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EVALUATING THE RESISTANCE OF SORGHUM LANDRACES TO ANTHRACNOSE IN HOT-HUMID AGRO-ECOLOGIES OF ETHIOPIA

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ABSTRACT:

Sorghum (*Sorghum bicolor* L.) is crucial for food security and farmers' livelihoods in Ethiopia. However, biotic stresses like anthracnose (*Colletotrichum sublineola*) hinder its production. This study evaluates the resistance of 42 sorghum landraces and breeding lines to anthracnose stress across three locations over two years in the hot-humid agro-ecologies of Ethiopia. The results confirm significant genotype variation in response to anthracnose, with notable differences in agronomic traits and grain yield. The genotypes Mok079 (G4) emerged as the top-performing landrace, showcasing high yield and a moderately resistant to anthracnose, while the landraces Bmb097 (G5) and Y047 (G18) exhibited stability and lower anthracnose severities. This study highlights the importance of environmental factors in anthracnose severity, emphasizing the necessity for multi-environment trials to enhance the stability of sorghum performance. The findings provide a foundation for breeding strategies to develop superior sorghum varieties that can sustainably bolster food security for smallholder farmers in hot-humid agro-ecologies of Ethiopia.

KEYWORDS: *Anthracnose, Colletotrichum sublineola, landraces, resistance, Sorghum bicolor, Sorghum.*

INTRODUCTION:

Sorghum (*Sorghum bicolor* L.) is a crucial crop in Ethiopia, significantly contributing to food security and the livelihoods of many farmers. It is adapted to diverse agro-ecologies and thrives in both arid and humid regions (Menamo et al., 2021; Mohammed & Misganaw, 2022). It is used for various purposes, including food, feed, and traditional beverages (Yali & Begna 2022; https://globalsorghumandmillet.com/ethiopia/). However, sorghum production faces significant challenges due to various biotic and abiotic factors, with anthracnose, caused by the fungal pathogen *Colletotrichum sublineola*,being one of the most devastating diseases affecting sorghum yields (Aragaw & Tefere, 2024; Dessalegn et al., 2022; Menamo et al., 2021; Mohammed & Misganaw, 2022; Tsedaley & Alemu, 2024).

Anthracnose is prevalent in regions with frequent rainfall and high humidity, such as the hot-humid agro-ecologies of Ethiopia (Birhanu et al., 2024; Chen et al., 2024). The disease manifests as dark lesions on leaves, stems, and panicles, leading to reduced photosynthetic capacity, weakened plants, and ultimately, lower grain yields (Birhanu et al., 2024; Chen et al., 2024; Dessalegn et al., 2022). The development of anthracnose-resistant sorghum genotypes is crucial for improving sorghum productivity and ensuring food security in affected regions (Menamo et al., 2021; Yali & Begna, 2022).

Recent studies have focused on identifying sorghum genotypes with resistance to anthracnose. For instance, Aragaw and Terefe (2024) evaluated 49 sorghum genotypes under field conditions and their results revealed that some genotypes showed lower disease levels and better yield performance in Eastern Ethiopia. Field trials conducted at Bako and Jimma locations in Ethiopia, had reported a consistent resistance in some genotypes and their findings highlighted the importance of selecting genotypes with both resistance to anthracnose and desirable agronomic traits for breeding programs (Dessalegn et al., 2022). Moreover, Birhanu et al. (2024) identified several loci associated with anthracnose resistance in Ethiopian sorghum accessions.

These studies underscore the need for continuous research and breeding efforts to develop anthracnose resistant sorghum varieties. By leveraging the genetic diversity of Ethiopian sorghum landraces, researchers can identify and promote resilient genotypes that can thrive in the hot-humid agro-ecologies of Ethiopia, ultimately enhancing sorghum production and contributing to food security (Mengistu et al., 2019). Therefore, this study aimed in evaluating sorghum landraces to anthracnose under field conditions across hot-humid agro-ecologies of Ethiopia.

MATERIALS AND METHODS:

Description of the study

The study was conducted in 2020 and 2021 main cropping season under natural anthracnose

infestation at Assosa (10° 02’ 33’’N latitude, 34° 34’ 05.89’’E longitude, altitude of 1550 m.a.s.l and mean annual rain fall of 1275 mm), Bako (9° 6’N latitude, 37° 09’E longitude, altitude of 1650 m.a.s.l and mean annual rain fall of 1150.10 mm) and Jimma (10°2’33’’N latitude, 34°34’05.89’’E longitude, altitude of 1550 m.a.s.l and mean annual rain fall of 1275 mm). These locations represent hot spot areas for sorghum anthracnose diseases in Ethiopia.

Planting materials and trial description

As total of 42 sorghum genotypes, including 36 sorghum landraces collected across western Ethiopia, one susceptible check (BTx378), and five resistant checks (PML981442, PML981446, PML981475, PML981488, and Bonsa varieties). The BTx378 was used as a spreader rows for initiating anthracnose epidemics.

The trials were laid out in a 42 x 5 row-by-column complete block design with three replications. Each plot included two rows, 5 m long with inter-row spacing of 75 cm and intra-row spacing of 15 cm. All sorghum genotypes were planted at 13 June 2020 and 10 June 2021 at Assosa, 25 May 2020 and 08 June 2021 at Jimma, and 03 June 2020 and 09 June 2021 at Bako test sites. Fertilizer was applied at the rate of 100 kg ha^{-1} for urea and 100 kg ha^{-1} for NPS (19% N, 38% P_2O_5 and 7% S). Urea was applied in two splits, half at planting and half at knee height (about 35 days after planting).

Data collection

Number of days to 50% flowering, days to 95% physiological maturity, panicle length (cm), plant height (cm), head weight (g), thousand grains weight (g), grain yield (tons ha^{-1}). Anthracnose disease severity was recorded sorghum dough stage using 1-9 scales described by Kumari and Singh (2014) and Sharma (1983).

Data analysis

The areas under the disease progress curve (AUDPC) were used to quantify and summarize disease severity over time. AUDPC was calculated for each genotype from the severity data obtained during different assessments following a method described by Madden et al. (2008).

$$\text{AUDPC} = \sum_{i=1}^{n-1} \left(\frac{X_i + X_{i+1}}{2}\right)(t_{i+1} - t_i)$$

Where, AUDPC is area under disease progress curve, n is total number of assessment times, ti is time of the i^{th} assessment in days from the first assessment date, and Xi is percentage of disease severity at i^{th} assessment. The overall disease progress during different assessment periods were used as the total AUDPC% day at the end of the epidemiological period. AUDPC total% day values were then used in different analysis packages in the study to compare disease prevalence among plots with different genotypes. The standardized relative area under disease progress curve

(rAUDPC) were calculated as a ratio of the actual AUDPC of each accession to the AUDPC of a susceptible landrace (ETSL101515) in order to obtain a better visual comparison among host genotypes across testing locations (Campbell & Madden, 1990).

Analysis of variance

AUDPC and rAUDPC data were transformed using Arcsine and subjected to analysis of variance (ANOVA) using general linear model (GLM) in R program (R core Team, 2023). Mean separations were conducted using Tukey's range test at 5% level of significance.

For yield and yield components, the combined analysis of variance across locations and years was done using linear mixed model of the R program (R core Team, 2023), where genotypes and locations were fixed while years, all the interactions, replications, errors were random. For the combined ANOVA, the following model was utilized:

$$Y_{ijkl} = \mu + Env_i + Rep_j(Env_i)_{ik} + Gen_l + Env_i \times Gen_l + \varepsilon_{ijkl}$$

Where, Y_{ijkl} is the yield of the i^{th} genotype in the j^{th} location and the k^{th} year in the i^{th} block within the l^{th} replication, μ is the grand mean, *r*1(*pt*)*jk r*l (*pt*)jk is the effect of the lth replication within locations and years, *bm*(*ptr*)*jkl* is the effect of the m^{th} block within the lth replication that is also within locations and years, *g*i, *p*j, and *t*k are the main effects of the genotype, locations, and years, (*gp*)ij, (*gt*)ik, (*pt*)jk are the first order interactions and (*gpt*)ijk is the second-order interaction, and finally *e*ijkm(l) is the pooled error term. The terms I = 1, 2, 3 … 20; j = 1, 2, 3, 4, 5; k = 1, 2; l = 1, 2, 3 and m = 1, 2, 3, 4, 5.

AMMI and Stability analysis were done using GEA-R software.

RESULTS AND DISCUSSION:

Analysis of variance for sorghum agronomic traits and anthracnose resistance

The results of the combined analysis of variance for sorghum landraces evaluated across three environments over two years showed significant findings (Table 1). Environmental factors had a highly significantly impact on the agronomic performance of sorghum and anthracnose disease severity. This indicates that environmental conditions, such as temperature, rainfall and humidity, play a vital role in influencing the performance of sorghum landraces.

The genotypes also showed significant variation for all traits, highlighting the genetic diversity among the studied sorghum landraces (Table 1). This genetic variation is crucial for breeding programs aimed at developing anthracnose-resistant varieties. This variability is consistent with findings of Mengistu et al. (2020), who reported the significant genetic variation in grain yield, plant height, and anthracnose resistance.

The year-to-year climatic variations had a significant effect on most traits, emphasizing the importance of considering annual climate fluctuations in sorghum breeding programs. The interactions between genotype and environment (G*E), environment and year (E*Y), and genotype and year (G*Y) were significant for several traits (Table 1). These interactions suggest that the combined effects of these factors influence sorghum's agronomic performance and anthracnose resistance. This aligns with the findings of Dessalegn et al. (2022), who reported significant G*E interactions for anthracnose severity and grain yield traits. Likewise, Mengistu et al. (2020) also emphasized the need to understand annual variations in genotype performance. This is why Coe (2012) highlighted the importance of multi-environment trials to select stable and high-performing genotypes.

Significant interactions among environment, genotype, and replication for some traits (Table 1) indicate the complexity of interactions between these factors, suggesting that genotype performance can be influenced by specific environmental conditions and experimental setups. The significant interaction of environment, genotype, and year for most traits (Table 1) reinforces the complexity of genotype responses under varying conditions, emphasizing the need for comprehensive evaluation.

Table 1. Means squares for combined analysis of variance for sorghum landraces evaluated in three environments for two years

Sources of variation	df	Grain yield (t ha^{-1})	Days to flowering	Days to maturity	Plant height (cm)	Plant aspect (1-5)	1000 grain weight (g)	Anthracnose severity
Environment (E)	2	16.72***	53920***	136129***	189065***	21.02***	2194.2***	11.231***
Genotypes (G)	41	11.11***	7086***	1741***	53326***	4.45***	155.9***	6.122***
Year (Y)	1	378.77***	1475***	39433***	28477***	5.42***	3459.0***	4.922*
Replication (R)	2	0.01	551**	3	8918***	2.08**	8.3	4.454**
E*G	82	1.93***	208***	166***	1802*	1.54***	106.5***	1.761***
E*Y	2	19.78***	14053***	19200***	81666***	69.90***	4668.1***	279.303***
G*Y	41	1.79***	352***	206***	4485***	0.77***	46.2***	1.412**
E*Y*R	10	0.62*	438***	131**	2470*	0.22	17.7	5.493***
E*G*Y	82	1.24***	313***	109***	1294	0.92***	40.6***	2.285***
Residual	492	0.33	89	47	1271	0.30	18.2	0.797
Error	584	0.53	173.44	122.62	1552.29	0.62	37.05	2.04

df degree of freedom; *** Significant at 0.001; ** Significant at 0.01; * Significant at 0.05

Performance of sorghum agronomic traits

The grain yield showed considerable variation, ranging from 1.53 t ha^{-1} to 4.57 t ha^{-1} (Table 2). This aligns with the findings of Mengistu et al. (2020), who reported significant genetic variation in grain yield for sorghum in Ethiopia. The landrace Mok079 (G4) exhibited the highest grain yield of 4.57 t ha^{-1}. This genotype had a 65.21% (1.6 t ha^{-1}) yield advantage over the most popularly adopted Assosa-1 variety across the study area. The second highest-yielding landrace is Ba066 (G16), which achieved a grain yield of 4.18 t ha^{-1}, providing a yield advantage of 1.2 t ha^{-1} over Assosa-1. The

third high-yielding landrace is SI01 (G10), with almost a 1 t ha^{-1} yield advantage compared to Assosa-1. These high-yielding landraces also exhibited promising agronomic traits, making them potential candidates for further breeding programs (Dessalegn et al., 2022; Mengistu et al. 2020) to improve food security and farmer income in the hot-humid agro-ecologies of Ethiopia.

Table 2. Performance of sorghum landraces for grain yield, and agronomic traits across three environments (Assosa, Bako, and Jimma) in 2020 and 2021 cropping seasons of Ethiopia

Genotypes	Sorghum landraces	Grain yield (t ha^{-1})	1000 grain weight (g)	Days to flowering	Days to maturity	Plant height (cm)	Plant aspect (1-5 scale)
G4	Mok079	4.57^{a}	21.15^{f-l}	144.83^{abc}	192.50^{defg}	306.61^{abcd}	2.6^{nop}
G16	Ba066	4.18^{b}	25.07^{b-f}	142.33^{abc}	200.94^{ab}	294.06^{cde}	2.4^{p}
G10	SI081	3.91^{bc}	25.68^{a-f}	143.06^{abc}	196.39^{abcde}	318.39^{abc}	2.4^{op}
G13	Mok085	3.66^{cd}	29.29^{ab}	144.50^{abc}	195.39^{abcdefg}	272.83^{efgh}	2.7^{lmnop}
G3	Mok087	3.65^{cd}	24.86^{b-g}	141.17^{bc}	195.00^{abcdefg}	293.22^{cde}	2.9^{ijklmno}
G1	NJ003	3.61^{cd}	27.81^{a-c}	137.72^{cd}	194.28^{bcdefg}	263.73^{fghi}	3.1^{hijklm}
G20	Qon072	3.57^{cde}	24.32^{c-h}	142.94^{abc}	201.78^{a}	294.44^{cde}	2.8^{klmnop}
G12	Bam075	3.56^{cde}	24.93^{b-g}	138.67^{c}	193.61^{cdefg}	305.89^{abcd}	2.7^{lmnop}
G14	Bmb095	3.52^{de}	18.81^{j-l}	138.89^{c}	190.94^{efgh}	301.72^{bcd}	2.8^{klmnop}
G17	Bs082	3.45^{def}	25.41^{a-f}	145.78^{abc}	197.61^{abcde}	288.89^{def}	2.7^{klmnop}
G15	Boj007	3.44^{def}	25.93^{a-e}	143.83^{abc}	195.56^{abcdefg}	304.89^{abcd}	2.9^{jklmnop}
G7	Bmb102	3.37^{defg}	23.91^{c-i}	143.22^{abc}	193.44^{defg}	288.94^{def}	2.8^{klmnop}
G5	Bmb097	3.23^{efgh}	25.58^{a-f}	141.33^{bc}	193.22^{defg}	288.83^{def}	2.8^{klmnop}
G18	Y047	3.21^{efgh}	25.24^{b-f}	138.28^{c}	195.17^{abcdefg}	288.28^{defg}	3.3^{defghij}
G9	Man069	3.08^{fghi}	25.25^{b-f}	144.22^{abc}	197.89^{abcde}	248.56^{hij}	3.0^{hijklmn}
G11	ETSC300382-1	3.02^{ghij}	23.56^{c-j}	150.67^{a}	200.83^{abc}	282.22^{defg}	3.1^{ghijklm}
G8	Ba119	2.96^{hij}	30.02^{a}	139.39^{c}	196.11^{abcdef}	327.17^{ab}	3.2^{fghijkl}
G35	ETSC10022-44-2	2.83^{ijk}	30.03^{a}	126.89^{e}	188.67^{ghi}	282.25^{defg}	3.6^{bcdefg}
G19	Qon070	2.68^{jkl}	25.07^{b-f}	138.94^{c}	194.50^{bcdefg}	298.44^{cde}	3.2^{fghijkl}
G6	ETSC300373-4	2.56^{klm}	22.92^{d-k}	141.28^{bc}	194.17^{bcdefg}	282.78^{defg}	3.4^{defghi}
G2	ETSC300376-1	2.53^{klm}	24.86^{b-g}	145.56^{abc}	195.22^{abcdefg}	329.38^{a}	3.5^{cdefgh}
G26	ETSL101515	2.51^{klm}	22.06^{d-l}	102.00^{hijk}	176.00^{klmn}	263.50^{fghi}	3.9^{abc}
G38	ETSC10020-22-1	2.27^{mno}	24.08^{c-h}	107.72^{ghi}	178.00^{jklm}	205.00^{lmno}	3.6^{bcdefg}
G37	ETSC10022-40	2.26^{mno}	26.77^{a-d}	113.67^{fg}	183.94^{hij}	248.06^{hij}	3.7^{abcdef}
G40	ETSC12004-11	2.24^{mno}	23.60^{c-i}	111.50^{g}	181.83^{ijkl}	251.94^{hij}	3.7^{abcde}
G25	ETSL100861	1.53^{s}	18.68^{kl}	93.17^{l}	170.61^{n}	172.20^{qrs}	3.8^{abcd}
G32	ETSL101699	1.60^{rs}	19.89^{h-l}	95.06^{kl}	173.44^{mn}	145.28^{t}	3.9^{abc}
G33	13MW6029	1.71^{qrs}	22.27^{d-k}	121.83^{ef}	178.11^{jklm}	200.72^{mnop}	3.7^{abcdef}
G21	ETSL100124	1.84^{pqrs}	24.48^{c-h}	100.17^{ijkl}	175.61^{klmn}	227.83^{jkl}	4.2^{a}
G22	ETSL100346	1.91^{opqr}	28.21^{a-c}	92.50^{l}	175.50^{klmn}	215.94^{lmn}	4.0^{ab}
G34	13MW6042	1.92^{opqr}	22.39^{d-k}	112.28^{g}	177.72^{jklmn}	182.82^{opqr}	3.8^{abcd}
G39	ETSC120051-3	1.93^{opqr}	24.62^{b-h}	129.22^{de}	189.06^{fghi}	245.57^{ijk}	3.2^{efghijk}
G24	ETSL100644	1.94^{opqr}	25.01^{b-g}	94.89^{kl}	174.69^{lmn}	193.51^{nopq}	3.7^{abcde}
G23	ETSL100620	1.95^{opqr}	23.72^{c-i}	110.50^{gh}	173.44^{mn}	221.56^{klm}	4.0^{ab}
G36	07MW6002	2.11^{nop}	21.18^{e-l}	114.83^{fg}	182.17^{ijk}	168.39^{qrst}	3.1^{ghijklm}
Standard checks							
G41	Assosa-1 (MR check)	2.98^{hij}	20.27^{g-l}	149.33^{ab}	198.22^{abcd}	185.33^{opqr}	2.6^{mnop}
G42	Bonsa (MR check)	1.73^{qrs}	17.46^{l}	113.56^{fg}	182.61^{ijk}	153.23st	3.6^{bcdefg}
G31	BTx378 (S check)	2.56^{klm}	23.87^{c-i}	97.44^{kl}	175.94^{klmn}	262.83^{ghi}	3.7^{abcde}
G28	PML981446 (R check)	2.42^{lmn}	19.30^{i-l}	96.39^{kl}	173.89^{mn}	164.71^{rst}	3.9^{abc}
G29	PML981475 (R check)	2.19^{mnop}	20.28^{g-l}	107.28^{ghij}	176.33^{klmn}	183.17^{opqr}	3.5^{bcdefgh}
G30	PML981488 (R check)	2.00^{opq}	21.40^{e-l}	102.72^{hijk}	175.72^{klmn}	177.33^{pqrs}	3.7^{abcdef}
G27	PML981442 (R check)	1.83^{pqrs}	23.48^{c-j}	98.67^{jkl}	175.94^{klmn}	176.00^{pqrs}	3.7^{abcdef}
CV%		21.22	17.73	7.55	3.66	14.39	16.5

Means with the same alphabets were not statistically different within the column; CV coefficient of variance.

The 1000 grain weight is a crucial indicator of grain size and overall yield potential. In this study, significant variations ranging from 17.46 g in Bonsa (G42) to 30.03 g in ETSC10022-44-2 (G35) (Table 2) were observed among the sorghum landraces for the 1000 grain weight trait. Similar findings were reported by Mengistu et al. (2020) and Asfaw et al. (2020), who found significant

genetic variation in 1000 grain weight among different sorghum genotypes in Ethiopia.

Higher grain weight is often associated with better grain quality and market value (Girma et al., 2024). Therefore, the high 1000 grain weight in certain landraces, such as ETSC10022-44-2 (G35), Ba119 (G8), and Mok085 (G13), could be prioritized for breeding programs aimed at improving grain size, marketability, and overall yield potential.

Days to flowering are a key phenological trait that affects the timing of grain development and overall crop productivity (Coe, 2012). In this study, sorghum genotypes showed a wide range of days to flowering, from 92.50 to 150.67 days (Table 2). The study area experienced long periods of rainfall lasting more than six months, which is why the long-maturing Assosa-1 variety was well-suited to the area. Therefore, sorghum genotypes with optimal flowering times (such as high yielding Mok079, Ba066, and SI081) should be prioritized for breeding programs in these agro-ecological conditions.

Days to maturity are another essential agronomic trait that affects the suitability of a crop for different growing seasons and environments. This study revealed significant differences in days to maturity, ranging from 175.94 to 201.78 days among the sorghum landraces (Table 2). A similar wide range of variations in maturity periods was reported by Birhanu et al. (2024). These variations are critical for breeding programs aiming to develop varieties that can thrive in diverse environmental conditions. Dessalegn et al. (2022) and Mengistu et al. (2020) emphasized the importance of selecting sorghum varieties with appropriate maturity periods to ensure optimal grain yield. The results of this study revealed that the high-yielding landraces Mok079, Ba066, and SI081 had appropriate maturity times across the study area.

Plant height is an important trait that influences both yield and the crop's ability to withstand lodging. The results showed a significant variation in plant height, ranging from 145.28 cm to 329.38 cm among the sorghum landraces, consistent with the findings of Kebede et al. (2001), Mengistu et al. (2020), and Reddy et al. (2007). This genetic diversity in plant height can be utilized in breeding programs to develop sorghum varieties with improved agronomic performance and resilience to environmental stresses. Taller plants may be more prone to lodging but can also provide more biomass for fodder, fencing and firewood. However, selecting genotypes with optimal height, like Mok079 (G4), SI081 (G10), and Ba066 (G16), can balance the need for grain yield and biomass production in the study area.

Plant aspect, which refers to the overall appearance and health of the plant, is an important trait for farmer preference and marketability (Wagaw, 2021). The findings of this study indicated significant differences in plant aspect among the landraces, highlighting the potential for selecting superior genotypes (Ba066, SI081, and Mok079) with desirable traits (Table 2). Landraces Ba066 and SI081

showed superior plant aspect compared to Assosa-1, while Mok079 exhibited a similar plant aspect to that of Assosa-1.

Table 3. Response of sorghum landraces to mean anthracnose severities under natural epidemics at Assosa, Bako, and Jimma during 2020 and 2021 main cropping seasons of Ethiopia

Entry	Genotypes	Anthracnose severity		Reaction	Entry	Genotypes	Anthracnose severity		Reaction
G5	Bmb097	3.9	l	MR	G39	ETSC120051-3	4.8	defghijkl	MR
G18	Y047	4.1	kl	MR	G12	Bam075	4.8	defghijkl	MR
G17	Bs082	4.1	kl	MR	G30	PML981488	4.8	defghijkl	MR
G41	Assosa-1	4.1	kl	MR	G32	ETSL101699	4.9	cdefghijk	MR
G8	Ba119	4.1	kl	MR	G19	Qon070	4.9	cdefghijk	MR
G7	Bmb102	4.1	kl	MR	G42	Bonsa	5.0	bcdefghij	MR
G20	Qon072	4.1	kl	MR	G28	PML981446	5.1	bcdefghi	MR
G27	PML981442	4.2	jkl	MR	G6	ETSC300373-4	5.1	bcdefghi	MR
G16	Ba066	4.2	jkl	MR	G38	ETSC10020-22-1	5.2	bcdefgh	MR
G9	Man069	4.2	jkl	MR	G37	ETSC10022-40	5.2	bcdefgh	MR
G4	Mok079	4.3	hijkl	MR	G2	ETSC300376-1	5.2	bcdefgh	MR
G29	PML981475	4.3	hijkl	MR	G24	ETSL100644	5.3	bcdef	MR
G36	07MW6002	4.3	hijkl	MR	G22	ETSL100346	5.3	bcdef	MR
G15	Boj007	4.3	hijkl	MR	G33	13MW6029	5.3	bcdef	MR
G14	Bmb095	4.4	fghijkl	MR	G35	ETSC10022-44-2	5.4	abcde	MR
G10	SI081	4.4	fghijkl	MR	G40	ETSC12004-11	5.4	abcde	MR
G3	Mok087	4.4	fghijkl	MR	G23	ETSL100620	5.6	abcd	S
G13	Mok085	4.6	efghijkl	MR	G25	ETSL100861	5.6	abcd	S
G11	ETSC300382-1	4.6	efghijkl	MR	G31	BTx378	5.8	abc	S
G1	NJ003	4.7	defghijkl	MR	G26	ETSL101515	5.9	ab	S
G34	13MW6042	4.8	defghijkl	MR	G21	ETSL100124	6.3	a	S
CV		18.65			CV		18.65		

Means with the same alphabets were not statistically different within the column; CV coefficient of variance; LSD is least significant difference; MR moderately resistant; R resistant; S susceptible.

Response of sorghum landraces to anthracnose infections

The anthracnose severity scores of 5.8 on susceptible check (BTx378) and 4.2 to 5.1 on the resistant checks included in this study indicate the presence of significant anthracnose infection, allowing for the categorization of sorghum landraces based on their resistance to anthracnose. This study identified sorghum landraces Bmb097, Y047, and Bs082 as moderately resistant to anthracnose, with lower severity scores ranging 3.9 to 4.1 (Table 3). These genotypes demonstrated superior anthracnose resistance compered to Assosa-1. Additionally, high-yielder Mok079, Ba066, and SI081 were found to be moderately resistant to anthracnose across the study area, providing an additional advantage for prioritizing these high-yielders in breeding programs. Conversely, genotypes like ETSL100124, ETSL101515, and BTx378 were found to be susceptible, with higher severity scores from 5.8 to 6.3. This result aligns with the findings that indicate genetic diversity influences anthracnose resistance (Birhanu et al. 2024; Reddy et al. 2007). Additionally, Aragaw and Terefe (2024) highlighted a range of anthracnose resistance levels among Ethiopian sorghum landraces.

Another study explored the genetic basis of anthracnose resistance in Ethiopian sorghum and identified several loci associated with anthracnose resistance (Girma et al., 2024), highlighting the

genetic diversity within Ethiopian sorghum germplasm. This genetic diversity is reflected in the present investigation, where genotypes show varying levels of resistance to anthracnose (Table 3).

Table 4. Response of sorghum landraces to anthracnose across Assosa, Bako, and Jimma during 2020 and 2021 main cropping seasons of Ethiopia

Assosa				Bako				Jimma			
Geno	Anthracnose severity	Std. Dev.	Reaction	Geno	Anthracnose severity	Std. Dev.	Reaction	Geno	Anthracnose severity	Std. Dev	Reaction
G27	3.5	0.8	MR	G17	3.3	0.5	R	G5	3.8	1.33	MR
G30	3.8	1.5	MR	G5	3.3	0.5	R	G41	4.0	1.90	MR
G17	4.0	1.1	MR	G7	3.3	0.8	R	G18	4.2	1.47	MR
G18	4.0	1.9	MR	G11	3.7	0.8	MR	G20	4.2	1.17	MR
G36	4.0	1.3	MR	G20	3.7	0.5	MR	G4	4.2	1.47	MR
G8	4.0	1.1	MR	G4	3.7	1.5	MR	G15	4.5	1.52	MR
G28	4.2	1.9	MR	G10	3.8	0.8	MR	G16	4.5	0.84	MR
G29	4.2	1.3	MR	G16	3.8	0.8	MR	G3	4.5	1.23	MR
G9	4.2	1.3	MR	G29	3.8	0.8	MR	G8	4.5	1.52	MR
G14	4.3	2.0	MR	G8	3.8	1.2	MR	G9	4.5	1.38	MR
G15	4.3	1.2	MR	G18	4.0	0.9	MR	G1	4.7	2.34	MR
G16	4.3	1.2	MR	G27	4.0	0.9	MR	G10	4.7	1.51	MR
G23	4.3	2.0	MR	G3	4.0	0.6	MR	G13	4.7	1.97	MR
G32	4.3	1.2	MR	G41	4.0	0.0	MR	G14	4.7	1.63	MR
G34	4.3	1.6	MR	G9	4.0	0.9	MR	G36	4.7	1.37	MR
G41	4.3	1.2	MR	G14	4.2	0.8	MR	G7	4.7	1.51	MR
G42	4.3	1.0	MR	G15	4.2	1.0	MR	G11	4.8	1.60	MR
G7	4.3	1.5	MR	G19	4.2	1.0	MR	G17	4.8	1.17	MR
G13	4.5	1.6	MR	G2	4.2	0.8	MR	G29	4.8	1.17	MR
G20	4.5	1.6	MR	G39	4.2	0.8	MR	G37	4.8	1.60	MR
G10	4.7	1.5	MR	G36	4.3	1.0	MR	G38	4.8	1.72	MR
G12	4.7	1.9	MR	G1	4.5	0.5	MR	G26	5.0	1.79	MR
G3	4.7	2.3	MR	G12	4.5	1.0	MR	G27	5.0	1.90	MR
G5	4.7	1.9	MR	G13	4.5	0.8	MR	G33	5.0	1.90	MR
G24	4.8	1.2	MR	G30	4.5	1.2	MR	G35	5.0	1.90	MR
G1	5.0	2.1	MR	G32	4.7	1.9	MR	G39	5.0	1.67	MR
G4	5.0	2.3	MR	G34	4.7	1.4	MR	G6	5.0	1.67	MR
G11	5.2	1.7	MR	G42	4.8	0.8	MR	G22	5.2	1.84	MR
G19	5.2	2.1	MR	G6	5.0	0.9	MR	G12	5.3	1.63	MR
G33	5.2	0.4	MR	G22	5.3	1.4	MR	G2	5.3	1.51	MR
G38	5.2	1.7	MR	G35	5.3	0.5	MR	G31	5.3	1.03	MR
G39	5.2	1.3	MR	G37	5.3	0.8	MR	G34	5.3	1.37	MR
G22	5.3	0.8	MR	G40	5.3	1.2	MR	G40	5.3	1.51	MR
G25	5.3	0.5	MR	G24	5.5	1.5	S	G19	5.5	1.87	S
G37	5.3	1.6	MR	G25	5.5	2.0	S	G24	5.5	1.52	S
G6	5.3	2.3	MR	G28	5.5	1.2	S	G28	5.7	1.51	S
G40	5.5	2.1	S	G38	5.5	0.8	S	G32	5.8	0.98	S
G21	5.8	1.6	S	G31	5.8	1.2	S	G42	5.8	1.33	S
G35	5.8	2.3	S	G33	5.8	1.0	S	G25	6.0	0.89	S
G2	6.2	2.0	S	G26	6.0	1.4	S	G21	6.2	1.33	S
G31	6.2	1.9	S	G23	6.2	1.5	S	G23	6.2	0.98	S
G26	6.7	1.9	HS	G21	6.8	1.0	HS	G30	6.2	1.17	S

Geno Genotypes, Rxn Reaction, R Resistant, MR Moderately resistant, S Susceptible, Std. Dev. Standard deviations

As illustrated in Table 4, the findings of this study demonstrate notable variability in anthracnose severity among the genotypes. Genotypes such as Bs082 (G17), Bmb097 (G5), and Bamb102 (G7) exhibited resistant to anthracnose in Bako, while 71.43% of the genotypes were moderately resistant, 19.05% were susceptible, and 2.4% were highly susceptible. In Assosa, 85.7% of the genotypes were moderately resistant, 11.9% were susceptible, and 2.4% were highly susceptible. At Jimma 80.9% of the genotypes were moderately resistant and 21.4% were susceptible in response to

anthracnose under field conditions. Anthracnose scores under 4.5 were exhibited by 42.9%, 50.0%, and 11.9% of genotypes at Assosa, Bako, and Jimma, respectively (Table 4). This variability might be due to the differences in *Colletotrichum sublineola* virulence (Mekonen et al. 2024) and sorghum genetic resistance (Afolayan et al. 2019; Birhanu et al. 2024; Dessalegn et al., 2022; Girma et al., 2024).

Stability analysis

The Additive Main Effects and Multiplicative Interaction (AMMI) analysis reveals significant insights into the genetic and environmental factors affecting yield (Table 5). The results of this analysis revealed that both the environment and genotypes were the primary sources of variation that significant (P<0.001) effect yield and anthracnose resistance. Moreover, the genotype-by-environment interaction also showed significant variation, indicating that the performance of genotypes is substantially influenced by the environments in which they are grown.

Table 5. AMMI ANOVA for yield of sorghum landraces across six environments

Sources of variation	df	MS	G*E explained (%)
Environment	2	16.72***	
Rep (Environment)	6	0.35	
Genotypes	41	11.11***	
Environment:Genotypes	82	1.93**	
IPCA1	42	1.26	67.12
IPCA2	40	0.65	32.88
Residual	624	1.22	

Rep replication; IPCA1 first interaction principal component axis; IPCA2 second interaction principal component axis; *** Significant at 0.001; ** Significant at 0.01; * Significant at 0.05; df degree of freedom; MS mean squares; G genotypes; E environment

The result of this investigation revealed that the first interaction principal component axis (IPCA1) captures the most significant portions of the interaction between genotypes and environments (Table 5). This finding align with previous reports of significant genotype-by-environment interactions in sorghum, emphasizing the necessity for multi-environment trials to identify stable genotypes (Bedru et al. 2024; Enyew et al. 2021; Wang et al. 2023).

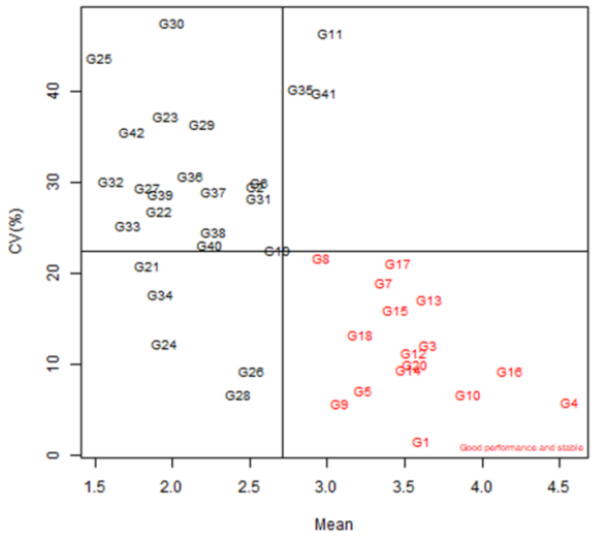

Figure 1. AMM bi-plot for yield across Assosa, Jimma, and Bako

The AMMI model found that 38.10 % of sorghum genotypes exhibited better performance and stability across the study area (Figure 1). Genotypes Mok079 (G4), Ba066 (G16), and SI081 (G10) perform consistently high yielders, while Bmb097 (G5) and Y047 (G18) maintained lower anthracnose severity values across Assosa, Bako, and Jimma. Studies by Enyew et al. (2021), Kumar et al. (2021), and Anisha et al. (2022) have demonstrated the effectiveness of the AMMI model in identifying stable, high-yielding, and stress-tolerant sorghum varieties.

Principal component (PCA) for sorghum agronomic traits

The principal component analysis reveals significant insights into the relationships between the agronomic and anthracnose diseases traits (Table 6). PC1 is highly correlated with days to flowering, days to maturity, plant height, and grain yield, indicating that these traits are closely related and contribute significantly to the overall variation observed in the sorghum genotypes. This finding aligns with previous studies that have highlighted the importance of these traits in sorghum breeding programs aimed at improving yield and disease resistance (Birhanu et al., 2024; Mengistu et al. 2019).

Table 6. Principal components (PCs) for sorghum agronomic traits and anthracnose severity during 2020 and 2021 in Assosa, Bako, and Jimma

Variables	PC1	PC2	PC3	PC4	PC5	PC6
DF (days)	-0.995	-0.006	1.000	0.175	0.963	-0.204
DM (days)	-0.995	0.075	0.985	0.018	-1.000	-0.056
PH (cm)	-0.995	1.000	-0.686	0.416	-0.003	-0.335
GY (t ha^{-1})	-1.000	0.172	-0.263	-1.000	0.135	0.850
AUDPC	0.976	0.588	0.500	-0.853	0.044	-0.709
rAUDPC	0.973	0.609	0.607	0.422	0.055	1.000

DF days to flowering; DM days to maturity; PH plant height; GY grain yield; AUDPC area under disease progress curve; rAUDPC relative area under disease progress curve, PC1 the 1st principal component, PC2 the 2nd principal component, PC3 PC4 the 4th principal component, PC5 the 5th principal component, PC6 the 6th principal component

The second principal component (PC2) shows a strong correlation with plant height and relative area under disease progress curve (rAUDPC), suggesting that taller plants may have a higher susceptibility to anthracnose. This observation is consistent with the findings of Aragaw and Terefe (2024), who reported that taller sorghum genotypes exhibited higher anthracnose severity under field conditions in eastern Ethiopia. The negative correlation between grain yield and AUDPC in PC4 further supports the notion that anthracnose significantly impacts sorghum yield, as previously documented by Mengistu et al. (2019).

Moreover, the positive correlation between days to flowering and days to maturity in PC1 and PC3 suggests that early-maturing sorghum genotypes may have a shorter flowering period, which could be advantageous in regions with shorter growing seasons. This finding is in line with the work of Birhanu et al. (2024), who emphasized the importance of selecting early-maturing sorghum genotypes for improved yield and disease resistance in Ethiopia.

CONCLUSIONS:

This study found that Mok079 (G4) was the high yielder and stable genotype across the six environments. Likewise, sorghum genotypes Bmb097 (G5), and Y047 (G18) showed high resistance to anthracnose and stable. These suggests sorghum breeding program to crossing the high-yielding Mok079 (G4) with disease-resistant Bmb097 (G5), and Y047 (G18) for the development of superior hybrids. By adopting the high-performing sorghum genotypes, smallholder farmers in Ethiopia can improve their productivity, resilience, and economic returns. This can lead to better food security, higher incomes, and more sustainable farming practices, ultimately contributing to the overall development of rural communities.

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