	-7.40 ns	5.06ns	2.11ns	11.30**	3.53**	13.87**	25.39**	69.06**
AS 13 x ICNSL2014-022-8	0.60ns	-16.96ns	0.84ns	1.95ns	-22.89**	48.67**	45.72**	115.67**
AS 13 x ICSV111	0.56ns	-26.26ns	8.21ns	-23.10**	17.34**	9.77**	-39.70**	-8.10**
AS 13 x Kurumbasau	-11.67**	3.52ns	-5.12ns	-11.08**	-13.33**	46.36**	17.44**	69.45**
AS 13 x Samsorg 40	0.58ns	54.84**	35.24**	25.45**	-19.43**	19.31**	24.87**	105.81**
AS 13 x Samsorg 7	-6.59ns	23.57ns	0.54ns	2.41ns	23.61**	-12.23**	41.02**	46.32**
AS 13 x Samsorg 9	0.24ns	22.83ns	19.50**	-30.53**	-11.21**	30.45**	17.42**	90.27**
AS 13 x SSV2008091	15.95**	-12.46ns	-23.08**	1.91ns	15.78**	16.29**	24.09**	64.18**
AS 13 x Masakwa	-0.78ns	-7.17ns	-20.66**	-9.05**	-2.20**	25.94**	71.39**	121.15**
AS 152 x Hindatu	5.41ns	-17.66ns	-4.51ns	-14.82**	66.85**	31.11**	27.74**	58.58**
AS 152 x ICNSL2014-022-8	-4.24ns	-6.51ns	11.62**	-1.02ns	29.90**	76.75**	57.94**	163.85**
AS 152 x Kurumbasau	-1.14ns	39.20**	37.53**	8.82**	29.73**	17.15**	13.49**	41.88**
AS 152 x Samsorg 9	10.87**	68.83**	24.90**	-17.17**	-15.86**	-20.70**	83.39**	78.07**
AS 152 x SSV2008091	1.17ns	18.43ns	15.61**	-0.31ns	32.75**	86.95**	13.79**	117.73**
CSR-02 x AS 152	-2.44ns	-35.64**	-15.11**	-0.68ns	-14.28**	9.10**	-41.85**	-28.21**
CSR-02 x Hindatu	-2.33ns	16.70ns	12.55**	-0.91ns	-56.78**	67.49**	-38.61**	12.30**
CSR-02 x ICNSL2014-022-8	6.93ns	9.28ns	0.04ns	-11.14**	-46.84**	-1.66ns	-14.51**	-5.87**
CSR-02 x ICSV111	0.49ns	-32.94**	6.11ns	-38.30**	3.50**	28.24**	-54.43**	-25.61**
CSR-02 x Kurumbasau	4.66ns	38.99**	16.86**	-22.74**	-61.67**	-28.76**	-11.06**	-24.13**
CSR-02 x Samsorg 9	8.82*	10.47ns	25.31**	4.59ns	-11.39**	0.18ns	-14.17**	-11.91**
CSR-02 x SSV2008091	-2.35ns	11.52ns	-15.44**	-0.19ns	-35.03**	54.04**	-22.52**	29.28**

Table 5.8: Continued

Crosses	Days to anthesis	Plant height (cm)	Panicle length (cm)	Weight of 1000 kernel (g)	Stay-green	Biomass yield (t/ha)	Harvest index	Grain yield (t/ha)
Hindatu x ICNSL2014-022-8	-0.49ns	-8.26ns	-32.88**	-8.93**	3.14**	11.06**	26.67**	52.10**
Hindatu x Kurumbasau	-1.84ns	-15.94ns	-26.87**	-34.01**	-18.72**	62.75**	-6.81**	72.36**
Hindatu x SSV2008091	-1.23ns	-1.23ns	-13.27**	1.69ns	-47.00**	40.57**	23.71**	85.36**
ICNSL2014-022-8 x SSV2008091	3.11ns	19.38ns	31.10**	-10.57**	-19.04**	13.25**	21.19**	45.65**
ICSV111 x AS 152	12.07**	-8.10ns	-15.16**	-18.51**	1.80**	68.37**	-40.20**	29.75**
ICSV111 x Hindatu	14.37**	-27.84*	9.90**	-15.19**	-3.10**	136.88**	-45.53**	62.40**
ICSV111 x ICNSL2014-022-8	12.86**	11.00ns	57.68**	-17.56**	-18.35**	104.65**	-22.34**	113.24**
ICSV111 x Kurumbasau	10.38**	-22.41ns	8.68**	-24.01**	-35.87**	-0.01ns	-19.95**	14.70**
ICSV111 x Samsorg 9	13.59**	-5.96ns	-2.61ns	-31.75**	2.44**	98.98**	-43.32**	33.03**
ICSV111 x SSV2008091	6.95ns	-36.13**	-1.39ns	-23.67**	-19.50**	48.61**	-32.74**	30.16**
Kurumbasau x ICNSL2014-022-8	-7.87 *	-5.79ns	-27.07**	-16.01**	29.09**	36.10**	37.72**	88.68**
Kurumbasau x SSV2008091	-6.74ns	56.49**	-24.87**	4.07ns	53.11**	24.97**	-9.40**	26.20**
Samsorg 40 x AS 152	-1.46ns	11.79ns	-29.21**	28.40**	-24.34**	105.87**	-9.74**	134.82**
Samsorg 40 x CSR-02	11.69**	10.70ns	3.00ns	1.44ns	3.46**	126.27**	-35.30**	61.59**
Samsorg 40 x Hindatu	-4.59 ns	-24.34ns	-23.49**	-2.29ns	12.56**	62.88**	-2.11**	73.49**
Samsorg 40 x ICNSL2014-022-8	1.01 ns	45.45**	15.02**	2.21ns	-22.08**	50.28**	-0.14*	85.38**
Samsorg 40 x ICSV111	13.22**	6.06ns	-1.77ns	8.12**	-29.03**	156.32**	-40.58**	59.75**
Samsorg 40 x Kurumbasau	-4.25ns	8.65ns	-29.13**	-16.52**	4.71**	53.88**	5.93**	133.67**
Samsorg 40 x Samsorg 9	-5.23ns	-12.72ns	-12.86**	-10.24**	48.79**	-16.87**	54.63**	51.30**
Samsorg 40 x SSV2008091	5.68ns	-5.80ns	-26.15**	17.27**	-27.34**	28.47**	12.87**	59.63**
Samsorg 7 x AS 152	1.34ns	49.07**	7.97**	4.57ns	24.71**	77.00**	-11.83**	82.48**
Samsorg 7 x CSR-02	-3.81ns	8.78ns	-0.19ns	6.40**	2.73**	24.02**	-8.25**	25.79**
Samsorg 7 x Hindatu	12.65**	22.67ns	5.86ns	2.79ns	-39.05**	101.66**	-26.22**	67.09**
Samsorg 7 x ICNSL2014-022-8	2.10ns	10.13ns	48.80**	1.64ns	-13.53**	40.06**	9.93**	63.64**

Table 5.8: Continued

Crosses	Days to anthesis	Plant height (cm)	Panicle length (cm)	Weight of 1000 kernel (g)	Stay-green	Biomass yield (t/ha)	Harvest index	Grain yield (t/ha)
Samsorg 7 x ICSV111	7.37*	-24.65ns	13.28**	2.79ns	-5.69**	135.74**	-46.69**	41.86**
Samsorg 7 x Kurumbasau	-5.34ns	-3.58ns	-10.04**	-15.25**	-0.81*	41.75**	27.31**	129.78**
Samsorg 7 x Samsorg 40	-3.10ns	-18.75ns	-5.70ns	-5.70*	-1.97**	52.10**	17.40**	85.65**
Samsorg 7 x Samsorg 9	-6.42ns	39.92**	23.46**	21.24**	-20.13**	26.47**	22.99**	73.82**
Samsorg 7 x SSV2008091	10.97**	24.42ns	5.58ns	-0.99ns	43.15**	98.70**	-30.88**	61.10**
Samsorg 7 x Masakwa	-3.40ns	-1.34ns	-5.55ns	-10.60**	12.40**	17.11**	11.30**	89.94**
Samsorg 9 x Hindatu	-1.84ns	-16.58ns	-28.66**	-29.35**	33.53**	16.09**	17.77**	43.57**
Samsorg 9 x ICNSL2014-022-8	-1.91ns	-22.05ns	-11.46**	1.87ns	23.85**	39.80**	31.78**	100.27**
Samsorg 9 x Kurumbasau	-5.68ns	-15.00ns	2.55ns	-5.99*	-17.82**	-19.96**	1.81**	-0.50*
Samsorg 9 x SSV2008091	0.16ns	24.51ns	-7.34*	-16.47**	9.30**	27.78**	31.97**	73.82**
Masakwa x AS 152	-0.15ns	-3.15ns	18.07**	-0.92ns	10.82**	-29.72**	6.00**	-23.75**
Masakwa x CSR-02	2.81ns	-15.51ns	-1.49ns	-0.35ns	8.12**	23.85**	-21.54**	38.56**
Masakwa x Hindatu	-1.00ns	19.44ns	-23.38**	-4.66ns	0.67ns	-14.69**	98.52**	125.60**
Masakwa x ICNSL2014-022-8	0.12ns	-21.32ns	-14.85**	-3.67ns	-10.49**	7.70**	71.73**	93.77**
Masakwa x ICSV111	17.98**	3.15ns	32.65**	-1.59ns	11.16**	22.55**	-46.49**	8.81**
Masakwa x Kurumbasau	-5.84ns	-1.74ns	29.57**	-4.96ns	-16.74**	30.47**	41.22**	101.77**
Masakwa x Samsorg 40	-1.10ns	0.39ns	-4.93ns	-9.58**	7.73**	-5.05ns	-15.35**	13.60**
Masakwa x Samsorg 9	5.55ns	-24.84ns	17.02**	1.06ns	-47.20**	13.69**	20.53**	81.40**
Masakwa x SSV2008091	20.01**	3.45ns	6.63*	4.94ns	2.52**	42.30**	-26.79**	37.96**
SE	4.152	16.345	3.790	3.112	0.440	3.630	0.082	0.294
CD (5%)	6.847	26.954	6.250	5.132	0.725	5.987	0.135	0.485
CD (1%)	8.163	32.135	7.452	6.119	0.864	7.137	0.161	0.579

*, **, Significant at 0.05 and 0.01 probability levels, respectively, ns = non-significant; SE = standard error, CD = critical difference

5.4 Discussion

The yield gap of sorghum in SSA is approximately 3.0 t/ha, which to some extent is attributed to the cultivation of low-yielding varieties. There is need for pre-breeding and breeding of sorghum to develop and deploy best-performing varieties for sustainable and high-profit sorghum production in the region. The present study estimated the combining ability, gene action and heterosis among sorghum genotypes for grain yield and related agronomic traits to select contrasting parental genotypes and unique families for breeding and genetic advancement.

The study revealed higher genotypic variation among the parental genotypes and their crosses for the assessed agronomic traits (Table 5.3). Variation for the assessed agronomic traits was high among the newly-developed crosses compared to parental genotypes (Table 5.3), which suggested successful gene recombinations that favor the expression of agronomic traits in the crosses. These will aid the selection and advancement of potential crosses for release and commercialization. In agreement with the present findings, genetic variation for grain yield and related agronomic traits has also been reported in sorghum genetic resources (Kanfany et al., 2018; Kante et al., 2019; Yahaya et al., 2023).

The testing environment had an impact on all measured traits except panicle length (Table 5.3). Previous studies have reported the environmental effect on days to anthesis, above-ground biomass yield, grain yield, and harvest index (Ndjeunga et al., 2015; Kante et al., 2019; Ignatius et al., 2021). The three environments in the current study represent sorghum production systems in sub-Saharan Africa, where rainfall is available during the vegetative growth stage followed by declining water supply from flowering through to crop physiological maturity (Ajeigbe et al., 2018; Kanfany et al., 2018). The high genotype x environment interaction effects recorded for grain yield and associated traits (e.g., days to anthesis, above-ground biomass, and harvest index) suggested the need for extensive testing of the crosses in multiple environments for recommendations of narrowly or broadly adapted cultivars. The present finding agrees with other studies which reported varied performance of sorghum genotypes under varied testing environmental conditions (Ndjeunga et al., 2015; Ajeigbe et al., 2018; Kanfany et al., 2018; Kante et al., 2019).

The successful development of high-performing varieties requires understanding the underlying gene action for the trait of interest to guide appropriate breeding approaches for the selection of parental genotypes for breeding (Hill and Mackay, 2004). In the present study, both additive and non-additive gene actions were important in the inheritance of days to anthesis, plant height, stay-green trait and grain yield (Table 5.4). The greater proportion of the SCA variances over GCA variances for most traits indicated a predominance of non-additive gene action (Table 5.4). In agreement with the present findings, several studies have reported that both GCA and SCA condition the expression of desirable traits in sorghum, including grain yield (Kenga et al., 2004; Makanda et al., 2010). Therefore, the selection for superior crosses should be delayed to the advanced generations to improve genetic gains and to select homozygous and stable pure lines.

Combining ability analysis allow the identification of parents for future breeding and crosses for genetic advancement. General combining ability is associated with additive gene effects, whereas specific combining ability is governed by non-additive gene effects (Sprague and Tatum, 1942). Due to the presence of additive genetic influences, high GCA reflects the inherent genetic value of a parent and is fixable. According to Welsh (1981), parents that are good general combiners have several advantages, as they often have a high probability of good SCAs, which allows the development of synthetic varieties, and are the ideal choice as parents in a hybrid program. Therefore, the parental genotype possessing high GCA values for traits of interest could serve as vital sources of beneficial alleles to develop superior segregants in the later generations (Mangena et al., 2022; Kante et al., 2019).

In the present study, the parental genotypes AS 13, Samsorg 7, Samsorg 40, and Samsorg 9 with significant negative GCA effect for days to anthesis suggests that these parents are useful in developing crosses with early flowering in sorghum (Table 5.6). This is confirmed by the early flowering of crosses AS 13 x SSV2008091, AS 152 x Samsorg 9, Samsorg 40 x CSR-02 and Samsorg 7 x Hindatu were derived from these parental genotypes (i.e., AS 13, Samsorg 7 and Samsorg 40). Therefore, the earliness gene in AS 13 and Samsorg 7 could be effectively introduced into elite cultivars using pedigree selection, marker assisted-backcrossing, and recurrent selection methods. Early flowering is an important drought-adaptive mechanism in drought-prone areas which allows for the successful cultivation of crops by reducing exposure to dehydration during the critical growth stages, including flowering and grain-filling (Assefa et al., 2010; Ignatius et al.,

2021). In areas with low and erratic rainfall, sorghum farmers prefer early flowering cultivars (Ignatius et al., 2021).

Plant height is a critical yield-determining agronomic trait. The present study identified genotypes AS 13, Samsorg 9, AS 152 and Samsorg 40 with negative and significant GCA effects for plant height (Table 5.6) for developing crosses with short-plant stature (e.g., CSR-02 x AS 152, and Samsorg 7 x Samsorg 40). Conversely, parental genotypes such as ICSV111, and SSV2008091 with positive GCA effects for plant height (Table 5.6) aided the development of crosses such as Samsorg 40 x ICSV111 and Kurumbasau x SSV2008091 with taller plants (Table 5.7). Sorghum plants with short stature are suitable for mechanical harvest and have enhanced lodging resistance. In Nigeria, farmers cultivate taller sorghum varieties for enhanced biomass production, which are utilized for livestock feed and grains for human food. Sorghum varieties that are taller tend to be late maturing but have higher yields compared to dwarf varieties. However, the tall varieties are susceptible to lodging and drought, which can significantly yield loss to farmers in SSA (Fernandez et al., 2009).

Panicle length influences grain yield and other agronomic traits (i.e., number of grains per panicle) in sorghum. The present study identified parental genotypes SSV2008091, ICSV111, and Kurumbasau with desirable impact on panicle length (Table 5.6) in the resultant crosses (e.g., Hindatu x ICNSL2014-022-8, ICSV111 x ICNSL2014-022-8, Samsorg 7 x ICNSL2014-022-8 and Masakwa x Kurumbasau) (Table 5.5). These are valuable germplasm for breeding novel sorghum cultivars with longer panicles. Longer panicles have more branches carrying more seeds per panicle, resulting in higher grain yield (Tolk and Schwartz, 2017).

The stay-green trait is useful and allows for extended vegetative periods. Stay-green genotypes have enhanced yield potential and drought tolerance under water-limited conditions (Xu et al., 2000). Genotypes including Kurumbasau, ICNSL2014-022-8, Samsorg 7, AS 13 and SSV2008091 with negative GCA effects for stay-green character can be utilized to develop the hybrids that can maintain their green leaves and photosynthesis capacity for a longer time after anthesis, especially under drought and heat stress conditions. Among the newly-bred crosses, AS 152 x ICNSL2014-022-8, Samsorg 9 x ICNSL2014-022-8, and Samsorg 9 x SSV2008091, which retained greener leaves were also high-yielding (>5.0 t/ha) which may be suited for cultivation in drought-prone areas.

Thousand kernel weight directly and positively impacts grain yield and nutritional quality in sorghum, thus making it a prominent character for selection (Yang et al., 2009). Parental genotypes ICSV111, Hindatu, and Masakwa, were identified with favourable alleles for improving kernel weight (Table 5.6). The favourable SCA effects among most of the crosses indicated that significant breeding gains can be achieved by developing high-yielding varieties by improving kernel weight. For example, the crosses Samsorg 40 x ICSV111, Samsorg 7 x ICSV111, AS 13 x Hindatu and AS 13 x Samsorg 40, had heavier kernels than their respective parents. However, the poor association between thousand kernel weight and grain yield suggests that simultaneous improvement of both traits is impossible in the current sorghum population. The present findings are inconsistent with the findings of Kadam et al., (2001), Reddy and Patil, (2015), Narkhede et al., (2017), who reported that seed weight was positively correlated with grain yield. The result from this study revealed that the non-additive gene action was important for thousand kernel weight. To find stable, high-yielding genotypes, a variety of good general combiners should be utilized during hybridization, and the resulting family should be subjected to evaluation across different environments. Rajguru et al., (2004) reported non-additive gene action for thousand kernel weight.

Breeding for high above-ground biomass can enhance grain yield potential. Parental genotypes Samsorg 7, Samsorg 40, and Kurumbasau in the present study exhibited good GCA effects for above-ground biomass and grain yield. These implied that the parental genotypes could be used as a genetic resource for simultaneously improving stover and grain yield. Crosses such as Samsorg 40 x CSR-02, Samsorg 40 x AS 152, ICSV111 x Hindatu, Samsorg 7 x Kurumbasau, ICSV111 x ICNSL2014-022-8 and AS 152 x SSV2008091 were identified as best crosses for above-ground biomass and grain yield (Table 5.7). The majority of the crosses involved either good x good (e.g., Samsorg 7 x Kurumbasau) or good x poor (.e.g., Samsorg 40 x CSR-02) parental genotypes. Some crosses, including AS 152 x ICNSL2014-022-8, AS 152 x SSV2008091, ICSV111 x ICNSL2014-022-8, and AS 13 x ICNSL2014-022-8 were among the top yielders for above-ground biomass (>25.0 t/ha) and grain yield (>6.0 t/ha). These crosses could be exploited for producing desirable transgressive segregants in breeding for superior grain and stover yield in sorghum.

Harvest index measures reproductive efficiency and increasing the index can significantly boost genetic yield gains (Kelly and Rao, 1993). Cross combinations such as Masakwa x Hindatu, AS 152 x Samsorg 9, which are tall and late-maturing, recorded higher harvest index (<3.0). Similarly, genotypes that are short and early such as Samsorg 40 x Samsorg 9, AS 13 x Samsorg 7 and Samsorg 7 x Kurumbasau, also recorded high harvest index (<3.0) values greater than that of the check hybrids (0.24). The response of the diverse sorghum genotypes to the harvest index suggested that the harvest index maybe significantly affected by environment and genotype. In addition, the efficiency of assimilate partitioning to the panicles need further studies. The positive correlation between harvest index and grain yield indicated that the higher yields in sorghum cultivars were due to panicle size and large grains associated with higher harvest indices (Carcedo et al., 2021). This will allow for the improvement of both traits in the studied population. Carcedo et al., (2021) reported that an increased harvest index in sorghum was responsible for higher grain yield in hybrids. The present study showed that dominant gene effects significantly influenced the inheritance of harvest index. Hence, exploiting heterosis and creating a composite variety would successfully improve the sorghum harvest index.

The high broad-sense heritability found for plant height (92.0%), grain yield (70.3%), and the majority of the assessed traits show that additive gene action controlled trait expression predominantly than the test environments. Similar results have been reported by Mangena et al., (2022) when assessing heterosis among sweet sorghum F_1 hybrids for ethanol production and associated traits. The high broad-sense heritability estimates indicate that the phenotypes accurately reflected the genotypes for the studied attributes and that phenotypic selection could be reliable. In contrast, days to anthesis showed moderate broad-sense heritability estimates of 53.9% suggesting that the environment impacted on the expression of days to anthesis and further highlights that genotype selection under specific environmental conditions is necessary for accelerating genetic advancement.

Narrow-sense heritability was very low (>30.0%) for all measured traits suggesting that non-additive gene effects were primarily responsible for the genetic variation in these traits, which suggests that selection will be effective in advanced generation. The variable magnitude of broad-sense and narrow-sense heritability of the different traits indicates the influence of the test environments (Owusu et al., 2020). The wider difference between the broad- and narrow-sense

heritability for all traits measured suggests a greater is environmental influence and, therefore, difficulty in artificial selection.

The crosses exhibited substantial high parent heterosis for grain yield and other agronomic traits (Table 5.8), revealing that hybrid breeding provides an effective strategy for boosting sorghum production in Africa. The crosses such as AS 152 x SSV2008091, Samsorg 7 x Kurumbasau, AS 152 x ICNSL2014-022-8, and Masakwa x Hindatu were among some top yielders (>6 t/ha) in the present study (Table 5.4) and recorded heterosis exceeding 120%. The magnitude of high-parent heterosis estimates for grain yield, above-ground biomass yield and harvest index in the present study was greater than reported in other studies (Makanda et al., 2010; Mindaye et al., 2016; Kante et al., 2019; Mangena et al., 2022). According to Cress (1966), the heterosis of the F_1s produced by parents with a more diverse genetic background is greater. Therefore, the derived F_1s expressed significant genetic diversity, and yielded heterosis, implying transgressive segregation for combining ability in the desirable direction in the early breeding generation.

5.5 Conclusions

The present study determined the combining ability, heterosis and gene action conditioning grain yield and related agronomic traits among sorghum genotypes to select the most suited parental genotypes for future breeding and desirable crosses for genetic advancement and commercialization. Parental genotypes Samsorg 7, Masakwa, and SSV2008091 were identified as useful germplasm resources for breeding for high-yielding capacity to improve yield gains and reduce the yield gap of sorghum in SSA. Crosses AS 152 x SSV2008091, Samsorg 7 x Kurumbasau, AS 152 x ICNSL2014-022-8, and Masakwa x Hindatu with high SCA effects for grain yield are recommended for further selection and multi-environment testing for future release and deployment for cultivation in drought-prone areas of Nigeria and similar agro-ecologies of SSA.

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Introduction and objectives of the study

Drought or limited water availability is the leading cause of poor agricultural productivity globally. Drought stress has been exacerbated in recent years by climate change. Nigeria is the largest producer of sorghum [*Sorghum bicolor* (L.) Moench] in Africa, accounting for about 26% of the continent's sorghum output in 2021. Sorghum is the second cereal crop in terms of production quantity in the country, serving food security and the economic well-being of resource-poor farmers. However, about 80% of Nigeria's rainfed sorghum production area faces drought stress, resulting in 40-100% yield losses. Genetic gains for yield and yield-contributing traits are low in sorghum, especially under low soil moisture conditions, contributing to the high yield gaps. The major causes for sorghum's low production and product development, especially in Nigeria, include lack of high-yielding and locally adapted varieties with farmer-preferred traits; declining soil fertility; drought stress; *Striga* infestation; limited access to production inputs; credit facilities, and finance. Thus far, sorghum has not garnered research and development support compared to other conventional cereal crops such as maize (*Zea mays* L.) and rice (*Oryza sativa* L.). There is a need to explore the extent of genetic variation of local cultivars for yield-determining traits to guide cultivar selection for production and variety design with farmer- and market-preferred traits to accelerate yield gains targeting increased production of sorghum in drought-stressed environments. This study was, therefore, executed with the following primary objectives:

1. To present the current opportunities and constraints to sorghum production in Nigeria and make recommendations as a guide to new variety design and sustainable production;
2. To determine drought tolerance and genotype-by-environment interaction (GEI) effect on grain yield of a population of African sorghum genotypes to identify high-yielding and drought-adapted genotypes for production and breeding;
3. To assess the genetic diversity and deduce the population structure among 200 sorghum accessions to guide the selection of contrasting parents for pre-breeding and breeding of drought-tolerant sorghum cultivars;
4. To determine the combining ability, heterosis, and gene action conditioning agronomic traits and grain yield among sorghum genotypes to select genetically superior and contrasting parental genotypes and new families for breeding, cultivar release and commercialization.

Research findings in brief

Sorghum production in Nigeria: opportunities, constraints, and recommendations

A participatory rural appraisal (PRA) study was conducted using semi-structured interviews and focus group discussions involving 250 farmers in three selected sorghum growing zones in Northern Nigeria (the Sub-humid Southern Guinea Savannah, the Northern Guinea Savannah and the Sahel Savannah). The main findings of the study were:

- Sorghum was cultivated mainly by males (80%) who had grade 6-12 levels of education (31.3%), with a productive age of 21-45 years (75.7%) and a household family size of below five members (52.3%).
- Low-yielding landrace varieties such as Kaura (37.4%) and Fara-fara (29.3%) were the most widely cultivated types across the study zones due to their good grain quality.
- Amongst production constraints, farmers rated drought stress as the major and significant challenge to the productivity of sorghum.
- The major farmers' preferred traits from a sorghum variety were high yield, drought tolerance and *Striga* resistance.
- Sorghum breeding programs in Nigeria should incorporate the farmer-preferred traits and the highlighted constraints while developing improved sorghum varieties suitable for production in semi-arid regions.

Drought tolerance response of African sorghum [Sorghum bicolor (L.) Moench] genotypes under variable environments

Two hundred and twenty-five sorghum genotypes were evaluated under non-stressed (NS), pre-anthesis drought stress (PreADS), and post-anthesis drought stress (PoADS) conditions under field and greenhouse environments using a 15 × 15 alpha lattice design with two replicates. The three water regimes and two environments resulted in six testing environments for this study. The following major outcomes were obtained:

- Sorghum genotypes showed a highly significant difference in grain yield response. The additive main effect and multiplicative interaction (AMMI) analysis of variance showed 44.6%, 38.7% and 16.7% of the total variation attributed to environment, genotype, and GEI effects.

- The mean grain yield of the best test genotypes under NS, PreADS, and PoADS were 3.70 t/ha, 1.76 t/ha, and 2.58 t/ha.
- The best genotypes adapted to non-stressed environments were G09, and G109 yielding 6.1 t/ha and 6.7 t/ha, respectively. G114 (6.3 t/ha) and G56 (5.6 t/ha) displayed the best performance in PreADS conditions, whereas genotypes G114 and G115 were identified as high performers under PoADS with grain yields of 3.8 and 4.2 t/ha, respectively.
- AMMI 4 was the best-fitting model for grain yield, and on the basis of AMMI 4 and the best linear unbiased predictions (BLUPs) calculations, genotypes G119 and G127 with a grain yield of 5.6 t/ha and 6.3 t/ha were selected as being suitable for NS conditions. Genotypes G8 and G71 with BLUPs of 2.5 t/ha and 2.6 t/ha were best-suited for PreADS conditions, whereas genotypes G115 and G120 with BLUPs of 4.2 t/ha and 4.3 t/ha are recommended for PoADS drought-prone environments, respectively.
- The identified sorghum genotypes are recommended for production or breeding population development in dry agro-ecologies of SSA characterized by PreADS and PoADS conditions.

Genetic diversity and population structure of African sorghum [*Sorghum bicolor* (L.) Moench] accessions assessed through single nucleotide polymorphisms markers

Two hundred sorghum genotypes advanced from the screening experiment with good drought tolerance and yield performance were genotyped using the diversity arrays technology (DArT) – derived single nucleotide polymorphism (SNP) markers. The main results of this study were as follows:

- The markers had moderate discriminatory power, with the polymorphism information content ranging between 0.09-0.38.
- The average gene diversity value (0.32) was high, while the average observed heterozygosity (0.15) was relatively low, which is a typical value for autogamous crop species like sorghum.
- The population structure and cluster analyses revealed four main clusters with a high level of genetic diversity among the accessions studied.
- The variation within populations (41.5%) was significantly higher than that among populations (30.8%) and between samples within structure (27.7%). The high genetic variation within population could be attributed to the preservation of sorghum landraces by farmers in Africa and suggested differences in adaptation and parentage.

- The study identified distantly related sorghum accessions such as Samsorg 48, Kaura Red Glume (Cluster 1); Gadam, AS 152 (Cluster 2); CSRO1, ICNSL2014−062 (Cluster 3); and Yalai, Kafi Mori (Cluster 4).
- The accessions that exhibited wide genetic diversity are selected to developing new gene pools and novel genotypes for the West and Central Africa (WCA) sorghum breeding programs.

Genetic analysis of agronomic traits and grain yield performance among African sorghum [*Sorghum bicolor* (L.) Moench] genotypes

Twelve agronomically complementary and drought-tolerant sorghum parents were crossed using a half-diallel mating design, and 66 F_1 progenies were developed. The F_1 progenies, the parents, and two check varieties were evaluated under three environments in Nigeria. The core findings of the study were:

- There was significant diversity among the parental genotypes and their crosses for the assessed agronomic traits, allowing for the selection of ideal parents and hybrids for traits of interest.
- Variation for the assessed agronomic traits was high among the newly-developed crosses compared to parental genotypes, which suggested successful gene recombinations that favor the expression of agronomic traits in the crosses.
- Parental genotypes Samsorg 7, Masakwa, and SSV2008091 were the most promising general combiners for grain yield with GCA effects of 0.425, 0.276 and 0.528, respectively.
- Crosses AS 152 x SSV2008091, Samsorg 7 x Kurumbasau, AS 152 x ICNSL2014-022-8, and Masakwa x Hindatu were selected based on their high specific combining ability effects and maximum grain yield across the three environments.
- Compared to the best parent (SSV2008091, 2.9 t/ha), AS 152 x SSV2008091 (6.4 t/ha) showed the most significant positive heterosis for grain yield at 163.9%.
- Higher variance due to specific combining ability for most of the studied traits indicates the preponderance of non-additive gene action.
- Broad-sense heritability values were greater than narrow-sense heritability values, indicating that the influence of additive gene activity was modest for each characteristic studied.
- The preponderance effect of non-additive gene action was useful for exploiting heterosis in sorghum breeding.

- The identified crosses, such as AS 152 x SSV2008091 and Samsorg 7 x Kurumbasau are recommended for further selection and multi-environment testing for cultivar deployment in Nigeria's drought-prone areas and similar agro-ecologies of SSA.

The implications of the research findings for population improvement and hybrid breeding of drought-tolerant sorghum

- The PRA study highlighted drought stress, *Striga* infestation, and bird damage as the most significant challenges smallholder farmers encounter in sorghum production in Northern Nigeria. These are key breeding goals requiring dedicated sorghum genetic improvement programs and a robust seed system in the country.
- Policymakers can address the identified production constraints of limited access to production inputs by providing sorghum farmers with subsidies and low-interest loans for purchasing production inputs.
- Current and future sorghum breeding programs should integrate the key production constraints and market- and farmer-preferred traits to develop and deploy new-generation cultivars to ensure sustainable production, productivity, and rapid adoption of the finished, improved products in the semi-arid regions of Nigeria.
- The presence of significant phenotypic variation for drought tolerance in both stressed and non-stressed sorghum genotypes suggested a considerable opportunity for selecting genotypes for higher grain yield with greater levels of drought resistance.
- The genotypes G56, G157, G8, and G152 were identified as highly tolerant to pre-anthesis drought stress based on yield performance and drought tolerance ranking, while the genotypes G144, G115, G157, and G08 were selected with tolerance to post-anthesis drought stress.
- The molecular markers had moderate discriminatory power, with the polymorphism information content ranging between 0.09-0.38. The average gene diversity value (0.32) was high, while the average observed heterozygosity (0.15) was relatively low, which is a typical value for autogamous crop species like sorghum.
- The results of STRUCTURE and PCoA analyses indicated a genetic structure comprised of four sub-populations of the sorghum accessions under study.
- The significance of both additive and non-additive effects in regulating grain yield and yield components and drought tolerance revealed that genetic gain can be attained through hybridization and selection.
- The selected F_1 populations, such as AS 152 x SSV2008091 (with mean grain yield of 6.4 t/ha) and Samsorg 7 x Kurumbasau (6.6 t/ha) are ideal for selecting transgressive

segregants for genetic improvement. The families are recommended as best experimental hybrids or for pure line breeding and variety release in drought-prone areas of Nigeria and similar agro-ecologies of SSA after continuous selection and multi-environment testing.