

CFAI & Dept Plant Sci

Plant Virology Seminar



Richard Kormelink

Wageningen University and Research

On the stories behind (a)typical dominant and recessive resistance genes against geminiviruses

Date: 10am-11am, 26 September, 2023

Venue: Lecture room #1 @ Aobayama commons

Tomato yellow leaf curl geminivirus (TYLCV) belongs to the most devastating plant viruses worldwide. One way to combat this virus is by resistance breeding. From the list of available resistance genes for introgression breeding in tomato against TYLCV, *Ty-1* to *-6*, several have been mapped and cloned in the past decade. Whereas *Ty-2* presents a typical dominant resistance gene of the “nucleotide-binding site Leucine-rich repeats” (NLR) class and is triggered by the Rep/C1 protein, *ty-5* presents a recessive resistance gene coding for pelota, an mRNA (translation) surveillance factor. On the other hand, *Ty-1* and its *Ty-3* allele present an a-typical dominant resistance gene, coding for an RNA-dependent RNA polymerase (RDR) of the gamma class and implicated in antiviral RNAi. While dominant resistance genes of the NLR class are the most commonly deployed genes for resistance breeding, they are pathogen specific and can easily be broken by the emergence of a new pathogen variant containing only one single point mutation in the pathogen effector. This presents a major drawback of using NLR resistance genes. In contrast, atypical dominant and recessive resistance genes often provide more durable and broad resistance, and for that reason receive a growing interest. The stories and underlying resistance mechanism behind *Ty-1* and DNA primase Large subunit (*PriL*), another recently identified gene in melon accessions correlated to a recessive resistance against Tomato leaf curl New Delhi virus (ToLCNDV), will be presented in support of their exploitation and implementation towards more durable resistance / disease management strategies. First of all, to combat geminiviruses.

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