AGRONOMY SCIENCE AND BIOTECHNOLOGY

Phenotypic stability and adaptability of sweet sorghum genotypes evaluated in different Brazilian regions

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ABSTRACT

Sweet sorghum is a special purpose sorghum with a sugar-rich stalk, almost like sugarcane. The objective of this work was to evaluate the phenotypic stability and adaptability of sweet sorghum genotypes, in different Brazilian regions, for the production of bioethanol. Twenty-five sweet sorghum genotypes were evaluated in 10 environments distributed in the Southeast, Midwest, Northeast, and Southern regions of Brazil. The experimental design was a randomized complete block design with three repetitions. The following agroindustrial traits were evaluated: fresh biomass yield (FBY), total soluble solids content (TSS) and tons of Brix per hectare (TBH). The adaptability and stability analyzes were performed with the methods GGEbiplot and Annicchiarico methodologies. The Annicchiarico and GGEbiplot adaptability and stability study methods presented satisfactory and consistent results and can be used separately or together in sweet sorghum breeding programs, and B005 and B008 sweet sorghum genotypes presented superior performance, with similar classification in both methods studied.

INTRODUCTION

The global demand for petroleum fuel and its associated environmental concerns, such as greenhouse gas emissions, increases the use of renewable crops for the production of bioenergy (Appiah-Nkansah, Li, Rooney, & Wang, 2019). Among the renewable energy sources, biofuels, especially ethanol produced by fermenting carbohydrates-rich crops, have gained prominence in the world energy market (Leite et al., 2019).

Brazil is the second-biggest producer of ethanol in the world, second only to the USA (Renewable Fuels Association [RFA], 2019). Several factors have combined to stimulate the development of Brazil's ethanol industry: an increased capacity to produce sugarcane as an ethanol feedstock, and greater incentive to research and investment with new and complementary energy cultures. Currently, the use of ethanol as biofuel in Brazil has been the most successful program to replace fossil fuels worldwide. Several countries have started their own programs for the production and use of ethanol as fuel to reduce oil dependence and greenhouse gas emissions. However, the Brazil still needs to sustain production growth in the ethanol sector in order to meet increasing domestic demand and maintain its export share.

Sweet sorghum [*Sorghum bicolor* (L.) Moench] is a special purpose sorghum with a sugar-rich stalk, almost like sugarcane. Besides having rapid growth, high sugar accumulation, and biomass production potential, sweet sorghum has wider adaptability (Souza, Parrella, Souza, & Parrella, 2016; Silva et al., 2017; Appiah-Nkansah et al., 2019; Leite et al., 2019). Besides, it is can be grown with less irrigation and rainfall and purchased inputs compared to sugarcane (Ribeiro, Salvador, Oliveira, & Menezes, 2021). The sugar content in the juice extracted from sweet sorghum varies from 16 - 23% Brix. It has also a great potential for jaggery, syrup, and most importantly fuel alcohol production (Silva et al., 2017; Teixeira et al., 2017; Klasson, Qureshi, Powell, Heckemeyer, & Eggleston, 2018).

The commercial release of new sweet sorghum cultivars requires understanding the performance of potential genotypes in different environmental conditions. The differential response of genotypes in different environments is known as the genotype x environment interaction (GxE), and when recommending sorghum cultivars in the face of GxE, it is necessary to annually test a large number of genotypes in different environments before the final recommendation and multiplication is made (Almeida Filho et al., 2014). GxE can complicate the recommendation of cultivars for different environments, making adaptability and stability analyses necessary. The study of adaptability and stability allows the identification of genotypes with predictable behavior in specific or general environments, and the identification of genotypes sensitive to positive environmental variations (Cruz, Regazzi, & Carneiro, 2012).

There are several methods for analyzing the adaptability and stability of genotypes when grown in different environments. The choice of using certain analytical methods of experimental data depends mainly on the number of environments available, the accuracy required, and the type of information desired. The GGE biplot analysis is efficient because it enables predicting the mean genotype yield per specific environment, as well as helps identifying the most stable genotype for the region of interest (Yan, 2014; Santos, Amaral Júnior, Kurosawa, Gerhardt, & Fritsche Neto, 2017). According to Badu-Apraku, Akinwale, Fakorede and Oyekunle (2012), this analysis is more versatile and flexible than other models based on simple linear regression and on segmented linear regression, as well as

than non-parametric methods, because it allows better understanding the G×E interaction. Already, the Annicchiarico (1992) method has the confidence index (Ii) as its statistical index whose result is expressed as a percentage of the mean of the environments. The confidence index allows us to estimate the risk of using each genotype.

Therefore, the objective of this work was to evaluate the phenotypic stability and adaptability of sweet sorghum genotypes, in different Brazilian regions, for the production of bioethanol.

MATERIAL AND METHODS

Environments and genotypes

The experiments were conducted in ten environments, distributed in different Brazilian regions: Southeast (Minas Gerais and São Paulo), Midwest (Distrito Federal, Mato Grosso do Sul and Mato Grosso), Northeast (Alagoas) and Sul (Rio Grande do Sul) in the 2015/2016 agricultural year (Table 1). Twenty-five sweet sorghum genotypes were evaluated, being 20 experimental hybrids, two experimental cultivars (CMSXS646 and CMSXS647), two commercial cultivars (BRS508 and BRS511), all belonging to the Embrapa Maize and Sorghum breeding program, and the commercial hybrid, CV198 (CanaVialis®). Sweet sorghum hybrids were developed using female sweet sorghum lines (A-lines) and restorative lines (R-lines) (Whitford et al., 2013).

Table 1. Geographic location of the environments and the mean cropping cycle of each sweet sorghum experiment evaluated in the 2015/2016 agricultural year.

Environment	Latitude	Longitude	Altitude	Cycle (days)
Sete Lagoas-MG[1]	19° 27' 57'' S	44° 14' 49'' W	767 m	110
Lavras-MG	21° 14' 43" S	44° 59' 59"W	919 m	112
Nova Porteirinha-MG	15° 47' 00'' S	43° 18' 00''W	533 m	103
Jaguariúna-SP	22° 42' 20" S	46° 59' 09"W	584 m	113
Planaltina-DF	17° 35' 03" S	47° 42' 30"W	1.100 m	117
Dourados-MS	22° 13' 16'' S	54° 48' 20''W	430 m	98
Sinop-MT	11° 50' 53" S	55° 38' 57'' W	384 m	116
Penedo-AL	10° 17' 25" S	36° 35' 11"W	27m	104
Passo Fundo-RS	28° 15' 46" S	52° 24' 24"W	687m	134
Pelotas-RS	31° 46' 19'' S	52° 20' 34'' W	7 m	136

[1]MG: Minas Gerais state; SP: São Paulo state; DF: Distrito Federal; MS: Mato Grosso do Sul state; MT: Mato Grosso state; AL: Alagoas state; RS: Rio Grande do Sul state.

Experimental planning and conducting

The experimental design was a randomized complete block design with three repetitions. The experimental unit consisted of two rows of five meters long, spaced 0.7 m between rows, except the Dourados environment, where the row

spacing used was 0.5 m and in Lavras 0.6 m. The plant population was 110,000 plants per hectare. The following agroindustrial traits were evaluated: fresh biomass yield (FBY; weight of all plants in the plot measured in kg using a digital hanging scale and expressed as ton. ha^{-1}); total soluble solids content (TSS; determined in the extracted juice using hydraulic press from a sample of six stalks using a digital automatic refractometer in °Brix); and tons of Brix per hectare (TBH; determined in t. ha^{-1} using the following expression: TBH = (FBY x TSS)/100).

Statistical analysis

Firstly, the analysis of variance was conducted for each environment. After verifying the homogeneity of residual variances using Bartlett´ test, the joint analysis of variance was performed, according to the following model:

$$Y_{ijk} = \mu + g_i + a_j + ga_{ij} + b/a_{jk} + e_{ijk}$$

where: Y_{ijk} is the observed phenotypic value of the i-th genotype, in the k-th block, within the j-th environment; μ is the general mean; g_i is the effect of the i-th genotype; a_j is the effect of the j-th environment; ga_{ij} is the interaction of the i-th genotype within the j-th environment; b/a_{jk} is the effect of the k-th block, within the j-th environment; e_{ijk} is the experimental error.

The averages of the genotypes were grouped by the Scott-Knott test (Scott & Knott, 1974), also at 5% probability. Then, the adaptability and stability analyzes were performed with the methods GGEbiplot (Yan, 2001) and Annicchiarico (1992). The methodology proposed by Annicchiarico is based on the Wi confidence index, which aims to demonstrate the risk of adopting a cultivar with performance below the general mean. Thus, the ideal cultivar is the one that presents the lowest risk and can be recommended, that is, the cultivar with the highest confidence index. The model used is as follows:

$$W_{i(g)} = \hat{\mu}_{i(g)} - Z_{(1-\infty)} \, \hat{S}_i,$$

where: $W_{i(g)}$ is the confidence index (%); $\hat{\mu}_{i(g)}$ is the mean percentage of the genotype i; S_i is the standard deviation of the percentage values; $Z_{(1-\infty)}$ is the percentile (1-α) of the cumulative normal distribution function, with α = 0.25.

For the GGE-Biplot analysis, only the main effect of genotype and G×E are important and must be considered together, and the main effect of the environment is not relevant for the selection of cultivars. The GGE biplot analysis was carried out according to the model expressed:

$$y_{ij} = \mu + \beta_j + y_{1\varepsilon i l\rho j l} + y_{2\varepsilon i 2\rho j 2} + \varepsilon_{ij}$$

where: y_{ij} is the mean grain yield of genotype i at environment j; μ is the overall mean of observations; β_j is the main effect of the environment; y_1 and y_2 are the errors associated to first (PC1) and second principal component (PC2), respectively; ε_1 and ε_1 are the values of PC1 and PC2, respectively, for the genotype of order i; ρj1 and ρj2 are the values of PC1 and PC2, respectively, for the environment of order j; and ε_{ij} is the error associated to the model of the ith genotype and j[th] environment (Yan, Hunt, Sheng, & Szlavnics, 2000).

This analysis was performed using the GGEBiplotGUI, package of the R software (R Core Team 2015) and the software Genes (Cruz, 2013).

RESULTS AND DISCUSSION

All plants that were exactly at the V2 developmental stage (V2+0D) showed epidermis with stomata and tector trichomes; angular collenchyma consisting of only one layer of cells; cortex of 6 to 9 layers, including aerenchyma and monocrystals were observed in the parenchyma cells of the primary phloem (Figure 1A). At this collection time (The significance was observed to effect of the genotypes at individual analysis. Then, the joint analysis of variance is shown in the Table 2. There was significance (p<0.01) for the sources of variation (genotype - G, environment - E, and the interaction GE) according to F test. A significant environmental effect (P<0.01) for all the traits was found, indicating differences among environments. These differences may be due to variations in macro-environmental aspects, such as soil type, climate, altitude, geography, or differences related to the crop cycle in the studied environments (Table 1).

The effect of genotype was significant (P<0.01) for all the traits, demonstrating that the observed differences in performances had genetic causes and, thereby, offer the possibility of selection and genetic gains. There was significant GxE interaction (P<0.01), indicating differential response of genotypes to the environments evaluated, and there may even be genotypes that display specific adaptability (Table 2). The coefficient of variation was satisfactory, indicating precision experimental (Table 2) as demonstrated by Almeida Júnior et al. (2020) and Silva et al. (2020).

Table 2. Summary of joint analysis of variance for fresh biomass yield (FBY), content of total soluble solids (TSS) and tons of Brix per hectare (TBH) of 25 genotypes of sweet sorghum, grown in different environments, in 2015/2016 agricultural year.

Source of variation	DF	Mean square		
		FBY	TSS	TBH
Block/E	20	545.54	7.38	16.68
Block	2	3203.43	5.37	101.38
Block x E	18	250.21	7.6	7.27
Genotypes (G)	24	497.64[**]	26.23[**]	22.29[**]
Environments (E)	9	28347.11[**]	453.50[**]	769.73[**]
G x E	216	206.24[**]	4.29[**]	7.54[**]
Error	480	112.09	2.76	4.04
Total	749			
Mean		54.73	15.91	8.73
CV(%)		19.35	10.45	23.01

[**]: significant at 1% probability by the F test. DF: Degrees of freedom; CV: coefficient of variation, in %.

The mean of fresh biomass yield (FBY) evaluated in each environment ranged from 34.72 t ha^{-1} in Pelotas to 94.69 t.ha^{-1} in Dourados, showing higher yield when compared to other studies, such as Souza, Parrella, Tardin and Costa (2013), where the yield was 27.31 t.ha^{-1} in Pelotas and 55.06 t.ha^{-1} in Goiânia,

thus validating the bioenergetic potential of these cultivars. The mean for total soluble solids (TSS) ranged from 11.80° Brix in Pelotas and 19.03° Brix in Sete Lagoas. And for TBH, ranged from 4.09 t.ha^{-1} in Pelotas to 14.35 t.ha^{-1} in Dourados.

According to the Scott-Knott test, the genotypes were classified into four groups. Then, the following genotypes were highlighted for FBY: B002, B004, B007, B008, B009, B012, B018, B020, CMSXS 647, CV198, which presented above mean yield in Dourados, Lavras, Nova Porteirinha, Penedo and Sete Lagoas. For TSS, genotypes with above mean values were B004, B007, B008, B010, B011, B012, B014, B015, B016, B019, B020, CMSXS 646, BRS 508 and BRS 511 in the environments of Sete Lagos, Sinop, Jaguariúna and Nova Porteirinha. These genotypes presented good quality of the juice, being these values higher than the one recommended for processing according to Masson et al. And for TBH, the genotypes that presented above mean values were B004, B005, B006, B007, B008, B011, B012, B015, B020, CMSXS 646, BRS 508 and CV198, in Dourados, Nova Porteirinha, Lavras and Sete Lagoas.

According to the environment classification, by Annicchiarico (1992) methodology, the estimation of the environmental index (Ij) was calculated for the traits FBY, TSS, and TBH (Table 3). This estimation of the environmental index validated the mean results obtained in the experiments classified as favorable or unfavorable.

Table 3. Environmental indices (Ij) and classification of favorable or unfavorable environments for cultivation, according to the methodology of Annicchiarico (1992). Values obtained by evaluating the traits of fresh biomass yield (FBY), content of total soluble solids (TSS) and tons of Brix per hectare (TBH), for 25 sweet sorghum genotypes evaluated in 2015/2016 agricultural year.

Environment	FBY		TSS		TBH	
	(Ij)	Class	(Ij)	Class	(Ij)	Class
Penedo	1.16	Favorable	-0.19	Unfavorable	0.08	Favorable
Dourados	39.96	Favorable	-0.82	Unfavorable	5.62	Favorable
Jaguariúna	-11.61	Unfavorable	2.42	Favorable	-0.76	Unfavorable
Lavras	20.67	Favorable	-0.78	Unfavorable	2.68	Favorable
Nova Porteirinha	15.35	Favorable	1.18	Favorable	3.20	Favorable
Passo Fundo	-12.26	Unfavorable	-3.46	Unfavorable	-3.46	Unfavorable
Pelotas	-20.01	Unfavorable	-4.11	Unfavorable	-4.64	Unfavorable
Planaltina	-17.99	Unfavorable	-0.06	Unfavorable	-2.90	Unfavorable
Sete Lagoas	-4.88	Unfavorable	3.12	Favorable	0.73	Favorable
Sinop	-10.38	Unfavorable	2.69	Favorable	-0.55	Unfavorable

Given these results, it was observed that for the Pelotas, Passo Fundo and Planaltina the lowest *Ij* values were estimated and, consequently, unfavorable for all the traits. And the Nova Porteirinha presented the favorable classification for all the traits. Then, the confidence index (Wi) was calculated for favorable environments $W_i(f)$ and for unfavorable environments $W_i(d)$. It is considered the

ideal genotype that provides the lowest risk of being adopted, in other words, the genotype that presents the greatest absolute value for the confidence index. The results are demonstrated in Tables 4, 5 and 6.

The genotypes CV198, B020, B004, B008, B005, B006, B009, B012, B019, B002, B017 and B014 had the lowest risk of having behavior below mean for FBY, considering 75% confidence (Table 4). For TSS, genotypes B008, BRS 508, B012, CMSXS647, B011, BRS511, B016, B015, B007, CMSXS646, B019 and B004. And for TBH, genotypes CV198, B006, B008, B005, CMSXS646, B010, B019, B009, B022, B017, B012, B016 and B004. Similar results were observed by Souza et al. (2013), that validate the use of the Annicchiarico method, using sweet sorghum genotypes.

The authors considering this methodology that is easy to implement and interpret, and it was possible through the reliability index to select genotypes that have adaptability and stability. The genotypes CV198 and B005 in favorable environments, and CV198 in unfavorable environments presented high Wi for FBY, with performances de 34.40% and 13.45% higher than mean. For TSS, the genotypes (B008 and BRS508) in favorable environments and (B008 and CMSXS647) in unfavorable environments. And for TBH, the genotypes (CV198 and B008) in unfavorable environments (B008 and B004). Thus, the CV198, B006, B008, B005 genotypes, in the general analysis, presented the lowest behavioral risks, the CV198 and B008 genotypes were the most responsive to environmental improvements, and the B008 genotype was highlighted because even in an unfavorable environment, it presented a behavior superior to the other genotypes.

The B008 genotype showed high Wi for TSS and TBH in the classification of the general analysis, in favorable and unfavorable environments, demonstrating that this genotype is widely adapted, in addition to having an mean content of SST 17.60° Brix, presenting quality agronomic potential in the juice. Thus, the B008 genotype is a promising sweet sorghum hybrid, developed through the research of the sweet sorghum breeding program of Embrapa Maize and Sorghum.

For the FBY the genotypes more adapted and stable, were CV198, B005, B006, B020 (Figure 1A). For TSS it was B012, B008, BRS 508, and CMSXS 646 (Figure 1B) and for TBH, B008, B012, B005, B020 (Figure 1C). The B008 and B012 genotypes were the more stable for both TSS and TBH, and B005 and B020 genotypes were the more stable for FBY and TBH. Some authors have found similar results when working with sweet sorghum. Alvels et al. (2020) aiming to select simultaneously, pre-commercial sweet sorghum hybrids with high adaptability and stability, via mixed models, in six different environments, evaluated 16 pre-commercial sweet sorghum hybrids, in the off-season of 2015/16 and 2016/17 in environments of the Brazilian Cerrado. This study demonstrated the possibility of obtaining high ethanol yield from sweet sorghum cultivated in the sugarcane off-season, using GGE biplot methodologies. Rono et al. (2016) evaluated eight sweet sorghum genotypes at five different locations in two growing seasons of 2014, and the GGE biplot showed high yielding genotypes EUSS10, ACFC003/12, SS14, and EUSS11 for cane yield; EUSS10, EUSS11, and SS14 for juice yield; and EUSS10, SS04, SS14, and ACFC003/12 for ethanol yield.

Based on the behavior of different genotypes in different environments, the formation of mega-environments is possible, where the mean of the genotype is compared to the mean of the mega-environment (Figure 2). For the FBY the environments were divided into two groups, starting from the blue lines that came from the origin of the biplot. For this trait, the environments were grouped as follows: Mega-environment 1: Penedo, Lavras, Pelotas, Sete Lagoas, and Sinop, where the best genotypes were those at the vertex of the group of environments,

highlighting the CV198 genotype. And the Mega-environment 2: Jaguariúna and Planaltina, highlighting the B007 genotype (Figure 2A). For the TSS, only one mega-environment was formed, consisting of Dourados, Lavras, Nova Porteirinha, Pelotas, Planaltina, Sete Lagoas and Sinop. For this mega-environment the genotypes B008 and B012 highlighting (Figure 2B). And for TBH two mega-environments were grouped as follows: Mega-environment 1: Penedo, Lavras, Passo Fundo, Pelotas, Sete Lagoas, and Sinop, highlighting the CV198 genotype. And in the second mega-environment: Dourados, Jaguariúna and Planaltina, highlighting genotype B019 (Figure 2C).

Table 4. Parameters of adaptability and overall stability (Wi) in favorable environments (Wi(f)) and in unfavorable environments (Wi(u)) of 25 genotypes of sweet sorghum for fresh biomass yield (FBY), based on the methodology of Annicchiarico (1992), for 25 sweet sorghum genotypes evaluated in 2015/2016 agricultural year.

| General		Favorable		Unfavorable	
Genotype	W_i	Genotype	$W_i(f)$	Genotype	$W_i(u)$
CV 198	122.27	CV 198	134.40	CV 198	114.18
B020	108.82	B005	113.45	B004	111.07
B004	108.40	B006	107.72	B009	110.59
B008	106.56	B020	106.58	B020	110.32
B005	106.28	B004	104.40	B012	109.24
B006	104.44	B010	104.40	B008	109.00
B009	103.57	CMSXS 647	103.30	B019	103.23
B012	102.54	B008	102.89	B006	102.25
B019	100.91	B002	102.31	B005	101.50
B002	100.72	B003	100.92	B017	101.05
B017	100.24	B014	100.50	B011	100.70
B014	100.18	B015	100.06	B014	99.97
B003	99.18	B017	99.02	B002	99.65
CMSXS 647	98.90	B018	97.71	BRS 511	98.29
B015	97.32	B019	97.42	B003	98.01
BRS 511	96.87	BRS 508	96.98	B016	96.87
BRS 508	96.25	B001	95.72	CMSXS 647	95.97
B011	95.99	CMSXS 646	95.46	B007	95.78
B010	94.83	BRS 511	94.73	BRS 508	95.77
B007	94.53	B009	93.03	B015	95.49
B018	94.48	B007	92.67	B018	92.34
B016	93.87	B012	92.48	CMSXS 646	92.13
CMSXS 646	93.46	B016	89.36	B001	90.13
B001	92.37	B011	88.93	B010	88.45
B013	87.04	B013	85.56	B013	88.02

Table 5. Parameters of adaptability and overall stability (Wi) in favorable environments (Wi(f)) and in unfavorable environments (Wi(u)) of 25 genotypes of sweet sorghum for total soluble solids (TSS), based on the methodology of Annicchiarico (1992), for 25 sweet sorghum genotypes evaluated in 2015/2016 agricultural year.

General		Favorable		Unfavorable	
Genotype	W_i	Genotype	$W_i(f)$	Genotype	$W_i(u)$
B008	111.15	B008	110.17	B008	111.80
BRS 508	109.83	BRS 508	109.58	CMSXS647	111.25
B012	107.40	B012	108.40	BRS 508	109.99
CMSXS647	107.37	B016	106.61	B011	107.93
B011	106.71	B007	105.46	B012	106.73
BRS 511	104.30	B011	104.88	B015	105.03
B016	104.27	B019	104.45	BRS 511	104.47
B015	103.19	BRS 511	104.06	CV 198	103.21
B007	102.70	CMSXS646	101.79	CMSXS646	102.75
CMSXS646	102.37	B009	101.78	B016	102.70
B019	102.15	CMSXS647	101.54	B004	101.97
B004	100.41	B015	100.42	B007	100.86
B005	99.22	B014	99.47	B019	100.62
B014	98.72	B005	99.26	B005	99.19
CV 198	98.55	B002	98.78	B010	98.83
B010	98.39	B004	98.06	B006	98.69
B002	97.81	B010	97.74	B014	98.22
B006	97.57	B003	97.39	B002	97.16
B009	94.94	B006	95.88	B018	94.48
B001	93.63	B001	95.27	B001	92.54
B003	93.40	B013	94.79	B017	92.06
B018	93.33	B018	91.61	B003	90.75
B017	91.42	CV 198	91.55	B009	90.37
B013	91.25	B022	90.60	B022	89.52
B022	89.95	B017	90.47	B013	88.88

Table 6. Parameters of adaptability and overall stability (Wi) in favorable environments (Wi(f)) and in unfavorable environments (Wi(u)) of 25 genotypes of sweet sorghum for tons of Brix per hectare (TBH), based on the methodology of Annicchiarico (1992), for 25 sweet sorghum genotypes evaluated in 2015/2016 agricultural year.

General		Favorable		Unfavorable	
Genotype	W_i	Genotype	$W_i(f)$	Genotype	$W_i(u)$
CV 198	121.04	CV 198	134.98	B008	120.50
B006	118.27	B008	116.03	B004	117.73
B008	111.21	CMSXS 646	108.61	CMSXS 646	113.81
B005	110.08	B005	108.50	B012	113.58
CMSXS 646	109.13	B012	106.58	BRS 508	110.54
B010	106.13	B006	105.61	B009	110.12
B019	105.40	CMSXS 647	104.55	B011	108.52
B009	103.78	B010	102.62	CV 198	107.10
B022	101.97	BRS 508	101.72	B019	107.04
B017	101.90	B004	100.53	BRS 511	103.70
B012	100.98	B019	100.51	B015	102.67
B016	100.86	BRS 511	100.23	B005	102.31
B004	100.19	B014	98.82	B007	100.07
B007	99.62	B002	98.72	B014	99.46
B014	99.14	B003	96.78	B016	97.53
B003	98.12	B016	96.61	B002	97.51
B011	97.68	B015	96.56	CMSXS 647	97.17
BRS 511	97.07	B007	95.29	B006	96.35
B001	94.02	B011	95.28	B017	91.92
B015	92.10	B018	92.55	B022	89.07
B002	90.16	B009	90.25	B003	87.41
B018	87.90	B001	89.77	B010	85.42
BRS 508	87.53	B017	88.40	B001	83.45
CMSXS 647	86.61	B022	85.99	B018	83.26
B013	79.13	B013	84.51	B013	73.75
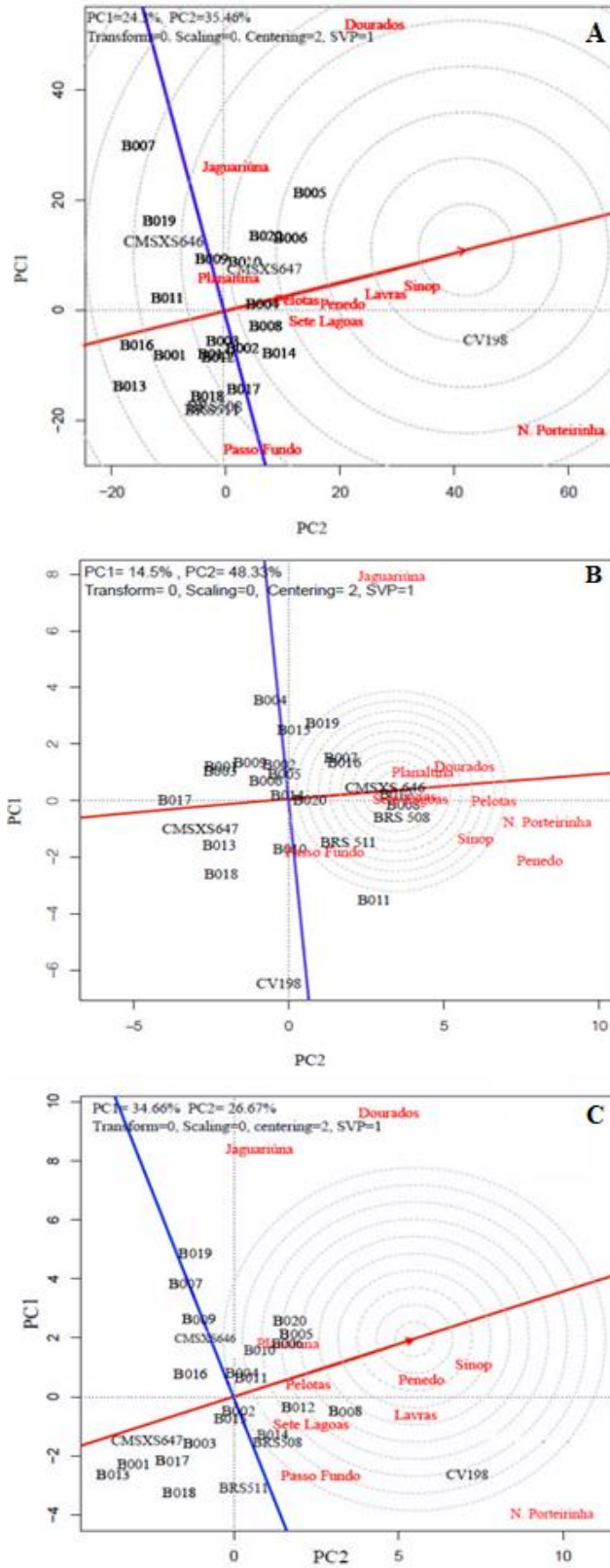
Figure 1. Classification of 25 sweet sorghum genotypes according to the GGE biplot model in ten environments during the 2015/2016 agricultural year. A: fresh biomass yield (FBY); B: content of total soluble solids (TSS); and C: tons of Brix per hectare (TBH).

Figure 2. Groups of mega-environments according to the GGE biplot model in ten environments during the 2015/2016 agricultural year. A: fresh biomass yield (FBY); B: content of total soluble solids (TSS); and C: tons of Brix per hectare (TBH).

Figueiredo et al. (2015) used the GGEbiplot method and found that the CMSXS 647 genotype presented the best stability and adaptability for FBY and TBH. This genotype was also used in the present work but did not obtain similar behavior. This can be explained by the fact that the genotype was evaluated in only six similar environments, Dourados, Nova Porteirinha, Passo Fundo, Pelotas, Sete Lagoas, and Sinop.

Thus, the adaptability and stability study methods used in this work presented satisfactory and consistent results, aiming at the selection of more adapted and stable genotypes for bioenergy production. Also, B005 and B008 sweet sorghum genotypes, showed superior performance, with similar classification in both methods. However, new studies of the adaptability and stability in the different agricultural year and new environments are important to obtain more complete information on the performance of sweet sorghum genotypes for bioenergy production.

CONCLUSIONS

The Annicchiarico and GGEbiplot adaptability and stability study methods presented satisfactory and consistent results and can be used separately or together in sweet sorghum breeding programs.

B005 and B008 sweet sorghum genotypes presented superior performance, with similar classification in both methods studied.

ACKNOWLEDGMENTS

REFERENCES

Almeida Júnior, J. J., Smiljanic, K. B. A., Matos, F. S. A., Perozini, A. C., Sousa, J. V. A., Junior, L. F. R., ... & Liberato, P. V. (2020). Utilização de fertilizante agroecologicamente correto no sorgo granífero BRG 21320 em diferentes doses, plantado em segunda safra no Sudoeste Goiano. *Brazilian Journal of Development*, 6(11), 87904-87915. https://doi.org/10.34117/bjdv7n9-352

Almeida Filho, J. E., Tardin, F. D., Daher, R. F., Silva, K. J., Xavier Neto, J. B., Bastos, E., Lopes, V. S., Barbé, T. C., & Menezes, C. B. (2014). Avaliação agronômica de híbridos de sorgo granífero em diferentes regiões produtoras do Brasil. *Revista Brasileira de Milho e Sorgo*, 13, 82-95.

Alvels, J. A. G., Cabral, P. D. S., Teodoro, P. E., Candido, L. S., Silva, F. H. L., Neto, J. H., & Reis, E. F. (2020). Adaptability and Genotypic Stability of Sweet Sorghum in the Brazilian Cerrado. *Sugar Tech*, 1-20. https://doi.org/10.1007/s12355-020-008716

Annicchiarico, P. (1992). Cultivar adaptation and recommendation from alfalfa trials in Northern Italy. *Journal of Genetics and Plant Breeding*, 46, 269-278.

Appiah-Nkansah, N. B., Li, J., Rooney, W., & Wang, D. (2019). A review of sweet sorghum as a viable renewable bioenergy crop and its techno-economic analysis. *Renewable Energy*, 143, 1121-1132. https://doi.org/10.1016/j.renene.2019.05.066

Badu-Apraku, R. O., Akinwale, M. A. B., Fakorede, M., & Oyekunle, J. (2012). Relative changes in genetic variability and correlations in an early-maturing maize population during recurrent selection. *Theoretical and Applied Genetics*, 125, 1289-1301. https://doi.org/10.1007/s00122-012-1913-8

Cruz, C. D. (2013). GENES - A software package for analysis in experimental statistics and quantitative genetics. *Acta Scientiarum Agronomy*, 35, 271-276. http://dx.doi.org/10.4025/actasciagron.v35i3.21251

Cruz, C. D., Regazzi, A. J., Carneiro, P. C. S. (2012). *Modelos biométricos aplicados ao melhoramento genético – Volume 2.* (4ª ed.). Viçosa, MG: Editora UFV.

Figueiredo, U. J., Nunes, J. A. R., Parrella, R. A. C., Souza, E. D., Silva, A. R., Emygdio, B. M., Machado, J. R. A., & Tardin, F. D. (2015) Adaptability and stability of genotypes of sweet sorghum by GGEbiplot and Toler methods. *Genetics and Molecular Research*, 14, 11211-11221. http://dx.doi.org/10.4238 / 2015.em.22.15

Klasson, K. T., Qureshi, N., Powell, R., Heckemeyer, M., & Eggleston, G. (2018) Fermentation of Sweet Sorghum Syrup to Butanol in the Presence of Natural Nutrients and Inhibitors. *Sugar Tech,* 20, 224–234. https://doi.org/10.1007/s12355-018-0594-2

Leite, P. S. S., Botelho, T. T., Ribeiro, P. C. O., Schaffert, R. E., Parrella, R. A. C., & Nunes, J. A. R. (2019). Intrapopulation recurrent selection in sweet sorghum for improving sugar yield. *Industrial Crops and Production*. https://doi.org/10.1016/J.INDCROP.2019. 111910. 111910

Masson, I. S., Costa, G. H. G., Roviero, J. P., Freita, L. A., Đutton, M. A., & Mutton, M. J. R. (2015) *Ciência Rural*, (45), 9. https://doi.org/10.1590/0103-8478cr20130549

R Core Team (2015). *R: A language and environment for statistical computing*. Vienna, Austria: R Foundation for Statistical Computing. Retrieved from: www.R-project.org/

RFA - Renewable Fuels Association (2019). *World Fuel Ethanol Production*. URL: https://ethanolrfa.org/resources/industry/statistics/

Ribeiro, P. C. O., Salvador, F. V., Oliveira, I. C. M., & Menezes, C. B. (2021). Factor analysis and environmental stratification in the assessment of grain sorghum adaptability and stability. *Agronomy Science and Biotechnology*, *7*, 1–8. https://doi.org/10.33158/asb.r134.v7.2021

Rono, J. K., Cheruiyot, E. K., Othira, J. O., Njuguna, V. W., Macharia, J. K., Owuoche, J., Oyier, M., & Kange, A. M. (2016). Adaptability and stability study of selected sweet sorghum genotypes for ethanol production under different environments using AMMI analysis and GGE biplots. *The Science World Journal*, 1-14. https://doi.org/10.1155/2016/4060857

Santos, A. D., Amaral Júnior, A. T., Kurosawa, R. D. N. F., Gerhardt, I. F. S., & Fritsche Neto, R. (2017). GGE Biplot projection in discriminating the efficiency of popcorn lines to use nitrogen. *Ciência e Agrotecnologia*, 41, 22-31. https://doi.org/10.1590/1413-70542017411030816

Scott, A. J., & Knott, M. (1974). A cluster analysis method for grouping means in the analysis of variance. *Biometrics*, 30, 507-512. https://doi.org/10.2307/2529204

Silva, P. C., Silva, M. V., Pereira, A. D., Costa, A. R., Giongo, P. R., de Abreu, J. P., & Moraes, V. H. (2020). Produtividade e características biométricas de Sorgo Sacarino sob torta de Filtro. *Brazilian Journal of Development*, 6(10), 78212-78226.

Silva, M. J., Pastina, M. M., Souza, V.F., Schaffert, R. E., Carneiro, P. C. S., Noda, R. W., Carneiro, J. E. S., Damasceno, C. M. B., & Parrella, R. A. C. (2017). Phenotypic and molecular characterization of sweet sorghum accessions for bioenergy production. *PLoS One* 12, 1-19. 4. https://doi.org/0.1371/journal.pone.0183504

Souza, R. S., Parrella, R. A. C., Souza, V. F., & Parrella, N. N. L. D. (2016). Maturation curves of sweet sorghum genotypes. *Ciência e Agrotecnol*ogia, 40, 46-56. https://doi.org/10. 1590/S1413-70542016000100004

Souza V. F., Parrella, R. A. C., Tardin, F. D., & Costa, M. R. (2013). Adaptability and stability of sweet sorghum cultivars. *Crop Breeding Applied Biotechnology,* 13, 144 151. ISSN 1984-7033.

Teixeira, T. P. M., Pimentel, L. D., Dias, L. A. S., Parrella, R. A. C., Paixão, M. Q., & Biesdorf, E. M. (2017). Redefinition of sweet sorghum harvest time: New approach for sampling and decision making in field. *Industrial Crops and Products*, 109, 579-586. https://doi.org/10.1016/j.indcrop.2017.09.002

Yan, W. (2014). *Crop variety trials: data management and analysis*. Chichester: Wiley.

Yan, W. (2001) GGEbiplot-A windows application for graphical analysis of multienvironment trial data and other types of two-way data. *Agronomy Journal*, 93, 1111-1118. https://doi: 10.2134 / agronj2001.9351111x

Yan, W., Hunt, L.A., Sheng, Q., & Szlavnics, Z. (2000) Cultivar evaluation and mega environment investigation based on the GGE biplot. *Crop Science*, 40, 597-605. https://doi:10.2135 /cropsci2000.403597x

Whitford, R., Fleury, D., Reif, J.C., Garcia, M., Okada, T., Korzun, V., & Langridge, P. (2013). Hybrid breeding in wheat: technologies to improve hybrid wheat seed production. *Journal of Experimental. Botany*, 64, 5411–5428. https://doi.org/10.1093/jxb/ert333