Interference of genotypes x environments interaction in the genetic control of resistance to Asian rust soybean

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Abstract – The objectives of this work were to identify parents resistant to Asian soybean rust using diallel crosses, obtain information on the genetic control of soybean resistance to the pathogen and verify whether the combining ability estimates interact with the environment (year or time of assessment). The F_1 generation was obtained in a greenhouse from crosses between five contrasting parents for the trait resistance to soybean rust, in a complete diallel without reciprocals. Two rust-severity assessments were carried out on individual soybean plants of 25 treatments (parents and F_2 and F_3 populations) in 2006/2007 and 2007/2008, in an experimental field at Embrapa Soja, Londrina, PR, Brazil. Additive effects predominated in the genetic control of soybean resistance to Asian rust, and the interaction of the segregant populations with the environment, although significant, did not alter the genetic parameter's general combining ability (GCA) and specific combining ability estimates, indicating that estimates obtained in one year and one assessment can be extrapolated to others. BR01-18437 inbred line is resistant to Asian rust and showed high GCA effects. This line should be used as parent if the objective is the resistance to *Phakopsora pachyrhizi.*

Index terms: *Glycine max*, *Phakopsora pachyrhizi*, general combining ability, specific combining ability.

Interferência da interação genótipos x ambientes no controle genético da resistência à ferrugem asiática da soja

Resumo – Os objetivos deste trabalho foram identificar genitores resistentes à ferrugem asiática da soja por meio de cruzamentos dialélicos, obter informações sobre o controle genético da resistência ao patógeno e verificar se as estimativas da capacidade combinatória interagem com o ambiente (ano ou época de avaliação). A geração F_1 foi obtida por meio de cruzamentos entre cinco genitores contrastantes para a característica resistência à ferrugem da soja, em um dialelo completo, sem os recíprocos, em casa de vegetação. Foram realizadas duas avaliações quanto à severidade da ferrugem asiática da soja em plantas individuais de 25 tratamentos (genitores e populações F_2 e F_3) em 2006/2007 e 2007/2008, no campo experimental da Embrapa Soja, em Londrina, PR. Houve predominância de efeitos aditivos no controle genético da resistência à ferrugem asiática da soja, e a interação das populações segregantes com os ambientes, embora significativa, não alterou as estimativas dos parâmetros genéticos da capacidade geral de combinação (CGC) e da capacidade específica de combinação, indicando que as estimativas obtidas em um ano e uma avaliação podem ser extrapoladas para outros. A linhagem endogâmica BR01-18437 é resistente à ferrugem asiática e apresenta alta estimativa de CGC, e deve ser utilizada como genitora quando o objetivo é a resistência a *Phakopsora pachyrhizi*.

Termos para indexação: *Glycine max*, *Phakopsora pachyrhizi*, capacidade geral de combinação, capacidade específica de combinação.

Introduction

Asian soybean rust, caused by the *Phakopsora pachyrhizi* Syd. & P. Syd. fungus, is one of the main problems in soybean cropping in Brazil. It was reported for the first time in the 2000/2001 growing season (Yorinori et al., 2005) and, since then, its dissemination has been fast, causing expressive reduction in grain yield.

The control method used to date has been fungicide application, which increases production costs and environmental risks. For this reason, research to obtain resistance cultivars has been intensified. However, this strategy may be short lived, since the pathogen has shown great variability and a fast pathotype selection seems to occur. Therefore, it is expected that breeding for polygenetic resistance may be more effective for obtaining durable resistance or tolerance.

Having information regarding the genetic control of this type of resistance is of great importance, and some reports are already available (Arias et al., 2007; Ribeiro et al., 2007, 2008). However, whether the genetic parameter estimates vary with the environment must be investigated, as this information is not yet available in Brazil.

The objectives of this study were to identify parents resistant to soybean rust using diallel crosses, to obtain information on the genetic control of soybean resistance to rust, and also to verify whether the combining ability estimates interact with the environment (year or time of assessment).

Materials and Methods

The experiments were carried out at Embrapa Soja, Londrina, PR, Brazil, in a Latossolo Vermelho distroférrico (Rhodic Hapludox), with warm and wet subtropical climate and annual temperatures ranging from 11 to 29°C.

The soybean line BR01-18437 and the cultivars BRS 184, BRS 231, BRS 232 and Embrapa 48, used as parents, were obtained from the active germplasm bank at Embrapa Soja and selected based on previous studies in which they had expressed different responses to Asian soybean rust. Single plants of these materials were collected and multiplied for the crossings and for the evaluations.

Crosses to obtain F_1 seeds started out in a greenhouse in December 2004, following a complete diallel cross scheme, without reciprocals. The F_2 seeds were sown in a greenhouse to obtain the F_2 generations. In sequence, parents, F_1 and F_2 populations were advanced together in the winter of 2006 to obtain seeds of the parental and F_2 and F_3 populations with the same age (equal germination and vigor) for the 2006/2007 crop season. Similar procedures were followed to obtain the seeds for the 2007/2008 crop season.

The parents and the F_2 and F_3 populations were assessed under field conditions in the 2006/2007 and 2007/2008 crop seasons, in a completely randomized design with a total of 25 treatments. The number of replicates was 50 per parent, 160 per F_2 population and 200 per F_3 population. The experimental plots consisted of single-plant hill plots, with a spacing of 0.20 m between plants in a row and 1.50 m between useful rows. Two border rows were sown between the useful lines using seeds left over from the experiment to keep the plant population per area similar to that recommended for the commercial soybean crop (approximately 250,000 plants ha^{-1}). This procedure ensured a homogeneous level of competition among the plants in the useful plots (hill plot). It also facilitated the natural dispersion of the inoculum from the spray-inoculated border rows to the useful rows.

The growing conditions of the experiment were maintained similar to those commonly used in soybean cropping (Tecnologias de produção de soja, 2006), including fertilizing and weed and insect control. The experiment was irrigated to ensure normal plant development and favorable pathogen infection and reproduction after the inoculations (Del Ponte et al., 2006).

The pathogen was inoculated twice within a week interval, in the borders, using an isolate from Mato Grosso, which has been kept in a greenhouse on plants of the BRS Bacuri soybean cultivar. The procedures used to prepare the inoculum and for the actual inoculation were described by Ribeiro et al. (2008).

The severity of the disease obtained was scored using the diagrammatic scale proposed by Canteri & Godoy (2003), which considers the percentage of infected leaf tissue. The first assessment was carried out 30 days after detecting the pathogen in the useful plots (30 DAD) and the second one, seven days later (37 DAD). Both assessments were carried out on the 11th tri-foliolate leaf of each plant, when flowering had already started in all the plants.

A joint analysis of variance was carried out using the data obtained in the two years and two assessments for the 25 treatments after the arc sin $(x/100)^{0.5}$ transformation. The following model was used: $Y_{ijkl} = m + t_i + a_j + p_k + (ta)_{ij} + (tp)_{ik} + (ap)_{jk} + (tap)_{ijk} + (rp)_{l(j)k} + e_{ijkl}$, where: Y_{ijkl} is the observation of the i^{th} treatment in the j^{th} growing season in the k^{th} assessment averaged over the l replicate; m is the general mean; t_i is the effect of the i^{th} effective treatment (i = 1, 2, ..., 25); a_j is the effect of the j^{th} effective year (j = 1, 2); p_k is the effect of the k^{th} assessment (k = 1, 2); $(ta)_{ij}$ is the effect of the treatment and year interaction; $(tp)_{ik}$ is the effect of the treatment and assessment interaction; $(ap)_{jk}$ is the effect of the year and assessment interaction; $(tap)_{ijk}$ is the effect of the triple interaction among the treatments, years and assessments; $(rp)_{l(j)k}$ is the interaction between within-year replication effects and assessments; e_{ijkl} is the mean error associated to the estimates of the means obtained. The diallel cross analyses were carried out with the mean data according to Griffing's (1956) method IV, and the Scott & Knott (1974) test was used to compare the means.

The analyses were carried out running the SAS (SAS Institute, 1999) and Genes (Cruz, 2001) programs.

Results and Discussion

The individual analyses of variance of the parents, F_2 and F_3 generations within each year and each assessment detected significant differences ($p \leq 0.01$) among parents and among the segregant populations. The general combining ability (GCA) effects, estimated from the diallel crosses, were significantly different in all the environments, but the specific combining ability (SCA) effects were not significant in any of the years or assessment periods.

The joint analysis of variance involving the treatments in the two years and two assessments was made (Table 1), once the ratio between the highest (214.03) and lowest (51.26) error mean square in the analysis of individual variance was of less than seven (4.17) (Cruz & Regazi, 2001).

Table 1. Joint analysis of variance of *Phakopsora pachyrhizi* severity of the soybean parents and F_2 and F_3 populations, 30 and 37 days after detecting the pathogen in the 2006/2007 and 2007/2008 crop seasons[(1)].

Source of variation	Degree of freedom	Mean square	p
Year	1	509,036.03	<0.0001
Assessment	1	1,145,319.36	<0.0001
Year x assessment	1	2,085.29	0.0002
Error a (Replicates year^{-1} x assessment)	796	134.94	-
Treatment	24	3,460.90	<0.0001
Parents	4	3,471.13	<0.0001
F_2	9	4,237.56	<0.0001
General combining ability (GCA)	4	9,488.80	<0.0001
Specific combining ability (SCA)	5	379.39	0.0093
F_3	9	3,197.86	<0.0001
GCA	4	6,915.34	<0.0001
SCA	5	428.53	0.0043
Parents vs F_2	1	31,038.97	<0.0001
Parents vs F_3	1	40,396.28	<0.0001
Treatment x year	24	358.64	<0.0001
Parents vs year	4	577.38	0.0013
F_2 x Year	9	337.20	0.0039
GCA x year	4	679.57	0.0004
SCA x year	5	27.15	0.9530
F_3 vs year	9	269.20	0.0208
GCA x year	4	356.13	0.0213
SCA x year	5	200.40	0.1505
Parents vs F_2 x year	1	3,263.05	<0.0001
Parents vs F_3 x year	1	3,875.09	<0.0001
Treatment x assessment	24	322.56	<0.0001
Parents x assessment	4	272.07	0.0658
F_2 x assessment	9	335.95	0.0040
GCA x assessment	4	658.65	0.0005
SCA x assessment	5	103.05	0.5284
F_3 x assessment	9	378.51	0.0015
GCA x assessment	4	709.58	0.0003
SCA x assessment	5	114.02	0.5321
Parents vs F_2 x assessment	1	3,629.50	<0.0001
Parents vs F_3 x assessment	1	3,246.43	<0.0001
Treatment x year x assessment	24	188.38	0.0491
Parents vs year x assessment	4	122.78	0.5881
F_2 x year x assessment	9	261.71	0.0249
F_3 x year x assessment	9	144.15	0.3131
Parents vs F_2 x year x assessment	1	1,674.62	0.0005
Parents vs F_3 x year x assessment	1	2,732.69	<0.0001
Mean error - (Treatment x year x assessment x replicates year^{-1})	13,810	123.89	-
CV (%)		25.13	

[(1)]Data were transformed to arc sin $(x/100)^{0.5}$.

The experimental precision assessed by the coefficient of variation (CV) was considered good, similar to that obtained in several other experiments that assessed the same pathogen (Furtado, 2007; Koga et al., 2007). This evaluation was important, because soybean rust severity was assessed visually on individual plants in the present work.

The year effects were significant (Table 1). In the 2006/2007 crop season, the pathogen incidence was greater than in 2007/2008, with plants showing an average of more than 40% of leaf area infected at 30 DAD. It is known that some environmental factors have decisive influence on the greater and lesser pathogen infection. Prolonged wetting (10 h per day), night temperatures between 18 and 24°C and frequent rain have been shown to be determining conditions to establish the disease (Navarini et al., 2007). These factors are prevalent in the Brazilian soybean cropping regions. Rainfall seems to be the key factor that influences disease severity, because it prolongs the leaf wetting period, which promotes the germination of the deposited spores, reduces the temperature inside the canopy, and even releases the spores from spore clusters via turbulence – that is, the fungus uredospores that tend to remain together and are not easily released by wind action are freed to germinate more easily (Bergamim Filho, 2006; Del Ponte et al., 2006).

A significant difference was also detected between assessments, as expected (Table 1). The mean increase in the leaf area infected by the pathogen at 37 DAD (60.9%) was 74% greater than the estimates at 30 DAD (35%). This fact showed that the environmental conditions for the occurrence of the disease were favorable, and the daily increase in severity was of 3.7%. In a similar experiment, carried out in 2004/2005, the pathogen severity was of 4.52% in the first assessment and of 22.19% in the second assessment (Ribeiro et al., 2007).

It was also observed that the genotypes were better discriminated at 30 DAD, corroborating Ribeiro et al. (2007), who reported that the best assessment time for soybean rust severity was between 25 to 30 DAD. This has important consequences, because assessments made prior to the proposed assessment period may provide non-reliable estimates for a study of this nature.

The year x assessment interaction was significant (Table 1). However, there was no alteration in the genotypes classification between the assessments in terms of year. In 2006/2007, the soybean rust severity was 43.49 and 71.34% at 30 and 37 DAD respectively, while in 2007/2008 it was 26.57 and 50.38% at 30 and 37 DAD respectively.

There were significant differences among the treatments (Table 1), which is important for the breeder in experiments of this kind. After partitioning the source of treatment variation, significant differences were detected both among the parents and among the F_2 and F_3 populations.

Regardless of the year and assessment, BR01-18437 was the most resistant genotype, with the lowest percentage of infected leaf area (Table 2), as expected, because it carries a recessive allele that confers resistance to soybean rust (Pierozzi et al., 2008). BR01-18437 typically shows a reddish-brown resistant-type lesion that favors a lower incidence of the disease, because these lesions tend to produce a smaller number of

Table 2. Mean percentage of *Phakopsora pachyrhizi* severity of the soybean parents 30 and 37 days after detecting the pathogen (DAD) in the 2006/2007 and 2007/2008 crop seasons[(1)].

Year	30 DAD	37 DAD	Crop season mean
		BR01-18437	
2006/2007	35.62	65.64	50.63
2007/2008	24.74	36.51	30.63
Assessment mean	30.18	51.08	-
Parent mean		40.63E	
		BRS 184	
2006/2007	50.44	81.50	65.97
2007/2008	33.14	51.31	42.23
Assessment mean	41.79	66.41	-
Parent mean		54.10A	
		BRS 231	
2006/2007	32.12	74.86	49.39
2007/2008	29.08	47.66	37.98
Assessment mean	30.60	61.26	-
Parent mean		43.69D	
		BRS 232	
2006/2007	48.54	74.86	61.70
2007/2008	31.34	47.66	39.50
Assessment mean	39.94	61.26	-
Parent mean		50.60B	
		Embrapa 48	
2006/2007	43.92	68.83	56.38
2007/2008	28.90	45.33	37.12
Assessment mean	36.41	57.08	-
Parent mean		46.75C	

[(1)]Means followed by equal letters among parents do not differ by Scott & Knott test at 5% probability.

uredia with low or no spore production (Calvo et al., 2007; Pierozzi et al., 2008). The BRS 184 cultivar was the most susceptible genotype at 30 DAD and 37 DAD assessments. In previous studies, it had displayed low severity scores at 7 DAD and high scores at 39 DAD, showing that resistance performance may vary with time (Ribeiro et al., 2007).

In the populations with low pathogen incidence, the BR01-18437 parent was always present, what indicates its contribution to the reduction of the disease. The mean severity percentage, considering all the environments, for all the populations in the F_2 generations (48.5%) was very similar to that of the F_3 generation (47.6%) (Table 3). It can, therefore, be deduced that there was no endogamy depression and, consequently, that the presence of dominance or epistasis is less important in the expression of soybean resistance to this pathogen.

The partition of the sum of squares (SS) of the populations according to Griffing's (1956) method IV showed that both GCA and SCA effects were significant, regardless of year and assessment (Table 1). However, it was observed that the GCA effects explained 99.5% of the population SS in the F_2 generation. Similarly, 96.1% of the F_3 population SS was explained by the GCA. Therefore, it can be concluded that GCA effects were more important than SCA effects in explaining the total variation observed. Considering a single locus, the GCA estimate is given by the expression $(p_i - \bar{p})[a + (1 - 2t)d]$, where: p_i is the frequency of the favorable allele of the i^{th} parent; $\bar{p}$ is the mean allele frequency; t is the mean allele frequency of the testers, that is, the mean allele frequency of the parents, except for the i^{th} order parent; a is the homozygote deviation to the mean; and d is the heterozygote deviation to the mean. In the absence of dominance (d = 0), GCA effects will only be a function of the difference among the allele frequencies of the parents (Vencovsky, 1978). Also, in the complete absence of dominance, the mean explains all the variations due to the combining ability (Oliveira et al., 1996).

The SCA (s_{ij}) of the i^{th} and j^{th} parents, considering one locus, is given by the expression $2[(\bar{p} - p_i)(r_j - \bar{r})d]$, where $\bar{p}$, p_i and d have already been described, and r_j and $\bar{r}$ have the same interpretation of p_i and $\bar{p}$ for the other parent. The s_{ij} estimate depends on the divergence between the parents and on the presence of dominance (Vencovsky, 1978). As the parents were divergent for the trait in question, it can be inferred that the small contribution of SCA to the variation among the populations was due to the small contribution of the effects of dominance (d close to zero) for the expression of the trait.

The GCA and SCA estimates of rust severity obtained on average for the environments from the F_2 and F_3 populations are shown in Table 4. Negative g_i values indicated that the concerned parents contributed to reduce the severity of the pathogen in the crossings in which they participated (Cruz et al., 2004). It is interesting to have some parents with high, negative g_i values. This happened with BR01-18437, which contributed to reducing disease severity on the average of the crossings in which it participated. On the other hand, the BRS 184 cultivar presented the highest positive g_i estimates and was the parent that most contributed to increasing susceptibility to the pathogen in the crossings in which it participated. The SCA

Table 3. Mean percentage of *Phakopsora pachyrhizi* severity of the soybean F_2 and F_3 populations, 30 and 37 days after detecting the pathogen (DAD) in the 2006/2007 and 2007/2008 crop seasons[(1)].

Crosses	2006/2007		2007/2008		Mean	2006/2007		2007/2008		Mean
	30 DAD	37 DAD	30 DAD	37 DAD		30 DAD	37 DAD	30 DAD	37 DAD	
	F_2					F_3				
BR01-18437 x BRS 184	39.98B	69.22B	24.91B	48.79C	49.53	42.40B	70.31B	25.43A	48.04C	46.55
BR01-18437 x BRS 231	36.81C	66.93B	21.02C	44.34C	46.06	36.22D	66.14C	21.07C	46.48C	42.48
BR01-18437 x BRS 232	41.08B	67.40B	22.33C	44.15C	47.74	39.88C	67.48C	23.77B	45.94C	44.27
BR01-18437 x Embrapa 48	42.08B	71.23B	22.58C	45.52C	48.87	40.50C	67.45C	23.61B	45.51C	44.27
BRS 184 x BRS 231	46.68A	75.81A	27.58A	60.60A	56.96	46.55A	76.45A	28.34A	56.39A	51.93
BRS 184 x BRS 232	46.14A	71.49B	27.32A	56.41B	55.43	44.54A	71.59B	27.69A	57.89A	50.43
BRS 184 x Embrapa 48	48.90A	75.88A	27.86A	57.76A	56.80	46.73A	72.86B	27.65A	52.10B	49.84
BRS 231 x BRS 232	44.28A	73.92A	27.15A	53.78B	53.16	42.49B	71.26B	27.37A	53.71B	48.71
BRS 231 x Embrapa 48	47.87A	74.79A	27.01A	53.93B	54.55	42.56B	70.81B	26.98A	53.15B	48.38
BRS 232 x Embrapa 48	48.04A	74.81A	28.73A	53.75B	55.76	45.64A	70.21B	28.70A	53.45B	49.50
Total mean					48.47					47.63

[(1)]Means followed by equal letters on the same column do not differ by Scott & Knott test at 5% probability.

effects were always of small magnitude, indicating that the hybrids performed as expected based only on the GCA effects, which was an indication that the trait is little affected by dominance.

The contrast parents x populations was significant (Table 1), indicating that the means of the parents differed from that of the populations, regardless of the environment. This significant difference can be attributed to the presence of dominance or epistasia (Bernardo, 2002). However, by observing the total mean of the parents and the F_2 and F_3 populations (Tables 2 and 3) it can be observed that the mean of the populations (48.05%) was only 0.9% superior to the mean of the parents (47.15%). Therefore, if there was depression by endogamy, it was of small magnitude and, as previously commented, dominance is not important in the trait expression.

One of the objectives of this work was to verify whether the genetic combining ability estimates varied over the years and assessments. As there was a significant difference among the genotypes and among environmental factors (years and assessments), this is a favorable condition to argue whether there was an interaction. It was verified that the SCA estimates presented no significant interaction with years nor with assessments. However, the interactions involving GCA were significant in all cases (Table 1).

Although the GCA interaction with year and assessment period was significant, the g_i estimates varied little among the environments (Table 5). The BR01-18437 parent has always contributed most to reducing the soybean rust severity in the crosses in which it participated, and, in most cases, the BRS 184 cultivar was the parent that most contributed to susceptibility, with high, positive g_i. For the other parents, the fluctuations in the g_i estimates were not very expressive as well. It is possible to estimate the parameters that assess the combining ability in a single year and one assessment (preferably 30 DAD) (Ribeiro et al., 2007) to obtain information that can be extrapolated, and that would be sufficient for further selecting soybean parents for hybridization programs for their resistance to Asian soybean rust. This fact contrasts with observations made of other soybean traits, such as yield and days to maturity, for which there is great inconsistency among the parameters estimates due to genotype x environment interaction (Lopes et al., 2001; Rossmann, 2001).

The data presented indicated that, in the genetic control of resistance to Asian soybean rust, estimated in terms of disease severity (percentage of leaf area infected by the pathogen), the effects of dominance or endogamy were less important than the additive effects. There are other reports in the literature that corroborate these results according to which dominance was not important in soybean rust control (Arias et al., 2007; Ribeiro et al., 2007). The superiority of GCA over SCA was also reported for other soybean diseases, such as frogeye spot, caused by the *Cercospora sojina* pathogen (Gravina et al., 2003). Cho & Scott (2000) observed similar result for other traits.

The interaction of treatments with the environments (year or time of assessment), although significant, did not alter the genetic parameter estimates, which indicates that the estimates obtained can be extrapolated for this kind of study. Thus, a single assessment can be made at 30 DAD, the best assessment time to discriminate the treatments (Ribeiro et al., 2007).

Table 4. Estimates of the general and specific combining abilities of *Phakopsora pachyrhizi* severity of the soybean parents and F_2 and F_3 populations joint analysis, 30 and 37 days after detecting the pathogen (DAD) in the 2006/2007 and 2007/2008 crop seasons[(1)].

Parent	F_2	F_3
	General combining ability	
BR01-18437	-5.60A	-2.78A
BRS 184	2.48C	1.90B
BRS 231	0.58B	0.22B
BRS 232	0.43B	0.58C
Embrapa 48	2.10C	0.08D
Crosses	Specific combining ability	
BR01-18437 x BRS 184	0.04	0.12
BR01-18437 x BRS 231	-0.74	-0.72
BR01-18437 x BRS 232	0.39	0.10
BR01-18437 x Embrapa 48	0.31	0.50
BRS 184 x BRS 231	1.09	1.04
BRS 184 x BRS 232	-0.67	-0.48
BRS 184 x Embrapa 48	-0.46	-0.67
BRS 231 x BRS 232	-0.11	-0.06
BRS 231 x Embrapa 48	-0.24	-0.26
BRS 232 x Embrapa 48	0.39	0.44
	Standard deviation	
SD (s_{ij})	0.29	0.28
SD (s_{ij} - s_{ik})	0.48	0.46
SD (s_{ij} - s_{kl})	0.34	0.33
SD (g_i)	0.43	0.21
SD (g_i - g_j)	0.68	0.33

[(1)]Data transformed to arc sin $(x/100)^{0.5}$. Means followed by equal letters on the same column do not differ by the standard deviation of the difference between the two compared parents.

Table 5. Estimates of the general and specific combining abilities of *Phakopsora pachyrhizi* severity of the soybean F_2 and F_3 populations, 30 and 37 days after detecting the pathogen (DAD) in the 2006/2007 and 2007/2008 crop seasons[(1)].

Parent	2006/2007		2007/2008		2006/2007		2007/2008	
	30 DAD	37 DAD	30 DAD	37 DAD	30 DAD	37 DAD	30 DAD	37 DAD
	F_2				F_3			
BR01-18437	-3.37A	-3.51A	-2.76A	-5.67A	-2.34A	-2.41A	-2.29A	-4.07A
BRS 184	1.02B	0.68C	1.23D	4.08D	1.87E	2.26D	1.11D	2.35D
BRS 231	-0.19C	0.93C	0.07B	1.18C	-0.66B	0.65C	-0.26B	1.13C
BRS 232	0.52C	-0.38B	0.59BC	-0.19B	0.30C	-0.30B	0.84CD	1.47C
Embrapa 48	2.03D	2.27D	0.87CD	0.60BC	0.83D	-0.21B	0.59C	-0.89B
SD (g_i)	0.34	0.53	0.34	0.64	0.30	0.48	0.22	0.48
SD (g_i - g_j)	0.53	0.84	0.54	1.01	0.48	0.75	0.34	0.76
Crosses								
BR01-18437 x BRS 184	-0.13	0.35	0.99	-0.46	0.41	-0.07	0.92	-0.46
BR01-18437 x BRS 231	-0.87	-1.24	-0.45	-0.73	-0.88	-1.28	-1.05	0.25
BR01-18437 x BRS 232	0.91	0.31	-0.36	0.48	0.36	0.93	-0.06	-0.93
BR01-18437 x Embrapa 48	0.08	0.58	-0.18	0.71	0.11	0.43	0.19	1.15
BRS 184 x BRS 231	0.73	1.27	0.09	1.45	1.06	1.78	0.55	0.51
BRS 184 x BRS 232	-0.36	-1.50	-0.58	-0.76	-1.14	-1.20	-0.68	1.18
BRS 184 x Embrapa 48	-0.24	-0.12	-0.49	-0.23	-0.33	-0.50	-0.79	-1.23
BRS 231 x BRS 232	-0.28	0.81	0.31	0.02	0.19	-0.15	0.33	-0.54
BRS 231 x Embrapa 48	0.42	-0.84	0.05	-0.74	-0.37	-0.35	0.17	-0.21
BRS 232 x Embrapa 48	-0.27	0.37	0.63	0.26	0.59	0.43	0.42	0.29
SD (s_{ij})	0.46	0.73	0.47	0.87	0.41	0.65	0.29	0.66
SD ($s_{ij} - s_{ik}$)	0.75	1.19	0.76	1.43	0.67	1.07	0.48	1.08

[(1)]Data transformed to arc sin $(x/100)^{0.5}$. Means followed by equal letters on the same column do not differ by the standard deviation of the difference between the two compared parents.

Conclusions

1. The interaction of the F_2 or F_3 segregant soybean populations with the years, although significant, does not alter the genetic parameter estimates, indicating that the estimates obtained in one year can be extrapolated to other years.

2. The interactions between assessments and F_2 or F_3 segregant soybean population do not alter the parameter estimates.

3. A single assessment of severity of *Phakopsora pachyrhizi* can be made 30 days after detecting the pathogen, the best assessment time to discriminate the treatments.

4. The BR01-18437 line confirmed its resistance in all the environments and can be used in breeding programs for resistance to *Phakopsora pachyrhizi*.

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