Notas Científicas

Heritability of peach tree resistance to bacterial leaf spot

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Abstract – The objective of this work was to evaluate the broad-sense heritability reaction to bacterial leaf spot (*Xanthomonas arboricola* pv. *pruni*), in peach tree populations obtained from directed crosses. Disease severity and defoliation of the genotypes were evaluated in field conditions, with posterior measurement of the healthy leaf area duration (HAD). The observed average heritability (0.51) indicates that the use of the evaluated genitors can be effective for the development of cultivars with higher resistance to the disease.

Index terms: *Prunus persica*, *Xanthomonas arboricola* pv. *pruni*, cultivar development, healthy area duration.

Herdabilidade de resistência de pessegueiro à bacteriose foliar

Resumo – O objetivo deste trabalho foi avaliar a herdabilidade no sentido amplo da reação à bacteriose foliar (*Xanthomonas arboricola* pv. *pruni*), em populações de pessegueiro obtidas de cruzamentos dirigidos. A severidade da doença e a desfolha dos genótipos foram avaliadas em campo, com posterior mensuração da duração da área foliar sadia (HAD). A herdabilidade média observada (0,51) indica que a utilização dos genitores avaliados pode ser efetiva para o desenvolvimento de cultivares com maior resistência à doença.

Termos para indexação: *Prunus persica*, *Xanthomonas arboricola* pv. *pruni*, desenvolvimento de cultivares, duração da área foliar sadia.

In Brazil, peach tree [*Prunus persica* (L.) Batsch] breeding programs focus on the development of cultivars with high productivity, high-fruit quality, early maturation, and good adaptation to different climatic conditions for growth. The expansion to subtropical and tropical regions, using cultivars with low-chilling requirement, exposed orchards to conditions of high temperature and humidity, which favors the development of diseases (Citadin et al., 2014), such as bacterial leaf spot caused by *Xanthomonas arboricola* pv. *pruni* (Smith).

When the disease severity is high, it causes early defoliation and hinders plant development and productivity (Suesada et al., 2013). Chemical and biological control of the disease shows little efficacy and, therefore, the use of cultivars with higher resistance is recommended (Suesada et al., 2013). Several studies have reported the existence of superior genotypes as for the resistance to the disease (Medeiros et al., 2011; Sachet et al., 2013; Suesada et al., 2013). However, the degree of correspondence between the phenotype and the genetic value in populations under the cultivation conditions of Brazil is still unknown.

Therefore, the estimation of broad-sense heritability is necessary to determine whether the selection for the character is effective (Nishio et al., 2014). Characters with high heritability are less susceptible to the environment in which the variation occurs, mostly because of genetic factors that can be used in cultivar improvement. Therefore, heritability quantification has a strategic role in breeding programs because it allows of incorporating the trait of resistance to *X. arboricola* pv. *pruni* into the new selections.

The objective of this work was to evaluate the broad-sense heritability reaction to bacterial leaf spot in peach tree populations obtained from directed crosses among parents previously classified as resistant or susceptible.

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Evaluations were performed in the collection of peach tree genotypes from the experimental orchard of Universidade Tecnológica Federal do Paraná, Campus Pato Branco (26°10'S, 52°41'W, at 764 m altitude), in the state of Paraná, Brazil. The climate of the site is classified as Cfa – humid subtropical – by the Köppen-Geiger's classification. The mean annual maximum and minimum temperatures are 25.1 and 14.3°C, respectively.

Plants were transplanted in 2010 in 1.5×5.0 m spacing. Plant management consisted of pruning twice a year (winter and summer). The control of leaf rust [*Tranzschelia discolor* (Fuckel) Tranzschel and Litvinov] was performed by lime sulfur applications during winter, followed by the application of azoxystrobin, difeconazole, epoxiconazole, and pyraclostrobin during the growing season. No phytosanitary treatments were used for the control of the bacteriosis.

The utilized genotypes originated from directed crosses between genitors with different levels of reaction to the bacterial leaf spot, as reported by Medeiros et al. (2011) and Sachet et al. (2013). A completely randomized experimental design was used, and consisted of seven populations, totaling 95 individuals.

The reaction to leaf spot was evaluated during the vegetative growth, over a period of three years, from 2011–2013. Five representative branches were selected from each plant, and the diagrammatic scale developed by Citadin et al. (2008) was used to determine the bacteriosis severity on the leaves. The severity and defoliation values were used to estimate the healthy area duration (HAD) of the leaves, according to the method used by Sachet et al. (2013).

In 2011, the peach tree genotypes were evaluated between October and December, in three evaluations that enabled the estimate of 60 days as the maximum HAD. In 2012, the evaluations were conducted between September and February, with a maximum HAD of 155 days (five evaluations). In 2013, the evaluations were conducted between September and December, and provided a maximum HAD of 87 days (three evaluations).

The variation observed between individuals within each population was used to obtain the phenotypic variation (sf^2) of HAD. The environmental variation (se^2) was obtained between the replicates (branches) of each individual for the entire population evaluated, whereas the genotypic variation between individuals was obtained within each population, excluding the environmental effect, according to the following equation: $sg^2 = sf^2 - se^2$. The coefficient of genetic variation was estimated by the expression,

$$CVg = \left(\sqrt{sg^2} / \bar{x}\right) \times 100,$$

and the coefficient of residual variation was estimated by the expression:

$$CVe = \left(\sqrt{se^2} / \bar{x}\right) \times 100,$$

in which $\bar{x}$ is the population average. The overall heritability (H^2) of each population was determined using the Genes software (Cruz, 2013), according to the formula: $H^2 = (sf^2 - se^2)/sf^2$.

In the experiment, the average heritability in each year and the general heritability were calculated as the weighted average of each population´s heritability.

None of the evaluated populations showed the maximum potential HAD (Table 1), which indicated the absence of immune genotypes to the disease; however, this evaluation showed the presence of genotypes with different resistance levels. These different levels of resistance to bacterial leaf spot have been reported in other studies (Medeiros et al., 2011; Sachet et al., 2013).

The coefficient of genetic variation (CVg) ranged from 0.04 to 23.42%, whereas the coefficient of residual variation (CVe), related to the environmental variation, ranged from 5.37 to 33.61%. Both coefficients decreased over the years, which can be attributed to the increase of inoculum potential. For CVe, the reduction over time resulted in greater experimental precision. According to Mistro et al. (2004), CVg/CVe ratios greater than or equal to 1.0 indicate very favorable conditions for selection. In the present work, only the 'Olímpia' × 'Conserva 1127' (1.0) and 'Atenas' × 'BRS Libra' (1.1) populations had CVg/CVe greater than or equal to one; this result indicates that the employed populations did not have a broad genetic variability for the trait, which requires more reasonable selection methods.

Heritability for HAD ranged from 0.02% ('Olímpia' × 'Conserva 985') to 85.83% ('Atenas' × 'BRS Libra'). The average heritability value estimated was 51.40%, which falls within the interval reported by Topp & Sherman (1990), for Japanese-type plum trees (42–58%), and by Yang et al. (2013), for peach trees (14–84%) in the

United States. This average heritability of 51.40% for the three years of evaluation is classified as moderate.

However, it was observed a tendency towards heritability reduction over the years, with 70.70% in 2011, 54.11% in 2012, and 29.38% in 2013. This decrease may be related to the greater inoculum potential of the pathogen in the orchard, that is, strong inoculum pressure can reduce the difference between plants for their reaction to bacterial leaf spot, which would lead to a reduction of the genotypic variation of the population and, consequently, to a reduction of the heritability. In fact, according to Suesada et al. (2013), evaluations of heritability under field conditions can be affected by climatic changes and density of bacteria in the area.

Table 1. Healthy area duration (HAD±standard deviation), broad-sense heritability (H^2), coefficient of genetic variation (CVg), coefficient of residual variation (CVe), and CVg/CVe ratio in seven populations of peach tree (*Prunus persica*) evaluated for their reaction to bacterial leaf spot (*Xanthomonas arboricola* pv. *pruni*), during 2011, 2012/2013, and 2013.

Year	HAD (days)[1]	H^2	CVg	CVe	CVg/CVe
Olímpia (resistant) × Conserva 1127 (susceptible), 27 plants					
2011	44.0±9.4	83.42	18.34	18.28	1.00
2012/2013	132.2±10.4	43.46	5.29	13.51	0.39
2013	84.1±2.5	35.60	1.78	5.37	0.33
Olímpia (resistant) × Cascata 967 (resistant), 14 plants					
2011	40.1±8.2	74.00	18.29	24.24	0.75
2012/2013	125.7±14.1	62.30	9.18	15.97	0.58
2013	82.5±3.4	4.12	0.85	9.23	0.09
Olímpia (resistant) × Conserva 985 (resistant), 14 plants					
2011	49.5±5.1	63.67	8.46	14.28	0.59
2012/2013	143.4±8.3	38.02	3.71	10.61	0.35
2013	84.3±2.6	0.02	0.04	7.10	0.01
Olímpia (resistant) × Tropic Snow (resistant), 14 plants					
2011	42.7±6.6	77.20	14.11	17.14	0.82
2012/2013	135.9±10.5	56.30	6.03	11.87	0.51
2013	78.6±5.7	50.99	5.38	11.80	0.46
Atenas (susceptible) × BRSLibra (susceptible), 12 plants					
2011	30.2±7.6	79.00	23.42	27.00	0.87
2012/2013	126.0±19.7	85.83	15.12	13.73	1.10
2013	74.4±6.3	53.52	6.41	13.35	0.48
Tropic Snow (resistant) × Conserva 1216 (susceptible), 7 plants					
2011	30.1±4.9	48.60	12.29	28.26	0.43
2012/2013	120.7±13.1	74.14	10.08	13.32	0.76
2013	73.1±5.9	30.53	4.80	16.19	0.30
Atenas (susceptible) × Conserva 1127 (susceptible), 7 plants					
2011	30.5±7.6	68.89	22.37	33.61	0.67
2012/2013	102.2±11.8	18.73	5.40	25.18	0.21
2013	77.0±3.7	30.88	3.06	10.26	0.30
Mean					
2011	38.2	70.70	-	-	-
2012/2013	126.6	54.11	-	-	-
2013	79.1	29.38	-	-	-
General	-	51.40	-	-	-

[1]Maximum possible values for HAD: 60, 155, and 87 days for 2011, 2012/2013, and 2013, respectively.

High to moderate heritability estimates indicate the possibility of including the resistance to disease trait in breeding programs (Díaz et al., 2007). Besides, they indicate that genetic progress can be achieved through mass selection (Tambarussi et al., 2010). Even the average heritability estimated in 2013, which was the lowest one, is sufficient to ensure the efficiency of mass selection in the field, although the genetic gain in each cycle should be low.

The average heritability obtained (51.40%) implies the existence of genetic variability for HAD in the studied progeny, enabling us to infer that selection may be effective for obtaining genetic gains for the evaluated characteristic. Moreover, this heritability indicates that the use of the evaluated parents may be effective in the development of cultivars with higher resistance to bacterial leaf spot.

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