Joint scaling test to estimate genetic parameters of soybean resistance to frogeye leaf spot

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ABSTRACT

To study the inheritance of soybean resistance to *Cercospora sojina* Hara, genetic parameters were estimated using means and variances of populations derived from a cross between a resistant and a susceptible cultivar, namely, 'Uberaba' and 'Bossier', respectively. The parents and the F_1, F_2, BC_1 and BC_2 generations were evaluated for six characteristics associated with the disease: visually evaluated infection degree; number of lesions per leaflet; lesion mean diameter; percentage of lesioned leaf area, number of lesions per square centimeter and disease index. The additive genetic effect was the most important in the determination of all traits related to soybean resistance to frogeye leaf spot. The infection degree, a subjective trait that considers the set of all resistance related characteristics in its constitution, presented positive variance and lower influence of the environment, consisting in a useful variable in programs of soybean breeding aiming at the resistance to *C. sojina*. All traits presented at least one type (aa, ad or dd) of significant epistatic interaction and the full model (additive + dominant + epistatic) was more adequate to describe the resistance.

KEY WORDS: *Glycine max*, generation analysis, *Cercospora sojina* hara.

INTRODUCTION

In Brazil, diseases are responsible for annual losses of about two billion dollars in soybean (*Glycine max* (L.) Merrill) crop. Amongst these diseases, cercospora leaf spot, also known as frogeye leaf spot, caused by *Cercospora sojina* Hara fungus is distinguished (Yorinori, 1997). It is primarily a foliar disease, but infections also occur on stems, pods and seeds (Sinclair and Backman, 1989). The incidence of the disease is favored by hot and humid environment and its influence on yield reduction derives from the reduction of the photosynthetic area, premature defoliation and damages to the seeds (Akem and Dashiell, 1994).

This disease was responsible for large losses of soybean in Brazil (Yorinori, 1989). Currently, it is under control through genetic resistance and its occurrence is sporadic, being limited to the South (Balsas) of Maranhão State and North (Niquelândia) of Goiás State. More than 23 races have already been identified in Brazil and new epidemics are likely to occur (Yorinori and Klingelfuss, 1999).

Chemical control with fungicides, besides being expensive, is not the most efficient way to control this disease. The use of resistant cultivars is the most economic and efficient control method. Breeding resistant cultivars requires knowledge of the mechanism of inheritance of the character. The evaluation of the nature and magnitude of the genetic effects on characters associated with the resistance to *C. sojina* Hara is of great importance for the breeder that aims at incorporating genes of resistance in cultivated soybeans. It is paramount to investigate, in the genetic fraction, which proportions can be attributed to the additive, dominant and epistatic genetic factors. These evaluations are intimately related with the objectives of the genetic improvement (Cruz and Regazzi, 2001).

Estimates of the relative proportions of the additive, dominant and epistatic genic effects have been reported for several crops, using the most diverse types of hybrids and populations and a varied genetic-statistic procedures. Among other useful methodologies at this stage of improvement there is the generation analysis, based on the study of means and variances (Mather and Jinks, 1982).

The objective of this work was to estimate the genetic parameters associated with the resistance of soybean to *C. sojina* Hara, by means of generation analysis, described by Cavalli (1952) as the joint scaling test.

MATERIAL AND METHODS

An isolate of the race 04 of *Cercospora sojina* Hara fungus, supplied by the National Center for Soybean Research of the Brazilian Agropecuary Research Enterprise - Embrapa, Londrina-PR was used. Inoculation of the soybean plants was carried out in a greenhouse at the Plant Science Department of the Federal University of Viçosa, in Viçosa-MG.

Resistance reactions to the pathogen were studied on the parents and on the F_1, F_2, BC_1 (P_1xF_1) and BC_2 (P_2xF_1) generations. The Bossier (P_1) and Uberaba (P_2) varieties were the susceptible and resistant parents, respectively. Each of these populations was constituted by the following number of plants: P_1 26, P_2 26, F_1 23, F_2 124, BC_1 60 and BC_2 45 plants. A completely randomized statistical design was used.

Multiplication of *C. sojina* isolate was carried out in Petri dishes, containing agar-tomato juice (Superbom) without the spices culture medium, prepared similarly to the V8-agar medium, but substituting V8 by tomato juice. The inoculation was made when the soybean seedlings presented the third trifoliolate leaf completely developed, spraying about 10 ml per plant of a 40,000 conidia per milliliter suspension. Immediately after the inoculation, the pots were taken to a mist chamber for approximately 3 days under 100% relative humidity.

After the establishment of the disease symptoms, 20 days after the inoculation, the following characteristics were evaluated: a) infection degree (ID) – visually evaluating the symptoms and applying the score scale, ranging from1.0 – without apparent infection - to 5.0, the maximum infection degree; b) number of lesions per foliole (NLF) – on the most infected leaflet of the plant; c) lesion mean diameter (LMD) – average of the 10 largest lesions of the most infected foliole, in millimeters; d) Number of lesions per square centimeter (NLC) - by dividing the number of lesions per foliole by the area of the foliole; e) percentage of lesioned foliar area (PLFA) - by dividing the lesioned foliar area by the area of the foliole and multiplying by 100; and f) disease index (DI) - by multiplying the number of lesions per foliole by the square of lesion mean diameter, DI = NLF x LMD2. Items from a to f were evaluated in accordance to the methodology used by Cordeiro (1986), Veiga (1973) and Martins Filho (1999).

The studies of the genetic inheritance of resistance of soybean to *C. sojina* were carried out using the means and variances of the studied populations, applying the joint scaling test of Cavalli (1952), according to Jinks and Jones (1958) and Mather and Jinks (1982). The analyses were carried out with the aid of the computational programs SAS, version 8.0 (SAS Institute-online), using the GLM procedure, and the GENES version 2001 (Cruz, 2001).

RESULTS AND DISCUSSION

The means and variances of each studied character, related to quantification of the resistance to frogeye leaf spot are presented in Table 1. In the majority of the evaluated characters on the resistant parent (Uberaba - P_2) and on the BC_2 and F_1 populations, the means were smaller than those of the susceptible parent (P_1) and the BC_1 and F_2 populations, indicating the presence of dominance in the determination of the resistance to the fungus. Smaller means for F_2 and BC_1 are expected in the presence of dominance, once in these two populations an expression of the recessive alleles occurs. High variance of the mean for some characters was observed, as for number of lesions per foliole (NLF), including the F_1. This high variance, in the case of NLF, can be attributed to the fact that injuries coalesce and make it difficult to evaluate the real number of lesioned points in some leaves. For other analyzed characteristics, lower variances were observed, as in the case of infection degree (ID) which is one of the characteristics considered by some authors as the most reliable, although somewhat subjective.

Table 2 shows, for each studied character, the estimates and the significances of each mean parameter for the complete genetic model, which considers the following effects: mean (m), additive (a), dominance (d) and additive x additive (aa), additive x dominance (ad) and dominance x dominance (dd) epistasis. The estimates of the genetic parameters in this table were calculated proportionally to the mean, which turns the value of the mean into1.00.

The non-allelic interactions, epistasis, were significant for all studied characters in at least one of the types (aa, ad or dd). The three types of epistasis were significant for NLF at 5% of probability, by the t test.

The genetic effect associated with dominance was the one that presented, in relation to the mean of the evaluated character, the highest estimate, except for

PLFA, affecting the estimate of the respective variance.

In selected materials, the additive genetic effect is reduced, this effect being more important in characters of less complex inheritance. In characters of more complex inheritance, the contribution of the genetic effects related to dominance becomes bigger. Characters controlled by dominance effects cannot be

Table 1. Mean $(\hat{m})$, variance $(\hat{\sigma}^2)$ and variance of the mean $[\hat{v}(\hat{m})]$ of characters evaluated in the trial of soybean resistance to *C. sojina* Hara, involving the P$_1$, P$_2$, F$_1$, F$_2$, BC$_1$, and BC$_2$ generations.

Population[2/]	Character[1/]								
	ID			NLF			LMD		
	$(\hat{m})$	$\hat{\sigma}^2$	$\hat{v}(\hat{m})$	$(\hat{m})$	$\hat{\sigma}^2$	$\hat{v}(\hat{m})$	$(\hat{m})$	$\hat{\sigma}^2$	$\hat{v}(\hat{m})$
P$_1$	4.60	0.160	0.0062	139.69	1872.78	72.03	0.348	0.0041	0.00016
P$_2$	1.15	0.027	0.0010	1.46	2.66	0.10	0.060	0.0028	0.00011
F$_1$	1.86	0.450	0.0196	37.43	1976.17	85.92	0.124	0.0029	0.00013
F$_2$	1.81	1.102	0.0089	16.48	803.75	6.48	0.168	0.0149	0.00012
BC$_1$	2.29	1.769	0.0295	16.27	357.55	5.96	0.210	0.0406	0.00068
BC$_2$	1.06	0.035	0.0008	1.07	13.20	0.29	0.020	0.0035	0.00008
Population[2/]	PLFA			NLC			DI		
	$(\hat{m})$	$\hat{\sigma}^2$	$\hat{v}(\hat{m})$	$(\hat{m})$	$\hat{\sigma}^2$	$\hat{v}(\hat{m})$	$(\hat{m})$	$\hat{\sigma}^2$	$\hat{v}(\hat{m})$
P$_1$	23.08	148.6081	5.7157	2.3877	0.5604	0.02156	16.8823	47.9776	1.8453
P$_2$	0.02	0.0005	0.00002	0.0246	0.0008	0.00003	0.0151	0.0003	0.00001
F$_1$	1.41	4.7543	0.2067	0.7294	0.6072	0.02640	0.9738	2.5211	0.1096
F$_2$	2.38	30.3931	0.2451	0.3096	0.2517	0.00203	1.6524	15.7663	0.1271
BC$_1$	10.03	206.0280	3.4338	0.8250	0.8753	0.01459	2.6088	15.6133	0.2602
BC$_2$	0.10	0.1358	0.0030	0.0355	0.0144	0.00032	0.0373	0.0194	0.0004

[1/] ID – Infection degree; NLF – number of lesions per foliole; LMD – lesion mean diameter; PLFA – percentage of lesioned foliar area, NLC number of lesions per square centimeter and DI – disease index; [2/] P$_1$ (Bossier) , P$_2$ (Uberaba), BC$_1$ (F$_1$ x Bossier), BC$_2$ (F$_1$ x Uberaba). P$_1$ (N=26 plants); P$_2$ (N=26); F$_1$ (N=23); F$_2$ (N=114); BC$_1$ (N=60) and BC$_2$ (N=45).

Table 2. Estimates of the parameters, their variance and the t test for the full additive-dominant-epistatic model fitted on the means of six generations of soybean (P$_1$, P$_2$, F$_1$, F$_2$, BC$_1$, BC$_2$) evaluated in the trial of resistance reaction to *Cercospora sojina* Hara.

Parameter	Character								
	ID			NLF			LMD		
	Estimate	Variance	t	Estimate	Variance	t	Estimate	Variance	T
m	1.00	0.2649	6.65[1/]	1.00	146.75	8.41[1/]	1.00	0.00501	5.86[1/]
a	0.50	0.0018	40.64[1/]	0.68	18.03	16.28[1/]	0.35	0.00007	17.71[1/]
d	1.43	1.6933	-3.76[1/]	2.72	888.15	-9.30[1/]	1.68	0.03550	-3.70[1/]
aa	0.16	0.2631	-1.07ns	0.31	128.72	-2.76[1/]	0.51	0.00493	-3.00[1/]
ad	0.29	0.1282	-2.74[1/]	1.06	97.14	-10.94[1/]	0.22	0.00328	1.60ns
dd	0.97	0.7115	3.95[1/]	2.09	619.56	8.54[1/]	0.98	0.01474	3.35[1/]
Parameter	PLFA			NLC			DI		
	Estimate	Variance	t	Estimate	Variance	t	Estimate	Variance	T
m	1.00	19.10	0.18ns	1.00	0.0975	2.30[1/]	1.00	3.5383	5.19[1/]
a	14.41	1.43	9.65[1/]	1.64	0.0054	16.02[1/]	0.86	0.4613	12.42[1/]
d	7.14	152.48	0.46ns	2.29	0.7415	-1.91ns	2.42	21.7825	-5.07[1/]
aa	13.44	17.67	2.56[1/]	0.67	0.0921	1.59ns	0.14	3.0770	-0.75ns
ad	4.00	19.46	-0.73ns	1.08	0.0812	-2.72[1/]	1.20	2.8879	-6.90[1/]
dd	6. 38	65.45	-0.63ns	2.31	0.3982	2.63[1/]	1.52	8.4885	5.10[1/]

[1/] Significant a 5%; ns: non-significant; Parameters: m: mean of homozygous lines derived from F$_2$; a: measure of additive genic effect; d: measure of dominance deviation, aa: measure of additive x additive interaction; ad: measure of additive x dominance interaction; dd: measure of dominance x dominance interaction; Characters: ID: infection degree; NLF: number of lesions per foliole; LMD: Lesion mean diameter; PLFA: percentage of lesioned foliar area; NLC: number of lesions per square centimeter and DI: disease index.

fixed and the exploitation of heterozygosity, in this case, is the only solution (Gamble, 1962; Arias, 1986).

Dominance effects and their epistatic interactions are of lesser significance to autogamous species (Brim and Cockerham, 1961). In this sense, breeding techniques that take advantage of additive and additive x additive epistatic variances for the obtention of bigger genetic gains will be more important to the improvement of soybean aiming at developing resistance to frogeye leaf spot. Amongst the evaluated characters in this study, those that presented additive genic effect and additive x additive type of epistasis in an expressive way (ID and DI) can be used as references in breeding programs.

The partition presented in Table 3 is not orthogonal, but the relative contribution (RC) gives an idea of the importance of a particular genetic effect on the available variability of the studied character. Thus, it can be observed that the most important genetic effect in the determination of the ID character was the additive genetic effect (95.24%) whenever the effect of the mean (that takes the value of 1.0) was not considered; however, the dominance effect was of much smaller importance (0.81%). This fact evidences the possibility of obtaining superior homozygotic materials by means of selection from the generation F_2, and that the gains in the selection cycles will be satisfactory, once the component of additive nature is of high magnitude. Table 3 also shows that, for the ID character, the additive x additive, additive x dominant and dominant x dominant interactions influenced the determination of the means of the studied generations in only 1.40%. Results suggest that the additive-dominant model can explain most of the variations in this character because of the low contribution of the epistatic interaction effects. However, the use of this reduced model is subject to bias, since the ad and dd epistasis were significant (Table 3) and should not be disregarded. This same reasoning can be extended to the other characters.

According to literature review made by Arias (1986), dominance effect and genetic interactions are of lesser importance to autogamous species. However, interactions between non-allelic genes, epistasis, cannot be disregarded in basic genetic mechanisms. Genetic models that neglect epistasis can be somewhat biased (Cockerham, 1954). In the present work, reduction of the complete genetic model to the additive-dominant model significantly ($P < 0.01$, by the F-test) reduced the model sum of square from 11.84 to 30.75 percent.

Despite the great importance of the complete genetic model to describe the means of the generations for a broader knowledge of the causes and magnitudes of the genetic components that control the character, the additive-dominant reduced model can also be evaluated which, besides being simpler, has been routinely used in breeding programs, providing indispensable information on the evaluation of the efficiency of the methods employed and their success.

The estimates and significance of each parameter of the additive-dominant reduced model for the characters evaluated in this experiment are found in Table 4. In all characters, the mean was the parameter of greater estimated value; the dominance genetic effect showed the biggest variance; and all parameter estimates were significantly different from zero at 5% probability, by the t test.

Table 5 shows a study of the evaluation of the adequacy of the additive-dominant model (simpler) by simple linear correlation between the observed and the estimated mean values. It is verified that the additive-dominant model makes possible the attainment of predicted means, which correlates with the observed means in high magnitude for all the analyzed characters, varying from 85.0 % for the character with higher variability (NLF) to 98.0% for PLFA. In the case of ID, considered as the character most important amongst the evaluated ones, 95.0% correlation was observed. These values are equivalent to the determination of 72.0%, 97,0% and 90,0% for NLF, PLFA and ID characters, respectively.

By looking at Table 6, it can be inferred that the use of the additive-dominant genetic model is satisfactory to explain the performance of the generation means, for the characters in study, and that the additive variability, present in F_2, is relatively greater than the dominance deviations for all the evaluated characters. However, as a consensus exists among the researchers (Arias, 1986; Cordeiro et al., 1992; Martins Filho, 1999; Barbieri, 2001) on the use of infection degree (ID) and considering this as a working characteristic, the breeder will be able to get superior homozygotic materials starting from the F_2 generation.

CONCLUSIONS

The additive genetic effect was the most important genetic effect in the determination of all characters of soybean related to frogeye leaf spot resistance.

Table 3. Gauss method non-orthogonal decomposition of the sum of squares (SS) and the relative contribution (RC) of the parameters (m, a, d, aa, ad, dd) for the full model fitted on the means of six generations (P_1, P_2, F_1, F_2, BC_1, and BC_2) of soybean in the trial for resistance to *Cercospora sojina* Hara.

Source of variation	**Characters**					
	ID		**NLF**		**LMD**	
	SS	RC	SS	RC	SS	RC
m/a, d, aa, ad, dd	44.17	2.55	70.68	11.36	34.38	8.94
a/m, d, aa, ad, dd	1651.34	95.24	264.90	42.57	313.54	81.57
d/m, a, aa, ad, dd	14.11	0.81	86.41	13.89	13.69	3.56
aa/m, a, d, ad, dd	1.14	0.07	7.60	1.22	9.01	2.34
ad/m, a, d, aa, dd	7.50	0.43	119.70	19.24	2.56	0.67
dd/m, a, d, aa, ad	15.57	0.90	72.97	11.73	11.20	2.91
Sum	1733.83	100	622.26	100	384.38	100
Source of variation	**PLFA**		**NLC**		**DI**	
	SS	RC	SS	RC	SS	RC
m/a, d, aa, ad, dd	0.03	0.03	5.30	1.88	26.96	9.59
a/m, d, aa, ad, dd	93.07	92.33	256.76	90.87	154.18	54.86
d/m, a, aa, ad, dd	0.22	0.22	3.66	1.30	25.70	9.14
aa/m, a, d, ad, dd	6.55	6.50	2.53	0.90	0.56	0.02
ad/m, a, d, aa, dd	0.53	0.53	7.40	2.62	47.60	16.94
dd/m, a, d, aa, ad	0.40	0.40	6.91	2.45	26.05	9.27
Sum	100.80	100	282.56	100	281.05	100

$^{1/}$ Significant a 5%; ns: non-significant; Parameters: m: mean of homozygous lines derived from F_2; a: measure of additive genic effect; d: measure of dominance deviation, aa: measure of additive x additive interaction; ad: measure of additive x dominance interaction; dd: measure of dominance x dominance interaction; Characters: ID: infection degree; NLF: number of lesions per foliole; LMD: Lesion mean diameter; PLFA: percentage of lesioned foliar area; NLC: number of lesions per square centimeter and DI: disease index.

Table 4. Estimates of the parameters, their variances and the t tests for the reduced additive-dominant model, fitted on the means of six generations of soybean (P_1, P_2, F_1, F_2, BC_1, BC_2) evaluated in the trial for resistance to *Cercospora sojina* Hara.

Parameter	**Characters**								
	ID			**NLF**			**LMD**		
	Estimate	Variance	t	Estimate	Variance	T	Estimate	Variance	t
m	1.00	0.0017	68.55$^{1/}$	1.00	4.14	15.13 $^{1/}$	1.00	0.000056	25.78$^{1/}$
a	0.60	0.0016	42.10$^{1/}$	0.95	4.07	14.51$^{1/}$	0.84	0.000057	21.21$^{1/}$
d	0.62	0.0060	-22.72$^{1/}$	1.04	6.60	-12.04$^{1/}$	0.53	0.000180	-7.15$^{1/}$
Parameter	**PLFA**			**NLC**			**ID**		
	Estimate	Variance	t	Estimate	Variance	T	Estimate	Variance	T
m	1.00	0.50118	10.96$^{1/}$	1.00	0.002 86	17.50 $^{1/}$	1.00	0.1257	12.23$^{1/}$
a	0.99	0.50108	10.94$^{1/}$	0.97	0.00284	17.08$^{1/}$	0.99	0.1258	12.19$^{1/}$
d	0.97	0.52564	-10.41$^{1/}$	0.98	0.00500	-12.95$^{1/}$	0.98	0.1291	-11.90$^{1/}$

$^{1/}$ Significant a 5%; ns: non-significant; Parameters: m: mean of homozygous lines derived from F_2; a: measure of additive genic effect; d: measure of dominance deviation, aa: measure of additive x additive interaction; ad: measure of additive x dominance interaction; dd: measure of dominance x dominance interaction; Characters: ID: infection degree; NLF: number of lesions per foliole; LMD: Lesion mean diameter; PLFA: percentage of lesioned foliar area; NLC: number of lesions per square centimeter and DI: disease index.

Table 5. Observed and estimated means of characters evaluated on plants of six soybean generations (P_1, P_2, F_1, F_2, BC_1, BC_2) in the trial for resistance to *Cercospora sojina* Hara.

Population[2/]	**Character** [1/]					
	ID		**NLF**		**LMD**	
	Observed mean	Estimated mean	Observed mean	Estimated mean	Observed mean	Estimated mean
P_1	4.60	4.52	139.69	60.16	0.3481	0.3537
P_2	1.15	1.12	1.46	1.54	0.0600	0.0330
F_1	1.86	1.07	37.43	-0.13	0.1239	0.0971
F_2	1.81	1.94	16.48	15.31	0.1677	0.1452
RC_1	2.29	2.79	16.27	29.97	0.2100	0.2253
RC_2	1.06	1.09	1.07	0.66	0.0200	0.0650
$R(y_{obs}, y_{est})$		0.95		0.85		0.97
R^2		0.90		0.72		0.94
Population[2/]	**PLFA**		**NLC**		**DI**	
	Observed mean	Estimated mean	Observed mean	Estimated mean	Observed mean	Estimated mean
P_1	23.08	15.50	2.38	1.86	16.882	8.664
P_2	0.02	0.02	0.02	0.025	0.015	0.015
F_1	1.41	0.22	0.73	0.022	0.974	0.064
F_2	2.38	3.99	0.31	0.479	1.653	2.202
RC_1	10.03	7.86	0.83	0.935	2.609	4.364
RC_2	0.10	0.12	0.04	0.024	0.037	0.040
$R(y_{obs}, y_{est})$		0.98		0.91		0.93
R^2		0.97		0.84		0.86

[1/] ID – infection degree; NLF – number of lesions per foliole; LMD - Lesion mean diameter; PLFA – percentage of lesioned foliar area; NLC – number of lesions per square centimeter and DI – disease index; [2/] P_1 (Bossier), P_2 (Uberaba), BC_1 (F_1 x Bossier), BC_2 (F_1 x Uberaba).

Table 6. Gauss method non-orthogonal partition of the sum of squares (SS) and their relative contribution (RC) for the parameters (m, a, d) of the reduced-model fitted on means of six generations (P_1, P_2, F_1, F_2, BC_1, and BC_2) of soybean in the trial for resistance to *Cercospora sojina* Hara.

Source of variation	**Character**					
	ID		**NLF**		**LMD**	
	SS	RC	SS	RC	SS	RC
m/a, d	4700.11	67.25	228.92	39.16	665.06	57.02
a/m, d	1772.55	25.36	210.69	35.03	450.18	38.60
d/m, a	516.08	7.38	145.01	24.80	51.13	4.38
Sum	6988.75	100	584.61	100	1166.36	100
Source of variation	**PLFA**		**NLC**		**DI**	
	SS	RC	SS	RC	SS	RC
m/a, d	120.23	34.53	306.28	39.99	149.73	34.03
a/m, d	119.62	34.36	291.73	38.09	148.70	33.79
d/m, a	108.32	31.11	167.80	21.91	141.53	32.16
Sum	348.18	100	765.80	100	439.97	100

[1/] Significant a 5%; ns: non-significant; Parameters: m: mean of homozygous lines derived from F_2; a: measure of additive genic effect; d: measure of dominance deviation, aa: measure of additive x additive interaction; ad: measure of additive x dominance interaction; dd: measure of dominance x dominance interaction; Characters: ID – infection degree; NLF – number of lesions per foliole; LMD - Lesion mean diameter; PLFA – percentage of lesioned foliar area; NLC – number of lesions per square centimeter and DI – disease index.

Infection degree, a subjective observation that considers the set of all resistance characters in its attribution, presented positive variance and small environmental influence, consisting in a useful variable in soybean breeding programs aiming at the resistance to *Cercospora sojina.*

All characters presented at least one type (aa, ad or dd) of significant epistatic interaction and the full model (additive + dominant + epistatic) was more adequate to describe the resistance.

RESUMO

Teste de Escala Conjunta na Estimação de Parâmetros Genéticos da Resistência da Soja à Cercosporiose

Para estudar a herança da resistência à *Cercospora sojina* Hara em populações de soja, por meio da obtenção de parâmetros genéticos, com base na análise de médias e de variâncias, realizou-se o cruzamento de um cultivar resistente “Uberaba”, com um suscetível “Bossier”. Foram avaliadas seis características das plantas, nos progenitores e nas gerações F_1, F_2, RC_1 e RC_2, associadas com a doença: nota do grau de infecção avaliado visualmente, número de lesões por folíolo, diâmetro médio da lesão, percentagem de área foliar lesionada, número de lesões por centímetro quadrado e índice de doença. O efeito genético mais importante na determinação de todos os caracteres relacionados com a resistência à cercosporiose foi o aditivo. A nota do grau de infecção, uma observação subjetiva que considera o conjunto das características na sua atribuição, apresentou todas as estimativas de variância positivas e menor influência do ambiente, constituindo-se em variável útil em programas de melhoramento da soja visando resistência à *C. sojina.* Todos os caracteres apresentaram pelo menos um dos tipos de interação epistática significativa (aa, ad e dd), sendo mais adequada a avaliação da resistência pelo modelo aditivo-dominante-epistático.

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Received: June 17, 2002;

Accepted: December 08, 2002.