

# The potato microbiome and its potential impact on late blight resistance



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## Background

Late blight, caused by the oomycete *Phytophthora infestans*, is a major threat for potato production worldwide. In organic farming, late blight control relies on the use of copper-based fungicides, which are the only efficient products currently available. However, due to the toxicity of copper towards the environment, the need to develop alternative control methods for organic potato production is evident. Moreover, due to the introduction of new isolates of *P. infestans* in Europe, the diversity of the pathogen's population has strongly increased over the past three decades. However, little information on the pathogen diversity currently present in Switzerland is available.

### *P. infestans* on potato

Necrosis develop on leaves, stems and tubers of infected plants. Susceptibility varies among cultivars. Annually, the disease accounts for over €5 Billion in crop losses and control costs worldwide.



## Aim of the study

This study focuses on understanding the potential role of the potato microbiome in the protection against late blight and aims at :

...characterizing the potato leaf microbial communities in both healthy and diseased plants (1)

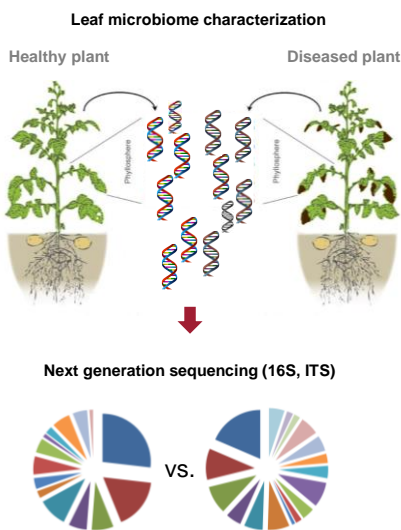
...identifying the genetic determinants of the anti-*Phytophthora* activity shown by a selection of potato-associated *Pseudomonas* isolates (2)

A third part of this project is devoted to characterizing the diversity of *P. infestans* isolates in Switzerland (3)

## Methods

### (1) Composition of the potato leaf microbiome

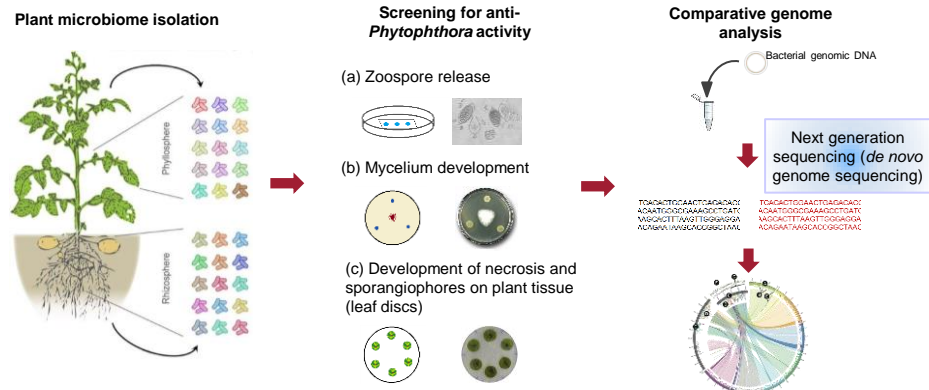
The leaf associated microbiome of different potato cultivars will be characterized different times of the year.



- **What is the composition of the potato microbiome?**
- **Do different potato cultivars shelter different bacterial communities?**
- **Does the microbiome composition change throughout the growth season?**
- **Does infection with *P. infestans* lead to shifts in the composition of the microbiome?**

### (2) Genomic determinants of the anti-*Phytophthora* activity

The antagonistic activity of bacterial strains isolated from potato plants and rhizosphere will be evaluated by analyzing their effect on virulence-associated features (a,b,c). Comparative genome analysis will be performed for a subset of active and non-active *Pseudomonas* strains.



- **Is the anti-*Phytophthora* activity attributable to specific loci within the genome?**
- **What are these loci encoding?**

### (3) Diversity of *P. infestans* in Switzerland

*P. infestans* isolates will be collected from naturally infected fields in Switzerland and characterized for :

- Mating type
- Genetic markers
- Virulence
- Fitness
- Sensitivity to antagonistic bacterial strains



- **What is the diversity and structure of the *P. infestans* population in Switzerland?**

## Expected Outcome

This study aims at providing a better understanding of the potential role and impact of the potato microbiome in protection against late blight. *De novo* sequencing of active strains and genome comparison between closely related active and less active strains should reveal the genetic basis of the anti-*Phytophthora* activity. This ultimately should enable us to better exploit the potential of antagonistic bacteria as components of late blight control strategies for organic production. Moreover, determining the diversity of *P. infestans* and its spatial distribution in Switzerland will bring essential new information that could be integrated in forecasting and disease management schemes for better protection against the disease.