

Relative contribution of expected sum of squares values for soybean genotypes × growing environments interaction

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Abstract

The objective of this work was to assess the effects and tendencies weighted by genotypes x environments interaction for soybean, as well as to employ a biometric approach through the relative contribution of the sum of squares expected values (RCSS) and to define which levels of the variation sources determine the differential effects of the interaction. The experimental design was randomized blocks arranged in a factorial scheme (four growing environments x 20 soybean genotypes). The relative contribution of expected sums of squares values to soybean genotypes x growing environments interaction defined that the environment Tenente Portela - RS significantly influence plant height, number of pods per plant, number of reproductive nodes in the main stem, number of reproductive nodes in the ramifications, number of grains per plant and grain yield. The variation factor soybean genotypes define that number of pods per plant, number of reproductive nodes in the ramifications, number of grains per plant and grain yield are potentiated by genotype TMG 7161 RR. The biometric approach is efficient to understand the treatment levels and the slicing of simple effects of a factorial experiment, being possible to apply this methodology extensively in soybean.

Keywords: *Glycine max* (L.), effects of treatment levels, traits of agronomic interest, variation factors

Abbreviations: FPIH_first pod insertion height; PH_plant height; NRNM_number of reproductive nodes on the main stem; NRRN_number of reproductive nodes in the ramifications; NPP_number of pods per plant; NGP_number of grains per plant; GY_grain yield; MTG_mass of one thousand grains; VF_variation factor; DF_degrees of freedom; SS_sum of squares; SM_square means; Fc_calculated F; MS_means square; CV_coefficient of variation; R²_determination coefficient; C²_determination coefficient of interaction G x E; rGE_Genotype correlation between growing environments; H²_heritability.

Introduction

Soybean yield is determined by the joint action of traits as plant height, number of pods and grains on the main stem and ramifications, number of grains per pod, and mass of these grains. In this context, it is necessary to quantify and to establish the effects, tendencies and contribution of each source of variation in the phenotypic expression of the traits of interest (Carvalho et al., 2017). The presence of significant interaction among the sources of variation intrinsic of the statistical model may hinder the interpretation of results, as the effects associated to genotype by environment interaction may assume a simple nature, resulting in subtle differences among genotype's performances. On the other hand, these effects might be designated as complexes, implying abrupt changes to the traits measured across different growing environment, which result in low genetic correlation of genotypes among environments (Szarecki et al., 2017). Likewise, the effects of G x E interaction may modify the tendencies of association between determining

traits for grain yield of soybeans (Silveira et al., 2016; Szarecki et al., 2018; Woyann et al., 2018).

Many biometric tools are available to infer about the interaction among sources of variation attributed to a linear stochastic statistical model. When properly used, they are able to explain the causes of the total variation of a trait of agronomic interest (Cruz et al., 2014). However, in some situations, it is not feasible to use any univariate or multivariate methodologies, since they require assumptions that are usually not meet great computational and iterative resource. In this context, it is possible to employ simple, easy-to-understand, explanatory models that reveal reliable responses, clearly presenting the differential effects in a genotype x environment interaction (Carvalho et al., 2016). Thereby, the use of relative contribution of sum of squares expected values to the interaction (RCSS) allows todetermine the importance of each treatment integrant of a factorial scheme. Thus, it becomes necessary to employ

simple but highly explanatory models with reliable answers to represent the differential effects in a genotypes x environments interaction. Thereby, the relative contribution of the sum of squares expected values allows understanding the magnitude of these effects (RCSS) and the significance of each treatment level integrant of a factorial experimental scheme. Therefore, the objective of this work was to assess the effects and tendencies weighted by genotypes x environments interaction for soybean, as well as to employ a biometric approach through the relative contribution of the sum of squares expected values (RCSS) and to define which levels of the variation sources determine the differential effects of the interaction.

Results and discussion

The analysis of variance revealed significant interaction between growing environments x soybean genotypes at 5% of probability (Table 2) for the traits first pod insertion height (FPIH), plant height (PH), number of reproductive nodes on the main stem (NRNM), number of reproductive nodes in the ramifications (NRNR), number of pods per plant (NPP), number of grains per plant (NGP), grain yield (GY) and mass of one thousand grains (MTG). The nature of genotype x environment interaction of the measured traits was determined through the genotypic correlation of genotypes among the growing environments tested (r_{GE}), which evidenced that all traits present complex interaction, with coefficients lower than 0.70 (Pupin et al., 2015, Rosado et al., 2012). The coefficient of determination of genotypes x environments interaction effects (C^2) indicates the participation of these effects in the phenotypic manifestation of determined trait. Thus, it is evident that number of pods per plant (NPP), grain yield (GY), mass of a thousand grains (MTG) and first pod insertion height (FPIH) were the traits most influenced by the differential effects attributed to genotypes x environments interaction (Carvalho et al., 2016). The broad sense heritability obtained through the ratio between total genotypic effects and phenotypic variation (H^2) determined that the number of reproductive nodes in the ramifications (NRNR), mass of a thousand grains (MTG), plant height (PH), grain yield (GY), number of reproductive nodes in the main stem (NRNM) and number of grains per plant (NGP) were influenced by more than 80% due to variations imposed by growing environments.

First pod insertion height (FPIH) indicate that the genotypes FPS Júpiter RR, BMX Potência RR, NA 5909 RR, A 6411 RR, BMX Turbo RR, were superior in the environments of Santa Rosa - RS, TenentePortela - RS, Campos Borges - RS and Sarandi - RS (Table 3). The great variation revealed by these results may be explained by environment factors such as air and soil humidity, quantity and quality of sunlight (Aumonde et al., 2017). Plant height (PH) is associated to productive potential of soybean, in Santa Rosa-RS the genotype BMX Potência RR presented the highest plant height, however, in TenentePortela - RS the genotypes FPS Netuno RR and BMX Potência RR were superior for this trait. In Campos Borges - RS the genotypes Fepagro 36 RR, FPS Netuno RR and BMX Potência RR presented the highest magnitudes, as well as in Sarandi - RS, the genotypes Don Mario 7.0i RR and A 6411 RR were superiors. In this view, the variation in plant height through growing environments is associated to

environmental peculiarities, such as, altitude, climate, air and soil humidity.

The number of reproductive nodes in the main stem (NRNM) and in the ramifications (NRNR) is agronomic traits-inherent to genotypes, genetic constitution, and strongly influenced by environment and management techniques (Ferrari et al., 2018). The Santa Rosa - RS for genotype FPS Solimões RR was superior (Table 4). In TenentePortela-RS, superiority was observed in genotype TMG 7161 RR, Campos Borges - RS with the genotypes FPS Solimões RR, Don Mario 5.9i RR and ROOS Camino RR. In Sarandi - RS, superiority was expressed for the genotype FPS Iguazu RR.

The number of pods per plant (NPP) indicates that Santa Rosa - RS the genotype NA 5909 RR was superior, in TenentePortela - RS the genotypes NA 5909 RR and TMG 7161 RR stood out, and in Campos Borges - RS and Sarandi - RS the genotype FPS Solimões RR evidenced superiority for NPP (Table 5). The trait number of grains per plant (NGP) is one of the main yield components of soybeans and is determined by the length of reproductive period (Carvalho et al., 2017). In Santa Rosa - RS the genotype NA 5909 RR presented superiority in TenentePortela - RS it was the genotype TMG 7161 RR, in Campos Borges - RS and Sarandi - RS the genotype FPS Solimões RR was superior to the others.

Considering grain yield (GY), indicates that the genotype NA 5909 RR was superior in Santa Rosa-RS. For TenentePortela - RS it was the genotype TMG 7161 RR, for Campos Borges - RS the superiority was verified for ROOS Camino RR and BMX Ativa RR and in Sarandi - RS (Table 6). For mass of one thousand grains (MTG), the genotype BMX Potência RR was superior in Santa Rosa - RS, however, in the environment of Sarandi - RS the highest magnitudes were expressed by the genotype A 6411 RR. In TenentePortela - RS by the genotype FPS Iguazu RR and in Campos Borges - RS by the genotype ROOS Camino RR. The MTG presents close relationship with grain yield and reveals compensatory capacity through dimensions, mass and magnitude of grains produced per plant.

The first pod insertion height (FPIH) revealed significance for all treatment levels of the variation factor growing environments, where Santa Rosa - RS influences the effects of G x A interaction in 56.28% (Tabela 7). Regarding the variation factor soybean genotypes, there is no significance for FPS Solimões RR, AMS Tibagi RR, Don Mario 5.8i RR, Roos Camino RR and BMX Ativa RR, being these genotypes defined as non-contributors to the differential effects of interaction, with responses assumed as predictable and stable for this trait. The genotypes most responsive to G x E interaction were BRS Tordilha RR, FPS Netuno RR and BMX Potência RR, being them destined to specific growing conditions with magnitudes not predicted for FPIH.

Plant height (PH) revealed significance for all treatment levels attributed to growing environments. The TenentePortela - RS contributed 47.05% for the differential effects of G x E interaction (Table 7), on the other hand for effects attributed to soybean genotypes, only Don Mario 5.9i RR did not reveal significance and assumed stable and predictable responses. Significance was verified for the other genotypes studied, with Don Mario 7.0 RR and FPS Urano RR being responsible for the greatest contribution to simple effects of interaction, and specificity is attributed to them regarding the most suitable growing environment for this trait.

Table 1. The parameters were obtained through the procedures.

VF	DF	SS	SM	Fc
Block (B)	(n-1)		$\frac{\sum(yij)2}{nE - nB} - C$	$\frac{SSB}{DFB}$
Environments (E)	(n-1)		$\frac{\sum(yi..j)2}{nG - nB} - C$	$\frac{SSE}{DFE}$
Genotypes (G)	(n-1)		$\frac{\sum(yi.j)2}{nE - nB} - C$	$\frac{MSG}{DFG}$
E x G	(E - 1) x (G - 1)		$\frac{\sum(yi.j)2}{nB} - C - SSE - SSG$	$\frac{MS_{ExG}}{DF_{ExG}}$
Error (ER)	(nB - 1) x (nE x nG) - 1)	SST - (SSE - SSG - SSB - SS _{ExG})		$\frac{MS_{ER}}{DF_{ER}}$
Total Sum of Squares (TSS)	(n - 1)		$\sum(yijk)2$	

VF: variation factor; DF: degrees of freedom; SS: sum of squares; SM: square means; Fc: calculated F.

Factor for experimental adjustment (C): $\frac{\sum yijk^2}{nijk}$

Table 2. Analysis and variance components of soybean genotypes x growing environments for the traits first pod insertion height (FPIH), plant height (PH), number of pods per plant (NPP), number of reproductive nodes on the main stem (NRNM), number of reproductive nodes in the ramifications (NRNR), number of grains per plant (NGP), mass of a thousand grains (MTG) and grain yield (GY).

VF	FPIH		PH		NPP		NRNM	
	DF	MS	DF	MS	DF	MS	DF	MS
Environment	3	1859.510*	3	35931.310*	3	12013.800*	3	77.450*
Genotypes	19	1989.020*	19	14864.830*	19	8615.150*	19	266.140*
E X G	57	2153.870*	57	20926.240*	57	9054.670*	57	279.640*
Block	2	30.250	2	191.910	2	339.940	2	4.790
CV (%)		14.660		10.150		25.050		15.860
R ²		0.860		0.900		0.700		0.570
C ²		0.460		0.570		0.110		0.140
rGE		0.340		0.210		0.640		0.540
H ²		0.240		0.150		0.210		0.170
VF	NRNR		NGP		MTG		GY	
	DF	MS	DF	MS	DF	MS	DF	MS
Environment	3	1308.630*	3	13920.030*	3	331166.570*	3	117785278.700*
Genotypes	19	1471.640*	19	9391.410*	19	282320.830*	19	41752937.600*
E X G	57	2436.940*	57	9519.430*	57	511408.670*	57	64373366.700*
Block	2	13.100	2	189.630	2	10332.390	2	168727.100
CV (%)		59.800		24.550		18.990		15.650
R ²		0.590		0.690		0.810		0.910
C ²		0.210		0.160		0.470		0.540
rGE		0.210		0.530		0.200		0.230
H ²		0.070		0.180		0.120		0.160

*VF: variation factor; DF: degrees of freedom; MS: mean square; CV: coefficient of variation; R²: determination coefficient; C²: determination coefficient of interaction G x E; rGE: Genotype correlation between growing environments; H²: heritability with broad sense.

Table 3. Means of interaction between 20 soybean genotypes grown in Santa Rosa-RS (SR), TenentePortela-RS (TP), Campos Borges-RS (CB) and Sarandi-RS (SA), for the traits first pod insertion height (FPIH) and plant height (PH).

Soybean genotypes	FPIH (cm)				PH (cm)			
	Growing environments							
	SR	TP	CB	SA	SR	TP	CB	SA
BRS Tordilha RR	33.06 b A	21.13 b B	15.00 bc C	15.76 cd C	83.65 b A	85.33 b A	58.40 bc B	93.13 cd A
FPS Paranapanema RR	16.93 cde AB	14.73 c B	12.93 bc B	21.23 bc A	54.46 d BC	63.40 cd B	48.20 c C	82.80 d A
Fepagro 37 RR	22.73 cd A	18.00 bc A	11.26 c C	12.80 d B	77.60 bc B	62.33 cd C	51.13 bc C	94.69 cd A
FPS Solimões RR	16.06 cde A	12.93 c A	12.26 bc A	13.73 d A	69.00 c B	69.61 c B	63.26 b B	91.20 cd A
Fepagro 36 RR	23.73 cd B	14.33 c A	12.20 bc C	14.20 d A	74.06 bc B	58.44 d C	65.80 ab BC	95.95 cd A
FPS Netuno RR	30.93 b A	20.03 bc B	14.53 bc C	12.60 d C	83.20 b B	105.54 ab A	77.53 a B	103.00 bc A
FPS Iguaçú RR	10.53 cde C	18.66 bc A	11.66 c B	16.06 cd A	71.00 bc B	82.33 bc B	56.93 bc B	106.80 bc A
FPS Urano RR	23.00 cd A	11.60 c B	14.00 bc B	14.90 d B	56.06 d B	43.40 e C	57.66 bc B	111.75 bc A
FPS Júpter RR	21.20 cd A	23.60 aA	14.26 bc B	15.60 d B	66.02 c B	92.89 b A	49.33 c C	72.45 de B
AMS Tibagi RR	14.06 f A	13.46 c A	14.20 bc A	15.06 d A	72.81 bc B	91.25 b A	54.20 bc C	60.89 e BC
Don Mario 7.0i RR	23.13 dc A	18.06b c BC	14.80 bc C	20.46 bc B	71.93 bc C	85.53 b B	54.93 bc D	129.34 aA
A 6411 RR	23.49 dc B	15.46 c C	13.53 bc C	29.73 aA	76.60 bc B	55.86 d C	53.26 bc C	118.40 ab A
Don Mario 5.8i RR	17.26 cde A	15.06 c A	15.26 bc A	18.98 cd A	66.66 c B	79.86 bc A	54.09 bc B	93.07 cd A
BMX Potência RR	38.06 aA	22.00 b B	20.86 a B	19.86 c B	99.60 a B	113.74 aA	68.86 ab C	98.80 c B
Don Mario 5.9i RR	21.14 cd A	14.33 c B	15.26 bc B	13.53 d B	68.48 c A	66.26 cd A	61.73 b A	68.45 e A
ROOS Camino RR	16.66 cde A	14.33 c A	17.26 ab A	15.70 cd A	66.82 c B	72.28 c B	60.93 bc B	102.26 bc A
BMX Ativa RR	20.53 cde A	15.80 c AB	15.40 b AB	17.73 cd AB	60.60 c B	50.60 de B	61.13 bc B	98.12 c A
NA 5909 RR	22.33 cd A	19.93 bc A	16.80 ab B	23.40 b A	70.53 bc C	85.46 b B	56.53 bc C	112.06 b A
BMX Turbo RR	29.26 bc A	21.96 b B	16.40 b C	24.96 ab AB	71.66 bc C	84.08 bc B	60.13 bc D	97.00 c A
TMG 7161 RR	26.33 c A	19.53 bc B	13.53 bc C	19.80 cd B	82.45 bc A	85.66 b A	58.71 bc B	91.55 cd A
CV %	14.67				10.12			

*Means followed by the same lowercase letters in the column and uppercase letter in the row do not differ by Tukey test at 5% of probability.

Table 4. Means of interaction between 20 soybean genotypes grown in Santa Rosa - RS (SR), TenentePortela - RS (TP), Campos Borges - RS (CB) and Sarandi - RS (SA), for the traits number of reproductive nodes in the main stem (NRNM) and number of reproductive nodes in the ramifications (NRNR).

Soybean genotypes	NRNM (units)				NRNR (units)			
	Growing environments							
	SR	TP	CB	SA	SR	TP	CB	SA
BRS Tordilha RR	7.80 bc B	7.40 c B	7.06 c B	11.73 ab A	6.31 ab A	6.13 c A	6.33 aA	8.93 aA
FPS Paranapanema RR	11.73 ab A	13.06 ab A	12.53 ab A	11.00 b A	5.26 ab A	5.66 c A	7.60 aA	6.33 aA
Fepagro 37 RR	8.86 bc B	8.13 c B	8.73 bc B	12.66 ab A	6.46 ab B	17.13 b A	16.51 aA	1.34 a B
FPS Solimões RR	13.06 aA	13.00 ab A	13.13 aA	12.00 ab A	6.33 ab A	9.06 c A	9.60 aA	9.13 aA
Fepagro 36 RR	9.66 bc B	8.33 c B	9.80 bc B	12.93 ab A	3.26 b B	10.33 bc AB	13.13 aA	3.13 a B
FPS Netuno RR	10.60 ab A	13.00 ab A	11.66 ab A	12.20 ab A	6.06 ab A	6.00 c A	3.40 aA	4.93 aA
FPS Iguaçú RR	12.73 ab A	12.00 ab A	11.20 ab A	13.80 aA	9.06 ab A	10.73 bc A	7.00 aA	5.46 aA
FPS Urano RR	7.33 c B	9.13 bc AB	10.80 ab AB	12.00 ab A	10.80 ab A	13.06 bc A	11.00 aA	8.73 aA
FPS Júpter RR	9.86 bc A	11.13 b A	10.20 b A	10.33 b A	9.80 ab A	6.86 c A	2.40 aA	3.40 aA
AMS Tibagi RR	10.33 ab A	12.26 ab A	11.26 ab A	10.46 b A	0.13 b A	4.00 c A	3.86 aA	3.73 aA
Don Mario 7.0i RR	9.66 bc A	11.73 ab A	11.00 ab A	10.60 b A	8.40 ab A	9.40 c A	8.20 aA	6.53 aA

A 6411 RR	9.00 bc A	9.06 bc A	11.20 ab A	9.91 b A	6.73 ab AB	12.40 bc A	12.86 aA	2.84 a B
Don Mario 5.8i RR	9.66 bc A	11.66 ab A	10.00 b A	11.08 ab A	1.33 b B	4.66 c B	14.60 aA	3.61 a B
BMX Potência RR	9.93 bc A	11.93 ab A	11.73 ab A	12.00 ab A	4.20 ab A	7.20 c A	11.86 aA	8.40 aA
Don Mario 5.9i RR	9.46 bc B	12.53 ab AB	13.53 aA	10.40 b B	6.80 ab AB	13.86 bc A	8.33 aA	2.46 a B
ROOS Camino RR	10.13 b A	10.86 bc A	12.73 aA	11.00 b A	4.66 ab A	12.13 bc A	9.46 aA	3.54 aA
BMX Ativa RR	9.80 bc A	9.40 bc A	11.80 ab A	11.46 ab A	3.93 ab B	11.66 bc A	10.00 a AB	3.80 a B
NA 5909 RR	10.86 ab B	13.66 ab A	12.00 ab A	11.00 b AB	11.33 a B	28.34 aA	7.44 a B	8.40 a B
BMX Turbo RR	7.60 bc B	10.8 bc AB	9.93 b AB	12.26 ab A	3.93 ab B	6.93 c AB	13.40 aA	3.80 a B
TMG 7161 RR	11.06 ab B	14.26 aA	12.33 ab AB	10.13 b B	10.86 ab B	27.93 aA	10.73 a B	5.13 a B
C V %	15.87				59.82			

*Means followed by the same lowercase letters in the column and uppercase letter in the row do not differ by Tukey test at 5% of probability.

Table 5. Means of interaction between 20 soybean genotypes grown in Santa Rosa - RS (SR), TenentePortela - RS (TP), Campos Borges - RS (CB) and Sarandi - RS (SA) for the traits number of pods per plant (NPP) and number of grains per plant (NGP).

Soybean genotypes	NPP (units)				NGP (units)			
	Growing environments							
	SR	TP	CB	SA	SR	TP	CB	SA
BRS Tordilha RR	17.11 b B	25.46 c AB	25.86 c AB	37.39 ab A	20.00 b B	25.73 d B	25.66 c B	41.93 ab A
FPS Paranapanema RR	32.66 ab B	45.20 b AB	54.80 ab A	50.82 ab AB	34.84 ab B	45.06 c AB	50.80 ab A	49.63 ab AB
Fepagro 37 RR	24.00 b B	49.93 b A	60.28 ab A	54.41 aA	24.94 ab B	49.85 bc A	45.53 ab A	38.26 ab AB
FPS Solimões RR	40.33 ab B	46.26 b B	64.33 aA	54.11 a AB	34.20 ab B	51.73 bc AB	60.23 aA	42.93 ab B
Fepagro 36 RR	22.80 b B	41.40 b A	44.53 bc A	40.33 ab A	22.41 b B	45.53 c A	46.50 ab A	39.73 ab A
FPS Netuno RR	27.26 ab B	52.26 b A	34.00 bc B	46.66 ab AB	26.31 ab B	49.40 bc A	31.40 bc B	46.53 ab AB
FPS Iguaçú RR	35.20 ab A	47.73 b A	44.00 bc A	41.20 ab A	33.78 ab B	50.13 bc A	43.57 b AB	41.01 ab AB
FPS Urano RR	28.53 ab B	58.40 b A	56.13 ab A	47.00 ab A	27.20 ab B	64.80 b A	46.33 ab A	51.18 aA
FPS Júpter RR	26.53 ab B	38.73 bc AB	47.08 ab A	35.46 ab AB	26.40 ab A	36.13 cd A	28.53 bc A	34.40 b A
AMS Tibagi RR	24.62 b A	39.00 b A	30.41 bc A	26.73 b A	21.93 b B	38.80 cd A	26.73 c AB	28.20 b AB
Don Mario 7.0i RR	27.66 ab B	49.53 b A	33.41 bc AB	29.11 b B	26.61 ab B	51.26 bc A	35.20 bc B	34.90 b B
A 6411 RR	26.00 ab B	46.60 b A	49.71 ab A	33.36 ab AB	25.86 ab A	42.06 c A	42.06 bc A	24.86 b A
Don Mario 5.8i RR	18.81 b B	33.86 bc B	59.01 ab A	33.91 ab B	20.40 b B	40.16 cd A	49.33 ab A	34.62 b A
BMX Potência RR	25.26 ab B	40.33 b AB	44.66 b A	48.80 ab A	23.80 b B	40.88 cd A	44.00 b A	45.60 ab A
Don Mario 5.9i RR	29.73 ab B	37.13 bc A	48.93 ab A	37.06 ab A	32.20 ab A	46.98 c A	47.20 ab A	36.60 ab A
ROOS Camino RR	26.66 ab B	41.40 b A	52.31 ab A	35.06 ab AB	22.70 b B	33.37 cd B	49.80 ab A	35.33 b AB
BMX Ativa RR	28.26 ab B	61.68 b A	48.93 ab B	34.80 ab B	31.26 ab B	56.80 bc A	47.06 ab A	36.20 ab B
NA 5909 RR	40.40 a B	64.73 aA	49.09 ab AB	47.00 ab B	40.33 a B	68.23 ab A	43.10 b B	43.65 ab B
BMX Turbo RR	16.40 b B	21.61 c B	51.40 ab A	38.46 ab AB	16.85 b B	37.93 cd A	53.06 ab A	41.73 ab A
TMG 7161 RR	35.40 ab B	82.58 aA	47.01 ab B	40.53 ab B	34.86 ab B	82.58 aA	48.98 ab B	40.30 ab B
C V %	25.05				24.55			

*Means followed by the same lowercase letters in the column and uppercase letter in the row do not differ by Tukey test at 5% of probability.

Table 6. Means of interaction between 20 soybean genotypes grown in Santa Rosa - RS (SR), TenentePortela - RS (TP), Campos Borges - RS (CB) and Sarandi - RS (SA) for the traits grain yield (GY) and mass of one thousand grains (MTG).

Soybean genotypes	GY (kg ha ⁻¹)				MTG (grams)			
	Growing environments							
	SR	TP	CB	SA	SR	TP	CB	SA
BRS Tordilha RR	1120.04 c B	2630.34 de A	862.28 d B	3868.23 ab A	164.33 c B	334.81 ab A	131.20bc B	288.52 bc A
FPS Parapanema RR	1133.45 c B	4300.09 bc A	2282.37 bc B	2524.43 cd A	129.66 c B	255.41 bc A	79.03 c B	247.17 bc A
Fepagro 37 RR	2067.94 ab B	4459.61 bc A	3203.25 ab B	3993.51 ab A	259.56 bc A	275.76 bc A	225.37 ab A	253.36 bc A
FPS Solimões RR	2253.79 ab B	4190.99 c A	3013.30 ab B	3159.12 bc AB	199.15 bc AB	270.88 bc A	138.58 bc B	207.72 c AB
Fepagro 36 RR	1670.09 bc B	2820.83 de A	1440.27 cd B	2815.83 c A	285.35 b AB	206.04 c B	89.88 c C	295.17 bc A
FPS Netuno RR	1889.25 bc B	3939.52 cd A	2718.47 bc B	3278.46 bc A	268.21 b A	301.13 bc A	183.53 bc B	316.58 b A
FPS Iguaçú RR	2580.16 ab C	5555.13 ab A	2706.15 bc C	4350.33 ab B	111.17 c C	423.25 aA	198.48 b C	311.78 b B
FPS Urano RR	1974.68 b B	4406.04 bc A	2501.76 bc B	3568.69 bc A	269.35 b B	229.00 c B	166.01 bc B	368.97 ab A
FPS Júpter RR	1524.67 bc C	3107.41 de B	2041.47 c C	4303.49 ab A	252.01 bc A	295.55 bc A	272.32 ab A	304.72 bc A
AMS Tibagi RR	1059.42 c B	3523.78 cd A	996.59 d B	3512.08 bc A	161.01 c B	292.41 bc A	147.78 bc B	331.74 b A
Don Mario 7.0i RR	2080.82 ab B	4421.54 bc A	1826.01 c B	3723.63 b A	207.29 bc AB	272.37 bc A	175.09 bc B	260.76 bc A
A 6411 RR	2697.77 ab C	3319.85 d B	2498.58 bc C	4700.54 aA	372.03 ab A	267.88 bc B	261.37 ab B	455.28 aA
Don Mario 5.8i RR	2375.41 ab B	3707.68 cd A	2490.24 bc B	3514.64 bc A	373.79 ab A	307.07 bc A	177.69 bc B	293.55 bc A
BMX Potência RR	2415.79 ab B	2553.27 e B	2429.80 bc B	3612.02 bc A	389.34 aA	209.60 c B	188.16 b B	447.87 aA
Don Mario 5.9i RR	2456.31 ab C	4571.16 bc A	3049.39 ab B	3505.38 bc B	253.37 bc AB	299.39 bc A	215.47 ab B	320.86 b A
ROOS Camino RR	2538.81 ab B	3806.06 cd A	3604.47 aA	4233.23 ab A	371.82 ab A	400.46 ab A	302.81 aA	347.84 ab A
BMX Ativa RR	1933.83 b C	4752.54 bc A	3863.44 a B	4698.15 aA	206.95 bc B	243.75 bc B	247.26 ab B	392.25 ab A
NA 5909 RR	2967.90 a B	5094.16 b A	2477.69 bc B	1829.23 d B	253.37 bc B	406.55 ab A	279.81 ab B	170.31 c B
BMX Turbo RR	1387.02 bc B	3375.93 cd A	2849.21 b A	2723.49 cd A	303.56 ab A	322.48 b A	186.37 b B	284.92 bc A
TMG 7161 RR	2590.42 ab B	6076.47 aA	1642.99 cd C	2101.37 cd B	213.27 bc AB	290.65 bc A	195.72 b B	210.62 c AB
CV %	15.65				18.99			

*Means followed by the same lowercase letters in the column and uppercase letter in the row do not differ by Tukey test at 5% of probability

Table 7. Slicing into simple effects and relative contribution of sums of squares expected values for soybean genotypes x growing environment interaction for the traits first pod insertion height (FPIH), plant height (PH), number of pods per plant (NPP), number of reproductive nodes on the main stem (NRNM), number of reproductive nodes in the ramifications (NRNR), number of grains per plant (NGP), mass of a thousand grains (MTG) and grain yield (GY).

FV	Traits															
	FPIH		PH		NPP		NRNM		NRNR		NGP		GY		MTG	
	SS	RCSS (%)	SS	RCSS (%)	SS	RCSS (%)	SS	RCSS (%)	SS	RCSS (%)	SS	RCSS (%)	SS	RCSS (%)	SS	RCSS (%)
Santa Rosa - RS	2325.7	56.2*	5737.3	16.1*	2217.7	12.1 ^{NS}	128.7	23.5*	547.5	14.0 ^{NS}	2156.2	11.4 ^{NS}	15795370.0	14.1*	282667.0	36.5*
TenentePortela - RS	633.7	15.3*	16681.0	47.0*	8506.5	46.6*	223.2	40.8*	2282.9	58.5*	9596.6	50.9*	39161305.0	35.1*	156924.0	20.2*
Campos Borges - RS	278.0	6.7*	2681.1	7.5*	4979.3	27.3*	136.1	24.9*	756.9	19.4*	4847.7	25.7*	30240429.0	27.1*	126170.0	16.3*
Sarandi - RS	894.6	21.6*	10350.0	29.1*	2529.7	13.8 ^{NS}	57.8	10.5 ^{NS}	309.7	7.9 ^{NS}	2217.2	11.7 ^{NS}	26287122.0	23.5*	208234.0	26.9*
BRS Tordilha RR	543.0	13.5*	2028.6	3.5 ^{NS}	414.4	1.8 ^{NS}	42.6	11.9*	16.1	0.4 ^{NS}	804.8	3.4*	13836393.0	7.6*	56831.0	6.8*
FPS Paranapanema RR	90.0	2.2*	2044.8	3.6*	777.9	3.4 ^{NS}	7.4	2.0 ^{NS}	9.4	0.2 ^{NS}	477.3	2.0 ^{NS}	12051721.0	6.6*	34103.0	4.1*
Fepagro 37 RR	198.3	4.9*	2626.2	4.6*	1939.4	8.6*	38.5	10.7*	418.8	11.5*	1070.4	4.5*	7669333.0	4.2*	3929.1	0.4 ^{NS}
FPS Solimões RR	24.7	0.6 ^{NS}	1359.4	2.4*	961.2	4.2*	2.5	0.7 ^{NS}	19.8	0.5 ^{NS}	1132.8	4.8*	4748536.0	2.6*	21629.0	2.6*
Fepagro 37 RR	240.6	6.0*	1784.7	3.1*	865.7	3.8*	34.2	9.5*	230.2	6.3*	1120.9	4.7*	3911325.0	2.1*	54115.0	6.5*
FPS Netuno RR	556.7	13.9*	1772.4	3.1*	1179.1	5.2*	9.0	2.5 ^{NS}	13.9	0.3 ^{NS}	1146.8	4.8*	4484084.0	2.4*	22032.0	2.6*
FPS Iguaçú RR	129.8	3.2*	4003.4	7.0*	251.2	1.1 ^{NS}	11.0	3.0 ^{NS}	48.0	1.3 ^{NS}	410.9	1.7 ^{NS}	12091725.0	6.6*	108747.0	13.1*
FPS Urano RR	219.4	5.4*	6113.1	10.8*	1659.9	7.4*	37.1	10.3*	28.2	0.7 ^{NS}	2178.7	9.2*	9072897.0	5.0*	43891.0	5.3*
FPS Júpiter RR	151.9	3.8*	2330.4	4.1*	536.8	2.3 ^{NS}	2.6	0.7 ^{NS}	102.9	2.8 ^{NS}	193.8	0.8 ^{NS}	9636355.0	5.3*	3636.0	0.4 ^{NS}
AMS Tibagi RR	3.9	0.0 ^{NS}	1813.2	3.2*	285.9	1.2 ^{NS}	7.1	1.9 ^{NS}	31.4	0.8 ^{NS}	455.1	1.9 ^{NS}	12386029.0	6.8*	55745.0	6.7*
Don Mario 7.0i RR	205.2	5.1*	6998.7	12.4*	864.0	3.8*	6.6	1.8 ^{NS}	12.7	0.3 ^{NS}	957.4	4.0*	11421186.0	6.2*	17279.0	2.0 ^{NS}
A 6411 RR	370.1	9.2*	3829.3	6.7*	938.8	4.1*	9.4	2.6 ^{NS}	169.6	4.6 ^{NS}	751.9	3.2 ^{NS}	6480582.0	3.5*	38527.0	4.6*
Don Mario 5.8i RR	24.7	0.6 ^{NS}	1781.0	3.1*	1332.3	5.9*	7.5	2.1 ^{NS}	303.0	8.3*	1318.4	5.6*	4241073.0	2.3*	51445.0	6.2*
BMX Potência RR	486.2	12.1*	2832.4	5.0*	948.5	4.2*	8.7	2.4 ^{NS}	90.4	2.4 ^{NS}	907.2	3.8*	2096112.0	1.1*	129267.0	15.6*
Don Mario 5.9i RR	107.6	2.6*	85.2	0.1 ^{NS}	567.9	2.5 ^{NS}	31.6	8.8*	199.5	5.4*	512.3	2.1 ^{NS}	5661180.0	3.1*	20038.0	2.4*
ROOS Camino RR	11.7	0.2 ^{NS}	3042.9	5.3*	1051.8	4.7*	10.9	3.0 ^{NS}	130.2	3.5 ^{NS}	1118.1	4.7*	3526321.0	1.9*	10178.0	1.2 ^{NS}
BMX Ativa RR	49.4	1.2 ^{NS}	2939.2	5.2*	1636.3	7.3*	12.8	3.5 ^{NS}	149.8	4.1 ^{NS}	1172.3	5.0*	15597219.0	8.5*	44080.0	5.3*
NA 5909 RR	75.6	1.8*	5079.5	9.0*	954.4	4.2*	15.0	4.1 ^{NS}	603.4	16.5*	1525.7	6.5*	12231291.0	6.7*	67178.0	8.1*
BMX Turbo RR	259.3	6.4*	2271.3	4.0*	2189.7	9.7*	34.3	9.5*	181.8	4.9 ^{NS}	2060.0	8.7*	5700821.0	3.1*	28910.0	3.4*
TMG 7161 RR	246.0	6.1*	1695.9	3.0*	3019.5	13.4*	28.7	8.0*	878.4	24.1*	4123.4	17.5*	24608872.0	13.5*	14486.0	1.7 ^{NS}

* significant at 5% of probability by the F test, NS: non-significant at 5% of probability by the F test. FV: factor of variation, SS: Sum of squares, RCSS (%): percentage of sum of squares relative contribution for interaction.

Number of pods per plant (NPP) revealed no significance for the simple effects through the treatment levels Santa Rosa - RS and Sarandi - RS, however, relative contributions of 46.65% for the sum of squares were obtained for TenentePortela - RS (Table 7). Regarding the variation factor soybean genotypes, absence of significance for simple effects was evidenced by BRS Tordilha RR, FPS Paranapanema RR, FPS Iguaçú RR, FPS Júpiter RR, AMS Tibagi RR and Don Mario 5.9i RR, being these genotypes defined as stable and predictable for the magnitude of reproductive structures per plant. However, superior contribution was expressed through the genotype TMG 7161 RR, requiring specific recommendation for growing environment.

Regarding number of reproductive nodes in the main stem (NRNM), there was no significance for simple effects in Sarandi-RS, however, relative contribution of 40.89% was observed for this variation factor in TenentePortela - RS (Table 7). Regarding the effects attributed to genotypes, it was defined absence of significance for FPS Paranapanema RR, FPS Solimões RR, FPS Netuno RR, FPS Iguaçú RR, FPS Júpiter RR, AMS Tibagi RR, Don Mario 7.0i RR, A 6411 RR, Don Mario 5.8i RR, BMX Potência RR, RoosCamino RR, BMX Ativa RR and NA 5909 RR, being these treatment levels assumed as predictable and stable for this trait. In contrast, superiority of sum of squares contribution for G x E interaction was verified to BRS Tordilha RR and FPS Urano RR, which are considered specific to certain growing environments.

The number of reproductive nodes in the ramifications (NRNR) evidenced the absence of significant simple effects for Santa Rosa - RS and Sarandi - RS. However, extreme contributions of 58.58% were expressed through TenentePortela - RS (Table7). When determining which treatment levels presented no significance, as stable and predictable the genotypes BRS Tordilha RR, FPS

Paranapanema RR, FPS Solimões RR, FPS Netuno RR, FPS Iguaçú RR, FPS Urano RR, FPS Júpiter RR, AMS Tibagi RR, Don Mario 7.0i RR, A 6411 RR, BMX Potência RR, Roos Camino RR, BMX Ativa RR and BMX Turbo RR are evidenced. On the other hand, contribution of 24.14% for differential effects of G x E interaction were presented by the genotype TMG 7161 RR, which is defined as of high specificity for this trait.

Regarding number of grains per plant (NGP), the environment TenentePortela - RS contributed in 50.99% to the differential effects of G x A interaction, however absence of significance was obtained for Santa Rosa - RS and Sarandi - RS, being these estimates indicative of stability for these treatment levels. Regarding genotypes, FPS Paranapanema RR, FPS Iguaçú RR, AMS Tibagi RR, A 6411 RR and Don Mario 5.9i RR were considered stable treatment levels for the magnitude of grains per plant. In contrast, the genotype TMG 7161 RR expressed 17.59% of contribution to the sum of squares and possibly it was the treatment level that caused significant G x E interaction for this trait. Grains yield (GY) expressed the significance of all treatment levels independent of the variation factor. For growing environments, it is evidenced that TenentePortela - RS, Campos Borges - RS and Sarandi - RS acted with greater emphasis on the sum of squares of G x E interaction (Table 7). Regarding genotypes, TMG 7161 RR, Roos Camino RR and BRS Tordilha RR are highlighted as the most contributors for the differential effects of G x E interaction.

Regarding mass of a thousand grains (MTG) for the variation factor growing environment, all treatment levels were significant. Also, it was determined that Santa Rosa - RS contributed with 36.52% to the differential effects of interaction (Table 7). Regarding genotypes Fepagro 37 RR, FPS Júpiter RR, Don Mario 7.0i RR, Roos Camino RR and TMG 7161 RR are defined as stable and predictable, which results are proven due to the lack of significance of simple effects and equality of variances of these treatment levels.

However, FPS Iguaçu RR and BMX Potência RR were the genotypes with the greatest influence on sum of squares expected values for G x E interaction.

The use of this biometric methodology allowed defining that the first pod insertion height and mass of a thousand grains were potentialized by the differential effects in the sum of squares of the G x E interaction through Santa Rosa – RS. In contrast, the environment TenentePortela - RS significantly influenced the phenotypic manifestation of plant height, number of pods per plant, number of reproductive nodes in the main stem, number of reproductive nodes in the ramifications, number of grains per plant and grain yield.

Absence of significance of simple effects with indication of stability and predictability was expressed in 25% of the genotypes tested for first pod insertion height and mass of one thousand grains, 60% of the genotypes for number of reproductive nodes in the main stem and ramifications. Regarding the variation factor soybean genotypes, it was verified that number of pods per plant, number of reproductive nodes in the ramifications, number of grains per plant and grain yield were potentiated by genotype TMG 7161 RR. Estimates of the relative contribution of sums of squares expected values to soybean genotypes x growing environments interaction were efficient to improve the comprehension of treatment levels, slicing of a factorial experiment into simple effects. Therefore, this new biometric approach provides a simple and quick interpretation of the differential effects of the interaction, in the same way, its use requires low computational resources and can be directed to other factorial experiments and crops of agronomic interest.

Materials and Methods

Conduction of study, experimental design and plant materials

This study was developed in the 2016/2017 agricultural year, with experimental design of randomized blocks arranged in a factorial scheme, being: four growing environments Santa Rosa - RS (27°52'15"S; 54°28'53"W, 277 meters of altitude), TenentePortela - RS (27°22'16"S; 53°45'30"W, 390 meters of altitude), Sarandi - RS (27°56'38"S; 52°55'23"W, 503 meters of altitude) and Campos Borges- RS (28°53'10"S; 52°59'55"W, with 513 meters of altitude) x 20 soybean genotypes (BRS Tordilha RR, FPS Paranapanema RR, Fepagro 37 RR, FPS Solimões RR, Fepagro 36 RR, FPS Netuno RR, FPS Iguaçu RR, FPS Urano RR, FPS Júpiter RR, AMS Tibagi RR, Don Mario 7.0i RR, A 6411 RR, Don Mario 5.8i RR, BMX Potência RR, Don Mario 5.9i RR, ROOS Camino RR, BMX Ativa RR, NA 5909 RR, BMX Turbo RR and TMG 7161 RR), disposed in three replicates.

The experimental unit consisted of four lines with 10 meters in length and spaced 0.50 meters. The traits of agronomic interest were measured in 10 plants randomly selected at the harvest. The population density used for all genotypes was 300 thousand plants per hectare, using no-tillage system. The base fertilization was 250 kg ha⁻¹ of N, P₂O₅, K₂O (10-20-20). The cultural treats, as well as the control of weeds, diseases and pest insects were carried out according to the crop demanding.

Traits measured

The measured traits were: first pod insertion height (FPIH, cm), plant height (PH, cm), number of reproductive nodes in the main stem (NRNM, units), number of reproductive nodes in the ramifications (NRNR, units), number of pods per plant (NPP, units), number of grains per plant (NGP, units), grain yield (GY, kg ha⁻¹) and mass of one thousand grains (MTG, g).

Statistical analysis

The data were submitted to analysis of variance, verifying the normality of residues (ShapiroWilk, 1965) and homogeneity of variances by Bartlett (Steel et al., 1997). Posteriorly checking the interaction between growing environments x soybean genotypes at 5% of probability. The statistical model used was: $\hat{Y}_{ijk} = m + b + E_j + G_i + (E_j \times G_i) + \hat{\epsilon}_{ijk}$, where: \hat{Y}_{ijk} : refers to the value observed in the experimental unit for the i^{th} genotype grown on j^{th} environment and k^{th} block; m: refers to the overall mean of the experiment; b: shows the effects of blocks; E_j : refers to the effects of the j^{th} growing environment; G_i : refers to the effects of the i^{th} soybean genotype; $E_j \times G_i$: refers to the differential effects of genotypes x growing environments interaction; $\hat{\epsilon}_{ijk}$: evidences the random effects of the experimental error (Table 1).

Traits that evidenced significant interaction were sliced into simple effects:

$$SSG = \left(\frac{(\sum(YGi1)^2 + \dots + (YGi20)^2)}{(N^{\circ}E * N^{\circ}B)} - C \right)$$

Where: SSG: Slicing of simple effects for the variation factor soybean genotypes, YG_i: means observed for the i^{th} genotype, N[°]E: number of growing environments tested, N[°]B: number of blocks contained in the experiment, C: factor for experimental adjustment.

$$SSE = \left(\frac{(\sum(YEj1)^2 + \dots + (YEj4)^2)}{(N^{\circ}G * N^{\circ}B)} - C \right)$$

Where: Slicing of simple effects for the variation factor of growing environments, YE_j: means observed for the j^{th} growing environment, N[°]G: number of tested genotypes, N[°]B: number of blocks contained in the experiment, C: factor for experimental adjustment.

Relative Contribution of Sum of Squares Expected Values for Genotype x Environments Interaction (RCSS):

$$RCSSG(\%) = \left(\frac{SSGGi1}{\sum GenotypesSS} \times 100 \right)$$

$$RCSSG(\%) = \left(\frac{SSEGi20}{\sum GenotypesSS} \times 100 \right)$$

Where: RCSS G (%): Relative contribution of sum of squares expected values for genotypes, SSGi: Sum of squares for each genotype by slicing into simple effects (SSG), \sum Genotypes SS: Summation of all sums of squares involved in the study for effects of genotypes.

$$RCSSSE(\%) = \left(\frac{SSEj1}{\sum EnvironmentsSS} \times 100 \right)$$

$$RCSSSE(\%) = \left(\frac{SSEj4}{\sum EnvironmentsSS} \times 100 \right)$$

Where: RCSS E (%): Relative contribution of sum of squares expected values for environments, SSEj: Sum of squares for

each environment by slicing into simple effects (SSE), Σ EnvironmentsSS: Summation of all sums of squares involved in the study for effects of environment.

Conclusion

The best performance regarding traits of agronomic interest is expressed by the genotype TMG 7161 RR in the growing environments tested, phenotype effects are affected by G x E interaction, and their tendencies must be adjusted by slicing into simple effects. The relative contribution of sums of squares expected values to soybean genotypes x growing environments interaction defined that the environment Tenente Portela - RS significantly influence plant height, number of pods per plant, number of reproductive nodes in the main stem, number of reproductive nodes in the ramifications, number of grains per plant and grain yield. The variation factor soybean genotypes define that number of pods per plant, number of reproductive nodes in the ramifications, number of grains per plant and grain yield are potentiated by genotype TMG 7161 RR. The biometric approach is efficient to understand the treatment levels and the slicing of simple effects of a factorial experiment, being possible to apply this methodology extensively in soybean.

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