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Deciphering the genetic basis of tolerance to Cucumber mosaic virus in pepper

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Plant defense against parasites can be divided into two distinct components: mechanisms that reduce parasite accumulation (resistance *sensu stricto*) and mechanisms that reduce the negative impact of infection on host fitness, health or yield without impacting parasite concentrations (tolerance). As it is expected to exert a weaker selection pressure on parasite populations, plant tolerance to pathogens appears as an interesting alternative to resistance *s.s.* for sustainable disease management. However, little is known about the genetic determinants controlling tolerance to parasites. We have chosen the interaction between pepper and Cucumber mosaic virus (CMV) as a model to study plant tolerance to viral pathogens. We performed a screen using a pepper doubled haploid (DH) mapping population to map CMV tolerance and resistance QTLs. Both virus titer and plant health were simultaneously evaluated for each DH line. Virus accumulation was quantified using serological methods (DAS-ELISA, Double Antibody Sandwich Enzyme Linked Immunosorbent Assay). The impact of infection on plant health was measured using different methods. These methods included calculating the AUDPC (Area Under the Disease Progress Curve) index, which combines time of symptom emergence and symptom intensity, measuring plant growth parameters, such as the reduction in fresh weight of infected plants compared to mock-inoculated plants, and measuring leaf chlorophyll content. Our screening efforts have shown that plant health and virus load are not correlated and allowed the identification of lines displaying contrasted levels of tolerance and resistance to CMV. Mapping efforts are underway to detect QTLs controlling tolerance or resistance *s.s.*, and to compare the genetic architecture of these two defense mechanisms.

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