Euphresco

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# Using High Throughput Sequencing to gain insights from virus collections and strengthening the infrastructure of Plant Virus Collections (VirusCurate)

## Funding

Non-competitive funding mechanism. Each funder only pays for the participation of their own national researchers. Total funding € 167 000

## Research consortium

Fera (GB), AVR (AU), UQ (AU), CISTA (CZ), JKI (DE), NVWA (NL), MPI (NZ), NIBIO (NO), KIS (SI), NIB (SI), UNIBL (BA), DSMZ (DE), NAIK (HU), Naktuinbouw (NL), OkState (US), UARK (US)

## Contact information

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## Goals

High Throughput Sequencing (HTS) is revealing large numbers of previously unknown viral sequences. However, in some cases these may not be ‘unknown viruses’ but may be viruses which have not been previously sequenced but are already held in reference collections and may have been previously characterised biologically and serologically. The aim of the project is to characterize historical isolates to support risk analyses of ‘novel’ viral species.

## Objectives

The project will address the following objectives:

- To generate sequences of viruses with no (or partial) known sequence, preferably where biological and serological data are available;
- To generate sequences of old isolates of more common virus species where there is limited sequence and a policy/regulation question;
- To harmonize the minimum expected requirements for identification of a novel virus. This objective will be addressed in liaison with ICTV for harmonization of nomenclature of novel 'sequence only' viral entities;
- To streamline the sharing of data within a network of reference collections and promote the publication of sequences, including utilising existing database infrastructures for depositing isolate information.

## Key outputs and results

The main expected results are:

- Collated list of isolates in collections in the partner countries;
- Annotated genetic sequence, genetic diversity and phylogeny of multiple isolates of known viruses