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Potato virus Y adaptation to various resistance QTL combinations in pepper and impact on host tolerance

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Plant resistance is one of the best strategies to control pathogens for an environmentally friendly agriculture. Resistances are of two types: monogenic or polygenic, the latter frequently controlled by resistance quantitative trait loci (rQTL). However, both resistance types face pathogen adaptation, leading regularly to a complete breakdown. Pathogen adaptation may also have an impact on the plant tolerance, which is the ability of the plant to reduce the damages caused by pathogen infection (i.e. the ability to reduce the pathogen virulence). Studies of viral molecular mechanisms linked with resistance breakdown are frequent for monogenic resistance but scarce for adaptation to rQTL. The main objectives of the current study are to (i) evaluate the adaptation of experimentally-evolved PVY strains on pepper lines containing various combinations of rQTL and tolerance QTL, (ii) determine tolerance changes induced by this adaptation, (iii) analyse mutations appeared during experimental evolution. Two PVY strains were experimentally evolved for nine months corresponding to nine successive passages on five doubled haploid lines, each containing one specific combination of rQTL and tolerance QTL. Following the experimental evolution, quantitative ELISA and fresh weight measurements were performed to compare the fitness and virulence of ancestral and evolved strains. Significant adaptation was only recorded on the most resistant doubled-haploid line. Two evolved strains from another treatment (strain-pepper line combination) showed a fitness decrease compared to the ancestral strain. Virulence increase was recorded for 2 treatments involving a non-tolerant doubled-haploid line, but they were not associated with a fitness increase. Actually, any evolved population showed both a change in fitness and in virulence. Sequencing of the viral population revealed at least one mutation related to either fitness or virulence changes. However, mutation validation is yet to be performed to confirm the impact of these mutations on the fitness and the virulence of viral populations.