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Genome-wide association mapping of loci implied in *Potato virus Y* resistance and tolerance in the pepper germplasm

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Plants have evolved two ways to decrease damage induced by parasite infections, resistance and tolerance. Resistance decreases the parasite load within plants whereas tolerance decreases the plant damage for a given parasite load. Resistance itself can be divided into qualitative resistance, usually conferred by a major-effect gene, and quantitative resistance conferred by quantitative trait loci. In this study, we used *Potato virus Y* (PVY; genus *Potyvirus*, family *Potyviridae*) and a core-collection representative of the pepper (*Capsicum annuum*; family *Solanaceae*) germplasm to test the following hypotheses:-Did resistance and tolerance evolve as independent, complementary or alternative defence mechanisms in pepper?-Similarly, did qualitative and quantitative resistance evolve as independent, complementary or alternative mechanisms?Using a genotyping-by-sequencing approach allowed to obtain 10,308 single-nucleotide polymorphisms (SNPs) in the C. annuum genome for a core-collection of 276 accessions. Two resistance traits were measured in this core-collection: the number of infection foci in plant cotyledons inoculated with a GFP-tagged PVY and within-plant PVY accumulation. Tolerance was measured as the slope of the regression line between PVY-induced damage (plant fresh weight of infected versus mock-inoculated plants) and within-plant PVY accumulation. Using genome-wide association, we identified three loci in the pepper genome that explained a significant proportion of resistance variation and one locus associated with tolerance variation. These four loci were located on four chromosomes. One resistance locus corresponded to the eIF4E (eukaryotic initiation factor 4E)-encoding gene, which comprises many major-effect alleles in pepper. At this locus, the resistance allele was associated more frequently than expected at random with resistance alleles at the other two resistance loci. Such associations could increase the durability of major-effect resistance genes. In contrast, the tolerance allele was less frequently associated with eIF4E resistance alleles than expected at random, suggesting that resistance and tolerance evolved as alternative defence mechanisms.
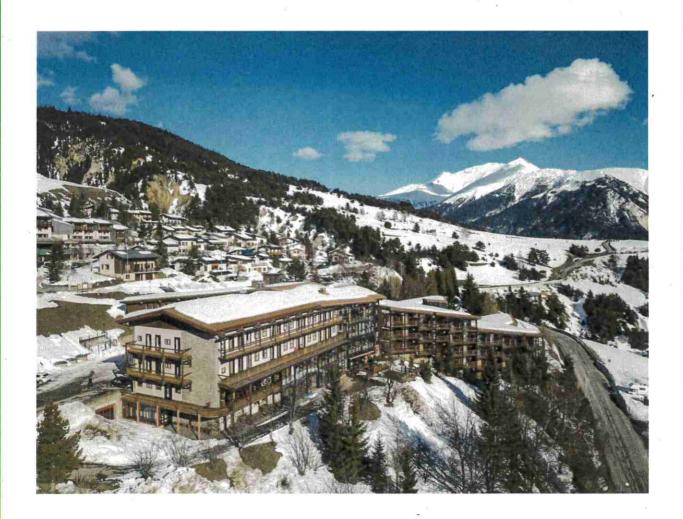
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