Development of sorghum hybrids for stable yield and resistance to grain mold for the Center and South-East of Senegal

Cyril Diatta [a,b,c], Thierry Klanvi Tovignan [a,b,d,*], Hubert Adoukonou-Sagbadja [b], Ousmane Aidara [c], Yagouba Diao [c], Mame Penda Sarr [c], Beatrice Elohor Ifie [d], Samuel Kwame Offei [d], Eric Yirenkyi Danquah [d], Ndiaga Cisse [a]

[a] Centre d'Etudes Régional pour l'Amélioration de l'Adaptation à la Sécheresse (CERAAS), BP 3320, Route de Khombole, Thiès, Senegal
[b] Département de Génétique et Biotechnologie, Faculté des Sciences et Techniques (FAST), Université d'Abomey-Calavi (UAC), BP 1947, Cotonou, Benin
[c] Centre National de Recherches Agronomiques (CNRA), BP 53, Bambey, Senegal
[d] West Africa Centre for Crop Improvement (WACCI), University of Ghana, BMP 30, Legon, Accra, Ghana

ABSTRACT

Panicle mold infestation is reported to cause 30–100% yield loss in sorghum. Therefore, breeding for mold resistance becomes a necessity. Due to difficulties in predicting genotype by environment interactions (GxE), multi-location tests are required in the breeding process to identify high-yielding and stable genotypes across environments. The present study aimed at assessing the performance and stability for yield and resistance to grain mold of five local sorghum hybrids evaluated over five years across four locations in the Center and South-East regions of Senegal. The combined ANOVA showed a strong effect of year, genotype and location on the days to anthesis, plant height, grain yield components and panicle grain mold rating score. The GxE interaction was significant for grain yield but not for panicle mold infestation. Year x location explained 25% of total variation of grain yield while year and location explained 22% and 19% respectively. With regard to panicle grain mold infestation, year explained 32% of total variation followed by year by location (29%), genotype (7%) and location (6%). Although year and location better explained the variation for the traits, broad-sense heritability was high, indicating a possibility to improve these traits through selection. For most of the traits, the hybrids had higher performance compared to the parental lines used as check, showing an expression of heterosis. The GGE biplot approach was used to identity hybrids with high performance and stability. Hence, hybrid G4 followed by G2 and G3, were the best in terms of yield performance and stability. Moreover, location STM15 followed by DAR15 were the best closest to an ideal location. Overall, G5 was pointed out as the best hybrid combining grain yield and mold tolerance across years and locations. These results in addition to providing details on the performance and stability of the five sorghum hybrids helped to identify the best hybrids to be released and disseminated in the Center and South-East regions of Senegal.

1. Introduction

Sorghum is a staple food crop for many people living in arid and semi-arid areas mainly in West-Africa. In Senegal, sorghum grain is the base of many local dishes and has recently been valorized in the bakery industry by partial replacement, about 20–30%, of wheat flour in bread (Sambe et al., 2017). Sorghum stem and leaf biomass are mainly used for animal feeding. Sorghum contributes both to food and financial security for the farmers as it represents an important source of income generation (Chepng'etich et al., 2014).

Despite its important role, sorghum production is influenced by climate variability, which induces biotic and abiotic constraints, mainly drought stress and pest damage (Das et al., 2012; Tovignan et al., 2016a). Sorghum is affected by a diversity of fungal diseases. Teferi and Wubshet (2015) reported in the South Tigray region of Ethiopia, a high incidence (37–94%) of various fungal diseases including anthracnose, leaf blight, long smut, head and loose smuts, and downy mildew. Mold attack is one of the major constraints hindering sorghum cultivation. Grain mold is caused by a complex of fungi which cause a reduction of grain yield from 30 to 100% (Ashok Kumar et al., 2011) and a cash loss

equivalent to US \$130 million per annum as reported by ICRISAT (1992) cited by Rao et al. (2016). Grain mold attack often occurs in sorghum varieties that reach maturity before the end of the rainy season. High humidity and temperature favor mold proliferation on the panicle which results in a decrease of grain filling and grain size along with chalky endosperm (Ingole et al., 2018; Rao et al., 2016). In addition, mold infestation can make plants susceptible to several diseases; mainly those caused by the mycotoxins secreted by pathogenic fungi which not only reduce the economic value of harvested grain but are especially harmful to humans and animals (Audilakshmi et al., 2011).

Several management strategies such as fungicide application, chemotherapy, physical treatments and varietal resistance are applied to control mold infestation (Indira et al., 2006; Navi et al., 2002). In contrast to other methods, the use of resistant varieties to control mold appeared to be cost-effective, efficient and eco-friendly (Mofokeng et al., 2017). Varietal resistance to mold is conferred by some physical and chemical plant properties including grain hardness or corneous endosperm, loose panicle, increased glum coverage, glum color, pigmented testa, red pericarp, phenolic compound, high levels of condensed tannin, phenolic acids and flavan-4-ols (Audilakshmi et al., 2005, 1999; Bandyopadhyay et al., 2000; Esele et al., 1995, 1993; Little et al., 2012; Menkir et al., 1996; Sharma et al., 2010; Thakur et al., 2006; Thirumala Rao et al., 2012). However, most of these resistance traits such as pigmented testa and high tannin content are less desired in Senegal where red grain sorghum varieties are rarely used for human consumption. Hence, they are not appropriate to develop resistant sorghum varieties to mold in Senegal. There is a need to identify new sources of grain mold resistance based on desirable agronomic traits (Thakur et al., 2007). Research on grain-mold resistance has focused on mechanisms of resistance that are suitable for food and feed quality sorghums (Klein et al., 2001). For this purpose, sources of resistance in white-grained sorghum were investigated. These traits included hard corneous endosperm, thin pericarp and thick wax layer, fast grain feeling, large glume coverage, pigmented glumes and open panicle (Ambekar et al., 2011; Audilakshmi et al., 2005; Reddy et al., 2000). Many studies have been carried out to improve grain mold tolerance in sorghum. Ambekar et al. (2011) identified superior lines with high yield and resistance to grain mold from crosses involving elite grain mold susceptible lines with resistance lines, and subsequent selfing generations. Nonetheless, to reduce the delay of selection and reach high yielding, uniform and stable genotypes across environments, hybrid breeding is encouraged (Almeida Filho et al., 2014a; Gasura et al., 2015). Rao et al. (2016) studied 168 hybrids and their parents across four environments in India in order to identify the good combiners for a breeding program aimed at improving grain mold resistance. Similarly, Ingole et al. (2018) studied ten divergent parents and their forty-five F_1 hybrids in India with the aim to study the inheritance of some mold resistance traits and identify useful parents for an efficient breeding scheme. Moreover, Almeida Filho et al. (2014a) studied twenty-five sorghum hybrids in seven locations in Brazil and identified some hybrids combining adaptability and stability across locations. In Senegal, several reports of Senegalese Agricultural Research Institute have identified grain mold and long smut as the most important diseases on improved sorghum varieties (Louvel, 1984; Luce, 1988). Recently, Prom et al. (2014) assessed the vulnerability of selected breeding lines and hybrids from the United States in two locations in Senegal across two consecutive years using inoculation and bagging contrary to the present study where the panicle infestation was natural. The authors identified 4 hybrids (Partners NK6638, Asgrow A571, AN600 × RN610 and Pioneer 83G19) with resistance to grain mold.

The present study aims to assess the performance and stability of five newly developed sorghum hybrids for yield and resistance to grain mold in the Center and South-East of Senegal. The findings will inform the subsequent release and dissemination of the best performing hybrid varieties in the targeted areas in Senegal.

2. Material and methods

2.1. Plant material

The plant material was made up of five sorghum hybrids and their parental lines used as checks (Table 1). The hybrids were obtained from crosses between the parental inbred lines Nguinthe, Darou, Nganda, Faourou and Dorado used as males with the cytoplasmic male sterile (CMS) line AVG1 used as female. All the parental lines have compact panicle with white grain without a pigmented testa, a corneous endosperm and belong to the caudatum botanic race. Details on the characteristics of these parental lines are available in Senegalese Institute of Agricultural Research database (ISRA, 2012) and also in a regional database (CEDEAO-UEMOA-CILSS, 2016). Data was collected taking into account all the five parents. However, complete data over all locations could only be obtained for Nganda used to compare the performance of the hybrids.

2.2. Experimental conditions and design

The trials were conducted in four sites located in the Center and South-East of Senegal. In Sinthiou-Maleme and Darou-Pakathiar, the experiments were set up at the Senegalese Agricultural Research Institute (ISRA) stations. In Guirigara and Sinthiou-Damba, the experiments were set up in two farmers' fields. Geographic coordinates of these locations and year of evaluation by location are presented in Table 2.

The climatic conditions of the studied locations are also presented on Fig. 1. The meteorological data were only recorded for Sinthiou-Maleme and Darou-Pakathiar. However, the experimental sites in Guirigara and Sinthiou-Damba are close to Sinthiou-Maleme (<30 km) and could be assumed to have weather conditions similar to Sinthiou-Maleme. The climate of the experimental sites is Sudano-Sahelian characterized by a short rainy season ranging from June to October with mono-modal rainfall distribution that peaks in August. In Darou-Pakathiar, over the five years, the annual average for rainfall was 822 mm with a temperature of 29 °C and a relative humidity of 74% whereas in Sinthiou-Maleme, the average rainfall was 677 mm with a temperature of 30.2 °C and a relative humidity of 71.2%. The year 2015 had the most rainfall (1044.5 mm) in Darou-Pakathiar. In Darou-Pakathiar, the variability of temperature and relative humidity between years was about 0.5 °C and 4% while in Sinthiou-Maleme it was about 1 °C and 3% for temperature and relative humidity respectively.

The soil type across sites was tropical ferruginous. The soil texture was predominantly sandy (88.1–91.7%) with low clay (2.6–5.8%) and low silt (4.0–6.8%). The content of organic matter was low for all location sites. However, it was more important in Sinthiou-Damba (0.81%) and Guirigara (0.45%) than Darou-Pakathiar and Sinthiou-Maleme where it was about 0.07%. The nitrogen content was also low but was higher for Sinthiou-Damba (0.30‰) and Guirigara (0.15‰) compared to Darou-Pakathiar (0.05‰) and Sinthiou-Maleme (0.04‰). The pH was slightly acid (5.3–6.0) for all the sites.

The experimental design was a randomized complete block with

Table 1
Characteristics of the studied hybrids and their parental lines.

N°	Type	Pedigree/original name	Status
G1	hybrid	AVG1 x Nguinthe	test
G2	hybrid	AVG1 x Faourou	test
G3	hybrid	AVG1 x Nganda	test
G4	hybrid	AVG1 x Darou	test
G5	hybrid	AVG1 x Dorado	test
G6	parent	Nganda (ISRA-S-622A[a])	check
G7	parent	Darou (ISRA-S-622B[a])	check
G8	parent	Nguinthe (ISRA-S-621A[a])	check
G9	parent	Faourou (ISRA-S-621B[a])	check

[a] , name in ISRA database (ISRA, 2012).

Table 2
Geographic position of the studied locations and year of evaluation by location.

Location code	Location name	Position in Senegal	Altitude (m)	Coordinates		Year of evaluation
				Longitude	Latitude	
DAR	Darou-Pakathiar	Center	31	15°50'W	13°55' N	2012, 2014, 2015, 2016, 2017
STM	Sinthiou-Maleme	South-East	23	13°55' W	13°49' N	2012, 2014, 2015, 2016, 2017
GUI	Guirigara	South-East	18	13°54' W	13°49' N	2015, 2017
STD	Sinthiou-Damba	South-East	47	13°54' W	13°55' N	2015, 2017
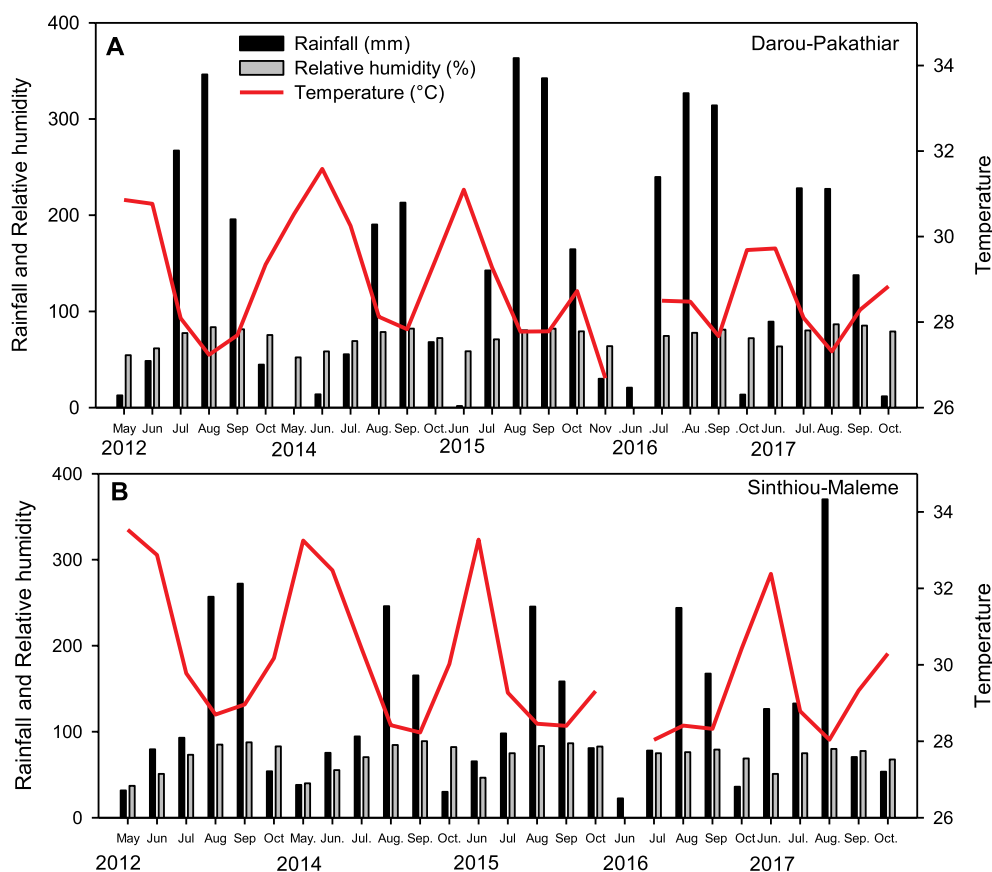
Fig. 1. Meteorological data (rainfall, relative humidity and temperature) of Darou-Pakathiar (A) and Sinthiou-Maleme (B) across the five studied years (2012, 2014, 2015, 2016, 2017).

three replications. Each experimental plot was composed of six rows of 5.2 m in length each, with 0.8 m between rows and 0.4 m between hills on each row. A walking space of 1.2 m was left between plots and the overall experimental area in each site was 510.4 m^2.

In the different sites, the trial was established at the beginning of the rainy season. Before sowing, the fertilizer NPK (15-15-15) was homogeneously applied on each plot at a dose of 150 kg per ha. The seeds were sown by placing four to ten seeds in each hill which was thinned to three plants two weeks after sowing. Urea (46% N) was supplied two weeks after sowing and during the vegetative phase (about 45 days after sowing) at a dose of 50 kg per ha. Weeding was done every two weeks.

2.3. Field monitoring and data collection

The seedling vigor (SV) was assessed two weeks after sowing using a visual scale of 1 (high plant vigor) to 5 (low plant vigor). Flowering time was recorded when 50% confluence was reached for each plot and by the same way the days from sowing to anthesis (TFLO) was estimated. At physiological maturity, plant height (PH) was measured on five plants per plot, from the soil surface to the top of the panicle. At physiological maturity, grain yield was estimated using the yield plot constituted by

the four central rows. Eleven hills were harvested per row. The harvested panicles were sun-dried for two weeks, and panicle dry weight (PDW) and grain dry weight (GDW) were measured. Grain yield (GY) was estimated by relating the grain production to the harvested area. Panicle grain mold score (PGMR) was rated in the field under natural infestation condition at physiological maturity. Disease assessment was done following Thakur et al. (2007) rating scale of 1–5 where a score of 1 means that no grain was molded while 5 means that more than 50% of the grains on the panicle were molded.

2.4. Data analysis

The data of the four locations and five years were pooled together for the analysis of variance (ANOVA) to test year (Y), location (L), genotype (G) and their interactions effects. To check assumptions for using ANOVA, primary statistical analyses were performed on the data using the Shapiro-Wilks test of normality and Bartlett's homogeneity test on residuals.

ANOVA was performed using the following model:

$$Z_{ijkl} = \mu + Y_i + L_j + G_k + B(YL)_{ijl} + (YL)_{ij} + (YG)_{ik} + (LG)_{jk} + (YLG)_{ijk}$$
$$+ \varepsilon_{ijkl}$$

(1)

with μ, the mean of the Z variable, Y_i, the random effect of the year i, L_j, the random effect of the location j, G_k, the fixed effect of the genotype k, YL_{ij}, the interaction between year i and location j, YG_{ik}, the interaction between year i and genotype k, LG_{jk}, the interaction between location j and genotype k, $B(YL)_{ijl}$, interaction effect between the bloc l within year i and location j, YLG_{ijk}, the interaction between year i, location j and genotype k, and $\mathcal{E}_{ijkl}$, the error term.

LSD test was performed for the mean comparison. Pearson correlations were estimated based on genotypes mean of the pooled data to evaluate the relationships between studied traits. All these analyses were performed using R v 3.5.1 (http://www.R-project.org/; R Core Team, 2018).

Broad-sense heritability (H^2bs) was calculated using the equation formulated by Allard (1960), which is given as follows:

- For one site:

$$H^2bs = \frac{\sigma_g^2}{\left(\sigma_g^2 + \frac{\sigma_e^2}{r}\right)} \text{ With } \partial^2 g = \frac{MS_g - MS_e}{r} \text{ and } \partial^2 e = MS_e$$

(2)

where $\partial^2 e$ = genotypic variance; $\partial^2 e$ = environmental variance; r = number of replications; *MSg* and *MSe* the genotypic and residual means squares respectively.

- For multiple years and multiple sites

$$H^2bs = \frac{\sigma_g^2}{\left(\sigma_g^2 + \frac{\sigma_{gl}^2}{l} + \frac{\sigma_{gy}^2}{y} + \frac{\sigma_{gly}^2}{ly} + \frac{\sigma_e^2}{rly}\right)}$$

(3)

with

$$\sigma_g^2 = \frac{MS_g - MS_{gl} - MS_{GY} + MS_{GLY}}{rly}$$

$$\sigma_{gl}^2 = \frac{MS_{gl} - MS_{gly}}{ry}$$

$$\sigma_{gy}^2 = \frac{MS_{gy} - MS_{gly}}{rl}$$

$$\sigma_{gly}^2 = \frac{MS_{gyl} - MS_e}{r}$$

$\sigma^2 g$ = genotypic variance, $\sigma^2 gl$ = variance of genotype x location (GxL) interaction, $\sigma^2 gy$ = variance of genotype x year (GxY) interaction, $\sigma^2 gly$ = variance of genotype x location x year (GxLxY) interaction, $\sigma^2 e$ = Error variance, l = number of locations, y = number of years, r = number of replications.

According to Robinson et al. (1949), the broad-sense heritability is categorized as low (0–0.3), moderate (0.3–0.6) and high (≥0.6).

GGE biplot analysis was used to decipher the genotype by environment interactions in order to identify ideal sorghum hybrids and suitable locations regarding grain yield and mold tolerance. For that, GGEBi-plotGUI package (Frutos-Bernal and Galindo, 2012) in R v 3.5.1 was used following the methods described by Yan and Tinker (2006). Data were tester-centered (G + GE) and scaled with the standard deviation of locations and the plots were drawn using column-preserving.

3. Results

3.1. Analysis of variance, mean performance and heritability

3.1.1. Mean performance and combined analysis of variance for the studied traits

The analysis of variance and means for plant vigor, phenology, morphology, grain production and panicle mold score is presented in Table 3. All the hybrids showed similar vigor that was significantly higher than that of the parent (G6) used as a check. Seedlings were significantly more vigorous in Sinthiou-Damba compared to the other locations. The days to anthesis (TFLO) was not significantly different between the hybrids whereas the parent (G6) reached its anthesis two to three days later compared to the hybrids. TFLO was longer in Darou-Pakathiar compared to Sinthiou-Damba (this trait was measured only at these two locations). There was a significant effect of year (Y), genotype (G), location (L), YxL, GxL and YxLxG interactions on TFLO. Plant height (PH) for hybrids G1, G2, G3 and G4 was similar (about 2 m). However, these hybrids were taller than G5 and the parent G6. The highest PH was recorded in Sinthiou-Maleme and Sinthiou-Damba. Grain yield components such as panicle dry weight (PDW) and grain dry weight (GDW) were similar for all the hybrids. However, they showed significantly higher performance than that of G6 in regard to these parameters. Hybrid G5 was the highest yielding (GY) followed by G2, G4, G1 and G3. All the hybrids had a significantly higher grain yield than the parent G6. G5 exhibited the highest P1000 while the other hybrids and the parent G6 had similar P1000. The highest PDW and GDW were recorded in Sinthiou-Damba and the highest GY was obtained in Sinthiou-Maleme. All the studied factors and their interactions were significant for all the grain yield components traits except LxG for PDW, YxG for GDW and YxLxG for PDW, GDW and P1000. PGMR was significantly different between G5 and other hybrids. However, their PGMR values ranged from 2.5 to 3.4, indicating that they were all tolerant. The parent G6 had a score of 3.5, characteristic of a susceptible genotype. Similarly, despite the significant difference among locations, the observed PGMR values ranked the hybrids as tolerant at these locations. PGMR was affected by all the studied factors and only the YxL interaction. Therefore, the interaction YxLxG representing the GxE in this multi-location study was not significant for PGMR.

3.1.2. Broad-sense heritability of the studied traits

Table 4 presents the broad-sense heritability (H^2bs) of traits in each location and across locations and years. Heritability was generally high for most of the traits across locations and years. However, for each trait heritability varied depending on year and location. Heritability for seedling vigor was low in Darou-Pakathiar, moderate in Sinthiou-Maleme in 2017 and high in Guirigara and Sinthiou-Damba in 2015. High heritability was recorded for TFLO for most of the years, but moderate in 2014 in Darou-Pakathiar and low in 2017 in Sinthiou-Maleme. Heritability for PH was high in Darou-Pakathiar for all years except in 2014 where it was moderate. However, in Sinthiou-Maleme, it was high in 2016 but low in 2017. For all the grain yield components traits (PDW, GDW, GY), high heritability was recorded in all the locations in 2015 and in Guirigara in 2017. However, it was low in Darou-Pakathiar in 2012 whereas moderate in Darou-Pakathiar and Sinthiou-Damba in 2017. Heritability was high for P1000 in 2016 and 2017 in Sinthiou-Maleme, high in Guirigara and Sinthiou-Damba in 2017 but moderate in Darou-Pakathiar. Heritability was low in 2012 and 2017 for PGMR, but high in 2016 in Darou-Pakathiar, moderate in 2012 and 2016 but high in 2015 and 2017 in Sinthiou-Maleme. It was moderate in Guirigara and Sinthiou-Damba in 2015 but low in Guirigara in 2017.

3.1.3. Contribution of the studied factors to the variation of grain yield and panicle resistance to grain mold

The relative contribution of each source of variation to the total variation measured for grain yield and panicle grain mold rating score

Table 3
Genotype and location *per se* performance and genetic variation among the five hybrids for the eight measured traits across locations and years.

| | Seedling vigor | Phenology | Morphology | Grain yield components | Grain mold score | | | |
	SV	TFLO	PH	PDW	GDW	GY	P1000	PGMR
Genotypes								
G1	1.9b	71.7bc	205.7a	3188.8a	2570.8a	2359.3 ab	16.5bc	3.03bc
G2	2.2b	71.2c	200.9 ab	3355.8a	2748.2a	2467.0 ab	17.0 ab	3.03bc
G3	1.9b	72.8b	203.5a	3022.5a	2432.6a	2294.7b	15.6c	3.13b
G4	2.1b	72.6b	202.9a	3226.9a	2559.2a	2450.3 ab	16.1bc	3.21 ab
G5	1.9b	72.5bc	193.2bc	3280.7a	2748.1a	2571.2a	18.1a	2.71c
G6	3.1a	74.2a	189.0c	2194.6b	1740.7b	1754.0c	16.2bc	3.51a
Locations								
Darou-Pakathiar	2.3a	76.2a	192.8b	2824.0c	2550.0b	2055.2c	15.7c	3.00b
Sinthiou-Maleme	2.3a	67.8b	209.2a	3297.0b	2644.6b	2852.6a	16.9b	3.17a
Guirigara	2.2 ab	–	185.9c	2029.2d	1367.6c	1491.9d	16.0c	3.23a
Sinthiou-Damba	1.9b	–	205.0a	3966.7a	3007.1a	2450.6b	18.2a	3.05 ab
Years								
2012	–	71.5b	213.8b	2902.6b	2092.4c	2514.8bc	–	2.31c
2014	–	72.8b	222.4a	3289.2a	2451.2b	2607.6 ab	–	–
2015	2.1a	72.2b	192.7d	2993.9b	1977.9c	1601.5d	–	3.65a
2016	–	77.1a	187.4e	–	–	2370.6c	14.0 b	3.47a
2017	2.2a	68.9c	198.4c	–	–	3193.3a	17.8 a	2.77b
Grand mean	2.2	72.5	199.2	3044.9	2467.5	2315.1	16.6	3.1
Year (Y)	ns	***	***	*	***	***	***	***
Location (L)	ns	***	***	***	***	***	***	*
Genotype (G)	***	***	***	***	***	***	***	***
Y x L	–	***	***	***	***	***	***	***
Y x G	*	***	ns	*	ns	***	***	ns
L x G	**	*	ns	ns	*	**	***	ns
Y x L x G	–	***	ns	ns	ns	***	ns	ns

*P < 0.05; **P < 0.01; ***P < 0.001; ns: not significant (P > 0.05).
SV: Seedling vigor, TFLO: the days to anthesis (d), PH: Plant height (cm), PDW: Panicle dry weight (g), GDW: Grain dry weight (g), GY: grain yield (Kg/ha), P1000: Thousand-seed weight (g), PGMR: panicle grain mold rating score.
For each trait, mean with different letters are statistically different (P < 0.05).

Table 4
Broad-sense heritability for the studied traits in each studied location in each year and on the pooled data.

| Research station | | | | | | | | | | | Farmer's field | | | | Pooled data |
| | Darou-Pakathiar | | | | | Sinthiou-Maleme | | | | | Guirigara | | Sinthiou-Damba | | |
	2012	2014	2015	2016	2017	2012	2014	2015	2016	2017	2015	2017	2015	2017	
SV	~	~	#	~	0.15	~	~	~	~	0.59	0.88	~	0.87	~	0.64
TFLO	0.6	0.56	0.92	0.83	0.88	0.66	~	#	0.65	0.18	~	~	~	~	0.81
PH	0.96	#	0.78	0.26	0.73	0.25	~	0.66	0.64	0.4	0.32	~	0.58	~	0.88
PDW	0.4	0.03	0.87	~	~	0.21	0.42	0.75	0.42	~	0.93	~	0.93	~	0.71
GDW	0.13	#	0.79	~	0.55	0.17	0.61	0.84	~	0.58	~	0.97	0.95	0.5	0.8
GY	0.13	#	0.82	0.96	0.55	0.17	0.61	0.96	0.99	#	0.95	0.78	0.95	0.45	0.88
P1000	~	~	~	#	0.56	~	~	~	0.82	0.75	~	0.81	~	0.81	0.35
PGMR	0.18	~	#	0.81	0.15	0.48	~	0.77	0.52	0.71	0.5	0.23	0.59	#	0.85

SV: Seedling vigor, TFLO: the days to anthesis (d), PH: Plant height (cm), PDW: Panicle dry weight (g), GDW: Grain dry weight (g), GY: Grain yield (Kg/ha), P1000: Thousand-seed weight (g), PGMR: Panicle grain mold rating score.
~ = these values were not measured in this year for this location.
# = these values were not calculated because their variance was negative.

are presented in Table 5. Grain yield was controlled to a large extent by YxL (25%) followed by Y (22%). The L, G and YxLxG interaction (GxE) accounted for 19%, 7% and 5%, respectively, in the overall variation of GY. Similarly, variation of PGMR was largely explained by Y (32%) followed YxL (29%), G (7%) and L (1%).

Results showed that location effect was strongly significant (P < 0.001) across the years for grain yield (Table 6). However, G effect was significant only in 2015 and 2016 and GxL was significant for all years except in 2012.

As for the relative contribution of each source to the total variation of grain yield, location was observed to be the most important source of variation across the years (>50%). The contribution of G was 28% and 26% in 2015 and 2016, respectively, but it was low (about 3%) in 2012

and 2017. The contribution of GxL to the total variation of grain yield was 15% in 2016 and 2017 while it was 4% and 7% in 2012 and 2015 respectively.

Mean squares and the relative contribution of the studied sources of variation to the total variation for PGMR are shown in Table 7. Results showed that G and L effects were significant across the years except in 2012. However, regardless of the year, there was no significant GxL for PGMR. The contribution of location to the total variation of PGMR was 38, 41, 62% and only 3% in 2015, 2016, 2017 and 2012, respectively. GxL accounted for 20, 15, 10% and only 2% in 2012, 2015, 2017 and 2016, respectively. The contribution of G was 15, 12, 8 and 3% in 2012, 2015, 2016 and 2017, respectively.

Table 5
Sum of squares and proportion of variation explained by Year (Y), Location (L), Genotype (G) and their interactions on grain yield (GY) and panicle resistance to grain mold infestation (PGMR).

	Grain yield			Panicle grain mold rating score		
	Df	Sum Sq	%SST	Df	Sum Sq	%SST
Year (Y)	4	53905834	21.6	3	56.93	32.4
Location (L)	3	47403534	19.0	3	2.38	1.4
Genotype (G)	5	17105243	6.9	5	11.97	6.8
YxL	6	61468089	24.6	5	51.3	29.2
YxG	20	9305550	3.7	15	4.67	2.7
LxG	15	5662615	2.3	15	5.66	3.2
YxLxG	30	12540166	5.0	25	7.52	4.3
YxLxRep	28	19985282	8.0	24	7.64	4.3
Residuals	133	22231077		118	27.7	
Total		249607390			175.77	

% SST, percentage relative to the sum of squares total.

3.2. GGE biplot analysis

3.2.1. Which-won-where pattern analysis

Fig. 2 shows the winning genotypes with their related locations through the GGE biplot analysis for grain yield. This figure indicates that the first two principal components (PC1 and PC2) of this biplot accounted for 70.6% the total variation of grain yield. The polygon view is divided in three mega-environments. The first was made up of DAR14, DAR16, STM14, STM15, GUI15, GUI17 and STD17 with G5 as the most favorable genotype in this mega-environment. The second mega-environment was composed of DAR12, DAR15, DAR17, STM16, STM17 and STD15 with G1 as the most favorable genotype. The third mega-environment had only STM12 with G6 as the best performing genotype. This finding showed that G6 was a low yielding genotype as it was far away from most of the tested locations and had poor yield at each location except STM12.

3.2.2. Performance and stability analysis of hybrid sorghum yield

Fig. 3 shows both the mean yield and stability performance of the studied genotypes. To identify the best performing genotype, the markers of the genotypes were projected on the horizontal axis, the single-arrowed line of the biplot. The closer the genotype is to the arrow, the better it is. Thus, G5 was the highest yielding genotype followed by G4, G1, G2, G3 and G6. To assess the yield stability of the genotypes, their markers were projected on the vertical axis. The most stable

genotype is the one whose absolute length of the projection is smaller. Hence, G4 was the most stable genotype followed by G3, G6, G2, G1 and G5.

3.2.3. Ranking of the studied genotypes to an ideal genotype

Fig. 4 depicts the ranking of the genotypes for grain yield in terms of ideal genotype. Ideal genotype combines stability and high performance across many environments. This genotype should be located in the center of the concentric circle on Fig. 3. The projection of the ideal genotype on the ATC horizontal axis is equal to the longest vector of all genotypes and its projection on the ATC vertical axis is obviously zero. Therefore, the genotype showing the shorter distance to the virtual ideal genotype represents an ideal genotype. The results indicate that genotypes G4 followed by G2 and G3, were the closest to the center of the concentric circle. Thus, they were the best genotypes in terms of yield performance and stability compared to the other genotypes.

3.2.4. Discriminating ability and representativeness of the studied environments

Fig. S1 displays the discriminating ability and representativeness of the studied environments for grain yield. The concentric circles on the biplot help to visualize the length of the environment vectors, which is proportional to the standard deviation within the respective environments and is a measure of the discriminating ability of the environments (Yan and Tinker, 2006). The longer the environment vectors length the more the discrimination. Thus, STM15 was the most discriminating environment followed by DAR12. However, the least discriminating environment for grain yield was STM12.

As for the environment representativeness, it is visualized by considering the angle between the environment vector and abscissa of average environment axis. The smaller the angle, the more representative the test environment would be. Thus, STM15 was the most representative environment following by DAR15, whereas STM12 was the least representative one for grain yield.

3.2.5. Ranking of the studied location to an ideal location

Fig. S2 depicts the ranking of the studied location to the ideal location. As described in the case of ideal genotype on Fig. 4, the ideal location is the location where the studied genotypes combined high performance and stability. This location should be located in the center of the concentric circle. Location STM15 was the closest to the ideal location followed by DAR15 whereas STM12, the furthest location from
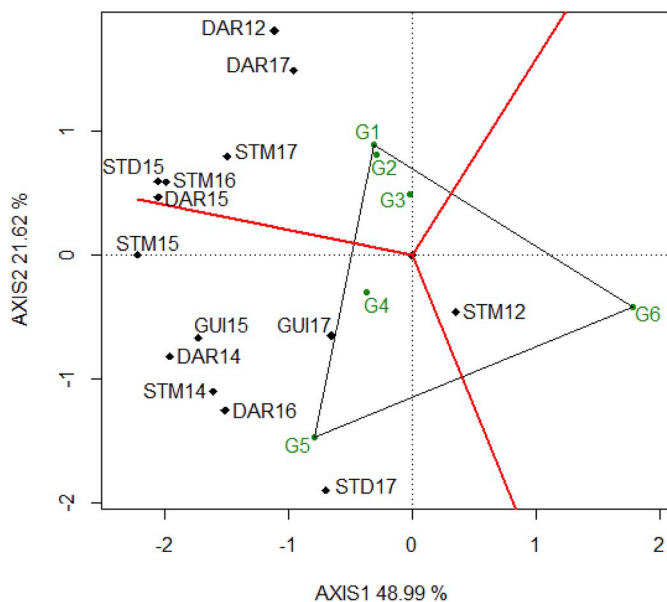
Table 6
Mean squares and proportion of variation explained by genotype (G), locations (L) and G × L interaction for grain yield in the different year of evaluation.

	2012			2015			2016			2017		
	Df	Mean Sq	%SST	Df	Mean Sq	%SST	Df	Mean Sq	%SST	Df	Mean Sq	%SST
Genotype (G)	5	357097ns	3.4	5	1855124***	27.8	5	1984604***	25.7	5	301765ns	3.2
Location (L)	1	4.2E+07***	80.5	3	6147558***	55.3	1	22183158***	57.5	3	8E+06***	51.4
GxL	5	367074ns	3.5	15	165188**	7.4	5	1167355***	15.1	15	459030*	14.8
Location x Rep	4	97982ns	0.8	8	174938**	4.2	4	42818ns	0.44	8	776532**	13.3
Residuals	20	303978ns		37	47967ns		20	22257ns		35	230263ns	

*P < 0.05; **P <, 0.01; ***P < 0.001; ns: not significant (P > 0.05).

Table 7
Mean squares and proportion of variation explained by genotype (G), Environment and G × E interaction for grain mold score (PGMR) in the different year of evaluation.

PGMR	2012			2015			2016			2017		
	Df	Mean Sq	%SST	Df	Mean Sq	%SST	Df	Mean Sq	%SST	Df	Mean Sq	%SST
Genotype (G)	5	0.2944ns	15.3	5	0.867*	11.5	5	1.412**	30.7	5	0.748**	7.7
Location (L)	1	0.25ns	2.6	3	4.763***	37.8	1	9.404***	40.9	3	9.92***	61.6
GxL	5	0.3833ns	19.9	15	0.387ns	15.3	5	0.087ns	1.89	15	0.335ns	10.4
Site x Rep	4	0.4722ns	19.6	8	0.291ns	6.15	4	0.395ns	6.87	8	0.23ns	3.8
Residuals	20	0.2056ns		40	0.277ns		20	0.227ns		38	0.21	

Fig. 2. Polygon view of the GGE biplot identifying which genotype had the best grain yield in which location.

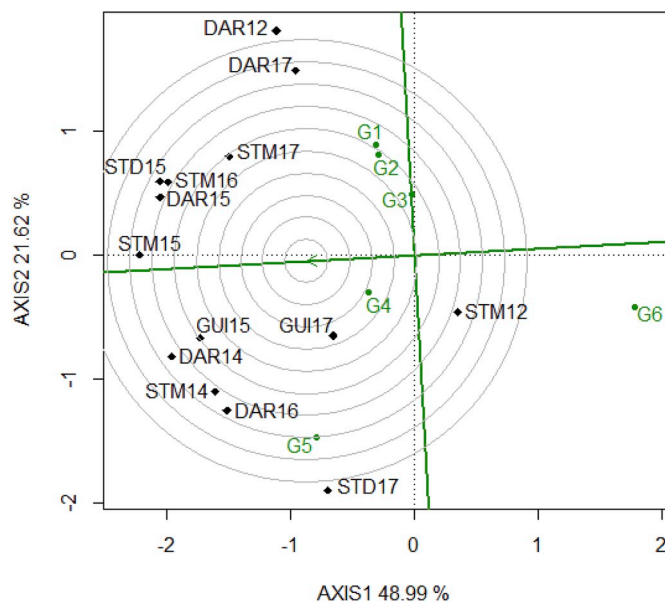**Fig. 4.** Ranking of genotypes based on both mean performance and stability relative to an ideal genotype for grain yield.
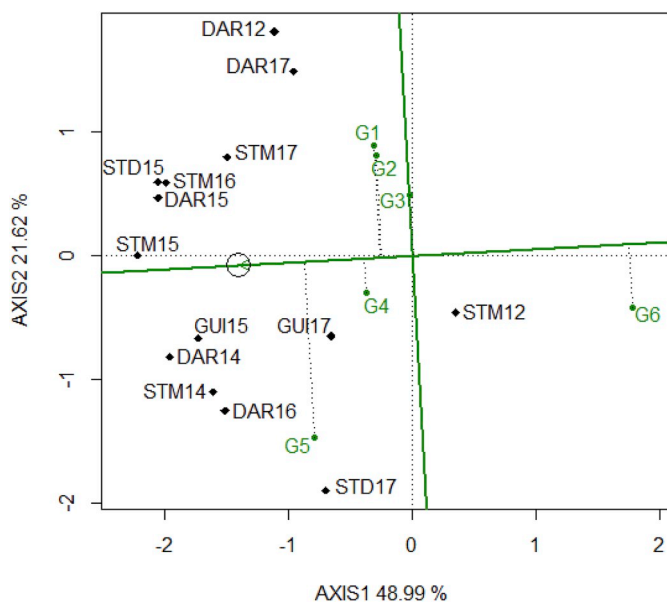
3.4. Sorghum hybrid ability to combine yield and resistance to grain mold infestation

Fig. 5 shows ability of the genotypes to combine grain yield and mold resistance compared among locations for each studied year. It also compares each genotype to the average yield performance (represented by vertical dash line) for a given year, irrespective of locations. For resistance to grain mold, the rating scale is from 1 to 5 with 1 being the most resistant. The horizontal dotted line indicates the limit between resistance and tolerance while the horizontal dash line indicates the limit between tolerance and susceptibility to grain mold infestation. In 2012, genotypes G2, G3 and G5 combined high GY and resistance to mold infestation in Sinthiou-Maleme whereas G1, G4 and G6 recorded a high GY and were tolerant to mold infestation. However, in Darou-Pakathiar, all the genotypes showed low GY and only G1 was resistant to mold infestation while other genotypes were tolerant.

In 2014, all the hybrids cultivated in Sinthiou-Damba recorded GY above the mean and were tolerant to mold infestation. A similar trend was observed for G5 cultivated in Sinthiou-Maleme. Most of the genotypes cultivated in Guirigara and Sinthiou-Maleme recorded low yield and they were susceptible to mold infestation. However, most of the genotypes in Darou-Pakathiar were susceptible to mold infestation but their grain yield was above the mean.

In 2016, all the hybrids in Sinthiou-Maleme combined high GY and tolerance to mold infestation. However, apart from G5, all the hybrids cultivated in Darou-Pakathiar were susceptible to mold with low GY.

In 2017, G1 and G2 cultivated in Darou-Pakathiar, combined GY and resistance to mold infestation. Similarly, hybrids G1, G2, G3, G5 cultivated in Sinthiou-Maleme and G3, G4, G5 cultivated in Sinthiou-Damba, were high yielding with tolerance to mold infestation. G1 and G2 cultivated in Sinthiou-Maleme recorded high yield but they were susceptible to mold infestation. The other genotypes in Darou-Pakathiar, Guirigara and Sinthiou-Maleme were tolerant to grain mold but low yielding.

Hybrid G5 was the most consistent genotypes in combining high grain yield and PGMR below 2.5 (Fig. 5). Fig. 6 shows G5 exhibiting a clean panicle with a PGMR score of 2 compared to the parental line G6 showing at the same stage a moldy panicle with a score of 5.

Fig. 3. GGE biplot of mean yield performance and stability of five sorghum hybrids with one parent cultivated in four locations across five years.

the ideal location.

3.3. Correlations between variables

Table 8 displays the Pearson bivariate correlation matrix computed on plant seedling vigor, plant phenology, morphology, grain yield components and panicle grain mold score across the genotypes, years and locations. TFLO was negatively correlated to PH and GY. However, PH and grain yield components traits such as PDW, GDW and P1000 significantly contributed to grain yield. PGMR was negatively correlated to GDW, GY and P1000. Moreover, plant vigor at seedling stage and grain mold score at maturity were moderately positively correlated (r = 0.37, p = 0.07).

Table 8
Correlation among traits related to seedling vigor, plant phenology, morphology, grain yield components and panicle grain mold score (PGMR) across the studied genotypes, years and locations.

	TFLO	PH	PDW	GDW	GY	P1000	PGMR
PH	−0.5584**						
PDW	−0.0798	0.3581					
GDW	0.0571	0.3331	0.9558***				
GY	−0.5417**	0.7825***	0.6646***	0.6642***			
P1000	−0.2248	0.2974	−0.0181	0.0623	0.4862*		
PGMR	−0.1285	−0.2007	−0.3645	−0.5050*	−0.4828*	−0.4806*	
SV	−0.0155	−0.2142	−0.0865	−0.1323	−0.2582	−0.2413	0.3745

*P < 0.05, **P < 0.01, ***P < 0.001.
SV: Seedling vigor, TFLO: Time to flowering (d), PH: Plant height (cm), PDW: Panicle dry weight (g), GDW: Grain dry weight (g), GY: Grain yield (Kg/ha), P1000: Thousand-seed weight (g), PGMR: Panicle grain mold rating score.
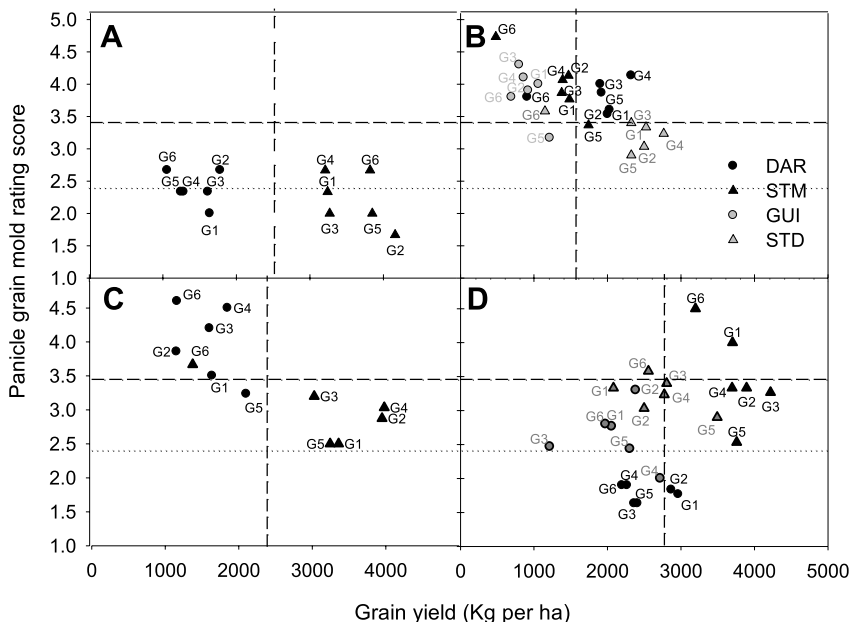
Fig. 5. Ability of the studied genotypes to combine grain yield and resistance to mold in each and across locations (DAR: Darou-Pakathiar, STM: Sinthiou-Maleme, GUI: Guirigara and STD: Sinthiou-Damba) for each year (A: 2012, B: 2014, C: 2016, D: 2017). Vertical dash line represents the average grain yield performance. Horizontal dotted line indicates the limit between resistance and tolerance while horizontal dash line marks the limit between tolerance and susceptibility to grain mold infestation.
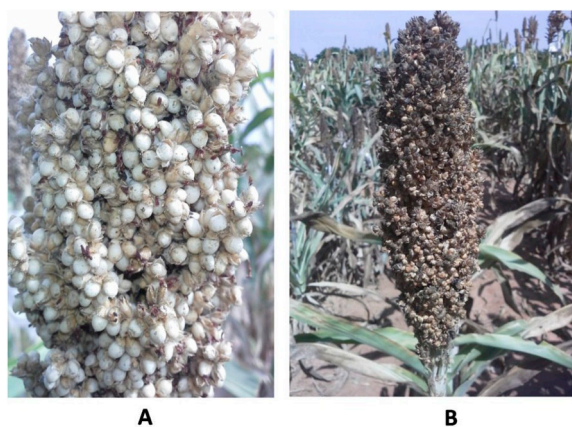
Fig. 6. Photo of panicle infestation compared between hybrid G5 (A) and parental line G6 (B) at physiological maturity.

4. Discussion

4.1. Performance of hybrids and heritability of studied traits

Location x year largely explained the variation of grain yield which contribution to the total variation was estimated at 25%. The influence of year was higher than that of location (22% *vs.* 19%). PGMR was mainly explained by years at 32% followed by years by locations at 29%. These results obtained for grain yield, PGMR and for most of the studied traits showing environment influence mainly year and to some extent, the location, corroborate many authors reporting a high environment influence on sorghum phenology, morphology and grain production traits (Bernal et al., 2014; Gasura et al., 2015; Kenga et al., 2006).

However, although environment explained most of the variation of the studied traits, their broad-sense heritability was generally high but differed depending on the locations and years. Many studies reported moderate to high heritability on days to anthesis and plant height (El Naim et al., 2012; Jimmy et al., 2017; Kenga et al., 2006) and on grain production traits (Almeida Filho et al., 2014b; Belay and Meresa, 2017; Mohammed et al., 2015; Phuke et al., 2017). Rodríguez-Herrera et al. (2007) found a high heritability (0.86) for panicle resistance to grain mold while Audilakshmi et al. (2011) reported a low heritability (0.24–0.26) on two hundred RILs population. The high heritability found in this study for most of the traits indicates the possibility to improve these traits through selection (Kamatar et al., 2015). In addition, the hybrids showed higher performance for all traits compared to the parental line, G6, used as a check. This denotes the superiority of hybrid over one open pollinated variety and inbred lines as reported in many studies on hybrid development (Hayes and Rooney, 2014; Mindaye et al., 2016; Park et al., 2010; Pfeiffer et al., 2010; Ringo et al., 2015; Rini et al., 2016; Soujanya et al., 2017).

4.2. GGE biplot analysis for grain yield performance and stability

Which-won-where is a very useful method to graphically address the GxE interactions, the differentiation of mega-environments and specific adaptation (Yan et al., 2000). It allows identification of the genotype suitable or not for one or more locations (Yan and Tinker, 2006). The GGE biplot indicates that the first two principal components (PC1 and PC2) accounted for 70.6% of the total variation in grain yield which is >60%, making the biplot useful (Yang et al., 2009). The first of the three mega-environments identified in Fig. 2, comprised of DAR14, DAR16, STM14, STM15, GUI15, GUI17 and STD17 with G5 as the most favorable genotype. As for the second mega-environment, it comprised DAR12, DAR15, DAR17, STM16, STM17 and STD15 with G1 as the most favorable genotype. The third mega-environment consisted only of STM12 with G6 as a corner genotype. This showed G6 as the lowest yielding genotype as it was far away from most of the tested locations and reached a poor yield at each location except at STM12. Many studies reported the use of which-won-where biplot to identify the best genotypes suitable for each location (Bernal et al., 2014; Rakshit et al., 2012; Rao et al., 2011).

From Fig. 3, G5 was shown to be the highest yielding hybrid but lacked stability. It was the least stable hybrid of this study. Many studies have reported that the highest yielding genotypes were not necessarily the most stable (Bose et al., 2013; Karimizadeh et al., 2013; Rakshit et al., 2012). In this study, G4 was the hybrid following the most yielding genotype and was the most stable. Therefore, G4 was the best hybrid combining yield and stability. This was confirmed by the ranking of the studied genotypes to an ideal genotype as G4 was the genotype closest to the ideal genotype (higher yielding and greater stability) followed by G3. G4 performed well in DAR14, DAR16, STM14, STM15, GUI15, GUI17 and STD17.

Location STM15 was identified as the most discriminating followed by DAR15 whereas STM12 was the least discriminating. Moreover, STM15 was again identified as the most representative location followed by DAR15 whereas STM12 was the least representative. Accordingly, Sinthiou-Maleme and Darou-Pakathiar were the most favorable for selecting stable hybrids.

4.3. Traits contributing to yield and resistance to grain mold in sorghum hybrid

Plant seedling vigor was positively correlated to grain mold score but negatively to yield component traits although it was not significant. Indeed, genotype with weak seedling vigor (G6) recorded the highest grain mold score. In a study carried out at Bambey (Senegal), Luce (1994) found that susceptibility to grain mold is linked to low germination rate at field and low seedling plant vigor. Similarly, Thirumala Rao et al. (2012) reported highly significant and negative correlation between field grain mold score and germination percentage on a panel of 25 sorghum hybrids.

Moreover, the cycle duration (TFLO) was negatively correlated to plant height and grain yield. This implies interestingly that long vegetative duration was not necessarily needed to achieve tall plant height and grain yield. This could be due to narrow diversity within the studied hybrids derived from parental inbred lines genetically close and accordingly having similar phenology and morphology. This result corroborates Tovignan et al. (2016b) who although having studied a diversified panel of 88 sorghum accessions from West Africa, did not find a significant correlation between plant height and cycle duration but showed a negative correlation between this latter and grain production. Contrary to the present study, Zou et al. (2011) found a significant contribution of cycle duration to plant height in a diversity panel of 436 recombinant inbred lines. PH and grain yield components traits such as PDW, GDW and P1000 significantly contributed to grain yield as shown in many studies (da Silva et al., 2017; Ezeaku and Mohammed, 2006; Tovignan et al., 2016b). Moreover, the high and

negative correlation between PGMR and yield component traits (GDW, GY and P1000) shows the damaging effects of the disease on sorghum grain. In fact, grain mold affects sorghum grain by degrading endosperm and germ, resulting in decreased grain density, germination and seedling vigor (Thakur et al., 2007). Similar results were reported by earlier researchers (Audilakshmi et al., 1999; Reddy et al., 2008). However, despite negative correlation found between the grain yield components traits and the mold tolerance, some genotypes mainly G5 and to a relative extent G4, G2 and G3 showed ability to combine grain yield and mold tolerance across locations and years. The high relative humidity (85–100%) and temperature (25–30 °C) that had prevailed during the study mainly in September, are likely to favor natural mold infestation as indicated by Tonapi et al. (2007). In this context, if some genotypes were able to show very low infestation or were not infested, this may be due to their ability to tolerate mold infestation compared to others. Interestingly, a good score of 2 for grain vitrosity for all the parental lines is reported in the ISRA database (ISRA, 2012). This may be one of the traits segregating in the parental lines that may confer the mold tolerance in some hybrids.

5. Conclusion

This study assessed the yield performance and stability of five sorghum hybrids evaluated over five years in the Center and South-East of Senegal with the aim to improve their tolerance to panicle grain mold infestation. The results showed a significant GxE interaction on grain yield but not on panicle mold infestation. The variation of the studied traits was mainly due to environment and despite this their broad-sense heritability was generally high, indicating a potential for high response to selection in these traits. The hybrids showed a higher performance compared to the parental line. The GGE biplot methodology used helped to identify hybrids G4 followed by G2 and G3 as the best in terms of yield performance and stability compared to the others. Moreover, many locations across years seemed to be favorable for the cultivation of these hybrids mainly the location STM15 followed by DAR15 that were shown to be the best close to the ideal location. Overall, across years and locations, G5 was the most stable hybrid combining high grain yield and mold tolerance. By providing further insight on the performance and stability of the five sorghum hybrids, this study helped to identify the best hybrids to be released and disseminated in the Center and South-East of Senegal.

Appendix A. Supplementary data

Supplementary data to this article can be found online at https://doi.org/10.1016/j.cropro.2019.02.001.

References

Allard, R.W., 1960. Principles of Plant Breeding. John Wiley Sons, Inc, New York, p. 485p.

Almeida Filho, J.E.D., Tardin, F.D., Daher, R.F., Barbé, T.C., Paula, C.M., Cardoso, M.J., Godinho, V.P.C., 2014. Stability and adaptability of grain sorghum hybrids in the off-season. Genet. Mol. Res. 13, 7626–7635. https://doi.org/10.4238/2014.March.24.24.

Almeida Filho, J.E.D., Tardin, F.D., Resende, M.D.V.D., Silva, F.F.E., Granato, Í.S.C., Menezes, C.B.D., 2014. Genetic evaluation of grain sorghum hybrids in Brazilian environments using the REML/BLUP procedure. Sci. Agric. 71, 146–150.

Ambekar, S.S., Kamatar, M.Y., Ganesamurthy, K., Ghorade, R.B., Saxena, U., Chand, P., Jadav, B.D., Das, I.K., Nageshwararao, T.G., Audilakshmi, S., Seetharamah, N., 2011. Genetic enhancement of Sorghum (Sorghum bicolor (L) Moench) for grain mould resistance: II. Breeding for grain mould resistance. Crop Protect. 30, 759–764. https://doi.org/10.1016/j.cropro.2010.06.024.

Ashok Kumar, A., Reddy, B.V.S., Sharma, H.C., Hash, C.T., Rao, P.S., Ramaiah, B., Reddy, P.S., 2011. Recent advances in sorghum genetic enhancement Research at ICRISAT. Am. J. Sci. 2, 589–600.

Audilakshmi, S., Stenhouse, J.W., Reddy, T.P., Prasad, M.V.R., 1999. Grain mould resistance and associated characters of sorghum genotypes. Euphytica 107, 91–103.

Audilakshmi, S., Stenhouse, J.W., Reddy, T.P., 2005. Genetic analysis of grain mold resistance in white seed sorghum genotypes. Euphytica 145, 95–101. https://doi.org/10.1007/s10681-005-0534-6 ?C.

Audilakshmi, S., Das, I.K., Ghorade, R.B., Mane, P.N., Kamatar, M.Y., Narayana, Y.D., Seetharama, N., 2011. Genetic improvement of sorghum for grain mould resistance: I. Performance of sorghum recombinant inbred lines for grain mould reactions across environments. Crop Protect. 30, 753–758. https://doi.org/10.1016/j.cropro.2010.12.024.

Bandyopadhyay, R., Butler, D.R., Chandrashekar, A., Kanaka, R., Navi, S.S., 2000. Biology, epidemiology, and management of sorghum grain mold. In: Chandrashekar, A., Bandyopadhyay, R., Hall, A.J. (Eds.), Technical and Institutional Options for Sorghum Grain Mold Management. ICRISAT, Patancheru, India, pp. 34–51.

Belay, F., Meresa, H., 2017. Performance evaluation of sorghum [Sorghum bicolor (L.) Moench] hybrids in the moisture stress conditions of Abergelle District, Northern Ethiopia. J. Cereals Oilseeds 8, 26–32. https://doi.org/10.5897/JCO2016.0168.

Bernal, J.H., Ligarreto, M., G, A., Hernández, R.S., 2014. Effects of the genotype and environment interaction on sugar accumulation in sweet sorghum varieties (Sorghum bicolor [L.] Moench) grown in the lowland tropics of Colombia. Agron. Colomb. 32, 307–314. https://doi.org/10.15446/agron.colomb.v32n3.45477.

Bose, L.K., Jambhulkar, N.N., Pande, K., Singh, O.N., 2013. Use of AMMI and other stability statistics in the simultaneous selection of rice genotypes for yield and stability under direct-seeded conditions. Chil. J. Agric. Res. 74 https://doi.org/10.4067/S0718-58392014000100001.

CEDEAO-UEMOA-CILSS, 2016. Catalogue Régional des Espèces et Variétés Végétales CEDEAO-UEMOA-CILSS, vol. 109p. http://insah.cilss.int/index.php/2017/12/07/catalogue_des_semences/.

Chepng'etich, E., Bett, E.K., Nyamwaro, S.O., Kizito, K., 2014. Analysis of technical efficiency of sorghum production in lower Eastern Kenya: a data envelopment analysis (DEA) approach, 5, 58–65.

da Silva, K.J., Teodoro, P.E., de Menezes, C.B., Júlio, M.P.M., de Souza, V.F., da Silva, M.J., Pimentel, L.D., Borém, A., 2017. Contribution of morphoagronomic traits to grain yield and earliness in grain sorghum. Genet. Mol. Res. 16, 1–10. https://doi.org/10.4238/gmr16029649.

Das, I.K., Audilakshmi, S., Patil, J.V., 2012. Fusarium grain mold: the major component of grain mold disease complex in sorghum (sorghum bicolor L. Moench). Eur. J. Plant Sci. Biotechnol. 6, 45–55.

El Naim, A.M., Ibrahim, I.M., Rahman, M.E.A., Ibrahim, E.A., 2012. Evaluation of some local sorghum (sorghum bicolor L. Moench) genotypes in rain-fed. Int. J. Plant Res. 2, 15–20. https://doi.org/10.5923/j. plant.20120201.03.

Esele, J.P., Frederiksen, R.A., Miller, F.R., 1993. The association of genes controlling caryopsis traits with grain mould resistance in sorghum. Phytopathology 83, 490–495.

Esele, J.P., Frederiksen, R.A., Miller, F.R., 1995. The importance of plant color and modifier genes in grain mould resistance in sorghum. East African Agric. For. J. 61, 31–37.

Ezeaku, I.E., Mohammed, S.G., 2006. Character association and path analysis in grain sorghum. Afr. J. Biotechnol. 5, 1337–1340.

Frutos-Bernal, E., Galindo, M.P., 2012. GGEBiplotGUI: Interactive GGE Biplots in R [Programa Informático]. Salamanca, España. Departamento de Estadística, Universidad de Salamanca. http://CRAN.r-project.org/web/packages/GGEBiplotGUI/index.html.

Gasura, E., Setimela, P.S., Souta, C.M., 2015. Evaluation of the performance of sorghum genotypes using GGE biplot. Can. J. Plant Sci. 95, 1205–1214. https://doi.org/10.4141/CJPS-2015-119.

Hayes, C.M., Rooney, W.L., 2014. Agronomic performance and heterosis of specialty grain sorghum hybrids with a black pericarp. Euphytica 196, 459–466. https://doi.org/10.1007/s10681-013-1047-3.

ICRISAT, 1992. ICRISAT Medium Term Plan 1994-98 Research Theme Datasets. Patancheru. A.P., India, p. 229, 502 324.

Indira, S., Muthusubramanian, V., Tonapi, V.A., Varanavasiappan, S., Seetharama, N., 2006. Utility of biocontrol agents in the suppression of seed borne pathogenic mycoflora and their effect on seed quality in sorghum (Sorghum bicolor (L.) Moench). Arch. Phytopathol. Plant Prot. 39, 379–387.

Ingole, D.G., Kalpande, H.V., Chinchane, V.N., More, A.W., 2018. Studies on combining ability for grain mould resistance parameters in sorghum (sorghum bicolor (L.) Moench). Int. J. Curr. Microbiol. Appl. Sci. 1361–1367.

ISRA, 2012. Catalogue officiel des espèces et des variétés cultivées au Sénégal. Dakar (Sénégal), 191p. http://www.fao.org/pgrf-gpa-archive/sen/docs/senegal_varieties/Catalogue_%20varieties.htm (consulted in October 2018).

Jimmy, M., Nzuve, F., Flourence, O., Manyasa, E., Muthomi, J., 2017. Genetic variability, heritability, genetic advance and trait correlations in selected sorghum (Sorghum bicolor L. Moench) varieties. Int. J. Agron. Agric. Res. 11, 47–56.

Kamatar, M., Biradar, B., Sowmya, H., Brunda, S., Deepakkumar, G.S., Rajaput, S., Hundekar, R., 2015. Genetic variability and selection for grain mold resistance in F3 progenies of sorghum. Int. J. Farming Allied Sci. 4, 334–340.

Karimizadeh, R., Mohammadi, M., Sabaghni, N., Mahmoodi, A., Roustami, B., Seyyedi, F., Akbari, F., 2013. GGE biplot analysis of yield stability in multi-environment trials of lentil genotypes under rainfed condition. Not. Sci. Biol. 5, 256–262.

Kenga, R., Tenkouano, A., Gupta, S.C., Alabi, S.O., 2006. Genetic and phenotypic association between yield components in hybrid sorghum (sorghum bicolor (L.) Moench) populations. Euphytica 150, 319–326. https://doi.org/10.1007/s10681-006-9108-5.

Klein, R.R., Rodriguez-Herrera, R., Schlueter, J., Klein, P.E., Yu, Z.H., Rooney, W.L., 2001. Identification of genomic regions that affect grain-mould incidence and other traits of agronomic importance in sorghum. Theor. Appl. Genet. 102, 307–319.

Little, C.R., Perumal, R., Tesso, T., Prom, L.K., Odvody, G.N., Mangill, C.W., 2012. Sorghum pathology and biotechnology - a fungal disease perspective: Part I. Grain mold, head smut and ergot. Eur. J. Plant Sci. Biotechnol. 6, 10–30.

Louvel, D., 1984. Phytopathologie du sorgho. Moisissures des grains du sorgho. Rapport d'activités 1383. CNRA Bambey, Senegal. Doc N: 38/84 multigraphie. 32 p.

Luce, C., 1988. L'amélioration du sorgho au Sénégal : acquis (1950-1986) et perspectives de recherches. Institut Sénégalais de Recherches Agricoles (ISRA) 1 (2), 22.

Luce, C., 1994. Influence des conditions de production des semences de sorgho sur la levée au champ. Agric. Dév. 43–45.

Menkir, A., Ejecta, G., Butler, L.G., Melakeberhan, A., Warren, H.L., 1996. Fungal invasion of kernels and grain mold damage assessment in diverse sorghum germ plasm. Plant Dis. 80, 1399–1402.

Mindaye, T.T., Mace, E.S., Godwind, I.D., Jordan, D.R., 2016. Heterosis in locally adapted sorghum genotypes and potential of hybrids for increased productivity in contrasting environments in Ethiopia. Crop J 1–11. https://doi.org/10.1016/j.cj.2016.06.020.

Mofokeng, M.A., Shimelis, H., Laing, M., Shargie, N., 2017. Sorghum [Sorghum bicolor (L.) Moench] breeding for resistance to leaf and stalk anthracnose, Colletotrichum sublineolum, and improved yield: progress and prospects. Aust. J. Crop Sci. 11, 1078–1085.

Mohammed, R., Ashok Kumar, A., Bhavanasi, R., Munghate, R.S., Kavi Kishor, P.B., Sharma, H.C., 2015. Quantitative genetic analysis of agronomic and morphological traits in sorghum,Sorghum bicolor. Front. Plant Sci. 6, 1–17.

Navi, S.S., Bandyopadhyay, R., Hall, A.J., 2002. Effects of crop season, storage conditions, cultivars, and fungicide on postharvest mold fungi infecting sorghum grain. ISMN 43, 65–68.

Park, S.E., Benjamin, L.R., Watkinson, A.R., 2010. Comparing biological productivity in cropping systems . J. Appl. Ecol. 39, 416–426.

Pfeiffer, T.W., Bitzer, M.J., Toy, J.J., Pedersen, J.F., 2010. Heterosis in sweet sorghum and selection of a new sweet sorghum hybrid for use in syrup production in Appalachia. Crop Sci. 50, 1788–1794.

Phuke, R.M., Anuradha, K., Radhika, K., Jabeen, F., Anuradha, G., Ramesh, T., Hariprasanna, K., Mehtre, S.P., Deshpande, S.P., Anil, G., Das, R.R., Rathore, A., Hash, T., Reddy, B.V.S., Kumar, A.A., 2017. Genetic variability, genotype × environment interaction, correlation, and GGE biplot analysis for grain iron and zinc concentration and other agronomic traits in RIL population of sorghum (sorghum bicolor L. Moench). Front. Plant Sci. 8, 1–13. https://doi.org/10.3389/fpls.2017.00712.

Prom, L.K., Perumal, R., Cissé, N., Little, C.R., 2014. Evaluation of selected sorghum lines and hybrids for resistance to grain mold and long smut fungi in Senegal, West Africa. Plant Health Prog. 15, 28–31. https://doi.org/10.1094/PHP-RS-13-0128.

Rakshit, S., Ganapathy, K.N., Gomashe, S.S., Rathore, A., Ghorade, R.B., Kumar, M.V.N., Ganesmurthy, K., Jain, S.K., Kamtar, M.Y., Sachan, J.S., Ambekar, S.S., Ranwa, B.R., Kanawade, D.G., Balusamy, M., Kadam, D., Sarkar, A., Tonapi, V.A., Patil, J.V., 2012. GGE biplot analysis to evaluate genotype, environment and their interactions in sorghum multi-location data. Euphytica 185, 465–479. https://doi.org/10.1007/s10681-012-0648-6.

Rao, P.S., Reddy, P.S., Rathore, A., Reddy, B.V.S., Panwar, S., 2011. Application GGE biplot and AMMI model to evaluate sweet sorghum (Sorghum bicolor) hybrids for genotype × environment interaction and seasonal adaptation. Indian J. Agric. Sci. 81, 438–444.

Rao, V.T., Reddy, P.S., Reddy, B.V.S., 2016. Combining ability for grain mold resistance in sorghum (Sorghum bicolor (L.) Moench). SABRAO J. Breed. Genet. 48, 240–246.

Reddy, B.V., Bandyopadhyay, R., Ramaiah, B., Ortiz, R., 2000. Breeding grain mold resistant sorghum cultivars. Technical and Institutional Options for Sorghum Grain Mold Management: Proceedings of an International Consultation. ICRISAT, Patancheru, Andhra Pradesh, India, pp. 195–224.

Reddy, B.V.S., Ramesh, S., Ashok Kumar, A., Wani, S.P., Ortiz, R., Ceballos, H., Sreedevi, T.K., 2008. Bio-fuel crops Research for energy security and rural development in developing countries. Bioenerg. Res. 1, 248–258. https://doi.org/10.1007/s12155-008-9022-x.

Ringo, J., Onkware, A., Mgonja, M., Deshpande, S., Rathore, A., Mneney, E., Gudu, S., 2015. Heterosis for yield and its components in sorghum (Sorghum bicolor L. Moench) hybrids in dry lands and sub-humid environments of East Africa. Aust. J. Crop. Sci. 9, 9–13.

Rini, E.P., Trikoesoemaningtyas, Wirnas, D., Sopandie, D., Tesso, T.T., 2016. Heterosis of sorghum hybrid developed from local and introduced lines. Int. J. Agron. Agric. Res. 8, 1–9.

Robinson, H.F., Comstock, R.E., Harvey, P.H., 1949. Genotypic and phenotypic correlation in corn and their implications in selection. Agron. J. 43, 282–287.

Rodríguez-Herrera, R., Rooney, W.L., Rosenow, D.T., Aguilar-González, C.N., Quero-Carrillo, A.R., 2007. Genetic control and heritability of resistance to grain mold in F2:5 sorghum families with non-pigmented testa. Plant Breed. Seed Sci. 55, 34–43.

Sambe, M., Tounkara, L.S., Lopy, M.J.F.S., N'Diaye, Y., 2017. Etude des comportements rhéologiques des mélanges de farine blé/sorgho sans tanins issue de trois nouvelles

variétés cultivées au Sénégal et mise au point de pains à base de farines composées (blé/sorgho). Agron. Africaine Sp. 29, 69–74.

Sharma, R., Rao, V.P., Upadhyaya, H.D., Reddy, V.G., Thakur, R.P., 2010. Resistance to grain mold and downy mildew in a mini-core collection of sorghum germplasm. Plant Dis. 94, 439–444.

Soujanya, T., Shashikala, T., Umakanth, A.V., 2017. Heterosis and combining ability studies in sweet sorghum [sorghum bicolor (L.) Moench] for green fodder yield and its contributing traits. Int. J. Curr. Microbiol. Appl. Sci. 6, 3434–3442. https://doi.org/10.20546/ijcmas.2017.610.405.

Teferi, T.A., Wubshet, M.L., 2015. Prevalence and intensity of economically important fungal diseases of sorghum in South Tigray, Ethiopia. J. Plant Sci. 3, 92–98.

Thakur, R.P., Reddy, B.V.S., Indira, S., Rao, V.P., Navi, S.S., Yang, X.B., Ramesh, S., 2006. Sorghum Grain Mold. Information Bulletin No. 72. International Crops Research Institute for the Semi-arid Tropics. Patancheru 502324, Andhra Pradesh, India, p. 32. ISBN 92-9066-488-6 32.

Thakur, R., Reddy, B., Mathur, K., 2007. Screening Techniques for Sorghum Diseases. Information Bulletin No. 76. Patancheru 502 324. International Crops Research Institute for the Semi-Arid Tropics, Andhra Pradesh, India, ISBN 978-92-9066-504-5, p. 92.

Thirumala Rao, V., Sanjana Reddy, P., Reddy, B.V.S., Ashok Kumar, A., 2012. Ergosterol as an indicator of mold resistance in white and colored grain sorghum hybrids. Crop Protect. 37, 7–12. https://doi.org/10.1016/j.cropro.2011.12.2.017.

Tonapi, V.A., Mundada, R.R., Navi, S.S., Reddy, R.K., Thakur, R.P., Bandyopadhyay, R., Varanavasiappan, S., Seetharama, N., 2007. Effect of temperature and humidity regimes on grain mold sporulation and seed quality in sorghum (Sorghum bicolor (L.) Moench). Arch. Phytopathol. Plant Prot. 40, 113–127. https://doi.org/10.1080/03235400500355626.

Tovignan, T.K., Fonceka, D., Ndoye, I., Cisse, N., Luquet, D., 2016. The sowing date and post-flowering water status affect the sugar and grain production of photoperiodic, sweet sorghum through the regulation of sink size and leaf area dynamics. F. Crop. Res. 192, 67–77. https://doi.org/10.1016/j.fcr.2016.04.015.

Tovignan, T.K., Luquet, D., Fonceka, D., Ndoye, I., Trouche, G., Cisse, N., 2016. Assessment of the variability of Senegalese landraces for phenology and sugar yield components to broaden the genetic pool of multi-purpose sorghum. Plant Genet. Resour. 14, 121–131. https://doi.org/10.1017/S1479262115000155.

Yan, W., Tinker, N.A., 2006. Biplot analysis of multi-environment trial data: principles and applications. Can. J. Plant Sci. 86, 623–645.

Yan, W., Hunt, L., Sheng, Q., Szlavnics, Z., 2000. Cultivar evaluation and mega environment investigation based on the GGE biplot. Crop Sci. 40, 597–605.

Yang, R., Crossa, J., Cornelius, P., Burgueno, J., 2009. Biplot analysis of genotype × environment interaction: proceed with caution. Crop Sci. 49, 1564–1576.

Zou, G., Yan, S., Zhai, G., Zhang, Z., Zou, J., Tao, Y., 2011. Genetic variability and correlation of stalk yield-related traits and sugar concentration of stalk juice in a sweet sorghum (Sorghum bicolor L. Moench) population. Aust. J. Crop. Sci. 5, 1232–1238.