



HAL
open science

Identification and characterization of new resistance to viruses in Cucurbitaceae

Aimeric Agaoua, Cecile Desbiez, Verane Sarnette, Vincent Rittener, Catherine Dogimont

► **To cite this version:**

Aimeric Agaoua, Cecile Desbiez, Verane Sarnette, Vincent Rittener, Catherine Dogimont. Identification and characterization of new resistance to viruses in Cucurbitaceae. 17. Rencontres de Virologie Végétale (RVV 2019), Jan 2019, Aussois, France. 127 p., 2019, 17èmes Rencontres de Virologie Végétale: RVV 2019. hal-02735260

HAL Id: hal-02735260

<https://hal.inrae.fr/hal-02735260>

Submitted on 2 Jun 2020

HAL is a multi-disciplinary open access archive for the deposit and dissemination of scientific research documents, whether they are published or not. The documents may come from teaching and research institutions in France or abroad, or from public or private research centers.

L'archive ouverte pluridisciplinaire **HAL**, est destinée au dépôt et à la diffusion de documents scientifiques de niveau recherche, publiés ou non, émanant des établissements d'enseignement et de recherche français ou étrangers, des laboratoires publics ou privés.



Distributed under a Creative Commons Attribution - NonCommercial - NoDerivatives 4.0 International License

Identification and characterization of new resistance to viruses in Cucurbitaceae

Aimeric Agaoua¹, Cécile Desbiez¹, Verane Sarnette¹, Vincent Rittener¹, Catherine Dogimont¹

¹GAFL INRA St. Maurice, 67 allée des Chênes. 84143 Montfavet

Cucurbitaceae are plants of agronomic interest in Europe and in the world. The species of this family are however very sensitive to viral diseases, mostly transmitted by different insect vectors.

Nowadays, a small number of viruses resistance genes are available in these species, like melon (*Cucumis melo*), where no E1F4e variant have been identified to potyviruses resistances.

In this context, using a collection of melon varieties, we study the genes of a highly conserved family in plants and their role in the viral cycle of ssRNA+ viruses. For this, we use an agro-infiltration approach to transiently induce the expression of a candidate gene and then, infect the leaves with *Watermelon Mosaic Virus* (GFP) transformed with GFP. In a second part, we generate a dominant-negative allele of my candidate gene to screen ssRNA+ needing the candidate to achieve their replication cycles. In a last approach, I use databanks to identify diversity in several species of my candidate gene and that I can associate with virus resistance.

In this study, we are characterising a new resistance allele in plant, to afterwards, use this new resistance for multiviruses resistance in several plant species.

17^{emes} Rencontres de Virologie Végétale

**27 au 31 janvier 2019
Aussois - France**

RVV 2019



**Aussois
du 27 au 31 janvier 2019**