



Field Evaluation of Sorghum Accessions and Improved Varieties for Resistance to Major Diseases under Natural Infection Conditions

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Authors' contributions

This work was carried out in collaboration between both authors. Both authors read and approved the final manuscript.

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Abstract

Sorghum is an important food and fodder crop in Eritrea, where production is constrained by several biotic and abiotic factors, including plant diseases. This study evaluated 23 sorghum accessions and three improved varieties for resistance to naturally occurring diseases under field conditions at Hamelmalo Agricultural College, Keren, using three replications. Genotypes were planted by the single-line method, and disease incidence and severity were assessed at the adult plant stage. Disease severity was rated on a 0–9 scale. Anthracnose, leaf blight, sooty stripe, target leaf spot, zonate leaf spot, and bacterial streak were recorded during the growing season. Disease occurrence and severity differed among the evaluated genotypes. Anthracnose was the most prevalent disease, occurring in 76.92% of entries, followed by leaf blight at 61.54%. Sooty stripe occurred in 23.08% of entries, zonate leaf spot in 11.54%, and target spot and bacterial streak each in 7.69%. Although target spot was less prevalent, relatively high severity was recorded in affected accessions. Anthracnose showed the highest overall severity, particularly in EG795, whereas zonate leaf spot and bacterial streak generally showed low incidence and severity. The variation observed among accessions and improved varieties indicates differential responses to natural disease pressure and identifies materials that warrant further evaluation as potential sources of disease resistance for sorghum improvement under Eritrean conditions.

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1. Introduction

Sorghum is a significant cereal crop in Eritrea and globally, ranking fifth among the major cereal crops (FAO, 1995). The origin and development of African agriculture are closely associated with the domestication and cultivation of sorghum (Smith, 1995). According to Doggett (1988), sorghum originated in Abyssinia. Following the spread of settled agriculture into Africa, which included the cultivation of wheat and barley and the domestication of sheep and goats, farming communities progressively adopted practices such as seed selection and the harvesting of whole grain inflorescences. Communities inhabiting areas along the Nile cultivated crops on seasonally flooded meadowlands and harvested them after maturity. During the late 1970s, considerable attention was given to the taxonomic classification of sorghum into species and subspecies (Rakshit & Wang, 2016; Wiersma & Dahlberg, 2007).

Distinct and true-breeding sorghum biotypes have evolved over a long period through the processes of speciation, intermingling, and natural selection. These processes resulted in the development and isolation of genetically diverse populations from the original gene pool. Through human migration and cultivation, sorghum was disseminated several thousand miles from its presumed Abyssinian centre of origin. Human selection subsequently influenced the natural processes of diversification and domestication. One of the major characteristics distinguishing wild, native, and domesticated sorghum is the degree of seed shattering. Consequently, shattering and non-shattering traits were important selection criteria during the early stages of sorghum domestication (Smith, 1995). The primitive sorghum race or biotype is considered to be *Sorghum bicolor* subsp. *bicolor*, from which the other cultivated races are believed to have evolved. *S. bicolor* race *aethiopicum* or *verticilliform* has been considered a probable early progenitor (Venkateswaran *et al.*, 2019). According to authorities who proposed West Africa as the centre of origin of *S. bicolor* subsp. *bicolor*, the probable progenitor was *S. bicolor* race *arundinaceum*. The race *bicolor* is widely distributed throughout Africa and is not considered native to Indonesia, India, or China (Singh & Upadhyaya, 2015). Other recognised races of *S. bicolor* include *caudatum*, *kafir*, and *durra*. The race *caudatum* is believed to have been selected by people of the Chari-Nile language group, while *durra* evolved within its region of origin. In contrast, the evolutionary origin of the *kafir* race remains uncertain. Recent SSR-based characterisation of sorghum genotypes further demonstrates genetic variability that may be useful in breeding programmes (Navyashree *et al.*, 2024).

According to Tesfamichael *et al.* (2013), various types of sorghum are cultivated in Eritrea, particularly in the Gash-Barka and Debub regions. The choice of sorghum type grown in a particular field is influenced by soil fertility and the availability of moisture. For example, *Koden*, a late-maturing sorghum type, is commonly cultivated in soils with high water-holding capacity or along riverbanks. In contrast, *Chimro*, an early-maturing type, is better adapted to relatively drier field conditions.

Sorghum is affected by numerous diseases that can substantially reduce crop productivity. Under humid and wet environmental conditions, losses caused by certain pathogens, including those associated with anthracnose and *Fusarium* diseases, may reach up to 50% (Khaskheli *et al.*, 2025). However, with appropriate crop management practices, these losses may be reduced to approximately 10% (Adugna, & Sethumadhava, 2023). Major diseases of sorghum include damping-off, seedling blight, charcoal rot, smuts, rusts, downy mildew, anthracnose, bacterial streak, and maize dwarf mosaic virus disease, among others (Sethumadhava, 2024). Screening of diverse sorghum accessions has also demonstrated differential responses to anthracnose, supporting germplasm evaluation as a practical approach for identifying resistance sources (Prom *et al.*, 2020).

Both pathogenic and saprophytic fungi play important roles in sorghum health by colonising plant surfaces, roots, cultivated soils, and infected plant tissues. Several fungal diseases and associated organisms have been reported in sorghum, including anthracnose or red leaf spot caused by *Colletotrichum* spp., rust caused by *Puccinia purpurea* Cooke, and grain smut caused by *Sphacelotheca sorghi* (Link) Clinton. In addition, several saprophytic fungi, including *Alternaria*, *Aspergillus flavus*, *Aspergillus niger*, *Rhizopus*, and *Mucor*, have been isolated from sorghum-associated soils and infected plant tissues (Kisanet *et al.*, 2024; Syed *et al.*, 2017). Although disease-resistant sorghum varieties continue to be developed and released, regular monitoring of these varieties remains essential because pathogen populations may evolve new virulence traits that enable them to overcome previously effective host resistance. Recent studies have identified additional sources and mechanisms of anthracnose resistance in sorghum (Cuevas *et al.*, 2023; Wolf *et al.*, 2024), while pathotype analyses have documented substantial variation in *Colletotrichum sublineola* virulence (Mekonen *et al.*, 2024). Accordingly, the research gap addressed in this study is the need for a comparative field evaluation of locally available sorghum accessions and improved varieties for their responses to naturally occurring diseases under Eritrean conditions. Therefore, this research aims to assess disease development in sorghum accessions and improved varieties under natural field conditions and to evaluate differences in their levels of resistance to major sorghum diseases. The study also aims to examine the stability of resistance in improved varieties and identify potentially resistant genotypes that may be useful for future breeding and disease-management programmes.

2. Methodology

2.1 Experimental Site and Planting

The study was conducted under field conditions at Hamelmalo Agricultural College (Fig. 1). Seeds of the available sorghum accessions and improved varieties were collected and sown using the single-line method. The resistance of the different accessions and improved varieties was evaluated under natural environmental conditions and natural disease pressure. Following seed germination, weeds were removed manually to minimise competition with the crop and reduce potential alternative sources of pathogen inoculum.

The field experiment was conducted at Hamelmalo, Anseba Zoba, from July until the end of crop harvest. The research area is located at an altitude of approximately 1,280 m above sea level, at 15°55'12.92" N latitude and 38°27'46.9" E longitude. The area receives an average annual rainfall of approximately 459 mm and is characterised by sandy loam soil with a pH ranging from 6.0 to 7.0. The mean temperature of the study area is approximately 24 °C (MoA, 2005).

Disease occurrence was assessed at various phenological growth stages, i.e., the seedling, vegetative, and panicle stages, in each plot of every sorghum accession. Disease incidence and severity were documented separately for each replication, and the mean values were subsequently calculated. No pesticides were applied during the cropping period to allow natural disease development. Only standard agronomic practices, including weeding and fertiliser application, were carried out throughout the experiment. Disease incidence was determined by assessing the number of infected plants among a total population of 120 plants in each experimental unit. In addition, disease surveys were conducted weekly for four months at specified phenological growth stages. Within each plot, 21 plants were selected using a diagonal random sampling method and assessed for disease occurrence and severity.

Samples of symptomatic leaves and other affected plant parts were collected from the field and brought to the Plant Pathology Laboratory for further examination. Laboratory observations were organised to confirm disease symptoms, estimate disease occurrence, and identify the associated causal organisms based on the available diagnostic characteristics. The causal organisms associated with the observed diseases were identified using standard taxonomic identification keys (Gilman, 1957; Nagamani et al., 2006). Fungal identification was based on both symptom characteristics and microscopic examination. Symptomatic plant tissues were examined, and fungal structures obtained from infected plant parts were observed under a compound microscope at 40x magnification. Identification was carried out using characteristic morphological features of the fungal colonies, hyphae, and other reproductive structures, such as conidia and spores, following standard mycological procedures (Aneja, 2003; Barnett & Hunter, 1972; Rifai, 1969). For pathogen isolation, the Moisture Plate Method (MPM), as described by Warcup (1950), and the Serial Dilution Method (SDM) were employed using potato dextrose agar (PDA) as the culture medium, following standard procedures (ISTA, 1985). The isolated fungi were characterised macroscopically on the basis of colony morphology, growth pattern, and mycelial characteristics, and microscopically on the basis of hyphal structure and conidial morphology. Data on the percentage occurrence of disease were analysed using MS Office Excel and subjected to analysis of variance.



Fig. 1. Aerial view of Hamelmalo Agricultural College Field

2.2 Disease Assessment

Disease incidence and severity were assessed at the adult stage of plant growth. The occurrence of naturally developing diseases was monitored on the different sorghum accessions and improved varieties, and disease severity was evaluated using a 0–9 rating scale.

2.2.1 Disease Incidence

Disease incidence was calculated by the following formula:

$$\text{Disease incidence} = \frac{\text{no. of infected plants assessed}}{\text{total number of plants observed}} \times 100$$

2.2.2 Disease Severity Rating Scale

Disease severity was scored according to the extent of symptomatic leaf area and the associated host reaction. A score of 0 indicated an immune or symptomless reaction. A score of 1 represented >0 to <1% of the leaf area affected, accompanied by hypersensitive reactions and mild yellow flecking. A score of 2 represented 1–5% of the leaf area showing a hypersensitive reaction without the

formation of acervuli, whereas a score of 3 represented 6–10% of the leaf area showing a hypersensitive reaction without acervuli. A score of 4 indicated 11–20% of the leaf area affected, with hypersensitive reactions and confined necrotic lesions containing acervuli. A score of 5 represented 21–30% of the leaf area affected, with hypersensitive reactions, confined necrotic lesions, and the presence of acervuli. A score of 6 indicated 31–40% of the leaf area affected, with coalescing necrotic lesions containing acervuli. A score of 7 represented 41–50% of the leaf area showing disease symptoms and coalescing necrotic lesions containing acervuli. A score of 8 indicated 51–75% of the leaf area affected, with extensive coalescing necrotic lesions containing acervuli, whereas a score of 9 represented 76–100% of the leaf area affected and covered by coalescing necrotic lesions containing acervuli (Marley *et al.*, 2002).

3. Results and Discussion

3.1 Disease Prevalence

There were substantial differences in the occurrence of the six diseases among the 26 sorghum entries evaluated (23 accessions + 3 improved varieties). The prevalence of the major diseases observed among the sorghum accessions and improved varieties varied considerably (Fig. 2). Anthracnose was the most prevalent disease, occurring in 76.92% of the evaluated sorghum entries (Fig. 3). This was followed by leaf blight, which occurred in 61.54% of the entries. In contrast, sooty stripe was recorded in 23.08%, zonate leaf spot in 11.54%, while target spot and bacterial streak each occurred in only 7.69% of the evaluated materials. These results indicate that anthracnose and leaf blight were the dominant diseases under the prevailing field conditions, whereas the remaining diseases occurred comparatively infrequently. Because 26 sorghum accessions and improved varieties were evaluated, the percentages in the figure approximately correspond to anthracnose being observed in 20 of the 26 entries, leaf blight in 16 entries, sooty stripe in 6 entries, zonate leaf spot in 3 entries, and target spot and bacterial streak in approximately 2 entries each. Thus, anthracnose had a particularly broad distribution among the tested genetic materials, suggesting that a large proportion of the accessions were susceptible to natural anthracnose infection under the environmental conditions prevailing during the experiment.

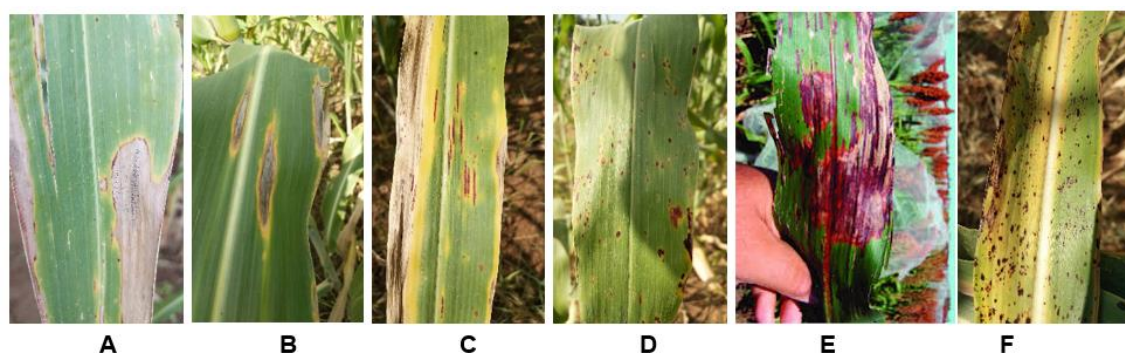


Fig. 2. Sorghum Anthracnose (caused by the fungus *Colletotrichum sublineola*) [A]; Sooty stripe caused by the fungus *Ramulispora sorghi* [B]; Bacterial Leaf Streak (*Xanthomonas vasicola*) [C]; Tar spot (*Phyllachora sorghi*) [D]; Zonate leaf spot (*Gloeocercospora sorghi*) [E]; *Bipolaris sorghicola* causes target leaf spot

The comparatively high prevalence of **anthracnose** is important because it indicates that the pathogen was able to infect a wide range of the sorghum genetic materials evaluated. This finding is consistent with Birhanu *et al.* (2024). The occurrence of disease in more than three-quarters of the tested entries may reflect a combination of favourable environmental conditions, availability of natural inoculum, and differences in host resistance. Since the experiment depended on natural infection rather than artificial inoculation, disease prevalence would have been influenced not only by the genetic susceptibility of the host but also by the amount and distribution of inoculum and the microenvironment around individual plants. Consequently, the high prevalence of anthracnose suggests that environmental conditions during the growing season were sufficiently favourable for infection and disease development. This result is consistent with Prom *et al.* (2015).

Leaf blight was the second most prevalent disease, affecting 61.54% of the evaluated entries. According to Prom *et al.* (2021), leaf blight was the most prevalent disease, followed by anthracnose, zonate leaf spot, rough leaf spot, sooty stripe, and target leaf spot across the regions. Although its prevalence was lower than that of anthracnose, its occurrence in more than half of the sorghum materials demonstrates that leaf blight was also an important disease in the experimental field. The relatively widespread occurrence of both anthracnose and leaf blight suggests that these two diseases should receive greater attention when sorghum accessions are screened for disease resistance under similar agroecological conditions.

Sooty stripe showed an intermediate prevalence of 23.08%, indicating that it occurred in considerably fewer entries than anthracnose and leaf blight. Its restricted distribution may indicate that a greater proportion of the evaluated accessions possessed resistance or that environmental conditions were less favourable for the development and spread of sooty stripe. However, prevalence alone cannot distinguish between these explanations. A disease may have low prevalence because few genotypes are susceptible, inoculum is limited, or environmental conditions are unfavourable for infection (Williams *et al.*, 1980; Haussmann *et al.*, 2001).

Zonate leaf spot was detected in only 11.54% of the sorghum accessions, whereas **target spot** and **bacterial streak** showed the lowest prevalence, with each occurring in 7.69% of the materials. Their low prevalence indicates that these diseases were relatively uncommon during the experimental period. Nevertheless, low prevalence should not automatically be interpreted as low disease importance. In particular, target spot, despite its low prevalence, showed a relatively high estimated marginal mean of disease severity in the accessions that became infected. This demonstrates an important distinction between prevalence and severity: a disease can occur in only a few accessions but cause severe symptoms in those susceptible genotypes (Prom *et al.*, 2023).

The variation in prevalence among diseases may also be related to differences in pathogen biology. The pathogens associated with anthracnose, leaf blight, sooty stripe, target spot, zonate leaf spot, and bacterial streak differ in their survival, dispersal, infection requirements, and dependence on environmental factors such as rainfall, relative humidity, leaf wetness, and temperature. Under rainfed field conditions, fluctuations in these environmental factors can favour some pathogens while restricting others. The relatively high occurrence of anthracnose and leaf blight, therefore, suggests that the prevailing environmental conditions were more conducive to these diseases than to target spot, zonate leaf spot, or bacterial streak. Host genetic variation is another likely contributor to the observed prevalence pattern. The sorghum accessions and improved varieties evaluated in the study were genetically diverse and therefore would not be expected to respond uniformly to infection. Some accessions may possess effective resistance mechanisms against particular pathogens, whereas others may lack such resistance. The high prevalence of anthracnose consequently suggests that effective resistance to this disease was relatively uncommon among the tested materials, while the low prevalence of bacterial streak and zonate leaf spot could indicate either greater resistance among the accessions or less favourable conditions for those diseases.

From a disease-management and crop-improvement perspective, the results emphasise the importance of anthracnose as a major disease constraint among the sorghum materials evaluated. Because anthracnose affected the largest proportion of accessions, selection and development of anthracnose-resistant sorghum genotypes would be particularly important. Leaf blight should also be considered a priority because of its high prevalence. At the same time, accessions that remained free from anthracnose or leaf blight under the same natural field conditions may represent useful materials for further resistance screening, although their resistance should ideally be confirmed through repeated trials and controlled inoculation (Stutts & Vermerris, 2020).

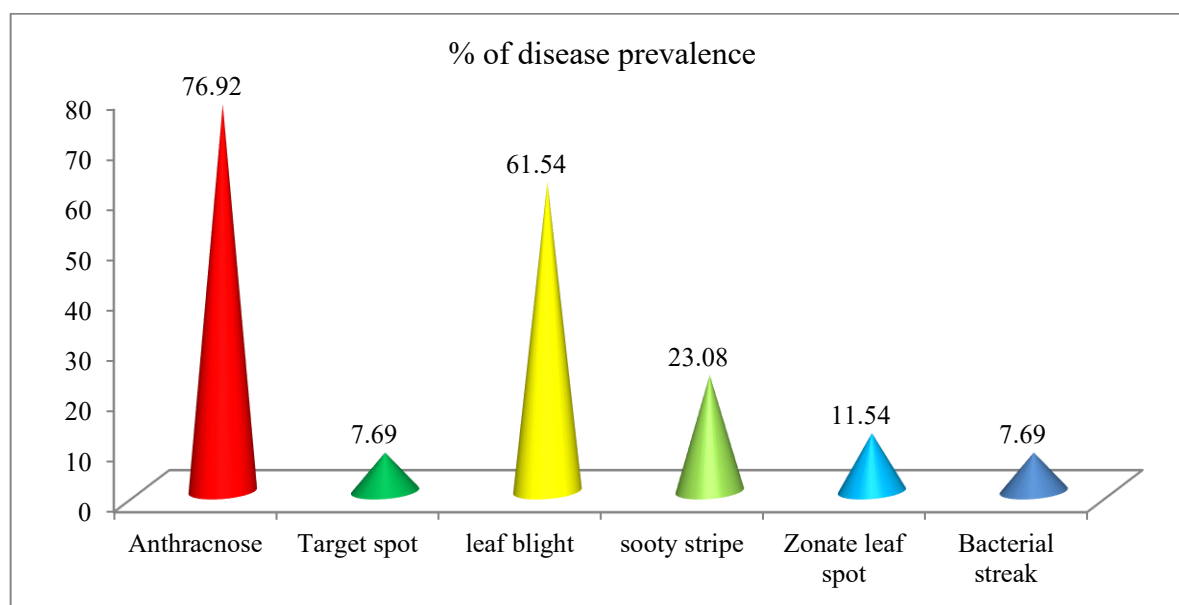


Fig. 3. Percentage of Disease Prevalence

Fig. 4 presents the estimated marginal means of disease severity for six diseases across the evaluated sorghum accessions and improved varieties. Estimated marginal means represent model-adjusted mean severity values, allowing comparison of disease responses among varieties after accounting for the other factors included in the statistical model. Overall, the figure shows clear variation in disease severity among both diseases and sorghum genotypes. Among the six diseases, target spot consistently exhibited the highest estimated marginal mean severity across most of the evaluated entries. Its severity values generally remained above those of the other diseases and showed pronounced peaks in some accessions, particularly around *EG795*, where the estimated marginal mean approached approximately 1.4, and again in *EG886* and *Maeloba*, where relatively high values were observed. This indicates that although target spot may not have been the most prevalent disease, the genotypes that became infected tended to exhibit comparatively severe symptoms.

Anthracnose generally showed the second-highest estimated marginal mean severity and followed a pattern similar to several of the other diseases across the different sorghum entries. Relatively high anthracnose severity was evident in accessions such as *EG471*, *EG484*, *EG729*, *EG795*, *EG845*, *EG881*, *EG886*, and *Maeloba*, although the magnitude of disease response varied substantially among genotypes. The high values observed in some accessions indicate greater susceptibility, whereas the lower values in others suggest comparatively stronger resistance or reduced disease development.

Leaf blight also showed considerable variation among accessions. Its estimated marginal means were generally lower than those of target spot and anthracnose but increased noticeably in some genotypes, particularly around *EG795*, *EG845*, *EG886*, and *Maeloba*. This suggests that susceptibility to leaf blight was not uniform across the evaluated sorghum materials.

The estimated marginal means for sooty stripe, zonate leaf spot, and bacterial streak were generally lower than those observed for target spot, anthracnose, and leaf blight, indicating that these diseases contributed comparatively less to the overall disease severity under the prevailing field conditions. Although their severity remained relatively low across most sorghum accessions, occasional increases in specific genotypes suggest differences in host susceptibility. The relatively greater importance of anthracnose and leaf blight observed in the present study is consistent with the findings of Prom et al. (2023), who reported 100% prevalence of leaf blight and 76% prevalence of both anthracnose and zonate leaf spot, with each of the latter diseases detected in 93 of 122 surveyed fields. They also reported lower prevalence of rough leaf spot (47%), covered kernel smut (32%), oval leaf spot (19%), and target leaf spot (19%). The similarities and differences between the two studies may reflect variation in sorghum genotypes, environmental conditions, pathogen distribution, and disease-conducive conditions across the study areas.

A notable feature of the disease-severity profiles is that they tend to rise and fall in a broadly similar pattern across many genotypes. This indicates that some sorghum accessions may possess general susceptibility or resistance tendencies that influence their response to several diseases. For example, accessions showing high severity for one disease sometimes also showed elevated severity for others, whereas some entries maintained relatively low severity across multiple diseases. Such variation is important for identifying potentially useful sources of broad-spectrum disease resistance. The pronounced peak observed for accession *EG795* appears to indicate relatively high estimated marginal means for several diseases simultaneously, suggesting a comparatively susceptible response under the field conditions of the study. In contrast, entries with consistently low marginal means across diseases may represent promising candidates for further resistance evaluation and breeding.

Fig. 4 also indicates that disease severity was influenced by both disease type and host genotype. The separation among the disease lines demonstrates differences in the aggressiveness or expression of the different diseases, while the fluctuations across varieties indicate substantial host-related variation. This pattern is consistent with a significant disease effect and a significant varietal effect in the statistical analysis.

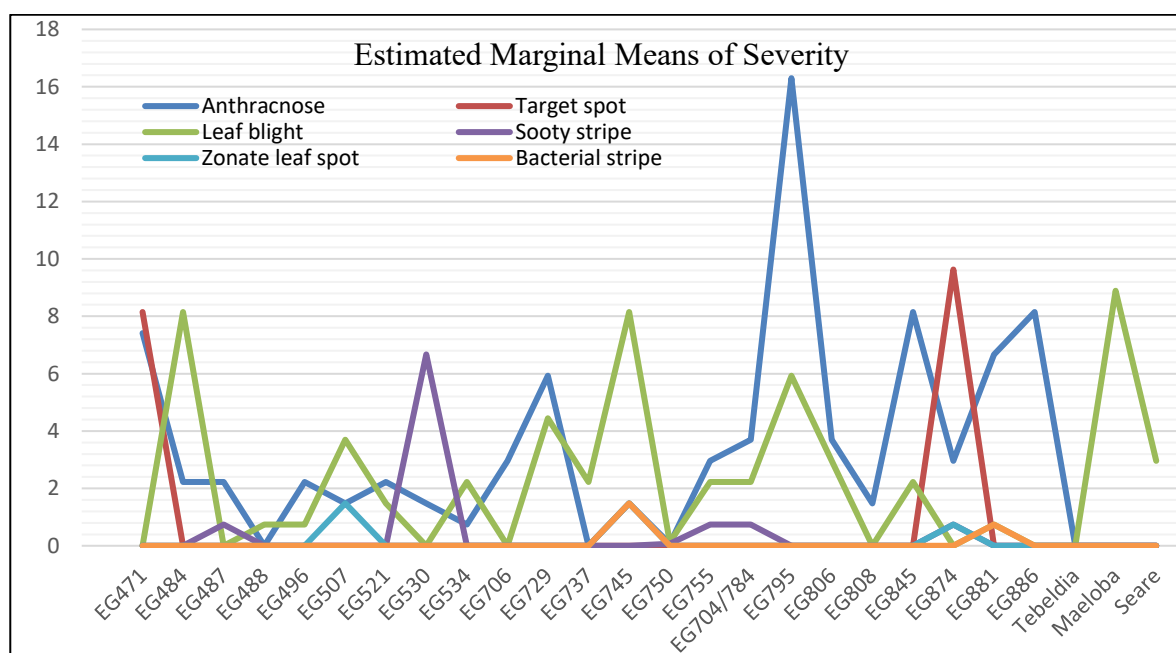


Fig. 4. Estimated Marginal Means of Disease Severity across Sorghum Accessions and Improved Varieties

3.1.1 Disease Incidence

The percentage disease incidence of the evaluated sorghum accessions and improved varieties varied markedly among both diseases and genotypes, indicating substantial differences in host response under the prevailing field conditions.

Anthracnose was the most widely distributed and generally the most important disease in terms of incidence. It occurred in a large number of accessions and reached the highest incidence values in several genotypes. The greatest anthracnose incidence was observed in accessions such as *EG795* and *EG845*, at approximately 66–67%, followed by *EG471* and *EG886*, at about 53–54%. Intermediate levels were observed in accessions such as *EG784*, *EG806*, and *EG881*. In contrast, several accessions, including *Tebeldia*, *Maeloba*, and *Seare*, showed minimal or no anthracnose incidence. This wide variation suggests considerable genetic diversity in susceptibility to anthracnose among the evaluated sorghum materials.

Target spot showed a much more restricted distribution but reached high incidence in a few accessions. The highest incidence was observed in *EG874*, at about 60%, followed by *EG471* and *EG745*, at approximately 40% and 37–38%, respectively. Most other accessions showed no detectable target spot. This indicates that target spot was not widely distributed across the germplasm but could cause substantial infection in particular susceptible genotypes.

Leaf blight was the second most broadly distributed disease after anthracnose. The highest incidence was recorded in *EG484*, at approximately 47%, and in *Maeloba*, at about 40%. Moderate incidence was also observed in accessions such as *EG729*, *EG795*, *EG507*, *EG534*, and *Seare*. The occurrence of leaf blight across a relatively large number of entries suggests that it was another important disease under the field conditions of the study.

Sooty stripe occurred at comparatively lower frequencies and generally at lower incidence levels. The highest incidence was observed in *EG530*, at approximately 33–34%, whereas most other affected accessions showed incidence values below 10%. This pattern indicates relatively localised susceptibility, with one accession showing a markedly stronger response than the others.

Zonate leaf spot and bacterial streak had the lowest incidence among the diseases assessed. These diseases were detected only in a few accessions, and incidence generally remained below 10%. Their limited occurrence suggests that either the majority of the evaluated sorghum entries were relatively resistant or the environmental conditions were less favourable for the development of these diseases during the study period.

A major feature was that some accessions were affected by several diseases, whereas others remained relatively free from infection. For example, accessions such as *EG471*, *EG745*, *EG795*, *EG845*, *EG874*, and *EG886* showed relatively high incidence for one or more diseases, indicating greater susceptibility. Conversely, entries such as *Tebeldia* and *Seare* showed generally low disease incidence across the evaluated diseases and may therefore represent potentially useful sources of resistance. However, anthracnose combined both broad distribution and high incidence in several accessions, whereas target spot had a narrow distribution but very high incidence in a few susceptible entries. Therefore, interpretation of disease importance should consider both the frequency of occurrence among genotypes and the magnitude of incidence within individual genotypes.

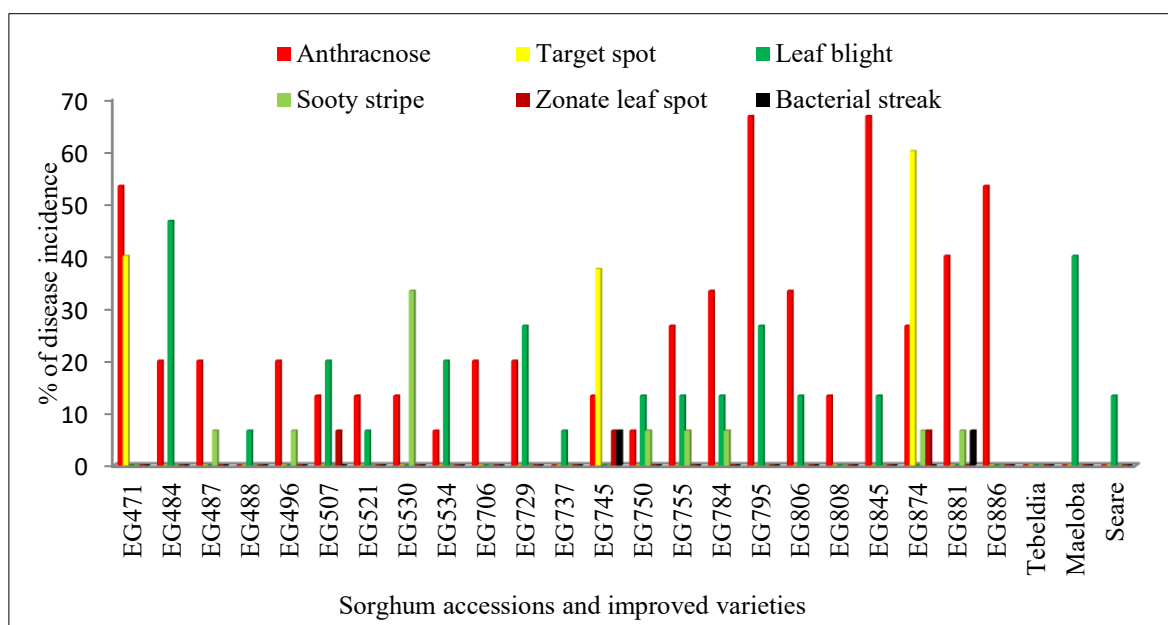


Fig. 5. Incidence of Major Diseases in Sorghum Accessions and Improved Varieties

3.1.2 Disease Severity

Anthracnose showed the highest overall severity and the widest distribution among the evaluated sorghum entries (Fig. 6). The greatest disease severity was recorded in *EG795*, reaching approximately 16.3%, which was the highest value observed in the dataset. Relatively high anthracnose severity was also recorded in *EG845* and *EG886* (about 8.1%), followed by *EG471* (7.4%), *EG881* (6.7%), and *EG729* (5.9%). In contrast, several accessions showed only low levels of anthracnose severity, while *Tebeldia*, *Maeloba*, and *Seare* exhibited little or no disease severity. This wide variation among genotypes indicates substantial differences in their response to anthracnose and suggests the presence of both susceptible and potentially resistant sources within the evaluated sorghum germplasm. These findings are consistent with Aragaw and Terefe (2024), who reported that the genotype *ETSL 101469* exhibited the highest anthracnose severity, followed by *BTX-623*. They further observed strong negative associations between anthracnose severity and both grain yield and thousand-seed weight, indicating that increased disease severity may adversely affect important yield-related traits.

Target spot was less widely distributed than anthracnose but produced relatively high severity in the few accessions that were affected. The highest target spot severity occurred in *EG874*, at approximately 9.6%, followed by *EG471*, at about 8.1%. Most of the remaining genotypes showed no detectable target spot severity. This pattern is important because it demonstrates that a disease may have low prevalence but high severity in susceptible genotypes.

High severity of leaf blight was recorded in *Maeloba*, at about 8.9%, and in *EG484* and *EG745*, at approximately 8.1%. Moderate levels were also observed in *EG795* and *EG729*, while many other entries showed relatively low severity. These results indicate that leaf blight was an important disease in particular susceptible accessions, although its overall severity was generally lower than that of anthracnose.

Sooty stripe severity was generally low across most entries, with one clear exception. Accession *EG530* showed a comparatively high severity of approximately 6.7%, whereas the majority of the other genotypes had values close to zero or below 1%. This suggests a highly genotype-specific susceptibility to sooty stripe.

Zonate leaf spot and bacterial streak exhibited the lowest severity values in this study. For zonate leaf spot, small severity values were observed in accessions such as *EG507*, *EG745*, and *EG874*, while bacterial streak was recorded at low severity in only a few entries. The generally low severity of these diseases suggests either higher host resistance or less favourable environmental conditions for their development.

A major feature of the graph is the strong genotype-by-disease pattern. *EG795* appeared particularly susceptible because it showed the highest anthracnose severity and also measurable leaf blight severity. Similarly, *EG845*, *EG874*, *EG886*, and *Maeloba* showed relatively high severity for specific diseases. In contrast, entries such as *Tebeldia* and *Seare* generally maintained low severity across the disease spectrum and may represent useful materials for further resistance screening.

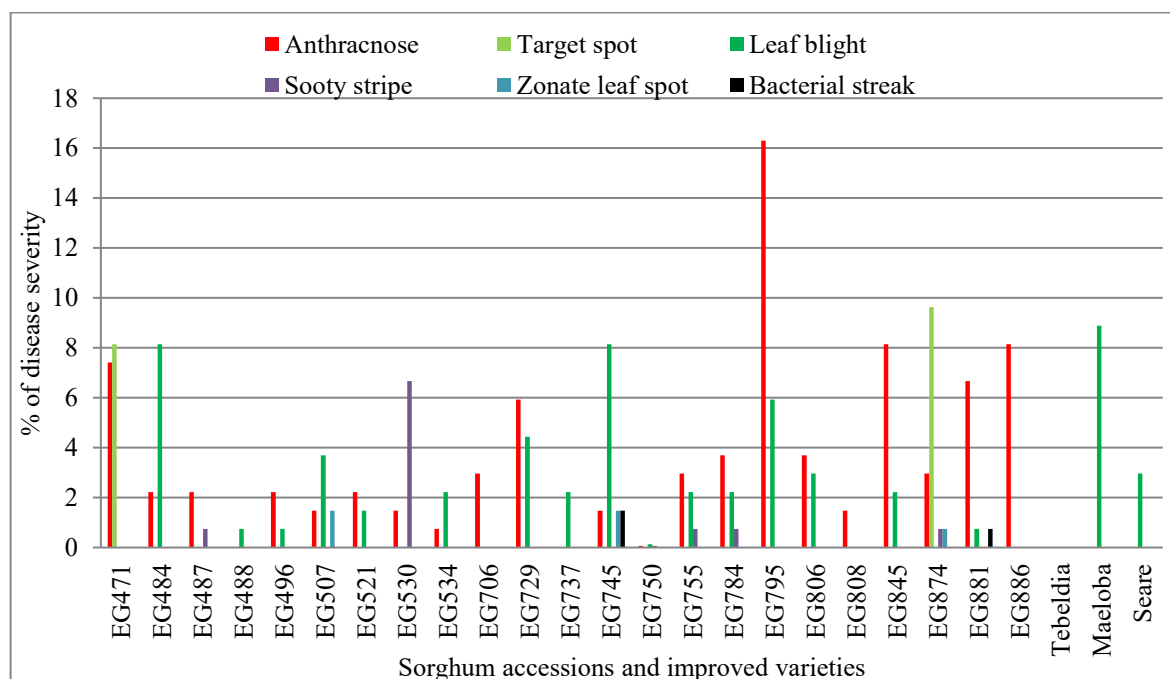


Fig. 6. Disease Severity of Major Diseases in Sorghum Accessions and Improved Varieties

The reactions of the experimental plants to the different diseases were highly significant ($P \leq 0.005$). Differences among the diseases were also highly significant ($P = 0.005$) (Table 1).

Table 1. Dependent Variable: Severity

Source	Type III Sum of Squares	df	Mean Square	F	Sig.
Corrected Model	43.624 ^a	29	1.504	3.478	.000
Intercept	21.094	1	21.094	48.766	.000
Variety	29.381	24	1.224	2.830	.000
Diseases	7.279	5	1.456	3.366	.005
Error	324.421	750	.433		
Corrected Total	368.045	779			

a. R Squared = .119 (Adjusted R Squared = .084)

3.2 Pairwise Comparison of the Diseases

The diseases occurring in the developing sorghum accessions were compared pairwise. Disease frequency varied considerably among the different accessions. As shown in Table 2, anthracnose differed significantly in disease intensity from target spot, sooty stripe, zonate leaf spot, and bacterial streak, with anthracnose being more prevalent. Target leaf spot also differed significantly in disease intensity from leaf blight, sooty stripe, zonate leaf spot, and bacterial streak; although its frequency was lower, target spot had a higher estimated marginal mean of severity. Leaf blight differed significantly in disease intensity from sooty stripe, zonate leaf spot, and bacterial streak. No significant differences were observed among sooty stripe, zonate leaf spot, and bacterial streak.

Table 2. Pairwise Comparison of Sorghum Diseases

	Anthracnose	Target spot	Leaf blight	Sooty stripe	Zonate leaf spot	Bacterial streak
Anthracnose	1					
Target spot	-.43*	1				
Leaf blight	.04	.47*	1			
Sooty stripe	.22*	.66*	.18*	1		
Zonate leaf spot	.25*	.69*	.21*	.03	1	
Bacterial streak	.27*	.70*	.23*	.04	.01	1

4. Conclusion

Overall, anthracnose was the most prevalent fungal disease among the evaluated sorghum accessions and improved varieties, followed by leaf blight, while target spot and bacterial streak were the least prevalent. The marked variation in disease prevalence suggests differences in host–pathogen relations and indicates that both genetic resistance and prevailing environmental conditions influenced disease progress under natural field conditions.

Estimated marginal means of disease severity varied considerably among diseases and genotypes. Target spot generally showed the highest adjusted severity, followed by anthracnose and leaf blight, whereas sooty stripe, zonate leaf spot, and bacterial streak showed comparatively lower severity. Some accessions showed high severity across multiple diseases, while others consistently sustained low severity, indicating substantial genetic variation in host response and the possible presence of useful sources of disease resistance.

Disease incidence also differed markedly among genotypes. Anthracnose was the most widely distributed disease, with the highest incidence recorded in *EG795* and *EG845*, approaching 67%. Leaf blight was the second most prevalent disease, with relatively high incidence in *EG484* and *Maeloba*. Although target spot occurred in fewer accessions, high incidence was recorded in *EG874*, *EG471*, and *EG745*, indicating strong genotype-specific susceptibility. Sooty stripe occurred mainly in *EG530*, whereas zonate leaf spot and bacterial streak were generally infrequent.

Disease severity followed a similar genotype-dependent pattern. Anthracnose showed the highest overall severity, particularly in *EG795*, followed by *EG845*, *EG886*, *EG471*, *EG881*, and *EG729*. Target spot caused substantial severity in *EG874* and *EG471*, while leaf blight was severe in *Maeloba*, *EG484*, and *EG745*. Overall, the observed variation demonstrates substantial differences in vulnerability and resistance among the evaluated sorghum germplasm, highlighting potentially valuable genotypes for disease-resistance breeding programmes.

5. Limitation

Because disease evaluation relied on natural infection, the level and distribution of pathogen inoculum were not experimentally standardised and may have differed among diseases and field positions. The findings therefore represent genotype responses under the prevailing environmental and disease-pressure conditions at Hamelmalo Agricultural College. Low disease incidence or severity may reflect host resistance, limited inoculum, or less favourable conditions for particular pathogens. Consequently, promising low-disease genotypes should be confirmed through repeated field evaluations and, where appropriate, controlled inoculation before resistance is considered stable.

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Declaration of AI Use

This manuscript was prepared through the intellectual contributions of the author(s) to the study design, data analysis, interpretation of results, and scholarly content. Grammarly and ChatGPT were used solely to assist with grammatical refinement and reference

formatting during manuscript revision. The author(s) accept full responsibility for the accuracy, integrity, and final content of the manuscript.

Competing Interests

The authors declare that they have no known competing financial or non-financial interests or personal relationships that could have influenced the work reported in this paper.

References

- Aneja, K. R. (2003). Experiments in microbiology, plant pathology and biotechnology (4th ed.). New Age International (P) Limited. https://opac.saulibrary.edu.bd/cgi-bin/koha/opac-detail.pl?biblionumber=656&shelfbrowse_itemnumber=25407
- Aragaw, G., & Terefe, H. (2024). Response of sorghum genotypes to anthracnose (*Colletotrichum sublineolum*) resistance under field conditions in eastern Ethiopia. *PLOS ONE*, 19(12), e0316016. <https://doi.org/10.1371/journal.pone.0316016>
- Barnett, H. L., & Hunter, B. B. (1972). *Illustrated genera of imperfect fungi* (3rd ed.). Burgess Publishing Company. <https://agris.fao.org/search/en/providers/122535/records/65de0c314c5aef494fd93d4b>
- Kisanet B. K., Ghedam, H., Arefaine, K., Ogbai, N., & Sethumadhava, R. G. (2024). Assessment of disease incidence, yield loss, and isolation of soil fungi from the sorghum fields in Anseba Region, Eritrea. *African Journal of Biological Sciences*, 6(Si4), 6169–6180. <https://doi.org/10.48047/AFJBS.6.Si4.2024.6169-6180>
- Birhanu, C., Girma, G., Mekbib, F., Nida, H., Tirfessa, A., Lule, D., Bekeko, Z., Ayana, G., Bejiga, T., Bedada, G., Tola, M., Legesse, T., Alemu, H., Admasu, S., Bekele, A., & Mengiste, T. (2024). Exploring the genetic basis of anthracnose resistance in Ethiopian sorghum through a genome-wide association study. *BMC Genomics*, 25, 677. <https://doi.org/10.1186/s12864-024-10545-2>
- Cuevas, H. E., Knoll, J. E., Prom, L. K., Stutts, L. R., & Vermerris, W. (2023). Genetic diversity, population structure and anthracnose resistance response in a novel sweet sorghum diversity panel. *Frontiers in Plant Science*, 14, 1249555. <https://doi.org/10.3389/fpls.2023.1249555>
- Doggett, H. (1988). *Sorghum* (2nd ed.). Longman Scientific & Technical. https://libcat.busitema.ac.ug/cgi-bin/koha/opac-detail.pl?biblionumber=8141&shelfbrowse_itemnumber=37080
- Food and Agriculture Organization of the United Nations. (1995). *Sorghum and millets in human nutrition* (FAO Food and Nutrition Series No. 27). <https://www.fao.org/4/t0818e/t0818e00.htm>
- Gilman, J. C. (1957). *A manual of soil fungi* (2nd ed.). Oxford & IBH Publishing Co. https://library.cnr.edu.bt/cgi-bin/koha/opac-detail.pl?biblionumber=1474&shelfbrowse_itemnumber=1909
- Adugna, H., & Sethumadhava, R. G. (2023). *Diseases of crops in Eritrea*. Clever Fox Publishing.
- Haussmann, B. I. G., Hess, D. E., Sissoko, I., Kayentao, M., Reddy, B. V. S., Welz, H. G., & Geiger, H. H. (2001). Diallel analysis of sooty stripe resistance in sorghum. *Euphytica*, 122(1), 99–104. <https://doi.org/10.1023/A:1012621729189>
- International Seed Testing Association. (1985). International rules for seed testing 1985. *Seed Science and Technology*, 13, 299–355. <https://www.fao.org/4/x5036e/x5036e00.htm>
- Khaskheli, M. A., Nizamani, M. M., Tarafder, E., Das, D., Nosheen, S., Muhae-Ud-Din, G., Khaskheli, R. A., Ren, M.-J., Wang, Y., & Yang, S.-W. (2025). Sustainable management of major fungal phytopathogens in sorghum (*Sorghum bicolor* L.) for food security: A comprehensive review. *Journal of Fungi*, 11(3), 207. <https://doi.org/10.3390/jof11030207>
- Marley, P. S., Gupta, S. C., & Aba, D. A. (2002). Assessment of sorghum genotypes for resistance to foliar anthracnose (*Colletotrichum graminicola*) under field conditions. *Samaru Journal of Agricultural Research*, 18, 17–24. <https://kubanni.abu.edu.ng/items/256c7804-0611-4049-a643-15c89daf857a>
- Mekonen, M., Tesfaye, K., Mengiste, T., Chala, A., Nida, H., Mekonnen, T., Abreha, K. B., & Geleta, M. (2024). Pathotype determination of sorghum anthracnose (*Colletotrichum sublineola*) isolates from Ethiopia using sorghum differentials. *Frontiers in Microbiology*, 15, 1458450. <https://doi.org/10.3389/fmicb.2024.1458450>
- Ministry of Agriculture. (2005). Statistical report.
- Nagamani, A., Kunwar, I. K., & Manoharachary, C. (2006). *Handbook of soil fungi*. IK International Publishing House Pvt. Ltd. https://library.cnr.edu.bt/cgi-bin/koha/opac-detail.pl?biblionumber=1476&shelfbrowse_itemnumber=1912
- Syed N. S. D. Y., Sethumadhava, R. G., Ghebrehiwet, Y., Isaac, M., Ogbai, R., & Ghebrehiwet, S. (2017). Soil borne fungi associated with groundnut, pearl millet and sorghum crops in Sub Zone Hamelmalo, Eritrea. *Indian Journal of Plant Protection*, 45(4). <https://epubs.icar.org.in/index.php/IJPP/article/view/105023>
- Navyashree, R., Mummigatti, U. V., Nethra, P., Basavaraj, B., & Hanamaratti, N. G. (2024). Evaluation of genetic diversity in sorghum genotypes via simple sequence repeat (SSR) markers. *Plant Cell Biotechnology and Molecular Biology*, 25(11–12), 1–9. <https://doi.org/10.56557/pcbmb/2024/v25i11-128833>
- Prom, L. K., Cuevas, H., Isakeit, T., & Magill, C. (2020). Screening sorghum accessions for resistance against anthracnose and grain mold through inoculating with pathogens. *Journal of Experimental Agriculture International*, 42(1), 73–83. <https://doi.org/10.9734/jeai/2020/v42i130453>
- Prom, L. K., Perumal, R., Isakeit, T., Radwan, G., Rooney, W. L., & Magill, C. (2015). The impact of weather conditions on response of sorghum genotypes to anthracnose (*Colletotrichum sublineola*) infection. *American Journal of Experimental Agriculture*, 6(4), 242–250. <https://doi.org/10.9734/AJEA/2015/14589>
- Prom, L. K., Sarr, M. P., Diatta, C., Ngom, A., Aïdara, O., Cisse, N., & Magill, C. (2021). The occurrence and distribution of sorghum diseases in major production regions of Senegal, West Africa. *Plant Pathology Journal*, 20(1), 1–10. <https://doi.org/10.3923/ppj.2021.1.10>
- Prom, L. K., Sarr, M. P., Diatta, C., Sall, M., Bodian, S., Fall, C., Dorego, G. S., & Magill, C. (2023). A survey of the major sorghum production regions for foliar and panicle diseases during the 2022 growing season in Senegal, West Africa. *American Journal of Plant Sciences*, 14(8), 829–844. <https://doi.org/10.4236/ajps.2023.148055>

- Rakshit, S., & Wang, Y.-H. (Eds.). (2016). The sorghum genome. *Springer*. <https://doi.org/10.1007/978-3-319-47789-3>
- Sethumadhava R. G., (2024). Sorghum pathology. *Iterative International Publishers*.
- Rifai, M. A. (1969). A revision of the genus *Trichoderma* (Mycological Papers No. 116). Commonwealth Mycological Institute. https://search.lib.utexas.edu/discovery/fulldisplay/alma991024986729706011/01UTAU_INST%3ASEARCH
- Singh, M., & Upadhyaya, H. D. (Eds.). (2015). Genetic and genomic resources for grain cereals improvement. *Academic Press*. <https://oar.icrisat.org/9323/>
- Smith, C. W. (1995). Crop production: Evolution, history, and technology. *John Wiley & Sons*. <https://catalog.libraries.psu.edu/catalog/1510365>
- Stutts, L. R., & Vermerris, W. (2020). Elucidating anthracnose resistance mechanisms in sorghum—A review. *Phytopathology*, 110(12), 1863–1876. <https://doi.org/10.1094/PHYTO-04-20-0132-RVW>
- Tesfamichael, A., Nyende, A. B., Githiri, S. M., Kasili, R. W., & Woldeamlak, A. (2013). Documentation of sorghum (*Sorghum bicolor* L. Moench) landraces: Production, utilization, and challenges in Eritrea. *ARPJ Journal of Agricultural and Biological Science*, 8(6), 498–508. https://www.arpnjournals.com/jabs/volume_06_2013.htm
- Venkateswaran, K., Elangovan, M., & Sivaraj, N. (2019). Origin, domestication and diffusion of *Sorghum bicolor*. In C. Aruna, K. B. R. S. Visarada, B. Venkatesh Bhat, & V. A. Tonapi (Eds.), *Breeding sorghum for diverse end uses* (pp. 15–31). Woodhead Publishing. <https://doi.org/10.1016/B978-0-08-101879-8.00002-4>
- Warcup, J. H. (1950). The soil-plate method for isolation of fungi from soil. *Nature*, 166, 117–118. <https://doi.org/10.1038/166117b0>
- Wiersema, J. H., & Dahlberg, J. (2007). The nomenclature of *Sorghum bicolor* (L.) Moench (Gramineae). *Taxon*, 56(3), 941–946. <https://doi.org/10.2307/25065876>
- Williams, R. J., Frederiksen, R. A., Mughogho, L. K., & Bengtson, G. D. (Eds.). (1980). Proceedings of the International Workshop on Sorghum Diseases, Hyderabad, India, 11–15 December 1978. International Crops Research Institute for the Semi-Arid Tropics. <https://oar.icrisat.org/475/>
- Wolf, E. S. A., Vela, S., Cuevas, H. E., & Vermerris, W. (2024). A sorghum F-box protein induces an oxidative burst in the defense against *Colletotrichum sublineola*. *Phytopathology*, 114(2), 405–417. <https://doi.org/10.1094/PHYTO-06-23-0184-R>

Appendix

	EG 471	EG484	EG487	EG488	EG496	EG507	EG521	EG530	EG534	EG706	EG729	EG737	EG745	EG750	EG755	EG704	EG795	EG806	EG808	EG845	EG874	EG881	EG886	Maeloba	Seare
EG 471	1																								
EG484	0.23	1																							
EG487	.57	0.33	1																						
EG488	.63	0.4	0.07	1																					
EG496	.57	0.33	0	-0.07	1																				
EG507	.50	0.27	-0.07	-0.13	-.57	1																			
EG521	.53	0.3	-0.03	-0.1	-0.33	0.03	1																		
EG530	0.33	0.1	-0.23	-0.3	0	-0.17	-0.2	1																	
EG534	.57	0.33	0	-0.07	0.07	0.03	0.23	1																	
EG706	.43	0.2	-0.13	-0.2	-0.07	-0.07	-0.1	0.1	-0.13	1															
EG729	0.23	0	-0.33	-0.4	-0.03	-0.27	-0.3	-0.1	-0.33	-0.2	1														
EG737	.50	0.27	-0.07	-0.13	-0.23	0	-0.03	0.17	-0.07	0.07	0.27	1													
EG745	.42	0.18	-0.15	-0.22	0	-0.08	-0.12	0.08	-0.15	-0.02	0.18	-0.08	1												
EG750	.59	.36	0.02	-0.04	-0.13	0.09	0.06	0.26	0.02	0.16	.36	0.09	0.17	1											
EG755	.52	0.29	-0.04	-0.11	-0.33	0.02	-0.01	0.19	-0.04	0.09	0.29	0.02	0.11	-0.07	1										
EG704	.50	0.27	-0.07	-0.13	-0.07	0	-0.03	0.17	-0.07	0.07	0.27	0	0.08	-0.09	-0.02	1									
EG795	-0.3	-.53	-.87	-.93	-0.15	-.80	-.83	-.63	-.87	-.73	-.53	-.80	-.72	-.89	-.82	-0.80	1								
EG806	.40	0.17	-0.17	-0.23	0.02	-0.1	-0.13	0.07	-0.17	-0.03	0.17	-0.1	-0.02	-0.19	-0.12	-0.1	.70	1							
EG808	.57	0.33	0	-0.07	-0.04	0.07	0.03	0.23	0	0.13	0.33	0.07	0.15	-0.02	0.04	0.07	.87	0.17	1						
EG845	0.23	0	-0.33	-0.4	-0.07	-0.27	-0.3	-0.1	-0.33	-0.2	0	-0.27	-0.18	-.36	-0.29	-0.27	.53	-0.17	-0.33	1					
EG874	.38	0.15	-0.18	-0.25	-.87	-0.12	-0.15	0.05	-0.18	-0.05	0.15	-0.12	-0.03	-0.21	-0.14	-0.12	.66	-0.02	-0.18	0.15	1				
EG881	.46	0.22	-0.11	-0.18	-0.17	-0.04	-0.08	0.12	-0.11	0.02	0.22	-0.04	0.04	-0.13	-0.07	-0.04	.76	0.06	-0.11	0.22	0.07	1			
EG886	-0.03	-0.27	-.60	-.67	0	-.53	-.57	-0.37	-.60	-0.47	-0.27	-.53	-.45	-.62	-.56	-.53	0.27	-.43	-.60	-0.27	-.42	-.49	1		
Maeloba	-0.1	-0.33	-.67	-.73	-0.33	-.60	-.63	-.43	-.67	-.53	-0.33	-.60	-.52	-.69	-.62	-.60	0.2	-.50	-.67	-0.33	-.48	-.56	-0.07	0.47	1
Seare	.43	0.2	-0.13	-0.2	-0.18	-0.07	-0.1	0.1	-0.13	0	0.2	-0.07	0.02	-0.16	-0.09	-0.07	.73	0.03	-0.13	0.2	0.05	-0.02	0.47	.53	1

Fig. A1. Pairwise comparison of sorghum accessions for disease resistance

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