

## ARTICLE

## Agronomic Application of Genetic Resources

# Identification of mega-environments for grain sorghum in Brazil using GGE biplot methodology

Karla Jorge da Silva<sup>1</sup>  | Paulo Eduardo Teodoro<sup>2</sup>  | Michele Jorge da Silva<sup>3</sup>  |  
 Larissa Pereira Ribeiro Teodoro<sup>2</sup> | Milton José Cardoso<sup>4</sup> |  
 Vicente de Paulo Campos Godinho<sup>5</sup> | José Hortêncio Mota<sup>6</sup> | Gustavo André Simon<sup>7</sup> |  
 Flávio Dessaune Tardin<sup>1</sup> | Adelmo Resende da Silva<sup>1</sup> | Fernando Lisboa Guedes<sup>8</sup> |  
 Cicero Beserra de Menezes<sup>1</sup> 

<sup>1</sup> Embrapa Milho e Sorgo, P.O. Box 151, Sete Lagoas, MG 35701-970, Brazil

<sup>2</sup> Departamento de Agronomia, UFMS, P.O. Box 112, Chapadão do Sul, MS 79560-000, Brazil

<sup>3</sup> Departamento de Biologia Geral, UFV, Viçosa, Minas Gerais 36570-000, Brazil

<sup>4</sup> Embrapa Meio-Norte, P.O. Box 112, Teresina, PI 64008-780, Brazil

<sup>5</sup> Embrapa Rondônia, P.O. Box 127 RO, Vilhena 76980-000, Brazil

<sup>6</sup> Departamento de Agronomia, UFJ, P.O. Box 03, Jataí, GO 75801-615, Brazil

<sup>7</sup> Faculdade de Agronomia, UniRV, P.O. Box 104, Rio Verde, GO 75901-970, Brazil

<sup>8</sup> Embrapa Caprinos e Ovinos, P.O. Box 71, Sobral, CE 62010-970, Brazil

## Correspondence

Cicero Beserra de Menezes, Embrapa Milho e Sorgo, P.O. Box 151, 35701-970, Sete Lagoas, MG, Brazil.

Email: [cicero.menezes@embrapa.br](mailto:cicero.menezes@embrapa.br)

Assigned to Associate Editor Madhav Bhatta.

## Funding information

Embrapa Maize and Sorghum; Centro Nacional de Desenvolvimento Científico e Tecnológico

## Abstract

The performance of genotypes in a wide range of environments can be affected by extensive genotype  $\times$  environment ( $G \times E$ ) interactions, making the subdivision of the testing environments into relatively more homogeneous groups of locations (mega-environments) a necessary strategy. The genotype main effects + genotype  $\times$  environment interaction biplot method (GGE) allows identification of mega-environments and selection of stable genotypes adapted to specific environments and mega-environments. The objectives of this study were to identify mega-environments regarding sorghum [*Sorghum bicolor* (L.) Moench] grain yield and demonstrate that the GGE biplot method can identify essential locations for conducting tests in different mega-environments. A total of 22 competition trials of grain sorghum genotypes were conducted over three crop seasons across several production locations in Brazil. A total of 25, 22, and 30 genotypes were evaluated during the first, second, and third crop seasons, respectively. After identifying the presence of  $G \times E$  interactions, the data were subjected to adaptability and stability analyses using the GGE biplot method. A phenotypic correlation network was used to express functional relationships between environments. The GGE biplot was found to be an efficient approach for identifying three mega-environments in grain sorghum in Brazil, selecting representative and discriminative environments, and recommending more adaptive and stable grain sorghum genotypes.

## 1 | INTRODUCTION

Sorghum [*Sorghum bicolor* (L.) Moench], native to Africa, is a cereal of the family Poaceae and was domesticated between 3,000 and 5,000 yr ago (Arendt & Zannini, 2013; Patil,

**Abbreviations:** GGE, genotype and  $G \times E$  interaction;  $G \times E$ , genotype  $\times$  environment; PCA, principal component analysis; SL, Sete Lagoas; GUA, Guaira; JAN, Janaúba; JAT, Jataí; RV, Rio Verde; SIN, Sinop; SOB, Sobral; TER, Teresina; UBE, Uberaba; VIL, Vilhena.

2016). It is the fifth most important cereal crop worldwide after maize (*Zea mays* L.), wheat (*Triticum aestivum* L.), rice (*Oryza sativa* L.), and barley (*Hordeum vulgare* L.) (FAOSTAT, 2018) and has a wide range of applications, including as food, feed, and fuel (Liu et al., 2013; Mathur et al., 2017; Tuinstra, 2008). In Brazil, the land area of grain sorghum is excessive, reaching a crop production of 3.3 Tg in an area of approximately 817,000 ha (CONAB, 2020).

In Brazil, sorghum is grown in several states, especially in the Midwest and Triângulo Mineiro in Goiás and Minas Gerais states (CONAB, 2020). Due to the great territorial extension of the country, different edaphoclimatic conditions are common among these sites. Sorghum has peculiarities that might interfere with its development depending on the latitude at which it is cultivated. Efforts have been taken in the genetic breeding of crops to establish cultivars adapted to the different cultivation regions (Ramos et al., 2017). This factor contributes to the occurrence of genotype  $\times$  environment ( $G \times E$ ) interactions, defined as the differential response of genotypes as a function of the environmental gradient. The  $G \times E$  interaction is one of the major bottlenecks in plant breeding because it causes difficulties in recommending genotypes for a group of environments or regions (Cruz et al., 2012).

The final step in sorghum breeding programs is to evaluate the genotypes annually in different environments, before their final recommendation and multiplication. Most of the time, the environments have distinct edaphoclimatic characteristics; therefore, there is a  $G \times E$  interaction. Identifying the magnitude of the  $G \times E$  interaction makes it possible to evaluate the selection strategies and ensures a high degree of reliability in recommending genotypes, and maximizing yield and other attributes of interest to a particular location or group of environments (Cruz et al., 2012). Because of the presence of  $G \times E$  interactions, none of the crop cultivars perform well in all environments (Ghaderi et al., 1980), and the interpretation of the performance of many genotypes in multi-location trials is generally affected by extensive  $G \times E$  interactions (Gauch & Zobel, 1996). Therefore, the planning of breeding and testing activities requires subdivision of the testing environments into relatively more homogeneous groups of locations, called mega-environments, where specific genotypes can be targeted for each of these groups of locations (Gauch & Zobel, 1997). Mega-environment differentiation is indicated when different genotypes perform best in different subregions across many years (Yan, 2014).

Several statistical analyses have been proposed to interpret the  $G \times E$  interaction to investigate these effects, including the genotype and  $G \times E$  interaction biplot method (GGE). The GGE biplot, proposed by Yan et al. (2000), has been widely employed in sorghum breeding (Batista et al., 2017; Figueir, 2015; Gill et al., 2014; Rakshit et al., 2012; Rakshit, Ganapathy, et al., 2014; Rakshit et al., 2016; Teodoro et al., 2016;

### Core Ideas

- Identifying mega-environments in Brazil for sorghum planting, during the off-season.
- Selecting representative and discriminative environments for sorghum in Brazil.
- Recommending more adapted and stable grain sorghum genotypes for the off-season in Brazil.

Rao et al., 2011). This method uses principal components applied to the effects of genotypes plus  $G \times E$  interaction to delimit mega-environments, identify testing locations, and recommend the best genotypes (Dalló et al., 2019; Singh et al., 2020). Shape and patterns are shown in the biplot, including the correlations between testing environment, depending on the relative magnitude of genotype and  $G \times E$  interaction effects. Biplots display both genotypes and  $G \times E$  interaction components, which are the two relevant sources of variation in cultivar evaluation and must be considered simultaneously for appropriate genotypic and environmental evaluation. Thus, it is crucial to identify groups of environments with similar edaphoclimatic characteristics and, within these, the location with the highest power to discriminate genotypes, which are called essential locations. The objective of the present study was to identify mega-environments in terms of sorghum grain yield and demonstrate that the GGE biplot method can identify essential locations for conducting tests in each mega-environment.

## 2 | MATERIAL AND METHODS

### 2.1 | Plant materials and multi-environment trials

Grain yield of 22 sorghum genotypes were evaluated in the crop seasons of 2016/2017, 2017/2018, and 2018/2019, in several production locations in Brazil. Detailed features of the testing locations (environments) and years are listed in Table 1. A randomized complete block design with three replications was used for each location. A total of 25 sorghum genotypes were evaluated in 2016/2017, of which 22 were pre-commercial hybrids of Embrapa Maize and Sorghum and 3 were commercial cultivars 50A70, BRS 373, and BRS 330. In 2017/2018, 22 genotypes were pre-commercial hybrids of Embrapa Maize and Sorghum and three were commercial cultivars 1G 100, BRS 373, and BRS 330. In 2018/2019, 30 sorghum genotypes were assessed, of which 28 were pre-commercial hybrids from Embrapa Maize and Sorghum and two were commercial cultivars 1G 100 and BRS 373. Each plot consisted of four 5-m rows, with 0.5-m spaces

TABLE 1 Characterization of sorghum genotype assessment environments in Brazil

Year	Local/State	Code	Altitude m	Latitude	Longitude	Average temperature °C	Accumulated rainfall mm
2016	Sete Lagoas/MG	SL	773	-19°28'	-44°15'	21.7	576
2016	Guaíra/PR	GUA	507	-20°03'	-48°06'	24.5	877
2016	Janaúba/MG	JAN	516	-15°48'	-43°19'	27.1	424
2016	Teresina/PI	TER1	81	-5°05'	-42°48'	26.7	219
2016	Teresina/PI	TER2	81	-5°05'	-42°48'	26.7	219
2016	Vilhena/RO	VIL	577	-12°44'	-60°08'	24.9	772
2016	Sinop/MT	SIN	345	11°51'	55°3'	26.3	1,131
2017	Sete Lagoas/MG	SL	773	-19°28'	-44°15'	21.3	337
2017	Janaúba/MG	JAN	516	15°48'	43°19'	26.9	191
2017	Guaíra/PR	GUA	507	-20°03'	-48°06'	24.9	260
2017	Uberaba/MG	UBE	752	19°45'	47°55'	22.3	366
2017	Rio Verde/GO	RV	754	-17°47'	-50°55'	22.5	618
2017	Jataí/GO	JAT	731	-17°52'	51°43'	22.3	408
2017	Teresina/PI	TER	81	-5°05'	-42°48'	26.9	200
2018	Sete Lagoas/MG	SL	773	-19°28'	-44°15'	23.0	726
2018	Guaíra/PR	GUA	507	-20°03'	-48°06'	24.7	472
2018	Jataí/GO	JAT	731	-17°52'	51°43'	23.5	799
2018	Rio Verde/GO	RV	754	-17°47'	-50°55'	22.7	663
2018	Sinop/MT	SIN	345	11°51'	55°3'	26.7	1,179
2018	Sobral/CE	SOB	66	-3°40'	-40°21'	26.0	647
2018	Teresina/PI	TER	81	-5°05'	-42°48'	26.5	837
2018	Vilhena/RO	VIL	577	-12°44'	-60°08'	24.0	780

Note. MG: Minas Gerais; SP: São Paulo; PI: Piauí; RO: Rondônia; MT: Mato Grosso; GO: Goiás; CE: Ceará.

between rows and 0.1-m spaces between the plants within each row. In each plot, the grain yield was evaluated in two central rows, corrected to 13% humidity, and estimated at tonnes per hectare. The experimental management system followed the technical recommendations for assessment environments in Brazil.

## 2.2 | Data analysis

Analysis of variance was performed for each environment (individual analysis) to assess the genetic variability among the sorghum genotypes during each crop season. After the individual analysis of variance, the feasibility of performing a joint analysis of variance was analyzed based on the reasoning proposed by Pimentel-Gomes (2009), who suggested that joint analysis of variance should only be performed if the relationship between the residual variances of the experiments is lower than seven. Thus, a joint analysis of variance of the trials was conducted for each crop season,

according to the statistical model described in Equation 1:

$$Y_{ijk} = \mu + B/E_{jk} + G_i + E_j + G \times E_{ij} + \varepsilon_{ijk} \quad (1)$$

where  $Y_{ijk}$  is the observation of the  $k$ th block evaluated in the  $i$ th genotype and  $j$ th environment;  $\mu$  is the overall mean of the experiments;  $B/E_{jk}$  is the effect of block  $k$  within environment  $j$ ;  $G_i$  is the effect of the  $i$ th genotype considered as random;  $E_j$  is the effect of the  $j$ th year considered as fixed;  $G \times E_{ij}$  is the random effect of the interaction between genotype  $i$  and environment  $j$ ; and  $\varepsilon_{ijk}$  is the random error associated with  $Y_{ijk}$  observation, assumed to be independent  $\varepsilon \sim N(0, \sigma^2)$ .

Once the presence of a  $G \times E$  interaction was confirmed in each crop season, the data were subjected to adaptability and stability analyses using a GGE biplot (Yan et al., 2000). The GGE biplot analysis was performed according to the model expressed in Equation 2:

$$Y_{ij} - y_j = \lambda_1 \alpha_{i1} \beta_{j1} + \lambda_2 \alpha_{i2} \beta_{j2} + \varepsilon_{ij} \quad (2)$$

where,  $y_{ij}$  is the mean grain yield of genotype  $i$  in environment  $j$ ;  $y_j$  is the overall mean of the observations;  $\lambda_1$  and  $\lambda_2$  are the singular values of the first and second principal components, respectively;  $\alpha_{i1}$  and  $\alpha_{i2}$  are the first two eigenvectors for the  $i$ th genotype;  $\beta_{j1}$  and  $\beta_{j2}$  are the first two eigenvectors for the  $j$ th environment; and  $\varepsilon_{ij}$  is the error associated with the model with normal distribution, with zero mean and variance  $\sigma^2/r$  (where  $\sigma^2$  is the variance of the error between plots for each environment and  $r$  is the number of replications) (Yan et al., 2000).

In the GGE biplot analysis, only the main effect of genotype and  $G \times E$  interaction is important and must be considered together, and the main effect of the environment is not relevant for the selection of cultivars. The GGE biplot was built on the first two principal components from principal component analysis. When the first component is highly correlated with the main effect of the genotype, the proportion of the yield is due only to the characteristics of the genotype. The second component represents part of the yield due to the  $G \times E$  interaction (Yan, 2011).

A phenotypic correlation network was used to express the functional relationships between environments. The thickness of the lines represents the absolute value of the correlation, which was controlled by applying a cut-off value of 0.5 to visualize the graph more easily. Values that were  $|r_{ij}| \geq 0.5$  had their lines highlighted proportionally to the intensity of the correlation. The fine lines had correlations lower than the cut-off point of 0.5 and were not highlighted to distinguish the values. Finally, positive correlations were highlighted in green, whereas negative correlations were represented in red.

Data were processed using R software (R Core Team, 2018) using the *metan* package (Olivoto and Lúcio, 2020) for multi-environment analyses and the *psych* package (Revelle, 2020) for the correlation network.

### 3 | RESULTS

The mean squares by the joint analysis of variance (Table 2), considering each crop season, showed significant ( $P \leq .05$ ) differences for genotypes, environments, and  $G \times E$  interaction effects, except for 2017/2018 when the effect of genotypes was not significant (Table 2). The coefficient of variation was low for the three crop seasons, emphasizing the satisfactory experimental quality of the trials (Table 2).

The mega-environments obtained for each crop season are shown in Figure 1, with this model defined in “which-one-where.” A polygon was generated that connected genotypes G2, G9, G13, G14, G15, and G16 in 2016/2017 (Figure 1a); G11, G12, G15, G17, G19, and G20 in 2017/2018 (Figure 1b); and G1, G18, G4, G6, G14, G15, and G25 in 2018/2019 (Figure 1c), further away from the biplot

**TABLE 2** Summary of joint analysis of variance for grain yield of sorghum genotypes evaluated in Brazil environments in three crop seasons

	2016/2017	2017/2018	2018/2019
<b>Source of variation</b>	<b>Mean squares</b>		
Blocks/ Environments	3.83ns	0.61ns	2.03ns
Genotypes (G)	4.10*	1.63ns	3.55*
Environments (E)	19.82*	80.73*	42.09*
$G \times E$	1.92*	1.28*	1.26*
Coefficient of variation, %	18.74	15.28	17.08
Mean, t ha <sup>-1</sup>	3.73	4.01	3.97

Note: ns: Not significant.

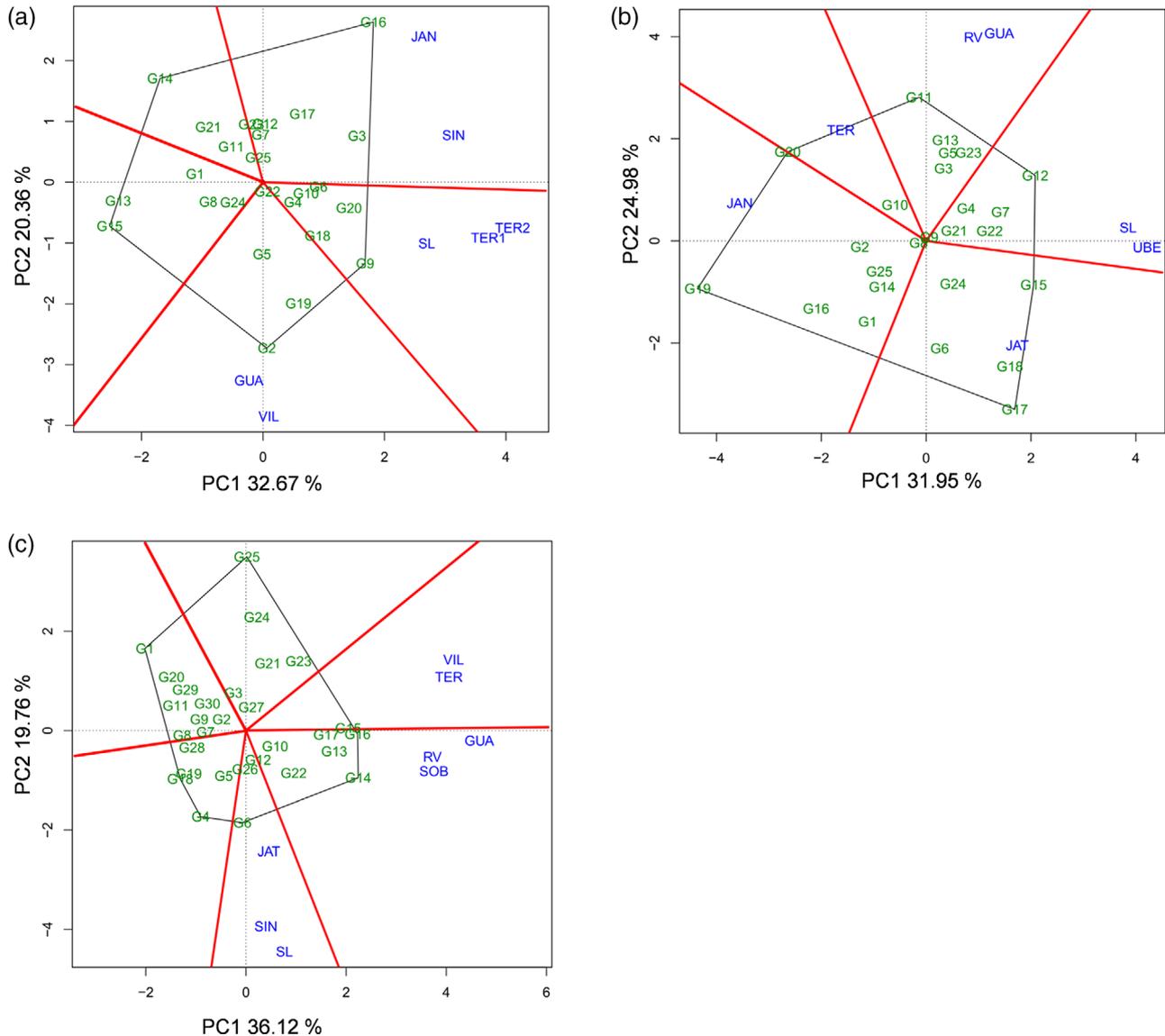
\*Significant at .05 probability by the  $F$  test.

origin. These genotypes had the largest vectors in each direction. The vector of length and direction is the extension of the genotype responsible for the tested environments. All other genotypes were contained within the polygon and had smaller vectors, that is, they were less sensitive compared to the interaction with the environments of each sector.

Figures 1a and 2a show that the seven environments could be divided into three mega-environments by the lines that came from the origin of the biplot in 2016/2017. The mega-environments were formed by (1) GUA and VIL; (2) SL, TER1, and TER2; and (3) SIN and JAN. The G2 genotype was the vertex of the mega-environment 1 sector, and it performed best in this group. G9 was the vertex of the mega-environment 2 sector, and it was the most adapted genotype in this group. Lastly, the G16 genotype was the most adapted in mega-environment 3 (Figure 1a).

For 2017/2018 (Figures 1b and 2b), there was a division into five mega-environments: (1) JAT, (2) SL and UBE, (3) RV and GUA, (4) TER, and (5) JAN. Genotypes G17, G12, G11, G20, and G19 were the most adapted in each of these mega-environments. In 2018/2019 (Figures 1c and 2c), there was a division into three mega-environments: (1) JAT, SIN, and SL; (2) RV, SOB, and GUA; and (3) VIL and TER. Genotypes G6, G14, and G16 exhibited better performance. If a GGE biplot was unsuitable for exhibiting  $G \times E$  interaction standards, the alternative was to build a GGE biplot based on a data subset, removing those genotypes that had not performed well in all or most test environments.

The GGE biplot graph of the “ideal genotype” is shown in Figure 3. Based on these criteria, of the 25 genotypes evaluated in the 2016/2017 crop season (Figure 3a), G22 was close to ideality, followed by G25, G24, G4, G7, and G11, whereas G3, G20, G9, G19, and G18 showed high averages. For 2017/2018 (Figure 3b), G8, G9, and G21 were close to



**FIGURE 1** Mega-environments obtained by the genotype main effects + genotype × environment interaction (GGE) biplot for grain yield of sorghum genotypes evaluated during the crop season of (a) 2016/2017, (b) 2017/2018, and (c) 2018/2019. SL: Sete Lagoas; GUA: Guaira; JAN: Janaúba; TER1: Teresina; TER2: Teresina; VIL: Vilhena; SIN: Sinop; UBE: Uberaba; RV: Rio Verde; JAT: Jatai; TER: Teresina; SOB: Sobral

ideality, and G17 and G19 were distant from ideality. For 2018/2019 (Figure 1c), G10 and G12 were close to ideality.

Therefore, during the 2016/2017 crop season, among the seven environments, TER1, TER2, and VIL were the most discriminating (most informative) (Figure 4a). In Figure 4b, UBE and SL were the most discriminating environments. During the 2018/2019 crop season, GUA was the most discriminating environment (Figure 4c).

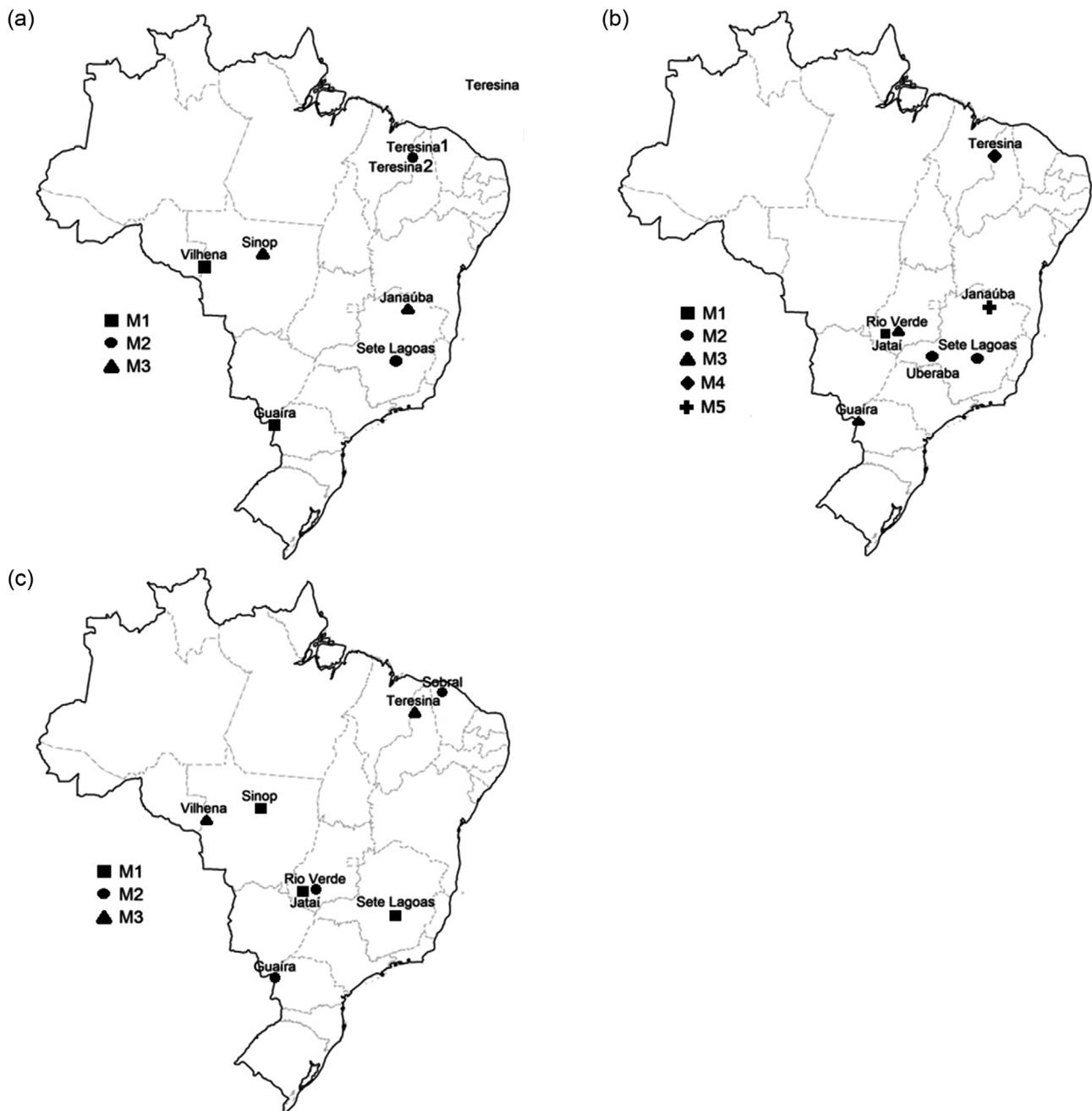
The phenotypic correlations between pairs of locations were estimated and expressed graphically using the correlation network (Figure 5). In mega-environment 1, there was a positive and moderate magnitude correlation between VIL and GUA. For mega-environment 2, there was a high and positive correlation between TER1 and TER2 and a moderate and positive correlation between SL and TER1

and SL and TER2. For mega-environment 3, there was a moderate and positive correlation between SIN and JAN (Figure 5a).

All correlations were classified as moderate for 2017/2018 (Figure 5b). In 2018/2019 (Figure 5c), there was a high and positive correlation between TER and VIL, and all other correlations were classified as moderate to low.

## 4 | DISCUSSION

A significant  $G \times E$  interaction indicates the differential response of genotypes across environments. This was confirmed in the present study by observing the climatic features of each environment (Table 1) that differed in

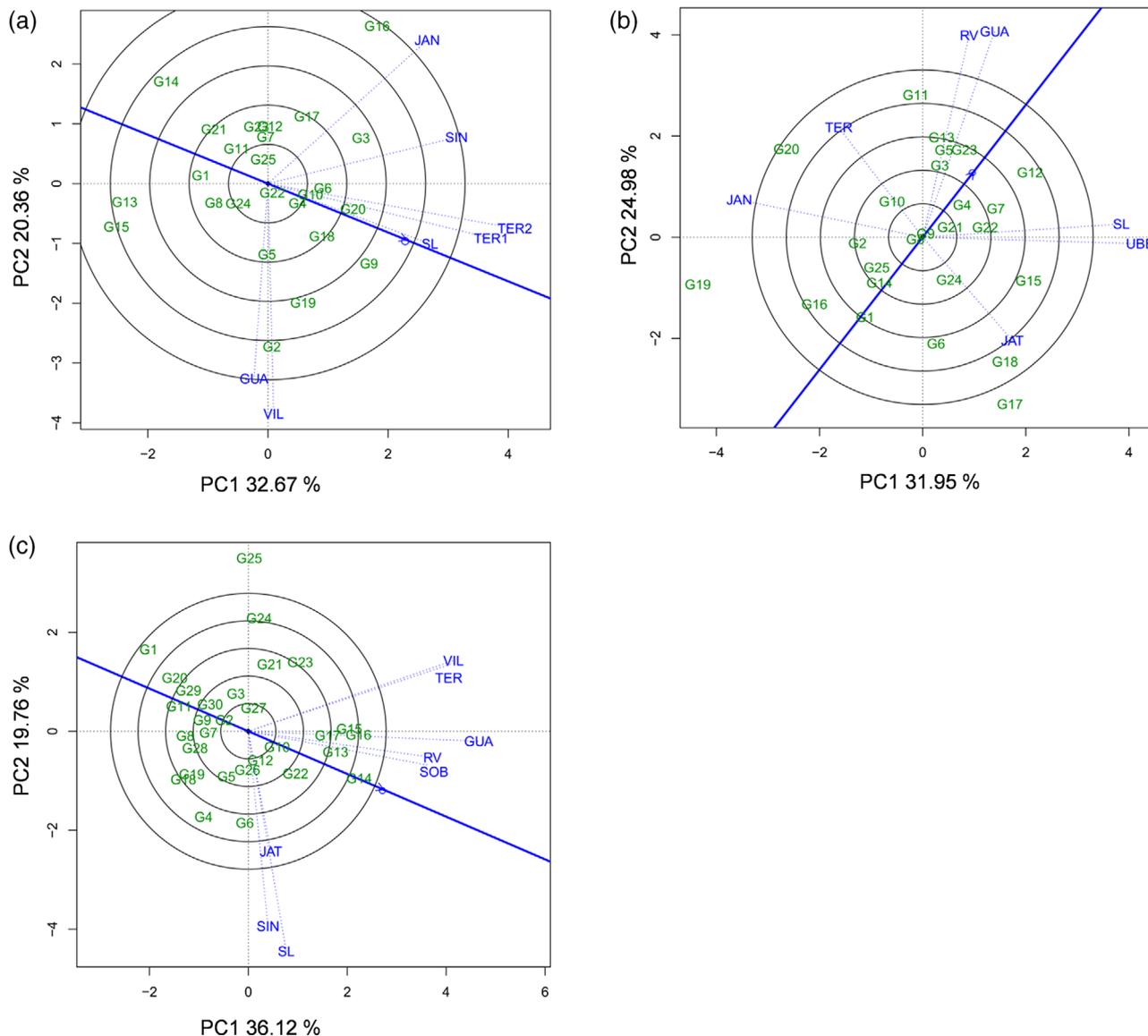


**FIGURE 2** Maps according to the evaluation locations and mega environments formed by GGE biplot for grain yield of sorghum genotypes evaluated during the crop seasons (a) 2016/2017, (b) 2017/2018, and (c) 2018/2019

altitude, latitude, longitude, and climate, including rainfall and temperature. A significant  $G \times E$  interaction can also be attributed to predictable factors, such as soil management, pests and diseases, irrigation, and fertilization, and unpredictable factors such as rainfall, temperature, relative humidity, and solar radiation. Rao et al. (2011) and Singh et al. (2020) reported that weather parameters and soil types are two principal factors determining genotypic performance in diverse locations. Similar results were obtained by Batista et al. (2017), Mare et al. (2017), and Teodoro et al. (2016).

They found significant differences in the genotype and environment effects and in the  $G \times E$  interaction after evaluating grain sorghum genotypes in multi-environment trials. To better understand the  $G \times E$  interaction, the growing regions of a crop must be divided into mega-environments.

Similar environments may be eliminated in the future from multi-location testing of sorghum hybrids to optimally allocating scarce resources. According to Yan and Kang (2003), when different cultivars are adapted to different groups of environments, and the variation between groups is

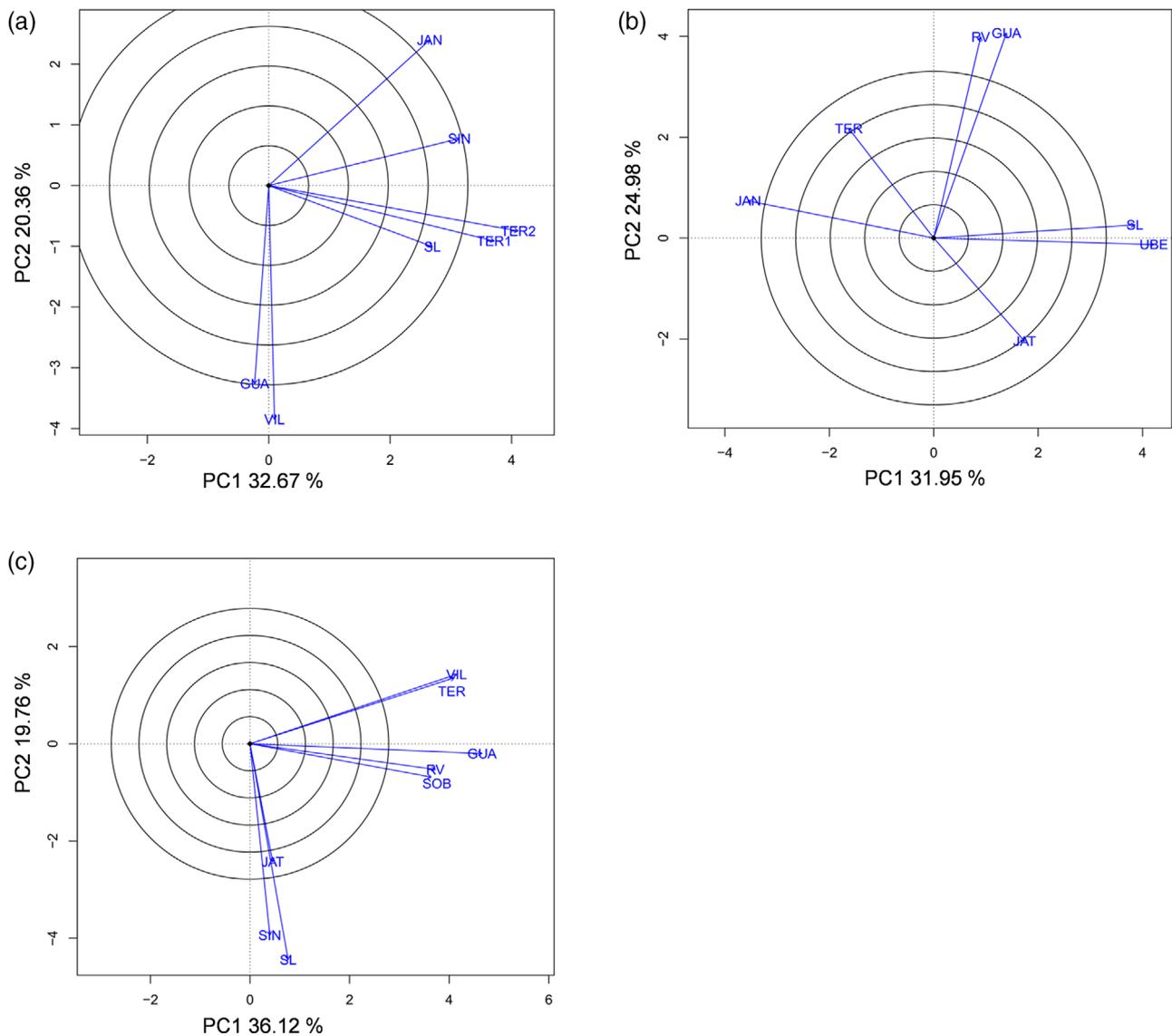


**FIGURE 3** GGE biplot “ideal genotype” for grain yield data of sorghum genotypes evaluated during the crop seasons: (a) 2016/2017, (b) 2017/2018, and (c) 2018/2019. SL: Sete Lagoas; GUA: Guaira; JAN: Janaúba; TER1: Teresina; TER2: Teresina; VIL: Vilhena; SIN: Sinop; UBE: Uberaba; RV: Rio Verde; JAT: Jatai; TER: Teresina; SOB: Sobral

higher than within groups, a mega-environment is formed. In the GGE biplot analysis, when studying mega-environments (Figure 1), the average graph was not related to the general average, but to the mega-environment average (Yan & Tinker, 2006). Therefore, the average of each cultivar was compared within its mega-environment. Alwala et al. (2010) reported that the compartmentalization of genotypes in various sectors indicates significant  $G \times E$  interactions. If this grouping of locations is repeatable year after year, the locations included within each sector can be considered a mega-environment. Mare et al., 2017 in a study to assess the  $G \times E$  interaction on grain yield stability of promising sorghum genotypes across five diverse environments of Zimbabwe. The results revealed that three mega-environments were identifiable.

Teodoro et al. (2016) using 20 hybrids grain sorghum, with the same methodology, in Brazil, identified two mega environments. Thus, the mega-environment identification involved a situation whereby one or more environments with similar or homogenous characteristics were bunched into one big location.

The GGE biplot method is very useful for studying performance patterns in genotypes according to the environment (Karimizadeh et al., 2013). Thus, a generally adapted environment and a specific environment can be identified conveniently (Teodoro et al. (2016). Closer relationships between the test environments indicate that the same information can be obtained from fewer environments. Thus, similar environments can be redefined in future multi-location testing



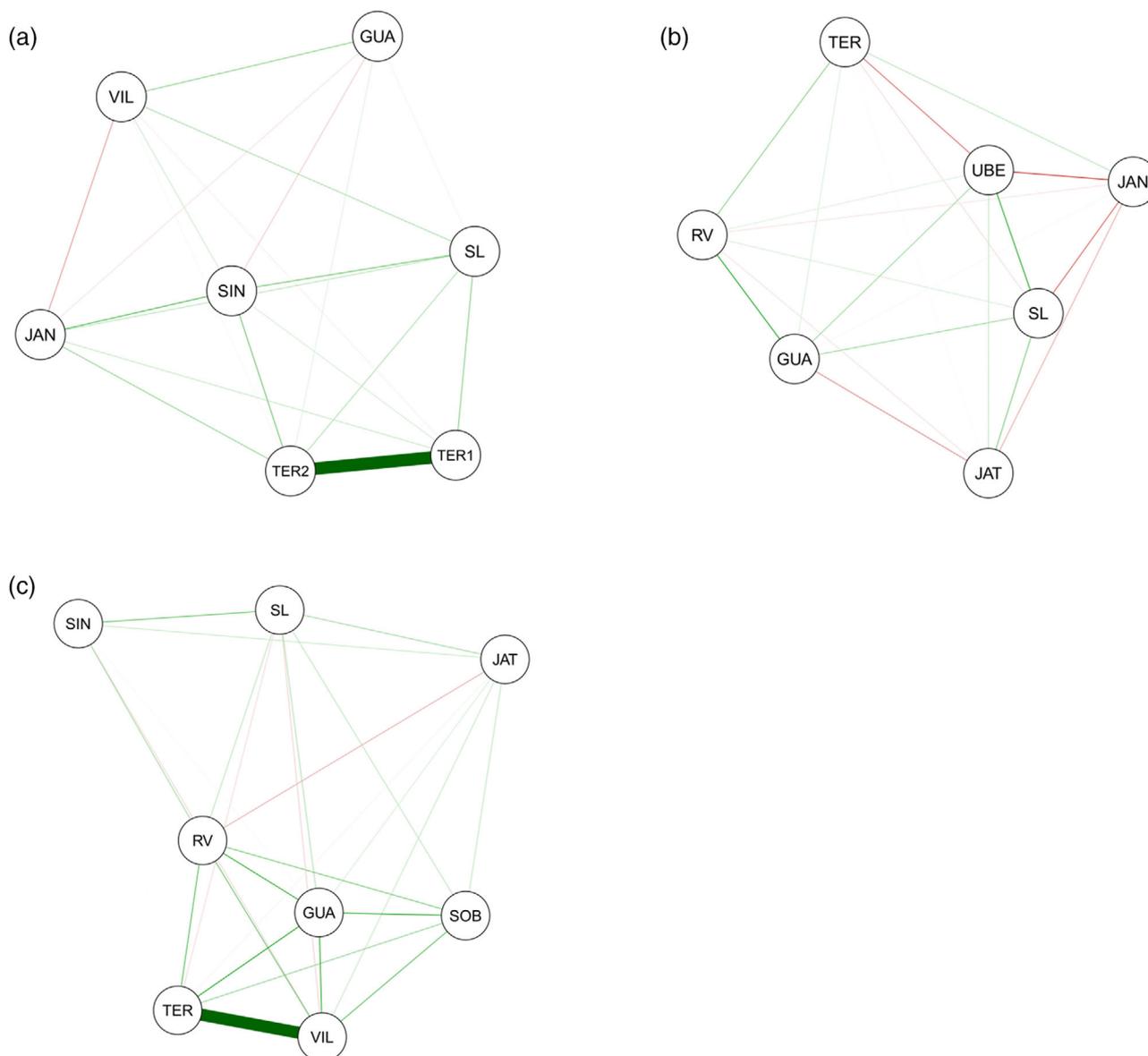
**FIGURE 4** GGE biplot “discrimination and representativeness” for grain yield data of sorghum genotypes evaluated during the crop seasons: (a) 2016/2017, (b) 2017/2018, and (c) 2018/2019. SL: Sete Lagoas; GUA: Guaira; JAN: Janaúba; TER1: Teresina; TER2: Teresina; VIL: Vilhena; SIN: Sinop; UBE: Uberaba; RV: Rio Verde; JAT: Jatui; TER: Teresina; SOB: Sobral

of sorghum grain (Rakshit et al., 2012; Rakshit et al., 2016; Rakshit, Ganapathy, et al., 2014; Rakshit, Hariprasanna, et al., 2014; Rao et al., 2011). Thus, based on the present analysis, the testing locations were partitioned into three, five, and three mega-environments during the crop season of 2016/2017 (Figure 1a), 2017/2018 (Figure 1b), and 2018/2019 (Figure 1c), respectively, suggesting that although the testing was conducted in many locations, a similar conclusion may be drawn from one or two representatives of each mega-environment. Thus, the cost of testing could be significantly decreased.

Under this scenario, it is extremely important that research aimed at developing efficient and responsive genotypes, since this is the best option for maintaining crop yields with less impact on production costs and the environment,

given that increasing technical recommendations, has been observed over past years (Meng et al., 2016). Thus, the mega-environments are formed for an environment that has the same pattern of G x E interaction, the exclusion of these environments should not significantly impact the gain with the selection, thus showing the efficiency of the assays net.

However, we verified a low repeatability of the mega-environments formed during the harvests. For example, the VIL and GUA environments formed mega-environments 1 for the 2016/2017 crop season (Figures 1a and 2a). However, in the 2018/2019 crop season these environments were grouped into different mega environments (Figures 1c and 2c). These results suggest that unpredictable factors (i.e., climatic conditions) affect the formation of mega-environments. Our results also indicate that there is no spatial pattern in the formation of



**FIGURE 5** Phenotypic correlation network between environments evaluated during the crop seasons: (a) 2016/2017, (b) 2017/2018, and (c) 2018/2019. SL: Sete Lagoas; GUA: Guaira; JAN: Janaúba. The red and green lines represent negative and positive correlations, respectively. The width of the line is proportional to the intensity of the correlation. TER1: Teresina; TER2: Teresina; VIL: Vilhena; SIN: Sinop; UBE: Uberaba; RV: Rio Verde; JAT: Jatai; TER: Teresina; SOB: Sobral

mega-environments, since environments belonging to the same state and close (such as RV and JAT) were grouped into different mega-environments in two crop seasons (2016/2017 and 2018/2019). Thus, this mega-environment pattern must be verified through multi-year and environmental trials (Aruna et al., 2015; Rakshit et al., 2012; Teodoro et al., 2016).

The GGE biplot “ideal genotype” graph (Figure 3) allowed inferences to be made about the ideal genotype (Yan & Kang, 2003). The ideal genotype must have high grain yield and stability across different environments (Dalló et al., 2019; Teodoro et al., 2016). According to Hongyu (2015), an ideal genotype is at the center of concentric circles; it can be a point on the axis media in the positive sense and has a vector

length equal to the longest vectors of the genotypes on the positive side of the axis media, that is, the highest average performance. Different authors such as Gasura et al. (2015), Mare et al. (2017), and Al-Naggar et al. (2018) used this stability parameter to identify suitable (high yielding and stable) sorghum genotypes.

The objective of evaluating the “ideal environment” is to identify test environments that can be used to select superior genotypes effectively for a mega-environment. An “ideal” test environment should be used for both genotype discrimination and representation of the target environment (Figure 4). Test environments with higher scores in principal component (PC1) are more discriminating among genotypes

and lower scores on principal component (PC2) (greater representation of all other environments) (Teodoro et al., 2016). Environments with short vectors in PC1 are less discriminating; therefore, all genotypes perform similarly, and little or no information about genotypic differences can be revealed in such an environment, and they should not be used as test environments.

In sorghum breeding programs, experiments with promising genotypes must be conducted in different environments, and the more heterogeneous the environments, the more representative the  $G \times E$  interaction assessments will be. According to Silva and Benin (2012), the GGE biplot method allows  $G \times E$  interactions to be explored with significant precision, favoring the identification of mega-environments and the selection of stable genotypes adapted to specific environments and mega-environments. The use of the GGE biplot methodology was an essential approach in the present study, mainly because of the large number of genotypes tested under different environmental conditions.

The GGE biplot method allows analysis of the environment, identifying favorable and unfavorable conditions, and setting the ideal number of environments to conduct tests for each recommended region, crucial for conducting and planning more efficient sorghum breeding programs. The GGE biplot was an efficient approach for identifying mega-environments, selecting representative and discriminative environments, and recommending cultivars that are more adaptive and stable to specific environments.

## 5 | CONCLUSION

Grain yield performance of the genotypes was significantly influenced by the environment, genotype, and their interaction. Seven locations in Brazil were representative for grain sorghum and can be reduced as three complex mega-environments. Therefore, a set of cultivars based on both mean yield and stability should be deployed. The separation of the testing sites in terms of discriminating ability and representativeness provided useful information on the effectiveness of each location for developing or recommending cultivars for specific or broad adaptation. The GGE biplot can be considered by sorghum breeders when breeding cultivars for varied geographical and climatic regions.

## ACKNOWLEDGMENTS

This research was supported by CNPq (Conselho Nacional de Desenvolvimento Científico e Tecnológico), CAPES (Coordenação de Aperfeiçoamento de Pessoal-Financeiro Code 001), and Embrapa (Empresa Brasileira de Pesquisa Agropecuária). The authors also thank all research and field assistants who helped to conduct field experiments at Embrapa Maize and Sorghum and at other Embrapa's stations.

## CONFLICT OF INTEREST

The authors declare that they have no conflict of interest.

## DATA AVAILABILITY STATEMENT

The authors declare that they have data availability directing readers to research data.

## ORCID

Karla Jorge da Silva  <https://orcid.org/0000-0002-6069-0619>

Paulo Eduardo Teodoro  <https://orcid.org/0000-0002-8236-542X>

Michele Jorge da Silva  <https://orcid.org/0000-0001-8648-8825>

Cicero Beserra de Menezes  <https://orcid.org/0000-0001-9437-6946>

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**How to cite this article:** da Silva, K. J., Teodoro, P. E., da Silva, M. J., Teodoro, L. P. R., Cardoso, M. J., Godinho, V. P. C., Mota, J. H., Simon, G. A., Tardin, F. D., da Silva, A. R., Guedes, F. L., & de Menezes, C. B. Identification of mega-environments for grain sorghum in Brazil using GGE biplot methodology. *Agronomy Journal*. 2021;113:1–12. <https://doi.org/10.1002/agj2.20707>