Exploring plant tolerance to viruses as a sustainable means of disease control

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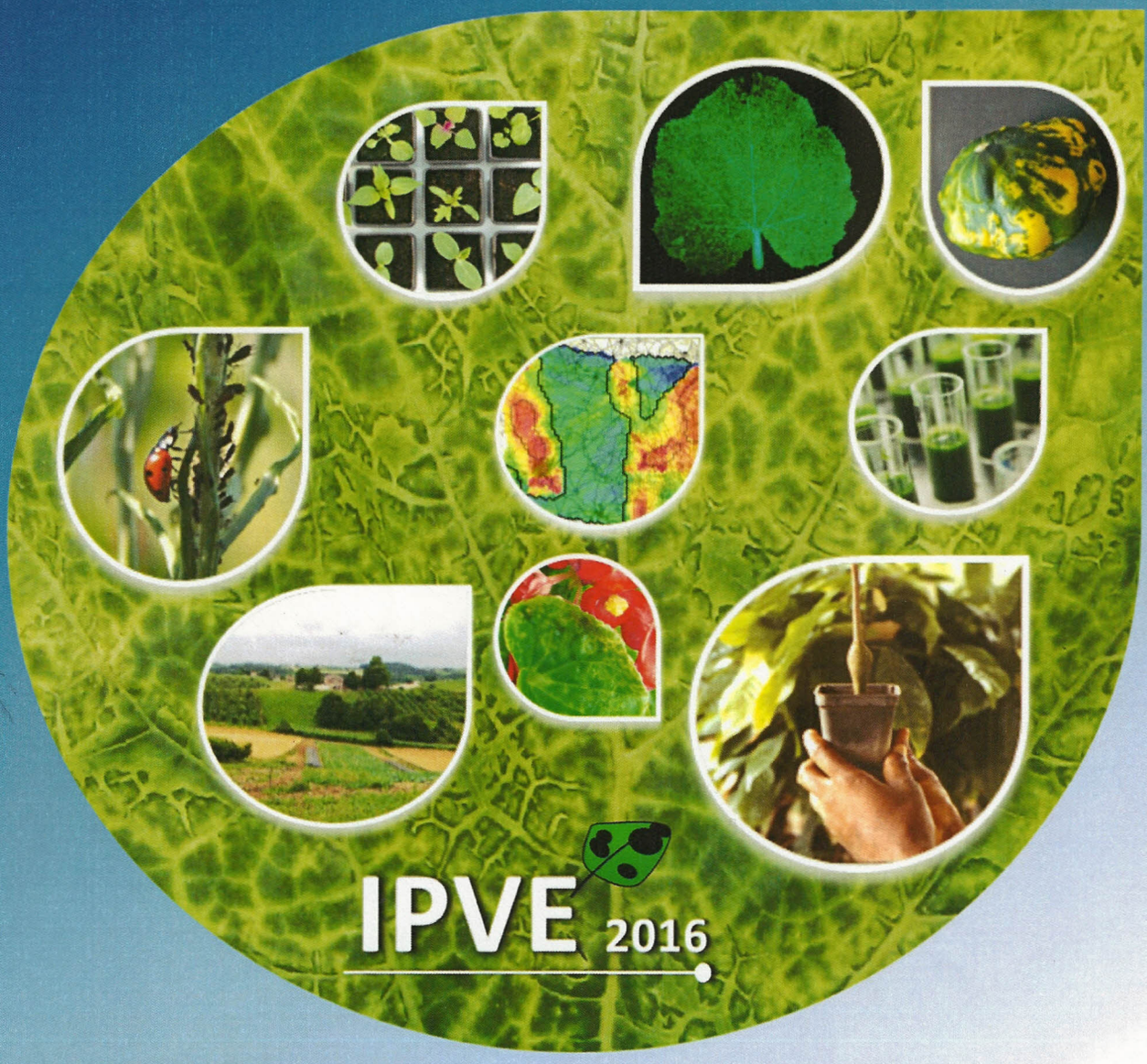
Building bridges between disciplines for sustainable management of plant virus diseases



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Programme and Abstracts

EXPLORING PLANT TOLERANCE TO VIRUSES AS A SUSTAINABLE MEANS OF DISEASE CONTROL

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BACKGROUND and OBJECTIVES

The use of resistant plant cultivars is an efficient, cost-effective and environmentally-friendly method of disease control, particularly against viral pathogens. However, resistance is subject to breakdown, through the often rapid adaptation of viral populations to newly deployed resistant genotypes.
As it exerts a weaker selection pressure on parasite populations, plant tolerance to parasites - the mechanisms that reduce the negative impact of infection on host fitness or yield, despite relatively elevated parasite concentrations - appears as an interesting alternative to resistance *sensu stricto* - mechanisms that reduce pathogen accumulation (1). However, the durability of tolerance has seldom been experimentally tested, and counter-examples exist (2). Moreover, little is known about the genetic determinants controlling tolerance to pathogens.
We have chosen the interaction between pepper and *Cucumber mosaic virus* (CMV) as a model to study plant tolerance to viral pathogens and evaluate the durability of tolerance.

MATERIAL and METHODS

We will exploit available pepper mapping populations in order to identify doubled haploid (DH) lines with contrasted levels of tolerance and resistance *s.s.* to a highly aggressive CMV isolate. Both virus titre and plant health will simultaneously be evaluated for each DH line. Virus accumulation will be quantified using serological methods (DAS-ELISA, Double Antibody Sandwich Enzyme Linked Immunosorbent Assay). The impact of infection on plant health will be measured using different methods, including the reduction in fresh weight of infected plants compared to mock-inoculated plants, and the AUDPC (Area Under the Disease Progress Curve) index, which combines time of symptom emergence and symptom intensity.
QTLs (Quantitative trait loci) governing symptom expression *versus* QTLs controlling virus accumulation will be mapped.
Tolerant DH lines will be exploited in experimental evolution assays, through serial virus inoculations, in order to evaluate the durability of this defense mechanism in controlled conditions.

RESULTS and CONCLUSIONS

We have recently initiated a screen using a pepper DH mapping population. Our preliminary screening efforts have allowed the identification of lines displaying different levels of resistance and tolerance to CMV. Screening of additional DH lines will allow us to map QTLs controlling tolerance or resistance *s.s.*, and to compare the genetic architecture of these two defense mechanisms.
Further efforts will aim at confirming tolerance and resistance levels of a small subset of DH lines with contrasted levels of resistance and tolerance to CMV, and testing their response to a set of isolates representative of CMV diversity.
Experimental evolution assays should indicate whether tolerance is evolutionarily more stable than resistance *s.s.* and whether breeding tolerant crops may contribute to sustainable control of plant viruses.

REFERENCES

(1) Råberg *et al.*, 2009, Phil. Trans. R. Soc. B, 364: 37-49.
(2) Desbiez *et al.*, 2003, Phytopathology, 93:1478-1484.