

Stability and Adaptation of Soya Strains Based on different Models in the North and Northeast Regions

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Received: 15 Oct 2023,

Receive in revised form: 25 Nov 2023,

Accepted: 06 Dec 2023,

Available online: 12 Dec 2023

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Keywords— *Glycine max.* **Heritability. REML/BLUP. Harmonic mean.**

Abstract— *In Brazil, soya is the most important annual crop and is grown in a variety of environmental conditions. The environmental effect segregates the growing regions, where each one has its own peculiarities, and it is therefore the responsibility of genetic improvement programmes to meet the demand for new cultivars that overcome the instabilities and take advantage of the beneficial conditions of these environments. The aim of this study was to assess the productivity, adaptation and stability of soya strains in VCU trials. A randomised block design with three replications was used, in which six strains and two commercial cultivars were part of the trials in the cities of Cariri-TO, Caseara-TO, Aparecida do Rio Negro-TO, Porto Nacional-TO, Balsas-MA and Barreiras-BA, in the 2022/23 harvest. The REML/BLUP variational modelling method was used to analyse the data, estimate genetic parameters and predict genotypic values via MHPRVG. Significance was observed for genotypic effects and double interaction. The average heritability was adequate for the type of data set, which showed high accuracy. The genotype x location interaction showed a high coefficient of determination and the opposite was observed for the correlation, demonstrating the great influence of this effect on the results, thus highlighting its importance for the study, according to genetic parameters estimated via various models. According to the BLUPs for MHPRVG, the SOY 03 strain showed the best behaviour compared to the others and could be used as a cultivar.*

I. INTRODUCTION

The soya bean, *Glycine max* (L.) Merrill, is an annual plant grown worldwide to produce oil and protein. Originally from the north-eastern Chinese region, it belongs to the Fabaceae family, where it has been cultivated for millennia. In this region, there are estimates that indicate that the plant has been used for human and animal consumption for more than 5,500 years and is

considered by local traditions to be one of the five sacred grains (SEDIYAMA, 2016).

Originally from a temperate climate, it has been widely adapted to subtropical and tropical regions, showing obvious plasticity, which has led to research into its behaviour in a wide range of fields of study, especially plant breeding (SEDIYAMA, 2016).

In Brazil, the first reports of its introduction and cultivation date back to 1882, in Bahia, for fodder use.

However, in this region the crop was unsuccessful because the cultivars came from the United States and did not adapt to the conditions. Later, in 1891, it was cultivated in São Paulo to produce food grains, and in 1914 in Rio Grande do Sul, with the aim of research. In both cases, the adaptation was superior to the first cultivation in Brazil, however, the best performance was obtained in the state of Rio Grande do Sul, as it had environmental conditions similar to the northern United States, where the cultivars originated (MIYASAKA; MEDINA, 1981).

Brazil is currently the largest exporter and producer of this oleaginous crop. In the 2023/2024 harvest, the forecast is that Brazil will harvest a total of approximately 162.003 million tonnes, in a territory of more or less 45.182 million hectares, with an average yield of 3586 kg ha⁻¹ (CASTRO, 2019; CONAB, 2023).

In this context, private and public genetic improvement programmes are largely responsible for this extraordinary advance in cultivation. Currently, this commodity is grown from north to south in the country, showing wide adaptation (CRUZ et al., 2012).

The aim of the following study was to assess the productivity, adaptation and stability of soya strains in the face of local variations and to identify promising strains for generating cultivars.

THEORETICAL REFERENCE

According to Cruz et al. (2012), for soya and many other crops, the main basis of genetic improvement programmes is the wide genetic variability contained in their segregating populations, which will give rise to future cultivars. This genetic variability is of great importance, as it allows for the selection of a wide range of traits, whether they be productivity, phenological or linked to biotic and abiotic factors. Among these traits, many are of quantitative inheritance and therefore of low heritability, showing complex behaviour and being highly influenced by the environment.

In addition to gathering all the desirable traits, genetic improvement programmes must meet market demands, which are not constant and change over the course of the harvest. In this way, there are cases in which productive cultivars are not necessarily successful cultivars, sometimes because they have characteristics that do not please producers and end consumers, so the breeder must be the bridge between research and the development and commercialisation of products, being aware of market trends (SEDIYAMA, 2016).

Because it is grown in a wide range of regions, one of the major challenges is separating genotypes, due to the presence of complex interactions between the environment

and the genotype. Understanding this phenomenon is essential for breeders to be able to make more assertive selections for the most diverse growing locations (MAIA et al., 2006).

Breeding programmes have been looking for strategies to carry out more reliable analyses of phenotypic and genomic data, thereby increasing the efficiency of genotype separation. Each year, new procedures and more robust methodologies are adopted to make this process more reliable and improve recommendations (PIMENTEL et al., 2014).

Similar to other crops, phenotypic variations are not constant over a wide range of environments, mainly due to frequent climate changes. This means that, today, most recommendations are for smaller and smaller regions. It is therefore essential to differentiate the types of cultivars with predictable behaviour that can be responsive to environmental changes (CRUZ et al., 2012).

Through Crop Value and Use (VCU) trials, one of the final stages of soybean genetic improvement, data is obtained that allows us to observe the behaviour of strains according to their productivity, adaptation and stability. For this type of analysis, the methodology using mixed models or REML/BLUP (Restricted Maximum Likelihood / Best Linear Unbiased Prediction) offers accurate predictions (RESENDE, 2006; SOARES et al., 2015).

This analysis consists of the following assumptions: the lower the standard deviation of genotypic behaviour across environments, the higher the harmonic mean of their genotypic values in these environments (Resende, 2006). Therefore, when selecting for the highest MHVG values, the breeder will separate for production and stability (CASTRO, 2019).

When this selection is made, it refers to the ability of genotypes to show highly predictable behaviour in the face of unfavourable environmental variations (CRUZ et al., 2012).

Adaptation refers to the relative performance of genotypic values (PRVG) across environments. In this bias, the predicted genotypic values are expressed as a proportion of the general average of each environment, then the average value of this proportion across these environments is obtained. This adaptability is related to the ability of genotypes to take advantage of environmental variations, resulting in good yields. Adaptation efficiency depends on a series of influences and interactions (RESENDE, 2016).

Simultaneous separation by productivity, stability and adaptation, on the other hand, is carried out using the harmonic mean of the relative performance of genotypic

values (MHPRVG) method, which makes it possible to select simultaneously for MHVG and PRVG attributes (RESENDE, 2006; CASTRO, 2019).

According to Resende (2004), Regitano Neto et al. (2013) and Soares et al. (2015), in their studies with other methodologies such as Lin and Binns (1988) and Annicchiarico (1992), they generally provide values similar to those of mixed model analyses. However, the MHPRVG, given that it is estimated by BLUP, offers results on the same scale of character evaluation and presents genotypic and non-phenotypic effects to select stable genotypes that are responsive to the improvement of each environment.

For Stefanova and Buirchell (2010), when considering that the aim of the analysis is to select the best performing genotypes based on their classification, assuming the effects of genotypes as random types and the consequent use of BLUPs is justified, as these maximise the correlation between the estimates obtained for the values of the random effects and the true planting and use values of the strains tested.

Furthermore, according to Resende (2007), assuming the heritability value of the character to be equal to 1 (an implicit assumption when considering the effects of genotypes as fixed and without effects weighted by reducing factors) is unrealistic within genetic improvement, especially for characters such as grain yield.

Therefore, no studies were found in the literature using mixed models to assess the productivity, adaptation and stability of soya strains in different locations and years. However, given its advantages, as well as its use in various allogamous species, this methodology has been widely used in some autogamous crops such as common bean (Carvalho, 2015) and rice (Borges et al., 2010; Colombari Filho et al., 2011; Regitano Neto et al., 2013). This highlights the relevance of this study and the use of this type of approach in soya strains.

II. METHODOLOGY

The test was carried out in the 2022/23 agricultural year in the cities of Cariri-TO, Caseara-TO, Aparecida do Rio Negro-TO, Porto Nacional-TO, Balsas-MA and Barreiras-BA (Table 1). Using the results related to the Crop Value and Use (VCU) trials for 06 experimental lines, all of which have Intacta RR2 PRO® technology.

The strains used come from the Soybean Genetic Improvement Programme developed by Genética SOY and two commercial cultivars that are widely accepted in the region of the experiments were also used (Table 2), resulting in 08 treatments. At the request of the

transferring company, the strains were coded for presentation in this work.

Table 1: Characteristics of the sites used in the state of Mato Grosso do Sul in the trials.

Order	Municipality	REC*	Altitude(m)
1	Caseara -TO	501	206
2	Balsas -MA	501	507
3	Cariri -TO	404	293
4	Aparecida do Rio Negro -TO	501	370
5	Santa Rosa do Tocantins -TO	404	284
6	Porto Nacional -TO	501	244
7	Barreiras -BA	405	820

*Edaphoclimat micro - region.

Table 2: Characteristics of the genotypes and commercial cultivars evaluated.

Table 2. Characteristics of the genotypes and commercial cultivars evaluated.

Order	Treatment	G.M.*
1	SOY 01	7.5
2	SOY AMPLA IPRO	7.9
3	SOY 02	7.9
4	SOY 03	7.9
5	SOY 04	7.9
6	SOY 05	7.8
7	SOY 06	8.2
8	BMX Olimpo IPRO	8.0

*Relative maturity group

The experiments were set up using a randomised block design (RBL) with three replications. The plots were made up of four rows of plants five metres long, with row spacing of 0.50 metres. For evaluation purposes, only the two centre rows were harvested, totalling a useful area of 5 m² per plot.

The crop was harvested using a plot harvester, after which it was cleaned to remove impurities. Subsequently, the grains were subjected to moisture determination and weighed on a digital scale, the moisture was converted to 13% and the yield results were transformed into kg ha⁻¹ in order to carry out the analyses.

These were carried out via mixed modelling, using model 54 of the Selegen REML/BLUP software, which includes a complete block design with several locations and one observation per plot - the MHPRVG method, as described by RESENDE (2006).

Using the mathematical-statistical model: $y = Xr + Zg + Wi + e$, the variance component estimates were calculated using the restrictive maximum likelihood (REML) method and the necessary genetic parameters were obtained from these values. Genotypic values were predicted using the best linear unbiased prediction (BLUP).

According to Resende (2006), BLUP's make it possible to identify genotypes with high stability and productivity, which is measured by the harmonic mean of genotypic values (MHVG), adaptation and productivity are obtained through the relative performance of genotypic values (PRVG) and simultaneous selection for productivity, adaptation and stability is achieved by the Harmonic Mean

of Relative Performance of Genotypic Values (MHPRVG) (RESENDE, 2006).

The MHPRVG indications that were used for selection correspond to:

$$MHPRVG_i = \frac{n}{\sum_{j=1}^n Vg_{ij}}$$

Source: Formula in Carvalho, Silva, Resende (2017).

where, n is the number of locations where genotype i was evaluated, Vg_{ij} is the genotypic value of genotype i in environment j, expressed as a proportion of the mean of that environment (RESENDE, 2016).

III. RESULTS AND DISCUSSION

Table 3 shows the deviance table (ANADEV) for the complete model and without the effects of genotype (g), genotype x location interaction (gl), as well as the likelihood ratio test (LRT) for their respective effects.

Table 3: Deviance Analysis (ANADEV) and Likelihood Ratio Test (LRT) for genotype and genotype x location effects for the yield trait in seven locations in the North and Northeast regions.

Table 3. Analysis of Deviance (ANADEV) and Likelihood Ratio Test (LRT) for genotype and genotype x location effects for the yield character in seven locations in the North and Northeast regions.

Effects	Deviances	LRT (χ^2)
Genotype (g)	2004,23+	4,75*
Genotypes x locations (gl)	2006,53+	7,05**
Complete Model	1999,48	-

* Deviance of the adjusted model without the corresponding effects.

* relative to a probability of 1% using the chi-squared test, with 1 degree of freedom.

** significant at 5% probability by the chi-squared test, with 1 degree of freedom.

According to the chi-squared test applied to the LRT, the genotype effect was significant at 1%, i.e. the genotypes differed statistically for the grain yield character. This means that there is genetic variability between the lines, thus favouring selection.

The effects of the double gl interaction were significant at 5%. According to Colombari Filho (2011) and Regitano Neto et al. (2013), in their studies with rice lines, the possible explanation for this behaviour in the results for the double interaction is that the variations in conditions that occurred between locations reflected a significant change in the behaviour of the genotypes studied.

Another probable explanation for the significance of this effect is that the environments are in different regions and have particular soil and climate conditions.

The overall average yield was approximately 3755.97 kg ha⁻¹. Table 4 shows the estimates of the variance components: genotypic (Vg), genotype x location interaction (Vint), residual (Ve) and phenotypic (Vf). Also shown are the genetic parameters of average heritability of the genotypic effects of the lines (h²g), selective accuracy

(Acgen), experimental coefficient of variation (CVe), coefficients of determination of the effects of the genotype x location interaction (c²int), as well as the genotypic correlation between performance in the various environments (rgloc), during the 2022/23 harvest.

Table 4: Estimates of variance and genetic parameters for the effects studied for the yield character in four locations and two harvests in the soya crop.

Effects	Variances (V)	Coefficients (%)	Correlations (r)
Genotype (g)	$V_g = 35435.94$	$h^2_g = 12,78$	
Genotypes x locations (gl)	$V_{int} = 58541.26$	$c^2_{int} = 21,11$	$r_{gloc} = 0,377$
Waste	$V_e = 183296.61$		
Complete model	$V_f = 277273.82$	$CV_e = 11,39$	$Acgen = 82,13$

The experimental coefficient of variation (CVe) was 11.39%, considered to be at an adequate level (RESENDE, 2004), demonstrating good experimental precision. However, it only depends on the residual variation as a proportion of the experiment mean, and in order to better assess the reliability of the data, genotype evaluation trials should be approached from a genetic and statistical point of view, and not just from a statistical perspective, i.e. validated in terms of experimental quality and precision.

Resende and Duarte (2007) and Henderson (1984) argue that one of the most relevant parameters for assessing the quality of an experiment via genotypic evaluation is accuracy. This parameter refers to both the genuine genotypic value for the genetic treatment and the value approximated using the data from the experiments.

According to Resende and Duarte (2007), analyses in different environments are essential for breeding programmes in order to select superior genotypes and subsequently generate improved cultivars. In these experiments, it is desirable to have high experimental precision and, consequently, accurate inference about the genotypic means, i.e. the genotypic values of the genetic treatments being evaluated.

Experimental quality measured by accuracy reflects the effectiveness of inferring genotypic values, i.e. predicting values via BLUP (BORGES et al., 2009). In this study, the Acgen obtained was 82.13%. This value is classified as high, demonstrating that the predictions made can be considered highly reliable, providing breeders with assertive selections (RESENDE; DUARTE, 2007).

According to Falconer (1981), heritability is the fraction of phenotypic variance equivalent to genetic origin. As can be seen, the average heritability of the strains (h²g) was 12.78%, a result considered to be of low magnitude. According to Candido (2016), this result is explained by the fact that productivity is a polygenic

quantitative character and is therefore strongly influenced by the environment, which in the case of this study was strongly influenced by variations between different locations.

The coefficient of determination c^2_{int} indicates how much each interaction component contributes to the phenotypic variance (Borges et al., 2010). The coefficients for the effects of the double interaction c^2_{int} contributed 21.11%, and were considered significant for the test levels estimated for each effect. These results mean that the phenotype of the strains contributed to the effects evaluated, i.e. there were statistically significant differences in the local stratum when analysed independently. These results are complementary to those observed in the variances in Table 4.

The rg_{loc} genotypic correlation estimates were of low magnitude (0.377), which was to be expected because if the coefficients of determination for these double interactions were high, it was probably because the behaviour of the genotypes across the sites varied so much.

These correlation values from this analysis reflect nothing more than the coincidence between the behaviour of the genotypes across each effect analysed (Resende, 2006). According to Torres et al. (2015), the genotypic correlations of the performance of genetic materials, across locations, provide the reliability of how constant the "ranking" of the genotypes is across the environments tested, thus, as discussed above, it is once again evident that genotype x location interactions are generally complex and significant interactions.

In order to demonstrate the behaviour not only of the data set in the environment evaluated (locations) but also of each genotype evaluated in the VCU trial, it is important to analyse the individual results of the average of each strain. This is best done by analysing adaptation and stability studies.

Table 5 shows the (MHVG), which refers to the Harmonic Mean of Genotypic Values, which indicates the predictions for stability and productivity of genetic values, relative performance of genotypic values (PRVG) which indicates the predictions for adaptability and productivity of genetic values, as well as the overall mean (PRVG*MG) and the harmonic mean of the relative performance of genotypic values (MHPRVG) which are the predictions for stability, adaptation and productivity of genetic values and also at the level of the overall mean (MHPRVG*MG) for the grain yield kg ha⁻¹ trait, in a joint analysis of four locations over two years.

Table 5: Stability and productivity of genotypic values (MHVG), adaptability and productivity of genotypic values (PRVG), (PRVG*MG), stability, adaptability and

productivity of genotypic values (MHPRVG), (MHPRVG*MG) for the productivity character grain yield kg ha⁻¹ in seven municipalities in the north and northeast of Brazil for soya.

Table 5 Stability and productivity of genotypic values (MHVG), adaptability and productivity of genotypic values (PRVG), (PRVG*MG), stability, adaptability and productivity of genotypic values (MHPRVG), (MHPRVG*MG) for the character grain yield kg ha⁻¹, in seven municipalities in the north and northeast of the country in soya cultivation.

Ord	Treatment	MHVG	PRVG	PRVG*MG	MHPRVG	MHPRVG*MG
1	SOY 03	3.979	1.081	4.061	1.081	4.058
2	BMX Olimpo IPRO	3.891	1.058	3.975	1.058	3.972
3	SOY AMPLA IPRO	3.696	1.006	3.777	1.004	3.772
4	SOY 02	3.676	1.007	3.782	1.004	3.770
5	SOY 04	3.668	1.001	3.759	0.995	3.737
6	SOY 01	3.562	0.970	3.642	0.969	3.640
7	SOY 06	3.492	0.955	3.587	0.954	3.584
8	SOY 05	3.377	0.923	3.466	0.921	3.460

Methodologies based on regression or multiplicative models AMMI and GGE Biplot show limitations in dealing with unbalanced data as well as the heterogeneity of variances between the environments analysed and these methods assume the genotypic effects are fixed, which is inconsistent when you want to predict variance components and parameters. The mixed model method is therefore more appropriate, as it assumes the effects of genotypes to be random, which makes it possible to obtain BLUPs as predictors of line behaviour (RESENDE, 2007).

Stability is verified according to the MHVG, which penalises the instability of genotypes when analysed in different environments. Furthermore, when the genotype shows negative behaviour in the face of adversity in the environments analysed, its stability is deflated (RESENDE, 2007). Instability due to climate and soil dissimilarity require the cultivars indicated to present a balance between productivity and stability (CRUZ et al., 2012).

Adaptation, verified by means of PRVG, is the ability of genotypes to respond in an advantageous way to variations in the environment when it increases productivity. Thus, adaptation is capitalised when the genotype responds positively to favourable situations (RESENDE, 2007).

The same ranking was observed (Table 5) for the treatments used according to MHVG, PRVG*MG, and then for simultaneous selection in MHPRVG*MG. In this case, the stable and productive lines showed similar levels of adaptation and productivity and for simultaneous selection, with the exception of the BMX Olimpo IPRO, SOY Ampla IPRO and SOY 02 treatments, which reversed their positions.

Of particular note is the SOY 03 strain, which has the highest BLUP or MHPRVG value. It is important to emphasise that this strain was superior to the commercial cultivars BMX Olimpo IPRO and SOY Ampla IPRO,

which are standouts for the locations evaluated. We can see that the genotype he obtained predicted MHPRVG about 2.3 per cent higher than the runner-up (BMX Olimpo IPRO). Therefore, according to the VCU trials evaluated, this is the most stable, adaptable and productive strain, with great potential as a cultivar.

According to Cruz and Carneiro (2006), the use of cultivars with broad adaptability and good stability is one of the options for reducing the influence of the G x A interaction, as the analyses provide detailed information on the behaviour of each genotype in the face of the most diverse environmental variations, and are therefore of great importance for genetic improvement programmes.

IV. CONCLUSION

The SOY 03 soya strain showed wide adaptation, stability and productivity, demonstrating higher predictions of genotypic values from varied models than commercial cultivars, and is therefore promising for use as a commercial cultivar in environments with similar characteristics to those studied.

Analyses involving genotype x location interaction are of great importance for studying the behaviour of lines in VCU trials, according to genetic parameters estimated from varied models.

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