**Late blight disease: *Phytophthora infestans***

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**Summary of the practical:**

The oomycete pathogen *Phytophthora infestans* causes late blight disease in potato and tomato plants. It has a hemibiotrophic lifestyle and can cause severe epidemics, destroying a whole crop in a few days. The late blight disease triggered the Irish Potato Famine in the 1845-1850 period. It is currently responsible for significant economic losses worldwide and its control relies on the extensive use of chemicals. Strategies based on the introgression of single resistance genes into cultivated potato did not prove to be durable in the field. *Phytophthora infestans* has a highly dynamic and plastic genome which allows rapid adaptation and evasion of control strategies. Availability of a large pool of diverse resistance genes together with knowledge of the pathogen and its populations can help design durable and sustainable approaches to control the late blight disease.

**Part 1: Overview of the biology of *Phytophthora infestans* and characteristics of the late blight disease. Observation of zoospores and sporangia under the microscope and demonstration of detached-leaf assays used for phenotyping resistance to late blight.**

We will discuss the impact of late blight disease, the lifestyle of *Phytophthora infestans* and the main characteristics of its genome structure. We will analyse current control strategies and the alternatives to achieve a more durable and sustainable disease management. Next, we will collect spores and sporangia from mycelia growing on plates to observe them under the microscope and, finally, we will demonstrate how to perform detached-leaf assays to test resistance to late blight in the lab.

**Part 2: Overview of RenSeq as a tool to accelerate the cloning of resistance genes.**

Standard map-based cloning of the resistance genes is slow, laborious and expensive. *R* gene enrichment and sequencing (RenSeq) is a method to capture and sequence only NLR-type resistance genes. Combined with long-read sequencing like PacBio or Oxford Nanopore, it allows the assembly of the full NLR repertoire from plants of interest, and in combination with bulked segregant analysis it allows the prediction of candidate sequences of functional resistance genes. We will discuss how we have used this approach to accelerate cloning of several late blight resistance (*Rpi*) genes.

**Part 3: Visit to the potato field trial site.**

We are currently testing transgenic plants carrying single *Rpi* genes and a 3-*Rpi*-gene stack in the field. We will visit the trial site and discuss the experimental and biosafety aspects of this study.