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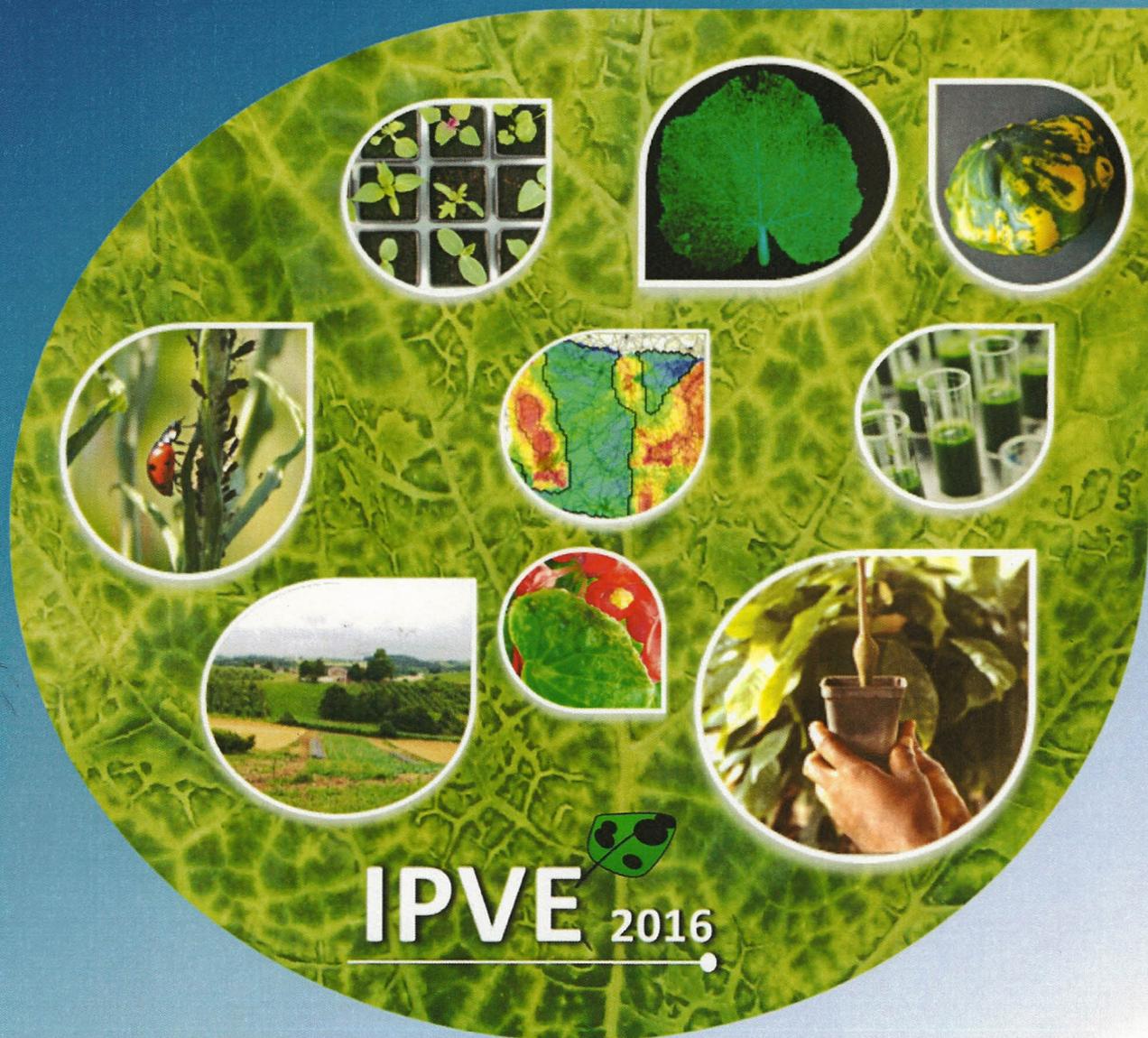
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Building bridges between disciplines for sustainable management of plant virus diseases



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Programme and Abstracts

IMPACT OF SELECTION, GENETIC DRIFT AND VIRAL ACCUMULATION ON THE EVOLUTION OF A PLANT RNA VIRUS

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BACKGROUND and OBJECTIVES

Genetic control is an efficient way to fight against crop disease, but this method is limited by the pathogen ability to evolve and break the resistance down. In the pepper-*Potato virus Y* (PVY) pathosystem, studies have demonstrated that the plant genetic background can increase the durability of the major resistance gene (Palloix et al., 2009), especially by constraining pathogen evolution (Quenouille et al., 2013). We conducted an experimental evolution to (i) measure the pathogen ability to adapt to plants combining major resistance gene and partially resistant genetic background and (ii) identify the role of the evolutionary forces induced by the genetic background on virus evolution.

MATERIAL and METHODS

We used six doubled-haploid (DH) lines of *Capsicum annuum* carrying the PVY resistance allele *pvr2³* and differing in their genetic background. All these lines were selected for their contrasted effects on viral accumulation, selection and genetic drift imposed to the viral population. Three variants of PVY isolate SON41p showing different levels of adaptation to the DH lines were chosen. Each variant carried one substitution in the VPg cistron, named 101G, 115K or 119N, allowing them to overcome the *pvr2³* resistance. We performed an experimental evolution by passaging serially the PVY variants on the six DH lines. The VPg of the viral lineages was sequenced at each evolutionary cycle and their final level of adaptation and aggressiveness was assessed.

RESULTS

We found that different evolutionary process occurred between the lineages resulting in fitness gains, extinctions or no evolution at all. The fitness gains were always observed in lineages showing at least one non-synonymous mutation in the VPg cistron. Genetic drift had a significant impact on virus evolution, since all the lineages that evolved in plants inducing a strong genetic drift did not adapt or became extinct.

CONCLUSIONS

Using experimental evolution, we demonstrated that genetic backgrounds inducing strong genetic drift reduced or prevented the virus adaption to the major resistance gene.

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