



Article

Response of African Sorghum Genotypes for Drought Tolerance under Variable Environments

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Abstract: Sorghum (*Sorghum bicolor* (L.) Moench) 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 rain-fed 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 Estimates (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 sub-Saharan Africa characterized by pre-and-post anthesis drought stress. In addition, the identified genotypes are valuable genetic resources to develop novel drought-tolerance material.

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



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1. Introduction

Sorghum (*Sorghum bicolor* L.) is a highly valued cereal crop native to Sub-Saharan Africa (SSA) and has been cultivated for centuries [1]. 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 [2]. 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 [2]. In terms of yield, sorghum is the third most important cereal crop in Africa with 26.3 million metric tonnes after maize (96.6 million metric tonnes) and rice (37.2 million metric tonnes) [2]. The grains are an important food source that is processed into a variety of traditional cuisines such as couscous, porridge, and semi-leavened bread [3,4]. 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 [1,5].

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 [6]. In addition, grains are widely used to prepare local beers and beverages [3]. According to Tenywa et al., [7] 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) [2]. 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 tons/ha and the 4.58 tons/ha achieved in the USA [2]. The lower yields in SSA are attributed to abiotic stresses (e.g., drought stress and poor soil fertility [1] and biotic factors e.g., anthracnose caused by *Colletotrichum graminicola* (Ces.) Wilson [8], stem borer (*Chilo partellus* (Swinhoe)), leaf blight (*Exserohilum turcicum* (Pass.) Leo and Suggs.) [9], and the parasitic weed (*Striga hermonthica* (Del.) Benth) [10]. 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 [6,11–14]. Drought stress is the most yield-limiting factor for sorghum production in SSA [12,14]. For example, drought caused yield losses of 36% and 55% during vegetative and reproductive growth stages, respectively [15]. Pre-flowering drought stress reduced grain yield of sorghum by more than 40% [16], whereas post-flowering drought stress caused grain yield losses by 50 to 90% [17]. Yield-component traits such as the number of grains per panicle and seed size are reduced by drought stress [14,18]. Drought stress occurring during the critical growth stages of the crop, including pre- and post-anthesis, has a detrimental effect on grain quality [16,19]. 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 [4,13,20]. 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 [21–25]. 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 [26]. 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-by-environment (GGE) biplots [26–29]. 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 [27]. 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 [16,30,31]. 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 rain-fed 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 [32–34]. 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 [25,32,33]. 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 genotype-by-environment interaction (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.

2. Materials and Methods

2.1. Plant Materials

Two hundred and twenty-five (225) sorghum genotypes assembled from diverse origins were used for the study. These comprised 235 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 Supplementary Materials Table S1.

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 [35]. The glasshouse 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%.

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 in two replicates. The three water regimes and two environments resulted in six testing environments, namely: glasshouse and non-stressed (E1); glasshouse and pre-anthesis drought stress (E2); glasshouse 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 glasshouse 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 tensiometers 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 glasshouse environments, pre- and post-flowering drought stress were imposed, according to Reddy et al. [33]. Pre-flowering stress 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 [36]. Post-flowering drought stress was imposed by withdrawing irrigation during the booting stage approximately 45 days after sowing [36]. In our case, post-flowering stress was imposed between 90 and 100 days after sowing in the glasshouse 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 at a recommended rate of 1 mL per 100 litres of water.

2.4. Data Collection

Grain yield (GY, in kg/plot) data under field conditions was recorded from 10–15 randomly selected plants from the inner middle rows of the plot and converted tons/hectare (t/ha) after adjusting to 12.5% grain moisture content. Under glasshouse conditions, GY was determined as the grain weight of all harvested sorghum heads in each pot. Subsequently, GY was calculated by dividing the total grain weight from each pot by the pot area using the formulae for the area of a circle: $A = \pi r^2$ (0.071 m²) adjusted to 12.5% moisture, expressed in kg ha⁻¹, and converted to t/ha.

2.5. Data Analysis

BLUPs and BLUEs 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 [37].

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

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

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 j th replicate within i th environment, $Block_k(Env_iRep_j)$ 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_{ijkl} = 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 [12,37].

2.6. Drought Tolerance/Susceptibility Indices

Based on the BLUPs data summary, the following 10 selection indices of drought tolerance were computed (Table 1): 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 (K₁STI), and modified stress tolerance index II (K₂STI).

Table 1. 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 [38]
2	Mean productivity	MP	$\frac{(Y_s + Y_p)}{2}$	Rosielle and Hamblin [38]
3	Harmonic mean	HM	$\frac{2(Y_p \times Y_s)}{(Y_p + Y_s)}$	Jafari et al. [39]
4	Stress susceptibility index	SSI	$1 - \left(\frac{Y_s}{Y_p} \right)$	Fisher and Maurer [40]
5	Geometric mean productivity	GMP	$\sqrt{(Y_p \times Y_s)}$	Schneider et al. [41]
6	Stress tolerance index	STI	$\frac{(Y_p - Y_s)}{(\bar{Y}_p)^2}$	Schneider et al. [41]
7	Yield Index	YI	$\frac{Y_s}{\bar{Y}_p}$	Gavuzzi et al. [42]
8	Yield Stability Index	YSI	$\frac{Y_p}{\bar{Y}_p}$	Bouslama and Schapaugh [43]
9	Modified stress tolerance index	MSTI/K ₁ STI	$\left(\frac{Y_p^2}{\bar{Y}_p^2} \right) \times \left[\frac{(Y_p + Y_s)}{\bar{Y}_p^2} \right]$	Farshadfar and Sutka [44]
10	Modified stress tolerance index	MSTI/K ₂ STI	$\left(\frac{Y_s^2}{\bar{Y}_s^2} \right) \times \left[\frac{(Y_p + Y_s)}{\bar{Y}_p^2} \right]$	Farshadfar and Sutka [44]

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

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 non-stressed vs pre-anthesis drought stress and NS vs post-anthesis drought stress conditions for field and glasshouse environments and across each drought condition and environment. This allowed grouping the sorghum genotypes for different levels of drought tolerance using the ggplot2 package [45] in R version 4.1.0 [46]. According to Fernandez [47], 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 condition; Group C genotypes which are relatively higher performers under drought stress condition; 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 glasshouse and field environments. Regression model diagnosis (e.g., fitted vs residual and quantile-quantile (QQ) plots) was performed in R using the ggfortify package [48,49].

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. [50] using the following relationship formula:

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

Standard deviation of rank (SDR) was measured as:

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

where S = sample standard deviation, n = number of observations, where R_{ij} is the rank of X_{ij} within the j th environment, $\bar{R}_i$ is the mean rank across all environments for the i th genotype.

2.9. AMMI Analysis

The Additive Main Effect and Multiplicative Interaction (AMMI) analysis was carried out using Genstat 20th edition [51]. 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 [52], 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 [53] 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 j th 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.

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. [54] as follows:

$$\text{AMMI Stability Value (ASV)} = \sqrt{\left[\frac{SS_{IPCA1}}{SS_{IPCA2}} (IPCA1score) \right]^2 + [IPCA2score]^2} \quad (5)$$

where SS = Sum of squares; $IPCA1$ = Interaction Principal Component Analysis axis 1; $IPCA2$ = 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 [55]. AMMI-1 biplot was constructed based on the genotype and environment mean yields and their IPCA1 scores to characterize the GE interaction.

3. Results

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 first 50 selected sorghum genotypes under six test environments are presented in Table 2, whereas BLUPs and BLUEs for all the test genotypes are provided in Supplementary Table S2. Under environment E1 (glasshouse environment, non-stress 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) (Table S2). Under a glasshouse environment and a pre-flowering drought stress 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 environment E2 (glasshouse environment, pre-flowering stress condition), 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 environment E3 (glasshouse and post-flowering drought stress), 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 environment E4 (Ukulinga and non-stressed condition) varied from 1.35 t/ha for G3 (Gadam) to 6.3 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, G114, G105, and G127 were the top yielders with >4.05 t/ha. The lowest yielders under E4 were G3, G190, G100, G199, G148, G155, and G113, which recorded grain yields of <1.50 t/ha. Under environment E5 (Ukulinga and pre-anthesis drought stress), 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 (Ukulinga and post-anthesis drought stress), 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 under environment E6. 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.

Table 2. Best linear and unbiased predictions (BLUPs) and best linear and unbiased estimates (BLUEs) for grain yield of 225 sorghum genotypes evaluated under non-stress conditions, pre- and post-anthesis drought stress in glasshouse and field environments.

Genotype Code	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
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
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
Mean	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		13.9	
Significance (G)	**		**		**		**		**		**		***	

CV = coefficient of variation, G = Genotype significance, E1 = greenhouse and non-stressed, E2 = greenhouse and pre-anthesis drought stress, E3 = greenhouse and post-anthesis drought stress, E4 = Ukulinga and non-stressed, E5 = Ukulinga and pre-anthesis drought stress, E6 = Ukulinga and post-anthesis drought stress, ** = Significant at the 5% probability level, *** = significant at the 1% probability level. See codes of genotypes in Supplementary Table S1.

Overall, drought stress 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 environments. The extent of grain yield reduction differed under glasshouse and field environments. Yield loss were detrimental under PreADS than PoADS compared with NS condition in a glasshouse 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.

3.2. Drought Tolerance Indices

The drought tolerance/susceptibility indices of 50 selected sorghum genotypes are presented in Table 3. In addition, Supplementary Table S3 presents drought tolerance/susceptibility indices values of all evaluated sorghum genotypes. 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 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 G89 (369.22) and G218 (135.93). Genotypes G108 (0.24) and G99 (0.51) recorded the lowest SSI values under PreADS compared with G30 G100 with an SSI of >1 . 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 sensitive.

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.

Table 3. Values of tolerance, susceptibility indices, and grain yield of the assessed sorghum genotype under stress and non-stress conditions in glasshouse and field environments.

Code	TOL		MP		HM		SSI		GMP		STI		YI		YSI		MSTI/k1STI		MSTI/k2STI	
	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
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

Table 3. Cont.

Code	TOL		MP		HM		SSI		GMP		STI		YI		YSI		MSTI/k1STI		MSTI/k2STI	
	PreADS	PoADS	PreADS	PoADS	PreADS	PoADS	PreADS	PoADS	PreADS	PoADS	PreADS	PoADS	PreADS	PoADS	PreADS	PoADS	PreADS	PoADS	PreADS	PoADS
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
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 denote pre-anthesis drought-stress and post-anthesis drought-stress, respectively; see codes of genotypes in Supplementary Table S1 and codes of drought tolerance indices in Table 1.

Indices such as k_1 STI and k_2 STI 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. Under PreADS, G144 (Kaura Short Panicle-1) and G9 (Yar Gumel) recorded high k_1 STI values of 1.42 and 1.31, whereas G3 (Gadam) and G100 (AS 97) recorded the lowest k_1 STI values of 0.02 and 0.03 under PreADS and were identified as drought sensitive. Under PoADS, high k_1 STI 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_2 STI 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_2 STI of 0.20 and 0.12, respectively, under PreADS. Under PoADS, the G3 (Gadam) genotype recorded the lowest k_2 STI 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).

3.3. Genotypes 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 glasshouse and field environments are shown in Figure 1. Grain yield performance under PreADS versus NS conditions in a glasshouse environment (Figure 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 G1 recorded relatively higher grain yield only under PreADS in a glasshouse 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 glasshouse environment (Figure 1B) revealed genotypes G08 and 144 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 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 glasshouse environment (Group D).

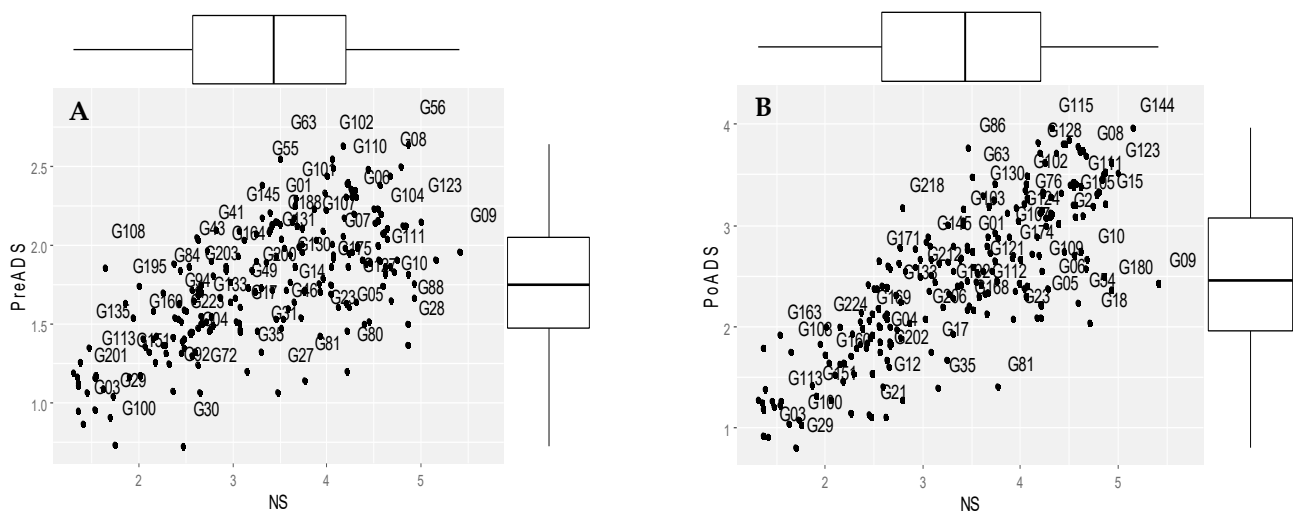


Figure 1. Cont.

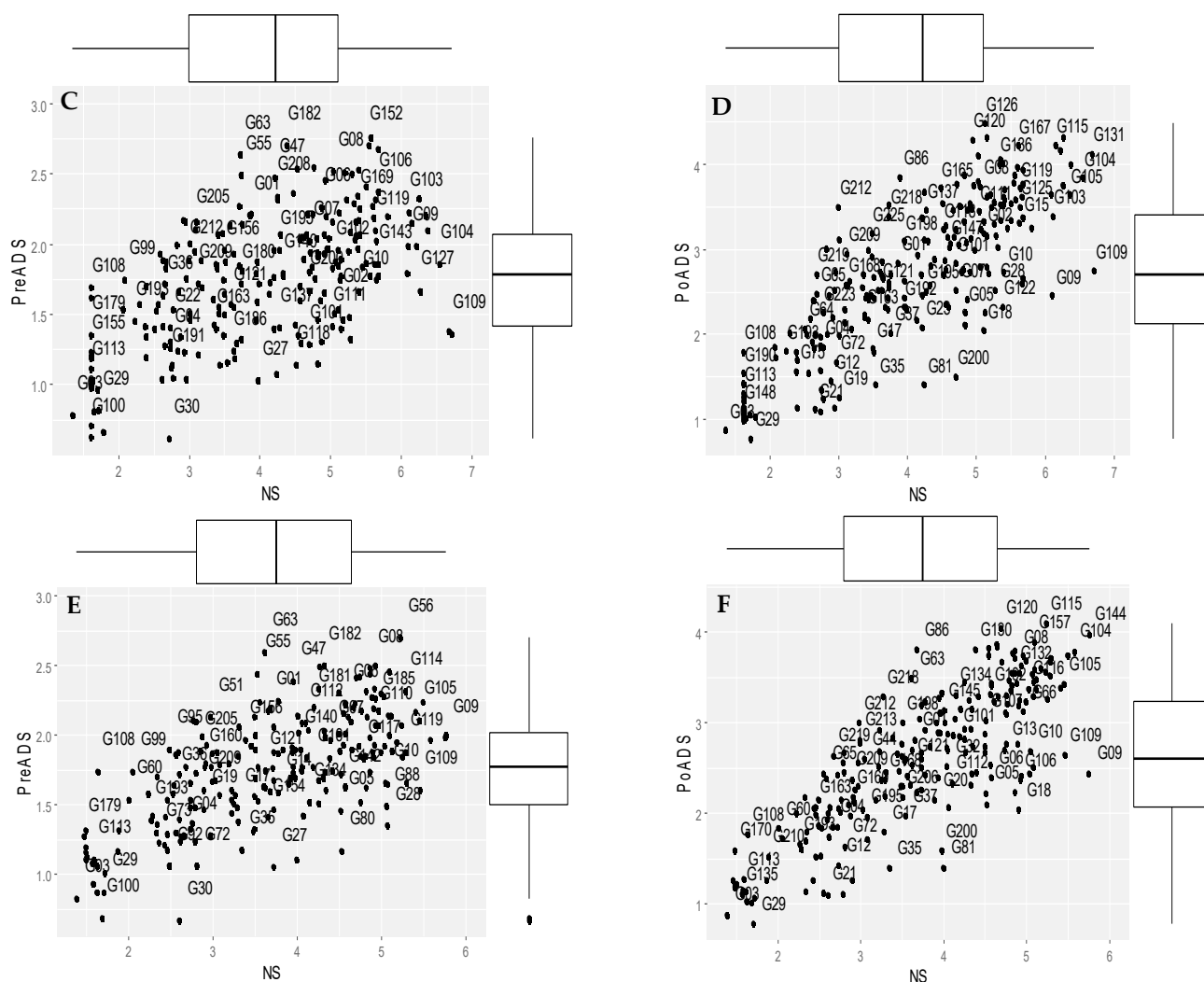


Figure 1. Scheme showing grouping of 225 sorghum genotypes for mean grain yield (t/ha) when evaluated under non-stressed (NS), pre-anthesis drought-stress (PreADS), and post-anthesis drought-stress (PoADS) conditions in the greenhouse (A,B) and field (C,D) environments, and across both glasshouse and 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.

Under the field environment (Figure 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 values (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 glasshouse environment (Figure 1C). Under PoADS in a glasshouse environment (Figure 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 glasshouse 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 glasshouse and field environments (Group D) (Figure 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 condition) (Figure 1F). 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 environments.

Simple linear regression models showing the relationships between grain yield under drought stress (e.g., PreADS and PoADS) and non-stress (NS) conditions in glasshouse and field environments are shown in Figure 2. For grain yield under PreADS vs NS conditions and PoADS vs NS conditions in a glasshouse 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 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 2C,D). Across glasshouse and field environments (Figure 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.

3.4. Genotype Ranking for Drought Tolerance

The drought tolerance/susceptibility presented in Table 3 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 4 and 5. 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 cultivars, while G3 (Gadam) and G100 (AS 97) were identified as the most drought sensitive genotypes (Table 4).

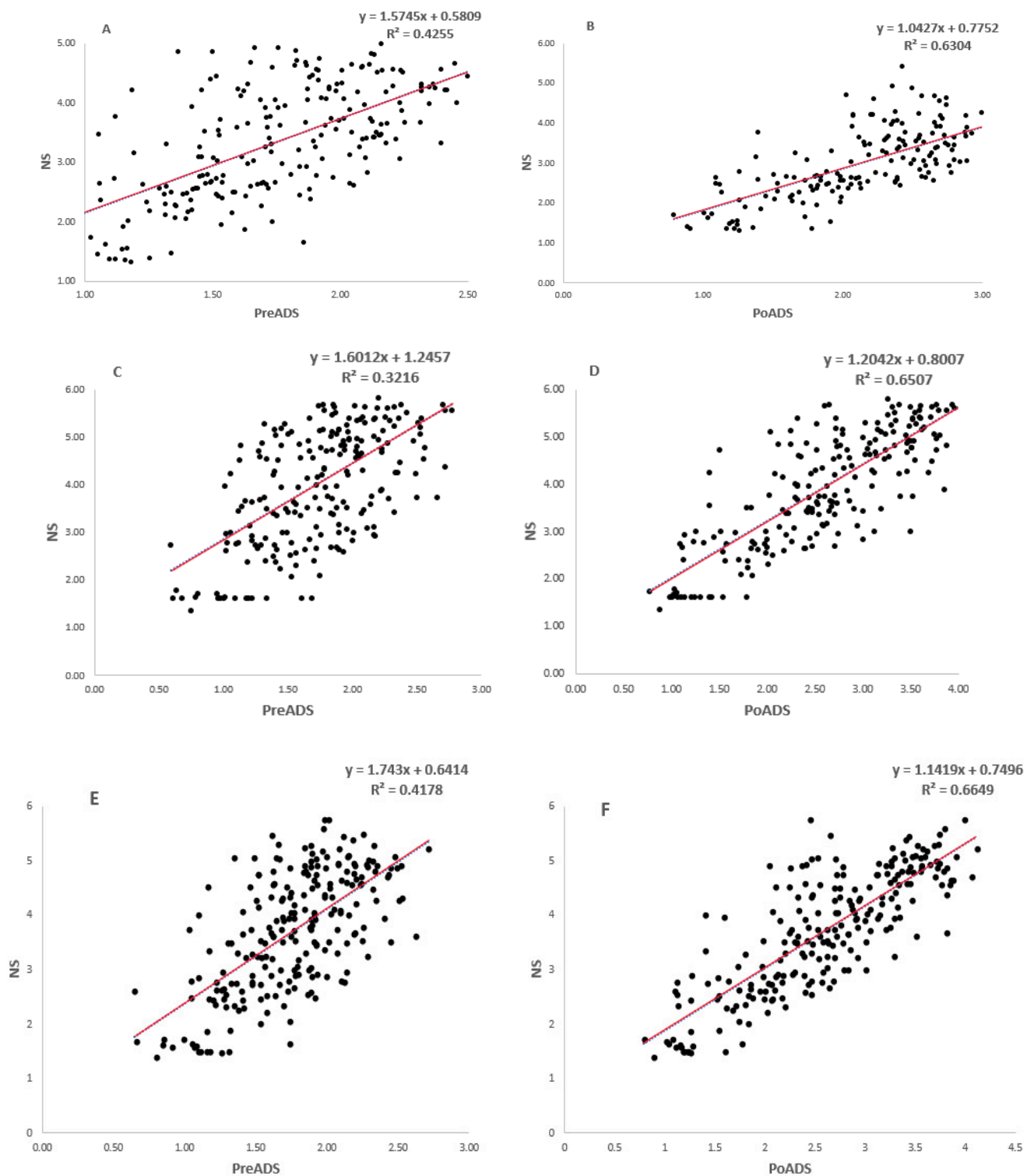


Figure 2. Simple linear regression model fitting grain yield (t/ha) performance of 225 sorghum genotypes evaluated under non-stressed (NS), pre-anthesis drought-stress (PreADS), and post-anthesis drought-stress (PoADS) in the glasshouse (A,B) and field (C,D) environments, and across both glasshouse and field (E,F) environments.

Table 4. Rank, rank mean ($\bar{R}$) and standard deviation of ranks (SDR) of drought tolerance indices of the sorghum genotypes in PreADS.

Code	Genotype Name or Designation	Yp	Ys	TOL	MP	HM	SSI	GMP	STI	YI	YSI	MSTI/ k1STI	MSTI/ k2STI	$\left(\bar{R}\right)$	SDR
Drought tolerant genotypes															
G56	CSRO1	8	1	152	1	7	43	74	74	1	43	5	1	34.17	44.62
G157	KAURA MAI BAKI KONA	15	3	163	4	22	68	63	63	3	68	10	2	40.33	45.72
G8	ICNSL2014-022-4	31	4	142	10	12	53	84	84	4	53	21	3	41.75	41.50
G152	BOG FARWA	33	5	149	12	19	61	77	77	5	61	24	4	43.92	41.43
G106	ICNSL2014-021-1	38	6	144	15	21	60	82	82	6	60	27	5	45.50	40.29
G114	JAR LAU	9	11	189	5	40	102	37	37	11	102	8	7	46.50	54.30
G128	BASSA DAWA	49	8	127	21	17	51	99	99	8	51	36	8	47.83	38.83
G184	CAPARLKSG20150291	29	12	158	16	29	74	68	68	12	74	26	10	48.00	41.35
G129	ICNSL2014-023-5	4	13	206	3	47	125	20	20	13	125	3	6	48.75	63.63
G178	YAR MAGOGO	20	15	170	13	35	88	56	56	15	88	17	13	48.83	45.41
G53	CAPARLGSG20150124	48	9	131	24	23	55	95	95	9	55	37	9	49.17	37.94
G136	TUNKURA	39	14	156	22	30	71	70	70	14	71	30	14	50.08	39.28
G116	JAR KAURA	21	18	176	14	41	92	50	50	18	92	19	15	50.50	46.42
G167	MAGARA	25	17	166	18	38	86	60	60	17	86	25	17	51.25	42.73
G182	GWAZA BANJI BORNO	74	7	92	41	10	29	134	134	7	29	66	11	52.83	45.09
G70	FARA FARA MAI-SHAHO	34	20	164	23	39	85	62	62	20	85	28	19	53.42	40.77
G120	GAGARAU-4	45	19	153	28	33	75	73	73	19	75	40	20	54.42	36.97
G71	TAKUMBO	81	10	89	49	11	27	137	137	10	27	70	16	55.33	45.29
G123	MASAKWA	6	24	207	6	65	136	19	19	24	136	7	18	55.58	64.10
G185	FARAFARA KADUNA	23	25	178	20	50	109	48	48	25	109	23	21	56.58	47.68

Table 4. Cont.

Code	Genotype Name or Designation	Y _p	Y _s	TOL	MP	HM	SSI	GMP	STI	YI	YSI	MSTI/ k1STI	MSTI/ k2STI	$\left(\bar{R}\right)$	SDR
Drought sensitive genotypes															
G215	ICSV 145	221	215	7	219	204	64	219	219	215	64	221	216	173.67	75.61
G191	KAURA BORNO	187	198	76	194	202	180	150	150	198	180	190	198	175.25	34.33
G73	ZAGO BLACK GLUME	200	200	52	204	201	151	174	174	200	151	200	202	175.75	41.86
G113	JAR BALAKWAMA	215	216	12	213	210	87	214	214	216	87	213	215	176.00	68.17
G211	GP11BR	209	209	24	210	205	115	202	202	209	115	210	211	176.75	57.40
G97	SAMSORG 7	179	201	87	190	208	199	139	139	201	199	184	201	177.25	35.20
G135	NDU VARI	218	217	11	220	212	98	215	215	217	98	216	217	179.50	67.04
G163	HIPUSINI	196	203	66	201	206	181	160	160	203	181	196	204	179.75	37.71
G26	MAI-GOJE	173	208	102	191	213	216	124	124	208	216	180	206	180.08	39.21
G222	IS 8268	199	206	59	206	207	176	167	167	206	176	201	205	181.25	39.98
G72	SAMBULMU- 3	176	210	103	195	218	218	123	123	210	218	183	207	182.00	40.30
G34	12KNICSV-297-4	214	218	17	216	216	128	209	209	218	128	212	218	183.58	59.59
G92	SAMSORG 42	194	211	84	205	217	207	142	142	211	207	197	208	185.42	39.15
G30	12KNICSV-297-2	193	224	124	209	224	225	102	102	224	225	205	223	190.00	47.82
G33	12KNICSV-176	211	219	25	214	219	182	201	201	219	182	211	219	191.92	51.94
G148	KOMA	217	220	22	221	220	190	204	204	220	190	222	220	195.83	53.64
G29	12KNICSV-293	212	222	39	222	222	219	187	187	222	219	214	222	198.92	49.77
G201	AKO VARIETY	216	221	27	223	221	211	199	199	221	211	219	221	199.08	52.50
G100	AS 97	213	225	50	224	225	224	176	176	225	224	224	225	200.92	48.83
G3	GADAM	225	223	21	225	223	215	205	205	223	215	225	224	202.42	55.16

Y_p = grain yield under NS condition, Y_s grain yield under drought-stress condition, $\left(\bar{R}\right)$ = Rank Mean, SDR = Standard Deviation of Rank. See codes of genotypes in Supplementary Table S1 and codes of drought tolerance indices in Table 1.

Table 5. Rank, rank mean ($\bar{R}$), and standard deviation of ranks (SDR) of drought resistance/tolerance indices of the sorghum genotypes (PoADS).

CODE	GENOTYPE	Yp	Ys	TOL	MP	HM	SSI	GMP	STI	YI	YSI	MSTI/ k1STI	MSTI/ k2STI	$\left(\bar{R}\right)$	SDR
Drought tolerant genotypes															
G115	DANYAR BANA	11	1	119	3	22	44	107	107	1	44	6	2	38.92	44.17
G157	KAURA MAI BAKI KONA	15	4	131	5	32	53	95	95	4	53	12	4	41.92	42.04
G120	GAGARAU-4	45	3	64	12	8	20	162	162	3	20	31	6	44.67	55.30
G144	KAURA SHORT PANICLE- 1	1	2	197	1	47	120	29	29	2	120	1	1	45.83	62.12
G152	BOG FARWA	33	6	109	15	27	45	117	117	6	45	25	7	46.00	41.54
G185	FARAFARA KADUNA	23	12	135	16	36	64	91	91	12	64	21	11	48.00	39.01
G68	PAM PARA-2	37	11	112	20	30	48	114	114	11	48	28	15	49.00	39.00
G8	ICNSL2014-022-4	31	13	123	18	33	56	103	103	13	56	26	14	49.08	37.96
G141	ICNSL2014-024-7	53	5	76	23	15	30	150	150	5	30	40	13	49.17	49.12
G178	YAR MAGOGO	20	15	141	14	42	74	85	85	15	74	18	12	49.58	39.85
G104	DAN YARA	3	7	196	2	61	130	30	30	7	130	2	3	50.08	63.09
G129	ICNSL2014-023-5	4	8	193	4	62	127	33	33	8	127	3	5	50.58	61.25
G78	E 29	54	9	79	28	17	33	147	147	9	33	43	16	51.25	46.88
G127	DANGAMA WULCHICHI	12	17	172	7	53	109	54	54	17	109	11	8	51.92	50.50
G126	JAN KAURA 1	59	10	70	33	14	26	156	156	10	26	51	19	52.50	49.81
G119	YAR LAZAU	10	20	179	6	59	115	47	47	20	115	9	9	53.00	53.06
G167	MAGARA	25	21	139	21	43	76	87	87	21	76	24	20	53.33	37.25
G128	BASSA DAWA	49	18	105	30	31	46	121	121	18	46	38	23	53.83	37.24
G56	CSRO1	8	22	186	8	69	125	40	40	22	125	8	10	55.25	56.60
G83	AS 152	62	19	80	35	18	34	146	146	19	34	53	27	56.08	44.02

Table 5. Cont.

CODE	GENOTYPE	Y _p	Y _s	TOL	MP	HM	SSI	GMP	STI	YI	YSI	MSTI/ k1STI	MSTI/ k2STI	$\left(\bar{R}\right)$	SDR
Drought sensitive genotypes															
G58	SAMSORG 49	190	197	99	196	203	183	127	127	197	183	194	198	174.50	33.93
G215	ICSV 145	221	214	19	216	197	86	207	207	214	86	221	215	175.25	66.62
G12	YARWASHA	180	204	138	194	210	206	88	88	204	206	186	200	175.33	43.27
G214	GPP4BR(H)C5	197	200	94	198	205	182	132	132	200	182	196	201	176.58	34.89
G199	YAR BURUNDUZU	223	215	20	219	201	92	206	206	215	92	223	216	177.33	65.68
G97	SAMSORG 7	179	210	183	201	222	224	43	43	210	224	189	206	177.83	62.00
G155	YAR KOMA	222	216	21	220	202	97	205	205	216	97	224	217	178.50	64.57
G21	GAGARAWA-3	192	212	156	204	220	219	70	70	212	219	199	208	181.75	52.67
G222	IS 8268	199	206	120	205	214	212	106	106	206	212	204	205	182.92	42.02
G30	12KNICSV-297-2	193	218	164	206	223	223	62	62	218	223	201	210	183.58	56.69
G211	GP11BR	209	207	50	210	208	176	176	176	207	176	209	211	184.58	43.30
G24	ADAMAWA-2	202	213	128	207	219	215	98	98	213	215	205	209	185.17	45.33
G148	KOMA	217	217	31	218	207	151	195	195	217	151	218	218	186.25	52.47
G135	NDU VARI	218	220	33	221	211	163	193	193	220	163	219	221	189.58	51.57
G201	AKO VARIETY	216	219	35	217	212	171	191	191	219	171	216	219	189.75	49.86
G33	12KNICSV-176	211	221	55	213	217	193	171	171	221	193	211	220	191.42	44.63
G34	12KNICSV-297-4	214	222	46	222	218	188	180	180	222	188	215	222	193.08	47.36
G100	AS 97	213	223	60	223	221	202	166	166	223	202	214	223	194.67	45.19
G29	12KNICSV-293	212	225	93	224	225	222	133	133	225	222	217	224	196.25	45.36
G3	GADAM	225	224	37	225	224	197	189	189	224	197	225	225	198.42	50.85

Y_p = grain yield under NS condition, Y_s grain yield under drought-stress condition, $\left(\bar{R}\right)$ = Rank Mean, SDR = Standard Deviation of Rank. See codes of genotypes in Supplementary Table S1 and codes of drought tolerance indices in Table 1.

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 5) 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 cultivars. 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 sensitive to drought stress (Table 5).

3.5. AMMI Analysis of the GE Interaction

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 6). Three interactive principal components axes (IPCA), including IPCA1, IPCA 2, and IPCA 3 were significant in the AMMI model (Table 6). 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 6. 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 non-stress, pre-flowering drought, and post-flowering drought stresses for grain yield are displayed in Table 7. 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 environment E1 (greenhouse and non-stressed condition) based on AMMI model families 1, 2, 3, and 4 in that order. Under 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 (Ukulinga and pre-flowering drought stress), 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 (Ukulinga and post-flowering drought stress) 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 7. Winning sorghum genotypes for grain yield based on additive main effects and multiplicative interaction (AMMI) model families.

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

Genotype (G) codes are presented in Supplementary Table S1. E1 = greenhouse and non-stressed (TN-NS); E2 = greenhouse and pre-flowering drought stress (TN-PR); E3 = greenhouse and post-flowering drought stress (TN-PO); E4 = Ukulinga and non-stressed (UK-NS); E5 = Ukulinga and pre-flowering (UK-PR); E6 = Ukulinga and post-flowering (UK-PO).

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. [54] to address this problem. The ASV of the top and poor performing genotypes in yield stability are shown in Table 8. 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 (Ged-dawaki 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 8. 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	0.03
G206	2.44	−0.01	0.02	0.05
G186	2.55	−0.02	0	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	1.97
G108	1.64	−0.6	−0.01	1.89
G9	3.47	0.54	0.48	1.77

Table 8. Cont.

Genotype Code	Means (t/ha)	IPCA1	IPCA2	ASV
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 Supplementary Table S1; IPCA1: The first interaction principal components axes; IPCA2: The second interaction principal components axes.

4. Discussion

Sorghum is an important cereal crop in the dry region 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 dispatch 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 [4,56]. The present study examined the response of African sorghum genetic resources (Supplementary Table S1) 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 6). Hence, the testing environments were distinct and discriminative of the genotypes for selection [22,23]. Grain yield response was significantly ($p < 0.01$) affected by the test environments, which accounts for 44.6% of the model's SS (Table 6). This agrees with the mean yield varying from 1.75 t/ha at environment E5 to 4.05 t/ha at environment E4 (Table 2), 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 [16,22,30,31]. 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., PrADS and PoADS) (Table 2). However, under both non-stressed and stressed conditions, the landraces and breeding lines from IAR-NG and ICRSIAT-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 2 and Supplementary Table S2). The high yield response of the collections from IAR-NG and ICRSIAT-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 6). The present results agree with previous studies that reported extensive variation in sorghum genetic resources for grain yield in east African, Indian, and Brazil [16,22,32,34].

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 [57], wheat [58] and rice [59], 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 7). 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 8). 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-flowering stages markedly decreased grain yield (Table 2). Pre-anthesis drought stress reduced grain yield significantly compared with post-flowering drought stress (Table 2), 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-flowering growth stages significantly reduced grain quantity and quality [16,60,61]. Emendack et al. [61] reported 55% and 52% sorghum yield reduction under pre- and post-flowering irrigation treatments, respectively. Rosenow et al. [62] 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. Water 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 [16,60–62]. Sorghum is relatively better adapted to drought stress and has genetic variability for pre- and post-flowering drought tolerance and related traits when compared with major crops such as maize and wheat [60–63].

Genotypes respond to water stress in various ways [16,39,44]. Regarding this, several criteria have been put forth to select genotypes based on their performance in an environment under stressed or non-stressed conditions [44]. Tolerant genotypes exhibit the lowest SSI, and TOL values while greater values were found for MP, HM, GMP, STI, YI, and YSI [38,39,44]. 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 PreADS condition, while genotypes G115, G157, G120, and G144 were the most tolerant to PoADS conditions (Table 5). This was supported by the biplot summary presented in Figure 1. The linear regression models (Figure 2) fitted the observed grain yield under non-stressed conditions and post-anthesis under glasshouse 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-flowering 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. [61] 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 [25,64–66]. In addition, G08 (ICNSL2014-022-4) is an elite and high-yielding breeding line developed at ICRISAT-Kenya with a drought tolerance [25,66]. 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 programmes to exploit heterosis.

5. Conclusions

The present study evaluated the drought-tolerance and genotype-by-environment interaction (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. Our findings have shown the existence of significant and intricate GE interactions, which suggests that genotype performance varied among the test conditions. This information can be used to enhance the selection and evaluation. 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 sub-Saharan Africa 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.

Supplementary Materials: The following supporting information can be downloaded at: <https://www.mdpi.com/article/10.3390/agronomy13020557/s1>, Table S1: Code, pedigree, and origin of 225 sorghum genotypes, Table S2: Best linear and unbiased predictions (BLUPs) and best linear and unbiased estimates (BLUEs) of 225 grain sorghum genotypes grown under non-water stressed conditions and with stress at pre- and post-flowering among six environments, Table S3: Values of tolerance, susceptibility indices, and grain yield of the assessed sorghum genotypes.

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