RESEARCH ARTICLE

Multivariate explanation of the establishment of soybean initial growth pattern via biostimulant seed treatment

Luiz Leonardo Ferreira¹, Juliano Macedo Resende¹, Ivan Ricardo Carvalho², Ariana Bertola Carnevale¹, Marilaine de Sá Fernandes¹, Núbia Sousa Carrijo dos Santos¹, Priscila Ferreira Batista³, Alexandre Igor de Azevedo Pereira⁴, Carmen Rosa da Silva Curvêlo⁴, Uirá do Amaral⁵, Rodrigo Vieira da Silva⁶ and Murilo Vieira Loro⁷

¹Mineiros University Center, Mineiros, GO, Brazil. ²Regional University of the Northwest of the State of Rio Grande do Sul, Ijuí, RS, Brazil. ³Goiano Federal Institute, Rio Verde campus, Rio Verde, GO, Brazil. ⁴Goiano Federal Institute, Urutaí campus, Urutaí, GO, Brazil. ⁵Brasília Federal Institute, Planaltina Campus, Planaltina, Brasília, DF, Brazil. ⁶Goiano Federal Institute, Morrinhos campus, Morrinhos, GO, Brazil. ⁷Federal University of Santa Maria, Santa Maria, RS, Brazil. Corresponding author, E-mail: carvalho.irc@gmail.com

ABSTRACT

Given the search for answers that improve soybean plant development, this study aimed to analyze the multivariate explanation about the establishment of the initial soybean growth pattern through seed treatment. The study was conducted at Luiz Eduardo de Oliveira Sales Experimental Farm, in the municipality of Mineiros-GO. The soil of the experimental area was classified as NEOSSOLO Quartzarenico. The experimental design was randomized blocks in factorial 10x5 corresponding to 10 soybean genotypes (Flecha, Bonus, TEC7548, M7739, 36B31, W791, M7198, M6210, Power and 48B32) and 5 seed treatments (Water, Sprint-Alga, Booster, Acorda and Stimulate), in 4 repetitions. The obtained data was submitted to the assumptions of the statistical model, verifying the normality and homogeneity of the residual variances, as well as the additivity of the model. Afterwards, the analysis of variance was performed in order to identify the interaction between soybean genotypes x seed treatment, applying uni and multivariate tests. The summary analysis of variance revealed significant interaction between cultivar x seed treatment. The seed treatment influenced the morphological components of soybean seedlings, showing their correlation with the fresh aerial and root mass, as well as different patterns that were observed according to the genetic variation.

Keywords: correlations, Glycine Max, canonical variables, genetic dissimilarity, UPGMA, Artificial Neural Networks.
INTRODUCTION

Soybean is most grown major crop in planted area in the country, and is currently consolidated as one of the most prominent products of Brazilian agribusiness (Zago et al., 2018). As the development of soybean has become important for the Brazilian economy, this sector is being one of the main pillars of the national economy.

The Brazilian territorial area corresponds to approximately 851.95 million hectares. The potential for national arable land is estimated at 152.5 million hectares, or 17.9% of the national territory. However, 62.5 million hectares are being used for agriculture, in which the soybean cultivation area represents 38 million hectares, the largest among the crops planted in the country (Empresa Brasileira de Pesquisa Agropecuária (Embrapa, 2018). In the 2020/2021 crop year, Brazil had an area of 38 million hectares of soybean planting, and production of 135 million tons.

According to Kryzanowshi et al. (2008) seed quality is defined as a series of genetic, physical, physiological and sanitary attributes that interfere with the ability to produce a uniform crop, consisting of representative vigorous plants and free from invasive or undesirable plants. Seed quality can be affected by several factors during the production process, as well as by the interaction between genotypes x environments (Carvalho et al., 2015). An example of this factor would be sowing under adverse environmental conditions such as inadequate temperatures, soil water deficit related to low quality seeds used in sowing.

The use of quality seeds and the use of products that improve their field performance are important elements for high agricultural production. In this case, biostimulants are components that favor plant growth and can act alone or in combination, interfering with various physiological and / or morphological processes, such as germination, vegetative growth, flowering, fruiting, senescence and abscission. In beans, Ferreira et al. (2021) showed that the use of foliar biostimulants enhances characteristics such as number of pods, seed weight and grain yield.

According to Binsfeld et al. (2014), soybean seed treatment with fungicides has been widely adopted allows the germination of infected seeds, control seed-borne pathogens and protect seeds from soil fungi, enabling greater potential for early crop development and initial stand establishment at reduced costs.

The use of biostimulants increases the components of plant development, even though there are few studies addressing the physiological characteristics of soybean related to the application of these products. Seed application may give rise to plants that are more vigorous, longer lengths, increased dry matter, and percentage of emergence in sand and soil adjusted for increased product doses in various crops (Marques et al., 2014). Kolling et al. (2016) points out that the results reported in the literature regarding the use of biostimulants indicate that the responses to the application of these products depend on the genotype used, the composition of humic substances present in the products, and the environmental conditions (Ferreira et al. (2019) and Silva et al. (2020).

Given the search for answers that improve soybean plant development, the objective of this study was to analyze the multivariate explanation about the establishment of the initial soybean growth pattern via seed treatment with biostimulants.
MATERIAL AND METHODS

The study was conducted at Luiz Eduardo de Oliveira Sales Experimental Farm, in the municipality of Mineiros-GO, located between the geographic coordinates of 17°34'10'' South latitude and 52°33'04'' West longitude, with an average altitude of 760 m. The average temperature is 22.7°C, the average annual rainfall is 1695 mm occurring mostly in spring and summer. The experimental area is classified as Aw (hot dry) climate. The soil of the experimental area was classified NEOSSOLO Quartzarenic, with medium texture, gently undulating to flat topography and good drainage (Embrapa, 2013).

Prior to the installation of the experiment, soil analysis was performed in the 0-20 cm layer and the following characteristics were observed: hydrogen potential 5.7; calcium 3, magnesium 0.8, aluminum 0.2, hydrogen + aluminum 2, cation exchange capacity 5.9, in cmol·dm⁻³; potassium 53, phosphorus 59, sulfur 1.7, boron 0.2, copper 1.4, iron 51, manganese 23, zinc 8.3, sodium 1.5, in mg dm⁻³; clay 223, silt 50, sand 728, organic matter 20 and organic carbon 12, in g dm⁻³. Data was taken according to Embrapa's methodology (2009).

The experimental design was randomized blocks in factorial 10x5 corresponding to 10 soybean genotypes (Arrow, Bonus, TEC7548, M7739, 36B31, W791, M7198, M6210, Power and 48B32) and 5 seed treatments (Water, Sprint-Alga, Booster, Acorda and Stimulate), in 4 repetitions, totaling 50 treatments and 200 experimental units. Each plot was sized with five rows spaced 0.5 m apart with and 1 m long. The main morphoagronomic characteristics of soybean genotypes are described in Table 1.

Table 1. Main morphoagronomic traits of soybean genotypes. Mineiros-GO, UNIFIMES, Brazil, 2020.

| Cultivar           | Commercial | Weight of a Thousand seeds (g) | Genetics | Maturation group | Architecture | Cycle (days after emergency) |
|--------------------|------------|---------------------------------|----------|------------------|--------------|-----------------------------|
| Bonus 8579 RSF IPRO| Bonus      | 190                             | Bramax   | 7.9              | Undetermined | 105 a 122                   |
| TEC7548 IPRO       | TEC7548    | 180                             | Bayer    | 7.5              | Undetermined | 116 a 124                   |
| Flecha 6266RSF IPRO| Flecha     | 190                             | Bramax   | 6.6              | Undetermined | 95 a 105                    |
| M 7739 IPRO        | M7739      | 175                             | Monsoy   | 7.7              | Undetermined | 105 a 115                   |
| CZ 36B31 IPRO      | 36B31      | 170                             | Bayer    | 6.6              | Undetermined | 105 a 112                   |
| W 791 RR           | W791       | 185                             | Bayer    | 7.7              | Undetermined | 105 a 120                   |
| M7198 IPRO         | M7198      | 175                             | Monsoy   | 6.8              | Undetermined | 99 a 107                    |
| BMX Power IPRO     | Power      | 170                             | Bramax   | 7.3              | Undetermined | 105 a 115                   |
| M6210 IPRO         | M6210      | 168                             | Monsoy   | 7.2              | Undetermined | 105 a 115                   |
| CZ 48B32 IPRO      | 48B32      | 140                             | Bayer    | 7.9              | Determined   | 115 a 120                   |

The tillage system was carried out with harrowing and plowing of the area on
11/23/2017. The seeds were treated one day before sowing in polyethylene bags, with the recommended label doses of each product (Table 2). Sowing was performed on 12/08/2017, manually distributing 15 seeds per meter in the furrow (300,000 plants ha\(^{-1}\)). The cultural treatments pertinent to weed control were performed whenever necessary. The main characteristics of the products used as seed treatments were described in Table 2.

### Table 2. Main characteristics of the products used as seed treatment. Mineiros-GO, UNIFIMES, Brazil, 2020.

| Nomenclature | Initial | Active Ing. | Dose (ml or g ha\(^{-1}\)) |
|--------------|---------|-------------|---------------------------|
| Water        | AGU     | Distilled water H\(_2\)O | 800                      |
| Sprint-Alga  | SPR     | Seaweed Extracts       | 40                       |
| Booster      | BOO     | Citric Acid + Potassium Hydroxide | 500          |
| Acorda       | ACO     | Organic carbon         | 500                      |
| Stimulate    | STI     | Cytokine + Gibberellin + Indolalcanoic Acid | 600       |

For the measures were taken on 20 seedlings per experimental unit and the following data was recorded: stand (STD) in units per linear meter, by counting vigorous plants; (COR) root length in cm, stem diameter (DIC) in cm, hypocotyl height (ALH) in cm, height of epicotylus (ALE) in cm and plant height (ALP) in cm, using a tape measure; aerial fresh matter (MFA) in g, and root fresh matter (MFR) in g.

The obtained data was submitted to the assumptions of the statistical model, verifying the normality and homogeneity of the residual variances, as well as the additivity of the model. Afterwards, the analysis of variance was performed in order to identify the interaction between soybean genotypes x seed treatment. Subsequently, the variables were subjected to linear correlation in order to understand the tendency of association, and their significance was based on 5% probability. The canonical correlations were estimated between group 1 (MFA and MFR) and group 2 (STD, COR, DIC, ALH, ALE and ALP), with significance between the character groups evaluated based on chi-square statistics. After genetic dissimilarity by the Mahalanobis algorithm where the residual matrix was weighted, after the phylogenetic tree of the distances was constructed through the UPGMA grouping, the biplot canonical variables method was used to visualize the general variability. of the experiment and multivariate trends. Character matrix data were subjected to unsupervised computational learning through Artificial Neural Networks using the K-means and Kohonen Map algorithms (Carvalho, 2018). The analyzes were performed in Rbio R interface (Bhering, 2017), in addition to Software Genes (Cruz, 2016).

### RESULTS AND DISCUSSION

The summary analysis of variance with the mean square QM and significance by the F test revealed significant interaction between G genotypes x TS seed treatment, in the variables STD stand, DIC stem diameter, height of epicotyl ALE, fresh air mass MFA and root fresh mass MFR (p <0.01) and the variables of root length COR and height of the hypocotyl ALH (p <0.05) (Table 3). Results found corroborate Carvalho et al. (2015), Toledo et al. (2015) and Tatt et al. (2018).
ASB JOURNAL

Table 3. Summary of analysis of variance (QM and CV (%)) for STD stand, COR root length, DIC stem diameter, ALH hypocotyl height, ALE epicotyl height, ALP plant height, MFA fresh air mass and mass fresh root MFR of G soybean genotype seedlings, submitted to different treatments of TS seeds. Mineiros-GO, UNIFIMES, Brazil, 2020.

| Factors | GL | STD | COR | DIC | ALH | ALE | ALP | MFA | MFR |
|---------|----|-----|-----|-----|-----|-----|-----|-----|-----|
| G x TS  | 36 | 260.16** | 7.64* | 0.00** | 0.09* | 0.41** | 12.98ns | 14.87** | 0.27** |
| G       | 9  | 969.79** | 13.18** | 0.00** | 0.36** | 4.42** | 185.49** | 12.89** | 0.38** |
| TS      | 4  | 456.05** | 3.63ns | 0.00ns | 0.05ns | 0.76** | 10.21ns | 3.10ns | 0.40* |
| Blocks  | 3  | 101.55ns | 111.29** | 0.07** | 0.65** | 0.10ns | 38.97** | 38.64** | 0.63** |
| Residue | 147| 106.32 | 5.00 | 0.00 | 0.06 | 0.13 | 9.51 | 2.62 | 0.13 |
| CV (%)  | -  | 23.30 | 11.02 | 8.81 | 12.21 | 11.89 | 9.09 | 16.44 | 15.49 |

** significant at 1% probability by F test; * significant at 5% probability by F test; nsignificant at 5% probability by F test.

Understanding the magnitude of existing associations between agronomic traits is important to help obtain improved genotypes that meet market expectations of high performance (Nardino et al., 2016). Pearson’s correlation coefficients arranged in the correlation networks revealed 7 positive correlations between soybean variables, among the different seed treatments. Correlations were diagnosed in pairs (DICxMFA) in the AGU; (ALPxALE and MFAxMFR) in SPR; (DICxMFA) for BOO; (MFAxALP) present in ACO; and (ALExALP and ALPxMFA) in TS STI (Figure 1). The use of correlation networks can increase the effectiveness of selection in soybean breeding, once it allows us to quickly identify the pairs of traits that present higher magnitude correlations; and determine which groups of variables most significantly influence the most important characters for the breeding program and identify the correlated variable groups.

Figure 1. Simple linear correlation applied to STD stand, COR root length, DIC stem diameter, ALH hypocotyl height, ALE epicotyl height, ALP plant height, MFR root fresh mass and MFA aerial fresh mass of soybean genotype seedlings of soybean genotypes submitted to different seed treatments. Mineiros-GO, UNIFIMES, Brazil, 2020.
According to the results obtained in the canonical correlation analysis, it was observed the formation of two significant canonical pairs (p≤0.01), by the chi-square test for each seed treatment, with high canonical correlation (r≥0.99), corroborating with Carvalho et al. (2015), where the high magnitude of the canonical correlation coefficients shows high dependence between the two trait groups. The information was described taking into consideration only the first canonical pair in the AGU, SPR and BOO seed treatments. However, the performance of the variables in OAC and STI were described with the two canonical pairs (Table 4).

It was observed that the increase of MFR and MFA variables in soybean seedlings were explained by the increase in COR and DIC for all seed treatments in question, as well as for ALT except SPR, following a trend for all reduction in STD. In other words, it has been described that seedlings with higher COR, DIC and low seedling population contribute to the increase in MFR and MFA (Table 4).

The interaction sequence between the 10 soybean genotypes and 5 seed treatments were arranged for the phylogenetic tree construction identifying the formation of 7 significant clusters with emphasis on I (48B32 Stimulate and M7739 Booster), IV (36B31 Stimulate and Bonus Stimulate), V (48B32 Wake), VI (48B32 Booster) and VII (48B32 SprintAlga) (Figure 2). According to Cruz et al. (2004), the establishment of groups containing genotypes with homogeneity within and heterogeneity across groups is the starting point for a more thorough evaluation of them, in order to make their use in the breeding programs. The 48B38 genotype had its performance highly influenced by seed treatment management, being present in 5 distinct and possible groups. Its sensitivity and expressiveness contributed to the formation of 3 clusters (V, VI, and VII). STI and BOO participated in 4 distinct groups each, showing potential change in the performance of the soybean genotypes under study, opening new possibilities for further studies with these active ingredients for further work (Figure 2).

The canonical axes add up to a total explanation equivalent to 67.9, 76.8, 73.2, 76.9 and 77.3% of the total data variation in the AGU, SPR, BOO, ACO and STI seed treatments.

Table 4. Canonical loads of fresh mass (group 1) and morphological (group 2) traits in the canonical correlations (r) between soybean genotype groups submitted to different seed treatments. Mineiros-GO, UNIFIMES, Brazil, 2020.

| Character | Group 1 | AGU | 1º | 2º | SPR | 1º | 2º | BOO | 1º | 2º | ACO | 1º | 2º | STI | 1º | 2º |
|----------|--------|-----|----|----|-----|----|----|-----|----|----|-----|----|----|-----|----|----|
| MFR      | 0.59   | 0.21| 0.63| -0.10| 0.47| 0.19| -0.17| -0.34| -0.32| -0.53|
| MFA      | 0.73   | -0.09| 0.53| 0.20| 0.78| -0.06| -0.81| -0.10| -0.82| -0.04|
| STD      | -0.42 | 0.51| -0.33| 0.22| -0.20| -0.24| -0.10| 0.58| -0.14| 0.40|
| COR      | 0.53   | -0.21| 0.22| -0.54| 0.71| 0.10| -0.13| 0.25| -0.24| -0.71|
| DIC      | 0.92   | 0.11| 0.92| -0.14| 0.83| -0.09| -0.55| -0.19| -0.55| -0.49|
| ALH      | 0.38   | 0.35| -0.17| 0.41| -0.13| 0.05| 0.03| 0.56| 0.07| 0.41|
| ALE      | -0.03  | -0.80| -0.47| -0.22| -0.14| -0.70| -0.61| 0.44| -0.26| 0.22|
| ALP      | 0.43   | 0.08| -0.01| 0.41| 0.68| -0.25| -0.86| 0.18| -0.82| 0.09|
| r        | 1.00   | 0.99| 1.00| 1.00| 1.00| 1.00| 1.00| 1.00| 1.00| 1.00|
| p        | <0.01  | <0.01| <0.01| <0.01| <0.01| <0.01| <0.01| <0.01| <0.01| <0.01|

Group 1: MFA aerial fresh mass and MFR root fresh mass; Group 2: DIC stem diameter, ALH hypocotyl height, ALE epicotyl height, ALP seedling height and CRA root length.
treatments, respectively. The traits that most influenced the genotype distinction among seed treatments were MFA and DIC (Figure 3).

Figure 2. Phylogenetic tree of dissimilarity of soybean genotypes submitted to different seed treatments, obtained by UPGMA clustering method, using the generalized Mahalanobis distance. Mineiros-GO, UNIFIMES, Brazil, 2020.

Similarities were addressed between ALP, MFA, MFR, ALH and DIC, as well as for MFA, MFR and DIC in the treatments of AGU and SPR seeds, respectively, which were positively expressive in both canonical variables in the Flecha genotype. The Bonus genotype presented high means in MFA, MFR and DIC traits in BOO seed treatment, as well as the TEC7548 genotype for MFA, ALP and DIC traits (Figure 3). Silva et al. (2015) stated that multivariate analysis techniques are efficient to verify similarities or differences in yield variability based on chemical and physical soil attributes in study.

For this study, the Kohonen Map was employed using 50 inputs (neurons) represented by soybean cultivar interaction and seed treatment. The phenotypic matrix was submitted to interactive procedures that defined a neural network with nine centroids topologies, establishing associative patterns among the tested characters (Figure 4). The standards set by the traits (Centroid I) UL-CR and UL-FO, (Centroid II) BK-CR, BO-ST and EX-FO, (Centroid II) EX-ST, BO-FO, BK-ST and BO-FI, (Centroid IV) BK-FI, (Centroide V) UL-FI, EX-CR and UL-AG, (Centroide VI) BK-AG and EX-AG, (Centroide VII) BO-AG, BK-FO and EX-FI and (Centroide VIII) UL-ST and BO-CR (Figure 4).
Figure 3. Analysis of canonical variables based on Mahalanobis distances for STD stand, COR root length, DIC stem diameter, ALH hypocotyl height, ALE epicotyl height, ALP plant height, MFR root fresh mass; and fresh aerial mass MFA of soybean genotype seedlings of soybean genotypes submitted to different seed treatments. Mineiros-GO, UNIFIMES, Brazil, 2020.

Figure 4. Artificial Neural Networks obtained by Kohonen Map defining centroids (blue) and neurons (yellow) and synaptic links (blue lines), as follows: 1-Flecha_APR, 2-Flecha_BOO, 3-Flecha_ACO, 4-Flecha_AGU, 5-Flecha_STI, 6-Bonus_APR, 7-Bonus_BOO, 8-Bonus_ACO, 9-Bonus_AGU, 10-Bonus_STI, 11-TEC7548_APR, 12-TEC7548_BOO, 13-TEC7548_ACO, 14-TEC7548_AGU, 15-TEC7548_STI, 16-M7739_APR, 17-M7739_BOO, 18-M7739_ACO, 19-M7739_AGU, 20-M7739_STI, 21-36B31_APR, 22-36B31_BOO, 23-36B31_ACO, 24-36B31_AGU, 25-36B31_STI, 26-W791_APR, 27-W791_BOO, 28-W791_ACO, 29-W791_AGU, 30-W791_STI, 31-M7198_APR, 32-M7198_BOO, 33-M7198_ACO, 34-M7198_AGU, 35-M7198_STI, 36-
Multivariate explanation of the establishment of initial soybean growth pattern via seed treatment with bio stimulants.

The seed treatment influenced the morphological components of soybean seedlings, showing their correlation with the fresh aerial and root mass, and different patterns were observed according to the genetic variation.

REFERENCES

Bhering, L. L. (2017) Rbio: A tool for biometric and statistical analysis using the R platform. *Crop Breeding and Applied Biotechnology*, 17(2), 187-190. https://doi.org/10.1590/1984-70332017v17n2s29

Binsfeld, J. A., Barbieri A. P. P., Huth C., Cabrera, I. C., & Henning L. M. M. (2014) Use of bioactivator, biostimulant and nutrient complex in soybean seeds. *Search Agriculture Trop*, 44(1), 88-94. https://doi.org/10.1590/S1983-40632014000100010

Carvalho, I. R., Souza, V. Q., Nardino, M., Follmann, D. N., Schmidt, D. & Baretta, D. (2015) Correlações canônicas entre caracteres morfológicos e componentes de produção em trigo de duplo propósito. *Pesquisa Agropecuária Brasileira*, 50(8), 690-697. https://doi.org/10.1590/S0100-204X2015000800007

Carvalho, I. R., Szareski, V. J., Demari, G. H., & Barbosa, M. H. (2018) Artificial Neural Network and Multivariate Models Applied to Morphological Traits and Seeds of Common Beans Genotypes. *The Journal of Agricultural Science*, 10(11), 572-580. DOI:10.5539/jas.v10n11p572

Carvalho, I. R., Souza, V. Q., Nardino, M., Follmann, D. N., Demari, G., Schmidt, D., Szareski, V. J., Pelegrin, A. J., Ferrari, M., Pavan, M., & Olivoto, T. (2015) Efeitos de fungicidas na soja com hábito de crescimento determinado. *Revista Sodebras*, 10, 30-34.

Carvalho, I. R., de Souza, V. Q., Nardino, M., Follmann, D. N., Silva, A. D. B., Szareski, V. J., & Olivoto, T. (2016) Associações fenotípicas entre caracteres fisiológicos da soja contrastante ao hábito de crescimento. *Global Science and Technology*, 8(3), 30-40. http://dx.doi.org/10.14688/1984-3801/gst.v8n3p30-40

Cruz, C. D. (2016) Genes Software-extended and integrated with the R, Matlab and Selegen. *Acta Scientiarum. Agronomy*, 38(4), 547-552. https://doi.org/10.4025/actasciagron.v38i4.32629

Cruz, C. D., Regazzi, A. J., & Ram S. P. C. (2004) Genetic divergence. *Biometric models*
applied to genetic improvement (1): 377-413.

Embrapa - Empresa Brasileira de Pesquisa Agropecuária (2009) Manual of chemical analysis of soils, plants and fertilizers. (2nd ed.). Technological Information: 628. Brasilia, DF: Embrapa Solos.

Embrapa - Empresa Brasileira de Pesquisa Agropecuária (2013) Brazilian system of soil classification. (3rd ed. rev. ampl.). - Brasilia, DF: Embrapa Solos.

Ferreira, L. L., Barbosa, H. Z., Carvalho, I. R., Prado, R. L. F., Curvêlo, C. R. S., Pereira, A. I. A., & Carnevale, A. B. (2019) Effect of Biostimulants in Late Seeding of Genotypes of Zea mays L. Journal of Experimental Agriculture International. 41(6), 1-9. DOI: 10.9734/jea/2019/v41i630431

Ferreira, L. L., Carvalho, I. R., Conte, G. G., Amaral, G. C. L., Campos, J. N., Tomazele, A. A. S., & Loro, M. V. (2021) Effect of biostimulant on yield characters of common bean cultivars under Southwestern Goiás conditions. Agronomy Science and Biotechnology, 8, 1-13. https://doi.org/10.33158/ASB.r148.v8.2022

Kolling, D. F., Sangoi, L., Souza, C. A., Schenatto, D. E., Giordani, W., & Boniatti, C. M. (2016) Seed treatment with biostimulant in corn submitted to different variability in the spatial distribution of plants. Rural Science, 46(2), 248-253. https://doi.org/10.1590/0103-8478cr20150504

Krzyzanowski, F. C., França Neto, J. D. B., Henning, A. D. A., & Costa, N.P. (2008) Soybean seed as technology and basis for high yields: seed series. Circular Technique (INFOTECA-E). Londrina, PR: Embrapa Soja.

Marques, M. E. R., Simonetti, A. P. M. M., & Rosa, H.A. (2014) Productive aspects of the use of biostimulants in soybean crop. Acta Iguazu, 3(4), 155-163. DOI: 10.22587/ajbas.2019.13.8.8

Nardino, M., Baretta, D., Carvalho, I. R., Follmann, D. N., Konflanz, V. A., Souza, V. Q., & Maia, L. C. (2016) Correlações fenotípica, genética e de ambiente entre caracteres de milho híbrido da Região Sul do Brasil. Revista Brasileira de Biometria, 34(3), 379-394.

Silva, S. E. M., Montanari, R., Panosso, A. R., Correa, A. R., Tomaz, P.K., & Ferraudo, A.S. (2015) Variability of soil physical and chemical attributes and yield of common bean cultivated in minimum crop system with irrigation. Brazilian Journal of Soil Science, 39(2), 598-607. https://doi.org/10.1590/1983-21252017v30n117rc

Silva, J. A. G., Mamann, A. T. W., Scremin, O. B., Carvalho, I. R., Pereira, L. M., Lima, A. R. C., & Norbert, L. (2020) Biostimulants in the indicators of yield and industrial and chemical quality of oat grains. Journal of Agricultural Studies, 8(2), 68-87. https://doi.org/10.5296/jas.v8i2.15728
Soares, F. C., Robaina, A. D., Peiter, M. X. & Russi, J. L. (2015) Predição da produtividade da cultura do milho utilizando rede neural artificial. *Ciência Rural*, 45(11), 1987-1993. https://doi.org/10.1590/0103-8478cr20141524

Tatto, L., Kulczynski, S. M., Bellé, C., Morin D., Rubin, F. M., & Uliana, M.P. (2018) Performance of biostimulant treated soybean seeds under different osmotic potential conditions. *UERGS Scientific Electronic Journal*, 4(3), 397-408. https://doi.org/10.1590/2317-1545v40n4199338

Toledo, M. Z., Fachin, C. A., & Zucareli, V. (2015) Physiological quality of green soybean seeds treated with biostimulant. *Agriculture Magazine*, 90 (1), 63-76. https://doi.org/10.1590/2317-1545v40n4199338

Zago, L. F., Lima, C. R., Cross, R. M. S., & Alberton, O. (2018) Inoculation by different doses of Bradyrhizobium by side dressing and its effect on soybean crop. *UNIPAR Archives of Veterinary Science and Zoolog*, 21(2), 65-69. https://www.cabdirect.org/cabdirect/abstract/20193037148