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Innovations in Genetics and Breeding of Capsicum and Eggplant

Proceedings of the 17th EUCARPIA Meeting on Genetics
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Deciphering the genetic basis of tolerance to *Cucumber mosaic virus* in pepper

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BACKGROUND 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. 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.

MATERIALS & METHODS We performed a screen using a pepper doubled haploid (DH) mapping population [1] 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 (semi-quantitative DAS-ELISA). 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.

RESULTS 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. Tolerance levels were measured as in [2] using the slope of the linear regression line between plant health and virus load. Based on the comparison of tolerance values calculated for 9 DH lines included in two independent screening rounds, broad sense heritability for this trait was estimated at $h^2=0.74$. Mapping efforts are underway to detect QTLs controlling tolerance or resistance *s.s.*

DISCUSSION & CONCLUSION Our screen has shown that tolerance is a highly heritable trait in the DH mapping population. Mapping of resistance and tolerance QTLs will allow us 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 using these DH lines 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.

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