



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

### 1.1. Topic area

A: 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-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-2.1: to support data exchange, data use and re-use for the benefit of plant health research activities
- Objective 2017-C-3.1: to favour knowledge exchange and support common initiatives with relevant players

### 1.3. Topic title

Plant Health Bioinformatics Network (PHBN)

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

In the last decade, High-Throughput Sequencing (HTS), also referred to as Next Generation Sequencing (NGS), has revolutionized biology and medicine. The technology allows DNA and RNA sequencing data to be generated in huge amounts at a very low cost per base pair, enabling the processing of many samples for a large number of applications. The resulting large amounts of data have led to the blooming of a relatively new field: computational biology or bioinformatics. In medicine, NGS-based tests for disease diagnostics are already brought into routine practice, and plant disease diagnostics seems to follow this path, with virology as discipline with the furthest developments. During a successful and widely attended EPPO workshop on the use of NGS technologies for plant pest diagnostics (22-24 November 2017, Bari, Italy), co-organized by several members of this consortium, it became clear though that the wide adoption of NGS in a plant health diagnostics context is still limited. One of the main bottlenecks is the lack of expertise and consensus on the standardization of the data analysis. With this project we would like to join forces on a European scale by building a community network of bioinformaticians/computational biologists working in plant health. Most NPPOs currently tend to employ very small numbers (if any) of computational biologists, frequently supported by molecular biologists running bioinformatics pipelines. This situation puts significant pressure on a small number of specialists who are required to provide support across a wide and complex range of applications in many different disciplines (virology, bacteriology, mycology...). The applications and research goals are similar in different countries which can also lead to duplication of work, developing comparable bioinformatics pipelines in multiple organizations for the same purpose. Everything considered, this results in an inefficient use of national funds and has the potential to limit the development and deployment of the technology. With this project proposal, our ambition is to pave the way towards community-driven solutions in order to address the main challenges related to the use of HTS in a diagnostic context. We will work towards this objective by:

1. Developing reference datasets that can be used for validation of bioinformatics pipelines and for standardization purposes
2. Developing training materials to leverage the experience of less experienced laboratories during and after the project (training material available online)
3. Building a network including bioinformaticians and plant pathologists, stimulating communication, exchange of expertise and collaboration to further close the knowledge gap among them

In this way we aim to speed up the development of more robust and accessible HTS-based diagnostic tools in plant health.



### 1.5. Description of the expected results

The project we propose focuses on different actions to promote exchange of expertise, collaboration and training. It also includes a research component since we would like to develop reference datasets that can be used for validation, proficiency testing and training. Our strategy is to allow European project partners without (much) own funding to participate in as many work packages as possible to maximize the knowledge exchange.

The expected outcomes can be categorized into 3 major topics as described below.

#### 1. Development and proficiency testing of reference datasets

This part involves developing reference datasets of a variety of well-characterized plant diseased materials using different HTS techniques. We would ideally target several plant samples containing different pests and pathogens (bacteria, fungi, nematodes, insects, viruses/viroids, phytoplasmas), and whose presence is/was confirmed using non HTS-based method (e.g. (q)RT-PCR, ELISA, Northern blot). The choice of samples to be included will depend on the availability and interest/expertise of the consortium and will be decided once the full project is starting. Samples will be processed using a metabarcoding or a whole genome shotgun sequencing method in the case of bacteria, fungi, nematodes and insects. In the cases of viruses/viroids, RNA-seq based methods will be used. Data will be generated and will be transformed into (partially artificial) reference datasets suited for validation of data analysis pipelines. These reference datasets will then be analyzed by all partners using their own pipelines and made available as reference data to the scientific community. Comparing the results of each partner will help in identifying key parameters, common mistakes and strengths/weaknesses of each pipeline. The results will be reported as an A1 publication.

#### 2. Development of training materials

In this part we want to give less experienced people the chance to learn from others, either by one-to-one virtual coaching initiatives, or by facilitating larger in-person training events. The main deliverables are open source training materials based on selected pipelines from the developed reference datasets.

#### 3. Stimulating networking, improving communication and knowledge sharing

This includes the centralization and documentation of existing pipelines of the collaborators in a single repository. Ideally this action will result in a virtual community of computational biologists / plant pathologists where people get to know each other, where questions can be asked to relevant experts, and where information can be found on the different expertise of each project partner, as well as on the corresponding data analysis strategies. We also propose to organize a scientific meeting towards the end of the project to stimulate collaboration and improve communication between bioinformaticians and pathologists / diagnosticians. This can be the start of new collaborations and joint project proposals.

### 1.6. Beneficiaries of this research product

- Computational biologists / bioinformaticians working in plant health (interaction with colleagues, sharing of data analysis pipelines, meeting)
- Plant pathologists and diagnosticians (training materials, meeting, better communication with computational biologists)
- Students and teachers in plant pathology (training materials)
- National Plant Protection Organisations, EPPO and its members (validated reference datasets, training materials)

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

Funding organisation	Research activity and researchers involved
1. Federal Public Service of Health, Food Chain Safety and Environment, Belgium	- Project coordination; - Potentially, reference data preparation, PT organization, participation and analysis,



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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

Information to define the profile of sought partners could be useful (but not mandatory): country/region (if there are preferences), skills/expertise required, etc.

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

None.

## 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. FPS (BE)	VP	€ 75 000
2. ILVO (BE)	NC	€ 10 000
3. CFIA (CA)	NC	€ 70 000
4. AU (DK)	NC	€ 7 000
5. ANSES (FR)	NC	€ 16 500
6. INRA (FR)	NC	€ 10 000
7. MOAG (IL)	NC	€ 10 000
8. MKGP (SI)	NC	€ 28 000
9. INIA (ES)	NC	€ 10 000
10. APHIS (US)	NC	€ 10 000
11. DSMZ (DE)	NC	€ 10 000
12. GRE-NRI (GB)	NC	€ 11 600
13. CNR (IT)	NC	€ 12 000
14. NAK (NL)	NC	€ 7 200
15. NAKTUINBOUW (NL)	NC	€ tbc
16. UB (RS)	NC	€ 9 350
17. IPEP (RS)	NC	€ 1 000
18. VRI (TR)	NC	€ 1 357
19. NOHU (TR)	NC	€ 3 150
20. AGS (CH)	NC	€ 10 000
total		€

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

36 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

The project will be managed through a number of work packages. These will be further developed as the full proposal is being written, but a potential structure of the project could be as described below.

#### WP1 Project Management

The project management deals with the overall management of the work packages (progress of the work, timely submission of reports, organization of meetings). A responsible person will be appointed to each work package for coordination and planning.

#### WP2 Development of reference datasets and proficiency testing

In this work package the development of reference datasets that can be used to validate new data analysis pipelines is coordinated. These artificial datasets (based on real datasets) target different organism groups (such as viruses, bacteria, fungi) and are meant for diagnostic purposes. The developed datasets will be used in a proficiency test across laboratories.

#### WP3 Training

The objective of this work package would be to produce training materials based on selected pipelines.

WP4 Communication and dissemination

This work package promotes the communication between bioinformaticians and pathologists, as well as the dissemination of the results. The end goals envisaged are: an expert database, a repository of different pipelines used in different institutes, a repository of reference datasets, a repository of training materials developed on selected pipelines and an A1 paper on the results of the proficiency tests. We also plan to organize a (satellite) meeting to promote discussions and present results.

<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.