Inheritance of bacterial wilt resistance in tomato plants cropped in naturally infested soils of the state of Tocantins

Artur Ferreria Lima Neto[1]; Márcio Antônio da Silveira[2]; Ricardo Magela de Souza[3]; Sônia Regina Nogueira[2] and Claudomiro Moura Gomes André[2]

[1] Curso de Doutorado em Agronomia, Fitopatologia da Universidade de Brasília (UnB), Brasília, DF, Brazil; [2] Universidade Federal do Tocantins, Laboratório de Sistema de Produção de Energia a Partir de Fontes Renováveis (LASPER), AV.NS 15, ALCNO 14 C. Postal 114, CEP 77123-360, Palmas, TO, Brazil; [3] Universidade Federal de Lavras (UFLA), Dep.de Fitossanidade, Caixa Postal 37, CEP 37.200-000, Lavras, MG, Brazil. (* Corresponding Author. E-mail: silmarcio@uol.com.br)

ABSTRACT

Inheritance of resistance to bacterial wilt caused by *Ralstonia solanacearum* was studied in tomato plants using the P_1, P_2, F_1, F_2 and the two backcross generations obtained from the cross between the Drica and Santa Clara cultivars, which are considered standards for resistance and susceptibility, respectively. The experiment was set up in Palmas, TO, Brazil. The study was carried out in soils naturally infected by the pathogen. The scale of scores proposed by Winstead and Kelman (1952) was used to assess the disease incidence. Scores were attributed to individual plants and after six assessments the area below the disease progress curve (AACPD) was calculated and the bacterial wilt incidence (IMB) in the generations was obtained. Inheritance of resistance to bacterial wilt in tomato plants is quantitative with partial dominance of the alleles that express greater AACPD and IMB, which are oligogenic or polygenic traits.

KEY WORDS: *Lycopersicon esculentum* Mill, *Ralstonia solanacearum*, resistance, inheritance.

INTRODUCTION

Although there are reports of resistance sources to bacterial wilt, there are still no marketed cultivars that combine resistance with good yield and agronomic characteristics (Persley, 1985; Lopes and Santos, 1994). There have been several attempts to breed a resistant cultivar, but the great pathogen variability and the significant influence of the environment and the presence of a pathogen x genotype interaction (McCarter, 1991) have hindered the success of the breeders' work.

There are relatively few reports on inheritance of resistance to *R. solanacearum* in tomato plants. Even fewer papers refer to studies in soil naturally infested with the pathogen. Therefore, knowledge obtained from this study is of fundamental importance. This is especially true because this characteristic was assessed in localities where a resistance breeding program in tomato plant genotypes takes place and also where the materials will be recommended for use by farmers.

Resistance to bacterial wilt in tomato plants has been identified as monogenic (Scott et al., 1988; Grimault et al., 1995;) oligogenic (Acosta et al., 1964) or polygenic (Ferrer, 1984; Monna and Sakata, 1997). These various authors used different resistance sources in their studies. Reports concluding on a polygenic nature of the resistance, with the presence of partial dominance and epistasis, have been more frequent (Mew and Ho, 1976; Ferrer, 1984; Peter et al., 1992; Monna and Sakata, 1992). However, recessive resistance and linkage between the genes that control resistance and small fruit size were also reported (Acosta et al., 1964; Somodi et al., 1992). However, the association between fruit size and resistance, which appeared to be constant in this pathosystem, does not always seem to occur (Monna and Sakata, 1997), and it is possible to obtain lines that combine resistance and good-sized fruits for market. Thus, the main objective of this study was to investigate the genetic control of tomato resistance to bacterial wilt using the P_1, P_2, F_1, F_2 and two backcross generations from the cross between the Drica and Santa Clara cultivars, which are considered resistance and susceptibility standards, respectively. The experiments were carried out under the soil and climate conditions of Tocantins state, in areas naturally infested by the *Ralstonia solanacearum* bacteria.

MATERIAL AND METHODS

The experiment was carried out in the UNITINS, located in the county of Palmas, TO, at 10° latitude south and 48º longitude west and 213 m of altitude. The mean temperature is approximately 27.8º C and maximum temperature is around 36°C. The region has a wet tropical climate with two well-defined seasons, one dry and the other rainy, with relative humidity of approximately 69%. The experiment was carried out under field conditions, under plastic covering, in soil naturally infested with *R. solanacearum*. Two commercial tomato cultivars were used in this study, Santa Clara and Drica, as bacterial wilt susceptibility and resistance standards, respectively. The cultivars were named P_1 and P_2 respectively, with the following characteristics: P_1 (Santa Clara) cultivar of the Santa Cruz group released in 1986, which has dominated the Brazilian market for almost a decade due to its high fruit resistance to transport and handling. In the 1990s, however, 'long life´ hybrids that have bigger and higher quality fruits were introduced and currently dominate the market. They are usually susceptible to bacterial wilt, but P_2 (Drica) is a new table tomato cultivar developed specifically for the soil and climate conditions of Tocantins state, which shows resistance to bacterial wilt and tolerance to root knot nematodes. It originates from the cross between 'Dina´ (resistant to *R. solanacearum*) and 'Cometa´ (resistant to root knot nematode) and is the result of nine years of selection using the modified SSD breeding method. P_2 has determined growth habit and fruits similar to the Santa Clara type, with excellent color and flavor qualities.

The six generations were obtained in February 2000 from the cross between the Santa Clara and Drica cultivars. Thirty plants of each parent were cultivated in pots and crossed under controlled conditions in a greenhouse. The Drica cultivar was used as the male parent and the Santa Clara cultivar as the female. Thus, the pollen was collected from the Drica cultivar and then placed on the previously emasculated Santa Clara plants to obtain the F_1 genotypes. The other generations were then obtained: F_2 (F_1 selfing); RC_{11} (F_1 x P_1); RC_{21} (F_1 x P_2). The plants were grown individually in a greenhouse without air conditioning and all the management and phytosanitary treatments for tomato crops were applied.

The seeds of the six generations (P_1, P_2, F_1, F_2, RC_{11} and RC_{21}) were sown on July 6th 2000 in plastic seed trays containing the commercial organic substrate Plantmax and vermiculite. The seedlings were removed after 10 days to extruded polystyrene seedling trays with 128 wells, and they were kept for 30 days in a nursery. They were transplanted 30 days after sowing, to a greenhouse without air conditioning with 1.0m between rows and 0.50 m between plants spacing. The seedlings were planted in drills previously fertilized with chicken manure at 20 t/ha. The 5-25-15 NPK formula at 200g per drill meter, corresponding to 2 t/ha was applied as mineral fertilization. Side-dressing fertilization was later applied twice a week, together with drop irrigation at 10g.m^2 of a highly soluble 10-10-10 NPK formula. A randomized complete block design with four replications and six treatments was used. The plots had 20 plants for each generation. Special care was taken regarding the number of plants for each population. Thus, 80 plants were used for the P_1, P_2 and F_1 generations, 400 plants for the F_2 generation and 240 plants for each one of the backcrosses. The study was carried out in fixed size plots. Thus each block consisted of one P_1 plot (20 plants) one P_2 plot, one F_1 plot, five F_2 plots and three plots for each of the backcrosses, making a total of 14 plots completely randomized within each block. The experiments were used to estimate the genetic components of the F_2 and the backcross generations (Mather and Jinks, 1982 and 1984). The mean and variance components (Cavalli, 1952; Rowe and Alexander, 1980) were both estimated (Warner, 1952).

Bacterial wilt severity and incidence were assessed every 10 days after transplant during a 60-day period to follow the bacterial wilt progress. The scale of visual scores ranging from 1 to 5, proposed by Winstead and Kelman (1952), was used to assess severity: score 1 = no symptoms; 2 = up to 1/3 wilted leaves; 3 = 1/3 to 2/3 wilted leaves; 4 = all the plant wilted, except for the main terminal shoot, which may be normal; and 5 = irreversible wilt or dead plant. The bacterial wilt index was calculated for each plant as: IMB (score x no. of plants with this score)] / total number of plants per plot. Bacterial wilt incidence was also assessed weekly, the first five days after inoculation (D.A.I.) during a 25-day period to follow the progress of the disease. The data were analyzed using the area under the progress curve of the disease. The progression curves of the disease were constructed from the bacterial wilt severity data in the tomato genotypes obtained in the weekly assessments, based on a graph where the x axis corresponded to the assessment days and the y axis to the bacterial wilt index (IMB). Furthermore, the percentage of plants with bacterial wilt symptoms was calculated to provide an idea of the high level of

incidence of the disease in the experiment.

The inheritance of bacterial wilt resistance in tomato plants was also studied using the plant frequency distribution of scores of reaction to bacterial wilt in the parents and the F_1, F_2, RC_{11} and RC_{12} generations. These data were used to test the hypothesis of monogenic inheritance according to methodology used by Oliveira et al. (1999). In this case, a cut-off point was chosen (PT) for the bacterial wilt index (IMB) below which most of the P_1 parent plants were placed and above which most of the P_2 parent plants were placed. Score 2 was chosen as the cut-off point (PT = 2).

The hypothesis of monogenic inheritance was tested under several assumed degrees of dominance (GMD), based on the following assumptions and procedures: a) The score distribution (phenotypes) in each one of the generations (P_1, P_2, F_1, F_2, RC_{11} and RC_{21}) follows a normal distribution; b) For each one of the parent generations the true mean ($\overline{P_1}$, $\overline{P_2}$) was considered equal to the respective estimated mean, and the true variance considered equal to the respective estimated variance; c) Based on the respective normal curves, the expected percentages of plants in P_1 and P_2 with scores lower or equal to the cut-off point (PT) were estimated (PT = 2); d) The true mean of the F_1 population was taken as $\overline{F_1} = (\overline{P_1} + \overline{P_2})/2 + GMD(\overline{P_1} - \overline{P_2})/2$, where GMD is the average degree of dominance assumed. The true variance of the F_1 population was taken as being equal to the respective estimated variance; e) Based on the normal distribution of the F_1 population, the expected percentage of plants below or above the PT scores was calculated; f) Under the hypothesis of monogenic inheritance, the expected frequency of the number of plants with values greater than the PT scores was calculated for F_2, as being the weighted mean of the expected frequencies in P_1, F_1 and P_2, with weights 1:2:1, respectively; g) Under the hypothesis of monogenic inheritance, the expected frequencies of the number of plants with scores greater than the PT score was calculated for RC_{11} and RC_{21}, as the weighted mean of the expected frequencies in P_1 and F_1, with weights 1:1, respectively, for the RC_{11}, and the weighted mean of the expected frequencies in F_1 and P_2, with weights 1:1, respectively for RC_{12}; h) The expected frequencies of the plants with scores greater or equal to the PT score, obtained for P_1 (item c), P_2 (item c), F_1 (item d), F_2 (item e), RC_{11} and RC_{21} (item g), were multiplied by the number of plants assessed per generation, and the expected number of plants with scores greater or equal to the PT score was obtained, under the hypothesis of monogenic inheritance with the GMD degree of dominance considered; i) The expected numbers of plants in P_1, P_2, F_1, F_2, RC_{11} and RC_{21} with scores greater or equal to the PT score were compared to the numbers effectively obtained, calculating the chi-square value with five degrees of freedom; j) A significant chi-square value will lead to the rejection of the monogenic inheritance under the degree of dominance considered. On the other hand, the insignificance of the chi-square value obtained will lead to the non-rejection of this hypothesis, thus admitting the possibility of dealing with monogenic inheritance, under the considered GMS.

For the estimates of the genetic and phenotypic parameters, the mean and variances of the P_1, P_2, F_1, F_2, RC_{11} and RC_{21} populations were obtained to estimate the genetic ($\hat{\sigma}^2_G$), environmental ($\hat{\sigma}^2_E$), phenotypic ($\hat{\sigma}^2_{F_2}$), additive ($\hat{\sigma}^2_A$) and dominance ($\hat{\sigma}^2_D$) variances and to obtain the heritabilities in the broad (h^2_b) and narrow senses (h^2_n) (Mather and Jinks, 1984; Ramalho et al., 1993; Cruz and Regazzi, 1994).

The broad (h^2_b) and narrow sense (h^2_n) heritabilities were estimated based on the scheme proposed by Warner (1952) with their respective standard errors (Vello and Vencovsky, 1978).

The additive effect [a] and dominance effect [d] of the gene(s) which control the trait were estimated from the generation means. The mean degree of dominance (GMD) and the minimum number of genes (n) involved in the expression of the trait were also estimated (Mather and Jinks, 1984; Ramalho et al., 1993).

RESULTS AND DISCUSSION

The χ^2 values of the tests for monogenic inheritance of bacterial wilt resistance in tomato plants were significant for all average degrees of dominance considered (Figure 1), which lead to the rejection of the monogenic inheritance hypothesis and suggested a oligogenic or poligenic inheritance of tomato resistance to *R. solanacearum*.

The means obtained for the AACPD values of the different generations (Table 1) expressed the variation among the genotypes assessed. The Santa Clara parent (P_1) behaved as a bacterial wilt susceptible genotype, showing greater area below the disease curve than the other treatments.

The expression of the additive component [a] approximately four times greater than the dominance component [d] for AACPD and about six times greater for IMB was detected and suggested that bacterial wilt resistance may be incorporated in tomato genotypes, as the additive component can be fixed by selection because it depends only on the homozygote contribution. The additive and dominant model explained the variation among the generation means and there was no evidence of significant epistatic gene action from the estimates of the various parameters assessed, using a 5% level of significance for the χ^2 tests.

The F_2 generation showed a continuous asymmetric distribution curve, placed in an inferior scale to the RC_{11} curve and superior to the RC_{21} (Figure 2). This situation, allied to the mean degree of dominance (GMD) and the superiority of the F_1 mean compared to the arithmetical mean between P_1 and P_2, suggested the quantitative character of the resistance inheritance. The average degree of dominance result indicated that genes showing additive genetic effects predominantly control genetic resistance to bacterial wilt, although there may also be some dominance. These results are in line with the data reported by Acosta et al. (1964); Ferrer (1984); Nirmaladevi and Tikoo (1992); Anand et al. (1992) and Mohamed et al. (1997).

Acosta et al. (1964) also reported partial dominance and few genes associated to resistance to wilt in tomato plants. Data obtained by Mohamed et al. (1997) in crosses involving *L. esculentum* var. *cerasiforme* (LA 1421) x (LA 1421 x Cascade) indicated that resistance is controlled by dominant genes, as the number of days to wilt in the F_1 generation was greater than that shown by the means of the parents. However, resistance to bacterial wilt has also been reported as partially recessive (incomplete dominance), with expression depending on the degree of resistance of the resistant parent Monma and Sakata, 1997).

In this study, the variances obtained in P_1, P_2 and F_1 for AACPD and IMB (Table 2) are of discrepant magnitudes, indicating that the environmental variance depends on the population considered. The present results indicated that selection of tomato genotypes resistant to bacterial wilt in the F_2 generation is difficult due to the trait low heritability. This showed that resistance depends also on the population and on the environmental conditions to which the individuals of the populations were submitted. Thus, selection should use a high number of plants to increase the chances of success in obtaining resistant individuals. The narrow sense heritability indicated that the phenotypic variation is due to the additive genetic variation, that is, it is fixable by the selection. But this value is only valid for the environmental conditions where the materials were assessed.

The number of genes estimated varied from two to seven. These results reflect an oligogenic or even polygenic resistance. When compared with other results it is found that the data in this study is in line with the reports by Acosta et al. (1964), Mew and Ho (1976) and Oliveira et al. (1999), which suggested a small number of genes associated with tomato plant resistance to bacterial wilt. On the other hand, Ferrer

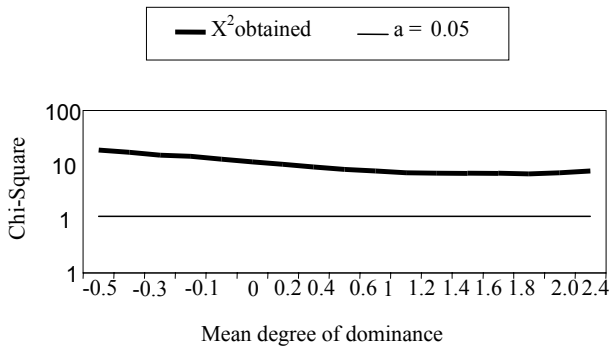

Figure 1. Values of X² for monogenic inheritance hypothesis, under different average degrees of dominance of bacterial wilt. Palmas, TO, 2000.

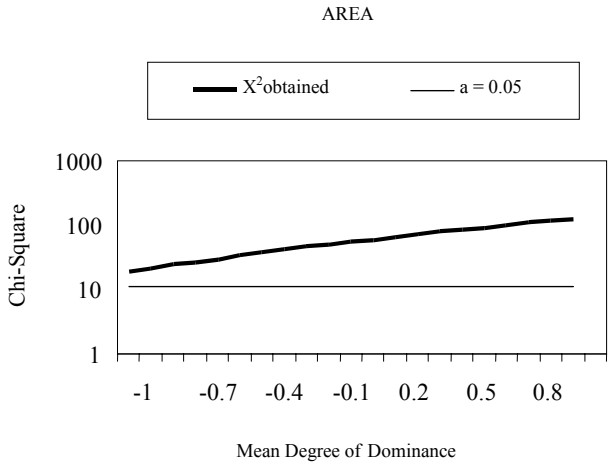

Figure 2. Values of X^2 for the monogenic inheritance hypothesis, under different average degrees of dominance for the area below the progress curve of the disease severity.

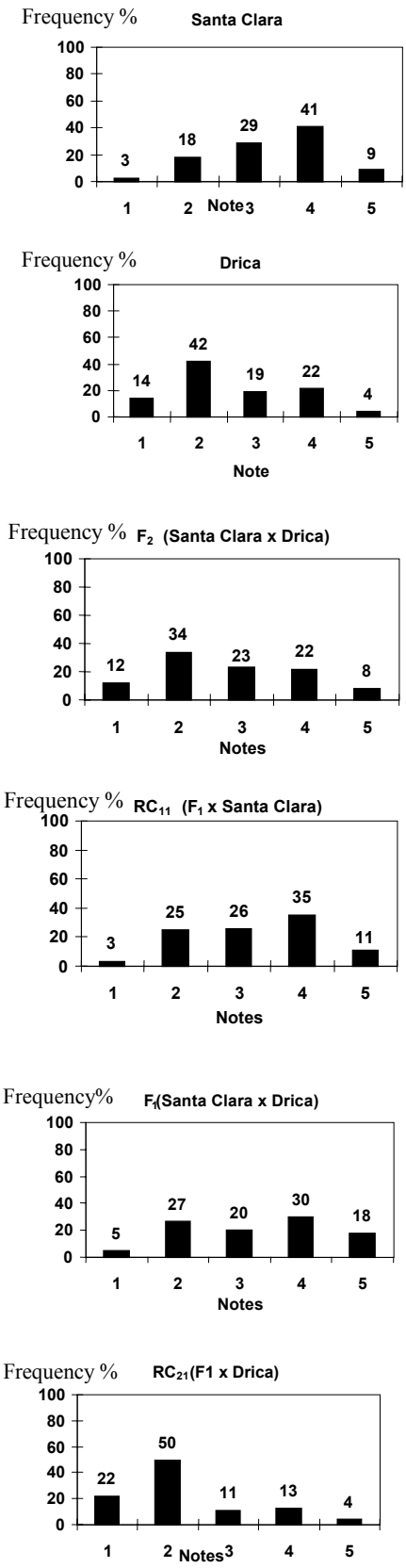

Figure 3. Observed frequency distribution of the generations P_1 (Santa Clara), P_2 (Drica), F_1(Clara Saint x Drica), F_2, RC_{11} and RC_{21}, obtained for tomateiro plants incidence of withered bacterin. Palmas-TO, 2000.

(1984) reported that the resistance is polygenic in nature, while authors such as Scott et al. (1988) and Grimault et al. (1995) when working with the Hawaii 7998 and Hawaii 7996 genotypes, reported that the resistance in these materials is controlled by a single gene. But these result variations reflect the difficulty

Table 1. Estimated values of the m, [a], [d] and average degree of dominance (GMD) parameters, number of genes (ng), area below the disease progress curve (AACPD) and bacterial wilt index (IMB) in tomato plants. Palmas, TO, 2000.

Parameters	AACPD	IMB
P_1 (Santa Clara)	109.3421	2.9123
P_2 (Drica)	78.4205	2.1350
F_1	111.1757	2.8761
F_2	90.2892	2.3815
RC_{11}	106.5933	2.8089
RC_{21}	71.1412	1.8580
[m]	88.0152 ± 4.7689	2.3572 ± 0.2478
A	24.0800 ± 4.0973	0.6296 ± 0.2144
D	7.2886 ± 9.4391	0.1164 ± 0.4907
χ^2	6.9983	1.1941
GMD	0.3026	0.1850

Table 2. Estimates of variance for the area below the progress curve of the disease (AACPD) and bacterial wilt index (IMB) in tomato plants. Palmas, TO, 2000.

Parameters	Área	IMB
P_1 (Santa Clara)	1743.055	0.9463
P_2 (Drica)	1753.827	1.1190
F_1 (Santa Clara x Drica)	2205.243	1.3075
F_2	1918.636	1.1857
RC_{11}	1761.089	1.0305
RC_{21}	1608.175	1.0340
Σ^2_E	1889.085	1.1145
$\Sigma^2 g$	29.55102	0.0712
$\Sigma^2 a$	468.0072	0.3069
$\Sigma^2 d$	-438.456	-0.2357
h^2_b	1.54	6.00
h^2_n	24.39	25.88
Ng	6.57	1.49

Table 3. Infestation and survival of tomato plants to bacterial wilt in naturally infested soil. Palmas-TO, 2000.

Generations	Survival	Infestation
	Mean	Mean
P_1 (Santa Clara)	10.99	97.80
P2 (Drica)	53.79	74.24
F_1	36.49	86.49
F_2	45.60	79.12
RC_{11}	27.56	93.33
RC_{21}	74.44	65.02

in selecting for resistance to bacterial wilt as there are several factors which impair an assessment process of this resistance. Among these are the partial nature of the resistance itself and the high variation of the pathogen in the environment. It also showed the plant death and bacterial wilt incidence. These parameters were assessed to show the magnitude of the bacterial wilt problem under the edafoclimatic conditions of Tocantins state. Table 3 shows the high number of plants that died due to the bacterial attack.

These results, besides indicating the superiority of the Drica cultivar compared to the susceptible parent, suggested that the stability of the resistance in the Drica cultivar should be assessed, as this is strongly associated with environmental factors.

CONCLUSIONS

The inheritance of bacterial wilt resistance in tomato plants under conditions of naturally infested soil is quantitative (oligogenic or polygenic) in nature, with partial dominance of the alleles which condition greater AACPD and IMB.

The low heritability suggests that selection of resistant tomatoes to bacterial wilt should be based on families instead of individuals.

The high number of plants killed by the bacteria under natural infestation conditions suggests that this procedure is safe to discriminate plant resistant to *R. solanacearum*.

The Drica tomato cultivar recommended for Tocantins state behaved as resistant, confirming its good performance under conditions of natural Biovar III occurrence.

Populations from the backcross for the Drica cultivar (RC_{21}) seem to be more promising than populations derived from the F_2 generation when selection of plants with low infestation index and high survival rate are required.

RESUMO

Herança da resistência à murcha bacteriana em plantas de tomateiro em solos naturalmente infestados do Estado de Tocantins

Estudou-se a herança da resistência à murcha bacteriana causada por Ralstonia solanacearum em plantas de tomateiro, a partir das gerações P_1, P_2, F_1, F_2 e os dois retrocruzamentos obtidas a partir dos cruzamentos entre as cultivares Drica e Santa Clara, consideradas padrões de resistência e suscetibilidade respectivamente.O experimento foi instalado em Palmas-TO. O estudo foi conduzido em condições de solo naturalmente infestado pelo patógeno.Foram utilizadas no processo de avaliação da incidência da doença, uma escala de notas proposta por Winstead e Kelman (1952).As notas foram atribuídas individualmente, e após seis avaliações calculou-se a área abaixo da curva de progresso da doença (AACPD) e a incidência de murcha bacteriana nas gerações.Verificou-se que a herança da resistência em tomateiro à murcha bacteriana é de natureza quantitativa com dominância parcial dos alelos que condicionam para maior AACPD e IMB, expressando-se como oligogênica ou poligênica.

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