Selection of tomato progenies $F_{2:3}$ for resistance to bacterial wilt via mixed modeling

Seleção de progênies $F_{2:3}$ de tomate para a resistência a murcha bacteriana via modelos mistos

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ABSTRACT
Bacterial wilt is among the major diseases of tomatoes and is currently considered the most important in Brazil. The development of resistant cultivars is the strategy that presents greater efficiency and viability, being the mixed modeling approach allows the selection of genetic materials with major accuracy. This work defines strategies for the development and selection of segregating strains F2:3 from the estimation of genetic parameters and individual mean components using mixed models. A greenhouse experiment was conducted in a randomized complete block design with four replicates, in which the resistance of 43 progenies F2:3 segregants obtained from the F2 generation from the cross between the parents was evaluated, having as parents Yoshimatsu (Resistant) and IPA-7 (Susceptible). Components of variance and genetic parameters were estimated, followed by ranking by additive genetic values. The selection of F2:3 progenies resistant to bacterial wilt was more effective when the household information was used. Mixed model procedures for the selective accuracy of 77.98%, verified efficiency in the selection of F2:3 progenies resistant to bacterial wilt evaluated at 20 days after inoculation. A total of 240 resistant and moderately resistant individual progenies were selected with severity scores between 1 and 2.49. Families presented the new averages between 1.0 and 2.87, making 23 families F2:3 that will continue the tomato breeding program.

Keywords: *Ralstonia solanacearum*, breeding value, families, resistance.

RESUMO
A murcha bacteriana está entre as principais doenças do tomateiro e atualmente é considerada a mais importante no Brasil. O desenvolvimento de cultivares resistentes é a estratégia que apresenta maior eficiência e viabilidade, sendo que a abordagem de modelagem mista permite a seleção de materiais genéticos com maior precisão. Este trabalho define estratégias para o desenvolvimento e seleção de linhagens segregantes F2:3 a partir da estimativa de parâmetros genéticos e componentes médios individuais usando modelos mistos. Foi conduzido um experimento em casa de vegetação em delineamento de blocos casualizados com quatro repetições, no qual foi avaliada a resistência de 43 progênies F2:3 segregantes obtidas da geração F2 do cruzamento entre os genitores, tendo como genitores Yoshimatsu (Resistente) e IPA- 7 (Susceptível). Componentes de variância e parâmetros genéticos foram estimados, seguidos de ordenação por valores genéticos aditivos. A seleção de progênies F2:3 resistentes à murcha-bacteriana foi mais efetiva quando utilizadas as informações entre familias. Procedimentos de modelo misto para acurácia seletiva de 77,98% verificaram eficiência na seleção de progênies F2:3 resistentes à murcha bacteriana avaliadas aos 20 dias após a inoculação. Um total de 240 progênies individuais resistentes e moderadamente resistentes foram selecionadas com escores de severidade entre 1 e 2,49. As famílias apresentaram as novas médias entre 1,0 e 2,87, perfazendo 23 famílias F2:3 que darão continuidade ao programa de melhoramento do tomateiro.

Palavras-chave: *Ralstonia solanacearum*, valor genético, família, resistência.

1 INTRODUCTION

The tomato (*Solanum lycopersicum L.*) is the second most cultivated vegetable in the world and the second in economic importance in Brazil with the production of 3.5 million tons in 72 thousand hectares (Ibge, 2016). Notwithstanding, this crop is highly vulnerable to the attack of several pathogens, these factors limiting productivity. Among the diseases incidental to the crop is bacterial wilt, caused by the bacterium *Ralstonia solanacearum*. This disease is Located between the main ones in the tropical regions and is considered currently the most important in the North and Northeast of Brazil (Félix et al. 2012), due to environmental conditions being highly favorable to its development (Lima et al. 2010).

Effective control of this disease is especially complex because of the wide host range of Ralstonia (Genin & Denny, 2012) and the complexity of soil bacterial survival. Few agricultural practices result in efficient control, except for the development of resistant cultivars, which usually present high control efficiency, and low cost, not requiring extensive knowledge of the user, and being more interesting from the ecological point of view, constituting the strategy of greater efficiency and viability in controlling bacterial wilt (Hanson et al. 2016; Zhao et al. 2016).

The use of resistant genotypes should be used in breeding programs to be incorporated as parents to obtain segregant populations for the advancement of generations and development of new resistant strains, in addition to desirable agronomic traits and to adapt to production systems (Oliveira et al. 2015; Silva et al. 2017). For this purpose, the Yoshimatsu tomato cultivar has been identified as highly resistant to bacterial wilt. According to Oliveira et al. (1999), when used in breeding programs, this cultivar allows for obtaining lines that combine resistance with good yields and agronomic traits. Several studies have reported monogenic, oligogenic, and polygenic genetic control with the most different types of allelic interactions (Oliveira et al. 1999; Sharma and Sharma, 2015).

Tomato breeding is conducted mainly using the pedigree method. This method for segregating generations is mainly characterized by the phenotypic selection between and within lines from individuals selected in F_2 (Oliveira et al. 2015). The selection of plants in segregating generations is more effective and accurate when they are taken based on the genotypic evaluation, which includes the estimation of genetic parameters such as heritability and the prediction of the additive genetic values, fundamental for the design of efficient breeding strategies (Resende et al. 2015; Oliveira et al. 2015; Amaral Júnior et al. 2017).

Estimation of components of variance made by the method of maximum likelihood constraint (REML) accommodates the properties of consistency, efficiency, sufficiency, and selection at the individual level, based on the genetic values predicted by the best non-biased linear predictor (BLUP). The mixed model for the selection of individual plants is a suitable methodology for the advancement of generations when the improvement of autogamous plants is being conducted (Resende et al. 2015). This new statistical approach in vegetables may mean greater robustness and reliability in the selection of segregating progenies (Oliveira et al. 2015).

In this context, a breeding program should have the information on the genetic parameters to define the breeding strategy most appropriate for the advances of segregating generations (Silva et al. 2017). This article defines strategies for developing and selecting F2:3 segregant resistant lines of tomato against bacterial wilt caused by Ralstonia, using the mixed model procedure.

2 MATERIALS AND METHODS

The experiment was conducted in a greenhouse at the Department of Agronomy of the Federal Rural University of Pernambuco (DEPA / UFRPE). It consisted of the evaluation of resistance in F2 progenies: from October 3/2016 to December 2016, with an average temperature of 27.38 °C and average relative humidity of 69.78%. The meteorological data were obtained at the Recife - Curado station.

To obtain the $F_{2:3}$ progenies, manual hybridizations were performed between the Yoshimatsu (Resistant) parent as the female parent and IPA-7 (Susceptible) as the male parent, obtaining the seeds of the F1 generation. From the seeds of the F1 plants, we obtained 400 plants in the F2 generation, of which 43 were resistant to *Ralstonia solanacearum*.

The isolate CRMRS185 used belongs to the Collection of The Phytobacteriology Laboratory of UFRPE. This isolate characterized as biovar 1, race IIA and dry IIA / 50 was originally collected from tomato plants in the Municipality of Petrolina of the State of Pernambuco, Brazil.

Seeding was carried out in 128-cell expanded polystyrene trays containing commercial substrate. Each cell has an approximate volume of 40 mL. At 21 days after sowing the plants were transplanted into 500 mL plastic pots containing substrate based on a soil and humus mixture in the proportion of 3:1, respectively. We evaluated 43 $F_{2:3}$ progenies along with the Yoshimatsu and IPA-7 parents. A randomized block design with four replicates was used and each $F_{2:3}$ progeny was represented by 16 plants in the plot.

For the preparation of the bacterial suspension, the isolates were rescued from water preservation and cultured in a TZC medium (triphenyl tetrazolium tetrachloride) (Kelman, 1954) for 48h at 30 °C ± 2 °C. The bacterial suspension was adjusted to the concentration of $1x10^8$ CF mL^{-1} using a spectrophotometer (Analyser 500 M, Brazil).

At 30 days after sowing, the plants were inoculated by the root-cutting method, using a scalpel a semicircular cut in the substrate near the stem of the plant, where 15 mL of the bacterial suspension ($1x10^8$ UFC mL^{-1}) (Felix et al. 2012) was inoculated. After inoculation, the irrigations were carried out in plastic containers located under the 500 mL pots, in order not to leach the inoculum and to always keep the substrate moist. Evaluations were performed on the 10th and 20th day after inoculation. The presence of the disease was measured using a descriptive scale of scores ranging from 1 to 5, adapted from Nielsen & Haynes (1960), where: 1 = absence of symptoms; 2 = plants with up to

1/3 of the wilted leaves; 3 = plants with up to 2/3 of the wilted leaves; 4 = totally wilted plants and 5 = dead plants.

The variables were analyzed using the Selegen REML / BLUP program (Selegen, Version 2016), using model 59, indicated in the one-site randomized block design, in single-line or F_2 population-derived strains, and the evaluations were made at the plant level within the plot. This model is appropriate for this work because it is the genealogical method, in which the evaluations are made based on individuals. The statistical model used was the mixed linear: y = Xr + Za + Wp + e, where y is the data vector, r is the vector of the repetition effects (assumed to be fixed) added to the general mean, a is the vector of the individual additive genetic effects (assumed to be random), p is the vector of plot effects, and is the vector of errors or residuals (random). Capital letters represent the incidence matrixes for these effects.

The estimated genetic parameters were as follows: genetic variance among families; environmental variance between plots; residual variance; individual phenotypic variance; individual heritability in the broad sense among families; individual heritability in the broad sense among families, adjusted for plot effects; coefficient of determination of plot effects; average heritability of the progeny; accuracy of progenies selection; additive heritability within the plot; coefficient of individual additive genetic variation; coefficient of residual variation and general mean of the experiment.

The data were interpreted by the estimation of the components of variance and genetic parameters, followed by the ranking of the new values in the improved population, resulting from the sum of the general average of the genetic gain.

3 RESULTS AND DISCUSSION

The overall mean severity score of 2.62 obtained at the evaluation at 20 DAI (days after inoculation) was higher than those found at the 10 DAI evaluations (1.51) (Table 1). Estimates of individual phenotypic variance and genetic variance among families show genetic variability. The variance of the genotypic effects among families for the evaluations at 20 DAI (0.1803) presented a magnitude higher than the genotypic variance at 10 DAI (0.0416), constituting 14.78% and 7.27% of the total phenotypic variability. For the environmental variance between plots, it was also verified that in the evaluations at 20 DAI (0.2735) the magnitude was higher than the variance at 10 DAI (0.1145), represented in the total phenotypic variance and in the determination coefficients of plot

effects, respectively, 22.43% and 20.02%. The residual variances at 10 DAI represented 72.68% of the total phenotypic variation, whereas at 20 DAI it represented 62.75% (Table 1).

Table 1. Variance components (REML Estimates) and genetic parameters estimative for resistance to *Ralstonia solanacearum*.

Components of Variance (Individual REML)	Evaluation at 10 days	Evaluation at 20 days
Genetic variance between families	0.0416	0.1803
Environmental variances between plots	0.1145	0.2735
Residual variance	0.4157	0.7652
Individual phenotypic variance	0.5719	1.2192
Individual heritability (in a broad sense) among families	0.0727 ++ 0.0284	0.1479 ++ 0.0405
Individual heritability (in a broad sense) among families, adjusted for the purposes of plots	0.0909	0.1907
Coefficient of determination of plot effects	0.2002	0.2243
Heritability of the average progeny	0.4324	0.6081
Accuracy of progeny selection	0.6575	0.7798
Additive inheritance within plot	0.0500	0.1178
Coefficient of individual additive genetic variation	13.4747	16.1715
Residual coefficients of variation	30.8755	25.9608
Overall average	1.5138	2.6263

Considering the heritability parameters obtained from the 10 and 20 DAI evaluations, estimates of individual heritability in the broad sense among families, as well as that adjusted for plot effects presented values up to 0.1907, considered as low to medium magnitude (Resende et al. 2015). While the average family heritabilities, values were significantly higher, ranging from 0.4324 for evaluation at 10 DAI to 0.6081 at 20 DAI, while the additive heritability within the plot presented values from 0.05 for 10 DAI and 0.1178 for 20 DAI (Table 1).

The coefficients of experimental variation were 30.87 for 10 DAI and 25.96% for 20 DAI, being considered high magnitude, as well as for coefficients of additive genetic variation that presented values for the two evaluation periods, respectively, 13.47% and 16.17% of the general average the amount of genetic variation available for selection. The selective accuracy values found for the evaluations at 10 DAI and 20 DAI (0.6575 and 0.7798, respectively) revealed high experimental quality and, therefore, efficiency in the selection of resistant $F_{2:3}$ progenies.

The effects of the environmental variances between plots (0.1145 and 0.2735) of the evaluations at 10 DAI and 20 DAI, respectively, represented 20.02% and 22.43% of the total phenotypic variation, reflected in the coefficients of determination of plot effects. Because the environmental effect between plots and plot coefficients was low in both

evaluations, there is a reasonably good selection efficiency for plots in terms of experimental precision.

The selection of the individuals was made considering the ordering based on the predicted additive genetic effect values (u + a). In this work, it was observed that the mean of the predicted additive values of each selected individual present values that are very close to their phenotypic values (f), being of interest for the selection of individuals in the pedigree method (Table 2). Genetic values predicted about the candidate individuals make it possible to establish the best strategy for increasing breeding efficiency (Oliveira et al., 2015). Approximately 35% of the individuals were selected for distribution in future experimental blocks (Table 3), including the Yoshimatsu cultivar. The number of plants selected within each family ranged from one to sixteen, which were selected to compose $F_{3:4}$ families that will continue the tomato breeding program.

Table 2. Predicted additive genetic values (u + a) of the 300 best F2:3 lines considering superior plants within the lines for resistance to *Ralstonia solanacearum* in tomato plants.

Order	Block	Family	F	u+a	Order	Block	Family	f	u+a
1	2	45 (4)	1.00	1.60	41	3	12 (2)	2.00	2.16
2	2	45 (3)	1.00	1.60	42	3	42 (1)	1.00	2.17
3	2	45 (2)	1.00	1.60	43	1	40 (2)	1.00	2.18
4	2	45 (1)	1.00	1.60	44	2	32 (1)	1.00	2.18
5	3	45 (4)	1.00	1.61	45	1	12 (3)	2.00	2.18
6	3	45 (3)	1.00	1.61	46	1	12 (2)	2.00	2.18
7	3	45 (2)	1.00	1.61	47	1	12 (1)	2.00	2.18
8	3	45 (1)	1.00	1.61	48	2	3 (2)	1.00	2.20
9	1	45 (4)	1.00	1.61	49	2	3 (1)	1.00	2.20
10	1	45 (3)	1.00	1.61	50	3	30 (4)	1.00	2.20
11	1	45 (2)	1.00	1.61	51	3	30 (3)	1.00	2.20
12	1	45 (1)	1.00	1.61	52	3	30 (1)	1.00	2.20
13	4	45 (4)	1.00	1.61	53	2	12 (4)	3.00	2.22
14	4	45 (3)	1.00	1.61	54	2	12 (2)	3.00	2.22
15	4	45 (2)	1.00	1.61	55	2	12 (1)	3.00	2.22
16	4	45 (1)	1.00	1.61	56	3	32 (4)	1.00	2.22
17	3	41 (2)	1.00	2.01	57	3	32 (3)	1.00	2.22
18	3	41 (1)	1.00	2.01	58	4	30 (4)	1.00	2.23
19	4	41 (3)	1.00	2.01	59	4	30 (3)	1.00	2.23
20	4	41 (2)	1.00	2.01	60	4	30 (2)	1.00	2.23
21	1	41 (3)	1.00	2.03	61	4	30 (1)	1.00	2.23
22	1	41 (2)	1.00	2.03	62	4	32 (2)	1.00	2.23
23	2	41 (3)	1.00	2.03	63	4	32 (1)	1.00	2.23
24	2	41 (2)	1.00	2.03	64	2	21 (4)	1.00	2.23
25	3	12 (1)	1.00	2.04	65	2	42 (4)	2.00	2.24
26	1	12 (4)	1.00	2.06	66	2	42 (2)	2.00	2.24
27	2	12 (3)	2.00	2.10	67	2	42 (1)	2.00	2.24
28	4	12 (4)	1.00	2.12	68	1	34 (2)	1.00	2.24
29	4	12 (3)	1.00	2.12	69	1	28 (3)	1.00	2.24
30	4	12 (2)	1.00	2.12	70	1	28 (2)	1.00	2.24
31	4	12 (1)	1.00	2.12	71	2	19 (1)	1.00	2.25
32	1	30 (4)	1.00	2.12	72	1	42 (4)	2.00	2.26
33	3	41 (3)	2.00	2.13	73	1	42 (2)	2.00	2.26

34	4	41 (4)	2.00	2.13	74	1	42 (1)	2.00	2.26
35	1	41 (1)	2.00	2.15	75	3	40 (4)	1.00	2.26
36	2	41 (4)	2.00	2.15	76	3	40 (3)	1.00	2.26
37	2	41 (1)	2.00	2.15	77	3	21 (4)	1.00	2.26
38	2	30 (2)	2.00	2.16	78	1	3 (2)	1.00	2.26
39	4	42 (4)	1.00	2.16	79	1	3 (1)	1.00	2.26
40	3	12 (3)	2.00	2.16	80	1	41 (4)	3.00	2.26
⋮	⋮	⋮	⋮	⋮	⋮	⋮	⋮	⋮	⋮
221	1	39 (4)	3.00	2.47	231	2	16 (1)	2.00	2.48
222	1	39 (3)	3.00	2.47	232	1	28 (1)	3.00	2.48
223	1	39 (2)	3.00	2.47	233	4	15 (4)	1.00	2.48
224	1	39 (1)	3.00	2.47	234	4	15 (3)	1.00	2.48
225	1	38 (3)	3.00	2.47	235	4	15 (2)	1.00	2.48
226	1	38 (1)	3.00	2.47	236	4	15 (1)	1.00	2.48
227	2	21 (3)	3.00	2.47	237	2	40 (2)	4.00	2.48
228	2	21 (1)	3.00	2.47	238	2	19 (4)	3.00	2.49
229	1	15 (4)	2.00	2.47	239	2	19 (3)	3.00	2.49
230	2	16 (2)	2.00	2.48	240	2	19 (2)	3.00	2.49

In this approach, the aim is to optimize methods to develop advanced lineages to evaluate and select resistant homozygous genotypes (recombinant inbred lines) combined with good agronomic and fruit quality characteristics to allow subsequent evaluations for resistance to multiple diseases, means pathogens inoculation assays. Estimates of individual phenotypic variance and genetic variance between families show the genetic variability, indicating that $F_{2:3}$ lines present potential for family selection, and this is higher in the evaluations at 20 DAI, where the genetic variation represented 14.78% of phenotypic variation.

It is remarkable that these heritabilities are higher when the plants are evaluated at 20 DAI and suffer greater effects in the plots than in plants within plots, that is, a greater genetic divergence between plots and between families than within families. In this situation, the selection of resistant progenies is more effective when using information from $F_{2:3}$ families, thus showing the existence of genetic variability that can be exploited in the tomato breeding program.

A scale used to classify estimated heritability for mixed models was proposed by Santos et al. (2017), which is considered as being of low magnitude when value heritability (h) is < 0.15; medium or moderate magnitude where $0.15 < h < 0.50$; and high magnitude when $h > 0.50$. Heritability has an important predictive role in expressing the confidence of the phenotypic value as a guide to the genetic value (Resende et al. 2015). The values of heritability found in this work express confidence in phenotypic and genotypic values for the selection of resistant progenies. This approach has been used to estimate heritability in several species such as papaya (Vivas et al. 2014) and the

development of new strategies for the improvement of self-pollinated plants such as pepper (Oliveira et al. 2015) and beans (Resende et al. 2015).

Table 3. Predicted additive genetic values (a) of the 43 $F_{2:3}$ lines considering for resistance to *Ralstonia solanacearum* in tomato plants.

Order	Evaluation at 20 days				
	Line	Number of selected plants	A	Gain	New mean
1	Yoshimatsu	16	-	-	-
2	41	16	-0.50	0.02	2.65
3	12	16	-0.46	0.03	2.66
4	42	16	-0.34	0.05	2.67
5	30	15	-0.34	0.06	2.68
6	32	16	-0.30	0.07	2.69
7	3	14	-0.27	0.08	2.70
8	34	14	-0.27	0.08	2.71
9	28	15	-0.27	0.09	2.72
10	40	15	-0.27	0.10	2.73
11	21	13	-0.23	0.11	2.74
12	39	12	-0.19	0.12	2.75
13	19	11	-0.19	0.13	2.76
14	38	13	-0.19	0.14	2.77
15	43	11	-0.15	0.15	2.78
16	37	9	-0.15	0.17	2.79
17	29	6	-0.11	0.18	2.80
18	16	5	-0.08	0.19	2.81
19	8	7	-0.08	0.20	2.82
20	15	7	-0.08	0.21	2.83
21	23	5	-0.04	0.22	2.84
22	13	3	-0.04	0.23	2.86
23	11	1	0.00	0.24	2.87
24	2	0	0.00	0.25	2.88
25	35	0	0.04	0.26	2.89
26	22	0	0.08	0.27	2.90
27	36	0	0.08	0.29	2.91
28	5	0	0.08	0.30	2.92
29	25	0	0.08	0.31	2.94
30	1	0	0.08	0.32	2.95
31	26	0	0.15	0.34	2.97
32	14	0	0.15	0.35	2.98
33	24	0	0.19	0.37	3.00
34	20	0	0.19	0.39	3.01
35	33	0	0.19	0.40	3.03
36	27	0	0.23	0.42	3.05
37	10	0	0.30	0.45	3.07
38	7	0	0.30	0.46	3.09
39	18	0	0.30	0.49	3.11
40	4	0	0.34	0.52	3.15
41	17	0	0.38	0.55	3.18
42	31	0	0.42	0.60	3.22
43	6	0	0.42	0.66	3.28
44	9	0	0.46	0.78	3.40
45	IPA-7	0	1.10	1.10	3.73

In any crop, when concerns the selection of characteristics of interest for breeding to take place, it is essential the availability of genetic variability within the population. In addition, the selection method uses the genetic and phenotypic correlations between characters, the type of gene action involved and the experimental accuracy also plays a relevant role in the success of a breeding program (Santos et al. 2017). This genetic and phenotypic correlation between characters is the basis for the mixed models approach, this was originally proposed for the estimation of heritability values in animal breeding. Later, for the improvement of perennial plants, as an opportunity to use this approach, considering the difficulties related to the selection of individual genotypes in unbalanced experiments. This statistical procedure generally produces lower heritability values than those observed when using variance components in traditional ANOVA (Amaral Júnior et al. 2017; Santos et al., 2017).

The use of mixed models in tomato breeding is still limited to a few works. For instance, Amaral Júnior et al. (2017), evaluated the prospection of single and double hybrids with dual industrial and fresh consumer aptitude, obtained from a diallel cross, However, this approach may also be interesting for the selection of segregating progenies for resistance to diseases in other crops, which suffer the great influence of abiotic factors and coexist with the imbalance of experimental data, being this phenomenon very common in plant breeding assays. Using this approach, for other vegetables, has only been reported work in a selection of progenies $F_{2:3}$ for pepper (Oliveira et al. 2015) and string bean (Sousa et al, 2017) for agronomic traits but not for selecting resistant progenies. In tomatoes using the REML / BLUP procedure for disease resistance, this work is pioneering.

One factor that affects disease evaluation and selection efficiency of resistant genotypes is the accuracy with which families are evaluated, especially in early generations, such as $F_{2:3}$. In this study, the experimental precision was evaluated through the coefficient of experimental and genetic variation, and the selective accuracy. The high values for these three parameters are expected, since the disease resistance characteristic is strongly influenced by the environmental conditions, and families $F_{2:3}$ show that there is genetic variability with the opportunity of selecting resistant individuals, especially in selections conducted to 20 DAI. However, what should be considered primarily is the simultaneous evaluation of the coefficients of genetic and experimental variation which are reflected in the parameter of selective accuracy of progenies, so that the higher the

accuracy, the better the relation between the predicted genetic values and the real values (Santos et al. 2017).

The accuracy obtained for the $F_{2:3}$ progenies presented a value of 77.98%, which indicates good experimental accuracy and, therefore, efficiency in the selection of genotypes resistant to bacterial wilt. Selective accuracy is one of the most relevant parameters for evaluating the quality of an experiment, taking into account not only the number of repetitions and the environmental variation but also the proportion between the genetic and residual variations associated with the evaluated character.

This parameter refers to the correlation between the true genotypic value of the genetic treatment and that estimated or predicted by the experimental information. Breeding programs should be approached from the genetic and statistical point of view, not only from the statistical perspective (Santos et al. 2017) since the evaluation of genetic treatments in field experiments has two objectives: to infer the genotypic values of these materials and to order them based on their genotypic values for selection purposes.

In this study, the phenotypic averages of progenies have values very close to the additive values (u + a) that are interesting for the selection of individuals in the experiments with artificial disease inoculation in greenhouses and/or in the field while driving the segregating generations. The additive values (u + a), that is, the reproductive values for individuals predict the genetic mean of future segregating generations from selection and establish the best strategy to increase reproductive efficiency (Resende et al. 2015; Santos et al. 2017). From the individual BLUPs, the selection was conducted between and within families, since in the $F_{2:3}$ generation in the study high heterozygosity persists, in such a way that it is still likely that plants inside the families differ from one another genetically, a fact that was also evidenced in the study of Oliveira et al. (2015).

Regards to the selection gain, the new mean of the 23 $F_{2:3}$ resistant families selected from the cross between Yoshimatsu x IPA7 was 2.76, resulting in a selection gain of 0.15%. While the genetic gain in the individual selection represented values -1.32%, due to the means of the selected ones being inferior to the general average of the population, which constitutes the efficiency in the gain of selection, practicing individual among and within families. In this work, the smallest genetic gains are desired, since it is a resistance to disease in which the objective is to decrease the severity of the disease in tomato leaves caused by Ralstonia. It is important to highlight the possibility of increasing

the efficiency of selection when selecting a smaller proportion of individuals, that is, those individuals, with disease severity scores between 1 and 2.

With this, the differential value is increased and, consequently, the gain of selection too. Certainly, choosing the intensity of such a strict selection index is convenient when looking at phytopathological issues. Individuals selected for having a lower severity score will have a reduced number of lesions caused by the bacteria in the leaf, resulting in a decrease in inoculum source and in the chance of disease spreading. On the other hand, rigorous selection intensity decreases the genetic variability of the selected population, which is not recommended for segregating generations in a breeding program at early stages as $F_{2:3}$ (Resende et al. 2015).

Although bacterial wilt resistance is an important character to be considered in the development of tomato cultivars, other characteristics will also be evaluated in segregating generations, such as agronomic characteristics and fruit quality, hence the relevance of genetic variability which allows use as a resource for selecting other traits such as qualitative ones, being yield one of the most important for every breeding program. In this work, the individual progenies selected were those with severity scores between 1 and 2.49 and families were those that presented the new averages ranging from 1 to 2.87 (Tables 2 and 3). This option makes the selection intensity less stringent, maintaining greater genetic variability of the population selected for later testing in the field for agronomic characters and future segregating generations.

Selection of $F_{2:3}$ progenies resistant to bacterial wilt is more effective when using family information. The procedures of the mixed models verified efficiency in the selection of $F_{2:3}$ progenies resistant to bacterial wilt in tomatoes. Here, 240 individual progenies resistant to bacterial wilt were selected from 23 families $F_{2:3}$ that will continue the tomato breeding program for releasing future varieties able to satisfy farmers and the market.

4 CONCLUSION

Mixed model procedures for the selective accuracy of 77.98%, verified efficiency in the selection of $F_{2:3}$ progenies resistant to bacterial wilt evaluated at 20 days after inoculation. A total of 240 resistant and moderately resistant individual progenies were selected with severity scores between 1 and 2.49 and families were those that presented

the new averages between 1.0 and 2.87, making 23 families $F_{2:3}$ that will continue the tomato breeding program.

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