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Evaluation and selection of passion fruit progenies resistant to collar rot disease

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Abstract

The objective of this work is to evaluate and select backcrosses of passion fruit progenies resistant to soil diseases. This selection contributes to the improvement of the passion fruit genetic improvement program. A cross of the interspecific hybrid UNEMAT 124-3 resistant to *Fusarium solani* was carried out. The hybrid arose from crossing the resistant species *P. nitida* with a commercial cultivar of *P. edulis*. *P. edulis*, cultivar BRS Sol do Cerrado, was a recurrent parent. The BC1 resistance tests were evaluated twice. The first test was carried out with BC1 adducts that are in the field; for this, clone seedlings were produced from cuttings of each plant for the resistance test. The second test comprised inoculation directly into BC1s that were planted in pots without replications. In addition, clones of *P. nitida* and HI were used as a positive (resistant) control and clonal seedlings of *P. edulis* as a negative (susceptible) control. The evaluation of resistance of the genotypes to *F. solani* was quantified considering ten resistance variables. In the first trial with plants from cuttings, it was possible to identify the BC1s 02, 14, and 24 as resistant to *F. solani*. In the second trial with *Passiflora* spp. seedlings, considering the results of UPGMA, hierarchical methods of torch optimization and graphical dispersion per genotype considering the importance of characters, it was possible to identify the BC1s 25, 26, 27, 28, 31, 43, 45, 48, 53, 57, 58, 61, 63, 66, 68, 71, 72, 73, 74, 80, 81, 83, 84, 86, and 87 as resistant. These should be selected to continue the passion fruit improvement program.

Keywords: *Passiflora* spp., complex species *Fusarium solani,* genetic resistance.

Introduction

The Passifloraceae family counts about 520 species (Wohlmuth et al., 2010). They are found mainly in tropical and subtropical regions of the world (Dhawan et al., 2004; Araújo et al., 2017). Brazil is the world's largest producer and consumer of passion fruit (Faleiro and Junqueira, 2016). However, *Passiflora edulis* Sims, known as sour passion fruit, represents 90% of all planted area in Brazil (Viana et al., 2016). Over the years, this species has suffered decreases in production, from 922,334 tons in 2010 to 593,429 tons in 2019 (IBGE, 2020).

One of the possible causes for such a decrease are injuries suffered by pests and diseases. Among diseases, those caused by fungi of the *Fusarium* genus stand out. Species of this genus have a wide geographic distribution and cause significant losses in several economically important crops (Summerell, 2019). In passion fruit, species of the *F. solani* complexes are causal agents of collar rot disease (Fischer and Resende, 2016). This disease causes great damage to the passion fruit crops. Infection by this pathogen starts in the plant cervix or roots through wounds (Fischer and Resende, 2016). Symptoms of these diseases are characterized by sudden wilt, collapse, and death of plants at any stage of development (Fischer and Resende, 2016).

As there is no record in the literature of cultivars resistant to soil pathogens, one of the possible ways to solve this problem is the transfer of resistance genes present in wild *Passiflora* species using interspecific crossing (Silva et al., 2017) with commercial cultivars of *P. edulis*, such as the cultivar BRS Sol do Cerrado. This cultivar, in addition to having large yellow fruits, a pulp yield around 38% and a high productivity, is also tolerant to leaf diseases such as bacteriosis, anthracnose, and virus. However, it is highly susceptible to diseases caused by soil pathogens (Embrapa, 2008). Interspecific hybrids may have undesirable characteristics, such as development problems, male sterility, low pollen viability, difficulty in flowering, or the absence of some interesting agronomic characteristics for cultivation and marketing, such as slow growth and low productivity (Meletti and Bruckner, 2001). In this case, an alternative is to use backcrosses with commercial varieties of *P. edulis* as recurrent parents (Junqueira et al., 2005).

Given the scenario above, the objective of the work is to evaluate and select backcrossing progenies of passion fruit resistant to soil diseases, contributing to the improvement of the passion fruit genetic improvement program.

Results

The data from the analysis of variance (Table 1) of the first test, carried out with clonal seedlings from adult plants of BC1s (first generation of passion fruit backcrosses), showed a significant effect by F test at 1% probability in seven of the ten analyzed factors, with the exception of the factors SP (Survival Period), LL (Length of Lesion), and LW (Lesion Width).

The results found with the Scott Knott test ($p \leq 0.05$) showed that, of the ten BC1s evaluated, the BC1s 02, 14, and 24 presented fewer symptoms of the disease compared to the other BC1s. These other BC1s showed the lowest averages of NDM, AULAEC, and AULLEC and the highest averages of NPL-50%, PILA-50%, and PILA-100% in relation to resistance to *F. solani* (Table 2).

The results of BC1s 02, 14, and 24 were similar to those observed for controls (*P. nitida*, HI, and control). Therefore, these BC1s are the best options to further the passion fruit genetic improvement program.

The worst averages were for BC1 21. This BC1 obtained significantly similar averages to the susceptible control (*P. edulis*) for all resistance variables. The plants that were not inoculated with the fungus (control) did not develop symptoms of the disease, indicating that the *F. solani* isolate used was the agent causing the lesions.

As this is a breeding program with interspecific crosses aiming resistance, variability among genotypes was expected. This variability of genetic resistance to *F. solani* can be observed in the multivariate analysis, which allowed the formation of three groups with a cutoff point at 80% (Figure 1). Group I, formed by HI, *P. nitida*, the control, and the BC1s 02, 14 and 24, obtained the best values for the strength characteristics evaluated here. The BC1s in this group are considered to have a high genetic resistance to *F. solani* and should be selected to continue the breeding program, as they were grouped with the resistant species *P. nitida*, HI 124-3, and the control.

Thus, the hybrid HI-124-3 can be considered a resistant genotype, confirmed by the fact that this genotype originated individuals resistant to *F. solani* when backcrossed with susceptible species (*P. edulis*).

Groups II and III are formed by BC1s considered to have little or no genetic resistance to the fungus *F. solani*, as their means were similar to those of *P. edulis*, which is highly susceptible to *F. solani*. Therefore, these BC1s should no longer be used to continue the passion fruit genetic improvement program.

In the second test, which was carried out with direct inoculation in BC1s planted in pots without the use of replications, from a total of 320 seeds only 63 plants germinated (19.68% germination). Based on the relative magnitude of the values of Euclidean distance obtained by the characteristics of resistance to *F. solani*, the UPGMA grouping method showed the existence of genetic variability among the genotypes. There were four distinct groups formed (Figure 2).

Groups I, II, and III are composed of BC1s with the best means for resistance traits and considered resistant to *F. solani*. These groups are composed of BC1s with the best values for all strength characteristics evaluated, such as 11 to 33 SP, 20.73 to 44.30 mm LL, and 3.29 to 14.54 mm WL.

Group III counts the highest number of resistant BC1s (24). In addition to BC1s, this group is composed of HI-resistant controls, *P. nitida*, and the control (genotype that did not receive the inoculum). Therefore, all BC1s in groups I, II, and III can be selected to continue the passion fruit breeding program.

Group IV, composed of 30 BC1s and *P. edulis*, considered susceptible to *F. solani*, had the worst averages in relation to genetic resistance to the fungus. The BC1s of this group have no resistance and should no longer be used to continue the passion fruit genetic improvement program.

The Tocher optimization method provided a different result to that found by the UPGMA hierarchical method, with the formation of five groups (Table 3).

Groups I and II are composed of BC1s with the best results for genetic resistance to the fungus *F. solani*. Group I is formed by the BC1s 25, 49, 72, 73, and 63 as in the first grouping by the UPGMA method; however, in the Tocher grouping, BC1-31, which belonged to group II, was added to the first group (UPGMA).

Group II is formed by the largest number of BC1s (24). In addition to BC1s, this group is composed of HI-resistant controls, *P. nitida*, and the control (genotype that did not receive the inoculum). This group is composed of all BC1s contained in groups II and III (resistant) from the grouping of the UPGMA method; however, the BC1s 30, 34, 35, 37, 38, 39, 41, 42, 46, 47, 50, 51, 54, 56, 60, 64, 65, 67, 70, 75, 77, 78, 82, and 85, which were grouped as susceptible to the disease by the hierarchical method, were grouped as resistant by the Tocher method.

Groups III, IV, and V are formed by BC1s with the worst averages for resistance characteristics, and *P. edulis* was considered susceptible to *F. solani*.

The graphic dispersion of genotypes by importance of characters (Figure 3) showed a different behavior from the groupings by the UPGMA and Tocher methods. Groups I, II, and III are composed of BC1s that obtained the best averages for resistance characteristics and must be selected to continue the breeding program. However, the BC1s 54, 77, and 78 (group I) and 33 and 35 (group II), were classified as susceptible in the UPGMA grouping.

Group III is composed of the highest number of BC1s (43) and the controls HI, *P. nitida*, and the control. However, 17 of these BC1s (30, 32, 37, 38, 40, 42, 46, 47, 50, 51, 55, 62, 65, 70, 75, 79 and 85) were classified as susceptible by the UPGMA method. The BC1s in groups IV and V were classified as having the worst means and considered susceptible to the disease. Group IV, composed of the control *P. edulis* and ten BC1s, included three BC1s (49, 52 and 69) considered resistant by the UPGMA grouping. The same situation occurred with Group V, which included the BC1s 36 and 44 as susceptible. However, they were classified as resistant by the UPGMA method.

Discussion

The transfer of resistance genes to *F. solani* from BC1s was already expected since the species *P. nitida* is one of the main species to have a program to improve resistance to collar rot, according to several authors (Freitas et al., 2015a; Preisigke et al., 2015; Marostega et al., 2019).

P. nitida, in addition to having resistant genes to collar rot, has a successful hybridization with the recurrent species *P. edulis* (Menezes et al., 1994; Junqueira et al., 2008; Santos, 2013; Marostega et al., 2020, 2021). For a successful interspecific hybridization to occur, it is necessary that parent species are genetically close and have a certain chromosomal homology, reducing problems with self-

Table 1. Summary of analysis of variance of ten genetic resistance traits of *Passiflora* spp. to the fungus *Fusarium solani.* Cáceres, Mato Grosso, 2021.

Source of Variation	GL	QM				
		SP	NDP	LL	WL	NPL 50%
blocks	2	28.6668	0.3810	11.1696	1.0606	0.3810
Treatment	13	98.3412 ns	2.4835 **	81.6059 ns	19.3497 ns	2.7399 **
Residue	26	65.7037	0.7143	87.9529	10.8502	0.2784
CV %		29.20	110.93	37.41	64.90	27.70

(**) Significant at 1%, (*) Significant at 5% and (ns) not significant, according to the F test; SP: Survival period; NDP: Number of dead plants; LL: Length of the lesion; WL = width of the lesion; NPL-50% = Number of plants in which the lesion reached less than 50% of the circumference.

Source of Variation	GL	QM				
		PILA 50%	PILA 100%	AULAEC	AULLEC	AULWEC
blocks	2	42.4456	28.1059	6738.5874	14.4266	5.8275
Treatment	13	195.1018 **	174.8384 **	7324.4498 **	71.7317 **	6.6597 **
Residue	26	22.4628	24.8124	2345.9206	19.9079	2.1078
CV %		19.18	19.14	82.77	25.34	50.34

(**) Significant at 1%, (*) Significant at 5% and (ns) not significant, according to the F test; PILA 50% = Period of inoculation until the lesion reaches 50% of the circumference; PILA 100% = Period of inoculation until the lesion reaches 100% of the circumference; AULAEC = Area under the lesion area expansion curve; AULLEC = Area under the lesion length expansion curve; AULWEC = Area under the lesion width expansion curve.

Table 2. Means of resistance characteristics of BC1s and controls, evaluated for the fungus *Fusarium solani.* Cáceres, Mato Grosso, 2021.

Trea	NDP	NPL50%	PILA50%	PILA100%	AULAEC	AULLEC
BC1-02	0.66 b	2.33 a	31.22 a	31.22 a	32.39 b	17.63 b
BC1-03	1.33 a	2 a	24.88 a	24.88 b	52.04 b	14.74 b
BC1-09	2 a	0 c	8.08 c	8.08 d	23.43 b	11.60 b
BC1-12	2 a	1 b	16.99 b	18.11 c	72.87 b	17.51 b
BC1-13	0.66 b	1.33 b	24.77 a	28.10 b	58.71 b	17.17 b
BC1-14	0 b	3 a	33 a	33 a	21.33 b	14.90 b
BC1-16	1 b	1.33 b	22.16 b	23.05 b	27.37 b	11.93 b
BC1-20	0 b	1.66 b	20.88 b	25.22 b	120.97 a	20.72 b
BC1-21	0.33 b	1.33 b	19.38 b	24.22 b	130.60 a	25.41 a
BC1-24	0 b	2.66 a	31 a	32.77 a	41.12 b	16.27 b
HI	0 b	3 a	33 a	33 a	17.22 b	16.02 b
P. nitida	0 b	3 a	33 a	33 a	20.74 b	15.29 b
P. edulis	2.66 a	1 b	14.54 c	16.66 c	175.10 a	29.72 a
Control	0 b	3 a	33 a	33 a	25.33 b	17.54 b

The means followed by the same letter in the columns do not differ by the Scott Knott test ($p < 0.05$).

Table 3. Grouping of *Passiflora* spp. by the Tocher method, based on ten characteristics of resistance to collar rot. Cáceres, Mato Grosso, 2021.

Groups	Genotypes
I	BC1-25, BC1-49, BC1-72, BC1-73, BC1-63 and BC1-31
II	BC1-27, BC1-48, BC1-58, BC1-74, BC1-68, BC1-80, BC1-81, BC1-84, BC1-36, BC1-66, BC1-69, BC1-43, BC1-45, BC1-26, BC1-83, BC1-61, BC1-44, BC1-86, BC1-57, BC1-28, Control, BC1-71, HI, BC1-52, *P. nitda*, BC1-53, BC1-59, BC1-38, BC1-41, BC1-50, BC1-65, BC1-75, BC1-37, BC1-78, BC1-64, BC1-54, BC1-77, BC1-47, BC1-35, BC1-46, BC1-39, BC1-34, BC1-60, BC1-67, BC1-70, BC1-82, BC1-30, BC1-85, BC1-56, BC1-42 and BC1-51
III	*P. edulis*, BC1-79, BC1-55, BC1-40, BC1-29 and BC1-76
IV	BC1-32 and BC1-62
V	BC1-33

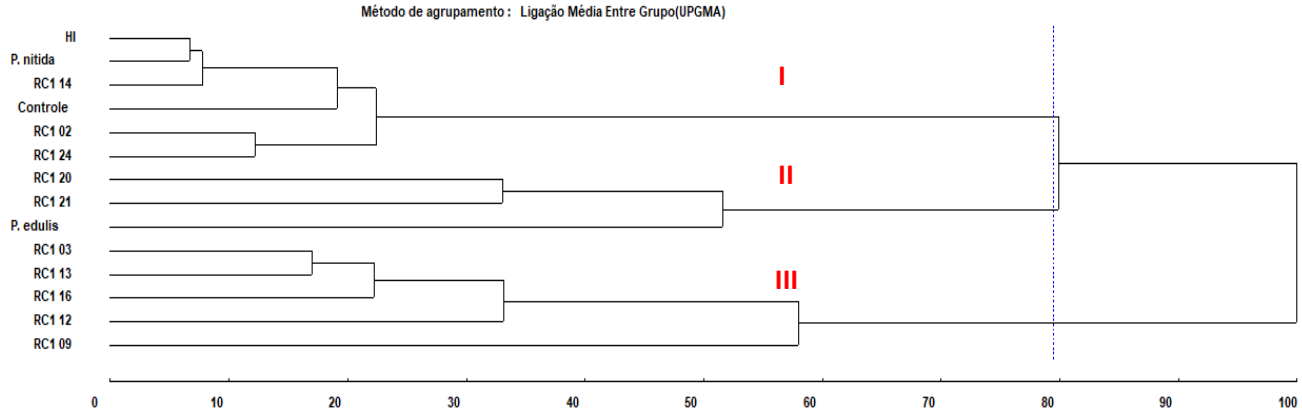

Figure 1. Dendrogram representing the genetic divergence between the 10 backcross genotypes of *Passiflora* spp. obtained by the UPGMA grouping method from ten characteristics of resistance to collar rot. Cáceres, Mato Grosso, 2021.

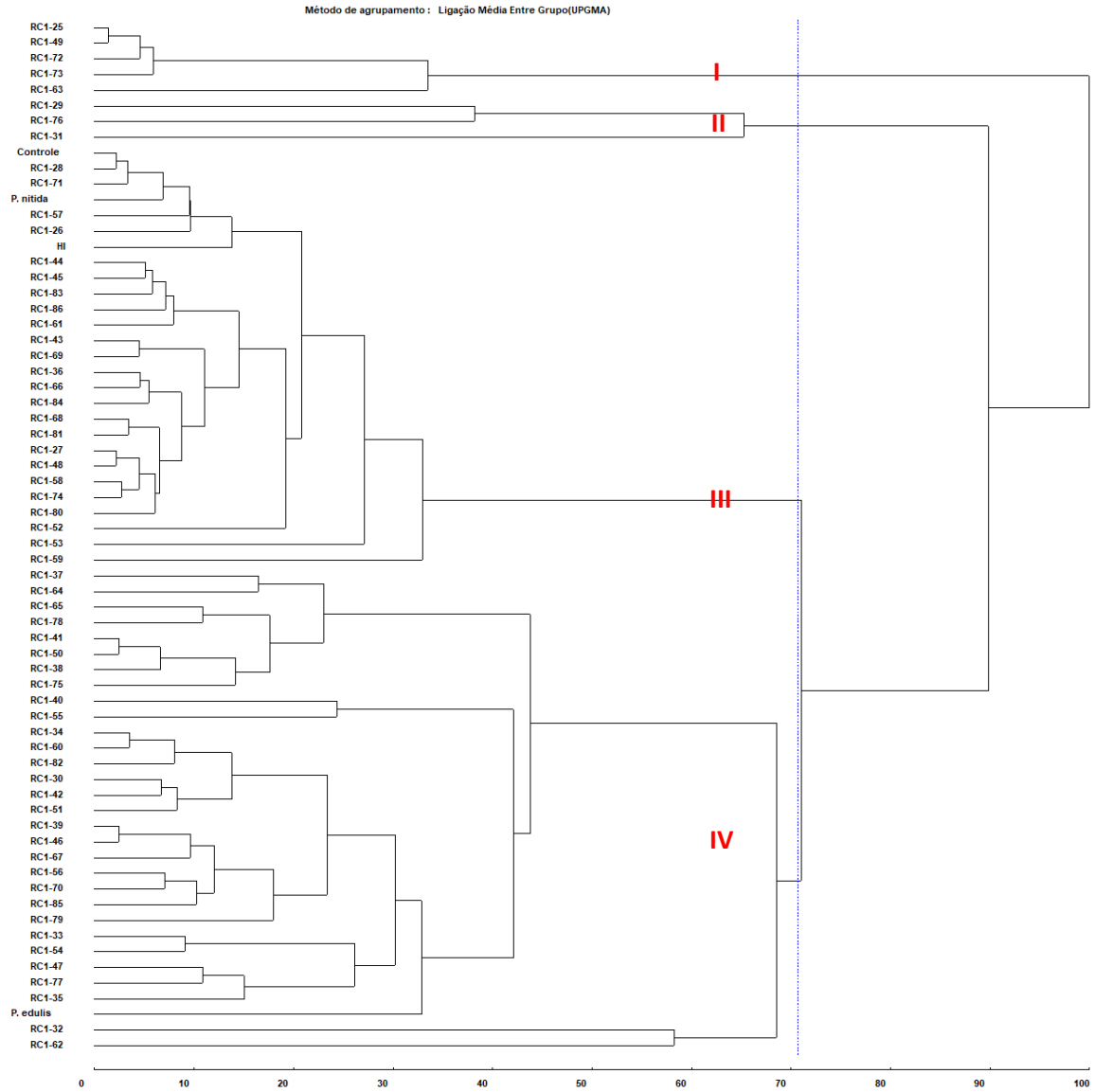

Figure 2. Dendrogram representing the genetic divergence between the 63 backcross genotypes of *Passiflora* spp. obtained by the UPGMA grouping method from ten characteristics of resistance to collar rot. Cáceres, Mato Grosso, 2021.

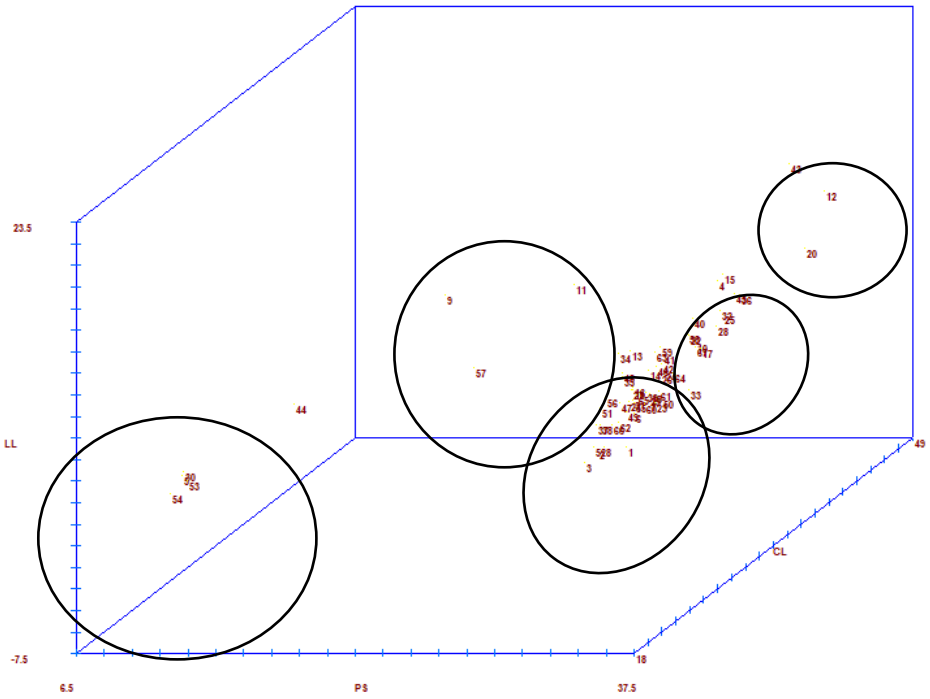

Figure 3. Graphical dispersion of genotypes for resistance to *Fusarium solani* (Survival period, Length of the lesion and width of the lesion), for the 63 BC1s of passion fruit and the controls (*P. nitida*, HI and *P. edulis*). Cáceres, Mato Grosso, 2021.

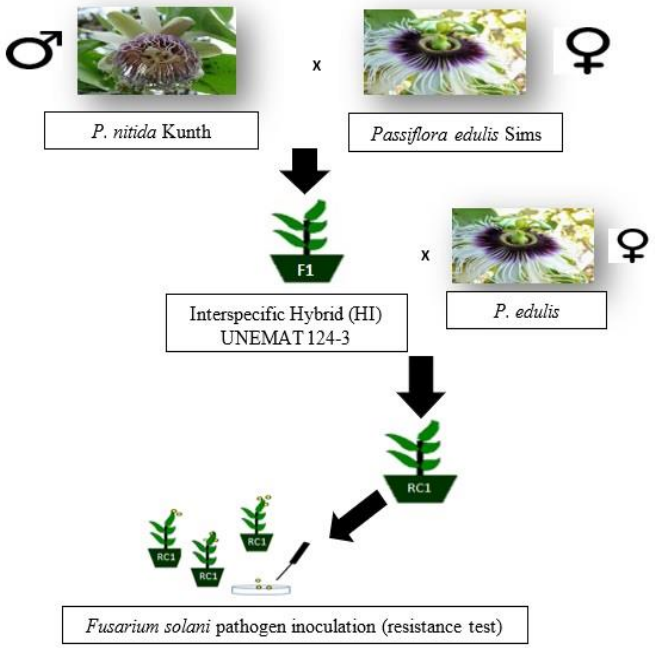

Figure 4. Genotypes of *Passiflora* spp. used in interspecific crossings to obtain families of complete siblings aiming resistance to collar rot. Cáceres, Mato Grosso, 2021.

incompatibility (Pereira et al., 2005). One of the possible causes of a successful hybridization is that the species *P. nitida* and *P. edulis* have the same number of chromosomes (2n=18) and that both belong to the subgenus *Passiflora* (Marostega, 2019).

The grouping by the UPGMA hierarchical method obtained an adjustment with the original distances of 72% (CCC of r=0.72). This value, according to Sokal and Rohlf (1962), is considered acceptable, demonstrating that the grouping method is in accordance with original distances, with no major distortions in the results.

Group I, formed by HI, *P. nitida*, the control, and the BC1s 02, 14 and 24, obtained the best values for the evaluated strength characteristics. The BC1s in this group have a high genetic resistance to *F. solani*, as they grouped with the resistant species *P. nitida* (Fischer et al., 2005; Preisigke et al., 2015; Freitas et al., 2016), the HI 124-3 (Marostega et al., 2020), and the control. Therefore, the BC1s 02, 14 and 24 should be selected to continue the passion fruit breeding program.

Regarding the test 2, the low germination percentage of hybrid seeds, according to Freitas et al. (2015b), may be due

to factors such as embryo death caused by endosperm degeneration. There were also problems with seed viability in interspecific hybridization using wild species and *P. edulis* (Junqueira et al. 2006; Freitas et al., 2015b; Marostega et al., 2020).

The cophenetic correlation coefficient obtained between the Euclidean distance matrix and the cophenetic distance matrix (r=0.92) revealed a good fit between the graphical representation of distances and its original matrix (Rohlf, 2000), enabling making inferences through a visual evaluation of Figure 2. In this type of graphical representation, the efficiency with which the original matrix of distance data is represented in the figure directly implies the possibility of its use.

Groups I, II and III are composed of BC1s with the best averages for resistance characteristics and are considered resistant to *F. solani*. Group III is formed by the largest number of resistant BC1s (24). In addition to BC1s, this group is composed of the resistant controls HI (Marostega et al., 2020), *P. nitida* (Fischer et al., 2005; Preisigke et al., 2015; Freitas et al., 2016), and the control (genotype that did not receive the inoculum). Therefore, all BC1s from groups I, II and III can be selected to continue the passion fruit breeding program.

Group IV, composed of 30 BC1s and *P. edulis* and considered susceptible to *F. solani* (Fischer et al., 2005; Preisigke et al., 2015; Pereira et al., 2019), had the worst means in relation to genetic resistance to the fungus. The BC1s of this group have no resistance and should not continue the passion fruit genetic improvement program.

The Tocher optimization method provided a different result from that found by the UPGMA hierarchical method: five groups formed (Table 3). This may have happened because in the UPGMA hierarchical method the genotypes are grouped using the arithmetic means of dissimilarity measurements, which avoid a characterization using extreme values (Cruz et al., 2011). Tocher's optimization method performs simultaneous grouping, which performs the separation of genotypes into groups at once. This method keeps the mean intragroup distance always lower than any intergroup distance (Cruz and Carneiro, 2006).

The method of importance of characters has the purpose of drawing a scatter plot that can identify similar genotypes, making it possible to simplify the interpretation of results. The feasibility of this interpretation is restricted to variables that exceed 80% (Cruz et al., 2004). In this study, the first three variables explain 82.95% of the total variation; therefore, the use of a three-dimensional graph is justified (Figure 03).

The graphic dispersion of genotypes considering the importance of characters (Figure 3) had a different behavior from that of groupings by the UPGMA and Tocher methods. This result is different from that found by Benitez et al. (2011), who, evaluating the genetic diversity of rice genotypes to salt tolerance, observed agreement in the grouping of genotypes by the Tocher optimization method and by graphical dispersion.

Genetic resistance evaluations of *Passiflora* spp. to *F. solani* using seedling inoculation method are scarce in the literature (Preisigke et al., 2015; Marostega et al., 2020, 2021). This study precisely identified 25 passion fruit genotypes that are resistant to *F. solani* depending on the inoculation method used.

The identification of resistance sources in germplasm banks is an interesting strategy for the development of disease-resistant genotypes (Freitas et al., 2016). In this study, the wild species *P. nitida* has a great potential for use in genetic improvement programs with interspecific hybridization since, in the crossing of HI 124-3 with susceptible plants, the resistance genes to *F. solani* were transferred to the progenies. Through multivariate analysis, UPGMA hierarchical method, torch optimization, and 3D graphic dispersion, it was possible to identify the BC1s 25, 26, 27, 28, 31, 43, 45, 48, 53, 57, 58, 61, 63, 66, 68, 71, 72, 73, 74, 80, 81, 83, 84, 86 and 87, as resistant to *F. solani*. Therefore, these BC1s should continue the passion fruit genetic improvement program.

Materials and methods

The experiments were carried out at the Plant Genetic Improvement Laboratory (LMGV) at the State University of Mato Grosso (UNEMAT), Cáceres campus. The location was at 16º 11' 42'' S and 57º 40' 51'' W, with an average annual temperature of 26.24 ºC, total annual precipitation of 1,333 mm, and altitude of 118 m. The municipality integrates the mesoregion of the Center-South of Mato Grosso and the microregion of Alto Pantanal, 215 km from the capital, where the climate is tropical hot and humid with dry winters (Neves et al., 2011).

Plant materials

The Interspecific Hybrid (HI) selected for generation improvement was the UNEMAT 124-3, which is described by Marostega et al. (2020) as resistant to *F. solani* and is deposited at the Active Germplasm Bank of the State University of Mato Grosso (UNEMAT). This HI is the result of the crossing of full brothers between the species *Passiflora edulis* Sims and the wild species *Passiflora nitida* Kunth., which has a high resistance to *F. solani* (Preisigke et al., 2015).

In order to recover the genotype of the recurrent parent, the crossing of HI with *P. edulis* was performed, obtaining the genotypes of the first generation of backcross (BC1). For the production of BC1 genotypes, the cultivar BRS Sol do Cerrado was used (Figure 4). In addition to having large, yellow fruits, pulp yield around 38% and a high productivity, it also has tolerance to leaf diseases, such as bacteriosis, anthracnose, and virus. However, it is highly susceptible to diseases caused by soil pathogens (Embrapa, 2008).

The transfer of pollen to the stigma was performed manually using tweezers, carefully rubbing the anther over the stigma of each flower protected in pre-anthesis with a paper bag according to the methodology described by Bruckner and Otoni (1999).

The period of anthesis of the genotypes involved in the crosses was 9 am for HI and 12 pm for *P. edulis*. Therefore, a technique of preserving pollen in silica gel at 4ºC for up to 24 hours was used (Almeida et al., 2011). The flower buds belonging to the recurrent parent were emasculated before anthesis. After crossing, the flowers were tagged and, five days after pollination, the setting rate was verified (Marostega et al., 2020).

The BC1 seeds were sown in Vivatto 128-cell Styrofoam trays and kept in a screen with a 50% shade. After three months, the seedlings were transplanted into plastic bags (15x25 cm) containing the same substrate. They were taken to the field, spaced 1.50 x 3.00 m apart, in an espalier system with two wires placed 1.50 and 2.00 m from the soil level. Normal soil preparation and culture treatments were adopted for the

crop (Carvalho et al., 2015), with a monthly fertilization of 25 g of N and 30 g of KCL and semiannual fertilization with 30 g of P2O5 per plant. The irrigation was by drippers previously installed in the experimental field.

Treatments

The BC1 resistance tests were carried out twice. The first test was carried out with ten BC1s adducts that are in the field; for this, clonal seedlings were produced in the form of cuttings from each plant for the resistance test. For evaluation, the clonal seedlings in the form of cuttings of each genotype were placed in a randomized blocks experiment with three blocks and three plants per plot.

The second test was carried out with direct inoculation into BC1s that were planted in pots with no replications. Resistance evaluation took place in 63 BC1s when the seedlings were 15 cm tall.

Furthermore, clones of *P. nitida* and HI were used as a positive (resistant) control and clonal seedlings of *P. edulis* as a negative (susceptible) control.

In both tests, a 3:1 mixture of substrate and sand was used. Fertilization was performed once a week with 1 g of P2O5, 0.5 g of N and 0.6 g of KCL per L.

Preparation of isolates

For inoculation, FSUNEMAT40 isolates from *F. solani* were used. This isolate was the most aggressive compared to the other *F. solani* isolates belonging to the LMGV mycotheca (Marostega et al., 2019).

For the production of the inoculum, the isolate preserved in filter paper was placed in Petri dishes containing PDA culture medium (potato-dextrose-agar) and kept at 25 ºC with a 12-hour photoperiod for seven days in a BOD.

Inoculation

Inoculation was carried out with a disc of pathogen mycelium, five millimeters in diameter, grown in PDA (potato-dextrose-agar), and fixed with PVC plastic over a small wound, three millimeters in diameter, on the plant's neck, at a height of two centimeters from the soil, by removing the PVC plastic after five days of inoculation (DAI), according to the methodology of Fischer et al. (2005). For treatments without inoculum, a culture medium disk (BDA) without the pathogen mycelium was used.

Traits measured

The evaluation of resistance of genotypes to *F. solani* was quantified considering ten resistance variables as described by Preisigke et al. (2015), namely:

- SP = Survival period;
- NDP = Number of dead plants;
- LL = Lesion length;
- WL = Lesion width;
- NPL-50% = Number of plants in which the lesion reached less than 50% of the circumference;
- PILA 50% = Period of inoculation until the lesion reaches 50% of the circumference;
- PILA 100% = Period of inoculation until the lesion reaches 100% of the circumference;
- AULAEC = Area under the lesion area expansion curve;
- AULLEC = Area under the lesion length expansion curve;
- AULWEC = Area under the lesion width expansion curve.

The evaluations were carried out five days after inoculation. They were carried out every two days until 33 days or until plant death. The lesions were measured as for their length and width of necrotic area using a digital caliper. The area of the lesion (AL, mm2) was estimated considering the formula for calculating the area of an ellipse ($\pi \cdot L \cdot W/4$), where L is the lesion length and W is the lesion width.

Statistical analysis

For test 1, the strength characteristics data were submitted to analysis of variance and significance tested by F test, and the means were compared by Scott Knott test ($p < 0.05$).

A multivariate analysis of resistance characteristics was performed by applying the grouping techniques through the generalized Mahalanobis distance (Mahalanobis, 1936) as a dissimilarity measure, and the delimitation of groups was done by the construction of a dendrogram using the grouping method of the mean link between groups (UPGMA). The fit between the distance matrix and the dendrogram was estimated by the Cophenetic Correlation Coefficient (CCC) (Sokal and Rohlf, 1962).

For test 2, a multivariate analysis of the strength characteristics was performed, applying the grouping techniques using the generalized Euclidean distance as a measurement of dissimilarity. In the delimitation of groups, a dendrogram was plotted using the grouping method of mean links between groups (UPGMA). The fit between the distance matrix and the dendrogram was estimated by Cophenetic Correlation Coefficient (CCC) (Sokal and Rohlf, 1962). A grouping was also formed using the Tocher optimization technique and a scatter plot was plotted using the importance of characters method.

All analyses were performed using the GENES software (Cruz, 2016).

Conclusion

The results show that there is genetic variability in backcrossing genotypes of *Passiflora* spp. in relation to genetic resistance to *Fusarium solani.*

The first test with plants from cuttings identified the BC1s 02, 14, and 24 as resistant to *F. solani*. The trial two with *Passiflora* spp. seedlings, considering the results of the UPGMA hierarchical methods of torch optimization and the graphic dispersion of genotypes through importance of characters, identified the BC1s 25, 26, 27, 28, 31, 43, 45, 48, 53, 57, 58, 61, 63, 66, 68, 71, 72, 73, 74, 80, 81, 83, 84, 86 and 87 as resistant and these BC1s should be selected to continue the passion fruit breeding program.

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Conflict of interest

The authors declare that they have no conflict of interest.

Ethical standards

The experiments shown in the manuscripts submitted for publication comply with the current laws of the country in which they were performed.

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