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13^{èmes} rencontres de virologie végétale

maréaux



Aussois du 16 au 20 janvier 2011



33- Genome-wide association genetics to identify loci involved in responses to Potyviruses in plants

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The aim of the project is to identify loci involved in susceptibility/resistance responses of *Arabidopsis thaliana* to Potyviruses using genome-wide association (GWA) mapping.

The project will allow, at once, designing a map of loci involved in quantitative response to two potyviruses, Turnip mosaic virus (TuMV) and Watermelon mosaic virus (WMV) in the species *Arabidopsis thaliana*. It will be an important first step towards the identification of candidate genes or quantitative traits loci (QTL) responsible for quantitative response and the cloning of the most important of them. The project will also contribute to an initial setting in understanding plant/virus co-evolution through the comparison of loci involved in the responses to the two challenged viruses.

In first steps, robust phenotyping protocols are developed on a narrow range of genotypes known to reveal a large variability of responses to TuMV.

We optimize :

- ✓ Standardization of plant culture, growth conditions and inoculation conditions, control of environment,
- ✓ Defining type of sample through the following of TuMV-GusGFP replication and movement,
- ✓ Defining scoring classes for symptoms,
- ✓ Defining sampling periods through analysis of virus accumulation by RT-QPCR,
- ✓ Optimizing mean-throughput sampling and RT-QPCR.

Based on the first data, we will measure on the whole plant set : (1) symptoms severity and distribution using a range of scoring classes, (2) length of floral hamp 21 days after inoculation, (3) virus accumulation in inoculated and systemic (further growing non inoculated) leaves by RT-QPCR, (4) infection kinetics by sampling inoculated leaves and systemic leaves 5, 7, 9 and 12 days after the inoculation and performing RT-QPCR.

Association between the phenotype and the genotype will then be performed using a 250k SNPs database.