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Specificity of resistance and tolerance to cucumber vein yellowing virus in melon accessions and evidence for resistance-breaking associated with a single mutation in VPg

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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, a member of the genus *Ipomovirus*), an emerging virus on cucurbits in the Mediterranean Basin (1), few resistances are available in melon. The melon accession PI 164323 was found to display complete resistance to the strain CVYV-Esp, and melon 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-11, while the tolerance is controlled by a recessive allele cvy-2 independent from Cvy-11. Upon inoculation with eight geographically diverse CVYV isolates corresponding to the known molecular diversity of the virus (2), 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 newly-obtained CVYV infectious clone (3). 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-11 allele alone.

References

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