Determinism of virulence of cucumber vein yellowing virus (CVYV) in melon and insights into the durability of resistance

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Genetic resistance is a sustainable way of controlling plant viruses, but it requires the presence of resistance genes in the host germplasm. Besides, its durability can be reduced by resistance-breaking isolates, either pre-existing in the environment or emerging after the deployment of the resistance. In the case of cucumber vein yellowing virus (CVYV, genus *Ipomovirus*), an emerging virus on cucurbits in the Mediterranean Basin, few resistances are available in melon. The accession PI 164323 was found to display complete resistance to the strain CVYV-Esp, and accession HSD 2458 presented a tolerance, i.e. very mild symptoms in spite of virus accumulation in inoculated plants. The resistance is controlled by one dominant allele *Cvy-1[1]*, while the tolerance is controlled by a recessive allele *cvy-2* independent from *Cvy-1[1]*. Upon inoculation with eight molecularly diverse CVYV isolates, the resistance was found to be strain-specific since many CVYV isolates induced necrosis on PI 164323, whereas the tolerance presented a broader range. A resistance-breaking isolate inducing severe mosaics on PI 164323 was obtained. It differed from the parental strain by a single amino-acid change in the VPg-coding region. The effect on the mutation was confirmed by reverse genetics using a CVYV infectious clone. Competition experiments suggested a fitness cost of the resistance-breaking mutation in susceptible melon. Our results highlight the need to combine cultural practices and/or additional genes to develop a more durable control of CVYV than the use of the *Cvy-1[1]* allele alone.