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CROP PRODUCTION

# Soybean adaptability and stability analyzes to the organic system through AMMI, GGE Biplot and mixed models methodologies

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**ABSTRACT**: This research determined the adaptability and stability of soybean yield for organic systems in different environments. Grain yield data (GY, kg ha$^{-1}$) from experiments with six soybean genotypes evaluated in six environments in Brazil and one environment in Paraguay were used. The experimental design used was randomized blocks, organized in an incomplete factorial scheme, with six environments in Brazil (Toledo- PR, Palotina- PR, Mangueirinha- PR, Três Passos- RS, Passo Fundo- RS, Major Vieira- SC) and one in Paraguay (Bela Vista do Norte-PY) with six soybean genotypes (BRS 284, BRS 391, BRS 511, BRS 523, BRS 525, BRS 535) arranged in four replications per environment. BRS 511 genotype was characterized by high average grain yield and stability by the AMMI method. BRS 284 genotype was identified as the ideal genotype in the GGE biplot method. WAASBY and BLUP index selected BRS511 and BRS284 genotypes.

**Key words**: *Glycine max*, Genotype x environment interaction, WAASBY.

# Análises de adaptabilidade e estabilidade da soja ao sistema orgânico por meio de metodologias AMMI, GGE Biplot e modelos mistos

**RESUMO**: O objetivo deste trabalho foi determinar a adaptabilidade e estabilidade da produtividade da soja para sistemas orgânicos em diferentes ambientes. Foram utilizados dados de produtividade de grãos (GY, kg ha$^{-1}$) de experimentos com seis genótipos de soja avaliados em seis ambientes no Brasil e um ambiente no Paraguai. O delineamento experimental utilizado foi blocos casualizados, organizados em esquema fatorial incompleto, com seis ambientes no Brasil (Toledo - PR, Palotina - PR, Mangueirinha - PR, Três Passos - RS, Passo Fundo - RS, Major Vieira - SC) e um no Paraguai (Bela Vista do Norte - PY) com seis genótipos de soja (BRS 284, BRS 391, BRS 511, BRS 523, BRS 525, BRS 535) dispostos em quatro repetições por ambiente. O genótipo BRS 511 foi caracterizado por alta produtividade média de grãos e estabilidade pelo método AMMI. O genótipo BRS 284 foi identificado como o genótipo ideal pelo método GGE biplot. Os índices WAASBY e BLUP selecionaram os genótipos BRS511 e BRS284.

**Palavras-chave**: *Glycine max*, interação genótipos x ambientes, WAASBY.

## INTRODUCTION

Soybean (*Glycine max* L.) is one of the most cultivated species in the world, with high agricultural, economic and social importance. Currently, the largest producer of this commodity is Brazil, followed by the United States. According to data from the 2020/2021 harvest, Brazil reached a productivity of 136 million tons of grains, in a cultivation area of approximately 38.5 million hectares (CONAB, 2022).

The crop has socioeconomic importance, since the applications of its grains are multiple, being considered an excellent source of income for the properties by boosting several agro-industrial sectors, such as fertilizers, seeds, vehicles, agricultural implements and pesticides (COSTA & SANTANA, 2013). In this context, new investments are crucial for research and development of new cultivars, management and technologies that result in greater sustainability for the national, state and regional soybean production chain.

In this context, the organic farming system becomes an alternative for economic and environmental sustainability. Allied to the demand for healthy foods and the added value to the final product,

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this system also contributes to increasing the income of the properties. Although, many advantages are observed in this system, there are still large gaps to obtain greater productivity and safety in the cultivation of crops. The positioning of genotypes in these systems requires specific studies, since chemical fertilization and pest and disease control are not used in this environment.

In addition, the major limitation of these systems is that they depend mainly on modern genotypes that were developed and selected by plant genetic improvement programs with the objective of cultivation in conventional systems that do not accurately represent the environmental conditions present in organic agriculture (MURPHY, et al., 2007).

Therefore, showing genotypes with behavior where they will be cultivated is essential for positioning safety. Evidencing genotypes with adaptation to the organic farming system and predictability in their performance, which characterizes the ideotype, promotes the advancement of these sustainable systems with greater economic return. In this way, the use of biometric models has promoted the identification of genotypes with desirable agronomic performance and provided the best positioning of these genotypes (CARVALHO et al., 2016; SILVEIRA et al., 2018; ROTTER et al., 2019) which guarantees better response to productivity with stability and adaptability. The identification of soybean genotypes for cultivation in the organic system can be optimized using models that estimate adaptability and stability. In this context, th this research determined the adaptability and stability of soybean yield for organic systems in different environments.

## MATERIALS AND METHODS

Grain yield data (GY, kg ha$^{-1}$) from experiments with six soybean genotypes evaluated in the states of Rio Grande do Sul, Santa Catarina and Paraná and one environment in Bela Vista do Norte -PY were used. The experimental design used was randomized blocks, organized in an incomplete factorial scheme, with six environments in Brazil (Toledo- PR, Palotina- PR, Mangueirinha- PR, Três Passos- RS, Passo Fundo- RS, Major Vieira- SC) and one in Paraguay (Bela Vista do Norte- PY) with six soybean genotypes (BRS 284, BRS 391, BRS 511, BRS 523, BRS 525, BRS 535) arranged in four replications per environment. The experimental units consisted of rows 15 meters long and 6 meters wide, spaced at 0.45 meters. Sowing was carried out in the first half of October 2019 and 2020, with a density of 10 seeds per linear meter, and cultivation was carried out organically without the addition of synthetic molecules.

When the plants were in full physiological maturity, the two central rows were harvested in each experimental unit to estimate grain yield in kg ha$^{-1}$, with grain moisture corrected to 13%. Posterior , the data of grain yield obtained were subjected to analysis of the assumptions of analysis of variance, such as homogeneity of residual variances by Bartlett's test and normality of errors by Shapiro Wilk. An individual analysis of variance was performed for each environment and the homogeneity of variances between environments was observed. The criterion considered to assess homogeneity was the maximum F test, in which the value of the division between the highest and lowest variance is less than seven. Subsequently, the joint analysis of variance was carried out to evidence the effects of the interaction, through the model:

$$Y_{ijk} = \mu + G_i + A_j + GA_{ij} + B/A_{jk} + \varepsilon_{ijk}$$

Where: $\mu$: general average; $G_i$: effect of the i-th genotype (i = 1, 2, ..., g); $A_j$: effect of the j-th environment (j= 1, 2, ..., e); $GA_{ij}$: effect of the interaction of the i-th genotype with the j-th environment; $B/A_{jk}$: effect of the k-th block within the j-th environment (k = 1, 2, ..., r); $\varepsilon_{ijk}$: random error.

With the presence of the genotypes x environments interaction, a study of adaptability and stability was carried out to identify genotypes with predictable behavior and that are responsive to environmental variations, under specific or broad conditions (CRUZ et al., 2012). For this, some methods were used to estimate stability and adaptability parameters.

The AMMI method (*Additive Main Effects and Multiplicative Interaction Analysis*) was used, and the scores obtained were later represented in Biplot graphs using the multivariate methodology of the main components (GAUCH, 1992). For this, the model was used:

$$Y_{ij=}\mu + g_i + e_j + \sum_{k=1}^{n} \lambda_k \gamma_{ik} \alpha_{jk} + \rho_{ij} + \varepsilon_{ij}$$

Where: $Y_{ij}$ is the average productivity of genotype i in environment j; $\mu$: general average; $g_i$: genotype effect; $e_j$: effect of the environment; $\lambda_k$: is the singular value for the k-th axis of the principal component; $\gamma_{ik}$: is the i-th element of the k-th eigenvector of genotypes; $\alpha_{jk}$: is the j-th element of the k-th eigenvector of environments; $\rho_{ij}$: is the additional error to be eliminated from the G x E interaction analysis; $\varepsilon_{ij}$: is the experimental error (DUARTE & VENCOVSKY, 1999).

Some studies portray the importance of the simultaneous use of adaptability and stability methods to obtain greater reliability in the selection of genotypes. HONGYU et al. (2015), SINGH et al. (2021) and KEHL et al. (2022) showed that the AMMI and GGE analysis used simultaneously is a strategy that can increase the assertiveness of genotype positioning. Thus, the Genotype and Genotype-by-Environment (GGE) method was also applied.

The *GGE* stands out for reproducing inferences regarding the performance of genotypes and environments, facilitating the visualization of the results in graphic outputs (YAN & KANG, 2003). In this way, it makes it possible to identify representative and discriminative environments, in addition to selecting genotypes that are more adapted and stable to a specific environment (SILVA et al., 2015). The *GGE* model was performed based on the grain yield of the different genotypes in the tested environments, using the following model:

$$\bar{Y}_{ij} - \mu_j = \sum_{k=1}^{t} \lambda_1\alpha_{i1}\gamma_{j1} + \lambda_2\alpha_{i2}\gamma_{j2} + \varepsilon_{ij}$$

Where: $\bar{Y}_{ij}$: represents the average productivity of the i-th genotype in the j-th environment; $\mu_j$: is the general average of genotypes in environment j; i=1, ..., g; j = 1, ... e, g and e being the numbers of genotypes and environments, respectively; t: is the number of main components used in the model; $\lambda_1\alpha_{i1}\gamma_{j1}$: is the first principal component; $\lambda_2\alpha_{i2}\gamma_{j2}$: is the second principal component; $\lambda_1$ e $\lambda_2$: are the eigenvalues associated with the first and second principal components, respectively; $\alpha_{i1}$ and $\alpha_{i2}$: are the scores of the first and second principal components, respectively, of the e-th genotype; and $\gamma_{j1}$ and $\gamma_{j2}$: are the scores of the first and second principal components, respectively, for the jth environment; $\varepsilon_{ij}$: is the model error associated with the i-th genotype and j-th environment (YAN & KANG, 2003).

In addition to these methods, the selection of promising genotypes was aided by the use of the superiority index (WAASBY) which is the simultaneous use of yield and stability by variable weighting of the yield and stability of genotypes (OLIVOTO et al., 2019).

Subsequently, the method based on Restricted Maximum Likelihood (*REML*) was used in order to estimate the variance components and genetic parameters, according to the following statistical model: y = Xb + Za + Wi + e, where y is the data vector; b is the vector of the block effects (assumed as fixed) added to the general average; a is the vector of individual genotypic effects (assumed as random); i is the vector of the effects of the genotype/environment interaction (with the environment corresponding to years); e is the vector of errors (random); and X, Z, and W represent the incidence matrices for the referred effects. The significance was obtained through the *Deviance analysis* at 5% probability by the *Chi-square* test.

This approach allowed of the following estimations: phenotypic variance (*σ²P*), broad sense heritability (*H²*), mean genotype heritability (*H²mg*), coefficient of determination of the effects of the genotype-environment interaction (*GEI*), genotypic correlation between performance genotypes x environments (*RGE*), coefficient of genotypic variation ($CVg^*$), residual coefficient of variation ($CVr^*$) and coefficient of variation of the proportion between genotypic and residual coefficient of variation ($CVratio^*$).

The meteorological information medium temperature (Tmed, °C), minimum (Tmin, °C) and maximum air temperature (Tmax, °C), precipitation (Prec, mm), relative humidity (RH, $g.kg^{-1}$) and incident radiation (Rad, $MJ.m^{-2}.day^{-1}$) were expressed in order to better understand the results obtained on the Nasa Power platform. To demonstrate the meteorological variables that determine the phenotypic expression of grain yield, multiple regression analysis was performed. This analysis was performed stratified by cultivation environment, setting the grain yield variable as a dependent character and Tmed, Tmin, Tmax, RH, Prec and Rad as explanatory independent of the model.

For the preparation of statistical analysis, the packages ExpDes.pt (FERREIRA et al., 2021), metan (OLIVOTO & LÚCIO, 2020) and ggplot2 (WICKHAM, 2016). The package “ggplot2” was used to develop the graphic performances of the genotypes, “ExpDes.pt” to verify the assumptions of the analyzes and “metan” for the application of Deviance analyses, BLUPs prediction and models of adaptability and stability. All statistical analyzes were performed with the used R software (R CORE TEAM, 2021).

## RESULTS AND DISCUSSION

According to the average air temperature variations over two years (Figure 1), in the 2019/2020 and 2020/2021 crop seasons, it was noticed that the lowest air temperatures occur from May to August, and during November, December, January and February the air temperatures tend to be higher, in which the month of February exhibited the greatest oscillation in relation to the average air temperature. It appears that Major Vieira- SC, Toledo-PR and Três Passos- RS had similar average air temperatures, that is, without major fluctuations throughout the year, especially in the period that is comprised of soybean cultivation, between October and April. According to Zanon et al. (2018), the optimal air temperature for soybean

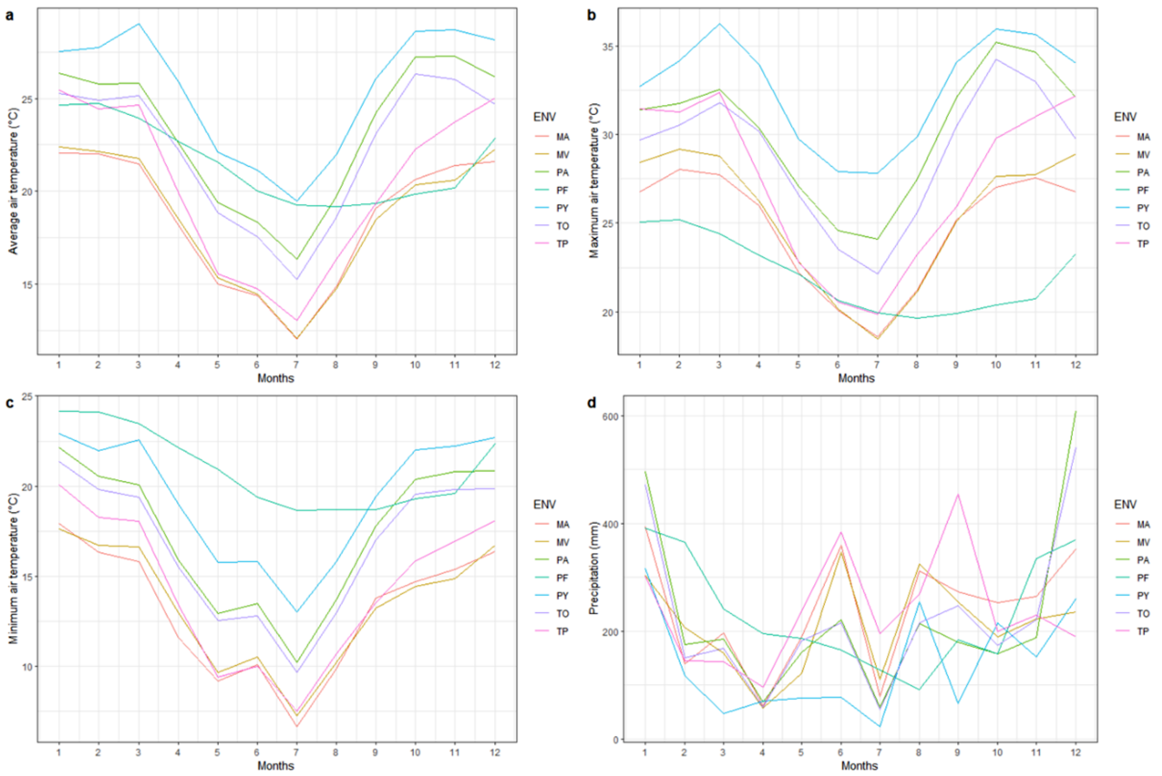

Figure 1 - Medium air temperatures (ºC) and average precipitation (mm) for the different environments. The circles represent the maximums and minimums values of the variable in each of the months.

cultivation throughout the vegetative and reproductive period is 25 to 31 ºC, an air temperature range that can be observed in all environments evaluated.

The soybean plant has approximately 90% of its mass made up of water, which operates in physiological and biochemical processes, being a determining factor in the development of the crop (ZANON et al., 2018). Thus, there was a discrepancy in precipitation volumes between 2019/2020 and 2020/2021, especially in January and February, where there were periods of drought (Figure 1). It is in this period that the grain filling phase begins (R5 stage), being considered the most sensitive stage to water deficit, with a water demand of 7 mm per day (ZANON et al., 2018). In this way, it was reported that the greatest variations occurred in January, mainly in Palotina- PR and Passo Fundo- RS, in which it can be considered a limiting factor to the crop's grain yield, given the importance of water demand for this species.

It is possible to demonstrate a better understanding of the similarity of environments as a function of meteorological variables through the analysis of principal components (Figure 2). It is observed that the accumulated precipitation was higher and similar in the Passo Fundo, Major Vieira and Mangueirinha environments. The higher altitudes observed in these environments may favor a greater accumulation of rainfall (AL-AHMADI & AL-AHMADI, 2013). However, Três Passos had the lowest rainfall; consequently, a higher incidence of radiation and maximum and minimum air temperatures. Lower minimum air temperature was observed between the Palotina, Bela Vista do Norte and Toledo environments.

It was observed that the contrasting environment corresponded to Palotina- PR (E3), whose genotypes BRS 525 (G5) and G6 (BRS 535) showed high grain yield, between 4.5 t ha$^{-1}$ and 5 t ha$^{-1}$ (Figure 3A). This indicated that these genotypes are promising for cultivation in an organic system in this environment. The environment that presented the lowest performance was Mangueirinha- PR (E1), where the genotypes BRS 391 (G2) and BRS 525 (G5) presented grain yield close to 2 t ha$^{-1}$,

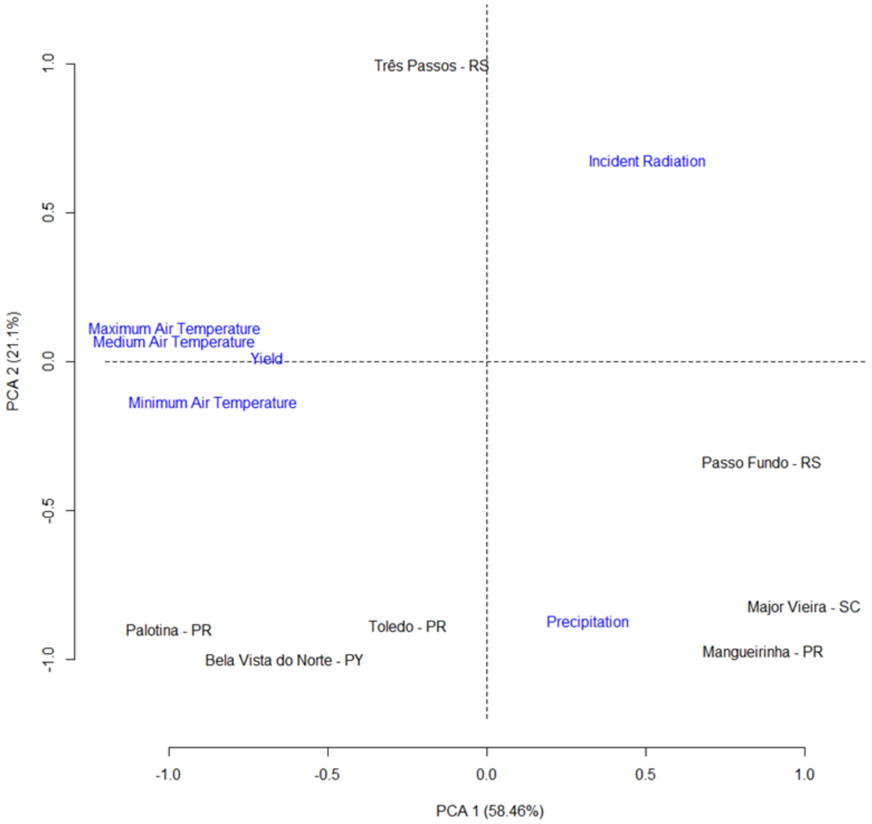

Figure 2 - Principal component analysis for minimum, average and maximum air temperature (ºC) and rainfall (mm) for the environments.

with minimum and medium air temperatures lower than the other environments. It can be observed that Palotina (state) kept air temperatures as close as possible to the optimal range, between 20 and 30 ºC, unlike Mangueirinha (state), where the minimum air temperature reached 10 ºC during the crop cycle. The environments Bela Vista do Norte- PY (PY), Palotina-PR (PA) and Mangueirinha- PR (MA), presented similar precipitation with a daily average of 4.22 mm, totaling approximately 506 mm along the cycle, which fits the values necessary for soybean development.

The analysis of variance (Table 1) revealed a significant interaction between the growing environments x soybean genotypes for grain yield at 5% significance by F test. This indicates the presence of variability between the genotypes and environments used, and also the occurrence of differential response of genotypes to environments, evidencing the need to carry out stability and adaptability analyzes.

About 73% of soybean grain yield was influenced by the environment in which the crop was exposed, and 27% by its genetic constitution, in other words, according to CARVALHO et al. (2017), the environment has a high effect on the expression of the phenotype, thus affecting the expression of different characters.

The occurrence of genetic variability can be seen (Table 2), in relation to grain yield, in the same way, there was an interaction between genotypes x environments for the analyzed variable. According to Taiz et al., (2017), the environment has a great effect on the expression of the phenotype, thus, environmental variations affect the characters through different stimuli and physiological mechanisms. In view of this, it can be said, according to table 2, that the heritability presented in the *REML* analyzes for the grain yield variable was considered low (9.31%), which indicated that the environment has an influence of 90.7% about the expression of this character. This result corroborates CARVALHO et al. (2018), who considered low heritability with values ranging from 0.09 to 0.15 for corn grain yield. For Rigon et al. (2012), because it is a quantitative character

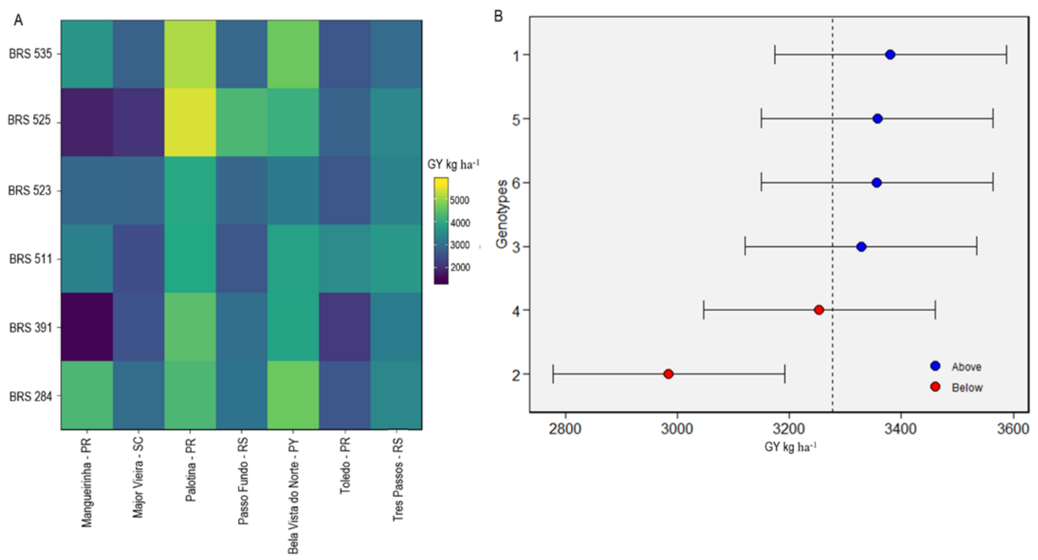

Figure 3 - Descriptive analysis of grain yield showing the interaction between genotypes x environments (A) and representation of estimates obtained by the method of analysis of restricted maximum likelihood/best unbiased linear predictor (*REML/BLUP*) (B), for the grain yield trait of six soybean genotypes. Genotypes: G1: BRS 284, G2: BRS 391, G3: BRS 511, G4: 523, G5: BRS 525, G6: BRS 535 (B).

and with large modifying alleles (small effect), it is strongly influenced by environmental conditions and; consequently, with low heritability.

The coefficient for determining the effects of the genotype-environment interaction (GEI) indicates the participation of the interaction effects in the total variation of the character (CARVALHO et al., 2018). The grain yield analysis indicated that 0.391 (39.1%) of the grain yield expression comes from this interaction, a value considered inconstant (Table 2). Interaction variation is the proportion of phenotypic variation determined by the effects of the interaction between different genotypes and the different environments in which these genotypes are inserted (CARVALHO et al., 2017).

Regarding the average heritability of the genotypes ($H^2mg$), this is estimated when using averages as an evaluation or selection unit (BARETTA et al., 2017). Thus, average heritability values of the genotypes were reported with an average magnitude of 59.6%, that is, this effect may come from the genotype, regardless of the environment in which it would be exposed. Within the *REML* analysis for the grain yield character, a high accuracy (77.2%) was identified.

Research defines that the simple interaction reveals a high genotypic correlation between the tested environments (PUPIN et al., 2015); however, when there are lower contributions of the genetic fraction to the phenotype cultivated in different environments, it results in the complex interaction with lower phenotypic stability for the environment. character (ROSADO et al., 2012).

Thus, it was observed that this correlation was low for the grain yield character (0.43), being less than 0.5. Low correlation indicated that a superior genotype in one environment may not present the same performance in another environment (PUPIN et al., 2015). Thus, it can be inferred that there is a predominance of complex interaction for grain yield, and it is not possible to indicate a single genotype for all environments.

The coefficient of genotypic variation (*CVg*) is a fundamental measure that makes it possible to infer the size of the genetic variability present in the population for the characters under study (Nardino et al., 2016). Thus, low values (5.93%) were observed, which indicates a low genetic contribution in the expression of variability, with the genotypes being strongly influenced by the environment in the expression of the phenotype. The residual coefficient of variation (*CVr*) refers to the experimental error, where an average value (14%) is observed, indicating the precision of the experiment. In relation to the coefficient of variation of the proportion between the coefficient of genotypic and residual variation (*CVratio*), for grain yield, it was low 0.425.

Table 1 - Meteorological variables, soil characteristics, relief and location of environments: Bela Vista do Norte- PY (PY); Palotina -PR (PA); Toledo- PR (TO); Mangueirinha- PR (MA); Major Vieira- SC (MV); Três Passos- RS (TP); Passo Fundo- RS (PF). Conjunct analysis of variance for grain yield evaluated in number of genotypes and environments.

------------Environmental characterization------------

| ENV | Lat$^{1}$ | Long$^{2}$ | Alt$^{3}$ | Soil Type | Tmax (ºC)$^{6}$ | Tmin (ºC)$^{8}$ |
|---|---|---|---|---|---|---|
| PY | 22º 7’ 48” S | 56º 31’ 12” O | 176 m | RL$^{12}$ | 32.32 | 18.45 |
| PA | 24°17'38.81" S | 53°48'03.77" O | 338 m | DRL$^{12}$ | 33.39 | 19.68 |
| TO | 24º 42’ 50” S | 53º 44’ 34” O | 550 m | DRL$^{12}$ | 32.27 | 18.61 |
| MA | 25º 56’ 27” S | 52º 10’ 33” O | 921 m | NLH$^{14}$ | 28.51 | 15.75 |
| MV | 26º 22’ 04” S | 50º 19’ 40” O | 786 m | LBDR$^{15}$ | 27.88 | 15.57 |
| TP | 27°29'52.30" S | 53°54'00.34" O | 438 m | DRL$^{12}$ | 31.95 | 17.64 |
| PF | 28º 15’ 46” S | 35º 24’ 25” O | 687 m | DRL$^{12}$ | 28.85 | 16.6 |

------------Analisys of Variance------------

| Variation | DF$^{9}$ | SS$^{10}$ | MS$^{11}$ | F value | Pr (>F) | Proportion | Accumulated |
|---|---|---|---|---|---|---|---|
| ------------Factor------------ | | | | | | | |
| ENV | 6 | 9.93E+07 | 1.70E+07 | 59.1 | 0.00E+00 | NA | NA |
| REP (ENV) | 63 | 1.76E+07 | 280031 | 1.34 | 5.73E-02 | NA | NA |
| GEN | 5 | 2.22E+07 | 4440065 | 21.2 | 2.80E-18 | NA | NA |
| GEN:ENV | 30 | 5.39E+00 | 1795940 | 8.58 | 2.82E-26 | NA | NA |
| PC1 | 10 | 2.76E+07 | 2763239 | 13.2 | 0.00E+00 | 51.3 | 51.3 |
| PC2 | 8 | 1.84E+07 | 2303634 | 11 | 0.00E+00 | 34.2 | 85.5 |
| PC3 | 6 | 5.90E+06 | 983804 | 4.7 | 1.00E-04 | 11 | 96.4 |
| PC4 | 4 | 1.52E+06 | 380660 | 1.82 | 1.25E-01 | 2.8 | 99.3 |
| PC5 | 2 | 3.91E+05 | 195630 | 0.93 | 3.96E-01 | 0.7 | 100 |
| RESIDUAL | 315 | 6.60E+07 | 209401 | | | | |
| Total | 449 | 3.13E+08 | 696774 | | | | |

[1] Lat - Latitude; Long - [2] Longitude; [3] Alt - Altitude; [4] Pre - Precipitation; [5] Rad - Radiation; [6] Tmax – Maximum Air Temperature; [7] Tmed – Medium Air Temperature; [8] Tmin – Minimum Air Temperature. [9] Degrees of Freedom (DF); [10] Sum of Squares (SS); [11] Mean Square (MS); [12] Red Latosol (RL); [12] Dystrophic Red Latosol (DRL); [14] Neosolo Litólico Húmico (NLH); [15] Latosol Bruno/Dark (LBDR).

The use of mixed models based on *REML/BLUP* and multivariate methods allow the exploration of different concepts of adaptability and stability of genotypes, thus increasing the efficiency of the selection of superior genotypes (ANDRADE et al., 2016). This efficiency is explained by the prediction of breeding values simultaneously with the estimation of variance components (RESENDE, 2000). The use of genetic evaluation techniques, based on mixed models such as *REML/BLUP* (Restricted Maximum Likelihood Analysis/Best Unbiased Linear Predictor), are fundamental for the prediction of additive and genotypic genetic values of individuals with potential for selection.

Thus, according to the BLUP (Figure 3B), for the genetic effect of the genotypes, 59.6% of the expression of the character is a genetic effect, it can be predicted that the additive genetic value (VGA) is equal to the heritability of the trait ($h^2$), multiplied by the individual’s performance (P), minus the overall mean of the experiment ($\mu$), ie, VGA= $h^2$. (P-$\mu$). Thus, with the selection via BLUP, it was observed that the genotypes BRS 284 (G1), BRS 511(G3), BRS525 (G5) and BRS 539 (G6) showed superior performance for grain yield and therefore are located above of the selection range.

It is possible to identify genotypes with predictable behavior in relation to grain yield and that are responsive to variations in environments, as with the *REML/BLUP* graph (Figure 4), it is possible to observe the behavior of the genotypes in each environment studied. In E1 environment (Mangueirinha- PR), the superior genotypes for this environment were BRS 284 (G1), BRS 539 (G6) and BRS 511 (G3), with grain yield above 3250 kg ha$^{-1}$. For the environment E2 (Major Vieira- SC), and E6 (Toledo- PR), none of the genotypes were superior in relation to grain yield, that is, all with low yield, which indicates an unfavorable environment, unlike Bela Vista do Norte- PY (E5), where all genotypes can be selected for this variable. In relation to Palotina- PR (E3), with the exception of the BRS 391 (G2) genotype, all the others showed high grain yield. In Passo Fundo- RS (E4), the genotypes BRS525 (G5), BRS 511 (G3) and

Table 2 - Estimates of variance components and genetic parameters for soybean grain yield in different environments in Brazil and Paraguay.

| VAR | MODEL | LOG LIK | AIC | LRT | PR (> CHISQ) |
|---|---|---|---|---|---|
| GY | GEN | -2744 | 5633 | 2.16 | 1.42E-01 |
| GY | GEN:ENV | -2798 | 5731 | 110 | 9.14E-26 |
| Parameters | | | | | GY |
| $\sigma^2P$ | | | | | 405829 |
| $\sigma^2G$ | | | | | 37782 |
| $H^2$ | | | | | 0.0931 |
| $GEIr^2$ | | | | | 0.391 |
| $H^2mg$ | | | | | 0.596 |
| Accuracy | | | | | 0.772 |
| RGE % | | | | | 0.431 |
| CVg % | | | | | 5.93 |
| CVr % | | | | | 14 |
| CVratio% | | | | | 0.425 |

Var: Variable; Model: Model; Log Lik: Restricted Maximum Likelihood Logarithm; AIC: Akaike Informative Criterion; LRT: Restricted Maximum Likelihood Ratio; PR: Probability by *Chi-Square* test: $\sigma^2P$: Phenotypic variance; $\sigma^2G$: Genotypic variance; $H^2$: broad-sense heritability GEI: coefficient for determining the effects of the genotype-environment interaction; $H^2$mg: Mean heritability of the genotype; RGE: genotypic correlation between genotypes x environments performance; CVg: Genotypic variation coefficient; Cvr: Coefficient of residual variation; CV ratio: coefficient of variation of the proportion between genotypic and residual coefficient of variation.

BRS 523 (G4) showed high productivity, and in the E7 environment (Três Passos- RS), only BRS 539 (G6) and BRS 391 (G2) with lower grain yield.

For the percentages of explanation of the axes of the AMMI2 model, it was observed that the first and second principal components presented an explainability of 51.3% and 34.2% of the general effects attributed to the G x E interaction (Figure 5A). Thus, it can be inferred that the closer to the origin of the data (0, 0), the more stable the genotype and, thus the BRS 284 (G1) genotype, is considered more stable and high yielding, consequently the most adapted to the E5 environment (Bela Vista do Norte- PY). After environments E6 (Toledo- PR) and E7 (Três Passos- RS), the genotypes were considered adapted to these BRS 391 (G2) and BRS 523 (G4).

It was possible to observe the formation of a polygon, it was observed that at the end there are genotypes of high productivity, being composed of all the genotypes studied BRS 284 (G1), BRS 391 (G2), G3 (BRS 511), BRS 523 (G4), BRS 525 (G5) and BRS 539 (G6) (Figure 5A). Environments located outside the polygon are considered to have high variability. Thus, it is possible to group these, the mega-environment I made it possible to gather the E4 (Passo Fundo- RS) and E7 (Três Passos- RS) environments, similar enough to compose a mega-environment of high variability, in addition to gathering the BRS genotype 525 (G5), considered high performance. Mega-environment II brought together environments E1 (Mangueirinha- PR), E3 (Palotina- PR) and E5 (Bela Vista do Norte- PY), the first two with high variability and the last one with low variability. Mega-environment III was composed of the environments. E2 (Major Vieira- SC) and E6 (Toledo- PR), with low performance and high variability, respectively. In this situation, genotypes BRS 391 (G2), BRS 511 (G3) and BRS 523 (G511) are positioned, which present high performance.

The WAASBY index (Figure 5B) makes it possible to identify genotypes that express high adaptability and phenotypic stability. Thus, / the genotypes BRS 511 (G3), BRS 284 (G1) and BRS 523 (G5) showed greater stability and adaptability in relation to environments when compared to genotypes BRS 391 (G2), BRS 525 (G5) and BRS 539 (G6), that is, the genotypes BRS 511 (G3), BRS 284 (G1) and BRS 523 (G5) showed higher WAASBY values, demonstrating their superiority when considering performance and stability.

The GGE (*Genotypes and Genptypes by Environmentes Interaction*) multivariate analysis method makes it possible to use a large number of genotypes and various environments, helping to understand the genotypes x environments interaction, which allows the identification of genotypes with high productivity (CARVALHO et al., 2017). The phenotypic stability analysis portrays the possibility of predicting possible responses in subsequent cultures, indicating the behavior of each genotype under certain culture

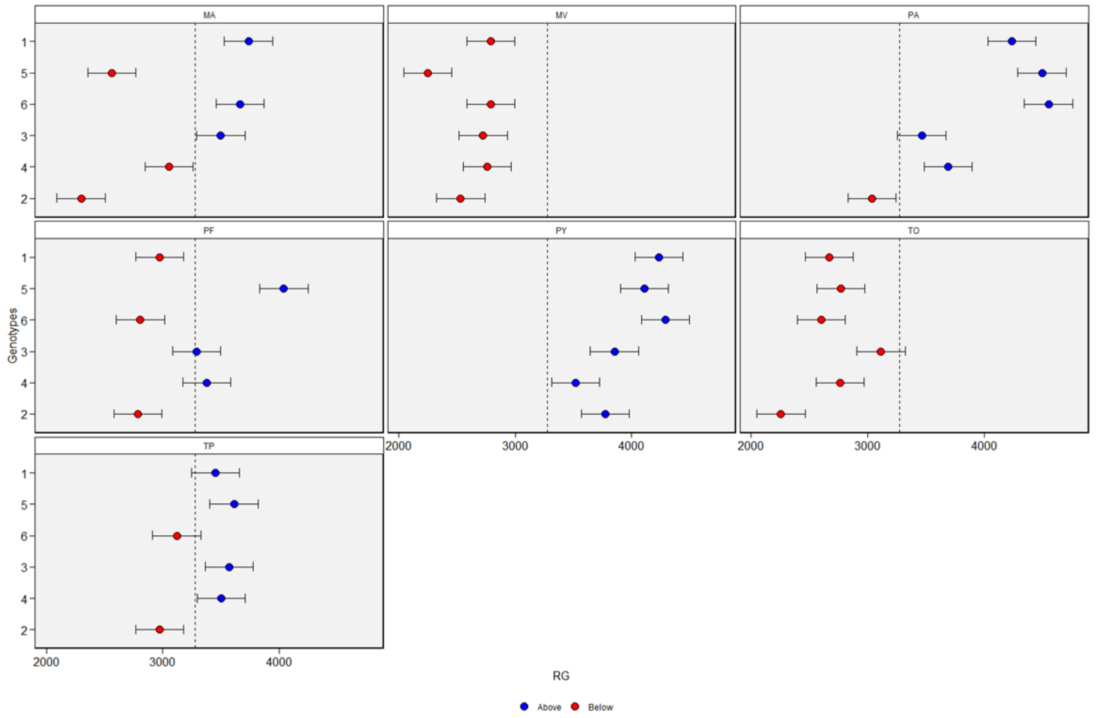

Figure 4 - Estimates of the components of yield averages by specific BLUP measured in six genotypes and six environments. Genotypes: G1: BRS 284, G2: BRS 391, G3: BRS 511, G4: BRS 523, G5: BRS 525, G6: BRS 535. Environments: E1-MA (Mangueirinha- PR), E2-MV (Major Vieira), E3-PA (Palotina- PR), E4-PF (Passo Fundo- RS), E5-PY (Bela Vista do Norte- PY), E6-TO (Toledo- PR), TP (Três Passos- RS).

conditions. These assumptions showed that the GGE method made it possible (PCI: 46.67% and PCII: 33.44%) representing 80.11% of the interaction effects on the grain yield variable (Figure 6A).

In this way, through the evaluation of the averages of the genotypes in each environment, it was possible to determine that the genotype BRS 284 (G1) was considered ideal, since it shows excellent stability

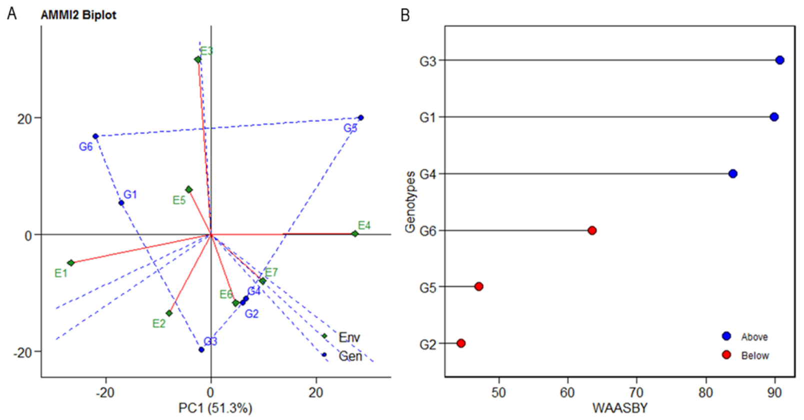

Figure 5 - Plotting the scores of the main components of the AMMI2 method (A) and estimating the WAASBY value (B) for soybean grain yield, relative to six genotypes (G) cultivated in six environments (E). Environments: Env E1: Mangueirinha- PR, E2: Major Vieira- SC, E3: Palotina- PR, E4: Passo Fundo- RS, E5: Bela Vista do Norte- PY, E6: Toledo- PR; E7: Três Passos- RS. Genotypes: G1: BRS 284, G2: BRS 391, G3: BRS 511, G4: BRS 523, G5: BRS 525 and G6: 535.

and performance regarding the variable grain yield. The BRS 391 (G2) genotype showed high stability, but with low grain yield. The BRS 525 (G5) genotype showed greater phenotypic instability in relation to the others. It was found that E5 (Bela Vista do Norte- PY) and E6 (Toledo- PR) showed high average and high stability, and Passo Fundo- RS (E4) was the most unstable, that is, an unpredictable environment.

The same magnitude was observed for environments E2 (Major Vieira- SC), E5 (Bela Vista do Norte- PY), E6 (Toledo- PR), E7 (Três Passos- RS), located near the origin of the data, that is, representative environments (Figure 6B). According to Yokomizo et al. (2020), the closer to the arrow, this environment can be considered as the most representative in relation to the others and; therefore, considered the most appropriate. For E1 (Mangueirinha- PR), E3 (Palotina- PR) and E4 (Passo Fundo- RS), dissimilarity between these environments was verified, in relation to the genotypes, there was dissimilarity in the grain yield variable for BRS 284 (G1), BRS 391 (G2), BRS525 (G5) and BRS 539 (G6), except for the genotypes BRS 511 (G3) and BRS 523 (G4).

The ideotype and the ideal environment are represented by the center of the circles and, thus, the best genotypes and environments are those that are in the closest circles (YOKOMIZO et al., 2020). The environment that is closest to high productivity is E3 (Palotina- PR), followed by E5 (Bela Vista do Norte- PY), E6 (Toledo- PR) and E7 (Três Passos- RS), after E1 (Mangueirinha- PR) and finally, the others that distanced themselves from high performance environments are Major Vieira- SC (E2) and Passo Fundo- RS (E4) (Figure 6C). Taking into account the ranking of genotypes, none of them showed high performance, but BRS 284 (G1) was above average and closer to the center of the circle (Figure 6D).

In the environmental multiple regression for grain yield (GY) (Figure 7), for genetic value for each environment, the Mangueirinha- PR (MA-

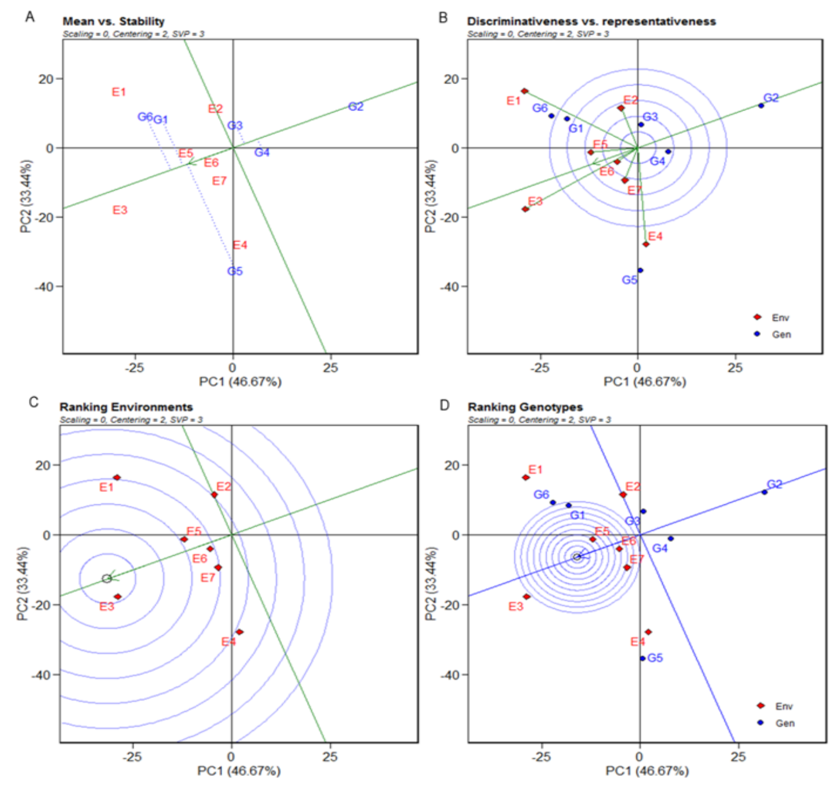

Figure 6 - GGE biplot (*Genotypes and Genptypes by Environmentes Interaction*) indicating the ranking of the seven environments (E) and six soybean genotypes (Gen), with their respective stabilities, discrimination and representativeness of production environments regarding the variable grain yield. Environments: Env E1: Mangueirinha- PR, E2: Major Vieira- SC, E3: Palotina- PR, E4: Passo Fundo- RS, E5: Bela Vista do Norte- PY, E6: Toledo- PR; E7: Três passos- RS. Genotypes: G1: BRS 284, G2: BRS 391, G3: BRS 511, G4: BRS 523, G5: BRS 525, G6: BRS 535.

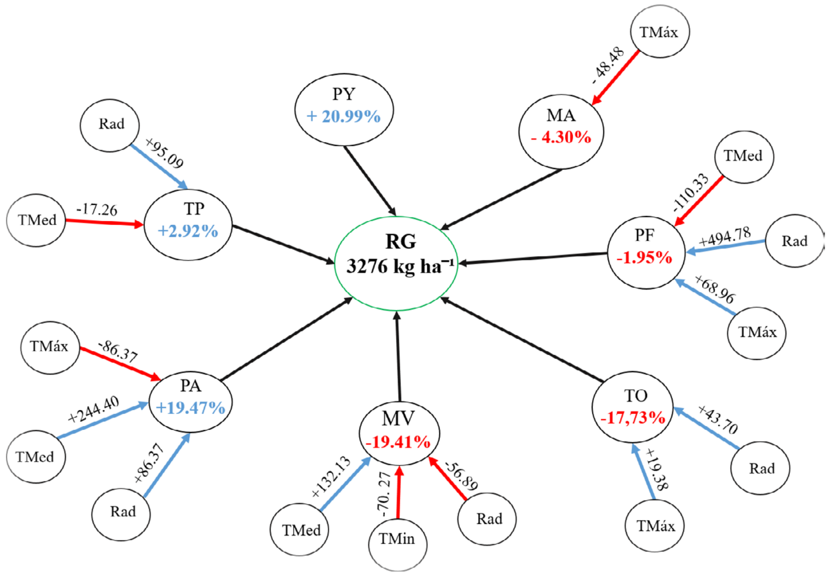

Figure 7 - Environmental predictor model for Grain Yield (GY). Tmed: Medium air temperature (ºC); Tmin: Minimum air temperature (ºC); Tmax: Maximum air temperature (ºC); Rad: Radiation (MJ m$^2$ day$^{-1}$).

PR) environment was negatively influenced by the maximum air temperature (Tmax). In relation to Major Vieira- SC (MV-SC), which was positively influenced by medium air temperature (Tmed), and negatively influenced by minimum air temperature (Tmin) and radiation (Rad) (Figure 7). Palotina- PR (PA-PR) showed a negative relationship for maximum air temperature (Tmax) and a positive relationship for meteorological conditions medium air temperature (Tmed) and radiation (Rad).

Passo Fundo- RS (PF-RS) environment had negative intervention for medium air temperature (Tmed) and positive for maximum air temperature (Tmax) and radiation (Rad). In Toledo- PR (TO-PR) a positive influence of the meteorological variables maximum air temperature (Tmax) and radiation (Rad) was observed. In Três Passos- RS (TP-RS) environment, a positive relationship was observed between radiation (Rad) and the predicted genetic value, and a negative relationship for medium air temperature (Tmed). According to Zanon et al. (2018) the main factor responsible for crop productivity are climatic elements.

From this study, it is possible to understand the responses of soybean genotypes in seven organic farming environments. In addition, it was possible to evidence the genetic parameters and select genotypes adapted and stable to the organic conditions in each environment. The results may encourage the specific use of these genotypes in genetic improvement programs as parents, for the development of genotypes superior to the conditions imposed for organic production. Subsequently, further research will be necessary in order to understand the performance of genotypes in other environments. This ensures progress in the development of plants with skills capable of adapting to ensure productivity, especially of grains. Thus, research has the potential to contribute to ensuring the sustainability of production, as well as mitigating food insecurity.

## CONCLUSION

BRS 511 genotype was characterized by high average grain yield and stability by the AMMI method. BRS 284 genotype was identified as the ideal genotype in the GGE biplot method. WAASBY and BLUP index selected BRS511 and BRS284 genotypes.The higher incidence of solar radiation tends to maximize grain yield.

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## DECLARATION OF CONFLICT OF INTEREST

The authors declare no conflict of interest. The founding sponsors had no role in the design of the study; in the

collection, analysis, or interpretation of the data; in the writing of the manuscript, and in the decision to publish the results.

## AUTHORS' CONTRIBUTIONS

All authors contributed equally for the conception and writing of the manuscript. All authors critically revised the manuscript and approved of the final version.

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