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Combining ability for common bacterial blight resistance in snap and dry bean (*Phaseolus vulgaris* L.)

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ABSTRACT. Common bacterial blight (CBB), which is caused by *Xanthomonas axonopodis* pv. *phaseoli* (Xap), is the main bacterial disease in snap beans and controlling this disease using resistant cultivars is still a challenge. This work aimed to study the combining ability for CBB resistance in *Phaseolus vulgaris* genotypes. Six parents (two genotypes of CBB-resistant dry bean and four susceptible snap bean accessions) were crossed in a complete diallel scheme without reciprocals to estimate the general and specific ability to Xap resistance. CBB resistance was evaluated by the inoculation with two Xap isolates, and its severity was evaluated based on the four following resistance components: area under the disease progress curve; scores in the leaves; latent period and diameter of pod lesion. Differences between the two isolates were observed considering all the disease components. Besides pathogen variability, significant GCA and SCA indicate that additive and non-additive effects are involved in Xap-resistance control for the evaluated genotypes, implying that CBC resistance is a trait with complex inheritance. For breeding purposes, the result demonstrates the need to apply breeding methods that are focused on advanced generations selection.

Keywords: *Xanthomonas axonopodis* pv. *phaseoli*, disease-resistance inheritance, genetic effects, general and specific combining ability.

Capacidade de combinação para resistência ao crestamento bacteriano em feijão comum e feijão-de-vagem (*Phaseolus vulgaris* L.)

RESUMO. O Crestamento Bacteriano Comum (CBC), causado por *Xanthomonas axonopodis* pv. *phaseoli* (Xap) é a principal doença bacteriana na cultura do feijão-de-vagem e o controle a essa doença usando cultivares resistentes é ainda um desafio. Esse trabalho tem como objetivo estudar a capacidade a capacidade combinatória para a resistência ao CBC em genótipos de *Phaseolus vulgaris*. Seis genitores (dois genótipos resistentes de feijão comum ao CBC e quatro acessos suscetíveis de feijão-de-vagem) foram cruzados em um esquema de dialelo completo sem recíprocos para estimar a capacidade geral e específica de combinação para a resistência a Xap. A resistência ao CBC foi avaliada por meio da inoculação com dois isolados de Xap e a severidade avaliada a partir de quatro componentes de resistência: área abaixo da curva de progresso da doença, notas de severidade nas folhas, período latente e diâmetro da lesão em vagens. Diferenças entre os dois isoladas foram observados considerando todos os componentes da doença. Além da variabilidade dos patógenos, CGC e CEC foram significativas, indicando que os efeitos aditivos e não-aditivos estão envolvidos no controle da resistência a Xap para os genótipos avaliados, implicando que a resistência a CBC é uma característica com herança complexa. Para fins de melhoramento, os resultados demonstram a necessidade de aplicar métodos de melhoramento que são focados em seleção de gerações avançadas.

Palavras-chave: *Xanthomonas axonopodis* pv. *phaseoli*, herança da resistência a doença, efeitos genéticos, capacidade geral e específica de combinação.

Introduction

Snap and dry beans are crops that are taxonomically classified in the same botanical species, *Phaseolus vulgaris* L. However, some important differences between these plants are related to plant management and their consumption. In dry bean, the final product is the grain, which is an important protein source for populations in less developed areas in the world. Snap bean sare cultivated as a vegetable crop, and their pods, with a juicy mesocarp and reduced fibre

content are the final products (BLAIR et al., 2010; SOTIRIOU; MAVRONA, 2008).

In Latin America and especially in Brazil, snap beans are primarily cultivated by small farmers who use few traditional climbing varieties and until the early 1980s, only climbing varieties were cultivated. Nowadays, few bush-type cultivars that have been adapted to different Brazilian conditions are available. The bush-type cultivars are derived from few genotypes, and some authors estimate that 76% of the bush snap bean germplasm is derived from the 'Tendercrop', 'Blue Lake' and 'Harvest' varieties (SILBERNAGEL et al., 1991; SOTIRIOU; MAVRONA, 2008; ZAUMEYER, 1972). This restricted genetic variability results in low productivity and high pathogen susceptibility (TRINDADE et al., 2011; VILELA et al., 2009).

Common bacterial blight (CBB), caused by *Xanthomonas axonopodis* pv. *Phaseoli* [Smith] Vauterin*et al.* (Xap), is the main bacterial disease that infects snap beans in many areas of the world (CHAN; GOODWIN, 1999; COYNE; SCHUSTER, 1974; FERREIRA et al., 2003; LIU et al., 2008). The disease occurs in all cultivation environments and proliferates under conditions of high temperature and humidity (SINGH; MUNOZ, 1999). The disease symptoms are brown spots surrounded by a yellowish halo and coalesce to form necrotic lesions on aerial plant organs. During early crop stages, the disease is associated with temperatures between 20 and 30ºC and an alternation between periods of rain and drought (MAHUKU et al., 2006; SAETTLER, 1989).

The most effective, economically viable and environmentally safe strategy for CBB control is the use of resistant cultivars. Unfortunately, no commercial snap bean varieties have been described as CBB resistant until now, and even for dry beans, it is still challenging to obtain resistant cultivars. Obtaining such cultivars demands the identification of sources of Xap resistance in both snap and dry beans as well as an understanding of the inheritance mechanism of this resistance.

One strategy to start a breeding program for disease resistance is the use of diallel crosses, which allows generating many combinations using a set of selected parents. Among diallel analyses approaches, one proposed by Griffing (1956), estimates the general and specific combining ability (GCA and SCA, respectively). The GCA is result of the average performance of each parent when crossed with other one while SCA represents the behaviour of two individuals (parents) in a number of hybrid combinations. Yet, GCA is related to additive effects while SCA is associated with non-additive effects (dominance and epistatic).

In dry beans, many sources of Xap resistance have been identified, and different types of molecular tools have been used to identify and study quantitative trait loci (QTL) that are associated with CBB resistance (DUNCAN et al., 2011; MAHUKU et al., 2006; MIKLAS et al., 2003; SINGH; SCHWARTZ, 2010; TAR'AN et al., 2001; VANDERMARK et al., 2008). However, few reports have described the inheritance of CBB resistance in snap beans (FERREIRA et al., 2003; FERREIRA et al., 2004; RODRIGUES et al., 1999; SANTOS et al., 2003). The aim of this research was to study the combining ability of six *Phaseolus vulgaris* parents, being four susceptible snap bean and two resistant dry bean genotypes, and their hybrids for CBB resistance.

Material and methods

Selecting parents and obtaining the F1

Four snap bean accessions coded as UENF 1482, UENF 1486, UENF 1487 and UENF 1579 (Table 1) based on previous results of germplasm evaluation (TEIXEIRA et al., 2004; TRINDADE et al., 2012) were selected. Two resistant dry beans genotypes, namely BAC 6 and PI 207262, which were previously used in snap bean breeding by Rodrigues et al. (1999), were also used in crosses considering a complete diallel scheme without reciprocals between July and October 2008 and February and May 2009, resulting in 15 F_1 hybrids.

Table 1. Description of the six parents of *Phaseolus vulgaris* L. used in the diallel crosses.

Genotypes	Flower color	Pods color	Seeds color	Cross section of the pod	Days to flowering
Dry bean (resistance to common bacterial blight)					
PI 207262	White	Green	Beige	Flat	41
BAC-6	White	Green	Beige	Flat	44
Snap bean					
UENF 1482	Purple	Yellow	Black	Flat	54
UENF 1579	Purple	Green	White	Elliptical	50
UENF 1487	White	Green	White	Flat	49
UENF 1486	White	Green	White	Flat	45

Evaluation of the resistance to the common bacterial blight in the F_1 generation

The evaluation of the F_1 plants and their parents for CBB resistance occurred in a greenhouse from May to September 2009. A randomised-block experimental design was adopted, and three replications and six pots for each genotype were used per experimental plot. The six parents and their 15 F_1 hybrids were assessed under inoculation by the

Xap isolates 1394-98 and 775-90, isolated from bean seeds, in 1998, and from bean plant, in 1990, respectively, were provided by the Instituto Biológico de São Paulo State, Brazil. These two isolates were used to represent genetic variability from different seasons and plant parts. The accessions were cultivated in 5-L pots with a substrate that was composed of 50 soil, 30 cattle manure and 20% sand.

Xap inoculation in the leaves was performed 25 days after planting. The isolates were cultivated separately in Petri dishes that contained solid DYGS medium (in g L^{-1}: dextrose, 2.0; bacteriological peptone, 1.5; yeast extract, 2.0; K_2HPO_4, 0.5; $MgSO_4.7H_2O$, 0.5; glutamic acid, 1.5 and agar, 18.0, pH 7.0) according to Rodrigues Neto et al. (1986) and Souza et al. (2008). After 36 hours, the bacterial colonies were suspended in distilled water, and the cell concentration was adjusted to 10^8 colony forming units per millilitre (cfu. mL^{-1}) using a spectrophotometer at 640 nm; the cells were diluted to 10^7 cfu. mL^{-1} for use on the same day. A trifoliate leaf was selected from each pot for inoculation. Two leaflets from each trifoliate leaf were previously identified by wool-yarn strings of different colours that were tied to the leaflet and indicated the strain that would be used. Each leaflet was inoculated with one of the Xap isolates (1394-98 or 775-90) by means of two 2-cm cuts that were made with scissors that were previously immersed in the bacterial suspension.

The pod inoculation was performed 45 days after planting during the beginning of pod filling. Two pods were selected from each pot and were previously identified by the presence of wool-yarn strings, which indicated which strain would be used to inoculate the pods. Each pod was inoculated with a different Xap isolate (1394-98 or 775-90) through the insertion of a hypodermic needle following method proposed by Rodrigues et al. (1999).

To evaluate the reaction to Xap in the leaves, daily assessments were performed for 30 days according to the following diagrammatic scale, and this variable was denominated Score: 1 = without symptoms, 2 = 1 to 5% necrosis, 3 = 6 to 25% necrosis, 4 = 26 to 50% necrosis and 5 = above 50% necrosis. The scores that were determined by the evaluation of the CBB advance in the leaves were used to calculate the area under the disease progress curve (AUDPC) (CAMPBELL; MADDEN, 1990). The response to Xap in the pods was evaluated by measuring the lesion diameter (DLP) in millimetres, which was measured with a high-precision calliper ruler from the point at which the needle was inserted. This evaluation was performedten days after the inoculation using the following classification (RODRIGUES et al., 1999): resistant = $0 < x \leq 1$ mm, moderately resistant = $1 < x \leq 2$ mm, moderately susceptible = $2 < x \leq 3$ mm, susceptible = $3 < x \leq 4$ mm and highly susceptibl e= $x > 4$ mm. In addition to these data, the latent period (LP) for the leaf inoculation (days between the leaf inoculation and the appearance of the symptoms) and the average of the scores for CBB progress in the leaves during the assessment period were recorded. During the experiment, the mean temperature was 27ºC and the relative air humidity was approximately 85%.

Statistical analyses and combining ability analysis

The method 2 of the diallel analysisthat was proposed by Griffing (1956) was used based on the average of the replications, which includes the parents and the F_1's and employs Model B, in which the effect of the genotypes is considered to be fixed. This model is represented as follows:

$$Y_{ij} = m + g_i + g_j + s_{ij} + \bar{\varepsilon}_{ij},$$

where:

in which Y_{ij} is the average value of the hybrid combination ($i \neq j$) or of the parent ($i = i$), m is the general average of all of the treatments, g_i refers to the effect of the general combining ability of the parent i, g_j refers to the effect of the general combining ability of the parent j, s_{ij} refers to the specific combining ability for the crossing of the parents i and j and $\bar{\varepsilon}_{ij}$: refers to the average experimental error. The analyses were performed with Genes software system (CRUZ, 2006).

Results and discussion

Differences between the two isolates were observed considering all the evaluated variables (AUDPC, Score, LP and DLP). The mean values for AUDPC and Score were higher for isolate 1394-98 (Table 2). For LP and DLP, higher average values were observed for isolate 775-90.These differences showed the complexity of this pathosystem and how difficult is to identify superior genotypes for CBC resistance.

The genotype significantly affected ($p < 0.01$) all of the evaluated traits (Table 2). The GCA and SCA displayed significant effects ($p < 0.05$) for all resistance components that were evaluated except when considering isolate 775-90, which was not significant for GCA in terms of LP and also for SCA in DLP (Table 2). The significant GCA and SCA indicate that additive and non-additive effects are involved in Xap-resistance control for the

evaluated genotypes, implying that CBC resistance is a trait with complex inheritance. For breeding purposes, the result demonstrates the need to apply breeding methods that are focused on advanced generations selection, in which we can select recombinant lines more efficiently since loci for the disease resistance will be fixed during inbreeding. Rodrigues et al. (1999) evaluated the inheritance of CBB resistance in the leaves and pods of snap and dry bean genotypes and only observed significant GCA effects for resistance in the leaves, while significant GCA and SCA effects were observed for Xap resistance in the pods. Silva et al. (2000) evaluated the CBB responses of common bean genotypes in the leaves using an unbalanced diallel model and observed GCA values of high magnitude for Xap resistance. In most of the evaluated crosses, by means of the SCA effects, the partial dominance of the CBB susceptibility of bean plants was observed in the leaves.

Table 2. Analysis of variance for the general (GCA) and specific (SCA) combination ability and average of the squares of the GCA and SCA effects for four components of resistance to bacterial blight (AUDPC = area under the disease progress curve; Score = average of the scores attributed to the advance of the disease over time; LP = Latent period; DLP = diameter of the lesion in pods in mm) evaluated in six parents and 15 F_1 hybrids of *Phaseolus vulgaris* L. inoculated by the isolates 1394-98 and 775-90 of *Xanthomonas axonopodis* pv. *phaseoli*.

SV	DF	Components of Resistance			
		AUDPC		Score	
		1394-90	775-90	1394-90	775-90
Replications	2	166.69	377.38	0.09	0.40
Genotype	20	36.17**	49.23**	0.05**	0.18**
GCA	5	77.70**	69.48**	0.11**	0.25**
SCA	15	22.33**	42.48**	0.03**	0.16**
Error	40	5.43	6.64	0.007	0.06
Mean		60.82	57.22	2.28	2.21
CV		3.83	4.50	3.58	10.71
		Quadratic components			
GCA		3.01	2.62	0.004	0.008
SCA		5.63	11.95	0.007	0.03
SV	DF	Components of Resistance			
		LP		DLP	
		1394-90	775-90	1394-90	775-90
Replications	2	4.17	19.01	0.02	0.70
Genotype	20	0.91**	1.46*	0.48**	1.63**
GCA	5	1.02**	1.30^{ns}	1.18**	3.59**
SCA	15	0.88**	1.51*	0.25**	0.98^{ns}
Error	40	0.18	0.78	0.06	0.53
Mean		10.93	13.35	2.41	3.42
CV		3.87	6.60	10.27	21.32
		Quadratic components			
GCA		0.035	0.022	0.047	0.13
SCA		0.23	0.24	0.06	0.15

The means of the squares of the SCA effects were higher than the averages of the GCA effects for the resistance components AUDPC, LP and Score. For DLP, higher square mean effect values were observed for SCA, however, these values were not significantly different from the GCA effects (Table 2). This result indicates the prevalence of non-additive effects in relation to the GCA effects for of the CBB-resistance components. Although the averages of the squares of the effects for GCA and SCA expressed prevalence of non-additive effects in relation to the GCA effects for all the components of resistance to CBB, Cruz et al. (2004) and Pereira et al. (2007) pointed out that the superiority of the quadratic component associated with SCA is common in diallels in which there is a previous selection for the character under study, which reduces the differential for the additive effects and increases the relevance of the non-additive effects. However, it is important to point out that, although the averages of the squares of the non-additive effects for resistance to Xap prevail, the significance and magnitude of the mean squares of the additive effects in the analysis of variance demonstrated higher influence of additive genes in the response to CBB (Table 2), increasing the possibility to achieve genotypes highly resistant to CBB in advanced generations. Ferreira et al. (2003), while comparing components of variance related to resistance to CBB in leaves of bean plants between the generations F_2 and F_7, observed increased heritability based on the average of families of 26.85% in F_2 for 91.77% in F_7, which proves the possibility of increased resistance to CBB with the advance of the segregant generations.

The estimates of the GCA effects ($\hat{g}_i$) revealed a lower AUDPC magnitude in the parents BAC 6, UENF 1487 and UENF 1486at the time of the inoculation with isolate 1394-98. For 775-90, negative $\hat{g}_i$ values were observed for AUDPC in the parents PI 207262 and BAC 6 (Table 3), which indicates that these genotypes contributed to the reduction of AUDPC and eventually to the increase the resistance level. The same result was observed for variable Score, i.e those two genotypes contributed for reduce the value of this variable. The values differed only for the negative estimate of $\hat{g}_i$, which was observed when the parent UENF 1487 was inoculated with isolate 775-90 (Table 3).

Positive values of $\hat{g}_i$ for LP were estimated when BAC 6, UENF 1579 and UENF 1487 genotypes were inoculated with 1394-98 and also for PI 207262 and BAC 6 when inoculated with 775-90. Negative estimates of $\hat{g}_i$ for DLP were observed when PI 207262, BAC 6 and UENF 1482 parents were inoculated with isolate 1394-98. The same parents displayed also negative estimates of $\hat{g}_i$ for isolate 775-90 along with UENF 1579 parent (Table 3). The results obtained for accessions UENF 1482 and

UENF 1579 corroborates with the data that demonstrate that the CBB-resistance genes in leaves are different from those that control CBB resistance in pods (ARNAUD-SANTANA et al., 1994; RODRIGUES et al., 1999; SANTOS et al., 2003) because these parents did not present high $\hat{g}_i$ estimates in the leaves (Table 3). The use of these accessions in combination with the common bean genotypes that are CBB-resistant in the leaves is highly recommended to generate snap bean genotypes that are Xap-resistant in advanced generations. The occurrence of negative $\hat{g}_i$ effects in PI 207262 and BAC 6 corroborates the existence of CBB-resistant genes in these genotypes.

Table 3. Estimates of the effects of general combination ability ($\hat{g}_i$) and standard deviations (SD) between two parents for four components of resistance to common bacterial blight (AUDPC = area under the disease progress curve; Score = average of the scores attributed to the advance of the disease over time; LP = Latent Period; DLP = diameter of the lesion in pods) evaluated in six parents of *Phaseolus vulgaris* L. intercrossed in diallel and inoculated with the isolates 1394-98 and 775-90 of *Xanthomonas axonopodis* pv. *phaseoli*.

Genitors	Components of resistance			
	AUDPC		Score	
	1394-98	775-90	1394-98	775-90
PI 207262	0.4479	-0.5221	0.0325	-0.0517
BAC 6	-3.1746	-3.1708	-0.1200	-0.1542
UENF 1482	1.9254	1.1367	0.0688	0.1183
UENF 1579	1.4179	1.4329	0.0463	0.0096
UENF 1487	-0.3308	0.2679	-0.0125	-0.0279
UENF 1486	-0.2858	0.8554	-0.0150	0.1058
SD (g_i-g_j)	0.6727	0.7437	0.0236	0.0684
Genitors	Components of resistance			
	LP		DLP	
	1394-98	775-90	1394-98	775-90
PI 207262	-0.0950	0.0688	-0.3729	-0.5304
BAC 6	0.2638	0.3900	-0.0179	-0.0904
UENF 1482	-0.2963	-0.3125	-0.0167	-0.0767
UENF 1579	0.0425	-0.1313	0.0171	-0.1517
UENF 1487	0.1838	-0.0063	0.0721	0.2396
UENF 1486	-0.0988	-0.0088	0.3183	0.6096
SD (g_i-g_j)	0.1223	0.2543	0.0716	0.2102

The estimates of $\hat{s}_{ii}$ for AUDPC and Score were positive for all parents that were evaluated for both isolate (with the exception of PI 207262) (Tables 4 and 5). For the variable Score, a different behaviour was observed for each isolate. Considering 1394-98, all of the parents displayed positive $\hat{s}_{ii}$ signals with the exception of PI 207262, while UENF 1482 and UENF 1486 parents presented negative $\hat{s}_{ii}$ values for 775-90 (Tables 4 and 5). Negative $\hat{s}_{ii}$ values were observed for LP in almost all parents for both isolates. The exceptions were PI 207262 for the two isolates and UENF 1579 inoculated with 775-90, although this genotype expressed a low $\hat{s}_{ii}$ magnitude. These results obtained for LP is closely related with AUDPC, which demonstrate that a higher LP can reduce the initial pressure of the pathogen (JEGER; VILJANEN-ROLLINSON, 2001). As for DLP, inoculation with 1394-98 resulted in $\hat{s}_{ii}$ values positive and of low magnitudes for all parents, which indicate predominance of additive genetic effects controlling the plant reaction to this isolate. For strain 775-90, negative effects among the parents were predominant with the exception of the UENF 1579 and UENF 1487 genotypes (Table 5).

Table 4. Estimates of the effects of specific combining ability ($\hat{s}_{ii}$ and $\hat{s}_{ij}$) achieved for four components of resistance to common bacterial blight (AUDPC = area under the disease progress curve; Score = average of the scores attributed to the advance of the disease over time; LP = Latent period; DLP = diameter of the lesion in pods) evaluated in six parents and 15 hybrids of *Phaseolus vulgaris* L. inoculated by the isolate 1394-98of *Xanthomonas axonopodis* pv. *phaseoli*.

Hybrids[1/]	Components of resistance			
	AUDPC	Score	LP	DLP
PI 207262	-2.8054	-0.0621	1.1457	0.1611
PI 207262 x BAC 6	-1.7629	-0.0796	-0.7731	0.1461
PI 207262 x UENF 1482	1.9771	0.0517	-0.2630	-0.0052
PI 207262 x UENF 1579	3.7346	0.1242	-0.8817	-0.0389
PI 207262 x UENF 1487	1.5634	0.0429	-0.3030	-0.0539
PI 207262 x UENF 1486	0.0984	-0.0146	-0.0706	-0.3701
BAC 6	2.9496	0.1129	-0.1318	0.1511
BAC 6 x UENF 1482	-0.6504	-0.0258	0.0382	-0.2002
BAC 6 x UENF 1579	-2.3929	-0.0833	0.5894	0.0361
BAC 6 x UENF 1487	-1.0641	-0.0346	0.2882	0.0011
BAC 6 x UENF 1486	-0.0291	-0.0021	0.1207	-0.2852
UENF 1482	4.3296	0.1654	-0.2918	0.3286
UENF 1482 x UENF 1579	-3.1628	-0.1121	0.4294	0.2648
UENF 1482 x UENF 1487	-2.4942	-0.0933	0.4582	-0.3101
UENF 1482 x UENF 1486	-4.3292	-0.1509	-0.0793	-0.4064
UENF 1579	1.6746	0.0604	-0.1893	0.0811
UENF 1579 x UENF 1487	-1.6566	-0.0608	-0.0505	-0.3339
UENF 1579 x UENF 1486	0.1284	0.0116	0.2920	-0.0902
UENF 1487	1.2621	0.0479	-0.4118	0.2611
UENF 1487 x UENF 1486	1.1271	0.0504	0.4307	0.1749
UENF 1486	1.5021	0.0529	-0.3468	0.4886

Large variation was observed among the hybrids in relation to the magnitude and signal of the $\hat{s}_{ij}$ values. For the crosses in which the parents had negative $\hat{g}_i$ values for AUDPC, the combinations BAC 6 x UENF 1487, BAC 6 x UENF 1486, UENF 1482 x UENF 1579, UENF 1579 x UENF 1487 and UENF 1579 x UENF 1486 for both isolates and the UENF 1579 x UENF 1487 for isolate 775-90 displayed negative $\hat{s}_{ij}$ values. For the variable Score, the crosses UENF 1482 x UENF 1579, UENF 1482 x UENF 1487 and UENF 1482 x UENF 1486 were noteworthy because they contained negative $\hat{s}_{ij}$ values and were derived from three parents with high and negative $\hat{g}_i$ values, which indicate that these genotypes contributed to reduce the disease in crosses, meaning less disease and more plant resistance.

Table 5. Estimates of the effects of specific combining ability ($\hat{s}_{ii}$ and $\hat{s}_{ij}$) achieved for four components of resistance to common bacterial blight (AUDPC = area under the disease progress curve; Score = average of the scores attributed to the advance of the disease over time; LP = Latent period; DLP = diameter of the lesion in pods) evaluated in six parents and 15 hybrids of *Phaseolus vulgaris* L. inoculated by the isolate 775-90 of *Xanthomonas axonopodis* pv. *phaseoli*.

Hybrids[1/]	Componentsofresistance			
	AUDPC	Score	LP	DLP
PI 207262	-0.9539	0.0200	0.2339	-0.5854
PI 207262 x BAC 6	-2.3551	-0.0575	0.7526	-0.5854
PI 207262 x UENF 1482	2.6673	0.0100	0.1751	0.8409
PI 207262 x UENF 1579	3.2011	0.1288	-1.2361	0.4259
PI 207262 x UENF 1487	-3.3839	-0.0938	0.6989	0.0846
PI 207262 x UENF 1486	1.7786	-0.0275	-0.8586	0.4046
BAC 6	0.8736	0.0650	-0.1285	-0.6154
BAC 6 x UENF 1482	0.1461	-0.0775	0.1839	0.3708
BAC 6 x UENF 1579	1.8499	0.1013	-0.1073	0.7058
BAC 6 x UENF 1487	-0.0652	0.0287	-0.6723	0.5246
BAC 6 x UENF 1486	-1.3226	-0.1250	0.1001	0.2146
UENF 1482	5.5085	-0.0100	-1.1636	-0.2329
UENF 1482 x UENF 1579	-4.9577	-0.2712	0.3751	-0.2579
UENF 1482 x UENF 1487	-5.2926	-0.2738	0.9101	-0.7592
UENF 1482 x UENF 1486	-3.5802	0.6325	0.6826	0.2708
UENF 1579	3.2461	0.1775	0.0239	0.1071
UENF 1579 x UENF 1487	-3.4989	-0.1150	0.4589	-0.6442
UENF 1579 x UENF 1486	-3.0864	-0.1988	0.4614	-0.4442
UENF 1487	5.6661	0.2525	-0.6161	0.1846
UENF 1487 x UENF 1486	0.9086	-0.0512	-0.1636	0.4246
UENF 1486	2.6511	-0.1150	-0.1111	-0.4354

The highest $\hat{s}_{ij}$ effects for LP were observed in the crosses UENF 1482 x UENF 1487 and UENF 1487 x UENF 1486 inoculated with 1394-98 and the crosses UENF 1482 x UENF 1579, UENF 1482 x UENF 1487 and UENF 1482 x UENF 1486 for isolate775-90 (Tables 4 and 5).

Focusing on the crosses among the PI 207262, BAC 6 and UENF 1482 genotypes, which contained negative $\hat{g}_i$ estimates for both isolates, for DLP negative $\hat{s}_{ij}$ values were observed in the following combinations: PI 207262 x UENF 1486, BAC 6 x UENF 1486, UENF 1482 x UENF 1487 and UENF 1482 x UENF 1486 for isolate 1394-98; and the crosses UENF 1482 x UENF 1579 and UENF 1482 x UENF 1487 for isolate 775-90. However, the crosses UENF 1579 x UENF 1487 and UENF 1579 x UENF 1486 were also noteworthy due to their high $\hat{s}_{ij}$ values for DLP.

Conclusion

Based on our results, it can be concluded that the snap bean genotypes UENF 1486 and UENF 1487 achieved the highest-ranked CBB resistance in the leaves, and they can be recommended along with the common bean genotype BAC 6 to obtain Xap-resistant snap bean cultivars. The complexity observed in this experiment for the inheritance of CBB resistance in snap bean, controlled by additive and non-additive gene effects, indicates the need to use breeding methods focused on parental control and selection in advanced generations of inbreeding, in order to obtain CBB resistant genotypes.

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