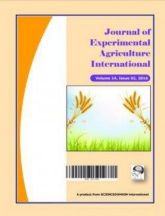

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Identification of Lines of Tomato Resistant to Bacterial Wilt

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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.

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ABSTRACT

The objective of this study was identifying lines of tomato plants resistant to the bacterial wilt**.** The work was accomplished was developed in the Laboratory of Bacteriology and in the greenhouse at Department of Agronomy of Federal Rural University of Pernambuco, during the months of August and September 2016. The experiment design was completely randomized in the factorial 30x3 with three repetitions. The treatments consisted of 30 genotypes submitted to three *Ralstonia solanacearum* isolates. The components were consistent after inoculation, in which the incidence of the disease was quantified. The data were submitted to analysis of variance and the averages were grouped by the Scott-Knott test at 5% probability, they were still obtained phenotypic, genotypic and environmental correlations and dendrogram of dissimilarity. Considering the bacterial wilt index, eight lines were classified as resistant. It was possible to observe high phenotypic, genotypic and environmental correlation coefficients between resistance components, demonstrating that the

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resistance and susceptibility characteristics are genetic and influenced by environmental conditions. It was observed through dissimilarity the formation of four groups and four subgroups, in which the "I" group was composed of four witnesses of resistance, which was resistant and moderately resistant strains. It was possible to observe that the results indicate that eight lines can be used in crosses to obtain hybrids resistant to bacterial wilt. The latency period can use as a reference in the selection of materials with resistance to *Ralstonia pseudosolanacearum*. The lineages that stood out for resistance to bacterial wilt were: L04, L42, L49, L53, L82, L120, L125 and L128.

Keywords: Solanum lycopersicum L.; Ralstonia pseudosolanacearum; resistance; dissimilarity.

1. INTRODUCTION

The tomato (*Solanum lycopersicum* L.), belongs to the family Solanaceae, is among the oleraceous of greater economic importance in the global market, both in value and in volume sold, being the second most produced solanaceae in the world, mainly the high technology in the cultivations and the development of new cultivars [1].

Despite the great productive potential of the cultivars on the market, the species has a high susceptibility to various pathogens such as bacteria, fungi and viruses, which can harm the development of culture and commit to full production [2].

In Brazil, due to the tropical climate, there are many diseases caused by bacteria, among which stands out the bacterial wilt that has as causal agents Ralstonia solanacearum *Ralstonia pseudosolanacearum* and *Ralstonia syzygii*, but the latter species does not occur in the country [3,4].

The entry of the pathogen into the plant occurs through wounds or through micro-injuries, such as the points at which emerge the secondary roots and partially exfoliated cells from the outer layer of the parenchyma, following the colonization of the timber vessel and consequent obstruction, which hinders the flow of water and nutrients to the plant [5].

The symptom of the disease is the wilting of older leaves to the younger leaves, especially during the hottest times of the day, developing into all the leaves [6]. Other symptoms that can be seen after the longitudinal section of the lower part of the plant, is the darkening of the xylem, due to degradation of walls and cells of the adjacent parenchyma, resulting in cavities in the phloem, spinal cord and cortical tissue [7].

There are no cultivars that meet the characteristics required by the market as fruit size, post-harvest time and firmness, at the same time, have wide resistance to bacterial wilt. Because hybrids available on the market provide incomplete resistance, varying effectiveness depending on the bacterial isolate and environmental condition [6].

Control of bacterial wilt is extremely difficult, especially when environmental conditions are favorable for disease and also due to the complexity involved in the survival of the pathogen in the soil and its wide host range [8]. According [9] for disease control, it is necessary to perform a set of measures such as grafting with resistant material, crop rotation, proper handling of irrigation, isolation of early foci of the disease, planting area with no history of bacteriosis.

As stated by [10], the development of genetically improved tomato cultivars is extremely important for cultivation in the humid tropics of Brazil that express the bacterial wilt resistance caused by the complex character *R. solanacearum*, being one of the largest components of the control strategies. The Hawaii 7996 and Yoshimatsu cultivars stand out as a source of resistance and can be used in breeding programs.

According [10] in evaluation of advanced progenies of the Yoshimatsu group, is resistant to bacterial wilt in favorable conditions for the development of the disease. As stated by [11], in the evaluation of 35 resistance sources in 12 countries were identified the locus of specific quantitative resistance of isolates in populations of Hawaii 7996.

Knowledge of the nature and magnitude of the correlations of bacterial wilt resistance components are of fundamental importance and may conduct studies to assess the genotypic, phenotypic and environmental correlations [12], allowing you to select indirectly. Only the genetic portion of phenotypic correlations is used to guide breeding programs, because it represents

the only component of hereditary nature and can be used on the orientation of research, being relevant separate and quantify the genetic and environmental correlations [13].

This study aimed to evaluate the resistance level of 30 tomato genotypes to three isolates of *R. pseudosolanacearum*, through the estimation of the resistance components and phenotypic, genotypic and environmental correlation coefficients.

2. MATERIALS AND METHODS

The experiments were conducted in a greenhouse of the Department of Agronomy at the Federal Rural University of Pernambuco (UFRPE), Recife-PE, between August and September 2016, with an altitude of four meters above sea level, the average temperature of 27 ± 4° C and relative humidity of 76 ± 5.5%. In the experiments we used three isolates of *R. pseudosolanacearum* obtained from the collection of bacterial cultures Rosa Mariano Fitobacteriologia from the Laboratory of Phytobacteriology of the Federal Rural University of Pernambuco: CRM74, CRM 76 and CRM 77, belonging to the phylotype I and sequevar 18; phylotype I and sequevar 17; phylotype I and sequevar 18, respectively. These isolates were used because they are frequently found in the research region.

For the preparation of bacterial suspensions, isolates were rescued from preservation in water and cultured on TZC (triphenyl tetrazolium tetrachloride) [14] for 48 h at 30 ± 2 °C and transferred to nutrient yeast dextrose agar medium (NYDA). Then the bacterial growth of isolates were suspended in sterile distilled water (SDW), the concentration of the suspension setting to $5x10^8$ CFU ml^{-1} in photocolorimeter (Analyzer 500M, Brazil). All isolates used were previously tested for pathogenicity in IPA-6 cultivating seedlings.

We evaluated 23 tomato lines for resistance to bacterial wilt. Also included in this evaluation three witnesses resistant: Hawaii 7996, Yoshimatsu and Woodstock, one moderately resistant: Tropithai and three susceptible witnesses: Cherry Red, Santa Clara and IPA-6.

The lines were obtained by the method of Single Seed Descent from F2 plants of the hybrid SE F1 1055, belonging to the East-West Seed Company, through Self-pollination until F7. The SE 1055 F1 hybrid is resistant to *Fusarium* wilt, the tomato mosaic, to Verticillium wilt and geminivirus. As well as the SE 1055 F1 hybrid presented, in previous experiments, resistance to bacterial wilt when grown in soil naturally infested with *R. pseudo solanacearum*.

The genotypes were sown in trays of expanded polystyrene with 128 cells, containing commercial peat-based substrate, peat, charcoal, vermiculite and enriched with NPK and micronutrients. The trays were kept in a greenhouse covered with an agricultural film of 150 microns and closed laterally with antiophidic screen. After 14 days, thinning was performed, maintaining only one plant per cell. The irrigation system was conducted through micro sprinkler.

Plants 21 days were transplanted to plastic pots containing a volume of 500 mL with the commercial substrate, and compound (soil, worm humus and coconut powder) at a ratio of 1: 1. After a week, when the roots are developed and spread through the vase, was made a cut in half moon about two centimeters around the plant lap with the aid of a stylet to damage the root system, serving gateway to the bacterium and then immediately placed 15 mL of the bacterial suspension.

To meet the water requirement of the plants, irrigation was performed in plastic containers placed in each pot, the objective of preventing the escape of inoculum, being effected according to the need and keeping the substrate always wet. The experiment was conducted in a completely randomized design, in 30x3 factorial design, with 30 genotypes and three isolates and three replicates. Each experimental plot consisted of four plants, that is, 12 plants per treatment.

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, 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) incidence (INC) of the disease, determined by the percentage of infected plants in relation to the total inoculated plants.

b) 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.

According to this index, the genotypes were classified for reaction to the pathogen as resistant 0.0 to 1.0; moderately resistant > 1.0 to 2.0; moderately susceptible > 2.0 to 3.0 and susceptible > 3.0 to 4.0 [15].

c) latency period (LP 50) determined by the number of days required for the onset of wilt in 50% of inoculated plants [16].

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.

Using statistical analysis program Sisvar version 5.6 [17], data were transformed to square roots, because they do not present a normal distribution and subjected to analysis of variance (ANOVA) and the grouped averages by the Scott-Knott test at 5% probability.

The genetic-statistical analysis program Genes version 2016.6.0 [18] was used to calculate the estimation of the phenotypic, genotypic and environmental correlation coefficients. It was also used to conduct the study of genetic diversity, calculating dissimilarity through the Mahalanobis distance (D2), generating the matrix of genetic distances between genotypes. Having the dissimilarity matrix, a dendrogram was constructed by the method of the unweighted arithmetic mean - UPGMA (Unweighted Pair Group Method with Arithmetic Average). For analysis of the dendrogram, it was considered the possibility of a significant cut, together with a visual examination of the dendrogram.

3. RESULTS AND DISCUSSION

According to the F test (*P* = .01) there was a significant difference for all the variables evaluated for the genotypes. The isolates showed a significant difference at 1% probability to BWI, LP 50 and AUDPC and was not significant for INC. The interaction Genotype x Isolates showed a significant difference (*P* = .01) for the variables LP 50 and AUDPC, indicating that the genotypes behave differently according to each bacterial isolate (Table 1).

Considering the three isolates, for the variable incidence (INC), Scott-Knott test at 5% probability demonstrated that three groups were formed. Resistant witnesses formed the group with the lowest INC, with the cultivar Hawaii 7996 (2.77%), Yoshimatsu (2.77%), Woodstock (5.55%) and Tropithai (19.44%). The intermediate group was composed of 10 lines (L04, L38, L42, L49, L53, L79, L82, L120, L125 and L128) with INC ranging from 36.11% to 55.56%, these values are considered high when seeking materials with high effectiveness for bacterial isolates. The cultivar IPA-6 presented 100% of plants with symptoms of bacterial wilt beginning from the 4th day, the same amount of cultivar Santa Clara and Cereja Vermelho, following the L166 (97.2%), L32 and L91 (91, 7%), L69 and L129 (88.9%) and L66 (83.3%), forming the group with the highest incidence. These values corroborate with [19] and [16], which classify Hawaii 7996 as resistant and IPA-6 as highly susceptible.

Considering the bacterial wilt index (BWI), resulting from the transformation of the notes scale readings, of the three isolates together, it was possible to classify the resistance reaction to

Table 1. Estimation of the mean squares for resistance components for 30 tomatoes genotypes

Sources of variation	DF	MS[(1)]			
		INC (%)	BWI	LP 50	AUDPC
Genotypes (G)	29	70.62**	2.15**	2.55**	17.24**
Isolates (I)	2	22.01^{ns}	1.95**	1.92**	16.78**
G x I	58	9.19 ^{ns}	0.20 ^{ns}	0.30**	1.63*
Residual	180	7.36	0.15	0.17	1.04
CV (%)		38.57	34.04	12.54	44.35

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

the pathogen according to [15]. Of the total 30 material (23 lines and 07 witnesses), twelve were classified as resistant, ten lines showed moderate resistance, four lines were moderately susceptible and four genotypes were considered susceptible.

Within the twelve classified as resistant was the formation of two groups, according to the Scott-Knott test, in which the Hawaii 7996, Woodstock and Yoshimatsu witnesses formed the group with the lowest values of BWI, differing statistically from the second group formed by the Thopithai witness and the lineages L04, L42, L49, L53, L82, L120, L125 and L128. The ten lines showed moderate resistance (L45, L12, L57, L27, L14, L24, L01, L79, L38 and L129) forming a third group. In the four moderately susceptible genotypes, grouped the lineages, L32, L66, L69 and L91 forming the fourth group. Among the genotypes susceptible, the IPA-6 witness formed the group with the highest BWI value, differing significantly (*P* = .05) of equally susceptible cultivars Santa Clara and Cereja Vermelho and also of lineage L116 (Table 2).

Considering the latent period (LP 50) and the area under the disease progress curve (AUDPC), there was a significant difference (P = .01) for genotype x isolates interaction, indicating that there aggressiveness difference between the three isolates used with lineages and witnesses.

For the unfolding of the variable LP 50 as a function of the isolates for each tomato genotype, different behaviors were observed for each of the isolates. For the CRM 74 isolate, three groups were observed, in which in the first group are resistance witnesses Hawaii 7996 and Woodstock with LP 50 of 16 days and did not differ from Yoshimatsu and lineages L24, L42, L49, L53, L82, and L128. The Tropithai witness was in an intermediate group with the lineages L01, L04, L12, L45, L57, L66 and L125. Then in the third group, the IPA-6 witness presented LP 50 of 3.33, not differing significantly from the other susceptibility witnesses and lineages L32, L69, L91, L116 and L129 (Table 3).

Regarding the CRM 76 isolate, most of the lineages did not differ from the resistance witnesses. Only IPA-6 behaved similar to the witness Cereja Vermelho forming the third group. The Santa Clara witness did not differ statistically from lineages L24, L38 and L116, staying in the intermediate group. Already with the CRM 77 isolate, the lineages that were in the same group as the resistance witnesses were the L38, L49, L82 and L125. The IPA-6 cultivar formed another group with Santa Clara and Cereja Vermelho witnesses, along with the lineages L01, L32, L66, L69, L91, L116 and L129.

Table 2. Reaction of tomato genotypes in relation to incidence and bacterial wilt index for three *Ralstonia pseudosolanacearum* isolates

Genotypes	INC (%) [1]	BWI[2]
IPA-6	100.00 c	3.86 f
SANTA CLARA	100.00 c	3.36 e
L116	97.22 c	3.03 e
C VERMELHO	100.00 c	3.01 e
L32	91.66 c	2.53 d
L91	91.66 c	2.36 d
L69	88.88 c	2.45 d
L66	83.33 c	2.19 d
L129	88.88 c	1.81 c
L01	88.88 c	1.83 c
L24	77.77 c	1.61 c
L14	75.00 c	1.72 c
L27	72.90 c	1.50 c
L57	69.44 c	1.39 c
L38	55.56 b	1.42 c
L79	50.00 b	1.31 c
L12	69.44 c	1.25 c
L45	63.88 c	1.33 c
L120	55.56 b	1.00 b
L04	44.44 b	0.97 b
L125	41.66 b	0.78 b
L82	47.22 b	0.78 b
L128	38.88 b	0.75 b
L49	47.22 b	0.67 b
TROPITHAI	19.44 a	0.61 b
L42	36.11 b	0.67 b
L53	47.22 b	0.64 b
YOSHIMATSU	2.77 a	0.17 a
WOODSTOCK	5.55 a	0.06 a
HAWAII 7996	2.77 a	0.03 a

[1] INC: incidence; [2] BWI: Bacterial wilt index. Scott-Knot test at 5% probability.

Unfolding the AUDPC variable for the isolates CRM 74, the Hawaii 7996 and Woostock genotypes were those that achieved the lowest average but did not differ statistically from Yoshimatsu and Tropithai witnesses and the lineages L49, L82, L53, L42, L04, L128, L24 and L01. As with all values of the treatments differed from IPA-6 witness, forming a single group. For CRM 76 isolate, most lineages behaved similar to the resistance witnesses, except the L116 lineage that behaved similarly to Cereja Vermelho and Santa Clara witnesses. And once

again, the IPA-6 witness was the one with the highest value of AUDPC, isolating themselves in a third group.

The CRM 77 isolate formed only three groups, in which the IPA-6, Santa Clara, Cereja Vermelho and L166 genotypes formed the group of higher susceptibility. The lineages L32, L69, L66 and L91 formed an intermediate group and the others behaved similarly to the resistant genotypes.

Considering the three isolates were observed that the lineages L49, L82, L53, L42, L04, L128, L24 and L01 obtained the lowest AUDPC values, not differing from the resistance witnesses. The progress of the disease in these materials was slower, slowing the onset of the epidemic, can be attributed to a possible resistance, since they were all kept in the same conditions. It was also observed that the L49 and L82 lineages were similar to resistance witnesses to the LP 50 and AUDPC characters, considering the three isolates.

They were also calculated the phenotypic, genotypic and environmental coefficients of correlation, between pairs of strength components which are stated in Table 4.

According to [20], plant breeders tend to value the sign and magnitude of correlation values, valuing estimates below -0.50 and above 0.50. In this way the values presented are all within such parameter, since negative values were between -1.00 and - 0.66 and positive values between 0.52 and 1.00.

Table 3. Reaction of tomato genotypes in relation to latency period and area under the disease progress curve for three *Ralstonia pseudosolanacearum* isolates

Genotype/isolate	LP 50[(1)]			AUDPC[(2)]		
	CRM 74	CRM 76	CRM 77	CRM 74	CRM 76	CRM 77
IPA-6	3.33 a	4.00 a	3.33 a	39.00 d	28.62 c	37.50 c
SANTA CLARA	6.66 a	7.00 b	4.33 a	20.75 c	15.38 b	28.00 c
C. VERMELHO	5.66 a	4.33 a	4.66 a	11.62 b	16.75 b	28.25 c
L116	5.00 a	9.33 b	5.33 a	25.25 c	11.99 b	31.37 c
L32	7.66 a	11.33 c	5.66 a	17.00 c	6.12 a	22.25 b
L69	6.00 a	12.00 c	5.66 a	19.12 c	6.50 a	17.37 b
L66	11.33 b	11.33 c	6.00 a	10.12 b	7.25 a	16.50 b
L91	8.66 a	10.33 c	7.00 a	14.87 c	7.50 a	15.75 b
L129	9.00 a	11.33 c	7.66 a	10.00 b	4.00 a	10.87 a
L01	11.66 b	11.66 c	9.00 a	5.00 a	4.13 a	13.12 a
L79	7.00 a	14.33 c	10.00 b	10.75 b	2.50 a	6.62 a
L24	13.33 c	9.33 b	10.33 b	2.62 a	10.25 a	5.37 a
L12	10.33 b	14.66 c	10.33 b	8.58 b	0.37 a	4.63 a
L57	12.00 b	12.66 c	10.66 b	9.87 b	2.50 a	10.12 a
L45	11.66 b	13.33 c	11.33 b	6.12 b	2.62 a	9.25 a
L27	9.33 a	12.66 c	12.00 b	10.50 b	3.88 a	6.88 a
L128	14.66 c	14.33 c	12.33 b	0.75 a	1.25 a	3.87 a
L04	12.00 b	12.66 c	12.33 b	2.62 a	2.37 a	4.12 a
L42	14.33 c	15.00 c	12.66 b	2.37 a	0.75 a	4.38 a
L53	15.00 c	15.00 c	12.66 b	2.00 a	0.50 a	2.88 a
L120	9.66 a	14.33 c	12.66 b	10.37 b	0.87 a	2.87 a
L14	7.66 a	12.00 c	13.33 b	16.12 c	8.25 a	4.50 a
L82	14.33 c	12.33 c	13.66 c	2.66 a	3.87 a	2.50 a
L125	10.33 b	14.33 c	14.33 c	6.87 b	1.25 a	1.87 a
L49	14.33 c	13.00 c	14.33 c	2.25 a	2.12 a	1.12 a
TROPITHAI	12.00 b	14.66 c	15.33 c	4.12 a	1.75 a	1.62 a
L38	6.00 a	7.66 b	15.66 c	16.50 c	9.50 a	0.75 a
YOSHIMATSU	14.66 c	16.00 c	16.00 c	1.25 a	0.00 a	0.00 a
WOODSTOCK	16.00 c	15.66 c	16.00 c	0.00 a	0.12 a	0.12 a
HAWAII 7996	16.00 c	16.00 c	16.00 c	0.13 a	0.00 a	0.00 a

[(1)] LP 50: latency period; [(2)] AUDPC: Area under the disease progress curve. Scott-Knot test at 5% probability

Table 4. Estimates of phenotypic (F), genotypic (G) and environmental (A) coefficients of correlation among four components of bacterial wilt resistance in 30 tomato genotypes

Characters	*r*	INC	LP 50	AUDPC
BWI	F	0.98*	-1.00**	0.99**
	G	0.99**	-1.00**	0.99**
	A	0.67^{ns}	-0.99**	0.97*
INC	F		-0.98*	0.96*
	G		-0.99**	0.98*
	A		-0.66 ^{ns}	0.52 ^{ns}
LP 50	F			-0.99**
	G			-0.99**
	A			-0.98*

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

It can be seen that the resistance components are highly correlated, since the coefficients presented significance by the t test at 1% or 5% probability for most cases, with the exception of environmental variance between characters INC x BWI, INC x LP 50 and INC x AUDPC. Note also that, generally in these combinations, the phenotypic correlations were of the same sign and slightly different from the genotypes correlations and superior to environmental correlations, confirming the greater contribution of genetic factors than above-mentioned environmental correlations.

With respect to the signs of the genotypic, phenotypic and environmental correlation coefficients were negative for the correlation between the latency period variable and the other resistance components. This indicates that the latency period decreases whenever the other characters increase in value and vice versa, demonstrating lower or higher aggressiveness of the bacterial isolate.

In 100% of character pairs, the genotype correlations were equal to or slightly higher than phenotypic correlations, as these two, in 50% of cases were slightly higher than the environmental correlations, showed that the environment favored in the same way for BWI x LP 50, BWI x AUDPC and LP 50 x AUDPC, since the values of the coefficients did not present difference in magnitude and signal. According to [21] that occurs due to bacterial wilt be strongly influenced by environmental conditions such as temperature, light intensity, day length, moisture and pH soil. However, the variable incidence had the lowest values of environmental correlation and high correlation values for bacterial wilt index, latency period and area below the disease progress curve. This shows that in these cases the genetic factors contributed more than the environmental factors and that the phenotype adequately reflects the genotype.

According to [22], in the occurrence of characters with a favorable genetic correlation, it is possible to obtain gains for one through indirect selection in the other associated. Thus, according to [23] in some cases indirect selection based on the correlated response, can lead to more rapid progress than the direct selection of the desired characteristic, besides that the observed associations can be valuable for the development of tomato hybrids involving the genotypes studied.

The dissimilarity dendrogram by UPGMA method between 23 lineages and the seven witnesses worked, based on the Mahalanobis distance, is shown in Fig. 1. The reliability of the data was confirmed by value of the cophenetic correlation coefficient (r), which obtained a result of 86.79%, expressing considerable reliability in the groupings.

For the dissimilarity observed by the dendrogram, a significant cut of 15.2% dissimilarity was performed, allowing the formation of four distinct groups and four subgroups.

The group “I” was the largest, consisting of genotypes considered resistant and moderately resistant according to the classification proposed by [15], containing witnesses Hawaii 7996, Woodstock, Yoshimatsu and Tropithai, besides the resistant lineages L04, L42, L49, L53, L82, L125 and L128 and the moderately resistant lineages L01, L12, L14, L24, L38, L45, 57, L79 and L129, totaling 21 genotypes, that is, 70% of the total. In this first group was observed the formation of two subgroups, the first being formed only by Hawaii 7996, Woodstock and Yoshimatsu and the second subgroup with the other genotypes of the group. It was also possible to observe that the first subgroup differed statistically from the second subgroup in the average grouping by the Scott-Knott test at 5% probability for the variable BWI with values between 0.03 and 0.17 for the first subgroup and values from 0.64 to 1.83 for the second subgroup.

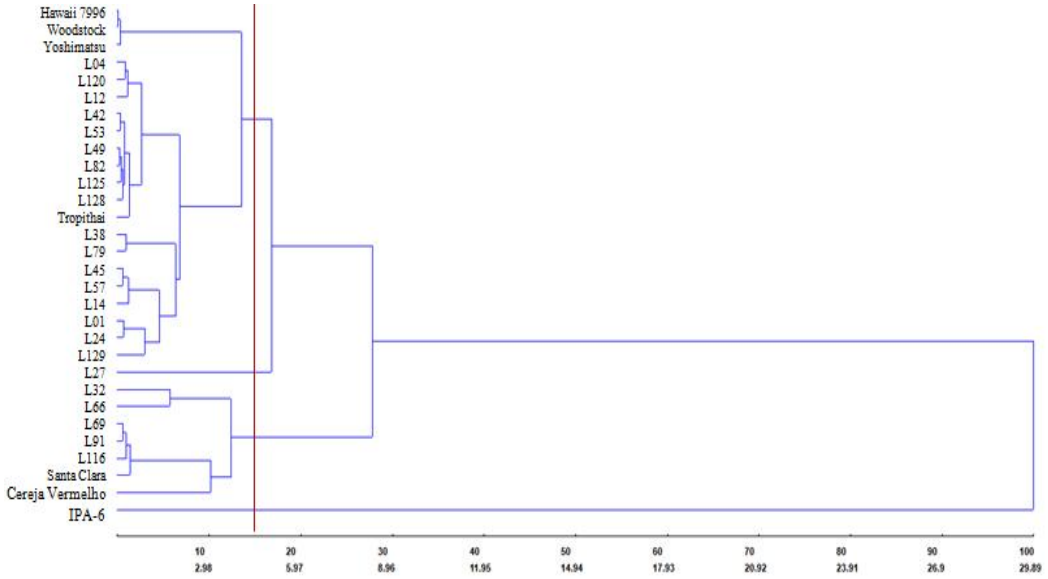

Fig. 1. Dendrogram obtained by the UPGMA method, based on measures of dissimilarity among 30 tomato genotypes, based on Mahalanobis distance

Group II was observed that L27 lineage formed a group, isolating themselves from other lineages. In group III are two subgroups, the first formed by lines L32 and L66 and the second subgroup with Cereja Vermelho and Santa Clara witnesses and L69, L91 and L116 lineages. Once again it was possible to observe that the first subgroup differed statistically from the second subgroup, by the average grouping of the Scott-Knott test at 5% probability for the variable BWI except the L69 and L91 lineages.

The IPA-6 witness is in the fourth group corresponding to only 3.3% of the materials, showing to be the most divergent genotype of all and statistically differing in the bacterial wilt index (3.86) and area under the disease progress curve for the isolates CRM 74 (39.00) and CRM 76 (28.62).

The higher dissimilarity was between the resistance witnesses Hawaii 7996 and Woodstock with IPA-6 witness, being this combination that has the greatest genetic divergence, expected result, since Hawaii 7996 and Woodstock are resistant to bacterial wilt and had the lowest values for INC, BWI and AUDPC and the highest values for LP 50, as the IPA-6 witness is highly susceptible to bacterial wilt, obtaining higher values for INC, BWI and AUDPC and the lowest values for LP 50. Among the lineages the greatest dissimilarity was between L49 and L82 with L116 lineage, showing that L49 and L82 were the ones that presented the lowest dissimilarity with the resistance witnesses and the L116 lineage with the lowest dissimilarity with the susceptibility witnesses. It also observed that the lineages L49 and L82 could be used in crosses involving the obtaining of resistant hybrids since they are in the same group as the resistance witnesses.

4. CONCLUSION

The latency period can be considered relevant to the breeding aiming at the resistance to *R. pseudosolanacearum* and to be used as a reference in the selection of materials. The lineages that stood out for resistance to bacterial wilt were: L04, L42, L49, L53, L82, L120, L125 and L128, and they can be used in crosses with resistant genotypes to provide the favoring of alleles that confer resistance to the isolates CRM 74, CRM 76 and CRM 77 from *R. psedosolanacearum*.

COMPETING INTERESTS

Authors have declared that no competing interests exist.

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