Silverleaf whitefly-resistant common beans: an investigation of antibiosis and/or antixenosis

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ABSTRACT: The silverleaf whitefly *Bemisia tabaci* biotype B is one of the most important sucking pests of common bean, which causes severe damages and requires frequently synthetic insecticides spraying to protect crop productivity. The use of common bean cultivars resistant to whitefly attack is an important strategy within an integrated pest management (IPM) program. The biological development of *B. tabaci* confined to 17 bean genotypes was evaluated in greenhouse trials to verify the occurrence of antibiosis. Whitefly adults were released on plants of these genotypes to oviposit, afterward the incubation period of eggs, nymphal period, complete development period (egg–adult), and viability of the silverleaf whitefly nymphs were recorded. As main results, genotype CHIP 300 prolonged the developmental period from egg to adult (~10 days) and BRS Estilo, Arcelina 4, IPR Garça, Tybatã, CHIP 300, IPR Eldorado, H96A102-1-1-1-52, SCS-202-Guará and CHIB 06 caused nymphal mortality, suggesting high levels of antibiosis and/or antixenosis. These genotypes may be helpful in common bean breeding programs aimed at developing commercial cultivars resistant to *B. tabaci* biotype B.
Key words: antibiosis, host plant resistance, *Phaseolus vulgaris* L.*, Bemisia tabaci* biotype B.

INTRODUCTION

Common bean (*Phaseolus vulgaris* L., Fabaceae) has great socioeconomic importance in Brazil, being widely consumed as a source of proteins and minerals for people´s diet (Carvalho et al. 2014), and besides that, it is a source of income for thousands of agricultural producers, especially family farmers (FAO 2015). The occurrence of insect pests and diseases of common bean are one of the main causes for the reduction of bean productivity (Moraes et al. 2006; Costa et al. 2018).

The silverleaf whitefly, *Bemisia tabaci* (Gennadius 1889) (Hemiptera: Aleyrodidae) biotype B, is one of the main sucking pests that colonize common bean crops (Musa and Ren 2005; Boykin et al. 2018). *Bemisia tabaci* is considered a complex of cryptic species that are morphologically indistinguishable, with a total of 43 identified species (De Barro et al. 2011; Tay et al. 2017). Some authors considered biotype B as Middle East-Asia Minor 1 (MEAM1) (Dinsdale et al. 2010; De Barro et al. 2011). However, the authors of the present study chose to use the older nomenclature that is still adopted by many researchers.

Bemisia tabaci biotype B can cause severe direct and indirect damage to the plants. The direct injury is due to feeding of nymphs and adults, which suck the phloem sap and inject toxins, impairing the vegetative and reproductive development of the plants (Villas Bôas 2005). Due to the large volume of honeydew excreted during feeding, there is usually an increase in the incidence of sooty mold (*Capnodium* sp.), with negative impacts on photosynthesis and crop productivity (Musa and

Ren 2005; Naranjo and Legg 2010). In addition, *B. tabaci* biotype B is an important vector of pathogens, as it can transmit virus species of various genera such as the Bean golden mosaic virus, which can cause losses of up to 100% in production (Garrido-Ramirez et al. 2000; Aragão and Faria 2009).

The management of silverleaf whitefly in common beans has been carried out almost exclusively using synthetic insecticides from different chemical groups. However, there are several reports of resistance of whitefly populations to active ingredients, jeopardizing the effectiveness of this control tactic (Horowitz et al. 2002; Alon et al. 2008; Houndete et al. 2010; Ma et al. 2010). Moreover, the abusive use of synthetic insecticides can negatively impact the environment, in particular the systemic insecticides that act by contact and ingestion (neonicotinoids based), cause undesirable effects on nontarget organisms, pollinators and natural enemies, as well as their leaching capacity in groundwater (Desneux et al. 2007; Furlan and Kreutzweiser 2015; Alford and Krupke 2017). Thereby, around the only control method used, it makes necessary searching for new control strategies in an efficient and environmentally safe manner, according to the integrated pest management (IPM) precepts. The IPM is a dominant paradigm that guides most aspects of implementation of insect pest management, whose philosophy and history are well documented (Perkins 1982; Kogan 1998; Pedigo 2002).

Among alternative methods to chemical control, genetic resistance is highlighted through the cultivation of resistant genotypes (Smith 2005), which allows the maintenance of the pest population below the level of economic damage being highly compatible with other management tactics (Panda and Khush 1995; Smith and Clement 2012). Resistance is divided into three categories: antixenosis, antibiosis, and tolerance (Painter 1951), the latter being less common (Smith 2005). During this process there are behavioral or biological changes in the insects, and, in other cases, there may be a reaction of the plant itself, but without even affect the pest-insect (Lara 1991). Antibiosis appear when the plant adversely affects the biology of the insect that attempts to use it as food, interfering in its cycle of development, reproduction, and survival, among other biological parameters (Painter 1951; Panda and Khush 1995; Smith 2005; Baldin and Beneduzzi 2010). Antibiotic genotypes generally promote high mortality in the early stages, reduction of adult fecundity, reduction in larval and nymph size and weight, and prolongation of the immature phase (Panda and Klush 1995). The present study focused on the category antibiosis-resistance.

However, studies involving the characterization of bean genotypes on whitefly still have not evaluated a wide range of germplasm (Oriani and Lara 2000; Oriani et al. 2005; Torres et al. 2012; Peixoto and Boiça Júnior 2014; Silva et al. 2014), which motivated the conduction of the present study. Some genotypes of *P. vulgaris* have already been evaluated for resistance to *B. tabaci* biotype B, and some have been characterized as having antixenotic and/or antibiotic factors (Oriani et al. 2005, Torres et al. 2012; Peixoto and Boiça Júnior 2014; Silva et al. 2014).

Thus, this study evaluated the biological performance of *B. tabaci* biotype B confined to 17 genotypes previous selected from 78 genotypes, in order to characterize the possible expression of antibiosis.

MATERIAL AND METHODS

The study was carried out in a greenhouse in Botucatu, SP, Brazil (22° 85'S, 48° 26' W), between November and December 2017. The experiments were conducted in the greenhouse under partially controlled conditions (temperature of 25.68 °C with a maximum of 35.99 °C and minimum of 15.37 °C, mean relative humidity of 59 ± 10%, and natural light).

Obtaining the genotypes

The 17 bean genotypes used in this study (Table 1) were selected from preliminary trials with *B. tabaci* (Santos 2018). The commercial genotype 'Pérola' was included as a whitefly susceptibility standard (Silva et al. 2014). The genotypes were provided by the Agronomic Institute of Campinas (IAC), SP, Brazil, and by the Agricultural Research and Rural Extension Company of Santa Catarina (EPAGRI), Chapecó, SC, Brazil, and are a part of the Germplasm Banks of these institutions. Before their use in the trials, the genotypes were grown in pots (1.7 L) containing a mixture of soil (dark red latosol),

washed coarse sand, and autoclaved organic matter (tanned manure), in a ratio of 1:1:1 (v/v/v), and commercial substrate (Plantamax, Joinville, SC, Brazil) in a ratio of 3:1 (v/v). The plants were housed in a greenhouse, free from insect infestation, and received the fertilization recommended for the crop (Fancelli 2010). When they reached the phenological stage V3-V4 (Valle et al. 2012), the plants were used in the trials.

Table 1. Common bean genotypes (*Phaseolus vulgaris* L., Fabaceae) evaluated for resistance to *Bemisia tabaci* biotype B and their respective genealogies.

Genotype	Germplasm bank	Genealogy/Origin/Characteristics	Resistance history
BRS Esplendor	EMBRAPA	It originated from the crossing CB911863/AN9123293	Not evaluated
SCS 204 Predileto	EPAGRI	Selected from population MN 13337 introduced from CIAT	Not evaluated
BRS Estilo	EMBRAPA	It originated from junction EMP 250/4/A769///A429/ XAN 252//V8025/PINTO VI114, carried out in 1991 at CIAT	Not evaluated
BRS Notável	EMBRAPA	Crossing lineages A769/4/A774///A429/XAN 252//V8025/ G 4449//WAF 2/A55//GN31/XAN 170	Not evaluated
CHIB 06	EPAGRI	Lineage obtained by the crossing between Ouro Branco and Iraí	Not evaluated
IPR Eldorado	IAC	Crossing from Carioca 99 × G.N. Nebraska 1 Sel. 27 × BAT 614	Antixenosis (Silva et al. 2014)
IPR Garça	IAPAR	Uninformed	Not evaluated
Iapar 81	IAC	A248/EMP117/4/Bat 93/2/Carioca Sel.99/ G.N.Nebraska 1#27/3/SelAroana	Antixenosis (Silva et al. 2014)
IPR Quero-Quero	IAC	Selection recurrent of genotypes BAT477, IAPAR 14, FT 84-29, Jalo EEP, A252, A77, Ojo de Liebre, ESAL 645, Pintado, Carioca, ESAL 645, P 85, P 103, H-4, AN910522, ESAL 624, Carioca MG	Not evaluated
SCS 202 Guará	IAC	Acess Jabola Bag IAC × IAC Tybatã	Not evaluated
Arcelina 4	IAC	Jalo Itararé × IAC Carioca Eté	Antibiosis (Oriani and Lara 2000)
CHIP 348	EPAGRI	Accession of the Epagri germplasm bank ("Guarapuava black"), collected in the agricultural area of São Carlos - SC (collected in 2002)	Not evaluated
CHIP 300	EPAGRI	Accession of the Epagri germplasm bank, collected in agricultural area of Chapecó - SC (collected in the 1980s)	Not evaluated
Tybatã	IAC	Emp 81 × H853-50-2	Not evaluated
IAC Carioca Eté	IAC	L933 × LM30630-12-2	Not evaluated
H96A102-1-1-1-52	IAC	(IAC Car. Aruã × G5686) × (Xan 251 . IAC Car. Akytã) × (IAC Car. Pyatã × Mar 1) × Pérola	Not evaluated
Pérola	IAC	Selection in 'Aporé'	Susceptible (Silva et al. 2014)

Colony of *Bemisia tabaci* biotype B

The initial population of *B. tabaci* biotype B was obtained from IAC and maintained in a greenhouse (2.5 × 2.5 × 2 m) closed on the sides and on the ceiling with glass and an anti-aphid screen. For the maintenance of the insects, cabbage plants [Brassica oleracea (L.) var. acephala] were grown in plastic pots (2.5 L), and were irrigated and replaced as needed, in order to maintain their nutritional quality and also the vigor of populations of *B. tabaci* biotype B. This population was also characterized was characterized before the start of the research to confirm the biotype (Walsh et al. 1991; Simon et al. 1994; De Barro et al. 2003).

Bioassays

The biological performance of *B. tabaci* biotype B on the different genotypes was evaluated to verify the possible expression of antibiosis-resistance. Accordingly, the leaves (of the middle third) of the genotypes were individualized with cages made of "fabric voile" tissue (15 × 15 cm), which were fixed to the petioles of the leaflets with a satin ribbon. With the aid of

a buccal aspirator, 150 pairs of whiteflies were collected from the breeding stock and released inside the cages, where they remained for 24 h, in order to obtain the eggs on the previously selected leaves. After this period, the cages were removed as well as the insects from the plants.

Under a stereoscopic microscope (40× magnification), the abaxial face of the leaflets was examined and an area containing 30 viable eggs per leaflet was delimited with Glitter (Acrilex, São Bernardo do Campo, SP, Brazil). Egg surplus was removed using cotton swabs (Cotonetes, Johnson & Johnson, São Paulo, SP, Brazil) (Cruz et al. 2014). Three pots per genotype were used and each leaflet (2 per plant) represented one replicate, totaling six replicates per genotype (n = 180), arranged under a randomized design.

The insects were daily observed to evaluate the following biological parameters: incubation period, duration of instars, total nymphal period, development period from egg to adult, mortality of nymphal instars, and nymphal viability.

Statistical analysis

The normality of residuals and homogeneity of variances were verified using the Shapiro-Wilk and Levene tests, respectively. When the assumptions were satisfied, the data were subjected to the analysis of variance using the F test and, when there was a difference between the treatments, the means were compared using the Fisher LSD test ($p > 0.05$). For all analyses, the statistical package PROC MIXED-SAS, version 9.2 (SAS Institute 2008) was used.

RESULTS

The duration of the embryonic development of *B. tabaci* biotype B in the different genotypes of common bean varied from 8.40 to 10.57 days, with the highest mean values observed in the genotypes SCS Predileto, BRS Notável, SCS 202 Guará, CHIP 300, and Arcelina 4 (Table 2). The genotypes Tybatã, Pérola, IPR Eldorado, and IPR Garça had the shortest incubation periods.

The genotypes BRS Estilo (2.48 days), Pérola (2.23 days), and Tybatã (2.20 days) differed from most of the genotypes (Table 2). For the second instar, the longest duration was observed in nymphs confined in CHIP 300 and CHIB 06 (7.54 and 6.15 days, respectively), differing from the other genotypes (Table 2). Genotypes Pérola (2.62 days) and Tybatã (3.03 days) provided the shortest periods for the second instar of the whitefly. The highest durations for the third instar were verified in genotypes CHIP 348 (10.76 days), CHIP 300 (10.57 days), and IPR Eldorado (10.21 days), differing from most of the evaluated genotypes (Table 2). Pérola (4.23 days) and CHIB 06 (5.12 days) had the lowest average lengths for the third instar nymphs (Table 2). In the fourth instar, the nymphs confined to the genotypes CHIP 300, H96A102-1-1-1-52, Pérola, Arcelina 4, and IPR Quero-Quero presented a significant prolongation of the duration (between 6.15 and 6.80 days), differing from most of the evaluated genotypes, mainly CHIB 06, SCS 202-Guará, SCS 204 Predileto, and CHIP 348 (Table 2).

There was a large variation in the total nymphal period of *B. tabaci* biotype B, with emphasis on the CHIP 300 genotype (24.91 days), which extended the nymphal period by approximately nine days in comparison to the standard susceptible genotype (Pérola) (Table 2), differing from all other genotypes. In CHIP 348 (21.84 days) and H96A102-1-1-1-52 (21.60 days), intermediate prolongation was observed compared with the standard genotype, differing from most genotypes (Table 2). The largest prolongation of the egg–adult period was observed in the CHIP 300 genotype (34.22 days), which differed from all other genotypes (Fig. 1). In turn, the susceptible standard genotype (Pérola) had the shortest egg–adult developmental period (24.36 days) (Fig. 1).

As for the four nymphal stages of *B. tabaci* biotype B, no significant differences in mortality were observed among the genotypes for the first and third instars of the whitefly (Fig. 2). However, there was a marked mortality of second-instar nymphs, especially CHIP 300 (38.89%), H96A102-1-1-1-52 (30.00%), BRS Estilo (26.11%), and BRS Esplendor (23.89%), which differed from most of the genotypes evaluated (Fig. 2 b). In the fourth instar, high mortality rates were observed in

IPR Eldorado (26.11%), BRS Estilo (22.22%), Tybatã (19.44%), and IPR Garça genotypes (19.44%), differing from most of the genotypes (Fig. 2 d).

Table 2. Means (± SE) for incubation period, nymphal instar, and nymphal period of *Bemisia tabaci* biotype B in 17 common bean genotypes, in a greenhouse trial.

Genotype	Duration (days)					
	Incubation[1]	1st instar[1]	2nd instar[1]	3rd instar[1]	4th instar[1]	Nymphal period[1]
SCS 204 Predileto	10.57 ± 0.25 a	1.84 ± 0.13 cde	3.40 ± 0.09 hg	9.00 ± 0.88 cdef	5.04 ± 0.28 ef	19.26 ± 0.71 ef
BRS Notável	10.35 ± 0.17 ab	1.78 ± 0.08 ed	4.18 ± 0.24 cdef	9.18 ± 0.25 bcde	5.63 ± 0.30 cde	20.50 ± 0.70 cde
SCS 202Guará	10.11 ± 0.20 abc	2.00 ± 0.06 bcd	3.58 ± 0.14 fgh	9.77 ± 0.26 abc	4.95 ± 0.02 ef	20.01 ± 0.33 ed
CHIP 300	10.05 ± 0.21 abc	1.66 ± 0.09 e	7.54 ± 0.39 a	10.57 ± 0.30 a	6.80 ± 0.35 a	24.91 ± 0.46 a
Arcelina4	9.96 ± 0.17 abc	1.84 ± 0.13 cde	4.44 ± 0.25 cd	7.72 ± 0.67 g	6.17 ± 0.23 abc	20.27 ± 0.74 ed
BRS Esplendor	9.80 ± 0.17 bc	1.84 ± 0.18 cde	4.23 ± 0.31 cdef	8.33 ± 0.54 efg	5.63 ± 0.36 cde	19.94 ± 0.21 ed
Iapar 81	9.72 ± 0.05 bcd	2.14 ± 0.05 bc	4.01 ± 0.03 defg	8.58 ± 0.07 defg	5.25 ± 0.08 de	19.74 ± 0.07 def
CHIP 348	9.72 ± 0.24 bcd	1.87 ± 0.04 cde	4.19 ± 0.12 cdef	10.76 ± 0.41 a	5.11 ± 0.30 e	21.84 ± 0.30 b
IAC Carioca Eté	9.69 ± 0.22 bc	1.65 ± 0.08 e	4.78 ± 0.29 c	8.57 ± 0.10 defg	5.69 ± 0.22 bcde	20.18 ± 0.13 de
IPR Quero-Quero	9.62 ± 0.19 cd	1.97 ± 0.07 bcd	3.91 ± 0.25 defg	9.29 ± 0.32 bcde	6.15 ± 0.32 abc	20.86 ± 0.39 bcd
H96A102-1-1-1-52	9.62 ± 0.30 cd	1.89 ± 0.07 cde	3.79 ± 0.26 defg	9.65 ± 0.34 abcd	6.74 ± 0.40 a	21.60 ± 0.46 bc
CHIB 06	9.53 ± 0.16 cde	2.05 ± 0.05 bcd	6.15 ± 0.35 b	5.12 ± 0.07 h	4.27 ± 0.04 f	18.53 ± 0.17 f
BRS Estilo	9.07 ± 0.43 def	2.48 ± 0.14 a	4.27 ± 0.40 cde	7.99 ± 0.78 fg	5.97 ± 0.64 abcd	20.58 ± 1.00 bcde
IPR Garça	8.92 ± 0.33 efg	2.14 ± 0.25 bc	4.11 ± 0.17 cdef	8.68 ± 0.30 cdefg	5.35 ± 0.19 de	20.14 ± 0.26 de
IPR Eldorado	8.86 ± 0.36 fg	2.04 ± 0.14 bcd	3.71 ± 0.08 efg	10.21 ± 0.22 ab	5.63 ± 0.10 f	20.51 ± 0.25 cde
Pérola	8.66 ± 0.17 fg	2.23 ± 0.00 ab	2.62 ± 0.01 i	4.23 ± 0.02 h	6.44 ± 0.02 ab	15.73 ± 0.02 g
Tybatã	8.40 ± 0.04 g	2.20 ± 0.05 ab	3.03 ± 0.03 hi	8.87 ± 0.04 cdefg	5.63 ± 0.07 cde	19.52 ± 0.07 ef
F	6.61	3.88	22.35	16.56	7.31	16.70
df	16.81	16.81	16.81	16.81	16.81	16.81
p value	<0.0001	0.0001	0.0001	0.0001	0.0001	0.0001

[1]Means followed by the same letter in the column do not differ statistically from one another by the Fisher LSD Test (p > 0.05).
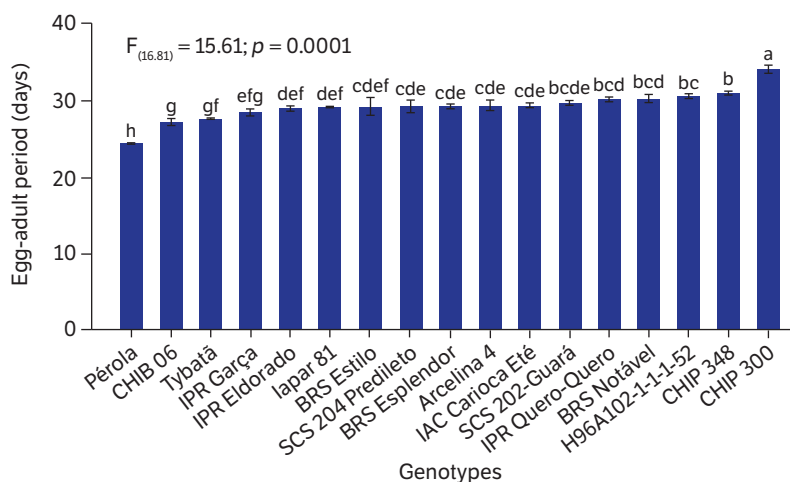

Figure 1. Means (± SE) of the development period from egg to adult (in days) of *Bemisia tabaci* biotype B in 17 common bean genotypes, in a greenhouse trial. Means followed by the same letter in the column do not differ statistically from each other by the Fisher LSD Test (p > 0.05).

The highest nymphal viability (85%) was observed in the Pérola genotype, which differed from the other evaluated materials (Fig. 3). The genotypes CHIB 06 (29.13%), Arcelina 4 (29. 44%), CHIP 300 (30%), BRS Estilo (34.16%), and IPR Eldorado (35.55%) showed the lowest viability indexes for the immature phase of the whitefly (Fig. 3).
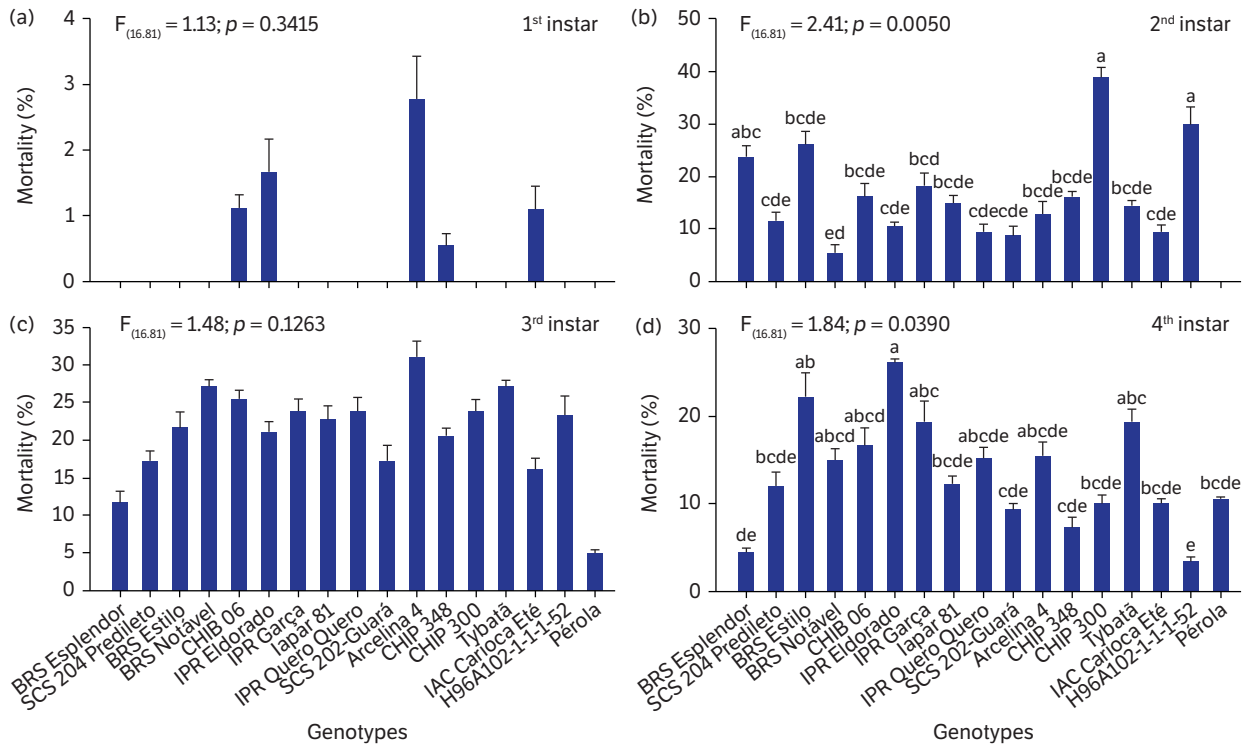

Figure 2. Means (± SE) of mortality per nymphal instar of *Bemisia tabaci* biotype B when confined in 17 common bean genotypes. Means followed by the same letter in the column do not differ statistically from each other by the Fisher LSD Test (p > 0.05).
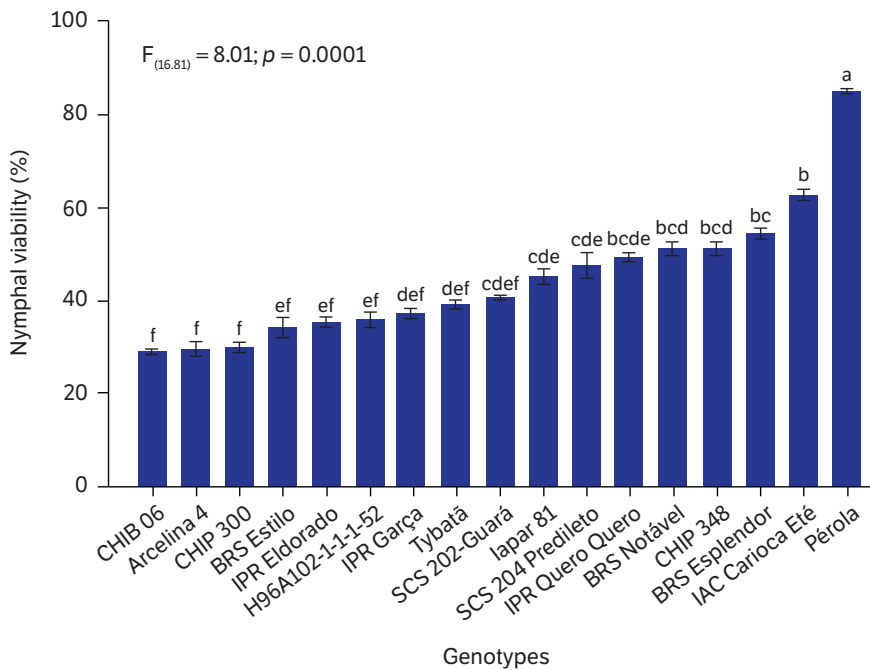

Figure 3. Means (± SE) of the percentage of nymphal viability of *Bemisia* tabaci biotype B in 17 common bean genotypes, in greenhouse. Means followed by the same letter in the column do not differ statistically from each other by the Fisher LSD Test (p > 0.05).

DISCUSSION

Reportedly, phytophagous insects consume large amounts of tissues and suck sap of various plant structures, despite the immense variation in the amount of nutrients, as well as the existence of innumerable physical and chemical barriers developed by plants to inhibit or prevent the attack (Bernays and Chapman 1994). However, the acceptance or rejection of host plants by insects depends on defense responses used by plants. Thus, successful colonization of pest insects depends on the presence or absence of various secondary metabolites associated with the possible host plant (Douglas 2018).

In general, insects attempting to colonize plants with antibiosis resistance, that is, plants with the capacity to affect their biology, present reductions in size and weight, diverse deformities, and prolongations in the lifecycle phases and, consequently, high mortality rates (Painter 1951). In the present study, the incubation period of the whitefly eggs in some of the evaluated genotypes was observed; in similar studies, the incubation period of the eggs of *B. tabaci* biotype B in bean genotypes ranged from 8.00 to 11.00 days (Torres et al. 2012; Peixoto and Boiça Júnior 2014). In the present study, the Tybatã and Pérola genotypes had the shortest incubation periods (8.40 and 8.66 days, respectively), consistent with the study by Peixoto and Boiça Júnior (2014), who observed that the incubation periods for these two genotypes ranged from 8.03 to 8.59 days. The change in the incubation period may be associated with biochemical causes related to common bean genotypes, or even to environmental factors (Smith 2005). Some authors suggest that the pedicel, besides fixing eggs on the plants, works absorbing water and even other compounds present on the plant, interfering on the whitefly embryonic development on common bean (Gameel 1974, Byrne and Bellows Junior 1991). In another study with *B. tabaci* biotype B in common bean, authors suggest that prolonged incubation periods might be influenced by low temperatures and humidity (Oriani and Lara 2000). However, in the present study these factors have not been evaluated and may be considered in further studies.

Genotype CHIP 300 (24.91 days) prolonged the nymphal period of the whitefly by approximately nine days compared with the susceptibility-standard genotype, Pérola (15.73 days). Such an extension may be associated with the presence of morphological factors, such as waxiness and/or trichomes (Glas et al. 2012), or even by chemical factors associated with resistance (Bernays and Chapman 1994; Smith 2005; Douglas 2018). The high prolongation of the instars from insect pests in the genotypes CHIP 300, CHIP 348, and H96A102-1-1-1-52 suggests the occurrence of antibiosis and/or antixenosis type resistance in the respective genotypes (Painter 1951).

The largest prolongation from egg to adult was observed in the genotype CHIP 300 (34.22 days), which required approximately 10 days more to complete the cycle compared with the susceptible Pérola genotype (24.36 days). This may be due to a lower nutritional adequacy or the presence of antibiotic factors in this genotype, which are aspects that must be better investigated in future studies. Based on the available literature, the duration of the egg to adult period varies between bean genotypes, and there are reports of periods between 16.20 and 41.00 days (Oriani and Lara 2000; Torres et al. 2012). Some references reported a large variation in the development period of the whitefly on cowpea genotypes (Cruz et al. 2014), cabbage (Villas Bôas et al. 1997), cotton (Prado et al. 2015), soybean (Cruz and Baldin 2016), tomato (Baldin et al. 2005), squash varieties (Baldin and Benduzzi 2010), melon (Baldin et al. 2012) and, more recently, peppers, where a duration of 30.25 days was observed (Pantoja et al. 2018), similar to the present study.

The genotypes CHIB 06 (29.13%), Arcelina 4 (29.44%), CHIP 300 (30.00%), BRS Estilo (34.16%), and IPR Eldorado (35.55%) caused low nymphal viability, also suggesting the expression of antibiosis resistance. However, some plants have combinations of chemical and morphological resistance factors with extremely inhibitory effects on insect-pest performance, making it difficult to isolate the causes related to antibiosis and/or antixenosis, as discussed by other authors (Panda and Khush 1995; Smith and Clement 2012).

In a study with the genotypes Iapar 81 and IPR Eldorado, high nymphal viability of whitefly was verified, with rates of 88.70 and 69.30%, respectively (Silva et al. 2014), in contrast to the present study, where viability in the two genotypes did not exceed 45%. These divergences are probably associated with the methodological or climatic differences (uninformed temperature) employed in the study of these authors. Other studies reporting low rates of nymphal viability of whitefly to antibiosis were also described in different hosts, such as cowpea (45.50 to 89.10%) (Cruz et al. 2014), soybean (68.60% to 89,60%) (Cruz et al. 2016), zucchini (36.10 to 100%) (Baldin and Beneduzzi 2010), and peppers (0 to 25%) (Pantoja et al. 2018). As they negatively affect the performance

of the insect's immature stages, the plants with antibiosis commonly cause high rates of nymphal or larval mortality, compromising the emergence of adults (Painter 1951; Panda and Khush 1995; Smith 2005), as verified in some genotypes in the present study.

The genotypes that demonstrated high levels of mortality in the different nymphal stages were CHIP 300, BRS Estilo, Arcelina 4, IPR Garça, and Tybatã. The mortality increased from the second instar, probably owing to increased insect feeding activity. Although the five genotypes showed a significant deleterious effect on the whitefly nymphs, it was observed in the CHIP 300 genotype that the effects were more intense, with common findings of individuals with deformities (Fig. 4 b), and difficulties in the molting processes (Fig. 4 d) and adult emergence (Fig. 4 f), compared with the same-stage individuals confined to the susceptible Pérola genotype (Fig. 4 a, c, e). The images (Fig. 4 b, d, f) indicate antibiosis as a mechanism of resistance in these genotypes. However, new studies are required to further elucidate the possible role of chemical resistance factors such as enzyme inhibitors or antibiotic compounds (alkaloids, flavonoids, and terpenoids) (Kubo and Hanke 1986) involved in the resistance of these materials.

Although the studies that characterized the expression of antibiosis in bean genotypes to whitefly are scarce, some authors have suggested that secondary compounds could be responsible for the negative effects on the biology of *B. tabaci* biotype B, as seeing in a study carried out with the Arcelina bean genotype 4 cultivated during the dry season, the nymphal mortality index of 80% of *B. tabaci* biotype B was verified (Oriani and Lara 2000). In the study, the authors suggested the presence of the arcelin protein as a possible resistance factor in the tested genotype, which may be responsible for the high mortality of insect nymphs. In soybean crop, it has been suggested that flavonoid-bearing genotypes may also negatively affect the biology of the whitefly (Vieira et al. 2016). In cotton genotypes, the presence of higher levels of gossypol in certain materials was negatively correlated with the biology of *B. tabaci* biotype B (Guo et al. 2013).
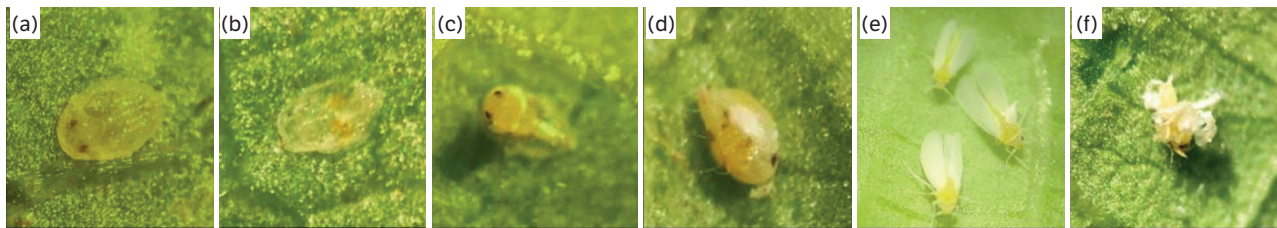

Figure 4. Different stages of development of *Bemisia tabaci* biotype B observed on leaflets of the susceptible bean genotypes Pérola (a, c and e) and of the CHIP 300 antibiotic resistant (b, d and f).

CONCLUSION

Considering all the results obtained in the biological performance tests of *B. tabaci* biotype B in common bean genotypes, it was verified that the CHIP 300 genotype caused a greater prolongation of the egg to adult period of *B. tabaci* biotype B, indicating the expression of antibiosis and/or antixenosis. In addition, CHIP 300 and the genotypes BRS Estilo, Arcelina 4, IPR Garça, Tybatã, IPR Eldorado, H96A102-1-1-1-52, and CHIB 06 negatively affected the development (viability) of the whitefly, indicating high levels of resistance through antibiosis and/or antixenosis. However, the resistance factors associated with these materials must be better investigated by characterizing the biochemical composition of these genotypes. Thus, these genotypes may constitute important sources of resistance to *B. tabaci* biotype B for breeding programs to obtain resistant cultivars.

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AUTHORS' CONTRIBUTION

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