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Screening of eggplant genotypes for resistance to bacterial wilt disease caused by *Clavibacter michiganensis* subsp. *michiganensis*

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Abstract: *Clavibacter michiganensis* subsp. *michiganensis* (*Cmm*) is one of the phytopathogenic bacteria causing bacterial wilt disease and severe yield losses in tomatoes and other solanaceous vegetables. Although there are some reports on *Cmm* infections in eggplants (*Solanum melongena*), there is no information available on the resistance sources and genetic control of the resistance to *Cmm* in this crop. We performed a search for resistance sources to *Cmm* in eggplants, in a set of 46 genotypes including landraces, inbred lines and cultivars and some cultivated and wild relatives, as well as an analysis of the genetic control of the resistance. A mixture of different *Cmm* strains from different genomic groups was used for the screening. Plants were inoculated through the injection of 10 µL of a *Cmm* suspension at a concentration of 10^7 cfu/mL in a single point of the stem. The symptoms were recorded at nine weeks after the inoculation with a 0–4 symptoms scale. The differences were observed in the symptoms in the collection evaluated, with the disease severity index of the genotypes ranging from 0.00 to 4.00. While 31 genotypes displayed no symptoms, three cultivated eggplant genotypes were highly susceptible. Reciprocal F1 and F2 generations were obtained from the crosses between the most susceptible genotype (CT30) and a resistant one (CT49). The genetic control of the resistance adjusted well to one dominant and one recessive gene model underlying the resistance to *Cmm*. These results are important for selection and breeding for resistance to *Cmm* in eggplants.

Keywords: bacteria; *Cmm*; genetic control; resistance resources; strain

The genus *Clavibacter*, which includes Gram-positive plant pathogenic bacteria, causes important economic losses in many crops (Davis et al 1984). One of the most relevant species in the genus is *Clavibacter michiganensis*, which is divided into five subspecies according to host specificity (Waleron et al. 2011). The subspecies *C. michiganensis* subsp. *michiganensis* (*Cmm*), *C. michiganensis* subsp. *sepedonicus* (*Cms*), and *C. michiganensis* subsp. *insidiosus* (*Cmi*) are considered quarantine organisms worldwide on tomatoes, potatoes, and alfalfa, respectively (van der Wolf et al. 2005). *Cmm* causes bacterial wilt and canker of tomatoes, while *Cms* causes potato ring rot, and both of them also

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cause damage to several other solanaceous crops (Nissinen et al. 1997; Louws et al. 1998; Waleron et al. 2011). *Cms* strains are virulent on eggplant (Louws et al. 1998), which is a natural host of this subspecies (Nissinen et al. 1997). Some recent studies have been published on *C. michiganensis* describing two new subspecies, named *C. michiganensis* subsp. *phaseoli* and *C. michiganensis* subsp. *capsici* for the causal agent of bacterial wilt on beans and peppers, respectively. Furthermore, two new subspecies isolated from tomato and pepper seeds produced in California and Chile were named as *C. michiganensis* subsp. *californiensis* and *C. michiganensis* subsp. *chilensis*, respectively. However, in a re-classification study, some of the subgroups of *C. michiganensis* mentioned above have been given the consideration of new species. These new species were called as *Clavibacter capsici*, *Clavibacter insidiosus*, *Clavibacter nebraskensis*, *Clavibacter sepedonicus* (Li et al. 2018; Méndez et al. 2020). Although the tomato is the primary natural host of *Cmm*, peppers (*Capsicum annuum*) and eggplants (*Solanum melongena*) can also be infected in the field (Yim et al. 2012). Highly virulent strains of *Cmm* were isolated from eggplants in Lithuania (Waleron et al. 2011) and in Turkey (Kara et al. 2018; Sen et al. 2018). These virulent strains have a considerable risk to be potentially spread globally (Ansari et al. 2019).

Cmm is xylem-inhabiting and the most common symptom is leaf wilting. Wilting appears first in the lower leaves and progresses to the upper leaves. Necrosis is commonly observed following the leaf wilting symptoms (Gleason et al. 1993). The pathogen can be spread by seed and agronomic practices (Westra et al. 1994; Sharabani et al. 2013). The usage of biocontrol agents and resistant cultivars might be alternative solutions to control the pathogen, but these methods have not been implemented in the field up to now (Mohd Nadzir et al. 2019). In this respect, there is a need to develop cost-efficient mass-scale production and registration procedures of these biocontrol agents for their commercial usage (Karthika et al. 2020). The copper-based chemicals, some antibiotics (such as streptomycin and kasugamycin) and plant activators can be significantly effective in reducing the population sizes and spread of *C. michiganensis* subsp. *michiganensis* (Milijašević et al. 2009). The application of combinations of copper compounds and antibiotics could display better performance to inactivate the pathogen (Khalid et al. 2019). Nevertheless, an intensive integrated management approach is essential to prevent serious economic losses (Catara & Bella 2020). Although it is known that *Cmm* can infect various solanaceous crops (the tomato, pepper, eggplant and potato), there are more studies regarding its damage in tomatoes than in other crops (Poysa 1993). In this way, several resistant resources were found in wild tomato types (Sen et al. 2013), and resistance to *Cmm* in tomatoes was identified as oligogenic or polygenic (van Heusden et al. 1999; Sen et al. 2015). Some interesting findings were mentioned in other studies performed on the genetic control of *Cmm* resistance in tomatoes. The genetic control of *Cmm* resistance in tomatoes differed according to the sources of resistance. While the genetic control of *Cmm* resistance from *Solanum habrochaites* accession LA407 was polygenic with an additive interaction, the resistance from *S. peruvianum* var. *humifusum* accession PI 127829 was controlled by one single dominant gene. These results are extremely promising for breeding studies (Yuqing et al. 2018). In eggplants, just a few studies are known on *Cmm* disease reporting and identification (Burokienė et al. 2005; Sen et al. 2018). In this way, there is not enough sufficiently detailed information on the prevalence and severity of the disease and the reactions of the eggplant against the pathogen, and there is a complete lack of information on the genetic basis of this resistance in eggplants. In this study, we performed a screening for resistance to *Cmm* in the eggplant gene pool and studied the genetic control of the resistance to this pathogen.

MATERIAL AND METHODS

Plant materials. A total of forty-six genotypes of cultivated eggplants (*S. melongena*), including landraces, inbred lines and cultivars, and some cultivated and wild relatives were used for screening to identify the resistance sources (Table 1).

For genetic analysis studies, the most susceptible and the most resistant genotypes were chosen. F_1 plants raised from reciprocal crosses between the susceptible and resistant parents were selfed to generate segregating F_2 populations. The crosses were performed by hand pollination. The female parent's buds were emasculated prior to the anthesis stage and isolated to protect them to alien pollen transmission. The manual pollination was undertaken the next day by using pollen collected from male plants. After they had been pollinated by hand,

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Table 1. List of the eggplants and the cultivated and wild relatives tested for screening the resistance to *Cmm*

No	Code	Biological status	Name or place of collection	Origin	Provider
1	CT1	cultivated relative	*S. integrifolium*	genebank	INRA
2	CT5	wild relative	*S. sisymbriifolium*	genebank	INRA
3	CT7	cultivar	Diamond	company	purchased
4	CT9	cultivar	LS1934	genepool	BATEM
5	CT10	cultivar	LS2436	genepool	BATEM
6	CT11	cultivar	Kemer	company	purchased
7	CT12	cultivar	Faselis	company	purchased
8	CT13	cultivar	Kocaş	grower	agricultural district office
9	CT14	landrace	Burdur -Gölhisar/Turkey	grower	collected in the field
10	CT15	landrace	Antalya-Kumluca/Turkey	grower	collected in the field
11	CT16	landrace	Burdur-Aglasun /Turkey	grower	collected in the field
12	CT17	landrace	Burdur-Aglasun /Turkey	grower	collected in the field
13	CT18	landrace	Burdur-Aglasun /Turkey	grower	collected in the field
14	CT19	landrace	Burdur-Aglasun /Turkey	grower	collected in the field
15	CT20	landrace	Burdur-Celtikci/Turkey	grower	collected in the field
16	CT21	landrace	Burdur-Celtikci/Turkey	grower	collected in the field
17	CT22	landrace	Burdur-Askeriye/Turkey	grower	collected in the field
18	CT23	landrace	Burdur-Askeriye /Turkey	grower	collected in the field
19	CT24	landrace	Burdur-Askeriye /Turkey	grower	collected in the field
20	CT25	landrace	Burdur-Askeriye /Turkey	grower	collected in the field
21	CT26	landrace	Muğla-Yatağan/Turkey	grower	collected in the field
22	CT27	landrace	Muğla-Milas/Turkey	grower	collected in the field
23	CT28	landrace	Mugla-Fethiye/Turkey	grower	collected in the field
24	CT29	landrace	Burdur-Karamanlı/Turkey	grower	collected in the field
25	CT30	landrace	Burdur-Karamanlı/Turkey	grower	collected in the field
26	CT31	landrace	Burdur-Karamanlı/Turkey	grower	collected in the field
27	CT32	landrace	Burdur-Gölhisar/Turkey	grower	collected in the field
28	CT33	landrace	Burdur-Yesilova/Turkey	grower	collected in the field
29	CT34	landrace	Burdur-Yeşilova/Turkey	grower	collected in the field
30	CT35	landrace	Burdur-Tefenni/Turkey	grower	collected in the field
31	CT36	cultivated relative	*S. aethiopicum*	genebank	INRA
32	CT37	cultivar	Long purple	company	purchased
33	CT38	cultivar	Black Beauty	company	purchased
34	CT39	landrace	Kayseri-Yamula/Turkey	grower	EUAF
35	CT40	landrace	Kayseri-Yamula/Turkey	grower	EUAF
36	CT41	landrace	Kayseri-Yamula/Turkey	grower	EUAF
37	CT42	landrace	Kayseri-Yamula/Turkey	grower	EUAF
38	CT43	landrace	Muğla-Koçarlı/Turkey	grower	collected in the field
39	CT44	landrace	Aydın-Köşk/Turkey	grower	collected in the field
40	CT45	landrace	Aydın-Köşk/Turkey	grower	collected in the field
41	CT46	cultivar	SM 43	genepool	BATEM
42	CT47	hybrid	*S. melongena* × *S. torvum*	crosses	BATEM
43	CT48	hybrid	*S. melongena* × *S. torvum*	crosses	BATEM
44	CT49	inbred line	TDC5/2	breeding	BATEM
45	CT50	inbred line	TDC21/21	breeding	BATEM
46	CT51	inbred line	TDC45	breeding	BATEM

INRA – French National Institute for Agricultural Research, France; BATEM – Bati Akdeniz Agricultural Research Institute, Turkey; EUAF – Erciyes University, Faculty of Agriculture, Turkey

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the emasculated flowers were isolated with paper bags until the fruit set to prevent alien pollination. This method is known to guarantee the hybrid nature of the seeds obtained after manual hybridisation (Kumar et al. 2014).

Pathogenic bacterial strains. The causal agent material belonging to the mixture of different strains of (*Cmm*) was provided by Cukurova University, Faculty of Agriculture, Plant Protection Department, Adana (Turkey), by Prof. Dr. Yesim Aysan. These strains are known to be in different genomic groups from aa multilocus sequence analysis (MLST) (Sen et al. 2018) and were originally isolated from diseased eggplant and tomato plants collected from different locations in Turkey (Antalya, Adana, Mersin, İzmir, Artvin and Tokat provinces) (Kabas et al. 2018; Sen et al. 2018). This mixture was also important for this experiment, as it included strains obtained from infected eggplant plants with *Cmm* (Sen et al. 2018). The selected ten *Cmm* strains by MLST isolated from Turkey over different years and their geographical origins are presented in Table 2. The pathogenicity of all the strains was verified on tomatoes.

Inoculum preparation and inoculation. After the *Cmm* strains were transferred to separate flasks including a YDC (yeast-dextrose-carbonate) medium and incubated at 25 °C and 250 rpm for 48 h (Lelliott & Stead 1987), they were inoculated into 1 L of King's B medium (Klement et al. 1990) separately under the same conditions for 24 hours. The bacterial concentrations were adjusted to 10^7 cfu/mL using spectrophotometer readings at 600 nm. A mixed culture was prepared from these different strains with equal amounts of their suspensions. All the plants used for the assays were produced from healthy seeds. They were grown in a growing substrate composed of 70% peat and 30% vermiculite until the seedlings reached the 3–4 true leaf stage. Then, each plant was inoculated through an injection of 10 µL of the *Cmm* suspension in a single point of the stem (Figure 1A). The genotype screening experiment was conducted with two replicates for each genotype, with five pots per replicate and two plants per pot. The plants were kept in a controlled glasshouse for eight weeks (Figure 1B). The disease scores were recorded at 9 weeks after the inoculation with the 0–4 rating scale described by Klement et al. (1990) as follows: 0 = no symptoms (resistant), 1 = wilting plant of 1–25% (tolerant), 2 = wilting plant of 26–50% (moderately tolerant), 3 = wilting plant of 51–75% (susceptible), 4 = wilting plant of 76–100% or dead plant (very susceptible). The visual disease symptoms scale on the inoculated plants due to the disease severity is presented in Figure 2. Then, the pathogenic bacterium was re-isolated from the diseased plants and confirmation of the *Cmm* as the causal agent was performed by species-specific polymerase chain reaction (PCR) tests with CMM-5 and CMM-6 primers (Dreier at al. 1995). The inoculated plants used in the screening assay were compared with the non-inoculated control plants for each genotype. The inoculated plants used in the determination of the genetic control were also compared with susceptible and resistance parents.

Data evaluation. The reactions of the genotypes were evaluated by assessing their disease severity. The mean of the disease severity index (*DSI*) of the genotypes was calculated for each genotype by using the following formula:

Table 2. *Clavibacter michiganensis* subsp. *michiganensis* (*Cmm*) strains used in this study*

Strains	Geographical origin	Coordinates of origin	Year isolated
Cmm 1	Karatas/Adana	36°41'77.7"N/35°05'24.2"E	1996
Cmm 2	province centre/Antalya	36°53'17.7"N/30°44'27.2"E	2002
Cmm 3	Dikili/Izmir	39°04'15.4"N/26°53'40.7"E	2003
Cmm 4	province centre/Artvin	41°11'07.9"N/41°49'43.7"E	2004
Cmm 5	Aydıncık, Mersin	36°08'55.2"N/33°17'36.5"E	2005
Cmm 6	Erdemli/ Mersin	36°30'37.8"N/34°11'10.3"E	2007
Cmm 7	Cicik/Mersin	36°30'29.9"N/34°08'02.5"E	2007
Cmm 8	Erdemli/Mersin	36°30'37.8"N/34°11'10.3"E	2010
Cmm 9	province centre/Tokat	40°20'01.2"N/36°35'02.3"E	2010
Cmm 10	province centre/Tokat	40°20'01.2"N/36°35'02.3"E	2010

*pathogenicity of all the strains was verified on tomatoes

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$$DSI = 5 \times \sum \frac{\text{severity rating} \times \text{ no. of plants in that rating}}{\text{total no. of plants}}$$

where: *DSI* – disease severity index

An ANOVA was performed for the *DSI*, and a separation of the means was performed with the Jump software package (version 5.0.1) using an LSD test at $P < 0.05$. For the F_2 segregating generation, the seedlings having scale values with ratings of 0, 1 and 2 were classified as resistant, while those with values 3 and 4 were considered as susceptible. The chi-square (χ^2) test method was used to determine the goodness-of-fit of the observed data to a theoretically expected segregation ratio for the proposed genetic model. The Yates correction for continuity was used to calculate the χ^2 values (Little & Hills 1978).

RESULTS

The tested eggplant genotypes displayed considerable differences in the severity of the symptoms resulting from the inoculation with *Cmm*. The symptoms appeared as foliar wilt in the susceptible plants (Figure 3A) within 25 days after the inoculation and the bacteria spread throughout the plant via the xylem (Figure 3B). In the re-isolation and identification studies, the disease symptoms were confirmed to be bacterial wilt disease caused by *Cmm* with the 614 bp amplificon product in the PCR tests.

The bioassay trial screening resistance to *Cmm* of forty-six eggplant genotypes resulted in highly variable responses. A significant difference among the reaction of the genotypes to the *Cmm* strains was found (Table 3). The disease severity index of the genotypes ranged from 0.00 to 4.00. While

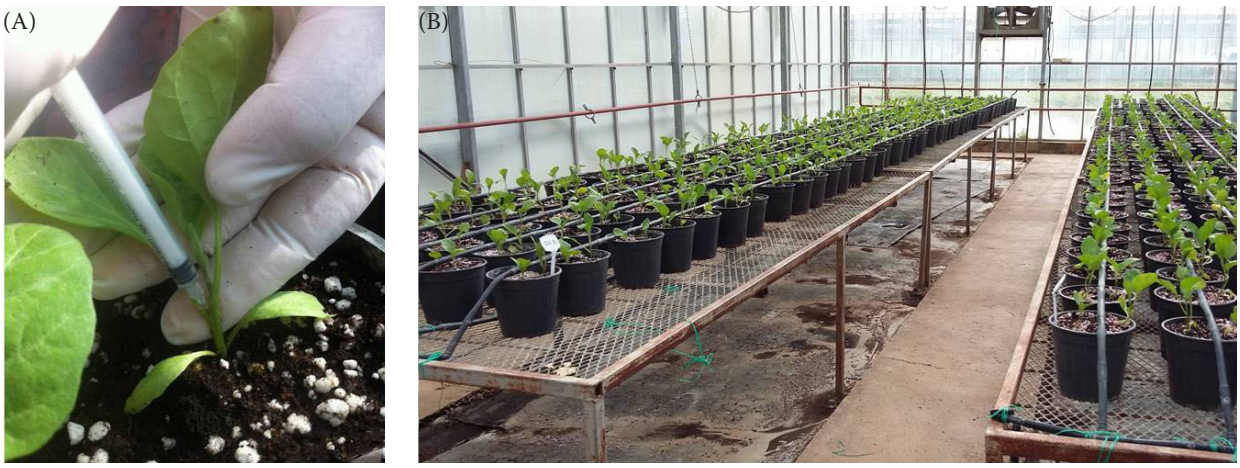

Figure 1. (A) Inoculation of *Cmm* to the eggplant vascular tissue by injection in the stem and (B) view of the tested plants

Figure 2. The varied visual disease symptoms occurred on the eggplants inoculated with *Cmm* due to the disease severity ranged from a (0) symptomless plant to a (4) dead plant

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(A) (B)

Figure 3. (A) Wilting symptoms and (B) pathogen damage caused by *Cmm* on the vascular tissue of the eggplant

Table 3. ANOVA of the disease severity index of 46 genotypes of eggplant and the relatives inoculated with *Cmm*

Source	*df*	Sum of squares	Mean square	*F* ratio	Probability > *F*
Model	46	70.830	1.5398	119.65	< 0.0001
Error	45	0.579	0.0129		
Total	91	71.410			

thirty-one showed no symptoms, fifteen genotypes displayed reactions consisting of symptoms of the disease caused by *Cmm*. Genotypes CT30, CT43 and CT35 were the most susceptible ones with highest average disease scores of 3.85, 3.20, 3.00, respectively. CT9, CT12, CT33 showed moderate resistance and their disease average scores ranged from 1.25 to 1.65. The average score of the nine other genotypes ranged between 0.05 and 0.50, indicating slight symptoms of the disease (Table 4).

The information obtained also provided some insight into the genetic control of the *Cmm* resistance on the eggplants. In this respect, all the plants of the susceptible parent CT30 displayed severe symptoms of bacterial wilt disease caused by *Cmm*. Conversely, all the plants of the resistant source CT49 did not display any symptoms as expected. Also, all the F_1 plants from both reciprocal crosses were resistant. In both F_2 populations, the plants displayed variation for the symptoms. While the F_2(RS) population showed a segregation of 132 resistant to 36 susceptible, the reciprocal F_2(SR) population showed a segregation of 173 resistant to 35 susceptible (Table 5). The χ^{22} tests revealed a close fit to a 13 : 3 ratio for the reciprocal F_2 populations. The expected ratios for the resistant (R) versus susceptible (S) are based on one dominant and one recessive gene model for controlling resistance to *Cmm* in the parental eggplant materials used.

Table 4. Average disease severity index of 46 genotypes of eggplant and the relatives after inoculation with *Cmm*, ordered by the decreasing values of the average score

Genotype	*DSI*	Host response
CT30	3.85^{a}	susceptible
CT43	3.20^{b}	susceptible
CT35	3.00^{b}	susceptible
CT33	1.65^{c}	moderately resistant
CT12	1.45^{cd}	moderately resistant
CT9	1.25^{d}	moderately resistant
CT5	0.50^{e}	resistant
CT38	0.45^{e}	resistant
CT7	0.20^{f}	resistant
CT13	0.10^{f}	resistant
CT29	0.10^{f}	resistant
CT22	0.05^{f}	resistant
CT25	0.05^{f}	resistant
CT39	0.05^{f}	resistant
CT46	0.05^{f}	resistant
CT50	0.05^{f}	resistant
CT1	0.00^{f}	resistant
CT10	0.00^{f}	resistant
CT11	0.00^{f}	resistant
CT14	0.00^{f}	resistant
CT15	0.00^{f}	resistant
CT16	0.00^{f}	resistant

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Table 4. to be continued

Genotype	*DSI*	Host response
CT17	0.00[f]	resistant
CT18	0.00[f]	resistant
CT19	0.00[f]	resistant
CT20	0.00[f]	resistant
CT21	0.00[f]	resistant
CT23	0.00[f]	resistant
CT24	0.00[f]	resistant
CT26	0.00[f]	resistant
CT27	0.00[f]	resistant
CT28	0.00[f]	resistant
CT31	0.00[f]	resistant
CT32	0.00[f]	resistant
CT34	0.00[f]	resistant
CT36	0.00[f]	resistant
CT37	0.00[f]	resistant
CT40	0.00[f]	resistant
CT41	0.00[f]	resistant
CT42	0.00[f]	resistant
CT44	0.00[f]	resistant
CT45	0.00[f]	resistant
CT47	0.00[f]	resistant
CT48	0.00[f]	resistant
CT51	0.00[f]	resistant

[a]means separated by different letters are significantly different according to the LSD test at $P < 0.05$; *DSI* – disease severity index

DISCUSSION

Bacterial diseases are one of the major phytopathological problems of solanaceous crops (Davis et al. 1984; Sen et al. 2015). *Cmm* is a seed borne pathogen of tomatoes that may cause important crop losses (Yang & Francis, 2007; Ansari et al. 2019). Information on the sources of the resistance and its inheritance are necessary to devise efficient and successful breeding strategies for developing resistant cultivars. In this way, in tomato resistance resources, polygenic inheritance (van Heusden et al. 1999), and quantitative trait locus (QTL) regions for *Cmm* resistance have been identified (Yang & Francis 2007). However, there is very little information available on this pathogen in eggplants, and this is limited to its detection in eggplants (Burokienė et al. 2005; Sen et al. 2018). Recently, Osdaghi et al. (2018) found that tomato *Cmm* strains from Iran did not cause symptoms in artificially inoculated eggplants and *Capsicum* peppers, revealing that *Cmm* strains display host specificity. Nevertheless, many cases of infections caused by *Cmm* in eggplants both in Asia and Europe have been reported (Waleron et al. 2011; Yim et al. 2012; Sen et al. 2018). In our study, we found that a mixture of ten *Cmm* strains can infect and cause disease symptoms on some eggplant genotypes, indicating that there are genetic differences for the resistance to *Cmm* in the eggplant genotypes studied that can exploited for selection and breeding.

Eggplant cultivars are susceptible to numerous pests and diseases, with breeding studies being concentrated on disease resistance breeding (Daunay et al. 2019; Kumar et al. 2020). The most significant research achievements have been made on breeding for resistance to soil-borne pathogens, with notable success (Barchi et al. 2018; Namisy et al. 2019; Saini & Kaushik 2019). The results presented herein show that many eggplant materials are resistant to *Cmm* and that resistance sources displaying no symptoms of infection are available in eggplants both in the cultivated species *S. melongena* as well as in its cultivated and wild relatives. This is contrast to tomatoes, where

Table 5. Segregation of eggplant *Cmm* resistant and susceptible plants in the parents CT49 and CT30, and reciprocal F_1s and F_2s generations

Population	Observed plants		Expected ratio	χ^2	*P*-value
	R	S			
CT49 (R)	20	0			
CT30 (S)	0	20			
F_1 (RS)	50	0			
F_1 (SR)	50	0			
F_2 (RS)	132	36	13 : 3 (136.5 : 31.5)	0.6257	0.4291
F_2 (SR)	173	35	13 : 3 (169 : 39)	0.387	0.3867

R – resistant; S – susceptible; RS – F1, generated from crosses of resistant parent × susceptible parent; SR – F1, generated from crosses of susceptible parent × resistant parent

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most materials of the cultivated species and their wild relatives are susceptible to *Cmm* (Sen et al. 2013). However, some eggplant genotypes are highly susceptible and this indicates that when susceptible varieties are cultivated in areas with a *Cmm* incidence, important crop losses may occur. The fact that many cultivated eggplant genotypes are resistant to *Cmm* facilitates the fast development of resistant varieties through intraspecific hybridisation, without the need to resort to wild relatives for introgression breeding, as has been the case of the tomato (van Heusden et al. 1999; Francis et al. 2001; Kabas et al. 2018).

Our results have provided the first available information on the genetic control of resistance to *Cmm* in eggplants. Intraspecific reciprocal crosses between the two extremes of symptoms (susceptible vs. resistant) in cultivated eggplants revealed that the resistance was compatible with one dominant and one recessive gene controlling the resistance. In several studies in tomatoes, resistance to *Cmm* has been found to be oligogenic or polygenic, with dominant, recessive or intermediate dominance depending on the materials and genetic background (Sen et al. 2015). It was reported by Yuqing et al. (2018) that the resistance to *Cmm* can be achieved with biotechnological methods thanks to the QTL mapping of resistance genes in tomatoes. Given the oligogenic and epistatic nature of the resistance to *Cmm* in eggplants, as in tomatoes (Yang & Francis 2007), marker assisted selection may be an efficient way for the introgression breeding of resistance to *Cmm* into susceptible genetic backgrounds and for the rapid development of new *Cmm* resistant cultivars of eggplants.

CONCLUSION

In this study, the reaction of eggplant genotypes has been evaluated against *Clavibacter*, an important pathogenic agent of some solanaceous crops. Although many genotypes were resistant, the presence of susceptible genotypes among the materials screened revealed the necessity to perform *Cmm* pathological and genetic resistance studies in eggplants. In addition to the first available information on the genetic control of the resistance to *Cmm* in eggplants, with our data adjusting to one dominant and one recessive gene genetic control model for the resistance, the resistant materials identified may be used for developing resistant F_1 hybrids and deriving new materials resistant to *Cmm*. In future studies, the identification of the genomic locations of the resistant genes and the development of markers linked may facilitate the marker assisted selection for resistance to *Cmm* in eggplants.

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