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Identification and characterization of new resistance to viruses in Cucurbitaceae

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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 theses species, like melon (*Cucumis melo*), where no EiF4e 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.

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