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▶ To cite this version:

Cecile Desbiez, Maria Luisa Domingo Calap, Michel Pitrat, Catherine Wipf-Scheibel, Gregory Girardot, et al.. Determinism of virulence of cucumber vein yellowing virus (CVYV) in melon and insights into the durability of resistance. 18. Rencontres de Virologie Végétale, Sep 2021, Aussois, France. hal-03555763

HAL Id: hal-03555763 https://hal.inrae.fr/hal-03555763

Submitted on 9 Feb 2022

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Oral Theme: Resistance Student: no

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 resistancebreaking 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 cvv-2 independent from Cvv-1¹. 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 resistancebreaking 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.

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