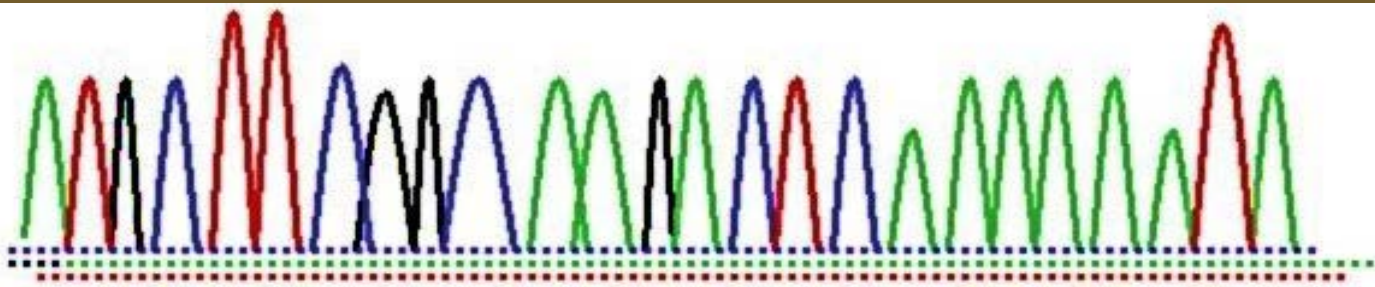


The application of Next-Generation Sequencing technology for the detection and diagnosis of non-culturable organisms: viruses and viroids



Funding

Non-competitive funding mechanism. Each funder only pays for the participation of their own national researchers. Total funding € 650 000

Research consortium

BMEL (DE), ILVO (BE), CFIA (CA), Aarhus (DK), ANSES (FR), INRA (FR), DEFRA (GB), BPI (GR), NFCSO (HU), AlphaTaxa (IE), CREA (IT), NVWA (NL), FGBU-VNIIKR (RU), INIA (ES), NIB (SI), CIP (PE), ARC (ZA)

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Key outputs and results

- Development and validation of a common pipeline from sample preparation to data analysis
- Developing reference sequence data for viruses and viroids (e.g. Q-bank) in a plant quarantine setting or certified scheme
- Aetiology of uncharacterized diseases

Goals

The existing molecular methods (PCR, real-time PCR, traditional gene sequencing) for the detection and identification of non-culturable organisms and particularly plant pathogen viruses and viroids don't always lead to the correct identification of the pathogen, especially in case of multiple infection. In some case, symptoms described as 'typical', e.g. Plum Pox Virus in stone fruits, may be associated to other viruses than Plum Pox Virus. In this case, using Next Generation Sequencing (NGS) technology can be helpful to save time and identify the aetiology of the symptoms. The collaborative evaluation of NGS can accelerate adoption of technology into routine diagnostics. An international consortium within Euphresco would also give broader support by including the methods into EPPO protocols. Collaboration at an international level would be beneficial to define new protocols for identification of plant pathogen viruses and viroids. The ultimate goal would be the development of reference sequence data for viruses and viroids and their inclusion in existing databases (Q-Bank Plant Viruses and Viroids Database; Roenhorst *et al.*, 2013).