

Assessment of a New Senegalese Sorghum (*Sorghum bicolor* (L.) Moench) Collection for Grain Yield and Tolerance to Anthracnose and Grain Molds

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Abstract

Sorghum is an important cereal crop for smallholder farmers' food security in many countries in West Africa. However, its production has stagnated due to several factors, such as anthracnose and grain molds. Thus, a study was conducted to identify local germplasms that combine high grain yield and resistance to anthracnose and grain molds under Senegalese environments. A set of 256 genotypes was assessed at Sefa, Sinthiou and Kolda research stations using an incomplete blocks design with two replications. Agro-morphological and phytopathological data were collected. The results revealed a huge phenotypic variation between the genotypes for all traits. The flowering time varied from 43 to 126 days after sowing, while the panicle length varied from 10 to 60 cm. The genotypes were generally more productive at Sinthiou (1653 Kg ha⁻¹) compared to Kolda (164 kg ha⁻¹) research stations. The disease parameters were significantly and positively associated, while the flowering time was strongly and positively associated to grain mold score. The genotypes were classified into three groups with plant height, panicle diameter and length, flowering time and grain mold score as the most discriminating parameters. The genotypes belonging to cluster 3, in addition of being more productive and more resistant to grain mold and anthracnose, have longer panicles. These genotypes present promising prospects for inclusion in breeding programs focused on advancing sorghum yield and disease resistance in Senegal.

Keywords

Sorghum, Grain Mold, Anthracnose, Yield, Resistance

1. Introduction

With a global production of 59.5 million tons per year (FAO 2023), sorghum (*Sorghum bicolor* (L.) Moench) is one of the most important cereals for human and animal consumption worldwide [1]. It is generally grown for its starch-rich grain, which is a staple food for millions of people in more than 30 countries [2]. In West Africa, sorghum is the basis of many local dishes and is valorized in bread-making [3]. It is also consumed in various forms such as couscous, the formulation of livestock and poultry feeds. In addition, sorghum fodder is used to make house fences and to feed livestock [3].

In Senegal, sorghum is an important source of energy, protein, vitamins, and minerals for many households. It is mainly grown in the central and southern parts of the country and represents the second most-grown cereal during the rainy season after pearl millet [4]. Indeed, the area cultivated with sorghum annually reaches approximately 247,648 hectares for an annual production of approximately 295,463 tons [4]. Despite the importance of this crop, the national average grain yield is low (around 1 ton ha⁻¹) compared with the potential of released varieties for sorghum cultivation in Senegal [5]. Indeed, sorghum is affected by several biotic and abiotic constraints, such as *Striga hermonthica*, insects, poor soil fertility, drought and various diseases [6]. Grain mold and anthracnose are among the most devastating diseases of this crop in Senegal.

A survey conducted during the rainy season of 2019 in Senegal identified up to 15 different sorghum diseases across seven production areas, with leaf blight and anthracnose being the most prevalent diseases [7]. The prevalence of grain mold was low because the survey was performed when most plants were assessed at soft-dough stage to the early hard-dough stage. However, for farmers, the most important diseases frequently observed in their fields were damping off, grain mold, and foliar diseases [6]. To overcome these constraints, considerable efforts have been made by the national program to develop varieties with high grain yields and resistance to biotic stresses using exotic sources of resistance. Breeding for resistance to grain mold is considered as top priority [8].

These efforts led to the release of six new tannin-free varieties in 2015. These varieties yield up to 4 tons ha⁻¹ and are highly appreciated by farmers for the quality of their grains. However, some farmers complained about their sensitivity to grain molds and anthracnose. In fact, these varieties were bred for earliness, grain yield, and disease resistance using genetic materials from the USA. Farmers' preferred varieties need to be improved using local materials. Therefore, searching for new sources of resistance for these diseases using local materials is essential

for a successful breeding program. This study was conducted to assess the existing genetic diversity of the Senegalese sorghum collection, estimate the phenotypic correlation among different agronomic variables, and identify the best lines that combine high grain yield, resistance to grain mold and anthracnose.

2. Materials and Methods

2.1. Plant Materials and Testing Sites

The plant material comprises 256 sorghum genotypes, including 251 accessions and 5 improved varieties. The accessions collected from farmers' fields were genotyped and phenotyped for drought tolerance at Bambey research station [9]. The improved varieties served as controls for disease tolerance and grain yield. (Table 1)

Table 1. Characteristics of checks used for this study.

Lines	Origin	Traits of interest
Nganda	Senegal	Improved variety for grain yield
Sureno	USA	Tolerance to grain molds
CE151-262	Senegal	Susceptible to grain molds
Sc728-5	USA	Tolerance to anthracnose
Rtx430	USA	Susceptible to grain molds

Field evaluations were conducted during two rainy seasons (2020 and 2021) at three locations. In 2020, the experiment was established at the Sinthiou (14° 43' 12" North, 16° 0' 36" East) and Kolda (12° 52' 48" North, 14° 39' 0" West) research stations. In 2021, it was conducted at Sefa Sefa (12° 49' 48" North, 15° 35' 24" West) research station (Figure 1).

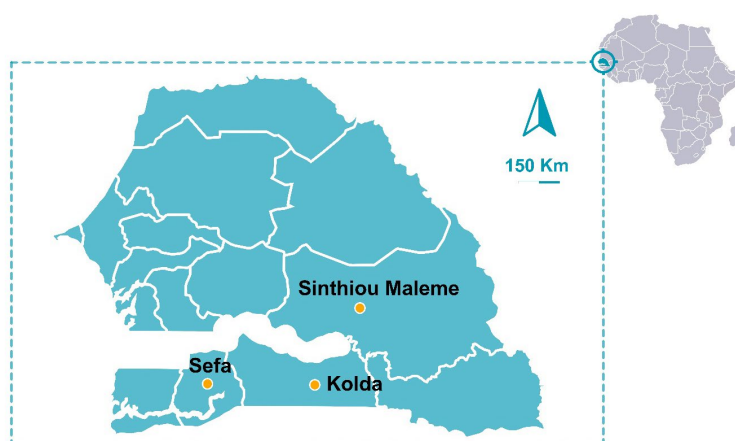


Figure 1. Map of Senegal showing the experimental locations.

The trials were conducted in sandy clay soil [10]. The rainfall conditions at the different sites are presented in Table 2.

Table 2. Precipitation at Sinthiou Maleme, Sefa and Kolda from June to October 2020 and 2021.

Location	Year	Precipitations	
		Quantity (mm)	Number of days
Sinthiou	2020	605.7	51
Kolda	2020	1475.8	84
Séfa	2021	986.95	62

2.2. Experimental Design and Field Management

The plant materials were arranged in 16×16 lattice design with two replications at each location. Each plot comprised one row of 4m length with inter-row spacing of 80 cm and intra-row spacing of 40 cm. All rows were thinned to three plants per hill fifteen days after sowing. The recommended cultural practices for sorghum production were applied across the study locations. After ploughing, NPK fertilizer (15-15-15) was applied as a basal dose at the rate of 150 kg ha^{-1} . Urea was applied at the rate of 100 kg ha^{-1} , in two split doses of 50 kg ha^{-1} , the first after thinning and the second at the booting stage.

2.3. Data Collection

At each location, agro-morphological parameters were recorded. Flowering time (FLO) was recorded by counting the total number of days from sowing until 50% of the plants in a plot flowered. The plant height (HEI) was measured as the length from the soil to the tip of the panicle. Data on panicle length (PAL) and its diameter (PDI), thousand-grain weight (TGW) and grain yield (GYI) were also recorded. Anthracnose (ANS) and Grain mold score (GMS) were recorded at physiological maturity using the 1 to 5 scale as described by [11]. The anthracnose and grain mold scores were performed on leaves and panicles, respectively, before harvest [11].

2.4. Statistical Analysis

Analysis of variance (ANOVA) was performed for the recorded data using R software to determine significant differences among locations, genotypes, and their interactions. The test of homogeneity of variances was confirmed using the Bartlett test for homogeneity of group variances before the combined analysis. Significant effects of treatments were determined by the magnitude of F values ($P \leq 0.05$). The phenotypic correlation between the observed parameters was also assessed using the `coef_cor()` function of `metan` R package [12]. A principal component analysis was performed to describe the agronomic data set using PCA function of `FactoMineR` package [13]. In order to classify genotypes according to the agronomic traits, hierarchical clustering was performed on the first two components of the previous principal component analysis using HCPC function of `FactoMineR` package [13]. Euclidean distance calculation and Ward clustering method were used. The optimal number of clusters was determined using the

inertia gain metric provided by the HCPC function, which identifies a balance between explained variance and the number of clusters. The decision to use three clusters was further supported by a visual inspection of the inertia gain plot (elbow plot in supplementary Figure S1), which showed a significant drop in gain beyond the three clusters. The projection of the data in the first two factorial components was rendered with the function `fviz_pca_biplot()` of the package `factoextra` [14].

3. Results

3.1. Agronomic Traits Variability and Analysis of Variance

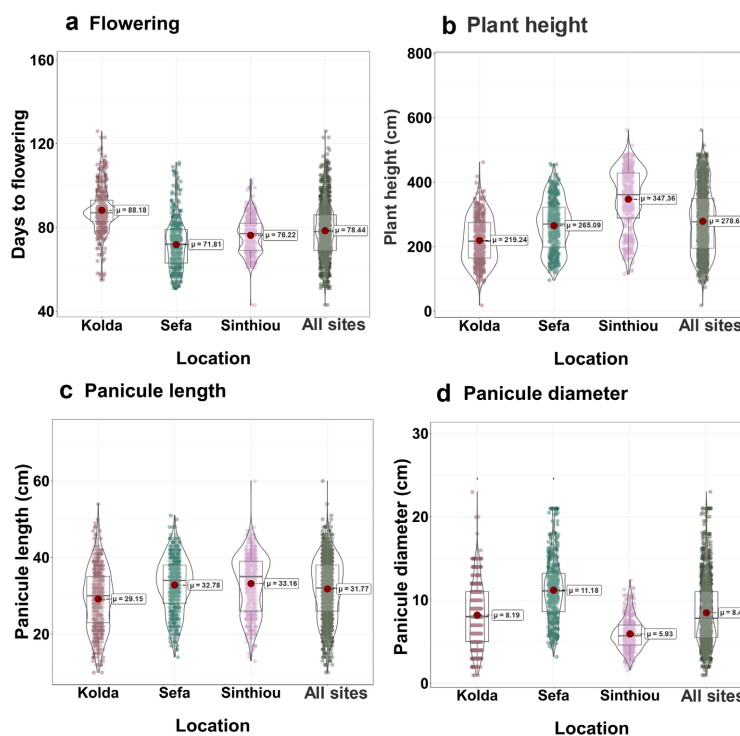


Figure 2. Boxplot representation of days to flowering, plant height, panicle length, and panicle diameter measured at Kolda, Sefa, Sinthiou, and all sites combined.

Table 3. Mean squares for studied traits across locations.

Source of variation	df	FLO	HEI	PAL	PDI	TGW	GYI	ANS	GMS
Genotype	255	316***	27060***	175.78***	19.9***	33.2***	812780***	1.442***	1.62***
Site	2	35742***	1849944***	2339.50***	3378.6***	3176.0***	295122695***	144.01***	375.78***
Genotype x site	510	85***	4203***	39.46***	11.4***	8.2***	610828***	1.193***	0.99***
Residuals	719	29	29	22.63	4.6	3.7	423841	0.910	0.33

All recorded traits were assessed for variability across genotype, location, and their interaction. Combined analysis of variance (ANOVA) across locations revealed significant phenotypic variation for all studied traits. A highly significant difference was observed between the mean square of sites, genotypes, and their

interaction for the traits (**Table 3**).

Time from sowing to flowering (FLO) varied from 43 days to 126 days (**Figure 2**). Genotypes were usually earlier at Sefa during the rainy season of 2021 compared to Kolda and Sinthiou during the rainy season of 2020. The average plant height of the genotypes was 279 cm. The tallest genotypes were noted at Sinthiou, while the shorter were noted at Kolda. The Panicle length ranged from 10 to 60 cm with an average length of 32 cm.

The thousand-grain weight varied from 4.1 g to 36.2 g (**Figure 3**). The genotypes were generally more productive at Sinthiou (1653 Kg ha⁻¹) compared to Kolda (164 kg ha⁻¹). For the panicle grain mold and anthracnose rating score, the lowest values were noted at Sinthiou compared to Sefa and Kolda.

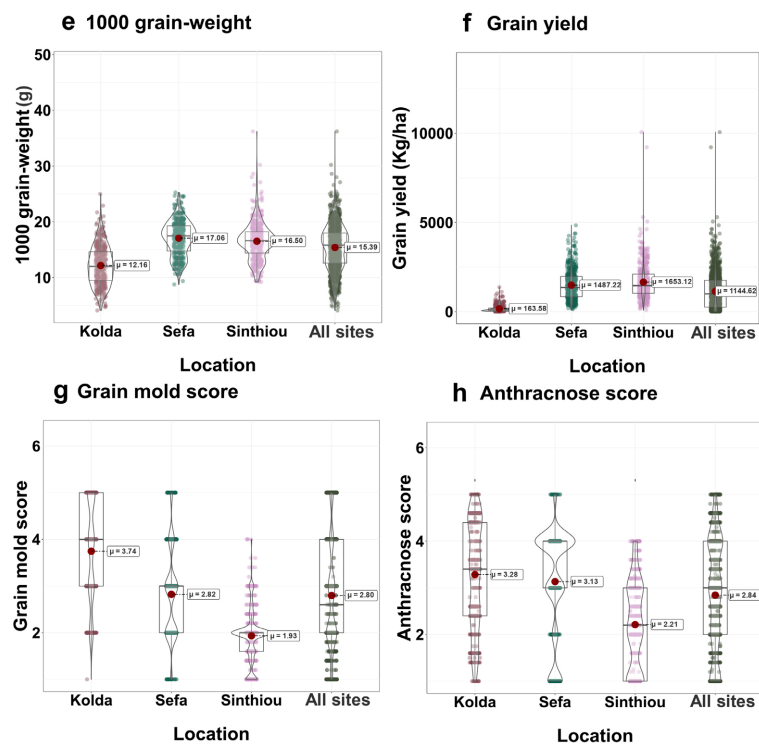


Figure 3. Boxplot representation of 1000 grain weight, grain yield, grain mold score, and anthracnose score measured at Kolda, Sefa, Sinthiou, and all sites combined.

3.2. Correlation among traits

Analysis of the phenotypic correlation revealed strong positive and negative associations between the studied parameters (**Figure 4**). Strong and positive correlations were detected between plant height and panicle length. Panicle diameter was also positively associated to panicle length. Furthermore, we observed that the disease parameters were significantly and positively associated, while the flowering time was strongly and positively associated to grain mold score. In contrast, flowering is strongly and negatively related to yield. Grain mold is negatively correlated with panicle length. Similarly, plant height and grain yield are negatively correlated with plant disease variables.

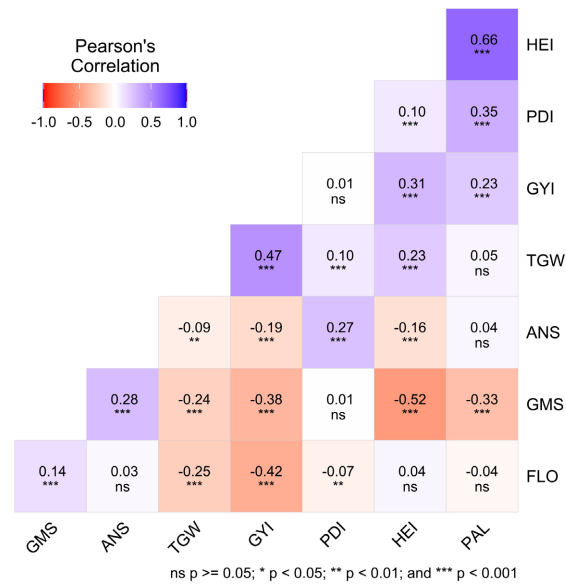


Figure 4. Pearson correlation coefficients between studied parameters.

3.3. Hierarchical Classification of the Tested Genotypes

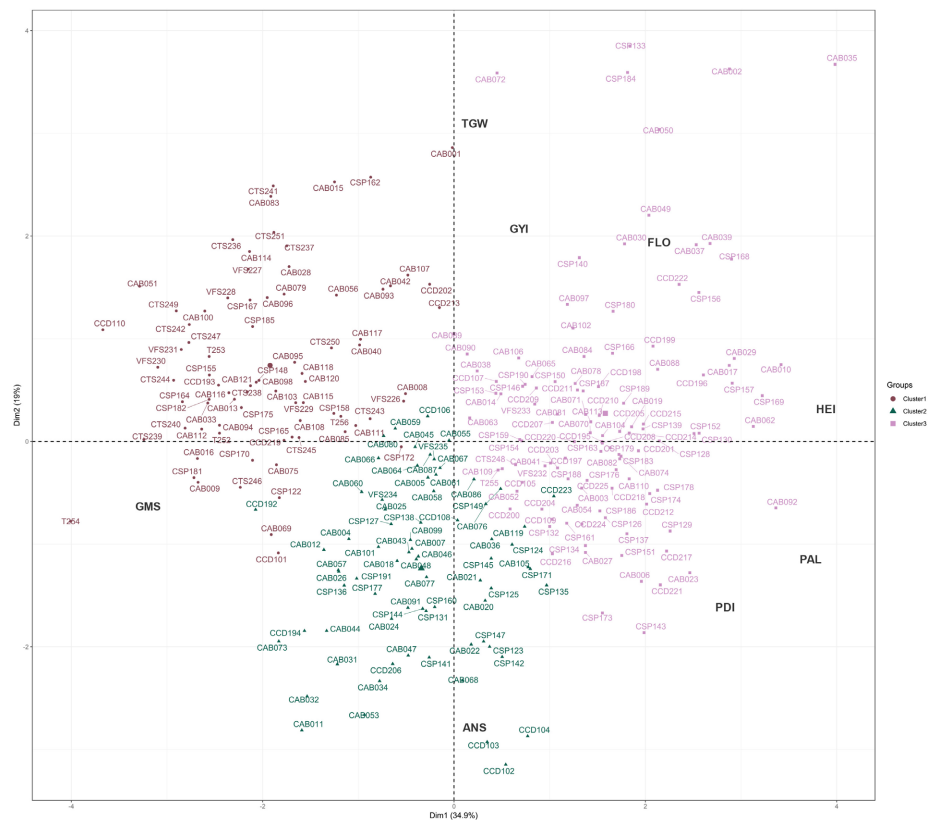


Figure 5. Projection of agronomic parameters and sorghum genotypes on the first factorial plane (Axis 1 and Axis 2).

Principal Component Analysis was used to classify the genotypes into three groups (Figure 5). The first two axes account for 54% of the total variance. Plant

height, panicle diameter and length, flowering time and grain mold score were the most discriminating parameters.

The first cluster comprises 80 accessions characterized by shortest plants with medium maturity cycle (78 das). The plants that belongs to this group had also the shortest panicle length (25 cm) and produce more than 1.2 tons ha⁻¹. Cluster 2 encompassed 73 genotypes that flower earliest (71 das) and are less productive (less than 987 kg ha⁻¹) compared to genotypes that belong to cluster 1 and 3. The 113 genotypes in cluster 3 are more productive (more than 1.2 t ha⁻¹) with long panicles (36 cm) and less susceptible to grain mold and anthracnose. They also had the longest plants (345 cm) with late growing cycle (84 das).

4. Discussion

The present study was conducted at the Kolda, Sefa, and Sinthiou research centers. These stations are representative of the main sorghum production zones in Senegal. The aim was to evaluate the new sorghum collection in Senegal, with the aim of identifying the best accessions combining high grain yield potential and resistance to grain mold and anthracnose.

The results of the variance analysis show a highly significant difference between the evaluated genotypes and between environments for all variables. Indeed, the sorghum genotypes displayed tremendous phenotypic variability for all the traits assessed. For instance, the flowering time varied from 43 to 126 days after sowing. This huge variation can be explained by the combinations of sorghums from different races. It may also be due to pedo-climatic conditions such as rainfall patterns among locations where the experiments were conducted. These results are in line with those of Sawadogo *et al.* [15] who explains that the genetic diversity in sorghum may be due to the genetic flows that exist in the farmers' environment. The results of the descriptive analysis confirm this diversity, with large differences between the minimum and maximum values of the variables.

The negative correlation between plant height and grain mold scoring indicates that genotypes with short plant height are more susceptible to grain mold than those that are tall. Indeed, the more the plant invests in growth, the more resistant it is. The study conducted by Thakur *et al.* [16] confirm that tall plants are more resistant to grain mold attacks. This can be explained by the fact that taller plants are closer to light radiation than shorter plants. These conditions are, therefore, unfavorable to fungus proliferation. Grain yield is negatively correlated with grain molds and anthracnose scores. In other words, the more susceptible the genotype, the lower the grain yield. This confirms that diseases have a negative influence on grain yield. Similar results have been reported [3]. Time from sowing to flowering is negatively correlated with grain yield, which mean that genotypes with long growing have a low grain yield potential. In fact, for late accessions, flowering coincides with the end of the rainy season or with the rain stopping, thus causing water stress. Nonetheless, post-flowering water stress can lead to total or partial abortion and poor grain filling, with a negative impact on grain yield. These

results corroborate those Diatta [8].

The considerable phenotypic variation observed in the present study allowed ranking the 256 entries into three clusters, which mainly contrasted in terms of flowering time, plant height, panicle length and grain mold score. Considering their productivity and resistance to diseases, cluster 3, contained the more productive genotypes, which are more resistant to the diseases. These findings are inconsistent with those of Derese *et al.* [17], who classified 196 sorghum landraces grown under rainfed and irrigated conditions in Ethiopia into five and six clusters, respectively. In this study, the genotypes belonging to cluster 3, in addition of being more productive and more resistant to grain mold and anthracnose; have longer panicles. Therefore, these lines can be good parental lines for improving sorghum for grain yield and disease resistance.

5. Conclusion

A comprehensive evaluation of a Senegalese sorghum collection has revealed significant phenotypic variability among the 256 genotypes assessed across different environments. The study identified three distinct clusters of genotypes, with cluster 3 emerging as the most promising group. These genotypes demonstrated superior grain yield and enhanced resistance to grain mold and anthracnose, along with longer panicles and taller plant height. The negative correlation between grain yield and disease susceptibility underscores the importance of selecting resistant genotypes to improve crop productivity. The findings highlight the potential of these genotypes as parental lines in breeding programs aimed at improving sorghum yield and disease resistance in Senegal.

Author's Contributions

GK and CD conceived and designed the study; MDS and SB performed the field experiments. GK and YABZ analyzed the data and wrote the manuscript. CD provided a critical review of the original manuscript. All authors read and approved the final version of the manuscript.

Data Availability

Data will be made available on request.

Conflicts of Interest

The authors report there are no competing interests to declare.

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