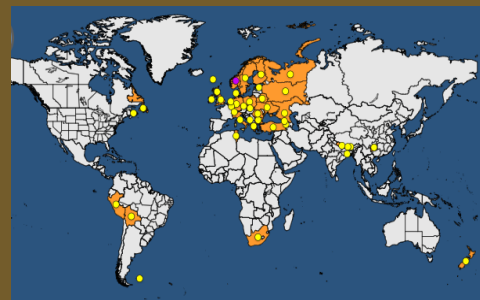


Molecular characterization of potato wart disease (SendoTrack)



Funding

Non-competitive funding mechanism. Each funder only pays for the participation of their own national researchers. Total funding € 272 000

Research consortium

NVWA (NL), BFSa (BG), CFIA (CA), AU (DK), JKI (DE), BPI (GR), DAFM (IE), VNIKR (RU), SBA (SE), SASA (GB), AAFC (CA), BSU (GE), LU (DE), APQA (KR), WUR (NL), CIP (PE), NAAS (UA)

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Goals

Potato wart disease is caused by the quarantine soil-borne fungus *Synchytrium endobioticum*.

As the pathogen develops new pathotypes which overcome varietal resistance, a thorough molecular characterization of the pathogen from European outbreak sites is essential. The project aims to collect data on the pest's genomic diversity, geographical origin and epidemiological traits, in order to track-and-trace the fungus and help support surveillance and management practices

Objectives

The project objectives are:

- To collect samples from all participating countries (warts, compost, soil, etc.);
- To molecularly characterize the samples (mitochondrial DNA and nuclear simple repeats-SSR);
- To validate a diagnostic test using the whole genome amplified DNA material

Key outputs and results

The main project's results are:

- Validated protocols for the detection and identification of *S. endobioticum* isolates;
- A public data platform in which the genomic diversity of *S. endobioticum* isolates can be accessed in the context of geographic distribution and other relevant metadata