

Scientific Journal. ISSN 2595-9433 Volume 5, Article n. 5, Jan/December D.O.I. http://dx.doi.org/10.35418/2526-4117/v5a5 Received: 04/17/2022 - Accepted: 06/21/2022



PERFORMANCE OF EARLY-CYCLE SOYBEAN GENOTYPES FOR USE IN A SUGARCANE ROTATION SYSTEM

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Abstract: Sugarcane and soybean are relevant crops for Brazilian agribusiness, and the demand for their products and by-products is growing worldwide. The Soybean x Sugarcane (SSC) production system operates with high efficiency and contributes to the sustainability of agribusiness. Soybean cultivars suitable for use in SSC must have an early cycle, adaptation to the edaphoclimatic region, and high yield. The Value of Cultivation and Use (VCU) assays are conducted in different edaphoclimatic regions, to identify promising soybean genotypes in an advanced stage of inbreeding. The objective of this work was to identify soybean genotypes with high adaptability and stability that are possible candidates for registration and protection of new commercial cultivars, for use in the SSC system in the São Paulo State, Brazil. Twenty genotypes and four commercial cultivars were evaluated in six environments, in a randomized block design with three replications. To verify adaptability and stability, the AMMI method was used. Using the adopted methodology, it was possible to identify superior genotypes for SSC that showed good adaptability and general stability between the evaluated environments, being possible recommendable candidates for SSC in the edaphoclimatic regions in which they were evaluated.

Keywords: Adaptability; Stability; Crop rotation.

Introduction

Soybean is the dominant Brazilian export product, and their importance has been steadily increasing. The country's position as the world's largest producer and exporter of soybean reinforces that. Soybean production in Brazil in the 2021/2022 crop year was 125.5 million metric tons

(Conab, 2022). Soybean also presents great benefits in crop rotation. For example, in the rotation system with sugarcane (Borges et al., 2013), São Paulo is the Brazilian state responsible for at least 50% of sugarcane production.

The practice of reforming sugarcane fields using the crop rotation system with le-



gumes such as soybeans represents a sustainable alternative capable of avoiding critical reductions in productivity (Ambrosano et al., 2011). This practice achieves a conservationist purpose that positively impacts soil and water. The soil degradation and loss of nutrients decrease, while the biodiversity and the incorporation of organic matter increase (Fancelli, 2009).

Soybean stands out in the crop rotation system with sugarcane due to its fast decomposition of plant residues and the availability of nutrients for the main crop. To provide nitrogen, an essential element for plant development, the root system of soybeans and other legumes fixes atmospheric nitrogen. The ability to fix nitrogen occurs due to the symbiosis established with nitrogen-fixing bacteria, which provide the nutrient for plants (Marchetti and Barp, 2015; Mylona, Pawlowski, and Bisseling, 1995).

The physiological and genetic traits of soybeans also generate economic benefits, as they can contribute to the amortization of around 40% of the cost of implementing a new sugarcane plantation (Oliveira, Pereira, and Vieira, 2012), in addition to reducing the need for fertilizer nitrogen, incorporation of organic matter and soil conservation (Oliveira, Pereira and Vieira, 2012). In addition, the high yields achieved underscore the viability of the technology of direct sowing of the soybean crop on sugarcane straw (Borges et al., 2013).

The soybean genotypes must have some traits to enable soybean cultivation in the sugarcane reforming time, the most desired trait being a short number of days to maturity (100 to 120 days). Also, other traits are required in commercial cultivation for soybean genotypes, such as adaptation to the edaphoclimatic region of cultivation, high yield potential, homogeneity, and phenotypic stability, among others (Embrapa, 2014).

Thus, the efforts of genetic breeding programs and research in search of a reduced number of days to maturity soybean cultivars for use in the Soybean x Sugarcane rotation system have become of great importance (Pavão et al., 2015). Based on the above, the objective of the present work was to evaluate the performance and stability of advanced inbreeding soybean genotypes, aiming to identify lines with potential for registration and protection of new commercial cultivars for use in the soybean x sugarcane rotation system (SSC).

Materials and methods

Value for Cultivation and Use (VCU) experiments were carried out in the agricultural years 2018/19 and 2019/20 following the requirements of the Ministry of Agriculture, Cattle and Supplying in three locations, one of them located in the Edaphoclimatic Region (REC) 203 in the municipality of Piracicaba (Latitude: 22° 43′ 30″ South, Longitude: 47° 38' 51" West, 524 meters altitude) and the others located at REC 302 in the municipalities of Pindorama (Latitude: 21° 11' 12" South, Longitude: 48 ° 54' 34" West, 542 meters of altitude) and Jaboticabal (Latitude 21°14'59" South and longitude 48°17'8" West, 575 meters of height), in São Paulo State (Kaster and Farias, 2012).

Sowing was the designated period of the agroclimatic zoning of risk for the crop and location. The management and cultural treatments occurred following the recommendations for the culture. After sowing was inoculated nitrogen-fixing bacteria (of the genus *Rhizobium*) were in the total area.

Twenty advanced inbreeding lines (F_{12}) were evaluated granted by the Soybean Breeding Program of the São Paulo State University "Júlio de Mesquita Filho" at Jaboticabal (UNESP/FCAV), from the previous selective process. Four commercial cultivars were the checks. The twenty soybean lines (1 - 20) and the checks (21 - 24) are classified according to the technology used in the development of the cultivar, being Conventional (no technology) and RR (Roundup Ready, gene insertion for herbicide resistance glyphosate) (Table 1).

A randomized block design was used, with three replications, the plots being composed of four 5m rows, spaced 0.5 m apart. The analyzed area was constituted by the two central 4m rows.

Genotype	Genealogy				
1	FT-Cometa x Bossier				
2	FT-Cometa x Bossier				
3	Tracy - M x Paraná				
4	FT-Cometa x IAC-11				
5	FT-Cometa x IAC-9				
6	FT-Cometa x IAC-8				
7	FT-Cometa x IAC-14				
8	BR-16 x Ocepar-4				
9	BR-16 x Ocepar-5				
10	FT-Cometa x Paraná				
11	FT-Cometa x Paraná				
12	FT-Cometa x Paraná				
13	Conquista x IAC Foscarin-31				
14	(BR-16 x Tainung-3) x (CAC-1 x BRS-137)				
15	(BRS -137 x Hartwig) x (IAC-8-2 x Embrapa 48)				
16	[[(BR-16 x Tainung-3) x (CAC-1 x BRS-137)] x [(Embrapa-59 x FT-2) x(Conquista x CD-204)]]				
17	[[Tainung-4 x Renascença) x (FT- Estrela x BRS - 134)] x [(Embrapa-59 X Coodetec-204) x (CAC-1 x BRS-137)]]				
18	JAB.00-05-5/4A2D x M 7908 RR				
19	JAB.00-05-8/2D3C x M 7211 RR				
20	JAB.00-02-3/6A4D x M 8360 RR				
21	M5947IPRO				
22	M6210IPRO				
23	AS3680IPRO				
24	TMG 1175 RR				

Table 1. Genealogy of evaluated genotypes.

The evaluations of the VCU trial were carried out following the minimum requirements for soybean registration in the National Register of Cultivars (RNC) - (Mapa, 2022). The genotypes were evaluated for the number of days to maturity (NDM) measured by counting days from planting to the date when 95% of their pods were dry (R8 on the scale of Fehr and Caviness, 1971) and grain yield (GY) per hectare.

The individual variance analysis was performed for the agronomic traits of a quantitative nature, with the significance of the sources of variation and the averages of the number of days to maturity and grain yield submitted by the Scott and Knott test at a level of 5% probability of error. The means and Genotype x Environment interactions (GxE) were calculated from joint analysis with the unfolding of the sources of variation to study the GxE for the variables evaluated.

An analysis of adaptability and stability tests using the AMMI method (Additive Main Effects and Multiplicative Interaction), the R program (R Core Team, 2020), ExpDes. pt (Ferreira et al., 2020), and lattice (Sarkar, 2008) packages.

Results and discussion

For each environment and agricultural year, there was a statistically significant difference (P < 0.05) between the means for NDM and GY (Table 2), indicating genetic variability among the evaluated genotypes. For NDM the genotypes showed a shorter cycle in Jaboticabal in the two seasons evaluated, this result indicated that the selection for precocity that has been carried out in the genotypes for the region has been effective, making the genotypes favorable for the soybean x sugarcane rotation system.

For NDM, check 21 was the earliest in 2018/19 in Jaboticabal (Table 3), presenting approximately 102 days. In Pindorama, genotype 1 was equal in 101 days with checks 21 and 23, being the most precocious genotypes of the 2018/19 crop for this environment. And in Piracicaba, genotypes 1, 19, and checks 22 and 23 stood out in precocity, all with 119 days to NDM.

In 2019/20 at Jaboticabal (Table 3), again, genotype 1 was the earliest, with 109 days to NDM. In Pindorama, genotypes 7 and 10 finished the cycle in 117 days, being the earliest of the 2019/20 crop in this environment. In Piracicaba, genotype 7 was the earliest to conclude its cycle with approximately 112 days.

Considering GY in the 2018/19 agricultural year (Table 4), genotypes 10, 5, and 18 were the most productive in Jaboticabal, Pindorama, and Piracicaba, respectively, obtaining a mean yield above 3.200 Kg.ha⁻¹. They stood out for having surpassed the means of the check that are commercial genotypes. In 2019/20 genotypes 17 (4605.08 Kg.ha⁻¹), 20 (2054.41 Kg.ha⁻¹) and 5 (4183.95 Kg.ha⁻¹) in Jaboticabal, Pindorama and Piracicaba respectively, also outperformed the checks.

The significance of the GxE interaction (Table 5) for the two evaluated traits indicates that there is a different performance of the genotypes between the environments. To

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Table 2. Mean squares and general means of 24 genotypes in six environments evaluated to number of days to maturity (NDM) and grain yield (GY) at São Paulo State, Brazil, agricultural years 2018/19 and 2019/20.

	C)/	DE	NDM	GY	NDM	GY
	SV	DF	2018/19		2019/20	
	Block	2	2.26	1580941.09	29.29	141618.60
	Treatment	23	84.26**	369179.19*	74.32**	520867.86*
Env.: Jaboticabal	Error	46	4.57	188445.52	15.62	233376.21
	Mean		110.36 ^c	3056.65 ^B	117.97 ^c	3656.32 ^A
	CV (%)		1.94	14.20	3.34	13.21
	Block	2	5.18	853195.92	47.16	605482.26
	Treatment	23	149.46*	413233.46*	69.96*	252173.76*
Env.: Pindorama	Error	46	9.58	435359.49	55.05	187646.98
	Mean		111.74 [₿]	2318.61 ^c	120.45 ^A	1440.72 ^c
	CV (%)		2.77	28.05	4.30	23.30
	Block	2	10.09	339666.50	15.45	214151.46
Env.: Piracicaba	Treatment	23	174.85**	472302.93*	26.47**	685111.47**
	Error	46	12.01	240045.97	5.32	212125.66
	Mean		130.33 ^A	3139.75 ^A	118.77 ^в	3550.14 ^B
	CV (%)		2.66	15.60	1.94	12.97

SV: Sources of variability; DF: Degree of freedom; Env.: environment; CV (%): coefficient of variation. *; **: significance level of 5% and 1% of probability respectively. For the same agricultural year in the columns, means linked by the same capital letter, do not differ statistically by the Scott- Knott test, with a significance level of 5% of probability.

Table 3.Means to number of days to maturity (NDM) in six environments at São Paulo State, Brazil, agricultural years 2018/19 and 2019/20.

	NDM							
Gen	Jaboticabal	Pindorama	Piracicaba	Jaboticabal	Pindorama	Piracicaba		
		2018/19			2019/20			
1	105.00 Pb	101.00 ^{Lc}	119.00 La	109.33 Nc	119.33 Da	115.33 ^{Gb}		
2	119.67 Ac	121.00 Ab	140.33 Aa	124.00 Aa	119.33 Dc	121.33 ^{Cb}		
3	112.33 ^{Gc}	116.00 Bb	135.33 ^{Ea}	116.00 ^{lb}	120.67 ^{Ca}	121.33 ^{Ca}		
4	105.00 Pb	103.00 ^{Jc}	122.67 ^{Ja}	114.67 ^{Jb}	119.33 Da	115.50 ^{Gb}		
5	114.67 Dc	121.00 Ab	135.00 Ea	122.00 ^{Ca}	122.33 ^{Ba}	121.33 ^{Ca}		
6	119.67 Ac	121.00 Ab	139.00 ^{Ba}	121.33 Da	121.67 ^{Ba}	119.50 ^{Ea}		
7	105.00 Pc	116.00 Bb	122.67 ^{Ja}	110.33 ^{Mc}	117.00 Fa	112.67 ^{Jb}		
8	108.33 Mb	107.00 ^{Hc}	130.00 Ga	117.00 Hb	120.67 ^{Ca}	115.00 ^{Hc}		
9	112.00 Hb	111.67 ^{Eb}	127.33 ^{Ha}	120.00 Fa	118.33 ^{Ea}	119.67 ^{Ea}		
10	113.67 ^{Eb}	110.67 ^{Fc}	126.00 la	119.33 Ga	117.00 Fa	119.33 ^{Ea}		
11	106.67 Nb	104.00 ^{lc}	131.00 Fa	114.33 ^{Jb}	120.33 ^{Ca}	119.33 ^{Ea}		
12	111.00 КЬ	111.67 Eb	136.33 Da	120.33 ^{Ea}	122.33 ^{Ba}	121.33 ^{Ca}		
13	113.00 Fb	112.00 Db	138.33 ^{Ca}	122.67 ^{Ba}	120.00 ^{Cb}	122.00 ^{Ba}		
14	119.00 Bb	114.00 ^{Cc}	138.33 ^{Ca}	124.33 ^{Aa}	122.33 ^{Bb}	122.00 Bb		
15	109.00 Lb	109.67 Gb	125.67 la	119.33 Ga	119.33 Da	118.50 Fa		
16	111.67 ^{Ic}	121.00 Ab	131.00 Fa	120.33 Eb	123.83 ^{Aa}	118.67 Fb		
17	111.33 ^{Jb}	112.00 Db	140.33 ^{Aa}	124.00 Aa	123.67 Aa	120.33 Db		
18	111.33 ^{Jc}	121.00 Ab	138.00 ^{Ca}	122.33 ^{Ca}	122.67 ^{Ba}	121.33 ^{Ca}		
19	105.67 ^{Оь}	102.00 ^{Kc}	119.00 La	112.50 ^{кс}	119.33 Da	114.33 ^{Ib}		
20	117.33 ^{Cc}	121.00 Ab	139.00 ^{Ba}	123.67 ^{Aa}	118.00 Eb	123.00 ^{Aa}		
21	102.33 Rb	101.00 ^{Lc}	120.67 ^{Ка}	110.33 ^{Mc}	119.33 Da	115.67 Gb		
22	103.00 Qc	107.00 Hb	119.00 La	112.00 ^{Lc}	123.33 ^{Aa}	116.00 Gb		
23	103.00 Qb	101.00 ^{Lc}	119.00 ^{La}	110.33 ^{Mc}	118.33 ^{Ea}	116.00 Gb		
24	109.00 ^{Lc}	116.00 Bb	135.00 ^{Ea}	120.67 ^{Ea}	122.33 ^{Ba}	121.00 ^{Ca}		

Gen.: Genotypes;For the same year, in the rows, means linked by the same lowercase letter and, in the columns, means linked by the same capital letter, do not differ statistically by the Scott-Knott test, with a significance level of 5% of probability.

Table 4. Grain yield(GY) means (Kg.ha⁻¹) in six environments at São Paulo State, Brazil, agricultural years 2018/19 and 2019/20.

	GY							
Gen	Jaboticabal	Pindorama	Piracicaba	Jaboticabal	Pindorama	Piracicaba		
		2018/19			2019/20			
1	2830.02 Ga	2319.81 Ea	2480.00 Ga	3602.24 Ga	1063.77 ^{Hc}	3358.37 Fb		
2	2811.39 Ga	2534.80 Db	2980.00 Ea	3435.90 Ha	1493.51 Eb	3631.99 ^{Ea}		
3	2745.82 Gb	2194.98 Ec	3593.33 ^{Ba}	4047.18 ^{Ca}	717.77 ^{Jc}	3625.90 Eb		
4	2965.72 Fa	1892.94 Fb	3148.00 Da	3699.08 Fa	1600.28 Dc	3205.69 Ga		
5	3120.67 ^{Ea}	3230.93 ^{Aa}	2808.00 Fa	3072.37 Jb	1570.64 Dc	4183.95 ^{Aa}		
6	2624.84 Ha	2771.07 ^{Ca}	3036.66 Ea	3539.41 Ga	1805.28 ^{Bb}	2017.04 ^{lb}		
7	3083.97 ^{Ea}	2320.40 Eb	3252.00 Da	3505.74 ^{Ha}	1730.30 ^{сь}	3684.43 Da		
8	3591.99 ^{Ba}	1960.02 Fc	3078.66 Eb	3692.79 Fa	1252.06 Gb	3621.80 ^{Ea}		
9	3110.03 ^{Ea}	2619.36 Db	3538.66 ^{Cc}	4313.76 ^{Ba}	1434.31 Eb	4014.91 ^{Ba}		
10	3945.15 Aa	1940.53 Fc	3234.66 Db	3761.86 Ea	1442.91 Eb	4053.76 ^{Ba}		
11	2544.42 ^{Hb}	2597.73 Db	3438.66 ^{Ca}	3924.61 Da	1128.93 ^{Hb}	3887.99 ^{Ca}		
12	3171.15 ^{Ea}	1914.99 Fb	3149.33 Da	3438.49 ^{Ha}	1358.11 ^{Fb}	3243.52 Ga		
13	3423.01 ^{Ca}	2598.65 Db	3444.00 ^{Ca}	3968.28 Da	1771.72 ^{Bb}	3902.76 ^{Ca}		
14	2860.52 Gb	2358.49 Ec	3666.66 Ba	3223.31 [™]	1643.81 Dc	3757.62 Da		
15	3367.33 ^{Ca}	2605.77 Db	2790.66 Fb	3927.81 Da	1175.96 ^{Hb}	4101.61 ^{Ba}		
16	3265.49 Da	2586.94 Db	3045.33 ^{Ea}	2553.73 ^{кь}	1552.33 Dc	3243.09 Ga		
17	3301.57 Da	2364.45 Eb	3405.33 ^{Ca}	4605.08 ^{Aa}	1227.77 ^{Gc}	3917.86 ^{вь}		
18	3263.45 Db	2989.79 Bb	3777.33 ^{Aa}	3770.25 ^{Ea}	1828.72 Bc	3093.05 ^{Hb}		
19	2637.95 Ha	2286.65 Ea	2332.00 Ga	3472.31 ^{Ha}	1680.82 ^{Cc}	3044.33 ^{Hb}		
20	2823.44 Ga	2028.04 Fb	3270.66 Da	3587.45 Gb	2054.41 Ac	3896.38 ^{Ca}		
21	2902.42 Ga	1603.91 Gb	2832.00 Fa	3652.11 Fa	851.00 ^{lc}	3248.05 Gb		
22	3042.73 Fa	1646.66 Gb	3001.33 ^{Ea}	3474.24 ^{Ha}	1694.18 ^{сь}	3547.76 ^{Ea}		
23	3400.07 ^{Ca}	2053.76 Fb	2404.00 Gb	4110.71 ^{Ca}	1100.12 нь	3852.86 ^{Ca}		
24	2526.42 Hb	2225.85 Eb	3646.66 Ba	3373.12 ^{Ha}	1398.99 Ec	3068.68 ^{Hb}		

Gen: Genotypes; For the same year, in the rows, means linked by the same lowercase letter and, in the columns, means linked by the same capital letter, do not differ statistically by the Scott-Knott test, with a significance level of 5% of probability.

Table 5.Summary of variance analysis for genotypes, decomposition of the GxE interaction using principal components (PC), and explained variation (%exp) to number of days to maturity (NDM) and grain yield (GY) traits in 6 environments at São Paulo State, Brazil. Agricultural years 2018/19 and 2019/20.

VS	DF	MS (NDM)	%exp	MS (GY)	%exp
Genotypes (G)	23	337.2**	-	585.06**	-
Environment (E)	5	3708.65**	-	49757.54**	-
GxE	115	37.52**	-	380.99**	-
PC1	27	89.11**	55.80	563.94**	34.80
PC2	25	33.43**	19.40	414.11 [*]	23.60
PC3	23	27.07**	14.40	362.52	19.00
PC4	21	14.91	7.30	285.27	13.70
PC5	19	7.24	3.20	205.58	8.90
Error	276	9.09	-	264.57	-

VS: Variation Sources; DF: Degree of freedom; CV (%): coefficient of variation; MS: Mean squares. *; **: significance level of 5% and 1% of probability respectively.

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understand this relationship, a more detailed study of this interaction is necessary so that the recommendation of superior genotypes be assertive and accurate.

AMMI analysis

The effects evaluated were significant for GY and NDM, indicating that the genotypes obtained alternate performances according to the evaluated environment (Table 5). The sum of squares was decomposed into 5 principal components (PC), with a significant difference between PC1, PC2, and PC3 for NDM and PC1 and PC2 for GY.

For NDM, the first three PCs explain 89.6% of the genotype variability, being sufficient and necessary to explain the sum of squares of the interaction. For GY, the first two PCs explain 58.4% of the genotype variability, also being sufficient to explain the GxE inter-

action for genotype grain yield in the 3 evaluated environments. Similar results for grain yield in the soybean crop were described in the literature by Krisnawati and Adie (2018) having observed by AMMI analysis that the first two PCs explained 57.41% of the variation for productivity in 12 genotypes in India.

Thus, considering the low noise of the interpretation, the AMMI (PC1 x NDM), AMMI (PC1 x GY), and AMMI2 (PC1 x PC2) models were considered, which presented greater precision for two-dimensional visualization (Figures 1 and 2). For Yang et al. (2009) if the first two principal components capture 60% of the total variation, there is greater reliability of the biplot analysis.

Figure 1a shows the environment Pnd_18/19 and Pnd_19/20 away from the other environments and genotypes, indicating that these environments were unfavorable for the pro-

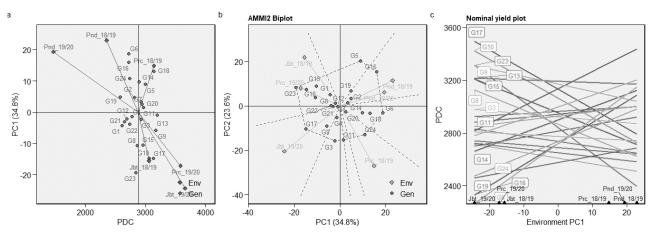


Figure 1. GGE biplot representing: (a) components 1 and grain yield (GY); (b) components 1 and 2 to GY.

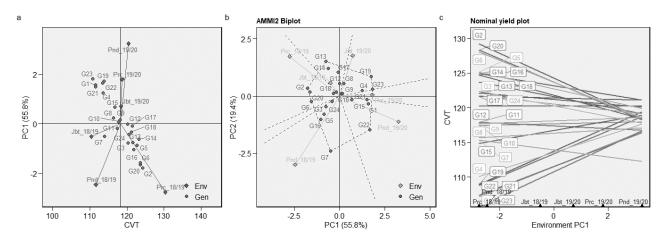


Figure 2. GGE biplot representing: (a) components 1 and number of days to maturity NDM); (b) components 1 and 2 to NDM.

ductivity of the genotypes. In Prc_18/19 genotype 18 stood out in productivity, and in Jbt_18/19 genotypes 10 and 17 were the most adapted. For GY, genotypes 4, 5, 7, and 20 were the most adapted and stable.

Therefore, the genotypes and environments were represented in a two-dimensional plane, in Figure 2a the NDM and the performance of the genotypes were combined. Genotypes close to the origin are considered more stable as they contributed little to the GxE interaction. According to Chaves (2001), combinations of genotypes and environments with scores of the same sign have positive interactions. Therefore, it can be considered that genotypes 8, 9, 10, 11, 12, and 17 were the most adapted and stable.

Figures 1b and 2b present the pattern of genotype interaction in the 6 environments, for GY and NDM, respectively. The shift along the vertical axis indicates differences in GxE interaction, while the vertical axis indicates differences in the main effects of genotype and environment. The genotypes present in the vertices of the polygon are the most distant from the origin of the other genotypes in the same sector, these are classified as more responsive. Genotypes located in the center of the polygon are considered less responsive to environmental stimuli.

Considering figure 1b, it is understood that the environments Jaboticabal (Jbt_18/19 and Jbt_19/20) and Pindorama (Pnd_18/19 and Pnd_19/20), even being from the same edaphoclimatic region, were allocated in different mega-environments. Uncontrollable environmental factors, such as rainfall, can be considered responsible for this event.

Conclusions

The genotypes showed a difference in performance when evaluated in different environments, indicating genetic variability among the advanced lines of the UNESP/FCAV Soybean Genetic Improvement Program. The selection process was efficient for the detection of genotypes with superior performance and suitable for the soybean x sugarcane rotation system. The AMMI method made it possible to group genotypes adapted and stable to each edaphoclimatic region, which is ideal for the registration and protection process of new commercial cultivars.

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