

1. Content of the 'Topic Description' document

1.1. Topic area

E: Pest/vector characterization: genetics, biochemistry, etc.

1.2. Links to the Euphresco Strategic Research Agenda

The topic addresses the following objective(s) of the 2017-2022 Euphresco Strategic Research Agenda:

- Objective 2017-R-1.2: to support taxonomic research for the unambiguous identification of pests
- Objective 2017-R-5.1: to understand the biological significance of a positive molecular diagnosis
- Objective 2017-R-5.4: to test and validate the use NGS (e.g. whole genome sequencing, metagenomics, deep sequencing, typing by sequencing) for routine diagnostics
- Objective 2017-I-1.1: to support knowledge exchange for efficient management and maintenance of collections
- Objective 2017-I-1.2: to improve access to collections of phytosanitary importance
- Objective 2017-I-1.3: to build a network of collections that fulfil minimum quality standards
- Objective 2017-I-2.1: to support data exchange, data use and re-use for the benefit of plant health research activities
- Objective 2017-I-2.2: to contribute to databases for plant pests identification and diagnostics

1.3. Topic title

VirusCurate: Using High Throughput Sequencing to gain insights from virus collections and strengthening the infrastructure of Plant Virus Collections.

1.4. Description of the problem the research should solve

Through the use of High Throughput Sequencing (HTS) in plant health we are revealing large numbers of previously unknown virus 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 isolate collections and may have been previously characterised biologically and serologically. Within existing virus collections are a range of unsequenced species which may be still listed as 'unknown virus' or may have been published before the advent of sequencing technologies. This has come sharply into focus recently with the detection of novel virus sequences in a niche crop *Ullucus tuberosus* where it is suspected that viruses detected through sequencing may be isolates of the same viruses previous detected and reported based on biology and serology (Fox *et al.*, in press). If these links can be made to virus isolates biologically characterized in previous reports then these linked data can be used to inform pest risk assessment of these 'novel' species, supporting the framework proposed by Massart *et al.*, (2017).

There are also situations where regulation is applied to some isolates of a species but not others (e.g. non-European isolates of common potato viruses, etc.). However, in many cases there is limited evidence of any clear difference between the isolates found in the EU and those from third countries. Sequence data from a range of isolates of such viruses, supported by phylogenetic analysis, could provide insights into the distribution isolates of such viruses considered to be a greater risk. An example of this work was published recently by Santillan *et al.*, (2018) using a range of newly sequenced historic isolates and sequence already on databases to give new insights into the evolutionary history of *Potato virus S*.

However, additional practical challenges will also need to be overcome, and the project should include sharing of best practice on methods for sequencing historic and ancient nucleic acid

and bioinformatics approaches. There will also be a need to create a common understanding on approaches to nomenclature with respect to sequence derived viruses.

Furthermore, this project will continue the efforts of the preceding VirusCollect I and II projects to share information and data on virus isolates resulting from other research projects. In the field of Plant Virology there is currently only one official ISO 17034-accredited collection at the Leibniz institute DSMZ German collection of Microorganisms and Cell cultures in Braunschweig. This collection includes only part of the currently regulated species (Roehorst *et al.*, 2013). This implies that isolates of many (regulated) viruses and viroids, if publicly available at all, are scattered over different collections at NPPOs, research institutes and universities. Therefore, this project also aims to establish a common collection of viruses and viroids by linking local collections of individual institutions via a common database (Q-bank). In this way the infrastructure will be improved by safeguarding of well-characterised virus isolates and making them available for diagnostics and research (Roehorst *et al.*, 2017).

References

- Fox A, *et al.* (2018, in press) Using High Throughput Sequencing in support of a plant health outbreak reveals novel viruses in *Ullucus tuberosus*. (Accepted, Plant Pathology)
- Massart, S., *et al.* (2017). A framework for the evaluation of biosecurity, commercial, regulatory, and scientific impacts of plant viruses and viroids identified by NGS technologies. *Frontiers in microbiology*, 8, 45.
- Roehorst JW, Boonham N, Winter S, Menzel W & Van der Vlugt RAA (2013). The plant viruses and viroids database and collections of Q-bank. *Bulletin OEPP/EPPO Bulletin* 43 (2), 238–243.
- Roehorst JW, Lacomme C, Nisbet C, Leichtfried T, Menzel W, Winter S, Van der Vlugt RAA (2017). Euphresco project VirusCollect – fulfilling the need for a common collection of plant viruses and viroids for reference. *EPPO Bulletin* 47, 41-47.
- Santillan, F.W., *et al.* (2018). The Biology and Phylogenetics of Potato virus S Isolates from the Andean Region of South America. *Plant Disease*, 102(5), pp.869-885.

1.5. Description of the expected results

Synergies will be pursued with previous Euphresco topics such as 2015-F-172 NGS-Detect, VirusCollect I, 2015-F-132 VirusCollect II, 2017-A-243 VIRFAST, and 2018-A-293 PRONC.

Following an assessment of isolates available within collections in the network, isolates will be prioritised for sequencing analysis. The aims of the project will be to provide sequence data for previously isolated viruses to be used for:

- Generating sequence for viruses/species with no (or only partial) existing sequence, preferably where they have existing biological and serological data;
- Generating sequence of old isolates of more common virus species where there is limited sequence and a policy/regulation question;
- Harmonization of minimum expected requirements for identification of a novel virus and liaison with ICTV for harmonization of nomenclature of novel 'sequence only' viral entities;
- Streamlining sharing of data within a collections network and promoting publication of sequences, including utilising existing database infrastructures for depositing isolate information such as that developed in support of VirusCollect I and II.

1.6. Beneficiaries of this research product

The project will benefit to research scientists, diagnosticians and regulators (policy makers and risk managers).

1.7. Research funders and research contribution/ distribution



Funding organisation	Research activity and researchers involved
1. Department of Environment, Food and Rural Affairs, United Kingdom Elspeth Steel Elspeth.steel@defra.gov.uk	-Project coordination; -Collections mapping; -Literature searching; -Isolates sequencing; Contact Person: Adrian Fox E-mail: Adrian.fox@fera.co.uk
2. Ministry of Agriculture and Water Resources, Australia Con Goletsos acppo@agriculture.gov.au	-Isolates sequencing; Contact person: Fiona Constable E-mail: Fiona.Constable@ecodev.vic.gov.au -Isolates sequencing; Contact person: Ralf Dietzgen E-mail: r.dietzgen@uq.edu.au
3. Central Institute for Supervising and Testing in Agriculture, Czech Republic Michal Hnizdil michal.hnizdil@ukzuz.cz	-Collections mapping; Contact person: Veronika Ševčíková E-mail: veronika.sevcikova@ukzuz.cz
4. Federal Ministry for Food and Agriculture, Germany Bettina Beerbaum bettina.beerbaum@bmel.bund.de Silke Steinmüller silke.steinmoeller@julius-kuehn.de	-Contribution to be detailed Contact person: Heiko Zeibell E-mail: heiko.ziebell@julius-kuehn.de Contact person: Wilhelm Jelkman E-mail: Wilhelm.Jelkmann@julius-kuehn.de
5. Netherlands Food and Consumer Products Safety Authority, The Netherlands Martijn Schenk m.schenk1@nvwa.nl	-Collections mapping; -Isolates sequencing; Contact person: Annelien Roenhorst E-mail: j.w.roenhorst@nvwa.nl Contact person: Carla Oplaat E-mail: A.G.oplaat@nvwa.nl
6. Ministry of Agriculture, Forestry and Food, Slovenia Erika Orešek erika.oresek@gov.si	-Isolates sequencing; Contact person: Mojca Virscek Marn E-mail: mojcavm@kis.si ; Contact person: Irena Mavric Plesko E-mail: irena.mavricplesko@kis.si -Isolates sequencing; Contact person: Maja Ravnikar E-mail: Maja.Ravnikar@nib.si



	Contact person: Denis Kutnjak E-mail: Denis.kutnjak@nib.si
7. University of Banja Luka, Faculty of Agriculture, Bosnia and Herzegovina Duska Delic duska.delic@agro.unibl.org	-Isolates sequencing; Contact person: Duska Delic E-mail: duska.delic@agro.unibl.org Contact person: Mariana Radulovic
8. National Agricultural Research and Innovation Center, Hungary Eva Varallyay varallyay.eva@abc.naik.hu	-Collecting materials with previously described symptoms (preferably grapevine, fruit trees, berries); -Isolates sequencing; -Validation of the sequences with independent molecular methods; Contact person: Eva Varallyay E-mail: varallyay.eva@abc.naik.hu
9. Leibniz Institute DSMZ, Germany Wulf Menzel wulf.menzel@dsmz.de	-Isolates sequencing; -Collection quality criteria; Contact person: Wulf Menzel E-mail: wulf.menzel@dsmz.de Contact person: Paolo Margaria E-mail: paolo.margaria@dsmz.de
10. Naktuinbouw, The Netherlands Marcel Toonen m.toonen@naktuinbouw.nl	-Collections mapping; -Isolates sequencing; Contact person: Ellis Meekes E-mail: e.meekes@naktuinbouw.nl
11. Oklahoma State University, United States of America Francisco Ochoa Corona ochoaco@okstate.edu	-Contribution to be detailed; Contact person: Francisco Ochoa Corona E-mail: ochoaco@okstate.edu
12. University of Arkansas, United States of America Ioannis Tzanetakis itzaneta@uark.edu	-Contribution to be detailed; Contact person: Ioannis Tzanetakis E-mail: itzaneta@uark.edu

1.8. Research project partnership outside Euphresco

Euphresco funding ensures a certain level of transnational collaboration among Euphresco member countries. It is possible, if the funding consortium is interested, to contact funding organisations or research groups outside the geographical area covered by Euphresco members. The Euphresco coordinator could advertise the research topic in order to have an enlarged collaboration. If funders are interested in this possibility, please check the case below:

The funding consortium of the topic mentioned in section 1.2 requires that the topic is advertised outside the Euphresco network

The project should be open to groups with a background or interest in high throughput sequencing, virus identification, and virus collections.

1.9. Any other relevant information on content

Close collaboration with other projects in the field is envisioned. Curators of Q-bank Plant Viruses and Viroids database will be involved in VirusCurate. The research partners will also look to interact closely with the project 2017-A-243 VIRFAST, the project 2018-A-289 PHBN and the project 2018-A-293 PRONC.

2. Euphresco management aspects of the project

2.1. Indication of the topic budget

Funding organisation ^a	Mechanism ^b	Total Budget ^c
1. Defra (GB)	NC	€
2. MoA (AU)	NC/In Kind	€
3. UKZUZ (CZ)	NC/In Kind	€
4. BMEL (DE)	NC	€
5. NVWA (NL)	NC	€
6. MKGP (SI)	NC	€
7. UNIBL (BA)	NC	€
8. NAIK (HU)	NC/In Kind	€
9. DSMZ (DE)	NC/In Kind	€
10. Naktuinbouw (NL)	NC	€
11. Okstate (US)	NC	€
12. UARK (US)	NC	€
total		€

2.2. Expected duration of the project (only for non-competitive topics)

24 months.

2.3. Identification of project coordinator

Has the research project coordinator been identified?

- Yes
 No

2.4. Any other relevant information on topic organisation and management

None.

^a First member is project coordinator. A minimum of two partners are necessary for each proposal. Add lines as needed.

^b Please indicate the preferred mechanism (e.g. real pot RP; virtual pot VP; non-competitive NC), or several mechanisms if there is flexibility.

^c Optional, as this amount can still change in the next phase. In-kind contribution should also be indicated in this column.