Research Article

Adaptability and stability of conventional soybean by GGE biplot analysis[1]

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ABSTRACT

The conventional soybean production has been re-establishing itself every year, due to the fact that the international market has demanded products with high agronomic performance and nutritional quality, free of genetically modified organisms. This study aimed to evaluate the adaptability of conventional soybean genotypes in the southwestern Goiás state (Rio Verde, Montividiu and Santa Helena de Goiás), Brazil, during the 2017/2018 and 2018/2019 crop seasons. A randomized blocks design was used, being tested eight genotypes (the cultivars BRS284, BRS283, BRS232, BRS317, NT11-1277, INT3459 and M6101 and the line NT1478SP). The grain and oil yields, as well as the oil and protein contents, were evaluated. Multi-environment analyses were performed using a heterogeneous residual variance model, and the GGE biplot analysis was used to describe the interrelationships between genotypes and environments. The most adapted and stable genotypes were BRS 317 for grain yield and BRS 283 for oil yield. They also corresponded more closely to the ideotype for the specific region, thus proving to be promising. NT1478SP showed the highest protein content. In the 2018/2019 crop season, Montividiu was more discriminating for the conventional soybean production, regarding grain and oil yields.

KEYWORDS: *Glycine max*, genotype x environment interaction, plant breeding.

RESUMO

Adptabilidade e estabilidade de
soja convencional pela análise GGE biplot

A produção de soja convencional vem se restabelecendo a cada ano, pois o mercado internacional tem exigido produtos com elevado desempenho agronômico e qualidade nutricional, livres de organismos geneticamente modificados. Objetivou-se avaliar a adaptabilidade de genótipos de soja convencional na região sudoeste do estado de Goiás (Rio Verde, Montividiu e Santa Helena de Goiás), nas safras 2017/2018 e 2018/2019. Utilizou-se delineamento de blocos casualizados e foram testados oito genótipos (as cultivares BRS284, BRS283, BRS232, BRS317, NT11-1277, INT3459 e M6101 e a linhagem NT1478SP). Foram avaliados a produtividade de grãos e de óleo, bem como os teores de óleo e proteína. Análises multiambientes foram realizadas utilizando-se um modelo de variância residual heterogêneo, e a análise GGE biplot foi utilizada para descrever as inter-relações entre genótipos e ambientes. Os genótipos mais adaptados e estáveis foram BRS 317 para produtividade de grãos e BRS 283 para rendimento de óleo. Além disso, eles se comportaram de forma mais próxima do ideótipo para a região específica, enfatizando serem promissores. NT1478SP apresentou o maior teor de proteína. Na safra 2018/2019, Montividiu mostrou-se mais discriminativo para a produção de soja convencional, quanto à produtividade de grãos e de óleo.

PALAVRAS-CHAVE: *Glycine max*, interação genótipos x ambientes, melhoramento genético.

INTRODUCTION

Brazil is the world's second largest soybean [*Glycine max* (L.) Merrill] producer (FAO 2020). In the 2019/2020 crop season, the Brazilian production reached around 104 million tons of grains, in a cultivated area of about 36.8 million hectares. The Goiás state is the third largest producer, averaging 12.4 million tons (Conab 2020). Areas cultivated with genetically modified (transgenic) soybean cultivars account for 35.3 million hectares, corresponding to around 96 % of the total soybean-grown area in the country. Therefore, the remaining 4 % (1.5 million hectares) are grown with conventional soybean crops (Céleres 2019).

The conventional soybean market has grown in Brazil, mainly for export to Europe and Japan. As a result, profitability has increased, if compared to that

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of transgenic soybean. Added to this, to encourage producers, the prices paid per bag of conventional grain have increased in the market (Brasilagro 2018). However, conventional soybean cultivation is restricted to a few cultivars, with BRS 218 being the most expressive one. Therefore, information is needed to support and expand the range of genotypes grown by farmers.

Conventional soybean crops have similar or, in some cases, greater growth rates than transgenic ones. It is up to farmers to decide what technology to use, aiming at cost reductions, as well as remuneration and grain yield increases (Felici 2017). In this context, soybean plant breeding programs have emerged, developing increasingly adapted and stable cultivars each year. Such a high production capacity in different environments allows the expansion and opening of new agricultural frontiers (Bisinotto 2013).

Productive genotypes with desirable traits are selected by experiments in diverse environments (years and sites). The performance of a cultivar may change from one environment to another because of genetic (G) and environmental (E) components, or their interaction (G x E) (Bornhofen et al. 2017). Environments are understood as edaphoclimatic conditions associated with crop practices that interfere with genotype performance (e.g., soil fertility, climatic factors, rainfall index and pest and disease attack) (Borém & Miranda 2013).

The G x E interactions effects can be mitigated by evaluating and recommending specific genotypes to homogeneous regions, thus providing more accurate results. Environment specification enables selecting and recommending genotypes to be explored at their maximum potential, thus capitalizing the G x E interaction effects (Yan 2016).

Multivariate statistics, together with biological knowledge, may improve the understanding of G x E interactions and help to propose alternatives to minimize or exploit them, so that improved cultivars may be released (Garbuglio & Ferreira 2015, Batista et al. 2017). Among the multi-environmental methods for evaluating and recommending genotypes, GGE biplot is effective in detailing the G x E interrelationship and environment and describing the genotype performance across environments (G + G x E). This approach uses biplot representations, what makes it easier to visualize and interpret results (Amira et al. 2013, Bhartiya et al. 2017).

The GGE biplot analysis is currently being used in several researches with soybean, due to its accuracy and versatility (Sousa et al. 2015, Golçalves et al. 2020, Silva et al. 2021), including evaluation related to grain chemical composition (Silva et al. 2015). However, there is little recent research with conventional soybean cultivars to provide relevant subsidies to technicians and farmers in the proper selection of the one that is most promising in a given cultivation environment.

Thus, the present study aimed to evaluate the adaptability and stability of conventional soybean genotypes at different growing environments in the southwestern Goiás State (Brazil) by GGE biplot analysis.

MATERIAL AND METHODS

Experiments were carried out during the 2017/2018 and 2018/2019 crop seasons, in the Brazilian soybean micro-regions 301, 302 and 401 (Kaster & Farias 2011), in the southwestern Goiás state. The soil type predominant in these micro-regions is Dystrophic Red Latosol (Santos et al. 2018), or Ferralsol (WRB 2015).

In the 2017/2018 crop season, the trials were conducted in three locations: Rio Verde (17º47'20"S, 50º57'29"W and 751 m of altitude); Santa Helena de Goiás (17º57'28"S, 50º28'50"W and 530 m of altitude); and Montividiu (17º11'04.7"S, 51º17'36.7"W and 930 m of altitude). In the 2018/2019 crop season, they were conducted in two locations: Rio Verde (the same as the previous crop season) and Montividiu (17º31'29"S, 51º13'27"W and 870 m of altitude).

Eight conventional soybean genotypes were tested, including seven cultivars (BRS 284, BRS 283, BRS 317, BRS 232, M6101, INT3459 and NT1478SP) recommended for the studied micro-regions (except INT 3459) and an experimental line (NT11-1277). These genotypes were selected because they are among the few conventional ones currently available for cultivation that are recommended for micro-regions, as well as being potential alternatives for farmers.

The trials were conducted in a complete randomized blocks design, with five replications. The plots comprised four 5-m-long rows spaced 0.5 m apart, corresponding to a total plot area of 10.0 m². The useful plot area consisted of the two central rows, excluding 0.5 m of the row ends, totaling

4.0 m^2. Tillage, seed treatment, population density and phytosanitary management were carried out according to the technical recommendations for the crop. Plants were harvested manually at the R8 stage, i.e., when 95 % of the pods display full mature color (Fehr & Caviness 1977). After harvesting, the plants were threshed using an SB04C threshing machine, and then the grain moisture was measured.

Grain samples were taken from the useful plot area and corrected to 13 % of moisture for measurements of grain yield (kg ha^{-1}) and 1,000-grain weight. Oil and protein contents were measured using near-infrared spectroscopy (NIR), with measurements calibrated by comparing them against analytical data from reference methods (Panero 2008). Lastly, the oil yield was calculated as the product of oil content and grain yield, extrapolated to kg ha^{-1}.

First, each environment or location-year combination (environment) was analyzed individually, using the *lm* function of the R statistical software (R Core Team 2019), according to the following statistical model: $y_{ij} = \mu + b_j + g_i + e_{ij}$, where y_{ij} is the phenotypic data of the plot in block j that received the genotype i; μ a general constant of the experiment; g_i the effect of the genotype i; b_j the effect of the block j; e_{ij} the effect of the experimental error associated with the observation y_{ij}; wherein $e_{ij} \sim N(0, \sigma_e^2)$. The coefficient of environmental variation was estimated from error variance estimates for each assay, as well as the Hartley's homoscedasticity test (Pimentel-Gomes & Garcia 2002).

As a metric of experimental environment quality, the coefficient of variation (CV) was estimated to measure experimental (Garcia 1989, Pimentel-Gomes 1991) and selection (AC) precision to check for genotype selection reliability (Resende & Duarte 2007).

A multi-environment analysis was performed using the heteroskedastic statistical model, with the aid of the gls function of the nlme package (Pinheiro et al. 2019): $y_{ijkm} = \mu + a_m + l_k + la_{km} + b_{j(km)} + g_i + ga_{im} + gl_{ik} + gla_{ikm} + \varepsilon_{ijkm}$, where y_{ijkm} is the observation of the plot in block j at location k and year m that received the genotype i; μ a general constant for the experiments; a_m the effect of year m; l_k the effect of location k; la_{km} the effect of the interaction between location k and year m; $b_{j(km)}$ the effect of the block at location k and year m; g_i the effect of the genotype i; ga_{im} the effect of the interaction between genotype i and year m; gl_{ik} the effect of the interaction between

the genotype i and location k; gla_{ikm} the effect of a triple interaction among the genotype i, year m and location k; and ε_{ijkm} the effect of the error associated with the observation y_{ijkm}, $\varepsilon_{ijkm} \sim N(0, \sigma_{\varepsilon km}^2)$.

The phenotypic means of genotypes adjusted to the crop seasons and locations were calculated using the means function of the MEANS package (Lenth 2019). The genotype means were compared by the Tukey test, using the *cld* function from the multcomp package (Torsten et al. 2008).

The genotype adaptability and stability in each environment were analyzed with the GGE biplot-Genotype Main Effects + Genotype by Environment Interaction method, using the two first principal components (Yan 2015). The biplot graphs or score plots based on the two first principal components were generated to describe the interrelationship between genotypes and environments (Yan & Tinker 2006). The GGE biplot analysis was performed using the GGE biplots package (Dumble 2017).

RESULTS AND DISCUSSION

The individual analysis of variance revealed significant differences among the genotypes for all the evaluated traits (p ≤ 0.01). Therefore, the observed genetic variation may be used to identify and indicate the best genotypes for each environment (Table 1). The experimental variation coefficients (CV) had a relatively low magnitude for all characters and, thus, a high experimental precision (Pimentel-Gomes & Garcia 2002). Accuracy estimates (AC ≥ 87 %) indicated a high reliability for genotype selection based on phenotypic information (Resende & Duarte 2007). However, all evaluated traits showed marked variations in CV estimates among the environments. Therefore, there was heteroscedasticity, which was attested by the Hartley's test (Pimentel-Gomes & Garcia 2002).

Notably, the years x locations interaction was found to be significant for grain and oil yields and oil content. These two factors are therefore interdependent. In short, the location effect varied with the crop year, and vice versa. Thus, the studied environments (i.e., a combination of year and location) combine predictable and unpredictable environmental factors, making it difficult to have a consistent characterization thereof.

Table 2 shows the effects of year and location on agronomic traits of the conventional

Table 1. F-calculated value for genotypes and coefficient of experimental variation and selective accuracy for grain yield (kg ha^{-1}), protein content (%), oil content (%) and oil yield (kg ha^{-1}), as a function of the eight conventional soybean genotypes evaluated in Montividiu (MTV), Rio Verde (RV) and Santa Helena de Goiás (SHG), Goiás state, Brazil, during the 2017/2018 and 2018/2019 crop seasons.

Trait	MTV - 2017/2018	RV - 2017/2018	SHG - 2017/2018	MTV - 2018/2019	RV - 2018/2019
			F-calculated genotype		
Grain yield	8.3**	3.5**	16.1**	12.5**	4.1**
Protein content	18.6**	32.1**	37.2**	7.5**	17.1**
Oil content	7.4**	11.9**	11.8**	4.2**	11.3**
Oil yield	12.3**	11.0**	9.1**	7.2**	5.7**
			Experimental variation		
Grain yield	8.67	7.64	6.01	7.65	7.91
Protein content	3.45	2.35	2.25	6.18	5.57
Oil content	6.94	6.13	6.22	7.00	8.50
Oil yield	10.69	8.60	10.03	12.50	12.00
			Selective accuracy		
Grain yield	93.7	84.4	96.9	95.9	87.0
Protein content	97.3	98.4	98.6	93.1	97.0
Oil content	93.0	95.7	95.7	87.4	95.5
Oil yield	95.8	95.3	94.4	92.8	90.8

** Significant at 1 % of probability by the F-test.

Table 2. Summary of the joint analysis of variance for the traits grain yield, protein content, oil content and oil yield of the eight conventional soybean genotypes grown in Rio Verde, Montividiu and Santa Helena de Goiás (Goiás state, Brazil), in the 2017/2018 and 2018/2019 crop seasons.

Source of variation	DF	F-calculated genotype			
		Grain yield (kg ha^{-1})	Protein content (%)	Oil content (%)	Oil yield (kg ha^{-1})
Year (Y)	1	255.1**	67.23**	0.52^{ns}	118.8**
Place (P)	2	240.4**	0.76^{ns}	13.99**	179.1**
Y x P	4	58.4**	0.02^{ns}	7.33**	11.9**
Genotype (G)	7	12.2**	61.57**	33.16**	24.7**
Y x G	7	1.6^{ns}	2.66**	3.59**	1.7^{ns}
P x G	14	10.0**	2.26**	2.03*	4.2**
Y x P x G	7	6.1**	1.81^{ns}	3.03**	2.5*

** and *: significant by the F-test at 1 % and 5 % of probability, respectively.

soybean genotypes in each environment. Except for protein content, the other traits showed a significant variation among the locations, which is associated with edaphoclimatic conditions in each micro-region. Thus, evaluating genotypes in different environments is essential for planting site recommendations. Regarding crop seasons, only the oil content did not show significant changes; therefore, unpredictable climatic factors influence crops in subsequent years (Cunha et al. 2013). Overall, while the genotype and crop year interaction is influenced by climatic factors (rainfall, temperature and light, among others), genotype and location interactions depend on altitude, fertility and other soil-related aspects.

By multi-environment analysis, the main effect of genotypes was significant for all the studied traits (Table 2). However, for some traits, the genotype (G) x environment (E) interaction had a significant effect. For the year (Y) x genotype (G) interaction, only grain and oil yields were not significant, while the location (L) and genotype (G) interaction was significant for all traits. Notably, there was also a triple interaction among year (Y), location (L) and genotype (G) for grain and oil yields and oil content. Then, the P x G interaction varied with agricultural season, or the Y x G interaction varied with location, directly impacting the genotype behavior predictability in the tested environments (Table 2).

Genotype interactions with crop season and local for most traits, but mainly grain yield, despite hindering the soybean breeders' work, may also help to identify adaptable and responsive genotypes to a given edaphoclimatic and technological condition. In this regard, a few results have been reported by some researchers (Branquinho et al. 2014, Dallo et al. 2019).

The main goal of soybean breeding programs is to develop highly productive genotypes. Genetic variability and environmental influence broadened the grain yield range, varying from 2,498 kg ha^{-1} for NT11-1277 in Santa Helena de Goiás, in the 2017/2018 crop season, to 5,810 kg ha^{-1} for BRS 317 in Montividiu, in 2018/2019 (Table 3). The cultivar INT3459 stood out in all evaluated environments; however, when considering the overall average, BRS 317, BRS 283 and BRS 284 also stand out. All these genotypes had overall grain yields higher than the average for the Goiás state (3,290 kg ha^{-1}) (Conab 2019). The average grain yield of conventional genotypes may be equal to or even higher than that

Table 3. Phenotypic means of the traits grain yield, protein content, oil content and oil yield of the eight conventional soybean genotypes grown in Rio Verde (RV1 and RV2), Montividiu (MTV1 and MTV2) and Santa Helena de Goiás (SHG) (Goiás state, Brazil), during the 2017/2018 and 2018/2019 crop seasons.

| Genotype | Grain yield (kg ha^{-1}) | | | | | |
| | 2017/2018 | | | 2018/2019 | | Mean |
	RV1	MTV1	SHG	RV2	MTV2	
BRS 232	3,958 ab*	3,245 cd	3,356 a	4,637 ab	4,753 b	3,990
BRS 283	4,297 ab	3,903 ab	2,804 cde	4,713 ab	4,939 b	4,131
BRS 284	4,346 ab	3,308 bcd	3,062 abc	4,736 ab	4,774 b	4,045
BRS 317	4,526 a	3,652 abc	2,920 bcd	4,651 ab	5,810 a	4,312
INT3459	4,120 ab	4,153 a	2,698 ab	4,397 ab	5,196 a	4,216
M6101	3,761 b	4,006 a	2,532 de	4,218 b	4,850 b	3,907
NT11-1277	4,011 ab	3,572 abcd	2,498 e	4,045 b	5,021 b	3,836
NT1478SP	3,866 b	3,005 d	3,215 e	5,083 a	3,689 c	3,628
	Protein content (%)					
BRS 232	41.8 bc	41.8 bc	40.8 c	37.7 bc	38.4 b	40.1
BRS 283	37.4 e	36.8 d	37.7 de	33.7 c	36.2 b	36.4
BRS 284	39.6 d	41.0 bc	41.2 bc	36.8 bc	39.7 b	39.6
BRS 317	40.2 cd	39.5 cd	40.7 c	37.2 bc	38.2 b	39.2
INT3459	39.3 de	40.7 bc	39.4 cd	36.6 c	37.5 b	38.7
M6101	38.8 de	39.0 cd	37.5 e	36.5 c	35.1 b	37.4
NT11-1277	43.0 ab	43.2 ab	43.1 ab	41.1 b	38.6 b	41.8
NT1478SP	44.7 a	45.7 a	44.8 a	46.7 a	44.9 a	45.4
	Oil content (%)					
BRS 232	13.6 d	14.2 c	13.2 c	15.7 c	13.7 bc	14.1
BRS 283	18.0 a	18.3 a	16.8 a	18.7 abc	15.7 a	17.5
BRS 284	17.2 ab	16.5 ab	16.0 ab	17.6 abc	14.7 abc	16.4
BRS 317	15.7 bc	15.8 bc	14.5 bc	16.4 abc	15.0 abc	15.5
INT3459	16.7 abc	15.6 bc	16.2 ab	17.0 ab	16.0 abc	16.3
M6101	17.3 ab	16.3 abc	17.2 a	18.2 a	16.6 ab	17.1
NT11-1277	14.7 cd	14.4 bc	13.8 c	15.3 abc	15.3 c	14.7
NT1478SP	15.0 cd	15.0 bc	14.6 bc	12.1 bc	14.1 d	14.2
	Oil yield (kg ha^{-1})					
BRS 232	536 c	457 cd	422 bc	729 ab	654 bc	560
BRS 283	769 a	714 a	470 ab	882 a	777 ab	722
BRS 284	748 a	560 bcd	490 ab	833 a	733 ab	673
BRS 317	708 a	578 bc	423 bc	760 ab	874 ab	668
INT3459	685 ab	641 ab	520 a	748 ab	829 ab	685
M6101	652 abc	654 ab	464 bc	808 b	805 ab	677
NT11-1277	590 bc	514 cd	350 c	616 b	768 ab	567
NT1478SP	580 bc	447 d	365 c	616 b	522 c	506

* Means followed by the same letter do not differ significantly by the Tukey test at 5 % of probability.

of transgenic ones. This is because only one or a few genes were inserted into transgenic genotypes, and for traits that are not directly related to grain production.

Protein is known to be inversely proportional to oil. In this sense, NT1478SP showed a better performance for protein, surpassing the others in all environments (~45.4 %), but had low oil contents (~14.2 %) (Table 3). Likewise, BRS 283 was superior in oil (17.5 %), but had low protein contents (36.4 %). BRS 283, BRS 284, BRS 317, INT3459 and M6101 stood out for oil yield, showing, respectively, 722, 673, 668, 685 and 677 kg ha^{-1}. The soybean chemical composition is strongly influenced by genetic and environmental factors, besides crop practices and water availability. All these factors may have directly interfered with the chemical compositions of the studied genotypes, which ranged 33-45 % for protein and 18-25 % for oil on a dry basis (Zarkadas et al. 2007, Silva et al. 2016).

Figure 1 shows the biplot representations, where the genotypes can be selected for adaptability and stability simultaneously, in an ideotype model. This ideotype was established based on the premise that, by estimating adaptability and stability, stable low-yielding genotypes can be ruled out (Yan 2015). An 'ideotype' is an ideal representation of a genotype for an environment, in terms of performance and stability. The genotypes found in the rightmost arrow-wise are the most adapted ones, while those close to this axis (arrowed axis) and hence the lowest in ordinate axis perpendicularly are the most stable. Thus, BRS 317 was the closest to the ideotype for grain yield (Figure 1a), while BRS 283 was the most promising for oil yield (Figure 1b). Gonçalves et al. (2020) concluded that the REML/BLUP and GGE biplot analysis are highly correlated, in terms of genotype ranking, for selection and recommendation purposes, what is reinforced by the discrimination of soybean genotypes with better estimates of adaptability and stability by the GGE biplot method of other researchers (Sousa et al. 2015, Silva et al. 2017, Silva et al. 2021).

Another aspect of the genotype-by-environment interaction is the interrelationship among the studied environments. Environments capable of distinguishing or discriminating the best genotype must be defined for breeding purposes. Likewise, redundant environments should be identified and avoided, to optimize resources. The studied environments were more positively

correlated for oil yield (Figure 1a) than for grain yield (Figure 1b). Overall, the environments showed higher and positive correlations in the 2017/2018 crop season rather than in the 2018/2019 one. The genotype discrimination potential also varied from one environment to another (i.e., environment vector length). This finding has also been observed in soybean by other researchers (Amira et al. 2013, Bhartiya et al. 2017).

In general, Montividiu was more discriminative than Rio Verde, mainly in the 2018/2019 crop
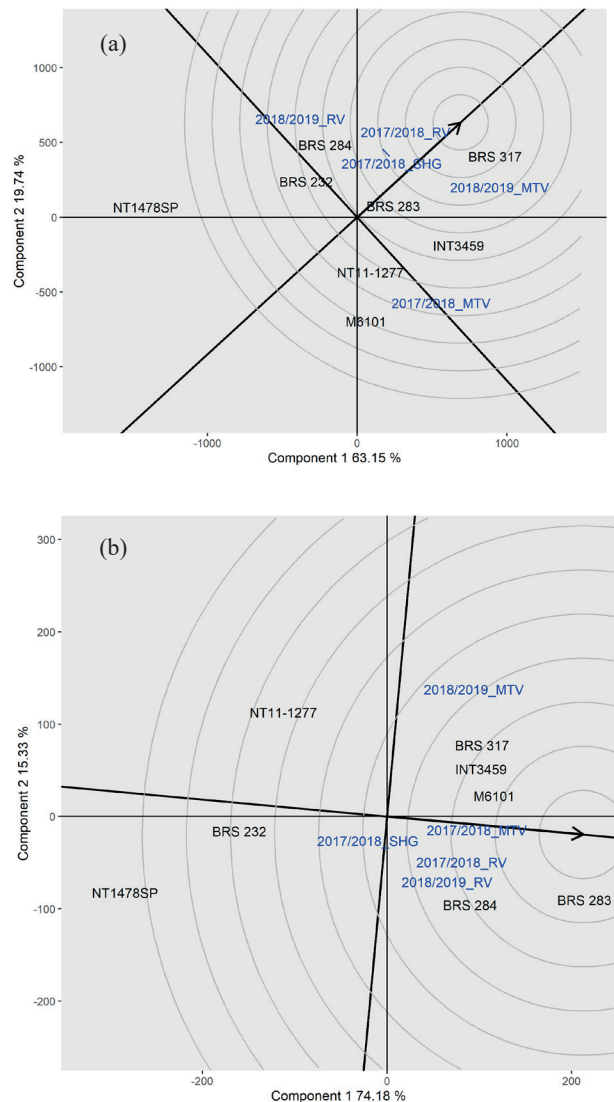

Figure 1. Biplot representation for the classification of the eight conventional soybean genotypes evaluated, concerning the 'ideotype' (in the center of the concentric circles), according to the traits grain yield (kg ha^{-1}) (a) and oil yield (kg ha^{-1}) (b). MTV: Montividiu; RV: Rio Verde; SHG: Santa Helena de Goiás.

season, for both grain and oil yields (Figure 2). The phenotypic standard deviation among the means for Montividiu in the 2018/2019 season was greater than for the other environments (Table 3). This might have occurred due to large amounts of straw and water availability during the trials, enhancing the plant photosynthetic capacity and hence the grain yield. These results may be explained by changes in the climatic conditions from one environment to another.
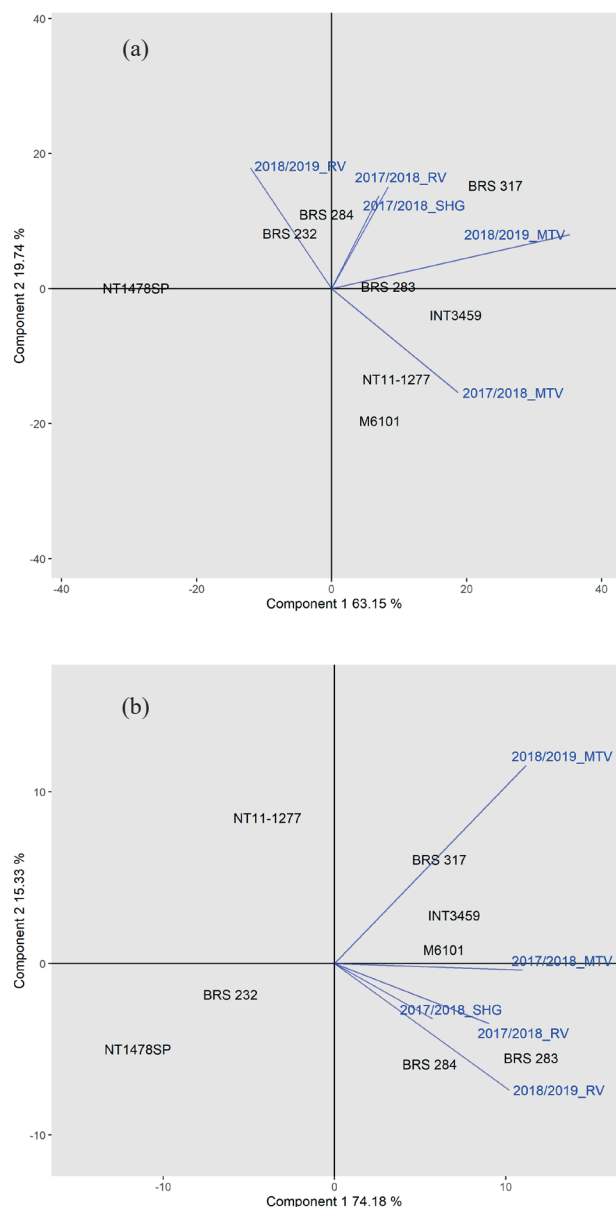

Figure 2. Biplot representation of the interrelationship between the environments and their ability to discriminate the best for the traits grain yield (kg ha⁻¹) (a) and oil yield (kg ha⁻¹) (b). MTV: Montividiu; RV: Rio Verde; SHG: Santa Helena de Goiás.

Among these, temperature, altitude, photoperiod and rainfall affected the early plant development, flowering and even grain filling.

Regarding grain yield, the most responsive genotypes were BRS 317 (Rio Verde during the 2017/2018 crop season, Santa Helena de Goiás in 2017/2018 and Montividiu in 2018/2019) and M6101 (Montividiu in 2017/2018) (Figure 2a). As for oil yield, BRS 317 performed well in Montividiu in 2018/2019, while BRS 283 and BRS 284 were superior in the other environments (Rio Verde during both seasons and Montividiu in 2018/2019) (Figure 2b). Likewise, Dallo et al. (2019) also used a GGE biplot analysis to discriminate genotypes for adaptability and responsiveness.

The identification of possible mega-environments may be done from biplots of the which-won-where type. According to Yan (2015), a mega-environment is defined based on the winner genotype. By the biplot representations, one can see the formation of two mega-environments for oil yield: Montividiu in 2018/2019 and the other environments (Figure 3b). However, for grain yield, three mega-environments were formed, the first one constituted by Montividiu in 2018/2019, Rio Verde in 2017/2018 and Santa Helena de Goiás in 2017/2018, while Rio Verde in 2017/2018 and Montividiu in 2018/2019 were separated into two other mega-environments (Figure 3a). It is worth to highlight that the mega-environments were of secondary importance in our study, since they were constituted by a year-local combination. Furthermore, the characterization of mega-environments needs validation by multi-environmental tests in various crops or agricultural years.

The accumulated percentage in the sum of the main components PC 1 and PC 2 exceeded in 80 % the studied traits, interfering with the reliability in the elucidation of the total variation in the performance of the genotype together with the environments interaction, being important to assume the existence of distinct mega-environments in one location. BRS 317, BRS284, INT3459, M6101 and NT 1478SP were more responsive in relation to grain yield and responsible for the formation of the polygon, and the continuous red lines delimited and formed five sectors, which defined three mega-environments, highlighting the cultivar BRS 317, which was promising in one of the main mega-environments (Figure 3a). Regarding the oil yield (Figure 3b), BRS 317, BRS 283, BRS 284, NT 1478SP and NT 11-
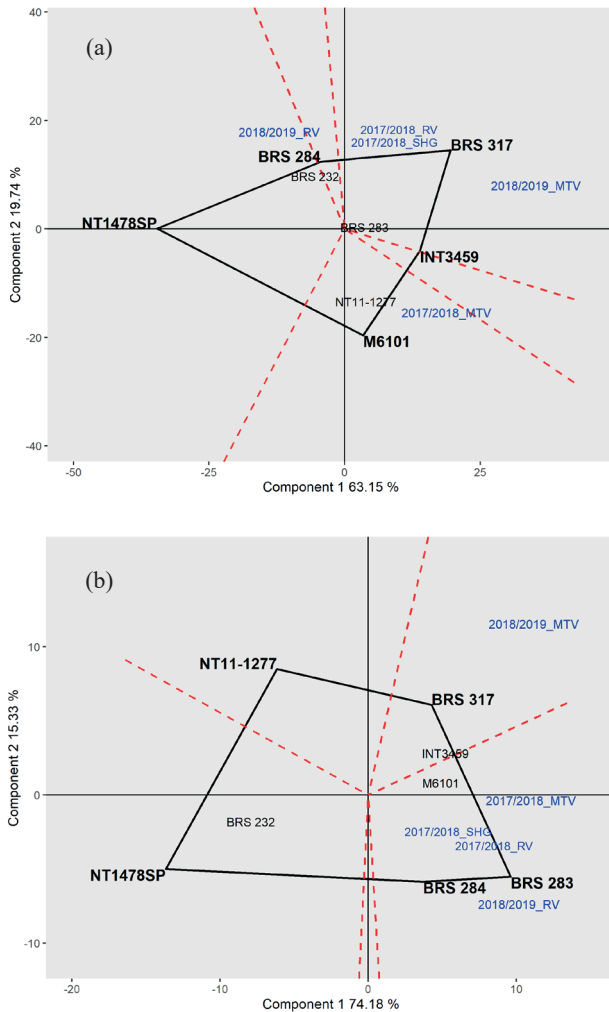
Figure 3. Biplot representation of the winning conventional soybean genotypes and sectors that form mega-environments for grain yield (kg ha⁻¹) (a) and oil yield (kg ha⁻¹) (b). MTV: Montividiu; RV: Rio Verde; SHG: Santa Helena de Goiás.

1277 participated in the formation of the polygon in which the continuous red lines delimited and formed four sectors that defined two mega-environments, evidencing the potential of the cultivars BRS 283 and BRS 284 for this trait.

CONCLUSIONS

1. The GGE biplot analysis accurately enables the selection of conventional soybean genotypes, in terms of environment adaptability and behavior predictability;

2. The cultivar BRS 317 is the most responsive and stable for grain yield, and BRS 283 for oil yield;

3. The environment composed by the city of Montividiu is favorable for the expression of variations among the soybean genotypes, allowing discrimination for selective purposes, in terms of grain and oil yields.

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