Diversity of Tobacco etch virus pathotypes faced with pepper resistance sources and durability potential of resistance genes

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Diversity of *Tobacco etch virus* pathotypes faced with pepper resistance sources and durability potential of resistance genes

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BACKGROUND Potyviruses are an important agronomic constraint to pepper (*Capsicum* spp.) production, worldwide. Compared to other potyviruses, *Tobacco etch virus* (TEV) has rather limited natural host range and geographical distribution. The main crops affected by TEV are tobacco (*Nicotiana tabacum*) and pepper and TEV is mostly prevalent in the Americas, Turkey and sporadically in China. In pepper, several recessive resistance alleles at the *pvr1/pvr2* locus, which encodes the eukaryotic initiation factor 4E (eIF4E), are available to control TEV and the corresponding resistance-breaking factor in TEV is the VPg (viral protein genome-linked). Until now, the spectrum of action of these different alleles has only been evaluated with a limited set of TEV isolates.

MATERIALS & METHODS We used a worldwide collection of 16 TEV isolates to evaluate the spectrum of action and durability potential of five *pvr1/pvr2* resistance alleles in laboratory conditions and under mechanical inoculation.

RESULTS The 16 TEV isolates infected the susceptible controls 'Yolo Wonder' and 'Yolo Y' homozygous at the $pvr2^{+}$ and $pvr2^{1}$ alleles, respectively. Phenotypes of resistance (i.e. no detectable TEV accumulation at the systemic level) and of susceptibility (i.e. presence of symptoms and TEV detection at the systemic level) were observed in the four remaining pepper genotypes homozygous at the $pvr2^{2}$, $pvr2^{7}$, $pvr2^{14}$ or *pvr1* alleles, depending on the TEV isolate. Some genotypes had heterogeneous responses to inoculation with some TEV isolates, with both resistant and susceptible plants. In several of these cases, the TEV populations in susceptible plants showed amino acid changes in the VPg, indicative of resistance breakdown. The $pvr2^{14}$ allele had the broadest resistance spectrum (14 of 16 isolates), followed by *pvr1* (10/16), $pvr2^{2}$ (9/16) and $pvr2^{7}$ (4/16). In all, eight different pathotypes of a theoretical total of 16 were observed (Table 1). VPg mutations associated with resistance breakdown have been observed at amino acid positions 109 and 119 for the pvr1 allele and at position 120 for the $pvr2^{2}$ allele.

DISCUSSION & CONCLUSION Although fewer *pvr2* alleles confer resistance to TEV than to the other potyvirus *Potato virus Y* (PVY) [1], there is a similarly high diversity of pathotypes in the two viruses. Such diversity is potentially driven by coevolution between pepper and potyviruses [2] but it is difficult to identify which potyvirus species has (or have) exerted a selection pressure on pepper. In addition, this study provides new informations about the resistance spectrum and potential of durability of different *pvr1/pvr2* alleles.

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Pathotype	*pvr2*^{2}	*pvr2*^{7}	*pvr2*^{14}	*pvr1*
1 (*n*=2)	R	R	R	R
2 (*n*=3)	R	S	R	R
3 (*n*=3)	S	S	R	R
4 (*n*=2)	S	S	S	R
5 (*n*=2)	R	R	R	S
6 (*n*=2)	R	S	R	S
7 (*n*=1)	S	S	PR	S
8 (*n*=1)	S	S	S	S

Table 1. The eight TEV pathotypes revealed by this study using four pepper genotypes with *pvr2*/*pvr1* resistance alleles.
R : resistant ; PR : partially resistant ; S : susceptible.
n : number of isolates belonging to each pathotype.

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