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### ► **To cite this version:**

Laurence Ouibrahim, André Moretti, Aurélie Salgues, Ana Giner Rubio, Hervé Lecoq, et al.. Towards the identification of new host factors required for plant susceptibility to potyviruses: novel routes to resistance. 13. Rencontres de Virologie Végétale, Jan 2011, Aussois, France. hal-02747103

**HAL Id: hal-02747103**

**<https://hal.inrae.fr/hal-02747103>**

Submitted on 3 Jun 2020

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# 13<sup>èmes</sup> rencontres de virologie végétale

maréaux



Aussois du 16 au 20 janvier 2011





## Towards the identification of new host factors required for plant susceptibility to potyviruses: novel routes to resistance

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As obligatory pathogens, plant viruses need to reroute host cellular factors in order to perform their infectious cycle. Such factors must cooperate with viral products to confer susceptibility, and the absence or mis-adequacy of appropriate host factors was shown to mediate recessive resistance mechanisms in plants. Strikingly, all virus recessive resistance genes characterized until now were demonstrated to encode translation initiation factors of the 4E and 4G families. However, knowing that the completion of the viral infectious cycle results from a complex interplay between virus-encoded and host-encoded factors together with the fact that a large number of natural resistance genes have yet to be characterized, we anticipate that there will be many more potential resistance targets that function as host susceptibility factors. In this context, our objectives are to identify and characterize new host factors required for the infectious cycle of RNA viruses (genus *Potyvirus*) using a combination of a map-based cloning approach and a candidate gene approach in the *Watermelon mosaic virus* (WMV) – *Arabidopsis thaliana* pathosystem. Phenotypic screening of selected *A.thaliana* ecotypes led to the identification in the Cape Verde islands (Cvi-0) ecotype, of a recessive resistance gene (*rwm1*) controlling a complete resistance phenotype. qRT-PCR experiments indicated that resistance occurs at an early stage of the infection, altering viral multiplication at the initial focus of infection. Using the genome-wide coverage near-isogenic line (NIL) population, with introgressed genomic regions from Cvi into the *Ler* (susceptible to WMV) genetic background, *rwm1* was mapped to the long distal region of chromosome 1, between the CIW1 and EC.88C markers. This genomic interval contains approximately 700 genes but none encoding eIF4E or eIF4G proteins. One candidate gene present in the *rwm1* interval is the TOR kinase (*Target Of Rapamycine*). According to its recently described role in plant-virus interactions, we investigated its potential role in the control of susceptibility to potyviruses. Interestingly, a significant decrease of susceptibility to WMV was shown for *A.thaliana* RNAi lines displaying partial TOR inactivation. Experiments aiming to elucidate the role of the TOR pathway in plant-potyvirus interactions are currently under way, and recent results will be presented.