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## Novel mechanisms of resistance to Plum pox virus are being unravelled in the model plant, *Arabidopsis thaliana*

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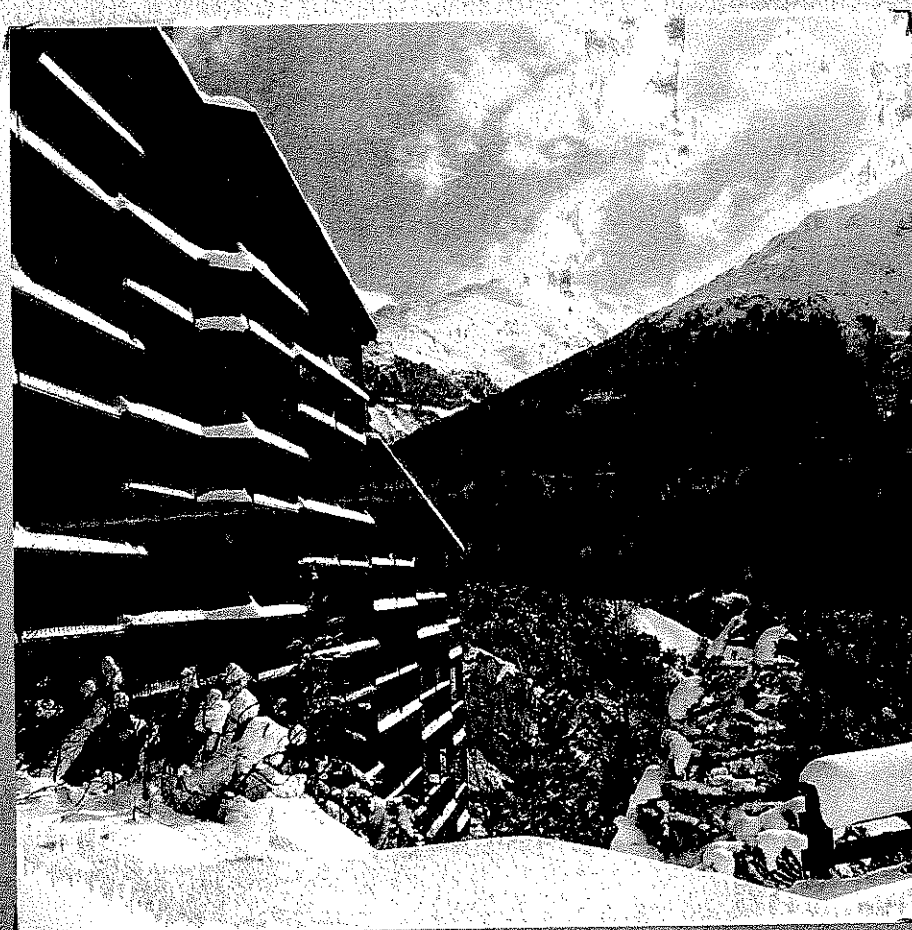
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# 13<sup>èmes</sup> rencontres de virologie végétale



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#### 45- Novel mechanisms of resistance to *Plum pox virus* are being unravelled in the model plant, *Arabidopsis thaliana*

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In plant-virus interactions, recessive resistance has been associated, up to now, to a passive mechanism in which virus infection is impaired due to the lack of a specific host factor. The identification of a recessive resistance gene and, symmetrically, of the corresponding susceptibility allele is thus expected to provide valuable information on the minimal requirements for successful virus infection of the host plant. Gaining access to such information is thus expected to result in new candidate genes for manipulation across species and genera and in the deployment of new resistance sources in agronomically important crop species, such as stone fruit trees. We showed few years ago that *Plum pox virus* (PPV) is able to infect the model plant *Arabidopsis thaliana* and that a large diversity of phenotypes was observed, from susceptibility with symptoms to complete resistance (Decroocq et al., 2006). Several still-unknown factors controlling recessive resistance mechanisms have been identified, their genetic characterization is in progress.

Genetic analyses of Cvi/Ler F2 population showed a digenic recessive resistance to PPV. Currently, isogenic lines (NIL) and backcross populations are using for fine mapping, in order to clone the recessive factor that have been mapped on linkage group 1.

The cloning and characterisation of *Arabidopsis* recessive resistance genes against PPV is an exciting project that has the potential to provide both important information on host-potyvirus interactions and new resistance genes that can be harness in stone fruit species.