

## INEXTVIR: High throughput sequencing of the virome of agricultural crops and ecosystems across Europe

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# INEXTVIR: High throughput sequencing of the virome of agricultural crops and ecosystems across Europe

MSCA ITN -Innovative Network for Next Generation Training and Sequencing of Virome



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Lighting



Scanning the

virome of selected

agricultural crops

ESR

Agronomic and

socio-economic

impact of virome

**ESR** 



WP3

Virus

ESR

characterization \_

WP4

Interactions

between virome

and environment

**ESR** 

ESR 11, 13

WP5

Developing and

validating NGS tools

**ESR** 







#### **BACKGROUND**

Plant Viruses cause 50% of the emerging plant diseases and pose an important threat to many agricultural crops worldwide, they are responsible for production losses estimated at € 15 to 45 billion per year.

INEXTVIR proposes a transdisciplinary research and training approach combining approach c agronomical, socio-economic and regulatory sciences.

Goal: Better understand, control and exploit the virome of selected agricultural crops and ecosystems across Europe. Benefits: Political, economic, industrial, social and environmental.

## **WP2** Scanning the virome of selected agricultural crops **ESR 1**: Investigating the European field

vegetable virome, University of Newcastle Upon Tyne, United Kingdom

ESR 4: Characterisation of tomato virome, National Institute of Biology, Slovenia

**ESR 6:** HTS-based viral indexing in Prunus species: virome characterization and validation of diagnostic approaches, Institut National de la Recherche Agronomique, France **ESR 10**: The cucurbits and lettuce viromes, ABIOPEP SL, Spain

### **WP6**

**Agronomic and socio-economic impact** of virome

**ESR 14:** Agronomic and socio-economic impact of virome, FERA Science Limited, United Kingdom

**ESR 15:** Risk-benefit communication and Knowledge exchange platform, Iniversity of Newcastle Upon Tyne, United 🔎 Kingdom



## **Developing and validating NGS tools**

WP5

Wp7 Dissemination and Exploitation

**ESR 11:** Development and validation of innovative HTS tools for the fast and efficient detection of virus and virus-like agents in the selected crops, DNAVision, Belgium

ESR 12: Bioinformatics pipelines development for virome classification, University of Bordeaux, France

ESR 13: Development and integration of decision-making tools in data analysis procedures for HTS-based plant virus diagnostics BioSistemika, Slovenia

#### **WP3 Virus Characterization**

**ESR 2:** Virome characterization of European germplasm resources of pome fruits for future breeding and risk analysis, University of Liege, Belgium

**ESR 3:** Survey and evaluation of the cultural practices impact on the virome of vegetable production systems and effect on sustainability, University of Liege, Belgium

### WP4

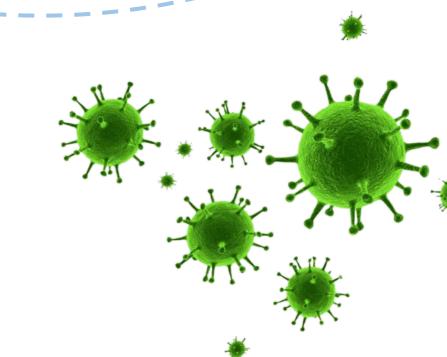
#### Interactions between virome and environment

**ESR 5:** Water as an important indicator of circulating plant viruses, National Institute of Biology, Slovenia

**ESR 7:** Ecological analysis of the plant virome structure and of reciprocal transfers between cultivated and wild host populations, Institut National de la Recherche Agronomique, France **ESR 8:** Effect of habitat biodiversity on the virome of wild plants and crops, *Universidad* Politécnica de Madrid, Spain

**ESR 9:** Effect of habitat biodiversity on virus host range evolution, Universidad Politécnica de Madrid, Spain





## Contribution to bioinformatic and software development segments of the project

## Developing of own bioinformatic methods

Finding alternative methods for plant virus detection

- Viral identification in HTS data from agricultural crops and ecosystems
- Generation of artificial HTS datasets for testing purposes Assessment of cross-contamination in sequencing dataset
- Obtain validation criteria on plant virus identification

## Virus related tools benchmarking

### Identify the most relevant HTS methods and tools

- Identify relevant use-cases in the project consortium (e.g. virus detection, virus classification ...) Identify the tools that seem relevant for the selected use-cases in our neutral study
- Use Docker images of tools (either existing or created) for testing and results dissemination
- Select datasets (artificial or natural) that meet test criteria
- Share the benchmark result highlighting tools performance

## Pipeline design

## **Pipeline testing**

Identify the most relevant **combination** of methods and tools

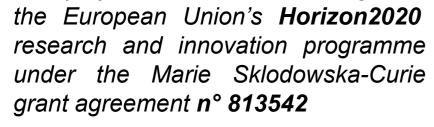
- Identify relevant steps in HTS data analysis (e.g. reads cleaning, identification ...)
- Create pipelines based on Docker images of the tools and test them
- Compare the pipelines performance
- The most suitable pipelines for each use case will be shared with project consortium in Docker images
- Document the pipeline for users and developers

## **Decision making**

Propose the most appropriate pipeline depending on the use case for the user

- Use performance comparison to make a recommendation
- Store relative performance metrics for each pipeline Access those metrics to be able to make a decision
- Update the performance metrics based on new tests and tools
- 2) Explain the recommendation to the users so that they make a final decision

Future consideration: Automated pipeline recommendation using a Machine Learning approach





INEXTVIR is implemented by a European Consortium of universities, research institutions and companies in **Belgium**, France, Spain, Slovenia and the UK.

























