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Agronomic Traits of Sorghum Cultivars from the US and Senegal and Their Response to Grain Mold Infection

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Abstract

Grain mold, incited by several fungal species, is the most destructive sorghum disease worldwide. In this study, the interrelationships among 9 agronomic traits and grain mold resistance were determined for 24 sorghum lines from the USA and Senegal, planted in two locations in Senegal, West Africa. The study revealed several negative correlations among many measured agronomic traits and grain mold. Intact-panicle grain mold rating was negatively correlated with yield, 1000-grain weight, grain weight, panicle length, and plant height, while threshed grain mold rating was negatively associated with panicle width, plant height, maturity, and flowering date. Machine learning techniques were implemented to construct predictive models for grain yield using the collected phenotypic data. The study identified several traits influencing yield and grain mold response. The work also identified two lines, PI570841 and Nganda, that may possess genes for grain mold resistance with high yield potential. These lines could be utilized in breeding programs to develop resistant lines and hybrids. Also, the work revealed that certain yield-related traits could be useful in selecting lines in sorghum grain mold improvement programs.

Keywords

Sorghum, Grain Mold, Plant Height, Panicle Length, Yield, Fungal Species

1. Introduction

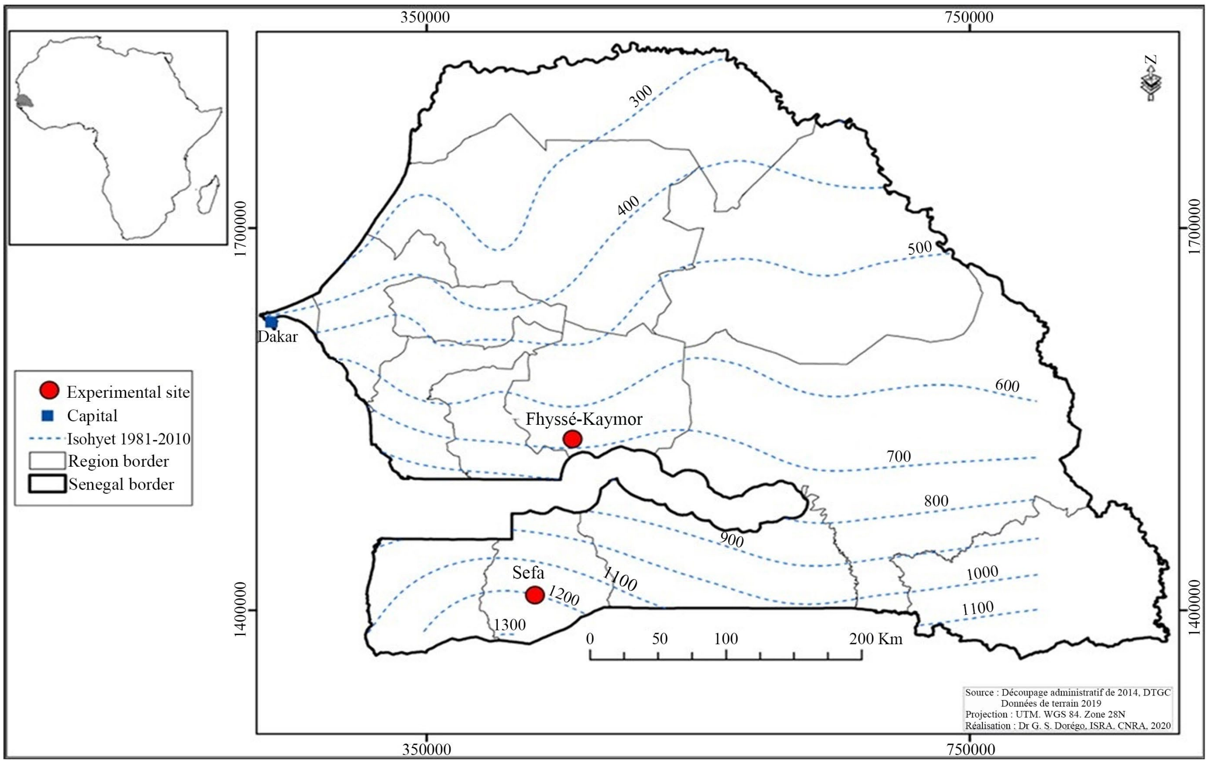
Sorghum [*Sorghum bicolor* (L.) Moench] ranks behind millet and maize in dryland cereal production and plays a crucial role in the daily lives of millions of inhabitants, especially subsistence farmers in Senegal, West Africa [1] [2]. In Senegal, 330,00 metric tons were produced during the 2024/2025 growing season [3]. In 2023, sorghum yield per hectare was 3.26 t/ha in the US, 3.65 t/ha in Mexico, 3.31 t/ha in Australia, and 4.67 t/ha in China, whereas in Senegal it was 1.71 t/ha [4]. Lower yields in Senegal and other African countries are attributable to Striga infestations, insect pests, sorghum landraces, unpredictable weather patterns, and diseases such as grain mold [5]-[9].

Grain mold is one of the major obstacles to sorghum productivity and profitability, and the disease is most severe when mature grains are not harvested on time and exposed to frequent rain later in the season [10] [11]. The disease is associated with many fungal species, including *Fusarium thapsinum* Klittich, Leslie, Nelson and Marasas, *Fusarium semitectum* Berk. & Ravenel, *Curvularia lunata* (Wakk.) Boedijin, *Colletotrichum sublineola*, *Phoma sorghina* and *Alternaria alternata* [10]-[12]. Losses in grain yield can reach 100%, and the crop's utilization is further limited for food and feed by the capability of some of the fungi associated with the disease to produce mycotoxins [12]-[15]. Furthermore, the fact that fungi associated with the disease complex vary across years and locations adds to the challenges in managing sorghum grain mold disease complex [16]-[19]. Grain mold management options include planting sorghum lines that mature during dry weather conditions, cultivars with colored grain high in tannins, or planting cultivars with high levels of resistance [10] [20] [21]. However, the best means for grain mold control is the use and development of genetically resistant sorghum lines [10] [21]-[24]. Thus, the aim of this study was to investigate grain mold response and agronomic characteristics of several sorghum cultivars/lines from the US and Senegal.

2. Materials and Methods

The field trials were conducted in two locations Thyssé-kaymor and Séfa, Senegal, West Africa. Thyssé-kaymor lies 13˚46'60"N and 15˚34'0"W, while Séfa lies 12˚46'58"N and 15˚32'46"W in the regions of Kaolack and Kolda, respectively (**Figure 1**) (https://www.getamap.net). Weather parameters for the two regions during the growing season are in **Table 1**. A total of 24 sorghum cultivars/lines from the US and Senegal were used in the study. Seeds of each cultivar/line were planted in 1.8 m rows with 0.8 m row spacing in each environment. The cultivars/lines were planted in a randomized complete block design, and each cultivar/line was replicated three times. Standard field operations were employed, and weeds were controlled by hand hoeing. The plant traits measured were: time of flowering, that is, when 50% of the plants in each row flowered [Fldate]; plant height [Pheight], measured in centimeters (cm) from the soil to the top of the plant; panicle length [Plength] (cm), measured from the first branch with racemes to the top of the panicle; panicle width [Pwide] (cm); time of maturity [Maturity] (days from planting); harvested plots grain weight [Gweight] (g); 1000 grain weight [TGWeight] (g); yield [Yield] (Kg/ha); and texture of endosperm, using a rating scale of 1 to 5, with 1 = completely corneous to 5 = completely starchy [25].

Grain mold rating (PGMR = Intact panicle grain mold severity rating and TGMR = Threshed grain mold severity rating) on a scale of 1 - 5, with 1 = clean grains and 5 = more than 50% moldy grains, based on Thakur *et al.* [11], was used to assess the disease on the intact panicles and threshed grain from the panicles.



Source : Découpage administratif de 2014, DTGC
Données de terrain 2019
Projection : UTM. WGS 84. Zone 28N
Réalisation : Dr G. S. Dorégo, ISRA, CNRA, 2020

Figure 1. Map of Senegal showing the locations of the trials.

Table 1. Rainfall, temperature, and relative humidity of the regions near the experimental sites in 2022.

Mean weather parameters (May to October)				
Region	Rainfall (mm)	Max temp (˚C)	Min temp (˚C)	Relative humidity (%)
Kaolack (near Thysse-Kaymor)	851.6	34.2	25.0	74
Kolda (near Sefa)	1340.1	33.5	23.5	76

Source: ANACIM and ISRA, 2022.

3. Statistical Analysis

Data analysis was conducted using JMP Pro 17 (SAS Institute Inc., Cary, NC). Initial comparisons of cultivar performance for each trait were made using one-way ANOVA. For subsequent correlation and multivariate analyses, continuous agronomic traits were log10-transformed to better approximate normality and ensure homogeneity of variances. Pearson correlations were used to summarize linear relationships among the log-transformed continuous traits. For correlation summaries involving ordinal disease ratings (PGMR, TGMR, and Tendo; 1 - 5 scales), log-transformed values were used for visualization, and rank-based (Spearman) correlations were used as a robustness check.

To gain more insights into the multivariate patterns, several analytical approaches were integrated. Principal Component Analysis (PCA) on the log-transformed data was performed. Hierarchical clustering, using Ward's linkage method, was applied to group cultivars with similar overall phenotypes and separately to understand the interrelationships among the measured traits. Additionally, t-Distributed Stochastic Neighbor Embedding (t-SNE) provided a non-linear method for visualizing cultivar relationships in a reduced-dimensional space (settings: 3 output dimensions, perplexity = 50, max iterations = 10,000, initial PCA = 100, convergence = 0.0001, initial scale = 0.0001, Eta = 200, inflate iterations = 250, random seed = 123).

To identify individual traits significantly associated with yield and TGMR, linear regressions were performed by the 'Response screening' function in JMP. The p-values from these regressions were adjusted using the False Discovery Rate (FDR) method to control for multiple testing errors; an FDR-adjusted p-value < 0.01 was the criterion for statistical significance.

Predictive modeling for yield and TGMR was carried out using machine learning techniques within JMP Pro 17's 'Model Screening' platform, trained on individual plot-level data (n = 135) to capture environmental variability. All measured traits were included as potential predictors. Model performance was rigorously evaluated and compared using 5-fold cross-validation. The algorithms tested under default settings comprised: Fit Stepwise, Generalized Regression (Lasso), Boosted Tree, Bootstrap Forest (Random Forest), Decision Tree, Neural Boosted, K-Nearest Neighbors (k-NN), Support Vector Machines (SVM with RBF kernel), and Fit Least Squares. Importantly, when modeling TGMR, the objective function was set to maximize resistance (minimize the score), achieved by reversing the scale of TGMR and PGMR scores (using 5 - score) to reflect higher desirability for lower values. Mathematical optima identified by the Prediction Profiler were interpreted subject to biological constraints.

4. Results

Analysis of variance (ANOVA) revealed significant phenotypic differences ($p < 0.05$) among the 24 sorghum cultivars evaluated for nearly all agronomic and disease resistance traits measured; however, Tendo was the only trait showing no significant variation ($p = 0.38$). For grain mold response specifically (TGMR), a wide range was evident, spanning from resistant lines like PI609251 (average = 2.33), PI570726 (average = 2.50), Nganda (average = 2.67), and PI570841 (average = 2.83) to highly susceptible cultivars such as BTx378, RTx2536, SC414-12E, SC328C, and SC112-14 (all with average score TGMR > 4.5) (**Table 2**). To explore the relationships between these traits and the distribution of cultivars, PCA was conducted on the log-transformed dataset. The first two principal components (PC1 and PC2) together accounted for 41.4% of the total variability, contributing 21.2% and 20.2%, respectively. The PCA score plot (**Figure 2(a)**) revealed considerable scatter among the data, without forming distinct clusters. The loading plot (Figure 2(b)) revealed strong positive associations between Yield, GWeight, and TGWeight, as well as close relationships between Maturity and Fldate, and between Pwide and Pheight. Further examination of component influence showed Maturity and Fldate were heavily weighted on PC1, whereas Yield, GWeight, and TGWeight were primarily driven by PC2. Pheight variation was most strongly associated with PC3. In contrast, Tendo was not influenced by PC1, PC2, or PC3, but rather by PC4 and PC5. These multivariate relationships were corroborated by factor analysis, which identified similar trait groupings driven by the first two factors, explaining 19.6% and 17.4% of the variance, respectively.

Table 2. Mean thousand-seed-weight, grain weight, yield, panicle grain mold rating, and threshed grain mold rating of 24 sorghum cultivars/lines from Senegal and the United States.

Cultivar/line	TGWeight	GWeight	Yield	PGMR	TGMR
PI570841	22.2a	550.4a	1158.2a	2.2a	2.8b
BTx398	21.6ab	290.9a	668.3a	2.6a	3.8ab
PI569979	20.4abc	552.0a	1534.8a	2.4a	3.5b
Nganda	19.9abcd	452.2a	1002.4a	2.5a	2.7b
BTx378	19.5abcd	301.1a	1071.3a	2.4a	5.0a
BTx623	19.5abcd	277.3a	710.1a	2.5a	3.7ab
SC326-6	19.2abcd	387.7a	1029.0a	2.5a	4.7ab
Brandes	18.7abcd	436.7a	1107.9a	2.4a	3.5b
SC414-12E	18.7abcd	290.3a	755.2a	2.1a	5.0a
SSD35	18.3abcd	154.9a	624.0a	2.1a	4.2ab
CE151262	18.2abcd	454.7a	1129.2a	2.8a	4.5ab
TAM428	18.1abcd	243.4a	683.8a	2.0a	4.0ab
SC328C	17.8abcd	323.5a	787.5a	2.3a	4.8ab
IC9V8803	17.6abcd	143.4a	451.9a	2.3a	3.2b
Payenne	17.3abcd	257.2a	730.9a	2.4a	4.0ab
IS18760	17.3abcd	257.2a	929.5a	3.1a	4.5ab
SC112-14	17.1abcd	151.3a	634.3a	2.6a	4.8ab
CE18033	17.1abcd	338.2a	908.7a	2.0a	3.3b
SC283	17.0abcd	170.2a	686.0a	2.5a	2.8b
RTx2536	15.3abcd	783.8a	1569.4a	2.5a	4.9ab
PI570726	15.3bcd	126.8a	495.8a	3.2a	2.5b
Theis	15.2bcd	216.6a	675.4a	2.1a	4.2ab
SC748-5	14.8cd	144.3a	574.1a	2.2a	4.7ab
PI609251	14.0d	209.4a	560.2a	2.6a	2.3b
Overall mean	17.9	313.1	854.8	2.4	3.9

Combined data from two locations Kaymor and Sefa, Senegal, West Africa; Thousand-seed weight in grams; Grain weight in grams for the harvested plots; Yield in kilograms per hectare; PGMR = Intact panicle grain mold severity rating based on a scale 1 = clean/no moldy grains, and 5 = more than 50% moldy grains (Thakur *et al.* 2007); TGMR = Threshed grain mold severity rating based on a scale of 1 - 5.

Pearson correlation analysis (based on plot-level observations, n = 135) highlighted several significant inter-trait relationships. As a robustness check for ordinal traits, Spearman rank correlations confirmed the key TGMR associations with Pheight ($\rho = -0.5325$, $p < 0.0001$), Maturity ($\rho = -0.4004$, $p < 0.0001$), and Fldate ($\rho = -0.3294$, $p < 0.0001$), as well as the positive association between PGMR and Pwide ($\rho = 0.2033$, $p = 0.018$). As expected, a strong positive correlation was found between Fldate and Maturity ($r = 0.97$, $p < 0.0001$) (Figure 3). Fldate also showed a significant negative correlation with TGMR ($r = -0.31$, $p < 0.0001$). Regarding Pheight, it was significantly positively correlated with Pwide ($r = 0.22$, $p = 0.01$) and negatively correlated with TGMR ($r = -0.49$, $p < 0.0001$). Pwide, in turn, exhibited a significant positive association with PGMR ($r = 0.24$, $p = 0.0057$). Maturity showed further significant negative associations with both Plength ($r = -0.23$, $p = 0.0076$) and TGMR ($r = -0.39$, $p < 0.0001$). Strong positive correlations were observed among Gweight, TGWeight, and Yield, with r values ranging from 0.42 to 0.80. Tendo's formed a weak positive correlation with PGMR ($r = 0.18$, $p = 0.034$).

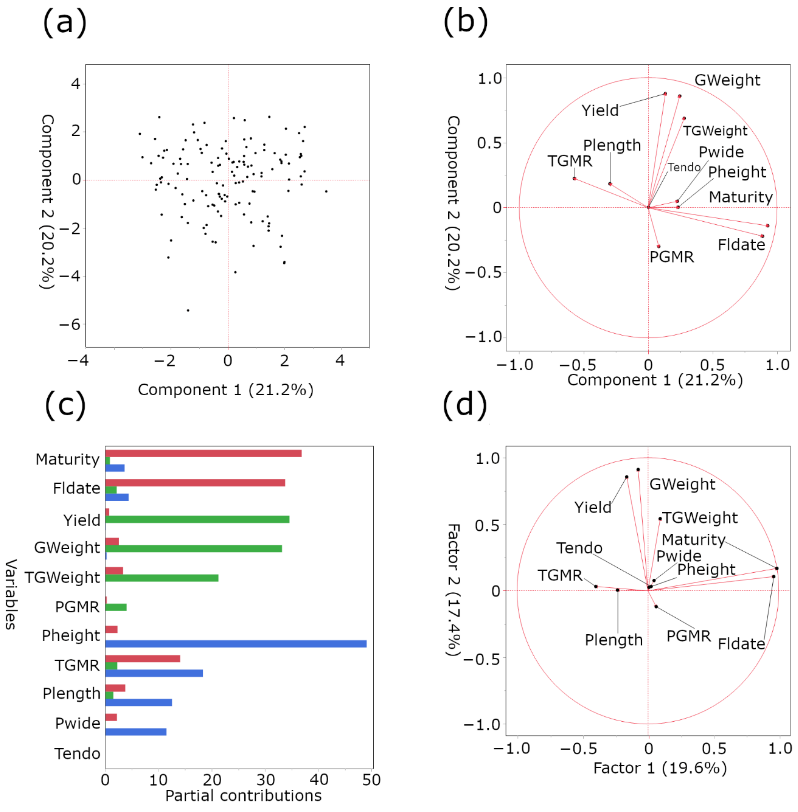


Figure 2. PCA and Factor Analysis of agronomic traits and grain mold response in 24 sorghum cultivars. (a) PCA score plot positioning cultivars based on PC1 (21.2% variance explained) and PC2 (20.2% variance explained). (b) PCA loading plot visualizing trait contributions (vectors) and correlations for PC1 and PC2. (c) Partial variance contributions of each trait to PC1 (red), PC2 (green), and PC3 (blue). (d) Factor analysis loading plot showing trait contributions to Factor 1 (19.6% variance explained) and Factor 2 (17.4% variance explained).

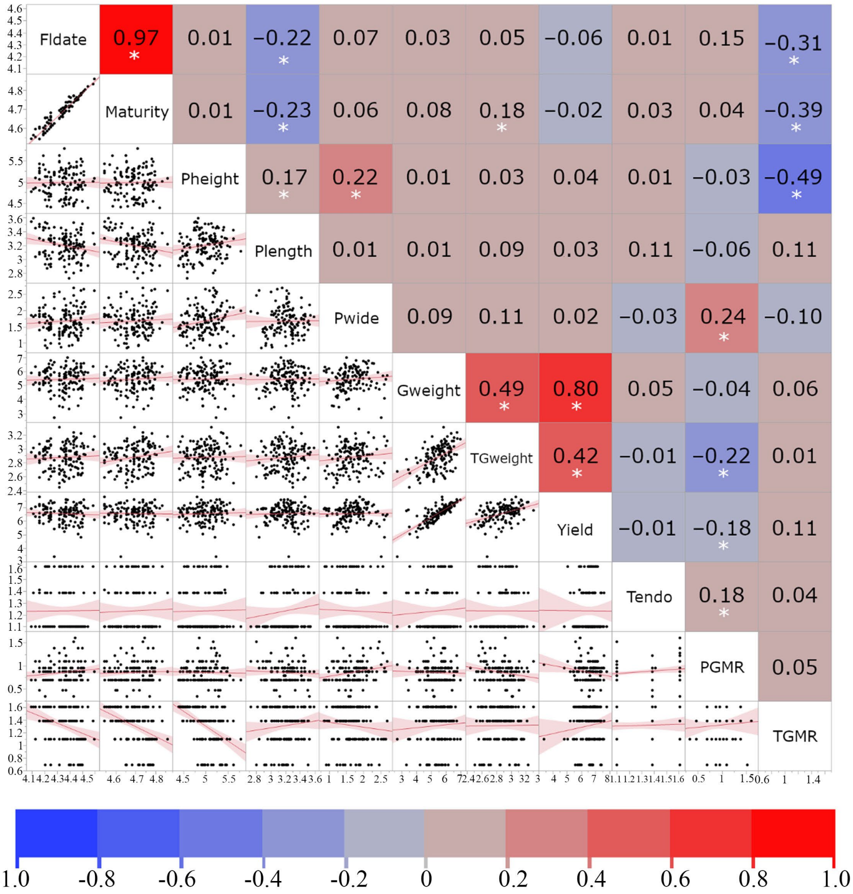


Figure 3. Correlation matrix illustrating pairwise Pearson correlations among log-transformed agronomic and disease traits based on plot-level observations (n = 135). The upper triangle presents a heatmap where color intensity signifies the strength and direction of correlation coefficients (Red = positive, Blue = negative), with asterisks (*) denoting statistical significance ($p < 0.05$). The lower triangle contains scatter plots for each trait pair, overlaid with linear regression lines. Rank-based (Spearman) correlations were additionally examined for pairs involving ordinal ratings (PGMR, TGMR, Tendo) as a robustness check (see Results).

Clustering and dimensionality reduction techniques were employed to gain a comprehensive understanding of the phenotypic relationships among the sorghum cultivars and the measured traits (Figure 4). Firstly, hierarchical clustering using Ward's method, applied to the average values of all traits, successfully grouped the 24 cultivars into three primary clusters (Figure 4(a)). A major cluster included lines like BTx623, SC328C, SC414, and TAM428 among its 17 members. The second distinct cluster contained BTx398, BVANDES (Brandes), PI569979, PI570841, and Nganda. PI570726 and PI609251 formed their own separate, smaller cluster. Secondly, hierarchical clustering was also performed on the traits themselves to investigate their interrelationships (Figure 4(b)). This analysis revealed groupings: Maturity and Fldate clustered together; Pheight and Plength formed another cluster; Pwide and PGMR showed a close relationship; Tendo grouped with TGMR; and the yield components Gweight, Yield, and TGWeight were clustered closely. As an alternative method for visualizing cultivar distribution, t-SNE projected the entries into a lower-dimensional space, revealing finer potential groupings (**Figure 4(c)**). This analysis suggested eight clusters, distinguished by color. One group (red) contained SC112-14 and SC748-5. Another (brown) comprised SC414-12E, SC328C, and SC326-6. A third distinct group (black) included PI570841, PI569979, RTx2536, and Brandes (BVANDES). Nganda, CE18033, and BTx398 formed a green cluster, while BTx378 and CE151-262 made up a pink cluster. The sky-blue cluster consisted of IC9V8803 and SC283. A blue cluster grouped BTx623, Theis, IS18760, TAM428, and Payenne. Finally, SSD35, PI609251, and PI570726 clustered together in purple.

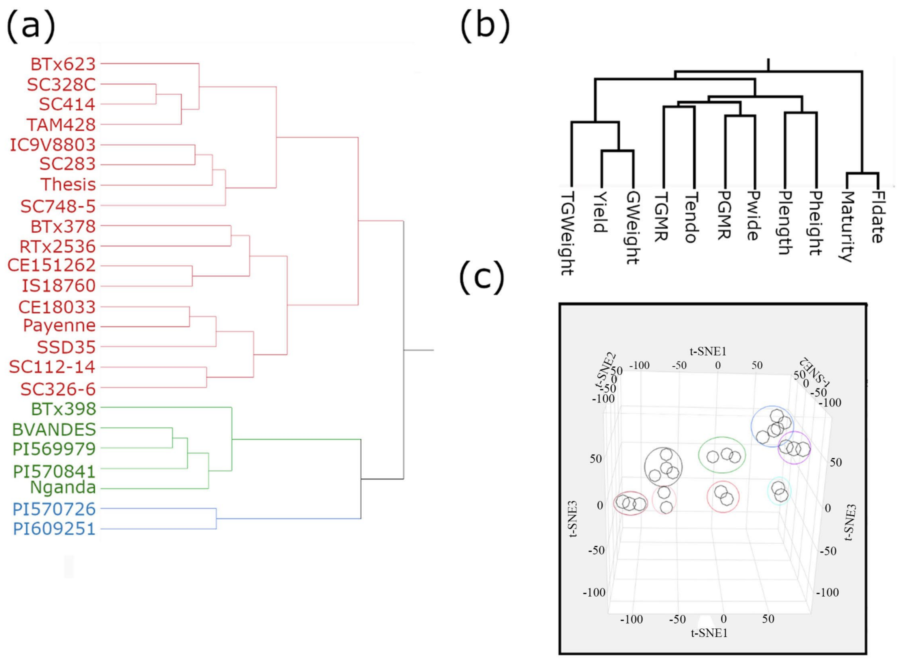


Figure 4. Visualization of cultivar and trait relationships in sorghum using clustering and t-SNE based on phenotypic data. (a) Hierarchical clustering (Ward's method) dendrogram grouping the 24 cultivars based on mean trait values, with the three main clusters highlighted by color. (b) Dendrogram showing the interrelationships among phenotypic traits based on their similarity profiles across cultivars. (c) t-SNE plot illustrating the distribution of the 24 cultivars in a reduced feature space (t-SNE1 vs. t-SNE2/t-SNE3). Points correspond to cultivars, and potential clusters identified through t-SNE are indicated by colors and circles (see text for details).

To pinpoint individual traits with significant effects on grain yield and TGMR, a Response Screening analysis was implemented using JMP Pro 17 (**Figure 5**). Significance was assessed after applying an FDR correction for multiple comparisons, using a threshold of FDR-adjusted $p < 0.01$. For grain yield (**Figure 5(a)**), two traits emerged as significant predictors: Gweight demonstrated the strongest association ($p = 9 \times 10^{-31}$), followed by TGWeight ($p = 4.68 \times 10^{-7}$). Regarding TGMR (**Figure 5(b)**), the analysis identified Pheight as having the most significant impact ($p = 2.41 \times 10^{-9}$), ahead of Maturity ($p = 3.4e \times 10^{-6}$) and Fldate ($p =$

0.0003). None of the other traits tested showed a statistically significant association with either yield or TGMR after FDR correction.

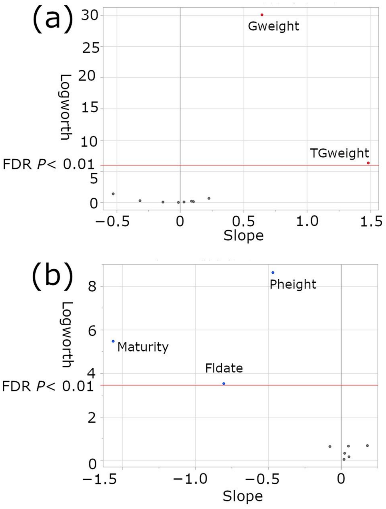


Figure 5. Volcano plots from JMP Pro 17 Response Screening, identifying traits significantly associated with (a) grain yield and (b) TGMR. Each plot displays statistical significance (-log10 (*p*-value), Logworth) on the y-axis versus the estimated effect size and direction (Slope) of predictor traits on the respective response variable (x-axis) (red: positive effect, blue: negative effect). Every point corresponds to a tested predictor trait. The horizontal red line marks the significance threshold based on an FDR-adjusted *p*-value of 0.01.

Table 3. Comparison of machine learning model performance in predicting sorghum grain yield, based on 5-fold (K = 5) cross-validation. Algorithms are ranked by their average coefficient of determination (RSquare) across validation sets. Mean Root Average Squared Error (RASE) and its standard deviation (StdDev RASE) are also reported for each model.

Models	RSquare	Mean RASE	StdDev RASE
Neural Boosted	0.6574	245.60	62.608
Fit Stepwise	0.5601	268.54	70.585
Generalized Regression Lasso	0.5563	273.19	76.925
Bootstrap Forest	0.5245	283.68	52.384
Fit Least Squares	0.5162	281.81	72.249
Decision Tree	0.5001	283.77	42.585
Boosted Tree	0.4962	293.79	58.483
Support Vector Machines	0.4756	305.63	76.008
K Nearest Neighbors	0.4466	311.92	58.406

Machine learning techniques were implemented to construct predictive models for grain yield using the collected phenotypic data. Several algorithms were assessed based on their performance during 5-fold (K = 5) cross-validation (Table 3). The Neural Boosted model demonstrated the highest average predictive capability across validation sets, yielding a cross-validation RSquare of 0.6574. While models such as Fit Stepwise (RSquare = 0.5601) and Generalized Regression Lasso

(RSquare = 0.5563) also showed competitive performance, Neural Boosted was selected for more in-depth analysis.

Table 4. Importance ranking of predictor traits in the finalized Neural Boosted model for sorghum grain yield (RSquare = 0.8231). This table quantifies the contribution of each trait, where 'Total Effect' represents the overall influence including interactions, and 'Main Effect' signifies the direct impact. The 'Importance score' visually depicts the magnitude of the 'Total Effect'.

Trait	Main Effect	Total Effect	Importance score
Gweight	0.753	0.784	
Maturity	0.086	0.107	
Fldate	0.06	0.082	
PGMR	0.013	0.024	
TGWeight	0.006	0.011	
Pheight	0.004	0.009	
Plength	0.003	0.007	
Pwide	0.003	0.007	
Tendo	0.003	0.007	
TGMR	0.001	0.004	

Table 5. Performance evaluation of different machine learning models for predicting TGMR, based on 5-fold (K = 5) cross-validation. Models are listed in order of their cross-validation coefficient of determination (RSquare). Mean Root Average Squared Error (RASE) and its standard deviation are also provided for comparison.

Model	RSquare	Mean RASE	StdDev RASE
Neural Boosted	0.656	0.58842	0.08904
Fit Stepwise	0.5046	0.70921	0.07286
Generalized Regression Lasso	0.4693	0.73342	0.0531
Fit Least Squares	0.461	0.73897	0.0553
Bootstrap Forest	0.4195	0.76678	0.11464
Support Vector Machines	0.3456	0.81822	0.09144
Boosted Tree	0.3357	0.81744	0.09238
K Nearest Neighbors	0.3316	0.81995	0.08787
Decision Tree	0.2894	0.84054	0.09453

The single best-performing Neural Boosted model from the cross-validation process achieved a high RSquare of 0.8231. Feature importance analysis conducted on this specific model (Table 4) indicated that Gweight was the primary contributor to yield prediction, exerting a total effect of 0.784. Maturity was the second most influential predictor, with a total effect of 0.107.

To assess the model's reliance on grain weight information, the Neural Boosted algorithm was retrained, excluding Gweight. This exclusion led to a significant drop in predictive power, reducing the average K = 5 cross-validation RSquare to 0.3243. In this modified model, TGWeight emerged as the most significant predictor (total effect = 0.634), followed by Pheight (total effect = 0.113), as detailed in Supplementary Data 1.

Finally, the prediction profiler of the validated Neural Boosted model was used to visualize directional effects of key predictors on Yield within the observed data range. Because profiler-based optima can produce biologically infeasible combinations when predictors are correlated, profiler outputs were interpreted qualitatively and subject to biological constraints.

Similarly, machine learning models were developed to predict TGMR using the measured phenotypic traits. Based on a 5-fold (K = 5) cross-validation comparison (Table 5), the Neural Boosted algorithm again emerged as the top performer, yielding an average cross-validation RSquare of 0.656. The next best model was Fit Stepwise (RSquare = 0.5046).

Table 6. Feature Importance analysis for the validated Neural Boosted TGMR Prediction Model (RSquare = 0.7308). Predictor traits are ranked according to their contribution to TGMR prediction within this final model. 'Total Effect' denotes the overall influence of each trait, including interactions, whereas 'Main Effect' represents its direct impact. The 'Importance score' serves as a visual representation of the 'Total Effect'.

Trait	Main Effect	Total Effect	Importance score
Maturity	0.522	0.57	
Fldate	0.314	0.348	
Pheight	0.061	0.101	
TGWeight	0.007	0.022	
Yield	0.006	0.016	
PGMR	0.003	0.008	
Gweight	0.003	0.007	
Plength	0.002	0.006	
Pwide	0.002	0.004	
Tendo	4×10^{-4}	0.001	

The optimized Neural Boosted model specifically for TGMR prediction achieved an RSquare of 0.7308 on its validation set. Feature importance analysis for this model (Table 6) identified Maturity as the most significant predictor (Total Effect = 0.57), followed by Fldate (Total Effect = 0.348) and Pheight (Total Effect = 0.101).

Furthermore, the predictive profiler of this validated TGMR model (RSquare = 0.7308) was employed to estimate the phenotypic profile associated with maximum grain mold resistance. A minimum TGMR score of 1 could potentially be achieved with a cultivar possessing the following traits: Maturity = 106.37 days, Fldate = 60 days, Pheight = 205.14 cm, Plength = 17.92 cm, Pwide = 12.27 cm, Gweight = 15 g, TGWeight = 17.23 g, PGMR = 2.12, Yield = 820.12 kg/ha, and Tendo = 4.05. As with the yield model, these results represent a mathematical phenotypic profile where practical breeding selection requires superimposing biological feasibility.

5. Discussion

The projected increase in global population to over 9 billion by 2050 will require increases in crop production, especially cereals, which include sorghum [9] [26]-[29]. Estimates of world food production increases by 2050 ranged from 60% to 110% [30]. Increases in crop production in the light of climate change will require robust and sustainable management strategies to mitigate the impact of emerging and novel microorganisms, including those that incite sorghum grain mold. Globally, the monetary loss due to grain mold on sorghum was estimated to be US$130 million annually, a figure that is considered an underestimation because of the unaccountability of quality losses due to mycotoxin contamination [31] [32].

Management of sorghum grain mold can be problematic due to the many fungal genera associated with the disease, variable weather or climatic conditions where the crop is planted, types of sorghum planted, and the types of fungal species present in the areas of production [10] [11] [14] [24] [32]-[34]. The best strategy for controlling grain mold is the use of resistant sources [10] [35]. Over the years, thousands of sorghum lines, cultivars, landraces, and hybrids have been evaluated in different agro-ecological zones to identify resistance either under natural infection or challenged with different grain mold fungi, and several resistant sources have been identified [36]-[43]. Herein, we report the results of grain mold response, agronomic traits, and their interrelationships on sorghum cultivars/lines from the US and Senegal evaluated in two different environments during the growing season in 2022 in Senegal, West Africa. According to Diatta [44], breeding for grain mold resistance is a top priority in Senegal.

In this study, several cultivars/lines PI570841, Nganda, SC283 and PI609251 were shown to be tolerant to grain mold. RTx2536 recorded the highest mean grain yield (1569.4 kg/ha), followed by PI569979 (1534.8 kg/ha), and PI570841 (1158.2 kg/ha) (**Table 2**). However, RTx2536 is a parental line used principally as a pollinator in commercial hybrid seed production and has been shown to be susceptible to grain mold [45]. Sorghum accessions PI 570011, PI 570022, and PI 569992 from Sudan were shown to possess high levels of resistance to grain mold while accessions PI525954, PI276841, and PI276840 exhibited lower grain mold severities and higher germination rates when inoculated with *F. thapsinum* and compared to the resistant controls Sureno and SC719 [21] [22]. Several sorghum accessions from Senegal revealed that accessions PI514302, PI514374, PI514420, and PI514467 may possess genes for resistance to grain mold when tested in Puerto Rico [24]. In the current study, yield was significantly and positively correlated with grain weight and 1000-seed weight. Goswami *et al.* [46] noted that sorghum yield per plant was significant and positively associated with 1000-grain weight. Correlation analysis for rice yield and other agronomic traits revealed a highly significant and positive association between grain yield and 1000-grain weight [47]. Similarly, a significant and positive association between the grain yield of red rice with grain weight per panicle and 1000-grain weight was noted by Sadimantara *et al.* [48]. Edet [49] also reported a highly positive correlation between maize grain yield and the number of kernels per row and 1000-grain weight. Aruna *et al.* [50] noted that flowering time, 100-grain weight, and plant height are factors in grain yield, while glume cover and plant height play a role in influencing grain mold resistance. This study also revealed an interrelationship between disease and agronomic traits. PGMR was negatively correlated with yield, 1000-grain weight, grain weight, panicle length, and plant height, while TGMR was negatively associated with panicle width, plant height, maturity, and flowering date. Prom *et al.* [51] noted that grain mold infection was negatively correlated with sorghum germination rate, seed weight, panicle length, and plant height. Further, research has shown negative correlations between relative yields of wheat and triticale infected with yellow rust and between grain yield and damaged leaf area, resulting from wheat sprayed with fungicides to control spots and leaf blight in Central Mexico [52] [53]. The principal trait in sorghum breeding is yield; however, other agronomic traits, including disease response, height, fresh weight, leaf and panicle architecture that influence yield, are also desirable [50] [54]-[56]. Mutezo *et al.* [54] noted that increased in sorghum yield was influenced by taller plants and those with higher biomass. Similarly, Aruna *et al.* [50] observed that improved grain yield was associated with plant height, flowering time, and 100-grain weight. While Aragaw [56] reported that leaf number, panicle length, panicle weight, and panicle width exhibited significant and positive association with sorghum yield.

In conclusion, this study has identified two lines PI570841 and Nganda that may possess genes for grain mold resistance with high yield potential which could be utilized in breeding programs. Also, the work revealed that certain yield-related traits could be useful in selecting lines in sorghum grain mold improvement programs.

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Conflicts of Interest

The authors declare no conflicts of interest regarding the publication of this paper.

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