

Estimate of general and specific combination capacity between two tomato groups for production of hybrids resistant to bacterial wilt

ABSTRACT

To estimate the combining abilities between two groups of tomato genotypes for the production of resistant hybrids to bacterial wilt. The experiments were carried out in phytobacteriology Laboratory and in greenhouse at Department of Agronomy of Federal Rural University of Pernambuco, between June and September 2016. A parental group was composed by the cultivars Yoshimatsu and Hawaii 7996 while the second group consisted of 10 lines and the cultivars IPA-6 and Santa Clara. The diallel analysis was according to the method of Geraldi and Miranda Filho, type G2, estimating the general (GCA) and specific (SCA) combination capacity besides the genetic parameters estimative. The crosses that showed the highest performance for resistance were the hybrids Yoshimatsu with the line L04 and Hawaii 7996 with the L125, because they obtained a positive CEC for the period of latency and negative for the other characters. It was observed that non-additive effects are involved in the four resistance components and that the additive effects are involved for bacterial wilt index (BWI), incidence (INC) and area under the disease progress curve (AUDPC). For the genetic parameters of BWI and the latency period with the isolate CRM 74 and AUDPC for the isolates CRM 74 and CRM 77 had the coefficients of genotype variation above the coefficient of environmental variation, with CVg/CVe above 1.0 and high genetic variance. The highest heritability was in AACP for both isolates with 88.24% and 75.90% respectively. The L125 line presented greater CGC to main resistance components for the main resistance components for CRM 74 and CRM77 isolated. The hybrid YOS x L04 combination stood out for having a higher CEC.

Keywords: *Solanum lycopersicum*. *Ralstonia pseudosolanacearum*. Crossing species mix

1. INTRODUCTION

The tomato (*Solanum lycopersicum* L.) is cultivated in all Brazilian regions, being the solanaceae most produced in the world, losing only to potato (*Solanum tuberosum* L.). In Brazil 3.7 million tons of tomatoes were produced in 2016, with an average yield of 63.8 t ha⁻¹, including tomatoes for the processing and consumption industry [1].

In the North and Northeast of Brazil, bacterial wilt is the main disease of the tomato, limiting its planting in several areas. Especially in the Northeast, the disease is more severe in plantations during rainy summers and in protected crops. Therefore, the need to develop genetically improved tomato cultivars with resistance to diseases for cultivation in the humid tropics of Brazil is immense [2].

There are no tomato cultivars with an adequate level of resistance and agronomic characteristics that the market requires. The resistance being strongly influenced by environmental conditions and linked to other undesirable characteristics such as nematode and Begomovirus susceptibility, besides small fruits and with concentric cracks [3].

Seed companies provide producers with cultivars resistant to bacterial wilt, but without desirable commercial characteristics indicating their use as graft holder. Despite the existence of these genotypes, some authors affirm that the use of resistant graft holder does not dispense complete resistance [4].

36 In Brazil, tomato production has been undergoing great technological transformations standing out
37 highlighting the use of hybrid cultivars, bringing the increase of desirable quantitative traits including
38 resistance to diseases [5]. To obtain hybrids with resistance to the disease, it is necessary to identify
39 the source to determine the genetic control, to establish strategies and to estimate the efficiency of
40 use of this source, in breeding programs [6].

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42 For the development of hybrid combinations with high potential, it is necessary to identify the genetic
43 lineages with good combining capacity, based on estimates of the general (GCA) and specific (SCA)
44 of combining ability [7].

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46 The GCA is related to the additive allele effects [8], representing the average behavior of the parents
47 in hybrid combinations whereas the SCA is related to the non-additive gene effects, characterizing the
48 deviations of hybrid combinations in relation to the average behavior of the parents [9]. The better
49 hybrid combination is the one with the highest SCA, where at least one of the parents has a higher
50 GCA and is divergent from the parent. According to previous literature, the resistance to *R.*
51 *pseudosolanacearum* in tomato was controlled by more than one gene or a gene block with
52 dominance [3].

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54 We aim was to estimate the general and specific of combining ability between two groups of tomato
55 genotypes to produce hybrids with resistance to bacterial wilt, in addition to the estimation of other
56 related genetic parameters.
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2. MATERIAL AND METHODS

The experiments were conducted in at Phytobacteriology Laboratory and in a greenhouse of the Department of Agronomy of the Federal Rural University of Pernambuco (UFRPE) in Recife-PE, with an average temperature of $26 \pm 5^{\circ}\text{C}$ and relative humidity of $80.4 \pm 5.5\%$.

The bacterial wilt resistant cultivars "Hawaii 7996" and "Yoshimatsu" were used as testers in Group I. Ten lines with the highest level of resistance to bacterial wilt (L04, L12, L42, L49, L53, L79, L82, L120, L125 and L128) and the two susceptible cultivars IPA -6 and Santa Clara were used as female genotypes in Group II, resulting in 24 F1 hybrids.

CRM74 and CRM77 isolates, both belonging to phylotype I and sequevar 18 of *R. pseudosolanacearum*, were obtained from cultures collection of at Rosa Mariano of the Phytobacteriology Laboratory of the Federal Rural University of Pernambuco.

Seedlings were produced in polystyrene trays with 128 cells, containing commercial substrate based on pine bark, peat, charcoal, vermiculite and enriched with NPK and micronutrients. In order to obtain enough pollen to perform the crossings, the proportion of pollinator plants for female plants was 1: 4. Testers were sown two weeks before the female plants to ensure availability of pollen from the start of the crossing operation.

After 21 days, the seedlings were transplanted in pots (5 L) containing coconut powder. The nutritional requirements were supplied with nutrient solution, according to the stage of development of the plants, daily through a pressurized drip system. The plants were conducted vertically and with only one main stem for the female parents and without sprout removal for the male parents, favoring a greater number of flowers.

The essential activities of removal of sepals, emasculation of flowers on the female parents (ten lines) and collection of pollen from male parents (testers) were done prior to hybridization. Hybridization was performed manually, by brushing the pollen grains on the surface of the stigma of the emasculated flower, repeating the process for two consecutive days. The pollinated flowers were marked with appropriate label with date, time and name of corresponding male parent.

Unused flowers were removed from the plant. The fruits from the crossings were harvested mature and the seeds extracted manually, the period between pollination and fruit harvest was on average 45 days.

Seeds of the hybrids and the parents were again planted following the same methodology as described above for lines and testers. The germinated seedlings were transplanted within 21 days to plastic pots of 500 ml with commercial substrate and soil containing earthworm, humus and coconut powder in the ratio of 1: 1.

For the preparation of the bacterial suspensions, the isolates were recupered from water preservation and cultured in TZC medium [10] for 48 h at $30 \pm 2^{\circ}\text{C}$ and transferred to agar nutrient-dextrose-yeast extract medium. The concentration of bacterial suspension was adjusted to 5×10^8 CFU (colony forming units) per ml in photocolorimeter (Analyzer 500 M, Brazil). All isolates were previously tested for pathogenicity in seedlings of IPA-6.

After a week of inoculation, when the roots developed symptoms of disease characteristic a half-moon cut, about two centimeters above the transition zone between the root and the stem of the plant was excised with the aid of a stiletto. A liquid (water) suspension of 15 ml was added to the infected tissue samples to collect bacterial suspension.

The experiment design is completely randomized with factorial split plot ($3 \times 10 \times 2 \times 2$), with three replications, with 10 strains, two suscetibile cultivars (IPA-6 and Santa Clara), two resistance cultivars (Hawaii 7996 and Yoshimatsu) and the 24 hybrids inoculated with the two bacterial isolates CRM 74 and CRM 77. Each plot consisted of four pots with one plant each.

The evaluations were performed daily for 15 days on the incidence and severity of the disease (SEV) using a descriptive scale of scores varying from 0 to 4 [11], where: 0 = absence of symptoms, 1 = plants with 1/3 of the wilted leaves, 2 = plants with 2/3 of the wilted leaves, 3 = totally wilted plants 4 = dead plants.

Following components of disease resistance were determined according to the data obtained:

a) **Bacterial Wilt Index** (BWI) at 15 days [12] was calculated by the formula: $BWI = \sum [(C \times P) / N]$, where C = symptom score given in each class; P = number of plants in each class of symptom and N = total number of inoculated plants;

b) **Incidence** (INC) of the disease, determined by the percentage of infected plants in relation to the total inoculated plants;

c) **Latency Period** (LP 50) determined by the number of days required for the onset of wilt in 50% of inoculated plants [13];

d) **Area Under the Disease Progress Curve** (AUDPC) calculated by the expression: $AUDPC = [\sum (y_i + y_{i+1}) / 2 \cdot d_{ii}] / n$, where y_i and y_{i+1} are the values observed in the severity of consecutive measurements and d_{ii} is the interval between evaluations [14].

The data collected were submitted to analysis of variance, considering the fixed model. Experimental hybrids were analyzed according to the diallel scheme according to the methodology of [15], type G2 analysis of Top cross with lines and testers, estimating of the general (GCA) and specific (SCA) of combining ability. The significance of the analysis of variance for GCA and SCA were tested by the F test. Genetic parameters were also estimated as phenotypic, genotypic and environment variability, genotypic and environmental coefficient of variation, ratio between the genotypic and environmental coefficient of variation, and broad-sense heritability. **Statistics analysis** was performed through the Genes program [16].

3. RESULTS AND DISCUSSION

Estimates of the mean squares relative to the contrast between the group of testers and the group of female parents showed a significant difference by the F test ($P = .01$) for all resistance components and for each of the isolates (Table 1) indicating that the genotypes used have different expressions according to the variation of the pathogen.

About the mean squares estimates of the combination SCA were significant by the F test ($P = .01$ or $P = .05$) for all characteristics evaluated with the two isolates (Table 1).

Estimates of GCA mean squares for the group of testers (**Group I**) with the CRM 74 isolate were significant for all variables, except for INC. For the female parents (Group II) only the variable LP 50 did not present significance. The ACG CRM 77 isolate showed mean squares of the testers (Group I) significant only for the AACPD and ACG of the female progenitors as well as (group II) for the INC and AACPD (Table 1).

The significance for GCA and SCA indicates the existence of variability between the effects of GCA ($\hat{g}_i$), associated with additive gene effects, and between the effects of **SCA** ($\hat{S}_{ii}$ and $\hat{S}_{ij}$), associated with non-additives [17]. The result obtained presupposes that the performance of the hybrids depends on both the ACG and the FA of the parents.

Table 1. Estimation of the mean squares of the general (GCA) and specific (SCA) of combining ability, mean and coefficient of variation (CV) for four components of bacterial wilt resistance for two isolates of *Ralstonia pseudosolanacearum*.

SV	DF	Mean Squares							
		CRM 74 Isolate				CRM 77 Isolate			
		BWI ⁽¹⁾	INC ⁽²⁾	LP 50 ⁽³⁾	AUDPC ⁽⁴⁾	BWI ⁽¹⁾	INC ⁽²⁾	LP 50 ⁽³⁾	AUDPC ⁽⁴⁾

Treatments	37	2.92**	4580.68**	94.90**	161.39**	2.98**	4864.27**	101.65**	133.22**
Groups (IxII)	1	24.80**	43924.22**	936.16**	1052.27**	27.21**	46783.63**	1067.30**	966.74**
GCA Group I	1	2.58*	527.34 ^{ns}	27.09*	201.75*	0.47 ^{ns}	104.17 ^{ns}	25.01 ^{ns}	200.54*
GCA Group II	11	1.03*	1549.81**	7.93 ^{ns}	74.13*	1.08 ^{ns}	1710.86**	8.06 ^{ns}	52.03*
SCA	24	2.89*	4499.40**	102.54**	161.95*	2.95**	4761.28**	107.50**	132.89**
Residual	74	0.47	396.75	6.69	35.30	0.7	425.32	8.16	49.97
Mean		2.17	78.08	8.70	16.37	2.11	77.69	10.12	13.90
CV (%)		31.61	25.51	29.72	36.28	38.88	26.55	28.22	50.81

* and ** significant at the 5% and 1% levels, respectively, of the probability by the F test and "ns" not significant by the F test. T: testers; F: female parents. (1) BWI: Bacterial wilt index; (2) INC: incidence; (3) LP 50: latency period; (4) AUDPC: Area under the disease progress curve.

For the CRM 74 isolate the mean squares for the BWI and AUDPC parameters were significant for the GCA and SCA of the testers and female parents, revealing the existence of variability resulting from the additive and non-additive gene action in the expression. The results favored the non-additive gene effects of studied parameters, since the mean squares of the SCA were superior to those of the GCA of the testers and the female parents for BWI, INC and LP 50, and superior to those of the female parents for AUDPC. For the isolated CRM 77, the variables BWI and LP 50 had their mean squares significant only for FA, predominating the nonadditive gene effects, this is, dominance.

Coefficients of variation presented values from 25.51% to 36.28% for the isolate CRM 74 and from 26.55% to 50.81% for the isolate CRM 77 (Table 1). It is noteworthy that the differences between treatments were highly significant for all variables, showing that the differences between treatments exceeded the experimental error. This is because the character of resistance to bacterial wilt is controlled by several genes being highly influenced by the environment contributing to raise the coefficient of variation [3].

Previous authors observed similar results with very high coefficients in identifying tomato progenies with resistance to bacterial wilt with a LP 50 of 34.55% [13] and a coefficient of variation from 18.76% to 29.00% for INC when studying the adaptability and stability of tomato in soil infested with *R. solanacearum* [2].

Hybrids should be produced from parents with positive and high magnitude GCA estimates for the LP 50 variable, unlike that required for BWI, INC and AUDPC.

The average GCA estimates of the four resistance components for the 12 genotypes inoculated with two bacterial isolates are presented in table 2. Several lines showed negative GCA indexes for IMB, INC and AACPD, demonstrating the capacity to contribute to the increase of resistance to bacterial wilt.

Table 2. Estimates of general combining ability (GCA) effects for four bacterial wilt resistance components in 14 tomato genotypes for two isolates of *Ralstonia pseudosolanacearum*.

Genotypes (̂i)	CRM 74 Isolate				CRM 77 Isolate			
	BWI	INC	LP 50	AUDPC	BWI	INC	LP 50	AUDPC
Yoshimatsu	0.16	2.34	-0.53	1.50	0.07	1.04	-0.51	1.45
Hawaii 7996	-0.16	-2.34	0.53	-1.50	-0.07	-1.04	0.51	-1.45
L04	-0.36	-18.75	-0.53	-2.77	-0.42	-20.83	-0.75	-2.69

L12	-0.39	-17.37	-0.53	-3.04	-0.41	-18.06	-1.08	-2.60
L42	0.04	2.08	-0.42	0.50	0.28	6.94	-0.36	1.99
L49	0.26	9.75	-0.59	2.01	0.05	2.78	-0.02	0.12
L53	0.11	2.08	0.52	0.79	0.06	4.17	0.14	0.83
L79	-0.08	4.86	0.69	-0.89	0.31	6.94	0.31	1.45
L82	-0.09	6.97	0.19	-0.97	0.09	6.94	-0.69	0.95
L120	0.04	-0.70	0.41	0.01	0.13	6.94	0.31	1.35
L125	-0.25	-4.87	1.30	-2.10	-0.21	-4.17	1.09	-1.66
L128	0.32	7.63	-0.98	3.54	-0.09	-1.39	0.92	-1.28
IPA - 6	0.01	3.47	0.25	1.00	0.01	5.56	0.48	-0.38
Santa Clara	0.28	4.86	-0.31	1.94	0.21	4.17	-0.36	1.93

BWI: Bacterial wilt index; INC: incidence; LP 50: latency period; AUDPC: Area under the disease progress curve.

According to [18] when GCA is negative and of high magnitude, demonstrates the highest positive potential of the investigated disease resistance trait contribution to progenies when used in crossing. The L04 and L12 lines showed the highest negative effects of GCA for BWI, INC and AUDPC parameters in both bacterial isolates. The L04 line was highlighted with the largest contribution to decrease INC (-18, 75) for the CRM 74 isolate and to decrease the BWI (-0.42), INC (-20.83) and AUDPC (-2.69) parameters for the CRM 77 isolate (Table 2).

For LP 50 the lines L79 (0.69) and L125 (1.30) showed the highest and positive values for the isolate CRM 74 and the lines L125 (1.09) and L128 (0.92) for the isolate CRM 77, with greater ability to transmit favorable alleles for the expression of character.

The L125 line with the CRM 74 isolate, in addition to the high and positive estimate of GCA effects for PL 50 (1.30), had its negatives estimates for IMB (-0.25), INC (-4.87) and AACPD (-2.10). This fact presents a good concentration of alleles that are favorable to the increase of days in which 50% of the plants exhibit symptoms of wilt and that there is no concentration of favorable alleles to increase the other characters. Similar observations were described with the lines L125 and L128 inoculated with the isolate CRM 77, indicating that the crossing made with these lines are important in contributing in resistance to bacterial wilt in tomato.

The isolate CRM 74 for the lines L49, L42 and L128 presented negative estimates of GCA for LP 50 and positive estimates for BWI, INC and AUPDC. Such values favor undesirable allelic frequency for those who are looking for materials that favor resistance. Similar results were observed for L49, L42 and L82 lines when inoculated with the CRM 77 isolate.

Low absolute SCA values mean that the F1 hybrids obtained between the parents in crossing behaved as expected based on the GCA of the parents. While high absolute values of SCA demonstrate that the behavior of a particular crossing is relatively better or worse than expected from the GCA of the parents [19].

According to [8] the better hybrids are those that have high effects of the SCA, positive or negative, depending on the traits interest, and that originate from the cross in which one of the parents has a high GCA. It is noteworthy that not always two parents of high overall combining ability when the crusaders resulted in the best hybrid.

SCA of the crosses of the lines with the testers positive and negative values were observed for all components of resistance to bacterial wilt, demonstrating that there are genes that increase the expression of the character as by others that reduce it (Table 3).

Table 3. Estimates of specific combining ability (SCA) effects for four bacterial wilt resistance components in 14 tomato genotypes for two *Ralstonia pseudosolanacearum* isolates.

Genotypes ($\hat{S}_{ij}$)	CRM 74 Isolate	CRM 77 Isolate
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	BWI	INC	LP 50	AUDPC	BWI	INC	LP 50	AUDPC
YOS x L04	-0.08	-17.16	9.40	-3.13	-0.23	-23.73	9.09	-3.20
YOS x L12	-0.97	-35.22	-6.27	-6.24	-0.91	-34.84	-6.24	-6.29
YOS x L42	0.68	28.67	-1.38	6.85	0.98	40.16	1.04	6.73
YOS x L49	0.88	37.67	1.45	6.71	0.38	19.33	1.70	2.23
YOS x L53	1.03	20.33	1.67	7.52	0.70	34.61	0.54	7.90
YOS x L79	0.22	17.56	4.51	0.62	1.12	31.83	2.37	6.02
YOS x L82	0.11	28.11	2.01	0.88	0.76	23.50	0.37	6.90
YOS x L120	0.35	14.78	4.78	-0.90	0.80	31.83	1.37	7.13
YOS x L125	0.22	27.28	2.90	-0.18	-0.27	9.61	4.92	-3.24
YOS x L128	0.32	14.78	1.17	3.68	0.19	-1.50	5.42	-0.25
YOS x IPA-6	0.79	18.95	2.28	6.85	-0.16	16.55	5.20	-3.14
YOS x SC	1.20	25.89	0.51	10.03	1.22	34.61	-0.96	10.55
HAW x L04	-0.67	-29.14	-7.33	-3.50	-0.76	-29.98	-7.60	-3.31
HAW x L12	0.11	-5.53	8.33	-1.48	-0.02	-7.75	6.40	0.14
HAW x L42	0.18	8.36	3.89	-0.40	0.87	17.25	2.01	5.50
HAW x L49	0.84	30.02	0.39	5.78	0.52	21.42	2.68	2.50
HAW x L53	0.11	16.69	4.61	0.07	0.26	11.69	4.51	-0.33
HAW x L79	0.13	30.58	2.44	0.25	0.84	25.58	3.35	4.04
HAW x L82	0.22	28.47	2.94	-0.31	0.31	33.91	1.35	1.17
HAW x L120	0.51	11.13	1.06	5.35	0.44	25.58	4.35	2.52
HAW x L125	-0.53	-18.03	6.50	-3.80	0.12	3.36	3.90	0.86
HAW x L128	1.65	44.47	-0.89	14.93	0.16	25.58	2.74	-0.61
HAW x IPA-6	0.29	23.63	2.89	1.60	0.90	35.50	1.18	5.87
HAW x SC	0.61	22.25	2.44	2.16	0.36	11.69	4.01	1.44

BWI: Bacterial wilt index; INC: incidence; LP 50: latency period; AUDPC: Area under the disease progress curve.
YOS: Yoshimatsu; HAW: Hawaii 7996; SC: Santa Clara.

It was observed that the hybrid YOS x L12 presented the highest negative values of SCA magnitude for three resistance components: BWI, INC and AUDPC in both isolates. This fact is observed in the CGC values of strain L12 for such characters with the greatest negative effects for BWI, INC and AUDPC.. with the isolate CRM 74 and the second largest negative GCA effect of the same three characters with the isolated CRM 77.

The BWI variable, the greatest negative effects of SCA were observed on the crossing YOS x L12, HAW x L04 (-0.67) and HAW x L125 (-0.53) for CRM 74 isolate and between HAW x L04 (-0.76) and YOS x L125 (-0.27) for the CRM 77 isolate. When Comparing CGC and BWI, it was observed that L04, L12 and L125 lines appear with the greatest negative effects, indicating that the additive gene effects also contributed to the good performance of these combinations for the two isolates.

In relation to the INC variable, the greatest negative effects of SCA were observed again in the YOS x L12 hybrid with a value of -35.22 for CRM 74 isolate and a value of -34.84 for CRM 77 isolate, in addition of the hybrid combination HAW x L04 with the second major negative effects of -29.14 and -29.98 for SCA with the isolates CRM 74 and CRM 77 respectively. In addition to the major negative effects of SCA, the L04 and L12 lines presented high and negative GCA values for both isolates (L04 = -18.75 and -20.83, L12 = -17.37 and -18.06 for CRM 74 and CRM 77 isolates respectively).

For the variable LP 50, the YOS x L04 and HAW x L12 hybrids with the CRM 74 isolates (9.40 and 8.33) and CRM 77 (9.09 and 6.40) presented the highest positive values of SCA. For this variable, it was observed that there was no significant difference in the estimation of mean squares with respect to GCA of the female parents besides the effects of GCA negative for LP 50 but it was observed that the lines L04 and L12 participated in the hybrid combination with the highest values of SCA, behaving differently than expected since they presented negative GCA estimates which may have a contribution of non-additive gene effects on the formation of higher hybrids for this variable.

According to [7], tomato hybrids with high SCA and the parents with low or negative GCA estimates were observed due to the major role of non-additive gene effects in determination of the characteristic in relation to the additive gene effects.

With respect to the AUDPC variable, both additive and non-additive gene effects were present, yet with non-additive gene effects with a greater magnitude in relation to GCA in the group of female parents. However, the hybrid combination YOS x L12 had the highest negative effect of SCA (-6.24 and -6.29) with both isolates. In addition, the L12 lineage was highlighted with a greater contribution towards decreasing the AUDPC with values of -3.04 and -2.60 for CRM 74 and CRM 77 isolates respectively.

The crossings that presented the greatest potential for resistance were the YOS x L04 with the two isolates and HAW x L125 with the isolate CRM 74, since they were the only ones with positive SCA for LP 50 and negative for the other characters, presenting intermediate to superior values. In addition to a high value for SCA, at least one of the parents had a high GCA value, which is desirable in these crosses.

In the literature, there are few results on the combining ability of tomato genotypes for resistance to diseases, especially in relation to bacterial wilt. However, it was observed in this study that the gene expression of the resistance phenotype in tomato is due to the action of additive and non-additive gene effects. Thus in which the non-additive gene effects are involved in the four resistance components and that the additive effects are involved for BWI, INC and AUDPC.

The components of phenotypic, genotypic and environmental variance, as well as broad-sense heritability, genotypic and environmental coefficient of variation and the ratio between the genotypic and environmental coefficient of variation are shown in table 4.

Table 4. Estimates of heritability and variance components for bacterial wilt resistance in tomato.

	Characters ⁽¹⁾							
	CRM 74 isolate				CRM 77 isolate			
	BWI	INC	LP 50	AUDPC	BWI	INC	LP 50	AUDPC
σ_F^2	0.77	417.48	10.25	100.04	0.67	416.87	7.07	69.10
σ_G^2	0.61	285.23	8.02	88.27	0.45	275.10	4.35	52.45
σ_E^2	0.16	132.25	2.23	11.77	0.22	141.77	2.72	16.66
CV_G (%)	36.11	21.63	32.55	57.38	31.68	21.35	20.61	52.12
CV_e (%)	31.61	25.51	29.72	36.28	39.11	26.69	28.23	50.60
CV_G/CV_e	1.14	0.85	1.10	1.58	0.81	0.80	0.73	1.03
h^2_a (%)	76.65	68.38	78.26	88.24	66.58	65.99	61.53	75.90

BWI: Bacterial wilt index; INC: incidence; LP 50: latency period; AUDPC: Area under the disease progress curve.

σ_F^2 - phenotypic variance; σ_G^2 - genotypic variance; σ_E^2 - environmental variance; CV_G - genetic coefficient of variation, CV_e - environmental coefficient of variation; CV_G/CV_e - ratio between the genotypic; h^2 - environmental coefficient of variation and heritability.

The estimated values of the genotypic variance were higher than the environmental variance for all the resistance components studied and for both bacterial isolates. This indicates that there are favorable conditions for genotype selection and breeding for the studied trait, indicating a high importance of the genetic components in comparison of the environmental components [6].

The environmental coefficient of variation indicates besides the magnitude of the experimental precision, the fluctuation within the blocks. The values obtained for the environmental coefficient of variation for the four characters evaluated were greater than 20%, ranging from 25.51% for INC with

CRM 74 isolate to 50.60% for AUDPC with CRM 77 isolate, showing that the resistance to bacterial wilt is influenced by environmental conditions.

The genetic coefficient of variation is used to make inferences and compare the genetic variability existing in different genotypes, environments and characters [20]. The genetic coefficient of variation ranged from 21.63% to 57.38% for the isolate CRM 74 and from 20.61% to 52.12% for the isolate CRM 77. According [21] values above 25% indicate that the genotypes have high potential for the selection of the character studied and significant selection gains.

Values greater than 1.0 were observed for the CVg / CVe ratio for almost all the resistance components studied with the isolate CRM 74, except for the INC. Regarding CRM 77 isolate only the AUDPC variable was higher than 1.0. Although the values were from 0.73 for the two isolates, indicating that the selection for these characters presents more favorable conditions in terms of immediate genetic gains.

The highest ratio of CVg / CVe (1.58) was observed for AUDPC with CRM 74 isolate, and a ratio greater than 1.0 for the CRM 77 isolate, indicating that the selection for this character presents conditions in terms of immediate genetic gains. The CVg / CVe ratio reflects the predominance of genetic effects expressed for the characters evaluated, and there is a very favorable situation to obtain gains in the selection when the CVg / CVe ratio is greater than unity and, therefore, provides a favorable situation for the improvement of its selection [22].

The CVg / CVe ratio results indicated that AUDPC for the two isolates presented the best indexes, with the highest genetic contribution in the phenotypic manifestation. For the LP 50 variable with the CRM 77 isolate, there was the greatest contribution of environmental factors, which requires more stringent selection.

It is important to emphasize that heritability is one of the most important genetic parameters, since it reflects how much of the phenotypic values are due to genetic causes, it quantifies the fraction of inheritable variation that can be explored, indicating the possibility of success with selection [23].

Broad-sense heritability values were moderate to high, varying from 68.32% to 88.24% for CRM 74 isolate and from 61.53% to 75.90% for CRM 77 isolate. The heritability values stood out for the AUDPC variable for both isolates with 88.24% and 75.90% respectively. It was observed that the heritability values of the resistance components were higher in the use of the isolate CRM 74 in comparison to the isolate CRM 77.

The heritability is of great importance in the selection of superior genotypes because it expresses the reliability of the phenotypic value as estimator of the genotypic value, the greater the heritability the greater the genetic gain by selection, indicating that the selection of genotypes has great probability of expression in the next generation [24].

However, the BWI and LP 50 characters with CRM 74 isolate and AUDPC for both isolates can be selected by simple methods, such as mass selection, since the genotype coefficients of variation were above the environmental coefficient of variation, with CVg / CVe above of 1.0 and high genetic variance. In the selection of the remaining characters, a more precise methodology should be adopted, because the genotype coefficient of variation was considered low.

4. CONCLUSION

The L125 line presented greater GCA to main resistance components for isolated CRM 74 and CRM77. The hybrid YOS x L04 combination stood out for a higher SCA.

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