

A new Bayesian approach to the Toler model for evaluating the adaptability and stability of genotypes

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Abstract: *This study aimed to apply, in unprecedented depth, a Bayesian approach to the non-linear regression model developed by Toler for evaluating the stability and adaptability of genotypes. Twenty-five soybean cultivars were evaluated in twenty-one plots across the midwestern of Brazil. A complete block design was employed, with three replications. The evaluated variable was grain yield. The proposed methodology was implemented in the R program by means of the BRugs package. The methodology was capable of differentiating the effect of the environment on soybean cultivars in terms of yield in the different environments, allowing exploration of the response of each genotype to environmental variations. Cultivars 6266RSF, NS6990, GD19I435, GD19I439, GD19C443, RC0496 and IA18661 presented good stability and general adaptability, being the most recommended for future evaluations. The other cultivars presented specific adaptability and high responsiveness to unfavorable environments.*

Keywords: Glycine max, non-linear models, genotype–environment interaction, non-linear regression

INTRODUCTION

Plant breeding programs aim to obtain genotypes that are high-yielding, stable and adaptable to a wide range of cultivation environments. Identifying widely adaptable genotypes may be difficult due to genotype–environment interaction ($G \times E$), defined as the differential response of genotypes to environmental variation. In addition, this interaction may inflate estimates of genetic variance, resulting in an overestimation of the expected genetic gains (Cochran 1954, Duarte and Vencovsky 1999).

Inconsistent genotype performance in different environments is one of the main challenges faced by breeders. The occurrence of the $G \times E$ interaction can be statistically detected by joint variance analysis using repeated trials in more than one environment. However, it is recommended to carry out a thorough study of genotype stability and adaptability in order to evaluate the $G \times E$ interaction effect in detail (Cochran 1954, Duarte and Vencovsky 1999).

Several methods for evaluating the $G \times E$ interaction have been developed over the years, involving simple linear regression models (Finlay and Wilkinson 1963, Eberhart and Russell 1966), segmented regression (Verma et al. 1978,

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Cruz et al. 1989), and non-parametric analysis (Lin and Binns 1988, Nascimento et al. 2010), as well as multivariate analysis methods such as GGE Biplot (Oliveira et al. 2016), additive main effects and multiplicative interaction (AMMI) (Gauch 2006, Bernardo Júnior et al. 2018, Rosa et al. 2022), extended centroid and, recently, Bayesian models (Couto et al. 2015, Nascimento et al. 2020, Oliveira et al. 2020).

With the same goal of better describing genotypic response to the environment, Toler and Burrows (1998) presented a non-linear regression model that allows joint estimation of parameters reflecting adaptation and stability (β_{1i} , β_{2i} , R_2) and the environmental index (μ_i). This model improves on methods that employ simple linear regression, as it allows classification of genotypes into different groups according to their response patterns. However, as it is based on frequentist principles, this model also has limitations, as responses are only in one dimension and hard to interpret when there is no linearity (Hamawaki et al. 2015, Jarquín et al. 2017). Bi-segmented multiple regression models, as described by Cruz et al. (1989), allow the performance of each genotype to be represented by a single curve constituted by two straight segments. However, such models also have limitations regarding the estimation of the parameters and the precision of estimates.

Unlike frequentist methods, the Bayesian approach naturally allows the incorporation of additional information into the model via the *a priori* probability distribution (Couto et al. 2015, Nascimento et al. 2020), which expresses one's assumptions about previously observed data before certain evidence is taken into consideration. Based on these premises and seeking to fill a gap in the world literature, this study aimed to, in unprecedented depth, apply the Bayesian approach to the Toler method in order to evaluate the stability and adaptability of soybean genotypes.

MATERIAL AND METHODS

The trials were carried out during the 2019/2020 crop season in 21 plots in various areas of midwestern Brazil (Goiás, Mato Grosso, and Maranhão states) (Table 1). Twenty-five soybean cultivars were evaluated: 6266RSF, 68168RSF, NEO680, 68169RSF, NS6990, GD19I435, GD19I439, GD19I434, GD19I438, GD19C443, RC0495, RC0496, RC6842, RC7904, RC0348, RC0349, SBC200381, RC5278, RC0377, CI8591, I10883, I17087, SBI200135, IA18617 and IA18661. A complete block design was employed with three replications. The experimental unit was represented by four rows 5.0 m long and

Table 1. Geographic characteristics of the 21 environments evaluated in the Midwest region of Brazil

Environment	Locations	Altitude (m)	Latitude	Longitude	Annual rainfall (mm)
1	Araguari	1013	-18.651	-48.1854	1566
2	Bom Jesus	1054	-9.075	-44.3573	985
3	Jatai 1	749	-17.8193	-51.1167	1541
4	Jatai 2	749	-17.8193	-51.1167	1541
5	Luziânia	930	-16.5246	-48.3016	1575
6	Mineiros	760	-17.6196	-52.1788	1675
7	Montividiu1	797	-17.1960	-50.6496	1500
8	Montividiu 2	797	-17.3839	-51.4535	1500
9	Morrinhos	771	-17.6198	-49.0938	1535
10	Nova Ponte	937	-19.1203	-47.8049	1149
11	Paraúna 1	790	-17.4888	-50.8912	1495
12	Paraúna 2	830	-17.4888	-50.8912	1495
13	Planalto Verde	1188	-17.3841	-51.4542	1468
14	Rio Verde 1	748	-17.7492	-50.7313	1663
15	Rio Verde 2	748	-17.6897	-50.8305	1663
16	Rio Verde 3	748	-17.7492	-50.7313	1663
17	Santa Helena	570	-17.8439	-50.6620	1454
18	São Miguel	679	-17.8439	-50.6620	1196
19	Serranópolis	696	-16.9361	-48.6965	1478
20	Turvelândia	470	-17.7264	-50.3460	1414
21	Uberlândia	887	-19.1559	-47.9777	1479

spaced 0.45 m apart. The useful parcel area for grain yield evaluation was 4.0 m²; the two central rows were evaluated, discarding 0.25 m at each end. Culture was carried out according to recommendations for soybean cultivation in this region (Seixas et al. 2020).

The grain yield data for each trial were subjected to standard individual variance analyses. Next, joint variance analysis was performed, for which the presence of heterogeneity between residual variances was evaluated using the Hartley test. When heterogeneity was detected, the degrees of freedom of the average error and interaction were adjusted according to the method described by Cochran (1954). The significance of the *F* test was interpreted only after these adjustments. In the presence of significant *G* × *E* interaction, analyses of stability and adaptability were carried out using the method described by Toler and Burrows (1998) via the Bayesian approach proposed by Nascimento et al. (2020), such that:

$$Y_{ij} = \alpha_i + [Z_j\beta_{1i} + (1 - Z_j)\beta_{2i}] \mu_j + e_{ij} \quad [1]$$

where:

Y_{ij} is the average response of genotype i in environment j ($i = 1, 2, \dots, 25; j = 1, 2, \dots, 21$);

α_i reflects the response of genotype i in the environment of average yield ($\mu_j = 0$);

β_{1i} and β_{2i} reflect the sensitivity of the response of genotype i in environments with yields lower ($\mu_j < 0$) and higher ($\mu_j > 0$) than average, respectively;

μ_j reflects environmental quality, that is, the effect of environment j ;

e_{ij} is the average experimental error;

Z_j is a dummy indicator variable, with $Z_j = 1$ when $\mu_j < 0$ and $Z_j = 0$ when $\mu_j > 0$.

The environmental quality parameter μ_j for this analysis was interpreted in the same way as the environmental index (I_j) of Eberhart and Russell (1966). The analysis was conducted according to the Bayesian approach adapted by Couto et al. (2015) and Nascimento et al. (2020). It must be pointed out that in linear regression models, environmental quality (the independent variable, I_j) is estimated separately before estimating the regression coefficients (b), whereas in Toler and Burrows (1998), μ_j is estimated simultaneously with the other regression parameters (favorable environment, $\mu_j > 0$; unfavorable environment, $\mu_j < 0$); the difference is that the use of μ_j ($j = 1, 2, 3, \dots, 21$) allows different genotype response patterns to be distinguished, even with a narrow genetic base, in addition to distinguishing the non-linear regression model from the linear one and facilitating hypothesis testing for the parameters being evaluated.

Equation (1), which describes the behaviour of a given genotype, can be reduced to $Y_{ij} = \alpha_i + \beta_{\mu_j} + e_{ij}$, when $\beta_{1i} = \beta_{2i} = \beta_{\text{common}}$. To determine whether this equation could be represented by a mono-segmented model (single straight regression line) or required a bi-segmented model, hypothesis testing was performed, with the null hypothesis H_0 being that $\beta_{1i} = \beta_{2i}$. Bi-segmented models can produce a convex, linear or concave response pattern (Figure 1). Toler and Burrows (1998) describes five categories of genotype response patterns based on hypothesis testing, as follows:

A: H_0 ($\beta_1 = \beta_2$) is rejected and $\beta_1 < 1 < \beta_2$ is accepted.

B: H_0 ($\beta_1 = \beta_2$) is not rejected and H_0 ($\beta = 1$) is rejected with $\beta_{\text{common}} > 1$.

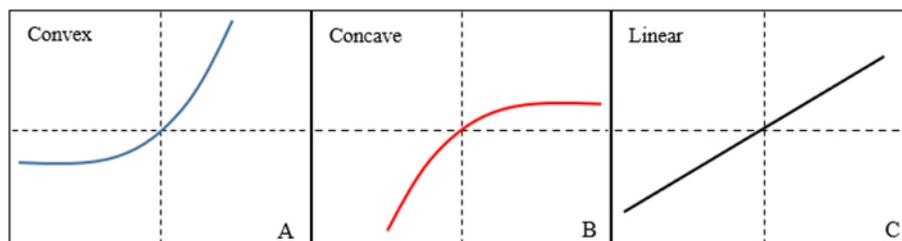


Figure 1. Graphic example of a doubly desirable (A), doubly undesirable (B) and average (C) response in the Toler model.

C: $H_0 (\beta_1 = \beta_2)$ is not rejected and $H_0 (\beta_{\text{common}} = 1)$ is not rejected.

D: $H_0 (\beta_1 = \beta_2)$ is not rejected and $H_0 (\beta = 1)$ is rejected, with $\beta_{\text{common}} < 1$.

E: $H_0 (\beta_1 = \beta_2)$ is rejected and $\beta_1 > 1 > \beta_2$ is accepted.

In practical terms, A represents a ‘doubly desirable’ response (good performance in both favorable and unfavorable environments) with a convex response pattern; B represents a desirable response only in favorable environments, with a simple linear pattern; C represents a simple linear pattern with no deviation from the average response, D represents a desirable response only in unfavorable environments, with a simple linear pattern; and E represents a doubly undesirable response with a concave pattern. In other words, a convex or doubly desirable response pattern is observed when the genotype has low responsiveness to unfavorable environments ($\mu_j < 0$) and starts to respond satisfactorily when conditions become favorable ($\mu_j > 0$), whereas a concave or doubly undesirable response pattern is observed when the genotype is highly responsive to unfavorable environments and only slightly responsive to more favorable environments. For each stability analysis, the genetic cultivars were assigned to groups A to E according to the criteria described above.

For the Bayesian analysis, non-informative *a priori* distributions were assumed for parameters β_{or} , β_1 , β_2 and σ_{di}^2 (stability), following Nascimento et al. (2020). For the parameter β_{common} , the model adopted by Couto et al. (2015) was followed. The proposed methodology was implemented in the R program (R Development Core Team 2022), and samples of the independent *a posteriori* conditional distribution were obtained using the *BRugs* function in OpenBUGS (an open-source Bayesian analysis program), which binds OpenBUGS to R by means of MCMC (Markov Chain Monte Carlo) procedures, considering 550,000 interactions via the Gibbs sampler. A burn-in (initial burning) of 50,000 iterations was adopted, as well as a skip of 10 iterations to eliminate potential self-correlations. The convergence of the chains was verified by means of Gebeke (1992)’s and Raftery and Lewis’s diagnostics using the coda package in R (Plummer et al. 2006).

To estimate the genetic parameters, their means and standard deviations were obtained *a posteriori*. These parameters were considered significant if their respective 95% credibility intervals did not contain a value of zero; that is, if the lower and upper limits of θ_1 and θ_2 exhibited a transition in value between positive and negative when $\theta_1 = \theta_2$ was rejected, or if β_{common} was greater than 1 when $\theta_1 = \theta_2$ was not rejected.

RESULTS AND DISCUSSION

There were significant differences among genotypes, environments and $G \times E$ interactions (Table 2). Due to these differences in environmental influence, it was difficult to recommend cultivars suitable for the whole region of study, and a thorough analysis of interaction effects was necessary (Duarte and Vencovsky 1999, Morais et al. 2008). The coefficient of variation (CV) for grain yield (kg ha^{-1}) was 14.20 (Table 2), indicating experimental control, and thus, it is suitable according to those reported in the literature (Morais et al. 2008, Hamawaki et al. 2015, Matei et al. 2017, Nascimento et al. 2020).

The Bom Jesus, Luziânia, Mineiros, Montividiu 2, Morrinhos, Nova Ponte, Planalto Verde, and Turvelândia plots had the the most negative environmental index estimates and the lowest yields compared to the general average for each genotype, with the environment in Morrinhos being the most unfavorable with the lowest yield ($2061.20 \text{ kg ha}^{-1}$), making it the least recommended area for the evaluated cultivars (Table 3). In the Araguari, Jataí 1, Jataí 2, Montividiu 1, Paranaú 1, Paranaú 2, Rio Verde 1, Rio Verde 2, Rio Verde 3, Santa Helena, São Miguel, Serranópolis, and Uberlândia plots, the environmental index estimates were positive and yields were high compared to the genotype averages, with São Miguel being the best with a yield of $5262.21 \text{ kg ha}^{-1}$. Thus, the difference between the plots with the highest and lowest yields was $3201.20 \text{ kg ha}^{-1}$ (Table 3), indicating

Table 2. Joint analysis of variance of soya yield (kg ha^{-1}) of 25 soybean cultivars evaluated in 21 environments in the Midwest region of Brazil

Source of variation	df	Mean of square	p-valor
Blocks/Environment	42	492364.5245	
Genotypes	24	3141329.5734	0.0000
Environment	20	42590326.099	0.0000
Genotypes x Environment	480	573604.9949	0.0268
Error	1008	328888.1694	
Total	1574		
Overall Average (kg ha^{-1})		4038.1435	
CV (%)		14.2018	

Table 3. Average results for grain yield (kg ha⁻¹) in soybeans and environmental quality indexes (μ_j) estimated by the Toler (1990)'s method, in cultivar competition tests, in 21 environments in the Midwest region of Brazil

Environment	Averages (kg ha ⁻¹)	Environmental Index (μ_j)	Classification
Araguari	4841.3760	803.2405	Favorable
Bom Jesus	3107.8763	-930.2592	Unfavorable
Jatai 1	4343.2800	305.1445	Favorable
Jatai 2	4250.3467	212.2112	Favorable
Luziânia	3480.5359	-557.5996	Unfavorable
Mineiros	2789.4000	-1248.7355	Unfavorable
Montividiu1	4202.0133	163.8779	Favorable
Montividiu 2	3848.3733	-189.7621	Unfavorable
Morrinhos	2061.2000	-1976.9355	Unfavorable
Nova Ponte	4031.1916	-6.9439	Unfavorable
Paraúna 1	4066.8533	28.7179	Favorable
Paraúna 2	4389.9867	351.8512	Favorable
Planalto Verde	3888.0000	-150.1355	Unfavorable
Rio Verde 1	4089.7067	51.5712	Favorable
Rio Verde 2	4893.8133	855.6779	Favorable
Rio Verde 3	5014.0091	975.8736	Favorable
Santa Helena	4254.8800	216.7445	Favorable
São Miguel	5262.2192	1224.0837	Favorable
Serranópolis	4425.5467	387.4112	Favorable
Turvelândia	3460.4933	-577.6421	Unfavorable
Uberlândia	4099.7435	61.6080	Favorable

a high discrepancy in environmental favorability among the plots, which reaffirms the need for more thorough studies of the $G \times E$ interaction (Duarte and Vencovsky 1999, Ferreira et al. 2006, Morais et al. 2008).

Convergence in all generated chains was verified. Parameters of adaptability and stability were estimated and are presented in Table 4. Most of the evaluated genotypes presented differential responses before the environments were classified as favorable and unfavorable ($\beta_1 \neq \beta_2$), except for cultivars 6266RSF, NS6990, GD19I435, GD19I439, GD19C443, RC0496, and IA18661, as $H_0 (\beta_1 = \beta_2)$ was not rejected in their case.

None of the genotypes in the present study could be classified in Toler's group A, as they were not highly responsive to favorable environments. Genotypes can be classified in group A if they are highly responsive to favorable environments but do not lose their potential in unfavorable environments; these can be considered the ideal genotypes in terms of adaptability. In general, these genotypes are demanding and require high environmental quality to express their full genetic production potential (Toler and Burrows 1998). Rosse and Vencovsky (2000) clarified that, in order to reach this potential, it is necessary to use advanced technologies to ensure good conditions (good fertilization, high hybrid availability, adequate handling and a favorable environment) because, under adverse conditions with $\mu_j < 0$, such genotypes produce relatively low yields. Genotypes such as these would not be the most recommended for environments where few technological resources are available.

Likewise, none of the genotypes in this study could be classified in groups B and D, as their response was not stable in different environments. Genotypes classified in group B present a linear response pattern before environmental favorability is determined, but their β_{common} value is above 1.0, indicating greater inclination of the line towards favorable environments. Such genotypes can be considered more stable in environmental response, as they tend to exhibit phenotypic plasticity, that is, a degree of change in individual traits in different environments (Bradshaw 1965). Genotypes classified in group D also present a linear response before environmental favorability is determined, but β_{common} is lower than 1.0, indicating greater inclination of the line towards unfavorable environments. It is important to point out that because the environmental favorability index (μ_j) highlights the divergences and contrasts among test locations, test locations as distinct as possible should be selected in order to maximize data regarding the adaptability

Table 4. Estimates for the mean *a posteriori* and credibility intervals (95% LB-UP) for the stability and adaptability parameters

Genotypes	LB	β_0	UP	LB	β_1	UP	LB	β_2	UP
6266RSF	3660.76	3801.32	3940.41	0.59	0.79	1.00	-0.25	0.25	0.76
68I68RSF	3639.32	3825.19	4009.10	0.71	0.99	1.26	-1.05	-0.37	0.29
NEO680	4285.58	4440.99	4594.77	0.74	0.97	1.20	-0.68	-0.12	0.43
68I69RSF	4171.68	4318.36	4463.51	1.03	1.25	1.47	-0.55	-0.01	0.51
NS6990	3628.87	3806.06	3981.40	0.65	0.91	1.17	-0.34	0.30	0.94
GD19I435	3617.37	3861.83	4103.74	0.41	0.77	1.13	-0.06	0.82	1.70
GD19I439	4141.62	4298.82	4454.37	0.63	0.86	1.09	-0.14	0.42	0.99
GD19I434	3563.70	3756.06	3946.40	0.70	0.98	1.27	-0.92	-0.21	0.47
GD19I438	4207.23	4380.70	4552.37	0.66	0.92	1.18	-0.83	-0.20	0.42
GD19C443	3723.69	3950.14	4174.22	0.62	0.95	1.29	-0.19	0.63	1.44
RC0495	3705.73	3874.13	4040.76	0.92	1.17	1.42	-0.63	-0.02	0.58
RC0496	3697.12	3872.10	4045.25	0.65	0.91	1.17	-0.32	0.31	0.94
RC6842	3367.31	3588.53	3807.43	0.65	0.97	1.30	-0.87	-0.06	0.72
RC7904	3828.48	4017.79	4205.11	0.76	1.04	1.32	-0.91	-0.22	0.46
RC0348	3897.46	4040.17	4181.38	0.78	0.99	1.20	-0.48	0.03	0.54
RC0349	3865.80	4040.14	4212.65	0.94	1.20	1.46	-1.18	-0.55	0.07
SBC200381	4052.65	4227.50	4400.51	0.85	1.11	1.36	-0.79	-0.15	0.47
RC5278	4034.37	4180.22	4324.54	1.03	1.25	1.46	-1.03	-0.49	0.02
RC0377	3656.58	3846.87	4035.16	0.72	1.00	1.29	-0.95	-0.26	0.42
CI8591	3982.42	4189.45	4394.30	0.57	0.88	1.18	-1.23	-0.47	0.26
I10883	4045.20	4182.34	4318.06	0.61	0.81	1.02	-0.67	-0.17	0.32
I17087	3987.64	4150.14	4310.93	0.81	1.05	1.29	-0.62	-0.03	0.55
SBI200135	4200.25	4331.77	4461.90	0.70	0.89	1.09	-0.28	0.19	0.66
IA18617	3813.70	3998.72	4181.80	0.82	1.09	1.36	-0.70	-0.03	0.63
IA18661	3794.43	3984.99	4173.56	0.85	1.13	1.42	-0.26	0.43	1.11

Genotypes	LB	$(\beta_1 - \beta_2)$	UP	LB	β_{common}	UP	LB	σ^2_{df}	UP
6266RSF	1.16	0.54	-0.08	0.64	0.84	1.03	-36328	14978	113023
68I68RSF	2.19	1.37	0.55	0.67	0.93	1.18	3793	93498	264927
NEO680	1.78	1.09	0.41	0.74	0.95	1.16	-24405	38312	158165
68I69RSF	1.92	1.24	0.62	1.05	1.25	1.44	-31562	24307	131072
NS6990	1.40	0.61	-0.16	0.72	0.96	1.20	-4744	76784	232584
GD19I435	1.03	-0.05	-1.13	0.54	0.91	1.26	72234	227412	523945
GD19I439	1.13	0.44	-0.25	0.71	0.93	1.15	-22885	41284	163910
GD19I434	2.05	1.20	0.35	0.69	0.95	1.20	10459	106543	290160
GD19I438	1.90	1.13	0.36	0.65	0.89	1.12	-8281	69868	219211
GD19C443	1.33	0.32	-0.67	0.73	1.06	1.38	49216	182375	436835
RC0495	1.95	1.20	0.45	0.94	1.17	1.39	-12996	60640	201358
RC0496	1.37	0.60	-0.17	0.72	0.96	1.20	-6857	72649	224584
RC6842	2.02	1.04	0.06	0.67	0.96	1.25	42848	169927	412773
RC7904	2.11	1.26	0.43	0.75	1.01	1.26	7300	100360	278200
RC0348	1.59	0.96	0.33	0.81	1.00	1.19	-34683	18197	119253
RC0349	2.53	1.75	0.98	0.85	1.11	1.36	-7472	71455	222286
SBC200381	2.04	1.26	0.49	0.85	1.08	1.31	-6988	72399	224107
RC5278	2.40	1.75	1.10	0.95	1.17	1.38	-32223	23016	128579
RC0377	2.11	1.27	0.43	0.70	0.96	1.22	8312	102341	282032
CI8591	2.27	1.35	0.44	0.51	0.80	1.08	26358	137660	350361
I10883	1.59	0.98	0.38	0.60	0.78	0.97	-38903	9939	103279
I17087	1.80	1.08	0.36	0.83	1.04	1.26	-18294	50271	181299
SBI200135	1.28	0.70	0.12	0.75	0.93	1.10	-43012	1898	87721
IA18617	1.94	1.12	0.30	0.84	1.09	1.33	2946	91838	261710
IA18661	1.55	0.70	-0.13	0.94	1.20	1.47	8599	102895	283093

and response stability of the genotypes being studied, thus enabling the best recommendations to be made (Cochran 1954, Bradshaw 1965, Ferreira et al. 2006).

In the present study, cultivars 6266RSF, NS6990, GD19I435, GD19I439, GD19C443, RC0496 and IA18661 were classified in Toler's group C, with β_i values that did not statistically differ from 1.0; that is, their performance followed the environmental average. According to Rosse and Vencovsky (2000), this pattern indicates good adjustment of the model to the dataset, which means high predictability. Other authors (Prado et al. 2001, Pacheco et al. 2003, Pacheco et al. 2005, Cotes et al. 2006, Couto et al. 2015) also verified this, reporting that genotypes in this group consistently yield within the expected average and show little variability even when cultivated in distinct environments, exhibiting high phenotypic stability and overall adaptability. Among the aforementioned genotypes, cultivar GD19I439 was found to have the highest expected average yield (4298.82 kg ha⁻¹). In this study, most of the genotypes that presented pattern C also presented high stability, with σ^2_{di} values that were not significant (Couto et al. 2015, Nascimento et al. 2020), particularly cultivars 6266RSF, GD19I435, GD19C443, RC0496 and IA18661.

Cultivars NEO680, 68I69RSF, GD19I438, RC0495, RC0348, RC0349, SBC200381, RC5278, I10883, I17087 and SBI200135, even though they presented good stability in terms of σ^2_{div} , proved to be extremely responsive to unfavorable environments; thus, they were classified under Toler's group E, with a doubly undesirable concave response pattern. A concave response pattern indicates a genotype with greater than desirable sensitivity in unfavorable environments and little response to environmental improvement under favorable conditions (Toler and Burrows 1998). These genotypes may be recommended for areas with limited technological access and suboptimal planting conditions, as they yield well in low-technology environments (Morais et al. 2008, Peluzio et al. 2010). However, cultivars NEO680, 68I69RSF, GD19I438, SBC200381 and SBI200135, despite presenting high expected average yields, cannot be recommended because of inconsistencies in their performance before accounting for environmental variations. All the other genotypes not previously mentioned in this section were also classified in group E, did not present good stability, and are not recommended for future evaluations.

CONCLUSIONS

The methodology described in this study was capable of differentiating the effect of the environment on soybean cultivars in terms of yield, allowing us to explore the response of each cultivar to environmental variations. Cultivars 6266RSF, NS6990, GD19I435, GD19I439, GD19C443, RC0496 and IA18661 presented good stability and overall adaptability, and are the most recommended for future evaluations. The other cultivars presented specific adaptability and high responsiveness to unfavorable environments; the higher-yielding of these may be recommended for future evaluations in low-technology environments.

AVAILABILITY OF DATA AND MATERIALS

The data generated and/or analyzed during the present study are available from the corresponding author upon reasonable request.

AUTHOR CONTRIBUTIONS

All authors contributed to study design, preparation of materials, data collection, data analysis and writing of the manuscript.

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