Association of genes from different sources of resistance to major cacao diseases[1]

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ABSTRACT

This study aimed to select genotypes resistant to witches' broom (WB) and black pod (BP), major cacao diseases in Brazil, as well as incorporate resistance genes to moniliasis supplemented by clones EET75 and UF273, forming populations of second-cycle recurrent selection. *Moniliophthora perniciosa* (2×10^5 basidiospores/mL) was inoculated on 30-day-old seedlings from 72 different progenies, being assessed 60 days later, and a mixture of four isolates of *Phytophthora palmivora* (3×10^5 zoospores/mL) was inoculated on leaf discs from 58 progenies, observing lesions after seven days. Significant effects of progeny were observed in the tests of resistance to both diseases ($p < 0.05$). Scavina-6 expressed resistance to both pathogens, 26 crosses did not differ from free-pollinated progenies of Scavina-6 for WB, and ten crosses were higher and 27 similar for BP. Eight crosses were largely resistant to both diseases.

Keywords: *Moniliophthora perniciosa; Moniliophthora roreri; Phytophthora palmivora*; plant breeding; *Theobroma cacao*.

INTRODUCTION

Witches' broom (WB) (*Moniliophthora perniciosa* (Stahel) Aime & Phillips-Mora) and black pod (BP), caused by three species of *Phytophthora* (*P. palmivora* Butler, *P. citrophthora* (RE Sm. & EH Sm.) Leonian, and *P. capsici* Leonian), are major cacao diseases in Brazil. Also, another pathogen, *Moniliophthora roreri* (Cif.) Evans, Stalpers, Samson & Benny, the agent of frosty pod rot (moniliasis disease) of cacao, is an A1 quarantine pest absent with imminent risk of arrival in Brazil (Oliveira & Luz, 2012).

Obtaining genetic material resistant to these diseases with desirable agronomic characteristics, as well as organoleptic qualities that contribute to obtaining adequate chocolate quality, is the main objective of genetic improvement at present (Moreira *et al*., 2016; Pimenta Neto *et al*., 2018).

Cacao (*Theobroma cacao* L.) is a species of Neotropical origin in the Americas that occurs spontaneously from southern Mexico to Bolivia (Monteiro & Ahnert, 2012). This wide geographical range shows distinct edaphoclimatic conditions that allowed the development of vast genetic diversity with a varied population, representing genetic resources with the potential to obtain varieties resistant to diseases. Several cacao populations have been generated at the Cocoa Research Center (Cepec) in Ilhéus, Bahia, to obtain improved genotypes aiming at selecting clones with more durable resistance, which carry genes from different sources of resistance, as well as increasing the genetic basis in order to hinder pathogen evolution (Paim *et al*., 2006; Yamada *et al*., 2008; Lopes *et al*., 2011; Benjamin *et al*., 2016; Gramacho *et al*., 2016; Pimenta Neto *et al*., 2018).

Thus, this study aimed to form populations of second-cycle recurrent selection for resistance to WB using the North Carolina II design, crossing first-cycle selections with genetically distant and productive materials and

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with other desirable genetic characteristics, including clones with resistance to moniliasis. The formed progenies were tested for resistance to WB and BP. From crosses carry out with the combination of genes from different sources of resistance, progenies and parents resistant to major cacao diseases were selected in the formed populations.

MATERIAL AND METHODS

1.1 Assessment tests for witches' broom

Twenty-two genotypes, fifteen mother plants selected in a first-cycle recurrent selection for resistance to WB, and the seven clones CSG70 (6A), BN34 (7A), SJ02 (9), MCB09 (10), RLF1938 (11), EET75 (12), and UF273 (13), being the first five clones selected in farms of the Bahia cacao region and the last two introduced in Brazil, previously selected as resistant to frost pod rot (FPR), were used as genitors. The mother plants were from the following crosses: CSUL3 x CCN10 (1), CAB301 x CCN10 (2), MO20 x CCN34 (3), CAB148 x MO20 (4), CAB157 x MO20 (5), NA33 x RB39 (6), SCA6 x P4B (7), SCA6 x RB36 (8), CEPEC86 x RB36 (1A), CA5 x RB36 (2A), CCN10 x CAB324 (3A), CCN34 x CAB301 (4A), MO20 x AMAZ15 (5A), TSH1188 x CAB169 (9A), and SCA6 x GU114 (10A). Crosses were carry out to associate genotypes with resistance genes from different sources of Scavina – selections in progenies from CSUL3 x CCN10, CAB301 x CCN10, MO20 x CCN34, CAB148 x MO20, CAB157 x MO20, NA33 x RB39, CEPEC86 x RB36, CA5 x RB36, CCN10 x CAB324, CCN34 x CAB301, and MO20 x AMAZ15; with resistant genotypes from Scavina – TSH1188 x CAB169, SCA6 x GU114, SCA6 x P4B, SCA6 x RB36, SJ02, MCB09, and RLF1938; and with genotypes selected as resistant to moniliasis – EET75 (12) and UF273 (13). These genotypes, selected for productivity, resistance to WB, resistance to FPR and other characteristics of interest, generated 72 progenies. The origin of the clones is shown in Table 1. Genotypes consisted of three genetic designs, composed as follows: diallel 01 with progenitors followed by simple numbers (1, 2, 3, 4, 5, and 6), which were crossed with 7, 8, 9, 10, 11, 12, and 13; diallel 02 with numbering followed by letter A were crossed with 6A, 7A, 9A, 10A, 11, 12, and 13; and the third diallel crossing only the clones. Diallel crossings between progenitors were carried out with unprotected pollination in a North Carolina II design. Clones Catongo and SIC23, used as susceptibility patterns, and Scavina-6 (SCA6), used as resistance pattern, were used as a control to assess the resistance.

After pollinations, the obtained seeds were planted in 288-cm^3 tubes containing a commercial substrate and soil in the ratio 3:1. Plants were maintained in a greenhouse until second leaf flushing was 15 mm (approximately 30 days), and then inoculated by depositing 30 μL of the suspension of 2×10^5 basidiospores/mL of *M. perniciosa* in an agar-water medium at 0.3% on the apical meristem. On the day before inoculation, leaves of first apical flushing were reduced to 1/3 to accelerate the growth of second flushing and better expose the area of the apical bud. After inoculation, seedlings were taken to the humid chamber at 25 °C and relative air humidity of 100% for 48 h. They were then transferred to a greenhouse, where they remained until the end of the assessments, *i.e.*, 60 days after inoculation. Because seeds from the 72 progenies were obtained at different times, ten inoculations were performed at different times, but all of them with the three progenies of the controls.

Plants with presence and absence of WB were assigned with scores 01 and 00, respectively. The type of brooms B, *i.e.*, terminal (TB), axillary (AB), dry (DB), and cotyledonary broom (CB), was also assessed. In addition, AB higher than 1 cm was quantified, and TB length was measured. For the data analysis, the disease index was calculated by the following Luz Index (Rodrigues *et al*., 2019): DI = TB + (0.1 × TBL) + AB + (0.2 × NAB) + CB + (4.3 × DB), where TB is the presence of terminal broom, TBL is the terminal broom length, AB is the presence of axillary broom, NAB = number of axillary brooms higher than 1 cm, CB is the presence of cotyledonary broom, and DB is the presence of dry broom. The coefficient that multiplies DB was defined to allow the plant with dry broom having a DI higher than all the others that did not die. The coefficient for TBL was defined to allow plants with larger terminal broom generating, together with TB, a value close to two, *i.e.*, the double the DI presented by a plant with a very small terminal broom. Similarly, the coefficient for NAB was defined to allow plants with the highest number of large axillary broom having a DI corresponding to twice the DI of plants with only axillary broom lower than 1 cm. The randomized block design was used at each inoculation or test, with 14 plants per replications (56 plants per crossing and inoculation time, repeated once with an equal number of samples).

A model with the sources of variation test or inoculation and progeny was used to analyze differences between progenies in an incomplete block system. Comparisons between the corrected means of progeny for the effects of test or inoculation were performed by the T-test (SAS, 2002). We did not consider to which genetic design or which of the diallels the progeny belonged.

Because progenitor-corrected means are not estimable in the model with the sources of variation mother, father, and test or inoculation (*i.e*)., the means of

mother corrected by principle of incomplete blocks are not estimable at the same time for effects of father and test or father, corrected for mother and test because the tests mixed progenies of the three genetic designs), DI correction was applied for each test to analyze differences between progenitors. In this case, the corrected index for each plant is equal to the original index (DI) multiplied by the inverse of the sum of the means of the indices of the three controls in that test and divided by the sum of the overall means of the controls in all tests. Thus, DIs of each plant were corrected for the effect of the test to which they belong by the ratio between the mean DIs of the controls in that test and their overall mean DIs for all tests. The effects of progenitors were analyzed in the model with the sources of variation father and mother for each of the three diallels from the corrected DI. The previous model was used to compare fathers within mothers or mothers within fathers, with uncorrected DI and model with the sources of variation test or inoculation and progeny. After the assessments, diseased plants were incinerated, and healthy plants were selected to further assessment of BP resistance.

1.2 Assessment tests for black pod

Fifty-eight progenies among surviving plants and without the presence of WB symptoms from the previous experiment were selected to be tested for resistance to BP using the leaf disc method (Nyassé *et al*., 1995). The isolates of *P. palmivora* used were 1744, 1778, 1845, and 1913, obtained from the Arnaldo Medeiros collection at Cepec, originated from cacao pods samples collected in the following counties and years: Uruçuca (2011), Camacan (2011), Mutuípe (2011) and Belmonte (2010), respectively. These isolates were selected based on their high aggressiveness to cacao among 100 *P. palmivora* isolates tested in previous studies (Lessa, 2017). Healthy leaves of surviving plants from crossings were collected and taken to the laboratory of *Phytophthora*, where they were sanitized and 15-mm diameter discs were cut from the leaf blade. These discs were arranged with the abaxial part up in boxes containing foam moistened with sterile water to form a humid chamber and provide favorable conditions for pathogen development.

A 10-µm aliquot of zoospore suspension from the mixture of four isolates, obtained according to the protocol

Table 1: Origin of clones used as parents or grandparents in the tested crossings

Clone	Abbreviation‘s mean	Genetic group	Origin
AMAZ15*	Amazon	Amazonian	Iquitos, Peru
BN34	Boa Nova	Trinitarian	Bahia, Brazil
CA5*	Careiro	Amazonian	Amazon, Brazil
CAB148	Cocoa from Brazilian Amazon	Amazonian	Acre, Brazil
CAB157	Cocoa from Brazilian Amazon	Amazonian	Acre, Brazil
CAB169	Cocoa from Brazilian Amazon	Amazonian	Acre, Brazil
CAB301	Cocoa from Brazilian Amazon	Amazonian	Amazon, Brazil
CAB324*	Cocoa from Brazilian Amazon	Amazonian	Amazon, Brazil
Catongo*	Mutation of common cocoa	Amazonian	Bahia, Brazil
CCN10*	Castro Naranjal collection	Trinitarian	Pichilingue, Ecuador
CCN34*	Castro Naranjal collection	Trinitarian	Pichilingue, Ecuador
CEPEC86*	Cocoa Research Center	Amazonian	Bahia, Brazil
CSG70	Conjunto Serra Grande	Trinitarian	Bahia, Brazil
CSUL3*	Southern cross	Amazonian	Acre, Brazil
EET75*	Tropical experimental station	Trinitarian	Pichilingue, Ecuador
GU114*	Guiana	Amazonian	Haut Camopi, French Guiana
MCBC9	Manoel Carlos Barreto	Trintário	Bahia, Brazil
MO20*	Morona	Amazonian	Morona, Peru
NA33*	Nanay	Amazonian	Nanay, Peru
P4B*	Pound 4 / B	Amazonian	Loreto, Peru
RB36*	Rio Branco	Amazonian	Acre, Brazil
RB39*	Rio Branco	Amazonian	Acre, Brazil
RLF1938	Romildo Luiz Fernandes	Trinitarian	Bahia, Brazil
SCA6*	Scavina	Amazonian	Ucayali, Peru
SIC23*	Cocoa institute selection	Amazonian	Bahia, Brazil
SJ02	São José Farm	Trinitarian	Bahia, Brazil
TSH1188*	Selected hybrid in Trinidad	Trinitarian	Saint George, Trinidad and Tobago
UF273*	United Fruit	Trinitarian	Limón, Costa Rica

(*Turnbull & Hadley, 2019).

of the Luz *et al*. (2008) was adjusted to a concentration of 3×10^5 zoospores/mL and placed on the center of each leaf disc. The boxes were closed and incubated at 25 °C in the dark for seven days, when the assessment was performed using a scoring scale developed by Nyassé *et al*. (2002) with values varying from 0 to 5. The disease severity index (DI) was determined for each genotype from the scores using the equation of McKinney (1923): Infection index (%) = [(Σ (scale degree × frequency) × 100] / [(total number of units × maximum scale degree)].

Two experiments were set up with all the 58 progenies in a randomized block design with four replications containing ten discs per clone, totaling 40 discs inoculated per clone and experiment. The analysis of differences between means of progenies was conducted under the model with the sources of variation experiment and treatment, without considering the genetic designs. The model experiment, mother, and father was used to analyze differences between progenitors for each of the three diallels. The previous model was used to analyze mother within father or father within mother.

RESULTS AND DISCUSSION

1.1 Assessment for witches' broom

The proposal presented here for defining the disease index for the early assessment of cacao seedlings took into account a very important factor: the dry broom. Therefore, plant death due to the disease was considered in this study. In addition, the methodology gives greater or lesser weight to the types of brooms formed according to the number of axillary broom and size of terminal broom. This formula also included the presence of cotyledonary broom because of the relatively high frequency of this type of symptom in plants from some genotypes.

Significant effects for inoculation test ($p = 0.0415$) and progeny ($P < 0.0001$) were observed by the F-test, with ten inoculations tests with different progenies in each test and three controls in all tests. As a primary and extremely important element, among the 72 crossings, 69 differed from the two susceptibility controls (Catongo and SIC23), showing the effectiveness of progenitor selection and prospects of gain with plant selection within these progenies (Table 2). Non-distinct crossings from one or both controls were [(MO20 x AMAZ15 (5A)) X UF273 (13)], [(CAB157 x MO20 (5)) X EET75 (12)], and (CAB148 x MO20 (4)) X UF273 (13)], all of them with one of the progenitors selected only for moniliasis and none of them with any Scavina ancestry.

At the other end of the list, 26 crossings did not differ from the control progeny of Scavina-6: [MCB09 (10) X EET75 (12)], [(CEPEC86 x RB36 (1A)) X RLF1938 (11)], [(CEPEC86 x RB36 (1A)) X (SCA6 x GU114 (10A))], [(CEPEC86 x RB36 (1A)) X CSG70 (6A)], [(CEPEC86 x RB36 (1A)) X (TSH1188 x CAB169 (9A))], [(CSUL3 x CCN10 (1)) X UF273 (13)] [(CSUL3 x CCN10 (1)) X MCB09 (10)], [(CSUL3 x CCN10 (1)) X (SCA6 x RB36 (8))], [(CA5 x RB36 (2A)) X UF273 (13)], [(CA5 x RB36 (2A)) X (TSH1188 x CAB169 (9A))], [(CAB301 x CCN10 (2)) X SJ02 (9)], [(CCN10 x CAB324 (3A)) X (SCA6 x GU114 (10A))], [(CCN10 x CAB324 (3A)) X (TSH1188 x CAB169 (9A))], [(MO20 x CCN34 (3)) X RLF1938 (11)], [(MO20 x CCN34 (3)) X (SCA6 x P4B (7))], [(MO20 x CCN34 (3)) X (SCA6 x RB36 (8))], [(MO20 x CCN34 (3)) X SJ02 (9)], [(CCN34 x CAB301 (4A)) X (SCA6 x GU114 (10A))], [(CCN34 x CAB301 (4A)) X (TSH1188 x CAB169 (9A))], [(CAB148 x MO20 (4)) X RLF1938 (11)], [(MO20 x AMAZ15 (5A)) X (SCA6 x GU114 (10A))], [(CAB157 x MO20 (5)) X RLF1938 (11)], [(CAB157 x MO20 (5)) X UF273 (13)], [(CAB157 x MO20 (5)) X (SCA6 x RB36 (8))], [(NA33 x RB39 (6)) X EET75 (12)], and [(NA33 x RB39 (6)) X (SCA6 x RB36 (8))]. Scavina-6 is a clone resulting from the first studies aimed at resistance to cacao diseases started in the 1930s in Latin America and the Caribbean, and from Pound collections (Pound, 1938) in Peru. Per se and in the progeny was practically immune to WB in their first assessment in Trindade (Bartley, 2005), which would indicate possession of more than one resistance allele – all progeny practically immune –, with an exceptional behavior until today depending on fungus population. Scavina-6 is still widely used as a source of resistance to *M. perniciosa* in current breeding programs with cacao clones, but new sources of resistance need to be incorporated as a strategy to obtain lasting resistance (Pinto & Pires, 1998).

Thus, these various progenies have a mean behavior equivalent to that of a progeny known to have resistance alleles in all plants. Others, with means not so favorable but distinct from susceptible progenies and, therefore, carrying resistance alleles, may be derived from heterozygous parents for resistance even with more than one allele (in this case, in different loci), which could segregate and generate non-resistant plants, which would raise the mean DI of the progeny.

All progenies that differed from susceptible controls may provide resistant plants for selecting clones for assessment and indication of commercial varieties or generation of a new selection cycle. However, this selection will be carried out with resistance and productivity field data, especially from plants selected as resistant in this early selection phase, considering, in addition to the per se plant performance, the combining ability of each parent and the mean progeny performance.

Among the progenitors involved in the 26 most resistant crossings, the mother plants SCA6 x GU114 (10A) and TSH1188 x CAB169 (9A) and clone RLF1938 (11) stood out since all of them appear in four of these

Table 2: Mean disease index of witches' broom in cacao seedlings from crossings (DI) and the probability of error (P) for rejecting the hypothesis of equality between means of each progeny and controls by the T-test

Crossings	Disease index (DI)	Controls		
		CAT 1.878526	SIC23 2.134295	SCA6 0.275166
MCB09 (10) x EET75 (12)	0.26236770	<.0001	<.0001	0.9676
MCB0 9 (10) x UF273 (13)	0.98332349	<.0001	<.0001	<.0001
RLF1938 (11) x EET75 (12)	1.21532022	<.0001	<.0001	<.0001
RLF1938 (11) x UF273 (13)	1.16995865	<.0001	<.0001	<.0001
CEPEC86 x RB36 (1A) x SCA6 x GU114 (10A)	0.26231648	<.0001	<.0001	0.9299
CEPEC86 x RB36 (1A) x RLF1938 (11)	0.30737087	<.0001	<.0001	0.8015
CEPEC86 x RB36 (1A) x EET75 (12)	0.77984161	<.0001	<.0001	0.0009
CEPEC86 x RB36 (1A) x UF273 (13)	1.27083093	<.0001	<.0001	<.0001
CEPEC86 x RB36 (1A) x CSG70 (6A)	0.17017603	<.0001	<.0001	0.4494
CEPEC86 x RB36 (1A) xTSH1188 x CAB169 (9A)	0.48887735	<.0001	<.0001	0.1512
CSUL3 x CCN10 (1) x MCBC9 (10)	0.10930392	<.0001	<.0001	0.4324
CSUL3 x CCN10 (1) x RLF1938 (11)	1.26759565	<.0001	<.0001	<.0001
CSUL3 x CCN10 (1) x EET75 (12)	0.82017957	<.0001	<.0001	<.0001
CSUL3 x CCN10 (1) x UF273 (13)	0.39253358	<.0001	<.0001	0.4163
CSUL3 x CCN10 (1) x SCA6 x P4B (7)	0.69903514	<.0001	<.0001	0.0010
CSUL3 x CCN10 (1) x SCA6 x RB36 (8)	0.55446115	<.0001	<.0001	0.0620
CSUL3 x CCN10 (1) x SJ02 (9)	1.23771981	<.0001	<.0001	<.0001
CA5 x RB36 (2A) x RLF1938 (11)	0.86136731	<.0001	<.0001	0.0001
CA5 x RB36 (2A) x EET75 (12)	0.82965478	<.0001	<.0001	<.0001
CA5 x RB36 (2A) x UF273 (13)	0.59216814	<.0001	<.0001	0.1580
CA5 x RB36 (2A) x TSH1188 x CAB169 (9A)	0.58292402	0.0001	<.0001	0.3568
CAB301 x CCN10 (2) x MCBC9 (10)	1.13292539	<.0001	<.0001	<.0001
CAB301 x CCN10 (2) x RLF1938 (11)	0.73288443	<.0001	<.0001	0.0003
CAB301 x CCN10 (2) x EET75 (12)	0.82615348	<.0001	<.0001	0.0054
CAB301 x CCN10 (2) x UF273 (13)	0.89303728	<.0001	<.0001	<.0001
CAB301 x CCN10 (2) x SCA6 x P4B (7)	0.84546700	<.0001	<.0001	<.0001
CAB301 x CCN10 (2) x SCA6 x RB36 (8)	0.64567362	<.0001	<.0001	0.0113
CAB301 x CCN10 (2) x SJ02 (9)	0.51708489	<.0001	<.0001	0.0546
CCN10 x CAB324 (3A) x SCA6 x GU114 (10A)	0.50806462	<.0001	<.0001	0.0695
CCN10 x CAB324 (3A) x RLF1938 (11)	0.54574495	<.0001	<.0001	0.0388
CCN10 x CAB324 (3A) x EET75 (12)	1.11338835	0.0004	<.0001	<.0001
CCN10 x CAB324 (3A) x UF273 (13)	0.84417142	<.0001	<.0001	0.0058
CCN10 x CAB324 (3A) xTSH1188 x CAB169 (9A)	0.47418613	<.0001	<.0001	0.1222
MO20 x CCN34 (3) x RLF1938 (11)	0.46385543	<.0001	<.0001	0.1493
MO20 x CCN34 (3) x UF273 (13)	0.80422209	<.0001	<.0001	0.0162
MO20 x CCN34 (3) x SCA6 x P4B (7)	0.28851720	<.0001	<.0001	0.9182
MO20 x CCN34 (3) x SCA6 x RB36 (8)	0.32270728	<.0001	<.0001	0.8318
MO20 x CCN34 (3) x SJ02 (9)	0.49044389	0.0021	0.0003	0.6339
CCN34 x CAB301 (4A) x SCA6 x GU114 (10A)	0.33895424	<.0001	<.0001	0.6306
CCN34 x CAB301 (4A) x RLF1938 (11)	0.77504600	<.0001	<.0001	<.0001
CCN34 x CAB301 (4A) x EET75 (12)	1.42855286	0.0080	<.0001	<.0001
CCN34 x CAB301 (4A) x UF273 (13)	0.80682535	<.0001	<.0001	<.0001
CCN34 x CAB301 (4A) x CSG70 (6A)	0.80651601	<.0001	<.0001	<.0001
CCN34 x CAB301 (4A) x BN34 (7A)	1.28318426	0.0025	<.0001	<.0001
CCN34 x CAB301 (4A) x TSH1188 x CAB169 (9A)	0.15517461	<.0001	<.0001	0.3753
CAB148 x MO20 (4) x MCBC9 (10)	1.55850781	0.0170	<.0001	<.0001
CAB148 x MO20 (4) x RLF1938 (11)	0.22898036	<.0001	<.0001	0.7639
CAB148 x MO20 (4) x UF273 (13)	1.97484709	0.8708	0.7878	0.0041
CAB148 x MO20 (4) x SCA6 x P4B (7)	1.40586739	0.0010	<.0001	<.0001
CAB148 x MO20 (4) x SJ02 (9)	0.98465817	0.0002	<.0001	0.0028

To be continued...

Continuation Table 2

Crossings	Disease index (DI)	Controls		
		CAT 1.878526	SIC23 2.134295	SCA6 0.275166
MO20 x AMAZ15 (5A) xSCA6 x GU114 (10A)	0.43917588	<.0001	<.0001	0.2079
MO20 x AMAZ15 (5A) x EET75 (12)	1.24824115	<.0001	<.0001	<.0001
MO20 x AMAZ15 (5A) x UF273 (13)	1.82716434	0.7939	0.1176	<.0001
MO20 x AMAZ15 (5A) x CSG70 (6A)	0.69640765	<.0001	<.0001	0.0494
MO20 x AMAZ15 (5A) x BN34 (7A)	1.26681025	0.0001	<.0001	<.0001
MO20 x AMAZ15 (5A) xTSH1188 x CAB169 (9A)	0.74904369	<.0001	<.0001	0.0086
CAB157 x MO20 (5) x MCBC9 (10)	0.93062792	<.0001	<.0001	0.0015
CAB157 x MO20 (5) x RLF1938 (11)	0.36615577	<.0001	<.0001	0.5336
CAB157 x MO20 (5) x EET75 (12)	1.80944936	0.5907	0.0109	<.0001
CAB157 x MO20 (5) x UF273 (13)	0.64574296	<.0001	<.0001	0.0569
CAB157 x MO20 (5) x SCA6 x P4B (7)	1.03421936	<.0001	<.0001	<.0001
CAB157 x MO20 (5) x SCA6 x RB36 (8)	0.50973135	<.0001	<.0001	0.1240
CAB157 x MO20 (5) x SJ02 (9)	0.61125419	<.0001	<.0001	0.0107
NA33 x RB39 (6) x MCBC9 (10)	0.78204961	<.0001	<.0001	0.0002
NA33 x RB39 (6) x RLF1938 (11)	1.13390423	0.0002	<.0001	<.0001
NA33 x RB39 (6) x EET75 (12)	0.52477423	<.0001	<.0001	0.0660
NA33 x RB39 (6) x UF273 (13)	0.62723668	<.0001	<.0001	0.0079
NA33 x RB39 (6) x SCA6 x P4B (7)	0.86889884	<.0001	<.0001	<.0001
NA33 x RB39 (6) x SCA6 x RB36 (8)	0.49357779	<.0001	<.0001	0.1651
NA33 x RB39 (6) x SJ02 (9)	1.33420130	0.0001	<.0001	<.0001
SJ02 (9) x EET75 (12)	1.00411401	<.0001	<.0001	<.0001
SJ02 (9) x UF273 (13)	0.94675223	<.0001	<.0001	<.0001
CATONGO[(1)]	1.87852665		0.0008	<.0001
SIC23[(1)]	2.13429554	0.0008		<.0001
SCA6[(2)]	0.27516669	<.0001	<.0001	

[(1)] Susceptibility control; [(2)]Resistance control.

crossings, and the first two presented the lowest corrected means of progenitors (0.3424 and 0.4985, respectively). Among the 26 crossings that were similar to Scavina-6, CEPEC86 x RB36 (1A) should also be highlighted, as it also appears four times in the list when combined with RLF1938 (11), CSG70 (6A), SCA6 x GU114 (10A), and TSH1188 x CAB169 (9A).

The two clones resistant to moniliasis used in the experiments (EET75 and UF273), formed five progenies as resistant as the standard: [MCB09 (10) X EET75 (12)], [(CSUL3 x CCN10 (1)) X UF273 (13)], [(CA5 x RB36 (2A)) X UF273 (13)], [(CAB157 x MO20 (5)) X UF273 (13), and [(NA33 x RB39 (6)) X EET75 (12)], which indicates their great potential also for WB. Pimenta Neto *et al*. (2018) also found that five of the offspring of the clones EET75 (12) and UF273 (13) crossed with other genetic materials generated progenies with very low WB index, three of them crossed with EET75 (12) and two with UF273 (13).

Regarding the performance of fathers and mothers used in the three tests, MO20 x CCN34 (3) was the best mother in diallel 01, with no difference only from NA33 x RB39 (6) (Table 3). Benjamin *et al*. (2016) used this last crossing in field assessments and concluded that RB39 is a highly promising source of resistance to WB, promoting the durability of this character when combined with other sources. This latter progenitor did not differ from the progenitors CSUL3 x CCN10 (1), CAB301 x CCN10 (2) and MO20 x CCN34 (3) which also showed low DI means.

The best father for crossings with MO20 x CCN34 (3) was SCA6 x P4B (7), but this crossing only differed significantly ($p < 0.05$) from the crossing with UF273 (13), which was, regarding resistance, selected only for moniliasis. The crossing [(MO20 x CCN34 (3)) X UF273 (13)] showed no ancestry of Scavina. The parents SCA6 x RB36 (8), RLF1938(11), and SJ02 (9), all with ancestry of Scavina, generated progenies with means close to that generated by the progenitor SCA6 x P4B (7) (means shown in Table 2 and probability of error for rejecting the hypothesis of equality between means not shown).

The best parents for crossings with NA33 x RB39 (6) were SCA6 x RB36 (8) and EET75 (12), both crossings significantly different from the two worst: SJ02(9) and RLF1938(11), which are very contrasting results when compared to those of the crossings with MO20 x CCN34 (3).

Regarding the overall means of parents of diallel 01, the best parents were the mother SCA6 x RB36 (8) and clones RLF1938 (11) and UF273 (13), not distinct from each other and significantly different from all others.

The father SCA6 x RB36 (8) was four times among the most resistant crossings when combined with mothers CSUL3 x CCN10 (2), MO20 x CCN34 (3), CAB157 x MO20 (5), and NA33 x RB39 (6). The father RLF1938 (11) also four times appeared, being the mothers CEPEC86 x RB36 (1A), MO20 x CCN34 (3), CCN34 x MO20 (4), and CAB157 x MO20 (5). Clone UF273 (13) appeared in this ranking with three satisfactory combinations with the mothers CEPEC86 x RB36 (1), CA5 x RB36 (2A), and CAB157 x MO20 (5).

The best mother in diallel 02 was CEPEC86 x RB36 (1A), which did not differ only from CCN10 x CAB324 (3A). The worst was the mother MO20 x AMAZ15 (5A), but the five did not present large differences in absolute values (Table 3).

The best fathers for mothers CEPEC86 x RB36 (1A) and CCN10 x CAB324 (3A) and overall means of diallel 2 were SCA6 x SGU114 (10A) and TSH1188 x CAB169 (9A). Clone RLF1938 (11), which is a selection carried out in a farm of the region, with probable ancestry of Scavina and also crossed with the first mother, as the two previous fathers, generated progenies with performance similar to that of the resistance pattern. In fact, the four crossings that had SCA6 x SGU114 (10A)

Table 3: Mean performance of *Moniliophthora perniciosa* infection of fathers and mothers for the three studied genetic designs and the probability of error (P) for rejecting the hypothesis of equality between means by the T-test

P	D	C	CM	C (1)	C (2)	C (3)	C (4)	C (5)	C (6)	
M	1	CSUL3xCCN10 (1)	0.814		0.9227	0.0348	<.0001	0.0522	0.6551	
		CAB301xCCN10 (2)	0.807	0.9227		0.0440	<.0001	0.0481	0.7343	
		MO20xCCN34 (3)	0.627	0.0348	0.0440		<.0001	0.0004	0.0821	
		CAB148xMO20 (4)	1.242	<.0001	<.0001	<.0001		0.0010	<.0001	
		CAB157xMO20 (5)	0.948	0.0522	0.0481	0.0004	0.0010		0.0193	
		NA33xRB39 (6)	0.784	0.6551	0.7343	0.0821	<.0001	0.0193		
F				C (10)	C (11)	C (12)	C (13)	C (7)	C (8)	C (9)
		MCBC9 (10)	1.019		<.0001	0.1705	0.0031	0.5228	<.0001	0.4087
		RLF1938(11)	0.666	<.0001		<.0001	0.3453	<.0001	0.4226	0.0004
		EET75 (12)	1.151	0.1705	<.0001		<.0001	0.0262	<.0001	0.0171
		UF273 (13)	0.743	0.0031	0.3453	<.0001		0.0053	0.0962	0.0156
		SCA6xP4B (7)	0.965	0.5228	<.0001	0.0262	0.0053		<.0001	0.7901
		SCA6xRB36 (8)	0.601	<.0001	0.4226	<.0001	0.0962	<.0001		<.0001
		SJ02 (9)	0.945	0.4087	0.0004	0.0171	0.0156	0.7901	<.0001	
M	2				C (1A)	C (2A)	C (3A)	C (4A)	C (5A)	
		CEPEC86xRB36 (1A)	0.635		0.0469	0.1747	0.0439	<.0001		
		CA5xRB36 (2A)	0.832	0.0469		0.4019	0.5620	0.2351		
		CCN10xCAB324 (3A)	0.744	0.1747	0.4019		0.6955	0.0171		
		CCN34xCAB301 (4A)	0.775	0.0439	0.5620	0.6955		0.0203		
		MO20xAMAZ15 (5A)	0.959	<.0001	0.2351	0.0171	0.0203			
F			C	(10A)	C (11)	C (12)	C (13)	C (6A)	C (7A)	C (9A)
		SCA6xGU114 (10A)	0.342		0.0003	<.0001	<.0001	0.0054	<.0001	0.0692
		RLF1938(11)	0.649	0.0003		0.0002	<.0001	0.7424	<.0001	0.0871
		EET75 (12)	0.977	<.0001	0.0002		0.0099	0.0005	0.0641	<.0001
		UF273 (13)	1.219	<.0001	<.0001	0.0099		<.0001	0.9858	<.0001
		CSG70 (6A)	0.616	0.0054	0.7424	0.0005	<.0001		<.0001	0.2508
		BN34 (7A)	1.222	<.0001	<.0001	0.0641	0.9858	<.0001		<.0001
		TSH1188xCAB169 (9A)	0.498	0.0692	0.0871	<.0001	<.0001	0.2508	<.0001	
M	3			C (10)	C (11)	C (9)				
		MCB09 (10)	1.069		0.3605	0.8606				
		RLF1938(11)	1.232	0.3605		0.2424				
		SJ02 (9)	1.035	0.8606	0.2424					
F				C (12)	C (13)					
		EET75 (12)	1.109	0.9711						
		UF273 (13)	1.115							

P: parental; D: diallel; C: crossings; CM: corrected mean; M: mother; F: father.

as father and four of the five with TSH1188 x CAB169 (9A) were as resistant as SCA6. The exception was observed for the crossing with the mother MO20 x AMAZ15 (5A), whose only resistant crossing was with 10A (Table 2).

Diallel 03 showed no significant difference between the means of the mothers SJ02 (9), MCB09 (10), and RLF1938 (11), all clones selected in farms of the cacao region of Bahia due to their productivity and resistance to WB, as well as probable ancestry of Scavina. No significant differences were also observed between the two fathers of diallel 03, EET75(12) and UF273(13).

1.2 Assessment for black pod

The tests with leaf discs suggested by Nyassé *et al*. (1995) has been widely used for the assessment of resistance to cacao diseases (Santos *et al*., 2011; Bahia *et al*., 2015; Barreto *et al*., 2015), showing a high reliability regarding BP behavior in fruits (Pires *et al*., 1997; Santos *et al*., 2009). The species *P. palmivora* was used in resistance tests because it is a common cosmopolitan species in all cocoa producing regions (Luz *et al*., 2001). In addition, Risterucci *et al*. (2003) demonstrated that the selection to a single predominant species, such as *P. palmivora* in Bahia (Luz *et al*., 2018), provides significant genetic gains of resistance to the disease.

The means of infection caused by *P. palmivora* showed that differences regarding susceptible controls were not as clear as those found for *M. perniciosa*. This result was expected because the selection in the previous cycle for BP was primarily indirect by the priority selection for resistance to WB or moniliasis. In addition, many of the progenies did not differ or even surpassed, in average, the controls: 16 crossings were similar and 11 crossings had means higher when compared to those found for the susceptibility controls Catongo and SIC-23 (Table 4). Progenies more susceptible than susceptibility patterns were also observed in other studies (Santos *et al*., 2011; Bahia *et al*., 2015; Barreto *et al*., 2015).

On the other hand, among the 58 crossings tested, 10 showed significantly lower means than Scavina-6 at 5% probability, namely: [RLF1938 (11) X EET75 (12)], [CSUL3 x CCN10 (1) X SJ02 (9)], [CA5 x RB36 (2A) X EET75 (12)], [CAB301 x CCN10 (2) X EET75 (12)], [CAB301 x CCN10 (2) X SJ02 (9)], [CCN34 x CAB301 (4A) X EET75 (12)], [CAB148 x MO20 (4) X MCB09 (10)], [CAB148 x MO20 (4) X RLF1938 (11)], [MO20 x AMAZ15 (5A) X EET75 (12)], and [CAB157 x MO20 (5) X SJ02 (9)]. Another 27 crossings had non-statistically different means to those of Scavina-6, with six crossings that did not differ from resistance or susceptibility controls: [MO20 x CCN34 (3) X SCA6 x P4B (7)], [MO20 x AMAZ15 (5A) X TSH1188 x CAB169 (9A)], [CAB157 x MO20 (5) X UF273 (13)], [NA33 x RB39 (6) X RLF1938 (11)], [NA33 x RB39 (6) X SJ02 (9)], and [SJ02 (9) X UF273 (13)].

Eight crossings presented exceptional values for both WB and BP, as follows: [(CSUL3 x CCN10 (1)) X UF273 (13)], [(CSUL3 x CCN10 (1)) X (SCA6 x RB36 (8))], [(CAB301 x CCN10 (2)) X SJ02 (9)], [(MO20 x CCN34 (3)) X RLF1938 (11)], [(CCN34 x CAB301 (4A)) X (SCA6 x GU114 (10A))], [(CCN34 x CAB301 (4A)) X (TSH1188 x CAB169 (9A))], [(CAB148 x MO20 (4)) X RLF1938 (11)] and [(NA33 x RB39 (6)) X EET75 (12)] (Tables 1 and 2). Two of these progenies, *i.e.*, [CSUL3 x CCN10 (1)) X UF273 (13)] and [(NA33 x RB39 (6)) X EET75 (12)], can carry resistance genes to moniliasis and are, therefore, essential for preventive breeding to this disease in Brazil. Fifteen crossings with sources of resistance to moniliasis stood out as resistant to BP, being eight with UF273 (13) and seven with EET75 (12).

Regarding the general combining ability in progenitors, the best mothers in diallel 01 were CAB148 x MO20 (4) and CSUL3 x CCN10 (1), not differing from each other and with significantly lower means than all other

Table 4: Mean disease index of black pod in cacao disc leaves (DI) and the probability of error (P) for rejecting the hypothesis of equality between means of each progeny and controls by the T-test

Crossings		Disease index (DI)	Controls		
			CAT	SIC23	SCA6
			51.71	52.54	37.29
MCBC9 (10) x	UF273 (13)	64.00	0.0070	0.0119	<.0001
RLF1938 (11) x	EET75 (12)	27.00	<.0001	<.0001	0.0238
RLF1938 (11) x	UF273 (13)	40.00	0.0102	0.0059	0.5511
CEPEC86 x RB36 (1A) x	RLF1938 (11)	55.50	0.4040	0.5150	<.0001
CEPEC86 x RB36 (1A) x	UF273 (13)	69.25	0.0001	0.0003	<.0001
CEPEC86 x RB36 (1A) x	TSH1188 x CAB169 (9A)	53.50	0.6933	0.8329	0.0004
CSUL3 x CCN10 (1) x	RLF1938 (11)	31.00	<.0001	<.0001	0.1664
CSUL3 x CCN10 (1) x	EET75 (12)	50.25	0.7482	0.6140	0.0045
CSUL3 x CCN10 (1) x	UF273 (13)	28.75	<.0001	<.0001	0.0605

To be continued...

Continuation Table 4

Crossings	Disease index (DI)	Controls		
		CAT 1.878526	SIC23 2.134295	SCA6 0.275166
CSUL3 x CCN10 (1) x SCA6 x P4B (7)	30.00	<.0001	<.0001	0.1089
CSUL3 x CCN10 (1) x SCA6 x RB36 (8)	39.50	0.0074	0.0042	0.6269
CSUL3 x CCN10 (1) x SJ02 (9)	22.75	<.0001	<.0001	0.0014
CA5 x RB36 (2A) x RLF1938 (11)	36.50	0.0009	0.0004	0.8617
CA5 x RB36 (2A) x EET75 (12)	22.00	<.0001	<.0001	0.0008
CA5 x RB36 (2A) x UF273 (13)	47.50	0.3544	0.2673	0.0249
CA5 x RB36 (2A) x TSH1188 x CAB169 (9A)	71.50	<.0001	<.0001	<.0001
CAB301 x CCN10 (2) x MCBC9 (10)	35.25	0.0003	0.0002	0.6531
CAB301 x CCN10 (2) x EET75 (12)	28.25	<.0001	<.0001	0.0469
CAB301 x CCN10 (2) x UF273 (13)	41.75	0.0287	0.0178	0.3266
CAB301 x CCN10 (2) x SCA6 x P4B (7)	61.75	0.0274	0.0430	<.0001
CAB301 x CCN10 (2) x SCA6 x RB36 (8)	55.00	0.4688	0.5884	0.0001
CAB301 x CCN10 (2) x SJ02 (9)	19.75	<.0001	<.0001	0.0001
CCN10 x CAB324 (3A) x SCA6 x GU114 (10A)	66.75	0.0010	0.0018	<.0001
CCN10 x CAB324 (3A) x RLF1938 (11)	42.25	0.0377	0.0238	0.2753
CCN10 x CAB324 (3A) x EET75 (12)	31.5	<.0001	<.0001	0.2027
CCN10 x CAB324 (3A) x UF273 (13)	29.50	<.0001	<.0001	0.0867
CCN10 x CAB324 (3A) xTSH1188 x CAB169 (9A)	67.00	0.0008	0.0015	<.0001
MO20 x CCN34 (3) x RLF1938 (11)	40.50	0.0139	0.0082	0.4801
MO20 x CCN34 (3) x UF273 (13)	61.50	0.0315	0.0490	<.0001
MO20 x CCN34 (3) x SCA6 x P4B (7)	44.00	0.0901	0.0605	0.1401
CCN34 x CAB301 (4A) x SCA6 x GU114 (10A)	37.75	0.0022	0.0012	0.9196
CCN34 x CAB301 (4A) x RLF1938 (11)	50.00	0.7069	0.5759	0.0053
CCN34 x CAB301 (4A) x EET75 (12)	26.50	<.0001	<.0001	0.0178
CCN34 x CAB301 (4A) x UF273 (13)	37.50	0.0018	0.0010	0.9634
CCN34 x CAB301 (4A) x CSG70 (6A)	54.75	0.5032	0.6269	0.0001
CCN34 x CAB301 (4A) x BN34 (7A)	57.50	0.2027	0.2753	<.0001
CCN34 x CAB301 (4A) xTSH1188 x CAB169 (9A)	34.25	0.0001	<.0001	0.5032
CAB148 x MO20 (4) x MCBC9 (10)	20.00	<.0001	<.0001	0.0002
CAB148 x MO20 (4) x RLF1938 (11)	20.00	<.0001	<.0001	0.0002
CAB148 x MO20 (4) x SCA6 x P4B (7)	35.00	0.0003	0.0001	0.6140
MO20 x AMAZ15 (5A) x EET75 (12)	27.00	<.0001	<.0001	0.0238
MO20 x AMAZ15 (5A) x UF273 (13)	56.75	0.2673	0.3544	<.0001
MO20 x AMAZ15 (5A) xTSH1188 x CAB169 (9A)	46.00	0.2092	0.1502	0.0556
CAB157 x MO20 (5) x MCBC9 (10)	37.25	<.0001	<.0001	0.9903
CAB157 x MO20 (5) x EET75 (12)	63.25	0.0113	0.0187	<.0001
CAB157 x MO20 (5) x UF273 (13)	45.00	0.1401	0.0973	0.0901
CAB157 x MO20 (5) x SCA6 x P4B (7)	68.25	0.0003	0.0006	<.0001
CAB157 x MO20 (5) x SCA6 x RB36 (8)	82.00	<.0001	<.0001	<.0001
CAB157 x MO20 (5) x SJ02 (9)	28.25	<.0001	<.0001	0.0469
NA33 x RB39 (6) x MCBC9 (10)	41.50	0.0249	0.0153	0.3544
NA33 x RB39 (6) x RLF1938 (11)	45.00	0.1401	0.0973	0.0901
NA33 x RB39 (6) x EET75 (12)	37.50	0.0018	0.0010	0.9634
NA33 x RB39 (6) x UF273 (13)	71.75	<.0001	<.0001	<.0001
NA33 x RB39 (6) x SCA6 x P4B (7)	36.75	0.0010	0.0005	0.9051
NA33 x RB39 (6) x SCA6 x RB36 (8)	49.00	0.5511	0.4357	0.0102
NA33 x RB39 (6) x SJ02 (9)	43.50	0.0712	0.0469	0.1721
SJ02 (9) x EET75 (12)	31.25	<.0001	<.0001	0.1839
SJ02 (9) x UF273 (13)	44.00	0.0901	0.0605	0.1401
CATONGO[(1)]	51.71		0.7315	<.0001
SIC23[(1)]	52.54	0.7315		<.0001
SCA6[(2)]	37.29	<.0001	<.0001	

[(1)] Susceptibility control; [(2)]Resistance control.

(Table 5). The mother CAB148 x MO20 (4) was present in three crossings classified as resistant, with MCB09 (10), RLF1938 (11), and SCA6 x P4B (7), the first two not differing from each other and both different from the latter at 5% probability (means shown in Table 2 and probability of error for rejecting the hypothesis of equality between means not shown).

The mother CSUL3 x CCN10 (1) was present in six crossings, five of them being the most resistant. The best combination of this mother was with clone SJ02 (9), not differing statistically from the combination with RLF1938 (11), UF273 (13), and SCA6 x P4B (7) (means shown in Table 4 and probability of error for rejecting the hypothesis of equality between means not shown).

For the fathers, the best performances were observed for clones SJ02 (9) and MCB09 (10), with means not statistically distinct and lower than those of the other progenitors. The third of the selections carried out in a farm, the clone RLF1938 (11), also presented a low mean infection, not differing from MCB09 (10). From the four crossings with SJ02 (9), two were among the best treatments, with the mothers CAB301 x CCN10 (2) and NA33 x RB39 (6).

In diallel 02, CCN34 x CAB301 (4A) was the best mother and EET75 (12) the best father, differing from the other progenitors. This mother, when combined with TSH1188 x CAB169 (9A), had a lower mean DI when compared to Scavina-6, with no statistical difference from each other.

Table 5: Mean performance of *Phytophthora palmivora* infection of fathers and mothers for the three studies genetic designs and probability of error (P) for rejecting the hypothesis of equality between means by the T-test

P	D	C	CM	C (1)	C (2)	C (3)	C (4)	C (5)	C (6)	
M	1	CSUL3xCCN10 (1)	32.157		0.0057	<.0001	0.2118	<.0001	<.0001	
		CAB301xCCN10 (2)	39.615	0.0057		0.0545	0.0008	<.0001	0.0081	
		MO20xCCN34 (3)	46.279	<.0001	0.0545		<.0001	0.0888	0.9639	
		CAB148xMO20 (4)	27.871	0.2118	0.0008	<.0001		<.0001	<.0001	
		CAB157xMO20 (5)	51.936	<.0001	<.0001	0.0888	<.0001		0.0222	
		NA33xRB39 (6)	46.428	<.0001	0.0081	0.9639	<.0001	0.0222		
F				C (10)	C (11)	C (12)	C (13)	C (7)	C (8)	C (9)
		MCBC9 (10)	31.407		0.1100	0.0003	<.0001	<.0001	<.0001	0.1395
		RLF1938(11)	36.655	0.1100		0.0664	0.0011	0.0031	<.0001	0.0043
		EET75 (12)	42.992	0.0003	0.0664		0.1779	0.3982	0.0004	<.0001
		UF273 (13)	47.181	<.0001	0.0011	0.1779		0.5265	0.0181	<.0001
		SCA6xP4B (7)	45.468	<.0001	0.0031	0.3982	0.5265		0.0021	<.0001
		SCA6xRB36 (8)	54.555	<.0001	<.0001	0.0004	0.0181	0.0021		<.0001
		SJ02 (9)	26.742	0.1395	0.0043	<.0001	<.0001	<.0001	<.0001	
M	2				C (1A)	C (2A)	C (3A)	C (4A)	C (5A)	
		CEPEC86xRB36 (1A)	62.160		0.0035	0.0052	<.0001	0.0041		
		CA5xRB36 (2A)	51.851	0.0035		0.8298	0.0047	0.8260		
		CCN10xCAB324 (3A)	52.516	0.0052	0.8298		0.0010	0.6749		
		CCN34xCAB301 (4A)	43.334	<.0001	0.0047	0.0010		0.0193		
		MO20xAMAZ15 (5A)	51.084	0.0041	0.8260	0.6749	0.0193			
F			C	(10A)	C (11)	C (12)	C (13)	C (6A)	C (7A)	C (9A)
		SCA6xGU114 (10A)	56.514		0.0089	<.0001	0.0349	0.2118	0.0838	0.6027
		RLF1938(11)	45.786	0.0089		<.0001	0.4511	0.0010	0.0002	0.0052
		EET75 (12)	30.515	<.0001	<.0001		<.0001	<.0001	<.0001	<.0001
		UF273 (13)	48.100	0.0349	0.4511	<.0001		0.0035	0.0006	0.0264
		CSG70 (6A)	63.605	0.2118	0.0010	<.0001	0.0035		0.6650	0.0820
		BN34 (7A)	66.355	0.0838	0.0002	<.0001	0.0006	0.6650		0.0242
		TSH1188xCAB169 (9A)	54.450	0.6027	0.0052	<.0001	0.0264	0.0820	0.0242	
M	3			C (10)	C (11)	C (9)				
		MCB09 (10)	57.562		<.0001	<.0001				
		RLF1938(11)	33.500	<.0001		0.0947				
		SJ02 (9)	37.625	<.0001	0.0947					
F				C (12)	C (13)					
		EET75 (12)	36.458	<.0001						
		UF273 (13)	49.333							

P: parental; D: diallel; C: crossings; CM: corrected mean; M: mother; F: father.

EET75 (12) appears as the father in two of the most resistant treatments.

For diallel 03, RLF1938 (11) and SJ02 (9) were comparatively better mothers than MCB09 (10), which presented a corrected mean higher than the others did. The fathers EET75 (12) and UF273 (13) did not differ from each other.

Clone SJ02 (9) contributed to the formation of three of the most resistant progenies to BP when crossed with mothers CSUL3 x CCN10 (1), CAB301 x CCN10 (2), and CAB157 x MO20 (5). The ancestry CSUL3 has been standing out as a progenitor in other tests for resistance to WB (Marita *et al*., 2001; Silva *et al*., 2010; Benjamin *et al*., 2016) and also for BP in field tests (Pires *et al*., 1997), as well as in the artificial inoculation on fruits with *P. palmivora* (Luz *et al*., 1996).

CONCLUSION

These results allow the early selection in the establishment of recurrent selection tests, future plant selection, which will be tested as clones and assessed regarding the possibility of becoming commercial varieties, and selection of progenitors for the next recurrent selection cycle. They also provide information on the potential of germplasm that can be used in other breeding programs. In addition to contributing to cacao farming in Bahia, they may also be useful for cacao farming in other regions.

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