Doi: 10.33158/ASB.r116.v6.2020

Neural network and canonical interrelationships for the physiological aspects of soybean seedlings: effects of seed treatment

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ABSTRACT

The objective of this work was to analyze the performance of soybean seedlings different seed treatments, with multivariate profiles and canonical interrelationships. The experiment was conducted in the county of Mineiros-GO. The soil was classified as a Quartzarenic Neosol. The experimental design used was a randomized block in a 5x4 factorial, corresponding to the seed treatments (Água, Fortenza, CruiserFipronil Alta and Standak Top) in 4 soybean cultivars (Bônus, Ultra, Extra and BKS7830), in 4 repetitions. Before sowing, pre-plant burndown was performed. The fertilizer used was 450 kg ha $^{-1}$ of fertilizer 05-25-15 applied in the furrow and in a single dose next to the seeding. During the conduct of the experiment, the control of pests, diseases and weeds were carried out as they became necessary, respecting good practices and integrated management. The data obtained were 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. Uni and multivariate tools were applied. The analyzes were performed on Rbio from R and Genes interfaces. The interaction of soybean cultivars and types of seed treatment led to variations in all analyzes evaluated in soybean seedlings. The best performances were found in the BRS 7380RR cultivar that expressed the highest shoot fresh mass when subjected to seed treatment with Cruiser, whereas the greatest root length was expressed in the Ultra cultivar with Fortenza seed treatment.

Keywords: Seed health, quality seed, phytotonic effect, active ingredient, plant growth and development, germinability.

INTRODUCTION

Soybean (*Glycine max* (L.) Merrill) is a legume originally from China and one of the main agricultural commodities in Brazil and the world. Its high importance is due to the fact that it has high levels of oil (20%) and, mainly, protein (40%), which justifies its economic importance, as it is used to manufacture animal feed (Lopes, Vello, Pandini, Rocha, & Tsutsumi, 2002; Ministério da Agricultura Pecuária e Abastecimento [MAPA], 2013; Nogueira, Nobre, Alves, Matsuo, & Macedo, 2020).

World soybean production in the 2017/2018 crop was 336,699 million tons, occupying a planted area of 124,580 million hectares. The United States is the main soybean producer in the world, with a percentage of 35.51% of world production and productivity of 3299 kg ha $^{-1}$ (Empresa Brasileira de Pesquisa Agropecuaria [EMBRAPA], 2018).

Soybean in Brazil has established itself as one of the outstanding products in agriculture, being one of the crops that has grown the most in the last three decades (MAPA, 2013). The country is the second largest producer of soybean in the world, being responsible for producing an average of 34.76% of the world production of the crop, with an average productivity of approximately 3333 kg ha $^{-1}$. Among the Brazilian states, the state of Mato Grosso is the largest producer of soybean, with an area of 9,519 thousand hectares, and the state of Paraná has the highest productivity in the country, with 3503 kg ha $^{-1}$ (EMBRAPA, 2018).

The application of products in the seed treatment, in order to increment production has become an increasingly constant agricultural practice. Among the products, fungicides, insecticides, inoculants, antibiotics, hormones and amino acids stand out (Avanzi et al., 2018; Messa, Nunes, & Mattei, 2019;

Santinoni et al., 2019).

Thus, it is becoming common to treat seeds with insecticides that have a physiological effect on plants, with a tendency for them to establish vigorous growth and better use of their productive potential. This growth is known as the phytotonic effect, which is characterized by the positive advantages in plant growth and development, provided by the application of some active ingredient (Castro, Bogiani, Silva, Gazola, & Rosolem, 2008).

The traits of physiological quality are acquired throughout the development of the seeds and begins in the maturation phase. Germination capacity (germinability) is the first to be acquired, followed by the acquisition of desiccation tolerance. Concomitantly, the vigor of the seeds is acquired, represented by the higher speed of germination, uniform establishment of seedlings and tolerance to stressful conditions during germination and emergence. Finally, longevity is increasingly acquired in the last stages of development (Bewley, Bradford, Hilhorst, & Nonogaki, 2013). Seed quality is defined as the expression of the interaction of genetic, physical, physiological and health components (Popinigis, 1985), among which stands out the importance of physiological seed quality as a key to improve and stabilize productivity (Leprince, Pellizzaro, Berriri, & Buitink, 2017).

The variety and diversity of products used for seed treatment has increased considerably in recent years, changing the timing of application of products that, commonly, were previously applied at sowing and currently have been carried out at the end of the processing, being stored and treated. There are few studies that analyze the performance of seed treatment in soybean crops, which generates a clear demand for research that evolves this theme. In this sense, the objective of this work was to analyze the performance of soybean seedlings in different seed treatments, with multivariate profiles and canonical interrelationships.

MATERIALS AND METHODS

The study was conducted from November 24 to December 19, 2018, at the Luís Eduardo de Oliveira Salles Experimental Farm, belonging to UNIFIMES, rural area of Mineiros county, GO, Brazil. Geographically it is at 17º 58 ’S latitude and 45º 22’ W longitude and approximately 800 m altitude. Average temperature of 22.7 °C and average annual rainfall of 1695 mm, occurring mainly in spring and summer. The experimental area is classified as Aw type (hot to dry) (Köppen & Geiger, 1936).

The results of chemical analyzes of soil samples in the 0-20 cm layer collected in the experiment area were: hydrogen potential 5.7; calcium 3, magnesium 0.8, aluminum 0.2, hydrogen + aluminum 2, cation exchange capacity 5.9, in cmolc 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 $^{-3}$. The data were taken according to the methodology of (Silva, 2009). The soil was classified as a sandy texture Quartzarenic Neosol (Entisol) (Santos et al., 2013).

A randomized block design organized in a 5x4 factorial scheme was used, totaling 20 treatments, corresponding to seed treatments ST (Água, Fortenza, CruiserFipronil Alta and Standak Top) in 4 soybean cultivars cv (Bônus, Ultra, Extra and BKS7830), in 4 repetitions, totaling 80 experimental units, where each unit was composed of 4 lines of 5 meters in length spaced every 0.45 m, with density of 15 seeds per meter of furrow according to Ferreira, Amaral, Silva, Curvêlo and Pereira (2019). The main morpho-agronomic characteristics of soybean cultivars have been described on Table 1.

Table 1. Main morpho-agronomic characteristics of soybean cultivars. Mineiros, GO, UNIFIMES, Brazil, 2019.

Cultivar		Maturity group	Seed genetics	Thousand seed mass (g)	Architecture	Cycle (days after emergence)
Commercial	Common					
Bônus 8579 RSF IPRO	Bônus	7.9	Brasmax	190	Indeterminate	105 to 122
Ultra IPRO	Ultra	7.5	Brasmax	175	Indeterminate	100 to 110
BMX EXTRA IPRO	Extra	7.4	Brasmax	157	Indeterminate	100 to 110
BRS 7380RR	BKS7830	7.3	Embrapa	174	Indeterminate	100 to 110

Before sowing, pre-plant burndown was performed (Cobucci, Stefano, & Kluthcouski, 1999). The fertilization used was 450 kg h a^{-1} of fertilizer 05-25-15 applied in the furrow and in a single dose next to the seeding. The seeds were treated one day before sowing in polyethylene bags, with the recommended doses of each product for 100 kg of seeds. The main characteristics of the products used as seed treatments were described on Table 2.

Table 2. main characteristics of the products used as seed treatments st. mineiros, go, unifimes, brazil, 2019.

ST description		Form.	Active ing.	g.a.i ha^{-1}	Dose
Commercial	Initials				(ml or g ha^{-1})
Water	WAT	H_2O	Distilled water	100	500
Fortenza	FOR	750 FS	Anthranilamide	600	40 to 200
Cruiser	CRU	350 FS	Thiamethoxam	350	100 to 300
Fipronil Alta	FIP	250 FS	Fipronil	250	80 to 200
Standak Top	STA	FS	Pyraclostrobin, Thiophanate-methyl and Fipronil	500	80 to 200

During the conduct of the experiment, the control of pests, diseases and weeds were carried out as they became necessary, respecting good practices and integrated management (Quintela, 2001). At the end of the experiment, 10 plants were collected at random from the useful area of the experimental plot and then taken the agronomic attributes: stem diameter SDI in cm, hypocotyl height HYH in cm, epicotyl height EPH in cm, seedling height SH in cm, root length RL in cm, shoot fresh mass SFM in g and root fresh mass RFM in g (Benincasa, 2004).

The data obtained were 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 carried out in order to identify the interaction between the soybean cultivars (cv) x seed treatment positions (ST). When verifying significant interaction, these were broken down to the simple effects through the Scott-Knott clustering test, at 5% probability. Subsequently, the variables of each fertilization method were subjected to Pearson's correlations in order to understand the association trend, with its significance based on a 5% probability by the t test. Canonical correlations were estimated between group 1 (SFM and RFM) and group 2 (SDI, HYH, SH, EPH and RL) for the ST, with significance between the groups of characters assessed based on the chi-square statistic. After the genetic dissimilarity was carried out jointly by the Mahalanobis algorithm, where the residual matrix was weighted, the distance dendrogram was constructed using the UPGMA grouping, then the biplot canonical variables method was used where it was possible to visualize the general variability of the experiment and multivariate trends. The character matrix data were subjected to unsupervised computational learning through Artificial Neural Networks, using the K-means algorithms and Kohonen self-organizing map (Carvalho et al., 2018). The analyzes were performed on Rbio from R interface (Bhering, 2017), in addition to the Software Genes (Cruz, Sena-Junior, Santos, Lunezzo, & Machado, 2016).

RESULTS AND DISCUSSION

The summary of the analysis of variance with the mean square MS and significance by the F test, revealed significant interaction between cultivar cv x seed treatment ST, in all variables ($p <0.01$) (Table 3). The results found corroborate with Dan, Piccinin, Ricci and Ortiz (2012), Silva, Oliveira and Neres (2018), and Barbosa, Radke and Meneghello (2017) when diagnosing changes in the averages of their respective works.

Based on the results found in Table 4, it was observed that the SDI in Ultra stood out among the others with an average of 0.21 cm in the ST CRU, which in turn was the ST that provided the highest averages among the STs in the studied cultivars. Silva et al. (2018) and Oliveira et al. (2015) found no statistical difference for the SDI, attributing this result to good quality seeds, a factor that standardizes this variable.

For the variable hypocotyl height HYH, it was observed that Ultra (4.69 cm) was the one that obtained the highest average in the ST CRU among the cultivars, and among the STs, FOR stood out, providing an increase in the HYH of the cultivars BKS7830, Bônus and Ultra (Table 4). For epicotyl height EPH, it was observed that in ST STA the cultivar Extra obtained the highest average with 4.22 cm. Seed treatment FIP was the one with the best performance among the others (Table 4).

Table 3. Summary of analysis of variance (calculated MS and CV (%)) for stem diameter SDI, hypocotyl height HYH, epicotyl height EPH, seedling height SH, root length RL, shoot fresh mass SFM and root fresh mass RFM of soybean cultivars submitted to different seed treatments. Mineiros, GO, UNIFIMES, Brazil, 2019.

SV	DF	SDI	HYH	EPH	SH	RL	SFM	RFM
Cv x ST	12	0.0005**	0.4499**	0.2852**	0.9312**	3.4522**	59.3619**	1.8430**
cv	3	0.0013**	0.9626**	1.3790**	0.8423**	0.4407	36.3333**	10.2138**
ST	4	0.0002	0.6887**	0.1382**	0.5080**	2.9414**	23.3328**	0.7930
Blocks	3	0.0001	0.0843	0.0052	0.0519	0.2200	1,7666	0.2338
Residue	57	0.0001	0.0311	0.0181	0.0549	0.1772	2,1635	0.3303
C.V		6.65	4.42	3.86	3.13	5.96	8.08	14.20

**significant at 1% probability by the F test. Cv: cultivar; ST: seed treatment.
SV: source of variation; DF: degree of freedom.

Table 4: Dismemberment of the interaction (Cultivar cv x Seed treatment ST) for stem diameter SDI, hypocotyl height HYH, epicotyl height EPH and seedling height SH of soybean cultivars submitted to different seed treatments. Mineiros, GO, UNIFIMES, Brazil, 2019.

Cultivars	-------------Seed treatment-------------				
	WAT	**CRU**	**FIP**	**FOR**	**STA**
	Stem diameter SDI (cm)				
BKS7830	0.16 bB	0.19 bA	0.18 aB	0.17 bB	0.16 bB
Bônus	0.20 aA	0.19 bA	0.19 aA	0.18 bA	0.20 aA
Extra	0.19 aA	0.17 bA	0.18 aA	0.19 aA	0.18 bA
Ultra	0.17 bB	0.21 aA	0.18 aB	0.19 aA	0.20 aA
//	**Hypocotyl height HYH (cm)**				
BKS7830	3.87 aB	4.34 bA	4.12 aA	4.26 bA	4.36 aA
Bônus	3.53 bC	3.61 cC	3.78 bC	4.54 aA	4.09 bB
Extra	4.08 aA	3.82 cB	3.42 cC	3.78 cB	3.47 cC
Ultra	4.02 aB	4.69 aA	3.82 bB	4.57 aA	3.60 cC
//	**Epicotyl height EPH (cm)**				
BKS7830	3.41 aA	3.47 bA	3.29 bA	2.91 bC	3.17 bB
Bônus	3.08 bC	3.00 cC	3.67 aA	3.48 aA	3.29 bB
Extra	3.50 aD	4.00 aB	3.77 aC	3.60 aD	4.22 aA
Ultra	3.63 aA	3.64 bA	3.74 aA	3.58 aA	3.25 bB
//	**Seedling height SH (cm)**				
BKS7830	7.28 bB	7.81 bA	7.42 aB	7.17 bB	7.53 aA
Bônus	6.61 cC	6.61 cC	7.46 aB	8.02 aA	7.38 aB
Extra	7.58 aA	7.83 bA	7.19 aB	7.39 bB	7.70 aA
Ultra	7.65 aB	8.33 aA	7.56 aB	8.15 aA	6.86 bC

Means followed by the same lowercase letter in the vertical and uppercase letters in the horizontal, do not differ from each other, by the Scott-Knott test, at 5% probability.

Regarding the seedling height SH, it was found that among the cultivars Ultra obtained the highest average (8.33 cm) in the ST CRU, and the same stood out among the other treatments (Table 4). In similar studies Dan et al. (2012) and Barbosa et.al (2017) also found differences between the analyzed STs. Some factors, such as genotype, vitality, longevity, viability, maturity and physiological potential of seeds, can influence seedling germination and growth (Ferreira and Borghetti, 2013).

When analyzing Table 5, it was possible to identify that the root length RL for Extra was reduced when submitted to ST WAT. The ST WAT had the lowest averages among the other STs for the RL. Results obtained in the work by Dan et al. (2012), observed that the RL in the ST CRU did not differ from the ST WAT, however, it reached an average higher than the other STs. However, the work of Cunha et al. (2015), demonstrated that the RL was not changed by the different analyzed STs.

Table 5: Dismemberment of the interaction (Cultivar cv x Seed treatment ST) for root length RL, shoot fresh mass SFM and root fresh mass RFM of seedlings of soybean cultivars submitted to different seed treatments. Mineiros, GO, UNIFIMES, Brazil, 2019.

Cultivars	-------------Seed treatment-------------				
	WAT	**CRU**	**FIP**	**FOR**	**STA**
	Root length RL (cm)				
BKS7830	6.60 aC	7.06 aB	7.90 aA	5.65 cD	7.79 bA
Bônus	6.43 aC	6.02 bC	7.35 aB	7.25 bB	9.03 aA
Extra	5.86 bC	7.11 aB	6.66 bB	7.67 bA	7.08 cB
Ultra	6.77 aC	7.38 aB	6.73 bC	8.45 aA	6.32 dC
//	**Shoot fresh mass SFM (g)**				
BKS7830	21.50 aB	26.25 aA	19.00 aC	17.75 bC	15.75 bD
Bônus	14.75 bB	23.00 bA	16.25 bB	16.62 bB	21.12 aA
Extra	19.75 aB	12.25 dD	16.50 bC	22.00 aA	15.75 bC
Ultra	13.75 bC	18.25 cB	15.25 bC	17.75 bB	20.75 aA
//	**Root fresh mass RFM (g)**				
BKS7830	4.75 aA	5.25 aA	4.75 aA	3.50 bB	3.75 bB
Bônus	3.25 bB	3.75 bB	3.25 bB	3.25 bB	4.95 aA
Extra	4.50 aB	4.25 bB	4.50 aB	5.75 aA	5.25 aA
Ultra	2.75 bA	3.50 bA	3.25 bA	3.25 bA	3.50 bA

Means followed by the same lowercase letter in the vertical and uppercase letters in the horizontal, do not differ from each other, by the Scott-Knott test, at 5% probability.

In the shoot fresh mass SFM, it can be observed that the cultivar BKS7830 had its SFM inferior to the others. Reduction in SFM was also seen in ST FIP. The highest averages in the root fresh mass RFM were noted in Extra and among the ST in STA (Table 5). In a study conducted by Barbosa et al. (2017) it was possible to observe that SFM and RFM differed from chemical ST in relation to ST WAT, concluding that treatments with mixtures of active ingredients and separated according to the combination have a positive action for the seed treatment in plant development.

Three factors must be considered to interpret the correlations: magnitude, direction and significance. Pearson's simple linear correlation matrix revealed positive pairs in ST WAT, negative in ST STA, in addition to negative and positive in STs FOR, CRU and FIP (Figure 1). The association between agronomic characteristics is important because it allows verifying the degree of interference of a characteristic on another of economic interest, as well as practicing indirect selection (Zuffo et al., 2016). In this context, Pearson's correlation coefficient is used to express the degree of association between two numerical variables.

The canonical loads of the 2nd pair of canonical correlations revealed that the SFM and RFM increased as the SDI decreased and the other variables increased in the ST WAT. Also in the 2nd canonical pair of the ST GRU, there was an increase in the variables of Group 1, only with the addition of HYH. Positive correlation of Group 1 for ST FIP and FOR were reported by HYH in the first, in addition to, SDI, EPH and RL for the second, in the 1st canonical pair. The reduction in SDI and HYH increased the RFM, whereas, SFM increased with decreasing HYH and SH, for the 1st and 2nd canonical pair of ST STA (Table 6). The responses of the SFM and RFM variables, correlated with the others analyzed in the experiment, varied according to the ST applied to soybean cultivars.

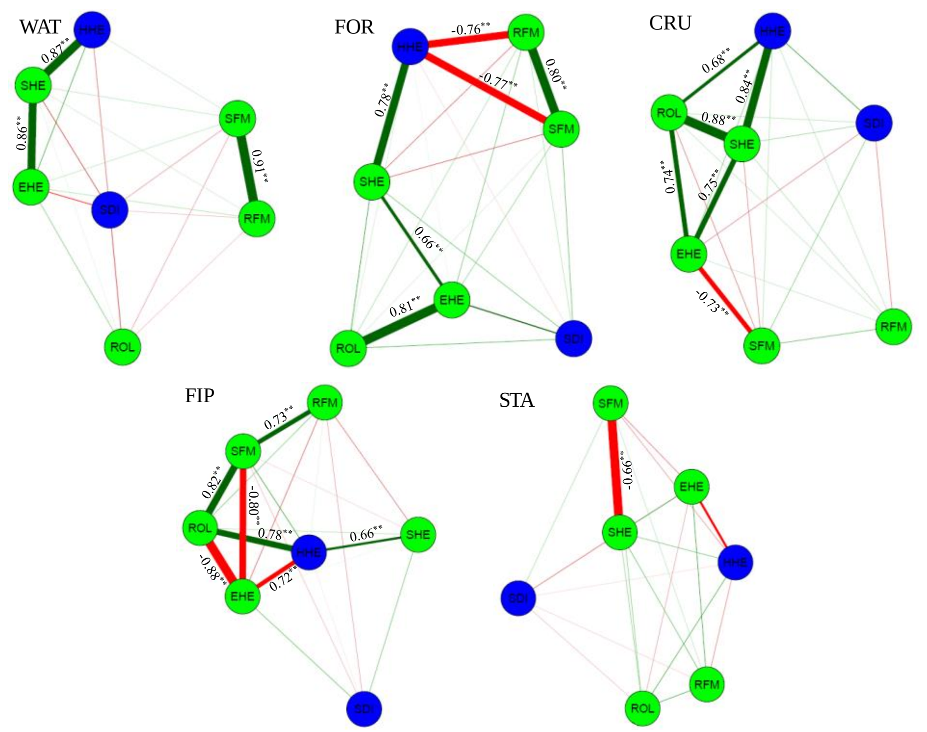

Figure 1. Network of linear correlations applied in different seed treatments of soybean cultivars.
Variables: stem diameter SDI, hypocotyl height HYH, epicotyl height EPH, seedling height SH, root length RL, shoot fresh mass SFM and root fresh mass RFM.
Mineiros, GO, UNIFIMES, Brazil, 2019.

Table 6. Canonical loads of fresh mass (group 1) and morphological (group 2) characters in canonical correlations (r) between groups of soybean cultivars submitted to different seed treatments. Mineiros, GO, UNIFIMES, Brazil, 2019.

Character[1]	Canonical pair		Canonical pair		Canonical pair		Canonical pair		Canonical pair	
Group 1	1st	2nd	1st	2nd	1st	2nd	1st	2nd	1st	2nd
	WAT		CRU		FIP		FOR		STA	
SFM	-0.54	0.84	0.55	0.84	0.93	0.36	0.99	0.17	-0.64	0.77
RFM	-0.65	0.76	-0.52	0.85	0.96	-0.27	1.00	-0.03	0.86	0.51
Group 2										
SDI	-0.66	-0.76	0.72	-0.05	-0.37	0.21	0.42	0.50	-0.44	0.81
HYH	0.18	0.48	0.08	0.10	0.30	0.83	-0.96	0.04	-0.17	-0.23
SH	0.33	0.47	-0.42	-0.14	-0.51	0.68	-0.50	0.05	0.92	-0.21
EPH	0.48	0.45	-0.84	-0.37	-0.76	-0.61	0.34	0.03	0.82	0.04
RL	0.87	0.06	-0.51	-0.12	0.59	0.81	0.16	0.33	0.27	0.44
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: shoot fresh mass SGM and root fresh mass RFM; Group 2: stem diameter SDI, hypocotyl height HYH, epicotyl height EPH, seedling height SH, root length RL.

The use of correlation networks can increase the effectiveness of selection in soybean breeding, since it allows to quickly identify the pairs of characteristics that present correlations of greater magnitude, to determine which groups of variables influence, in a more expressive way, the most important characters for the breeding program and to identify the groups of correlated variables. Silva, Rêgo, Pessoa and Rêgo, (2016) also observed the potential of using correlation networks to breed pepper (*Capsicum* spp.).

When analyzing the dendrogram representative of the dissimilarity for the variables, it can be noted that 4 distinct groups were formed, with emphasis on the individual groups Extra_CRU and BKS7830_CRU (Figure 2).

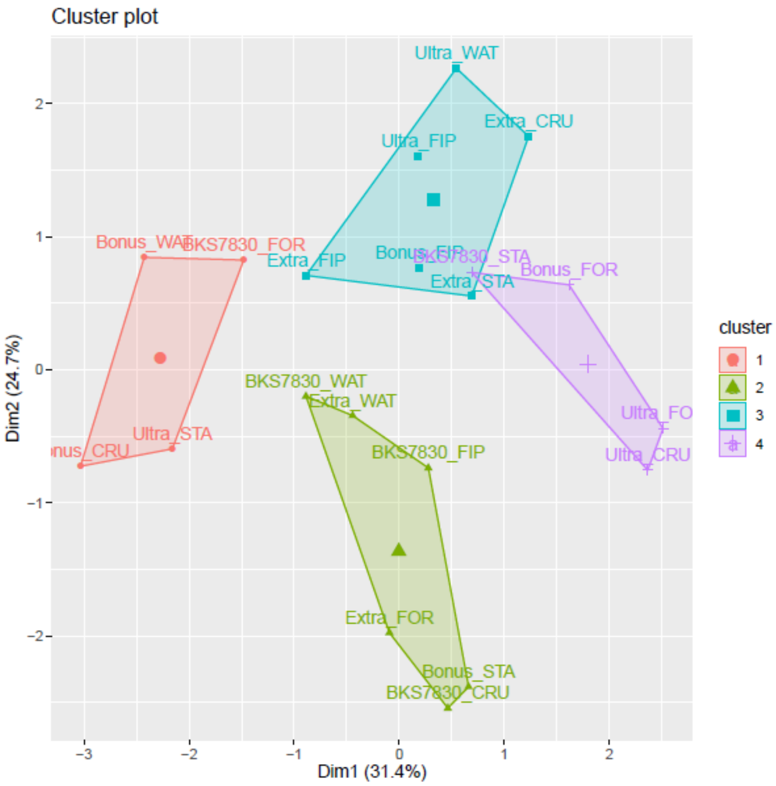

Figure 2. Dendrogram representative of the dissimilarity between soybean cultivars submitted to different seed treatments, obtained by the UPGMA clustering method, using the generalized Mahalanobis distance. The cophenetic correlation coefficient (r) was 0.80. Mineiros, GO, UNIFIMES, Brazil, 2019.
Variables: stem diameter SDI, hypocotyl height HYH, epicotyl height EPH, seedling height SH, root length RL, shoot fresh mass SFM and root fresh mass RFM.

The canonical axes added a total of explanation equivalent to 76.07% of the total variation of the data. The variables SFM, RFM and SDI showed similarities, where the cultivar BKS7830 with ST CRU presented the largest SFM and the cultivar Extra in ST FOR for SDI and RFM. Cultivar Ultra at ST FOR corresponded to the highest RL and SH (Figure 3). Silva et al. (2015) state that multivariate analysis techniques are efficient to verify similarities or differences in productivity variability, based on the chemical and physical attributes of the soil in the studied area. Also being added the influence of soybean genetic variability and seed treatment on the performance of the initial grubbing of its seedlings.

For this study, the Kohonen Map was used using 20 inputs (neurons) represented by the interaction of soybean cultivars and seed treatment. The phenotypic matrix was subjected to interactive procedures that defined a neural network with a topology of eight centroids, establishing associative patterns among the tested characters (Figure 5). The standards established by the characters (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, (Centroid V) UL-FI, EX-CR and UL-WA, (Centroid VI) BK-WA and EX-WA, (Centroid VII) BO-WA, BK -FO and EX-FI and (Centroid VIII) UL-ST and BO-CR (Figure 4).

Artificial neural network has already been addressed in soybean crop; however, studies involving the discussion of this tool with the use of seed treatment in soybean seedlings are precarious. Soares, Robaina, Peiter and Russi (2015) point out that artificial neural networks are efficient and can be used as a tool to estimate the grain yield of corn, thus adding to the conventional simulation models for agricultural crops.

In view of the results, it was observed that there was a significant interaction between cultivars and seed treatments, in all variables. In the simple linear correlation matrix represented by the correlation network and Pearson's coefficients, it presented positive and negative correlations for the STs. The dissimilarity dendrogram distinguished treatments in clusters. In the canonical variables, one can observe the magnitude of the variables depending on the treatments. Canonical correlations expressed significant values between the groups proposed within the STs. And the neural network expressed a synaptic dimension, bringing together in profiles the treatments proposed at this work.

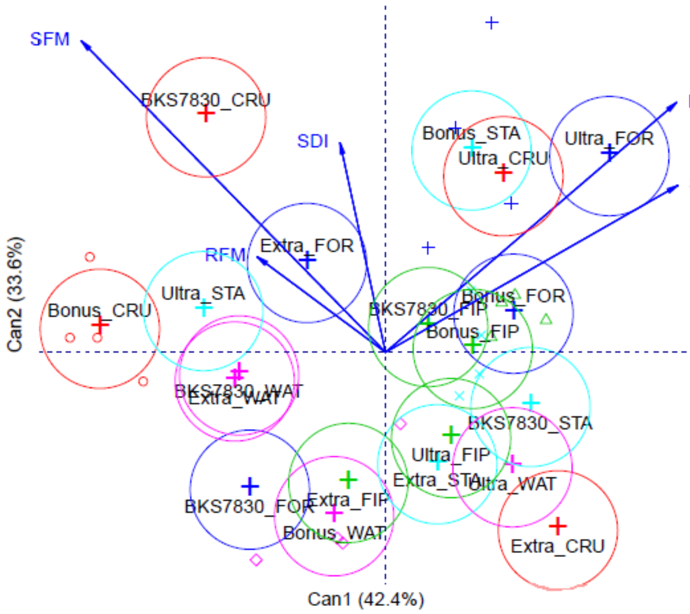

Figure 3. Analysis of canonical variables in soybean cultivars submitted to different seed treatments, based on Mahalanobis distances. Mineiros, GO, UNIFIMES, Brazil, 2019.
Variables: stem diameter SDI, hypocotyl height HYH, epicotyl height EPH, seedling height SH, root length RL, shoot fresh mass SFM and root fresh mass RFM.

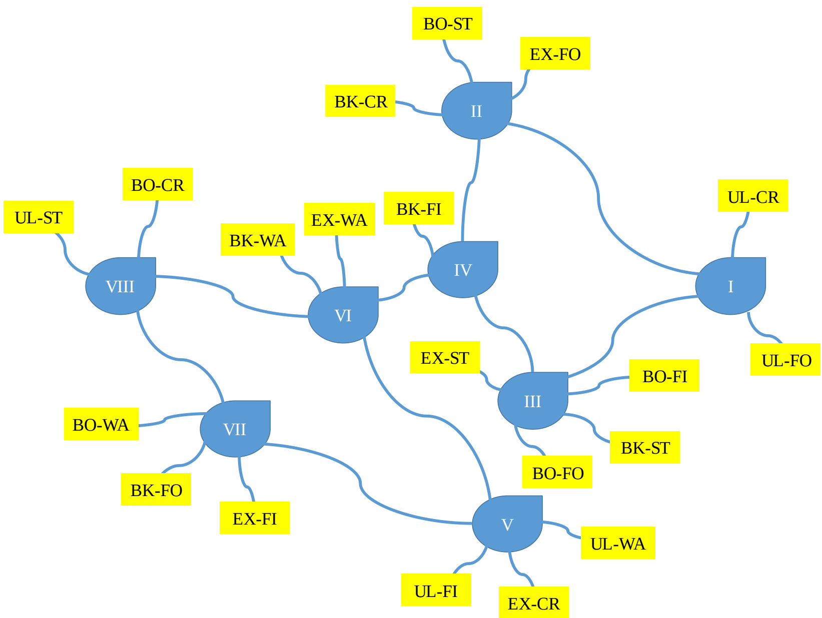

Figure 4. Artificial Neural Networks (ANNs) obtained by Kohonen's Map defining the centroids (blue) and neurons (yellow) and synaptic links (blue lines), being: BO-CR: cv Bônus in the ST CRU, BO-FO: cv Bônus in the ST FOR, BO-ST: cv Bônus in the ST STA, BO-FI: cv Bônus in the ST FIP, BO-WA: cv Bonus in the ST WAT, UL-CR: cv Ultra in the ST CRU, UL-FO: cv Ultra in the ST FOR, UL-ST: cv Ultra in the ST STA, UL-FI: cv Ultra in the ST FIP, UL-WA: cv Ultra in the ST WAT, EX-CR: cv Extra in the ST CRU, EX-FO: cv Extra in the ST FOR, EX-ST: cv Extra inthe ST STA, EX-FI: cv Extra in the ST FIP, EX-WA: cv Extra in the ST WAT, BK-CR: cv BKS7830 in the ST CRU, BK-FO: cv BKS7830 in the ST FOR, BK-ST: cv BKS7830 in the ST STA, BK-FI: cv BKS7830 in the ST FIP e BKS7830_WAT: cv BKS7830 in the ST WAT.

CONCLUSIONS

The interaction of soybean cultivars and types of seed treatment led to variations in all analyzes evaluated in soybean seedlings.

Hypocotyl height and root fresh mass have high correlations with the other variables.

The best performances were found in the BRS 7380RR cultivar that expressed the highest shoot fresh mass when subjected to seed treatment with Cruiser, whereas the greatest root length was expressed in the Ultra cultivar with Fortenza seed treatment.

ACKNOWLEDGMENT

To CNPq, for grating a Ph.D. scholarship.

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Received: January 20, 2021.
Accepted: March 6, 2021.
Published: March 31, 2021.

English by: Francine Lautenchleger