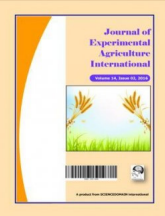

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Estimate of General and Specific Combination Ability in Tomato for Production of Hybrids Resistant to Bacterial Wilt

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Authors' contributions

This work was carried out in collaboration between all authors. Author AQM designed the study, wrote the protocol. Author DM guided the research. Author IDEC performed the statistical analysis. Authors AMFS and AOA provided guidance in phytotopathology. Authors EFFF, LBL and GGM participated in the execution of the experiment. All authors read and approved the final manuscript.

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ABSTRACT

To estimate the combining ability, two groups of tomato genotypes for the production of resistant hybrids to bacterial wilt were evaluated. The experiments were carried out in phyto bacteriology laboratory and in greenhouse facility of the department of agronomy at Federal Rural University of Pernambuco, between June and September 2016. A parental group with wilt resistant cultivars Yoshimatsu and Hawaii 7996 as testers and the second group consisted of 10 lines and the two susceptible cultivars IPA-6 and Santa Clara. The diallel analysis was according to the method of Geraldi and Miranda Filho, type G2, employed in estimating the general (GCA) and specific (SCA) combining ability and other genetic parameters. The crosses that showed the highest performance

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for resistance were the hybrids of Yoshimatsu with the line L04 and Hawaii 7996 with the L125, because they were observed with a positive SCA for the period of latency (LP-50) and negative for the other characters studied. It was observed that additive effects were involved for bacterial wilt index (BWI), incidence (INC) and area under the disease progress curve (AUDPC) and non-additive effects were involved for all the four resistance components (BWI, INC, LP-50 and AUDPC) studied. The genetic parameters of BWI and LP-50 for the isolate CRM 74 and AUDPC for the isolates CRM 74 and CRM 77 had coefficients of genotype variation above the coefficient of environmental variation, with a CVg/CVe above 1.0 and a high genetic variance. The highest heritability was in AUDPC for both isolates with 88.24% and 75.90% respectively. The L125 line presented greater GCA to main resistance components for the main resistance components for CRM 74 and CRM77 isolated. The hybrid Yoshimatsu x L04 combination stood out with a higher SCA.

Keywords: Solanum lycopersicum; Ralstonia pseudosolanacearum; crossing species mix.

1. INTRODUCTION

The tomato (*Solanum lycopersicun* L.) is cultivated in all Brazilian regions.In Brazil, 3.7 million tons of tomatoes were produced in 2016, with an average annual yield of 63.8 t ha^{-1}, including tomatoes used 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 cultivation in several areas. Especially in the Northeast, the disease is more severe in rainy summers and in protected crops. Therefore, there is immense need to develop genetically improved tomato cultivars with resistance to diseases for cultivation in the humid tropics of Brazil [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 fruit size and fruits with concentric cracks [3].

Seed companies provide producers with cultivars resistant to bacterial wilt, but without desirable commercial characteristics. Despite the existence of these genotypes, some authors affirm that the use of resistant cultivars as roots stocks in generating cultivars by vegetative means by grafting for complete resistance and better fruit quality [4].

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

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

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

Our aim was to estimate the general and specific of combining ability in tomato lines (ten) and testers (2 resistant cultivars) offering resistance in comparison to two susceptible cultivars in estimating gentic components controlling the resistance to bacterial wilt, by studying the chosen two groups of tomato genotypes with differential resistance to produce hybrids.

2. MATERIALS AND METHODS

The experiments were conducted in 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 ± 5ºC and relative humidity of 80.4 ± 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 collections at Rosa Mariano of the Phytobacteriology Laboratory of the UFRPE.

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 trrained vertically and with only one main stem for female parents and without sprout removal for the male parents, favoring a greater number of flowers for pollinations.

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 when 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 in 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 recuperated from water preservation and cultured in TZC medium [10] for 48 h at 30 ± 2ºC and transferred to agar nutrient-dextrose-yeast extract medium. The concentration of bacterial suspension was adjusted to $5X10^8$ 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 caracteristics resembling 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 knife. A liquid (water) suspension of 15 ml was added to the infected tissue samples to collect bacterial suspension.

The experimental design was completely randomized with factorial split plot (3X10X2X2), with three replications, with 10 lines, 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 in each pot.

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 = Σ [(C x 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 = $[\Sigma (y_i + y_{i+1}) / 2.d_{ti}]/n$, where y_i and y_{i+1} are the values observed in the severity of consecutive measurements and d_{ti} 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 methodology of [15], type G2 analysis of Top cross with lines and testers, estimating general (GCA) and specific (SCA) 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 by using the Genes software 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 having differential expressions due to variation of the pathogen strain.

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

For estimates of GCA, the mean squares for the group of testers (Group I) with the CRM 74 isolate were significant for all variables studied, except for INC. For the female parents (Group II) only the variable LP 50 did not present significance in difference. The GCA estimates for CRM 77 isolate showed significant differences for variable AUDPC mean squares of the testers (Group I) and the female progenitors and ten lines (group II) for the INC and AUDPC (Table 1).

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

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 different only for SCA, predominating the nonadditive gene effects, and this is considered as dominance.

The coeficient of variation (CV) was ranging 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 the 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 CV % in identifying the tomato progenies with resistance to bacterial wilt with a LP 50 of 34.55% [13] and a CV ranging from 18.76% to 29.00% for INC when studying the adaptability and stability of tomato in soil infested with *R. solanacearum* [2].

Present rsults revealed that 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.

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

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 BWI, INC and AUDPC, demonstrating the capacity to contribute to the increase of resistance to bacterial wilt.

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 [18]. 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 decreased INC (-18, 75) for the CRM 74 isolate and to decreased BWI (-0.42), INC (-20.83) and AUDPC (-2.69) parameters for the CRM 77 isolate (Table 2).

For LP 50 parameter, 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 LP 50 (1.30), had its negatives estimates for IMB (-0.25), INC (-4.87) and AUDPC (-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 expression of other characters. Similar observations were made with the lines L125 and L128 inoculated with the isolate CRM 77, indicating that the crossing made with these lines are important in contributing 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 indicate 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 demonstrates that the behavior of a particular crossing is relatively better or worse than expected from the GCA of the parents [19].

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 [8]. It is not always two parents of high overall combining ability resulted in the best hybrid.

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	CRM 74 Isolate				CRM 77 Isolate			
(ĝi)	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

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

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

The BWI variable was observed with, the greatest negative effects of SCA in YOS x L12, HAW x L04 (-0.67) and HAW x L125 (-0.53) for CRM 74 isolate and in HAW x L04 (-0.76) and YOS x L125 (-0.27) for the CRM 77 isolate. When Comparing GCA and SCA for 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 to 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).

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			
	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
YOSx 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
YOSx 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
HAWx L120	0.51	11.13	1.06	5.35	0.44	25.58	4.35	2.52
HAWx L125	-0.53	-18.03	6.50	-3.80	0.12	3.36	3.90	0.86
HAWx L128	1.65	44.47	-0.89	14.93	0.16	25.58	2.74	-0.61
HAWx PA-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

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 negatively for LP 50 but it was observed that the lines L04 and L12 participated in the hybrid combinations 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 in the formation of higher quality 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 comparison to the additive gene effects.

With respect to the AUDPC variable, both additive and non-additive gene effects were present, with a greater magnitude of non-additive gene effects in comparison to GCA in the group II (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 cross that presented the greatest potential for resistance was YOS x L04 with the two isolates and HAW x L125 with the isolate CRM 74, because these 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.

There are very few literature reports on the combining ability of tomato genotypes for resistance to wilt disease. However, it was observed in the present study that the gene expression of the resistance phenotype in tomato is due to the combined action of additive and non-additive genes. The non-additive gene effects are involved in all the four resistance components and the additive effects are involved for BWI, INC and AUDPC only.

The components of phenotypic, genotypic and environmental variance, 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^2_F	0.77	417.48	10.25	100.04	0.67	416.87	7.07	69.10
σ^2_G	0.61	285.23	8.02	88.27	0.45	275.10	4.35	52.45
σ^2_E	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^2_F - phenotypicvariance; σ^2_G - genotypicvariance; σ^2_E environmentalvariance; 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 to the environmental components [6].

The environmental coefficient of variation indicates 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. The values that were above 25% indicate genotypes with high potential for studied character selection and significant selection gains [21].

Values greater than 1.0 were observed for the CVg / CVe ratio for almost all the resistance components studied for the isolate CRM 74, except for the INC.For CRM 77 isolate only the AUDPC variable was higher than 1.0. The CVg / CVe values were ranging from 0.73 to 1.58 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 and 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 have greatest 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.

COMPETING INTERESTS

Authors have declared that no competing interests exist.

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