

## 1. Content of the 'Topic Description' document

### 1.1. Topic area

Diagnostics, field detection, surveillance

### 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-1.1: to improve knowledge on the biology, epidemiology and ecology of priority invasive and (re)emerging pests for early detection and pest management
- Objective 2017-R-1.2: to support taxonomic research for the unambiguous identification of pests
- 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-2.4: to use information technology in pest/pathogen surveillance programmes

### 1.3. Topic title

Baseline study on virus reservoirs in native plant species and crops

### 1.4. Description of the problem the research should solve

To adequately anticipate and respond to the detection of new viruses in the event of outbreaks and interceptions, it is necessary to have a better understanding of the current virus reservoir, the "baseline": knowledge on the species present, their host plants, and geographical distribution.

In the case of a new finding (e.g. a pest new to science, a new host or an area where the pest was previously not known to be present), the question often arises whether phytosanitary measures are necessary or not. If data were available to confirm that a virus is already present and distributed in the wider environment, phytosanitary measures are no longer an issue. On the other hand, identification of important reservoir hosts may need to be taken under consideration during regular crop management practices.

High-throughput sequencing (HTS) techniques are a useful tool to obtain these baseline data allowing to map the viruses and viroids that are present in a crop or crops of a specific area. It is evident that execution of these baseline studies and sharing of the output in an international setting will improve the quality and impact of these data: e.g. when the same virus is detected in different crops and areas.

A baseline study using HTS is conducted in a Belgian research project in which 17 000 plants of Solanaceae (native plant species, vegetable and ornamental crops) are sequenced with HTS and analysed to determine the virus reservoir in Belgium for this plant family ([SEVIPLANT](#)). The obtained data are shared with the community of virologists. We expect that virus species found during this project will also (partly) be present in the baseline of other countries.

Within this Euphresco project, contributors will generate and share new and existing data from surveys and diagnostics to determine which viruses are already present in a territory, in relevant crops or potential reservoir hosts. More specifically, key plant families relevant for such surveys should include economically important crop species as well as ornamental species and wild species that are present in agricultural areas and/or native to natural ecosystems. Priority could for example be given to Solanaceae and Cucurbitaceae as both families include important crop species. Moreover, introduction of viruses from crops into

native plants could impact biodiversity. Data from these baseline studies allow to prioritise research on findings.

New findings will be shared within the community of virologists via a form created during a data sharing initiative by BE, GB and NL (among others). As a result, all pieces of information about certain virus species that are present can be combined and lead to a more comprehensive insight into the geographical distribution and epidemiology of a certain virus. A selection of these findings from these baseline studies will be made available as joint publications in scientific journals and will contribute to and hopefully prompt other countries to start similar initiatives. Once published, these data can e.g. be used as input for pest categorizations or pest risk analyses and will help to anticipate outbreaks in new areas and reduce the impact on crops on the one hand and prevent unnecessary regulation on the other hand.

This project will maximise the value of the data by sharing these within the Euphresco Virology community network and other data sharing initiatives. In addition, new findings can feed back into the Euphresco project 2019-E-312 Virus Curate by examining whether there is interesting virus material in collections that can clarify uncertainties about the viruses found during these baseline studies.

### 1.5. Description of the expected results

- Data on the virus reservoirs: which virus species are present in which plant species and in which areas

### 1.6. Beneficiaries of this research product

- Policy makers
- National Plant Protection Organizations
- EPPO and its member countries
- EFSA
- Plant virologists and bioinformaticians
- Horticultural and agriculture sectors

### 1.7. Research funders and research contribution/ distribution

Funding organisation	Research activity and researchers involved
1. Netherlands Food and Consumer Products Safety Authority, the Netherlands  Martijn Schenk <a href="mailto:M.Schenk1@nvwa.nl">M.Schenk1@nvwa.nl</a>	-Sampling of Solanaceae and Cucurbitaceae and a selection of wild species from other plant families; characterising the viruses and viroids present in those samples using HTS on a Illumina platform; -Sampling for viruses in plants and fruits of Solanaceae that are imported from inside and outside the EU. Characterising the viruses and viroids present using HTS on a Illumina platform;  Contact person: Marleen Botermans E.mail address: <a href="mailto:m.botermans@nvwa.nl">m.botermans@nvwa.nl</a>
2. Research Institute for Agriculture, Fisheries and Food, Belgium  Kris De Jonghe <a href="mailto:Kris.dejonghe@ilvo.vlaanderen.be">Kris.dejonghe@ilvo.vlaanderen.be</a>	-Sampling of native Solanaceae, Vaccinium and (non-native) tuber crops, and testing for viruses/viroids present using HTS on a Illumina platform;  Contact person: Kris De Jonghe



	<p>E.mail address:  <a href="mailto:Kris.dejonghe@ilvo.vlaanderen.be">Kris.dejonghe@ilvo.vlaanderen.be</a></p>
<p>3. Federal Ministry of Food and Agriculture, Germany</p> <p>Silke Steinmüller  <a href="mailto:Silke.steinmoeller@julius-kuehn.de">Silke.steinmoeller@julius-kuehn.de</a></p>	<p>-Sampling of native Fabaceae for testing for viruses/viroids using HTS on ONT Minlon;</p> <p>Contact person: Heiko Ziebell  E.mail address: <a href="mailto:heiko.ziebell@julius-kuehn.de">heiko.ziebell@julius-kuehn.de</a></p>
<p>4. All Russian Plant Quarantine Center, Russian Federation</p> <p>Yuri Shneyder  <a href="mailto:yury.shneyder@mail.ru">yury.shneyder@mail.ru</a></p>	<p>-Contribution to be detailed;</p> <p>Contact person: Yuri Shneyder  E.mail address: <a href="mailto:yury.shneyder@mail.ru">yury.shneyder@mail.ru</a></p>
<p>5. Ministry of Agriculture Forestry and Food, Slovenia</p> <p>Erika Orešek  <a href="mailto:Erika.oresek@gov.si">Erika.oresek@gov.si</a></p>	<p>-Sampling wild plants, including weeds growing in the vicinity of vegetables or crops, and characterising the viruses present in sampled wild samples using HTS (detection, genome reconstruction, taxonomical placement);</p> <p>Contact person: Denis Kutnjak  E.mail address: <a href="mailto:denis.kutnjak@nib.si">denis.kutnjak@nib.si</a></p> <p>Contact person: Anja Pecman  E.mail address: <a href="mailto:anja.pecman@nib.si">anja.pecman@nib.si</a></p>
<p>6. Department for Environment, Food and Rural Affairs, United Kingdom</p> <p>Iain Dummett  <a href="mailto:iain.dummett@defra.gov.uk">iain.dummett@defra.gov.uk</a></p>	<p>-Identify crop of interest with appropriate wild /near wild relatives;</p> <p>-Sample a limited number of field sites to include both crop and relatives in vicinity;</p> <p>-Sequence and look for virus sources/ reservoirs linked to crop;</p> <p>-In addition, analysis of data from other sources to look for viruses (e.g. the BBSRC bacterial diseases work where we are sequencing to look for <i>Liberibacter</i> spp., pea viruses, etc.) could be undertaken;</p> <p>Contact person: Adrian Fox  E.mail address: <a href="mailto:Adrian.Fox@fera.co.uk">Adrian.Fox@fera.co.uk</a></p>
<p>7. Science and Advice for Scottish Agriculture, United Kingdom</p> <p>Fiona Highet  <a href="mailto:Fiona.Highet@sasa.gov.scot">Fiona.Highet@sasa.gov.scot</a></p>	<p>-Identify solanaceous crops and wild relatives in Scotland for sampling and inclusion in the study;</p> <p>-Additional samples from other projects and surveys (i.e. apiaceous crops and wild relatives) may be available;</p> <p>Contact person: Christophe Lacomme  E.mail address:  <a href="mailto:Christophe.lacomme@sasa.gov.scot">Christophe.lacomme@sasa.gov.scot</a></p>
<p>8. United States of America</p> <p>David Schimmelpfenning  <a href="mailto:david.schimmelpfenning@usda.gov">david.schimmelpfenning@usda.gov</a></p>	<p>-Seeds are reservoirs for viruses and viroids. They aid long-distant dispersal of these pathogens.</p>



	<p>-Viruses and viroids (old and new) can be found by extraction of both total RNA and DNA from seeds of tomato, pepper, eggplant, water melon, zucchini, cucumber, and squash seeds from different sources. The extraction will be enriched for the targets, if present, by removing most host plant nucleic acids prior to High-Throughput Sequencing (HTS), using the Illumina platform, followed by bioinformatic analysis to identify viruses and viroids contigs.</p> <p>-Specific primers will be used to amplify suspected viruses and viroids and amplicon sequenced to confirm it. If new viruses and viroids are discovered, specific primers will be designed, RT-PCR or PCR done, and amplicon sequenced to confirm the pathogen.</p> <p>Contact person: Bright Agindotan E.mail address: <a href="mailto:bright.agindotan@usda.gov">bright.agindotan@usda.gov</a></p> <p>Contact person: Schyler Nunziata E.mail address: <a href="mailto:schyler.o.nunziata@usda.gov">schyler.o.nunziata@usda.gov</a></p>
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**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

**1.9. Any other relevant information on content**

Close collaboration with other projects in the field is envisioned e.g. the Euphresco topic 2020-G-346 Data sharing initiative.

## 2. Euphresco management aspects of the project

### 2.1. Indication of the topic budget

Funding organisation <sup>a</sup>	Mechanism <sup>b</sup>	Total Budget <sup>c</sup>
1. NVWA (NL)	NC	€
2. ILVO (BE)	NC	€
3. BMEL (DE)	NC	€
4. VNIKR (RU)	NC	€
5. MAFF (SI)	NC	€
6. DEFRA (GB)	NC	€
7. SASA (GB)	NC	€
8. APHIS (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.

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

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

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