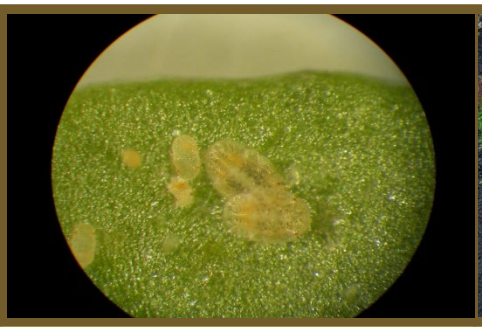
The biology and epidemiology of '*Candidatus* Liberibacter solanacearum' and potato phytoplasmas and their contribution to risk management in potato and other crops

Euphresco

04/2020-03/2022



Funding

Non-competitive funding mechanism. Each funder only pays for the participation of their own national researchers. Total funding € 201 000

Research consortium

SASA (GB), AGES (AT), ILVO (BE), CFIA (CA), ANSES (FR), DAFM (IE), CREA (IT), MPI (NZ), VNIIKR (RU), AGRIF (RS), Tarimormam (TR), FN3PT (FR)

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Goals

Phytoplasmas and '*Candidatus* Liberibacter solanacearum' are responsible for causing severe losses in a number of economically important crops worldwide.

The goals of the project are to facilitate and coordinate work between an established team of researchers working on phytoplasma and '*Candidatus* Liberibacter solanacearum' in order to further understand the impact of these insect-vectored bacteria on plant health

Objectives

Some of the objectives of the projects are:

- to monitor phytoplasmas and '*Candidatus* Liberibacter solanacearum' distribution and diversity in insect vectors, crop plants, weed species reservoirs and seeds
- to improve knowledge on how '*Candidatus* Liberibacter solanacearum' is transmitted plant to plant, plant to insect and insect to insect.
- to improve knowledge on the genetics and pathology of '*Candidatus* Liberibacter solanacearum' by genome and transcriptome sequencing
- to examine psyllid, leafhopper and planthopper diversity in carrot and potato fields
- to examine psyllid behavior and ecology to understand transmission of '*Candidatus* Liberibacter solanacearum' and the propensity for certain psyllid species to spread it to crops

Key outputs and results

Some of the key outputs of the project are:

- knowledge on '*Candidatus* Liberibacter solanacearum', phytoplasma, leafhopper and psyllid diversity from different regions
- knowledge on the prevalence of '*Candidatus* Liberibacter solanacearum' in seeds
- knowledge on disease entry pathways
- genome sequencing and MLST of novel and existing Lso haplotypes