

Research Article

Multienvironment Evaluation of Tannin-Free Photoperiod-Insensitive Sorghum (*Sorghum bicolor* (L) Moench) for Yield and Resistance to Grain Mold in Senegal

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Combining resistance to grain mold with high grain yield in tannin-free white-grained photoperiod-insensitive sorghum is of major interest for farmers in Senegal. In this study, GGE biplot analysis was used to assess the performance, adaptability, and stability of eleven sorghum parental lines and their hybrid combinations for yield and grain mold resistance under Senegalese environments. Eleven inbred lines along with their 22 hybrid combinations and one check were evaluated across three sites during the 2015 and 2016 rainy seasons under natural grain mold infestation. The results of this study showed strong genetic variability among studied genotypes for all measured traits. The highly significant $G \times E$ interaction effects for grain yield and panicle grain mold rating score (PGMR) indicated that both traits are influenced by genetics and to some extent by environment. Broad-sense heritability computed was high for all these traits except PGMR, showing a high environmental pressure on this later. The study showed that grain mold pressure in the studied sites decreased following a South-North gradient similar to the rainfall pattern, with the south region wetter, explaining the high disease pressure in Darou and Sinthiou Maleme contrary to Bambey. The GGE biplot analysis performed showed that the first two principal components explained 85.84% of the total variation of GGE sum of squares for grain yield. The which-won-where view of the GGE biplot for grain yield showed that the hybrid HB16 was the most adapted for Bambey area. The ranking of genotypes based on both yield performance and stability showed that HB16, HB5, HB21, HB18, and HB7 were the best hybrids combining high grain yield, high stability performance, and tolerance to grain mold disease across the test environments. These hybrids outperformed the best yielding inbred line P29 (2196.7 kg ha⁻¹) with grain yield advantages ranging 17–60%. Therefore, these hybrids could be recommended to farmers in order to improve sorghum yield in Senegal.

1. Introduction

Sorghum is an important cereal crop extensively grown in Senegal during the rainy season and along the Senegal River

Valley during the water flooding recession. In 2017, sorghum production in Senegal averaged 225,865 tons under a cultivated area of 221,329 ha [1]. The major growing regions in the country are Kaffrine, Tambacounda, and Kolda that

account for about 62.8% of the national sorghum production [1]. Sorghum has good adaptation to a wide range of ecological conditions, requires low inputs for cultivation, and amenable for various end uses [2]. In Senegal, sorghum is mainly used as food, feed, fodder, and more recently involved in food processing activities such as bread making [3]. Moreover, sorghum grain is an important source of energy, protein, vitamins, and minerals for many households [4]. However, the yield of sorghum in the farmer's field is very low (1020 kg ha^{-1}) and far below the needs of the population [1].

To reduce the yield gaps and to increase sorghum production, breeding for high yielding hybrids is known to be more productive than relying on landraces and purlines [5–7]. In Senegal, efforts have been made by the national sorghum breeding program to develop high yielding, tannin-free, photoperiod-insensitive cultivars belonging to the race *caudatum*. These efforts have led to the release of several tannin-free semicompact varieties such as CE151-262, CE196-7-2, 93B1057, F2-20, Nguinthe, Faourou, Nganda, and Darou whose yield is between 2 and 3 t ha^{-1} in farmer's field and are highly appreciated for their grain quality [8]. However, as these varieties were bred for earliness, in prolonged growing season, they mature before the end of the rainy season and are readily infected by grain mold that results in poor nutritional quality of the grain and poor germination rate when the contamination is high [9].

In Senegal, grain mold disease is one of the main constraints to the adoption of improved short- and medium-duration tannin-free photoinensitive sorghum varieties [10, 11]. The occurrence of the disease depends on the growing region, years, cultivars, and the prevailing weather conditions during the grain filling phase. Grain mold of sorghum is caused by a complex of more than 40 genera of pathogenic and saprophytic fungi [12, 13]. The most important genera infecting sorghum grain in Senegal are *Fusarium*, *Curvularia*, *Helminthosporium*, *Alternaria*, and *Phoma*, with *Fusarium verticillioides* and *Curvularia lunata* being more virulent [11, 14, 15]. These species, individually or in combination affect sorghum grain quality resulting in significant yield losses [16, 17]. The estimated field production losses due to grain mold ranges from 30% to 100% [18]. This results in a reduction in food availability, exposure to health risks through contaminated food, and income losses through lower prices [19]. Efforts in improving grain mold resistance in high yielding genotypes have been limited because the disease is governed by multiple mechanisms of resistance. Previous studies indicated that grain mold resistance in sorghum is governed by several major and minor genes that are influenced by genotype (*G*), environment (*E*), and *G* × *E* interactions [9, 16, 20, 21]. In this context, multi-environment trials (MET) are important for studying yield stability and adaptation, as well as for the prediction of yield performance of genotypes across environments [22].

The GGE biplot model has been considered as an effective method to identify genotype differences under several testing environments [23]. This methodology is composed of two concepts, the biplot concept [24] and GGE concept [25]. It is now widely used by crop breeders in MET analysis for

estimating mean performance, stability of cultivars, and discrimination of test sites [26, 27]. GGE biplot methods are graphical procedures that are able to interpret the *G* × *E* interaction in the site regression model [28]. This model assumes that the main effect of the environment is not relevant in the selection of genotype (*G*), with the *G* effect presented as a multiplicative *G* × *E* effect [29]. The popularity of the GGE biplot methodology is due to its flexibility and ability to analyze a range of data types with a two-way structure. It has been used in sorghum to investigate the *G* × *E* interaction for several traits such as yield, drought tolerance, stem sugar, grain iron, and zinc concentration [7, 29–31]. In a recent study, high yielding sorghum hybrids (AVG-1 × Nganda and AVG-1 × Darou) have been identified as the most stable and tolerant to grain mold infestation, suitable for the center and southeast regions of Senegal [8]. The present study was conducted to identify the suitable material for this zone and increase yield in farmers' fields in terms of improved varieties. The current study was conducted to (i) identify the best hybrids and parents having both high grain yield and resistance to grain mold, (ii) estimate the stability of the response of hybrids and parents to grain mold and grain yield, and (iii) identify genotypes with a broad or specific adaptation to the tested sites.

2. Materials and Methods

2.1. Plant Materials and Testing Sites. The 22 F_1 hybrids of the present investigation were obtained from the crosses between each of the 11 white-grained tannin-free photoinensitive lines Darou, Dorado, 93B1057, F2-20, Faourou, Macia, Nganda, Nguinthe, Sureño, CE151-262, CE196-7-2 used as male parents, with each of the two cytoplasmic male sterile (CMS) female parents CE310-31A and AVG-1, according to the line × tester mating design developed by Kempthorne [32]. The 22 F_1 hybrids, their 13 parental lines (11 male lines and 2 female B-lines), and one grain mold tolerant hybrid check (CE310-31A × 75-1) were evaluated during the rainy seasons in 2015 and 2016 under natural grain mold infestation at Bambey, Darou-Pakathiar, and Sinthiou Maleme research stations as shown in Figure 1.

In these three locations, the trials were laid out in a sandy-clay soil characterized by sand (86–90%), silt loam (2–5%), and clay (6–10%) [33]. The climatic conditions during the two years of evaluation are given in Table 1.

2.2. Experimental Design and Field Management. The 36 sorghum genotypes were arranged in a 6×6 lattice design with three replications at each location. Each plot comprised of two rows of 5.2 m length with interrow spacing of 80 cm and intrarow spacing of 40 cm. Fifteen days after planting, all rows were thinned to three plants per hill giving a population density of about 87740 plants per hectare. Standard cultural practices recommended for sorghum production were adopted across all locations. Before planting, 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 next at the booting stage.

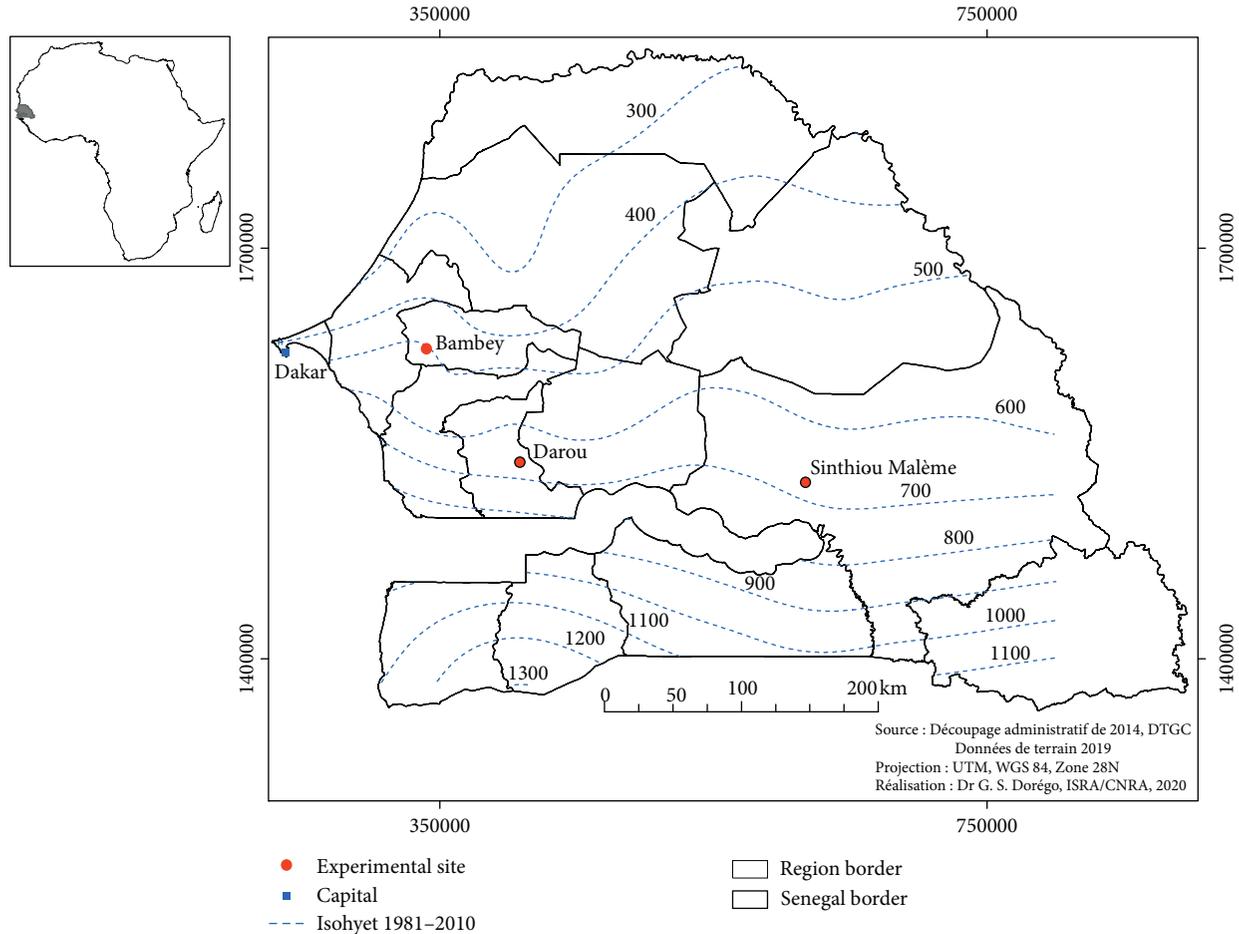


FIGURE 1: Map of Senegal showing the experimental locations, Darou = Darou-Pakathiar.

TABLE 1: Precipitation, temperature, and relative humidity for Bambey, Darou, and Sinthiou Maleme during the growing seasons between July and October in 2015 and 2016.

Location	Year	Precipitation		Temperature (°C)			Relative humidity (%)		
		mm	Days	Min.	Max.	Mean	Min.	Max.	Mean
Bambey	2015	689.4	35	24.3	34.4	29.3	54.8	97.7	76.0
	2016	363.9	36	24.1	35.5	29.8	53.9	97.0	75.4
Darou	2015	685.3	46	22.2	33.4	27.8	59.7	95.0	77.0
	2016	894.4	20	22.8	34.4	28.6	52.5	94.0	74.0
Sinthiou Maleme	2015	493.0	52	22.3	34.5	28.5	49.8	97.3	74.5
	2016	525.5	43	22.5	35.3	28.9	47.9	94.0	73.5

Min., minimum; Max., maximum; mm, millimeter; °C, degree Celsius; %, percentage.

2.3. Data Collection. At each location, climatic conditions such as temperature, relative humidity, and rainfall were recorded daily. Agromorphological parameters and observations recorded include number of days from planting to 50% flowering (TFlo), plant height (PH) as the length of the plant from the soil to the tip of the panicle, panicle length (LPan), thousand-grain weight (TGW), grain yield (GYield), and panicle grain mold rating score (PGMR). Grain mold score was recorded at physiological maturity on panicles before harvesting, using the 1-5 scale as described by Thakur et al. [34], where 1 = 0 to <1% of mold visible on the panicle; 2 = 1-10% of the panicle surface

covered by mold; 3 = 11-25% of the panicle surface molded; 4 = 26-50% of the panicle surface molded; and 5 = mold infestation with more than 50% of the surface molded.

2.4. Statistical Analysis. Data of each location were first subjected to analysis of variance using the command PROC GLM procedure implemented in SAS 9.4 (SAS Institute Inc., 2013). Due to the homogeneity of error variance, the combined analysis across environments was performed using the following linear additive model:

$$Z_{ijklm} = \mu + Y_i + S_j + YS_{ij} + R_k + B_l + G_m + B(YS)_{ijkl} + (YG)_{im} + (SG)_{jm} + (YSG)_{ijk} + \varepsilon_{ijklm}, \quad (1)$$

where Z_{ijklm} is the phenotypic observation of genotype m in replicate k of block l of site j and year i ; μ is the grand mean; Y_i is the effect of year i ; S_j is the effect of site j ; R_k is the effect of replication in site j and year i ; G_m is the effect of genotype m ; $B(YS)_{ijkl}$ is the effect of block l nested with replication k in site j and year i ; $(YS)_{ij}$ is the interaction between year i and site j ; $(YG)_{im}$ is the interaction between year i and genotype m ; $(SG)_{jm}$ is the interaction between site j and genotype m ; $(YSG)_{ijk}$ is the interaction between year i , location j , and genotype m , and ε_{ijklm} is the residual effect.

Broad-sense heritability (H^2) based on combined results across sites and years were estimated by the following formula:

$$H^2 = \frac{\sigma_g^2}{(\sigma_g^2 + \sigma_{gs}^2/s + \sigma_{gy}^2/y + \sigma_{gsy}^2/sy + \sigma_e^2/rsy)}, \quad (2)$$

where σ_g^2 is the genotypic variance; σ_{gs}^2 is the variance of genotype \times site interaction; σ_{gy}^2 is the variance of genotype \times year interaction; σ_{gsy}^2 is the variance of genotype \times site \times year interaction; σ_e^2 is the error variance; r is the number of replicates; y is the number of years; and s is the number of sites.

The presence of significant $G \times E$ interactions ($P < 0.001$) for grain yield (GYield) and panicle grain mold rating score was further analyzed by testing for $G \times E$ components using the GGE biplot analysis. Each location-year combination was considered as an environment. The GGE biplot model was constructed using the formula suggested by Yan [28].

$$Y_{ij} - \bar{Y}_j = \lambda_1 \varepsilon_{i1} \eta_{j1} + \lambda_2 \varepsilon_{i2} \eta_{j2} + \varepsilon_{ij}, \quad (3)$$

where Y_{ij} is the mean performance of genotype i in environment j ; \bar{Y}_j is the overall mean yield over all genotypes in environment j ; λ_1 and λ_2 are the singular value of axis₁ and axis₂, respectively; ε_{i1} and ε_{i2} are the axis₁ and axis₂ scores, respectively, for genotype i ; η_{j1} and η_{j2} are the axis₁ and axis₂ scores, respectively, for environment j ; and ε_{ij} is the residual of the model associated with genotype i in environment j . The multi-environment data were analyzed based on a tester-centered ($G + GE$) without any scaling (scaling = 0). It is a row metric preserving GGE biplot, genotype focused, using singular value partitioning (SVP = 1) for visualizing mean versus stability of genotypes. Environment-focused single value partitioning (SVP = 2) was employed for location evaluation, and “which-won-where” option was used to identify which genotype was the winner in a given set of environments. GGE biplot analysis was performed using GGEbiplotGUI package [35] implemented in R statistical software version 3.6.1 [36].

3. Results

3.1. Analysis of Variance and Descriptive Analysis. The combined analysis of variance (ANOVA) across sites and years showed that the mean squares for site, year, and

site \times year interaction were highly significant ($P < 0.001$) for all traits except for panicle length (Table 2). Genotype, genotype by year, and genotype by site interaction mean squares exhibited highly significant differences ($P < 0.001$) for all six measured traits across sites and years. Highly significant genotype \times year \times site interaction mean squares ($P < 0.001$) were also observed for grain yield (GYield), panicle grain mold rating score (PGMR), and all other measured traits.

3.2. Performance of Genotypes for the Six Measured Traits across the Tested Environments. Time from planting to flowering (TFlo) of parental lines and their hybrids varied from 61 days (HB1) to 78 days (P27) (Table 3). Hybrids were usually earlier than their parental lines. Among hybrids, the hybrids with the female parent CE310-31A were on average earlier than the ones with AVG-1. The average plant height of the genotypes was 202.2 cm with HB17 being the tallest hybrid combination (281.7 cm), and T36 (check), the shorter genotype (151.3 cm) followed by P30 and P27. Panicle length (LPan) ranged from 19.5 cm (P28) to 29.8 cm (HB12) with an average length of 26.3 cm. The thousand-grain weight (TGW) varied from 13.3 g to 19.0 g. The hybrid HB2 had the highest TGW, followed by HB5 and P24.

Hybrids were generally more productive than their parental lines. HB16 (3,516.2 kg ha⁻¹) recorded the highest grain yield followed by HB5 (2,983.9 kg ha⁻¹), HB21 (2,934.9 kg ha⁻¹), HB18 (2,855.0 kg ha⁻¹), and HB7 (2,822.3 kg ha⁻¹). Among the hybrids, HB22 (1,744.9 kg ha⁻¹) was the poorest yielding hybrid with a yield slightly superior to that of the check T36 (1,239.0 kg ha⁻¹).

For the panicle grain mold rating score (PGMR), the parental line P27 was the most resistant genotype (2.4 score), followed by the hybrids HB16, HB22, HB21, and HB6 in that order with a PGMR score inferior or equal to 3.

Broad-sense heritability was high for all six studied traits except for PGMR estimated at 0.26 (Table 3). PH was the most heritable trait (0.97), followed by TFlo (0.95). Heritability was also high for LPan (0.85), GYield (0.82), and thousand-grain weight (0.77).

3.3. GGE Biplot Analysis. The GGE biplot analysis was carried out by considering high yielding genotypes with PGMR score between 1 and 3.4 (Table 3). Thus, 22 genotypes consisting of 15 hybrids, 6 parental inbred lines, and the check were subjected to the GGE biplot analysis for GYield and PGMR.

3.4. Mean Performance and Stability of Genotypes across Environments. Figure 2 shows the average-environment coordination (AEC) view of the GGE biplot. Together, axis₁ (69.39%) and axis₂ (16.45%) explained 85.84% of GGE sum of squares for grain yield. The single-arrowed line (AEC abscissa), which connects to the biplot origin, points to a

TABLE 2: Mean squares ANOVA for six measured traits of sorghum parental lines and their hybrids evaluated at three sites in Senegal in 2015 and 2016.

Source	Df	TFlo	PH	LPAN	TGW	GYield	PGMR
Site	2	5621***	76264***	611.6***	1050***	4603737***	48.19***
Year	1	6026***	11213***	0.7 ^{ns}	120.2***	775988*	18.57***
Year (site)	2	7255***	178788***	492.9***	1952.1***	78572254***	20.48***
Rep	2	71***	3441**	1.4 ^{ns}	6.4 ^{ns}	402340 ^{ns}	0.91**
Block	5	23*	1451 ^{ns}	6.2 ^{ns}	5.4 ^{ns}	48824 ^{ns}	0.26 ^{ns}
Block (site × year)	10	13 ^{ns}	1294*	4.3 ^{ns}	2.7 ^{ns}	252333 ^{ns}	0.17 ^{ns}
Genotype	35	264***	20949***	118.4***	33.8***	5505741***	1.76***
Genotype × year	35	17***	1304***	14.0***	11.5***	1085452***	1.41***
Genotype × site	70	35***	1794***	15.0***	6.4***	828071***	0.46***
Genotype × year × site	70	38***	2525***	11.3***	10.0***	922533***	0.56***
Residuals	400	8	553	5.1	2.5	169149	0.16

ns, $P > 0.05$; * $P < 0.05$; ** $P < 0.01$; *** $P < 0.001$; TFlo, time to 50% flowering; PH, plant height; LPan, panicle length; TGW, thousand-grain weight; GYield, grain yield; PGMR, panicle grain mold rating score.

higher mean across environments for the trait analyzed [35, 37], which is here the grain yield. Thus, HB16 had the highest mean yield, followed by HB5, HB21, HB18, HB7, HB13, HB19, HB20, HB6, and HB11, whereas T36, P33, P27, P30, P23, HB22, HB14, P32, HB17, P25, and P22 recorded the lowest mean yield. The vertical axis (or AEC ordinate), which is perpendicular to the AEC abscissa and passes through the origin, represents the stability of genotypes in either direction. The shorter the absolute length of the projection of a genotype, the more stable it is [35]. Thus, HB19 was the most stable genotype for grain yield, followed by HB5, HB20, and HB18.

For panicle grain mold tolerance, Figure 3 shows the biplot presenting the mean performance and stability of genotypes across environments. As described for grain yield, the best performing genotype regarding grain mold tolerance was P27, followed by P29, HB16, HB6, HB21, P32, and HB17. Moreover, hybrid HB12 was the most stable, followed by HB16, HB20, and HB7. The parent P29 was the least stable for this trait.

3.5. Which-Won-Where Pattern Analysis. This approach locates the winning genotypes for each environment on the vertex of the polygon. The hybrids HB7, HB16, HB21, and HB13 were the winning genotypes for grain yield in the megaenvironment constituted by Bambey_2015, Darou_2015, Sinthiou_2015, and Bambey_2016 (Figure 4). During the rainy season of 2016, the parental line P29 was the vertex genotype at Darou, while no winning genotype was associated with Sinthiou_16. On the other hand, the hybrid HB12, parental line P23, and the check T36 were not associated with any of the test environments where the materials were evaluated.

The which-won-where pattern for grain mold tolerance is shown in Figure 5. The hybrid HB6 was the winning genotype for the megaenvironment constituted by Darou_16. The parental line P27 was the winning genotype for the megaenvironment constituted by Bambey_15, Bambey_16, Sinthiou_15, and Sinthiou_16. The parental line P29 was more associated with Darou_15. However, the genotypes HB5, HB7, and P33 were not associated with any tested environment.

3.6. Ranking Genotypes Relative to the Ideal Genotype. Ranking of the tolerant sorghum parental lines and hybrids for grain yield based on both mean and stability with regard to an “ideal” genotype is shown in Figure 6. The center of the concentric circle is where an “ideal” genotype should be. Its projection on the AEC x -axis was designed to be equal to the longest vector of all cultivars, and its projection on the AEC y -axis was obviously zero, meaning that it is absolutely stable [28, 35]. An “ideal” genotype should have the highest mean performance and be absolutely stable [38]. Thus, genotype HB16 was the best performing and more stable genotype followed by HB18, HB5, HB7, and HB21 for grain yield across the tested environments. However, the check T36 was the least yielding and unstable genotype across environments.

As for panicle grain mold tolerance, the parent P27 was the best performing and stable genotype, followed by HB16, HB21, P32, HB6, HB17, and P29. Whereas the hybrid HB7 was the least performing and stable genotype (Figure 7).

4. Discussion

The combined analysis of variance showed that the genotype effect was highly significant ($P < 0.001$) for all measured traits, suggesting the presence of genetic variability among the parental lines and their hybrids for the six measured traits. The highly significant effect of $G \times E$ interaction observed for both grain yield and grain mold score, which indicates that effect of environment, significantly determined both grain yield and genotype response to grain mold. Significant $G \times E$ interaction in multienvironmental trials has been previously reported in sorghum for both grain yield [29, 31, 39, 40] and grain mold score [9, 16, 20, 21]. Moreover, substantial differences in genotypic responses of the hybrids and their parental lines were observed between sites and between years on the same site. This differential response could be explained by differences in soil texture across sites [33], climatic conditions (temperature, relative humidity, and rainfall patterns) [19], and sucking insects [41], and the diversity of fungal species causing grain mold disease [11, 14, 42, 43]. A report in Senegal about forty years ago reported the fungi *Curvularia lunata* and *Fusarium spp*

TABLE 3: Mean per se performance of parental lines and their hybrids across the test environments.

Genotypes	Code	TFlo	PH	LPan	TGW	GYield	PGMR
CE 310-31 A × 93 B1057	HB1	61.3	239.3	28.6	17.7	2167.3	3.5
CE 310-31A × CE151-262	HB2	62.6	189.9	29.0	19.0	2249.0	3.8
CE 310-31A × CE196-7-2	HB3	65.1	253.3	25.7	15.6	2290.6	3.5
CE 310-31A × Darou	HB4	65.3	208.1	27.9	16.8	2370.6	3.5
CE 310-31A × Dorado	HB5	65.6	201.1	28.7	18.2	2983.9	3.3
CE 310-31A × F2-20	HB6	65.8	272.3	23.9	15.9	2414.7	3.0
CE 310-31A × Faourou	HB7	63.8	215.6	28.6	16.8	2822.3	3.4
CE 310-31A × Macia	HB8	63.1	204.8	28.6	17.1	2307.4	3.5
CE 310-31A × Nganda	HB9	64.6	208.1	28.9	16.7	2571.6	3.5
CE 310-31A × Nguinthe	HB10	64.2	221.5	28.8	17.2	2437.3	3.5
CE 310-31A × Sureño	HB11	68.8	235.8	25.5	16.5	2217.4	3.2
AVG-1 x 93B1057	HB12	68.2	194.6	29.8	15.5	2143.4	3.4
AVG-1 x CE151-262	HB13	65.3	188.3	28.9	16.3	2569.9	3.2
AVG-1 x CE196-7-2	HB14	69.9	273.4	26.2	14.0	1917.9	3.3
AVG-1 x Darou	HB15	70.7	203.4	29.0	15.7	2683.4	3.5
AVG-1 x Dorado	HB16	69.0	203.4	27.8	17.1	3516.2	2.8
AVG-1 x F2-20	HB17	70.7	281.7	23.7	14.7	1961.4	3.1
AVG-1 x Faourou	HB18	67.9	203.8	29.3	16.0	2855.0	3.2
AVG-1 x Macia	HB19	70.4	197.2	27.3	16.9	2456.0	3.2
AVG-1 x Nganda	HB20	68.6	203.6	28.7	14.5	2439.6	3.3
AVG-1 x Nguinthe	HB21	69.6	198.4	27.3	16.3	2934.9	3.0
AVG-1 x Sureño	HB22	70.6	243.8	24.1	13.4	1744.9	2.9
93B1057	P23	67.4	182.1	27.1	16.4	1755.2	3.1
CE151-262	P24	67.3	155.7	25.7	18.0	1975.7	3.6
CE196-7-2	P25	69.2	199.7	21.2	14.5	1916.7	3.4
Darou	P26	71.8	194.8	26.5	15.7	2072.3	3.6
Dorado	P27	77.8	152.8	23.3	16.4	1726.7	2.4
F2-20	P28	72.8	193.7	19.5	14.8	1522.9	3.6
Faourou	P29	72.8	171.9	23.8	16.0	2196.7	3.3
Macia	P30	72.4	152.7	23.5	15.1	1716.3	3.3
Nganda	P31	70.4	185.9	26.8	15.6	1608.6	3.7
Nguinthe	P32	70.5	170.2	24.9	15.6	1952.7	3.3
Sureño	P33	74.4	213.6	22.4	13.4	1605.0	3.0
CE 310-31B	P34	62.7	154.8	23.7	14.6	740.1	4.2
BVG-1	P35	71.9	160.5	25.8	13.3	1259.9	3.7
CE310-31A × 75-1	T36	73.8	151.3	26.5	14.7	1239.0	3.4
Mean		68.5	202.2	26.3	15.9	2148.4	3.3
Min.		61.3	151.3	19.5	13.3	740.1	2.4
Max.		77.8	281.7	29.8	19.0	3516.0	4.2
CV (%)		4.1	11.6	8.6	10.0	19.1	11.9
HSD		3.6	30.3	2.9	2.1	530.4	0.5
Heritability (broad sense)		0.95	0.97	0.85	0.77	0.82	0.26

TFlo, time to 50% flowering; PH, plant height; LPan, panicle length; TGW, thousand-grain weight; GYield, grain yield; PGMR, panicle grain mold rating score; Min., minimum; Max., maximum; CV, coefficient of variation; HSD, honest significant difference.

(*F. moniliforme*, *F. equiseti*, *F. longipes*, *F. flocciferum*, and *F. sporotrichioides*) being most frequently observed [14]. The high temperature (33.4–35.5°C) and humidity (94.0–97.7%) that prevailed during the growing season in the study areas in Senegal explain the rapid proliferation of the fungi. This also corroborates with the report of Tonapi et al. [19] in India, which reports a significant increase of fungal sporulation and grain mold severity with increasing incubation temperature (25–28°C) and relative humidity (95–98%). Moreover, the rainfall at Bambey decreased by 50% in 2016 compared to 2015, while at Darou, it increased by 209 mm. At Sinthiou, it increased slightly by 32 mm. In parallel, the degree of panicle infestation decreased slightly in Bambey by 6%, increased by 10% in Darou, and decreased by 25% in

Sinthiou Maleme. The decrease of the rate of mold infestation in Sinthiou Maleme could be due to the reduction in the relative humidity, since the mold infestation is controlled by the set made up of hygrometry, temperature, and rainfall. Otherwise, our previous study reported that the grain mold pressure in the studied sites decreased following a South-North gradient, with Sinthiou Maleme having the highest pressure and Bambey the lowest pressure [44]. The high influence of environments on the expression of grain mold reduces the accuracy for estimating disease resistance and selecting the appropriate germplasm [21].

Furthermore, this study showed that the broad-sense heritability estimates for agronomic traits such as time to 50% flowering, plant height, panicle length, thousand-grain

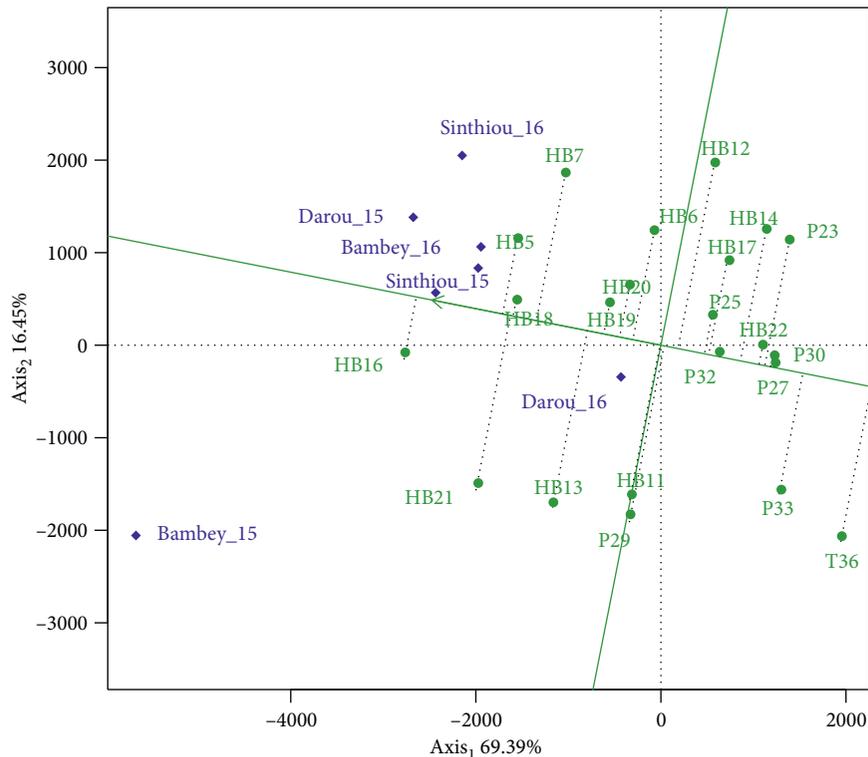


FIGURE 2: Average-environment coordination (AEC) view of sorghum hybrids and their parents for mean grain yield performance and stability based on GGE biplot analysis. The green single-headed horizontal line represents the AEC abscissa, and the green vertical line represents the AEC ordinate. The direction of AEC abscissa arrowhead indicates higher yield. The vertical projections on the AEC abscissa indicate stability of genotypes in either direction. Greater the projection, higher is the instability. Genotype and environment labels are represented in green and blue, respectively.

weight, and grain yield were high. This suggests that these traits were predominantly under genetic control, and their improvement can be realized through phenotypic selection. Similar results have been found by Phuke et al. [31]. However, in this study, the heritability estimate for panicle grain mold score (PGMR) at physiological maturity was low (0.26), as also observed by Audilakshmi et al. [16]. This denotes the strong influence of environment on the expression of this disease. However, a relatively high heritability estimate of 86% for grain mold has been reported by Rodríguez-Herrera et al. [21].

The parental lines P27 and P33 were identified as the most tolerant genotypes for grain mold disease. Although both varieties have the longest time to flowering, their resistance to grain mold disease has been previously reported by several studies carried out in Senegal and in other countries [43, 45]. Worldwide, the popularity of P33 was due to its resistance to lodging, grain mold, and most of the major foliar diseases such as grey leaf spot (*Cercospora sorghi*), zonate leaf spot (*Gloeocercospora sorghi*), rust (*Puccinia purpurea*), leaf blight (*Exserohilum turcicum*), anthracnose (*Colletotrichum sublineola*), and downy mildew (*Peronosclerospora sorghi*) [45, 46]. Additionally, in a recent study, Diatta [44] reported that the variety P27 has a good general combining ability for grain yield and grain mold resistance. Therefore, these varieties could be used by breeders to improve the resistance of susceptible elite

genotypes to grain mold disease. This study also identified HB16 and HB21 as the best hybrids combining both high grain yield and tolerance to grain mold disease. In addition to their free-tannin and white-grained status, these two hybrids outperformed the best yielding parental line P29 ($2,196.7 \text{ kg ha}^{-1}$) with a yield advantages ranging 10–60% and confirmed the yield superiority of the hybrids over their parental lines [6, 7, 47, 48].

Which-won-where analysis identifies the best genotype for a given megaenvironment and allows the breeder to recommend genotypes for a particular environment [40]. A megaenvironment could be defined as a group of sites that consistently share the same best cultivar (s) [49]. In this study, HB16 was identified as the most adapted hybrid combination for Bambey area. On the other hand, Darou_2015 and Darou_2016 as well as Sinthiou_2015 and Sinthiou_2016 environments did not fall into the same megaenvironment. This could probably be due to variability in weather conditions and rainy season patterns in these test sites from year to year. Such situations limit breeders' ability to recommend the most adapted cultivars to a given environment. Such situation demands increase in the number of years and sites of evaluation to ensure accurate decision making.

Furthermore, it can be said that one of the most exciting applications of GGE biplot methodology is the ranking of genotypes with reference to an "ideal" genotype. In this

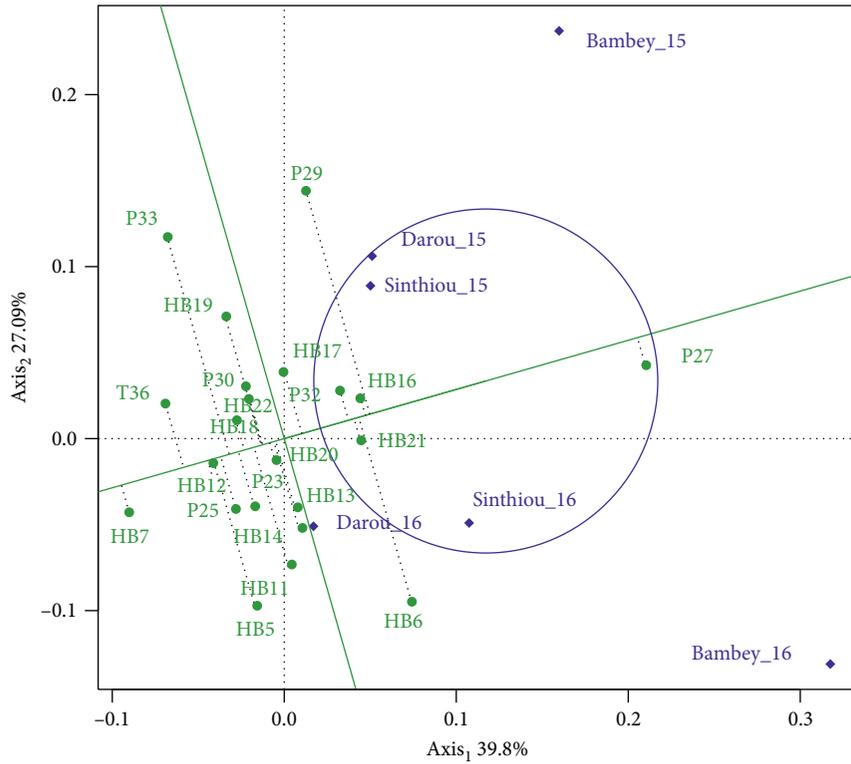


FIGURE 3: Average-environment coordination (AEC) view of sorghum hybrids and their parents for grain mold resistance performance and stability based on GGE biplot analysis. The green single-headed horizontal line represents the AEC abscissa, and the green vertical line represents the AEC ordinate. The direction of AEC abscissa arrowhead indicates higher yield. The vertical projections on the AEC abscissa indicate the stability of genotypes in either direction. Greater the projection, higher is the instability. Green and blue labels stand for genotypes and environments, respectively.

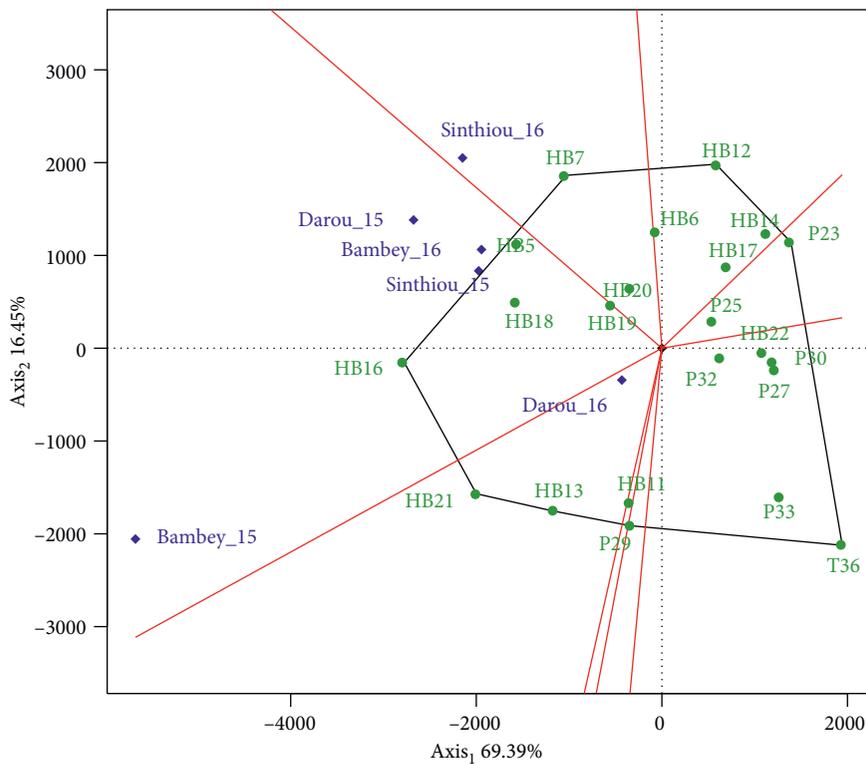


FIGURE 4: "Which-won-where" view of best grain mold resistant inbred lines and hybrid combinations based on grain yield. Red lines represent the megaenvironments; hybrids and inbred lines labels are written in green; locations labels are written in blue; dotted lines represent the axes.

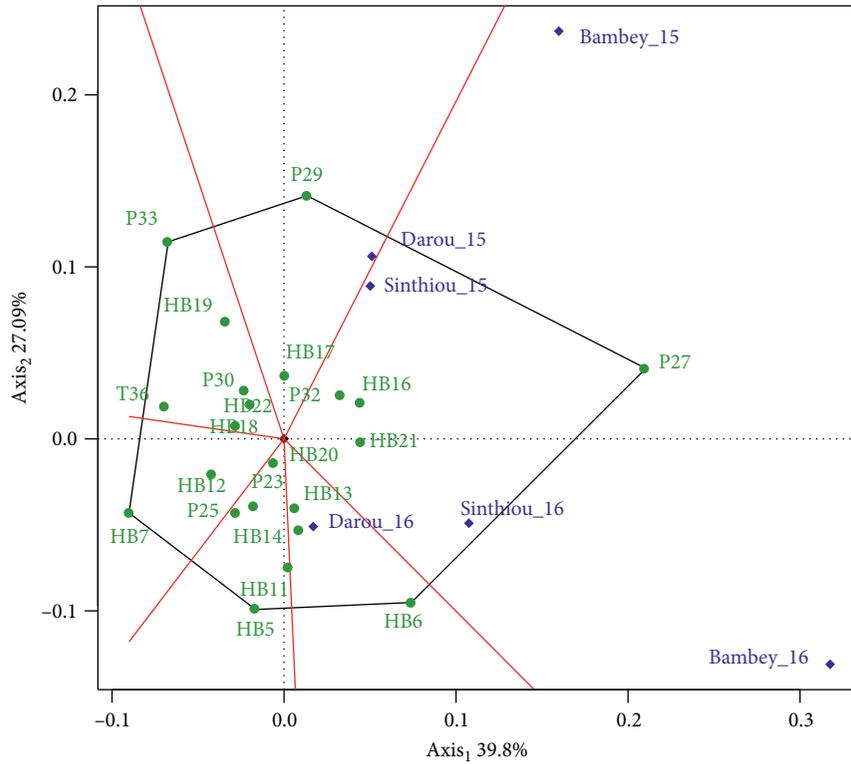


FIGURE 5: “Which-won-where” view of best grain mold tolerant inbred lines and hybrid combinations based on panicle grain mold resistance rating score. Red lines represent the megaenvironments; hybrids and inbred lines labels are written in green; locations labels are written in blue; dotted lines represent the axes.

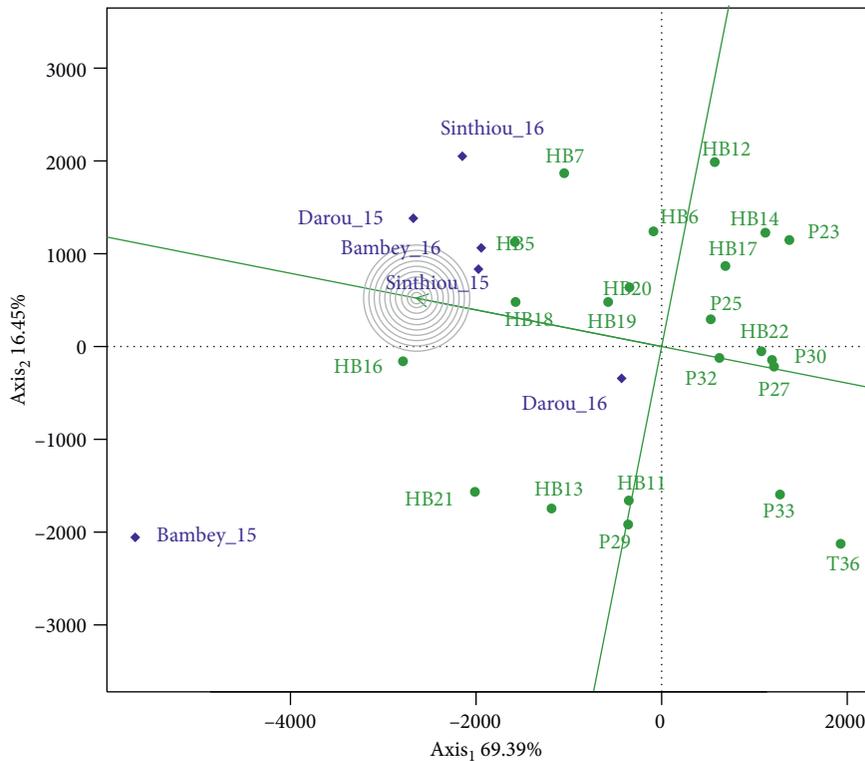


FIGURE 6: Ranking genotypes for grain yield based on both mean performance and stability with reference to an “ideal” genotype. The green single-headed horizontal line represents the AEC abscissa, and the green vertical line represents the AEC ordinate. The AEC abscissa arrowhead indicates where an “ideal” genotype should be. Its projection on the AEA was designed to be equal to the longest vector of all genotypes, and its projection on the AEC was obviously zero, meaning that it is absolutely stable. Genotypes located closer to the ideal genotype are more desirable than others. The concentric circles help to visualize the position of the genotype with respect to ideal genotype. Genotype and environment labels are represented in green and blue, respectively.

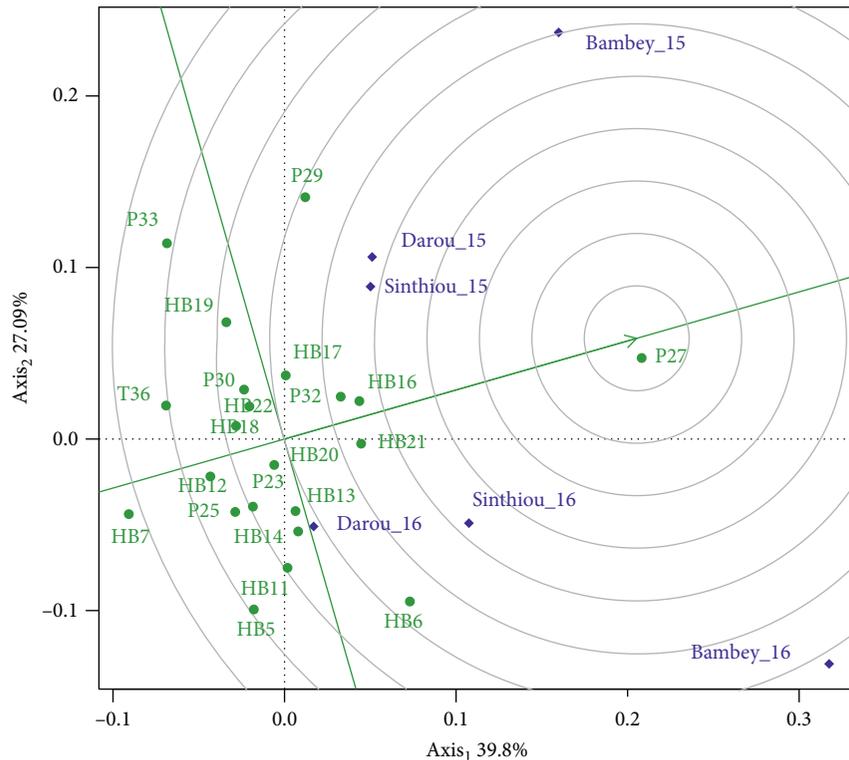


FIGURE 7: Ranking genotypes for grain mold resistance based on both mean performance and stability with reference to an “ideal” genotype. The green single-headed horizontal line represents the AEC abscissa, and the green vertical line represents the AEC ordinate. The AEC abscissa arrowhead indicates where an “ideal” genotype should be. Its projection on the AEA was designed to be equal to the longest vector of all genotypes, and its projection on the AEC was obviously zero, meaning that it is absolutely stable. Genotypes located closer to the ideal genotype are more desirable than others. The concentric circles help to visualize the position of the genotype with respect to ideal genotype. Genotype and environment labels are represented in green and blue, respectively.

study, the ranking of varieties with regard to the “ideal” genotype identified HB16, HB18, and HB5 as the best hybrids combining both mean performance and stability for grain yield. The stability and adaptability of varieties are important along with higher mean performance in determining the success of varieties [27]. In Senegal where the average sorghum grain yield in farmers’ fields is still very low (around $1,000 \text{ kg ha}^{-1}$), the promotion of stable high yielding and grain mold tolerant hybrids will significantly contribute to increase in sorghum grain production per unit of area, increase the price, and therefore contribute to eradicate hunger from rural areas.

5. Conclusion

This study confirmed the resistant status of the varieties P27 and P33 to sorghum grain mold disease in Senegal. It identified the hybrids HB16 and HB21 as the best combinations for high grain yield performance, stability, and tolerance to grain mold disease. These hybrids outperformed the best yielding inbred line P29 with grain yield advantages ranging 10–60%. For environment-specific adaptation, this study showed high intrasite variability in the response of hybrids at Darou and Sinthiou Maleme. The study identified promising hybrids that could positively boost sorghum production per unit of area in farmers’ fields in Senegal.

Data Availability

The data used to support the findings of this study are available from the corresponding author upon request.

Conflicts of Interest

The authors declare that they have no conflicts of interest.

Authors’ Contributions

CD, NC, EYD, and SKO conceived and designed the study; CD, OA, and MPS performed the research; CD and TKT analyzed the data and wrote the manuscript; DKD, JMF, and EDH contributed to the results interpretation and provided a critical review on the final manuscript. All authors read and approved the final version of the manuscript.

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