



## Virus discovery using HTS by plant virologists





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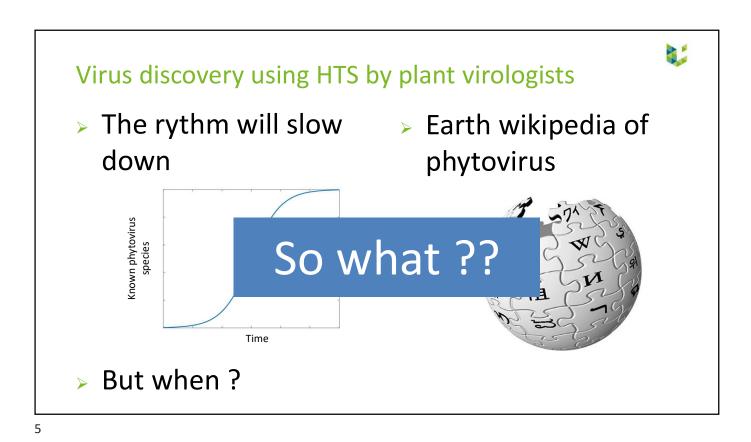
### Virus discovery using HTS by plant virologists



The virus discovery party!



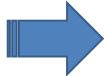
- Fruit tree viruses :
  - > >90 viral species discovered (until 06/2020)
  - > Exponential growth



### Downstream biological characterization







-> Impossible to evaluate biological properties of all new viruses



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Surviving kit for navigating and settling in the biological characterization desert

### 1. GPS for biological characterization



> Collective characterization framework in 2017:



PERSPECTIVE published: 24 January 2017 doi: 10.3389/fmicb.2017.00045

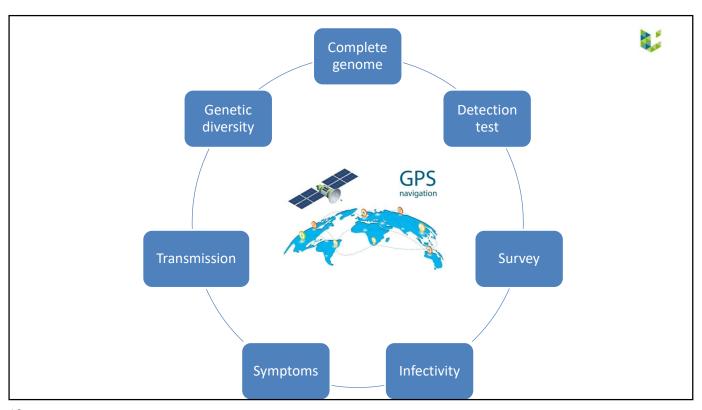




A Framework for the Evaluation of Biosecurity, Commercial, Regulatory, and Scientific Impacts of Plant Viruses and Viroids Identified by NGS Technologies

Sebastien Massart<sup>1\*</sup>, Thierry Candresse<sup>2</sup>, José Gil<sup>3</sup>, Christophe Lacomme<sup>4</sup>, Lukas Predajna<sup>5</sup>, Maja Ravnikar<sup>6</sup>, Jean-Sébastien Reynard<sup>7</sup>, Artemis Rumbou<sup>8</sup>, Pasquale Saldarelli<sup>9</sup>, Dijana Škorić<sup>10</sup>, Eeva J. Vainio<sup>11</sup>, Jari P. T. Valkonen<sup>12</sup>, Hervé Vanderschuren<sup>13</sup>, Christina Varveri<sup>14</sup> and Thierry Wetzel<sup>15</sup>

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### 2. Exploration of the desert: fruit tree & tomato





Is There a "Biological Desert" With the Discovery of New Plant Viruses? A Retrospective Analysis for New Fruit Tree Viruses

Wanying Hou<sup>1,2,3</sup>, Shifang Li<sup>3,4\*</sup> and Sebastien Massart<sup>2\*</sup>

- A decade of virus discovery by HTS
- 91 putative new viral species
- How have they been characterized ?
- Reviewing 1,000 publications



Global Advances in Tomato Virome Research: Current Status and the

Mark Paul Selda Rivarez<sup>1,2</sup>, Ana Vučurović<sup>1,3</sup>, Nataša Mehle<sup>1</sup>, Maja Ravnikar<sup>1,4</sup> and

Impact of High-Throughput

- A decade of virus discovery by sanger and HTS
- 45 putative new viral species

Sequencing

How have they been characterized ?

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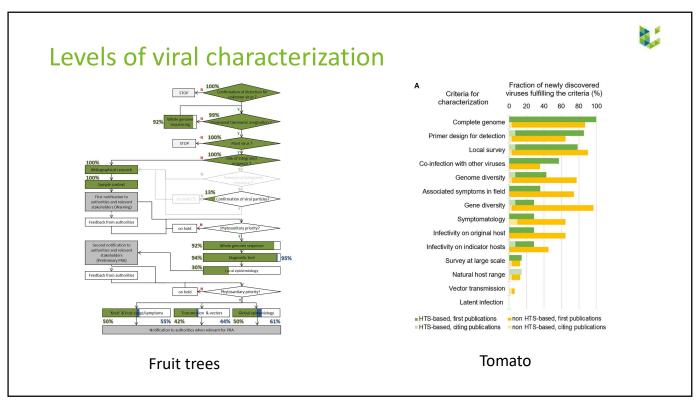
### How well the new viruses are characterized?



Have you explored the desert?

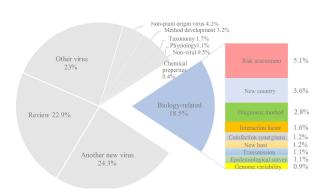
www.wooclap.com/RJLGUJ





### The citations forget biological characterization





Fruit tree viruses ~1,000 citations reviewed

- 69% = citation in review paper or with another virus
- Only 18% of citation bring biologically-relevant information
- Once the virus is published : no one cares about biology ?



### The Darwinian process of virus characterization

- Characterisation process = Darwinian
- Only the most threathening new viruses will be characterized and continue to live the characterization process

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### The Darwinian process of virus characterization

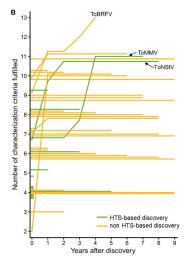


- Framework = 14 steps
- « Quite » after publication
- Strong selection pressure:

45 new viruses on tomato



13 for ToBRFV in 4 years 11 for ToMMV & ToNStV in 5 years (1st HTS)



### Darwinism creates oasis in the desert

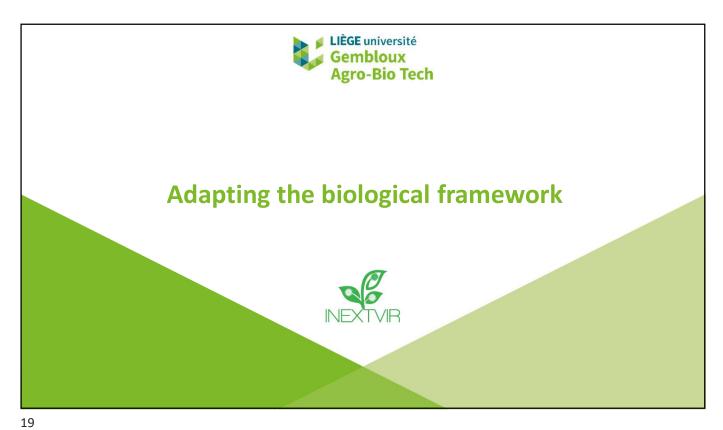


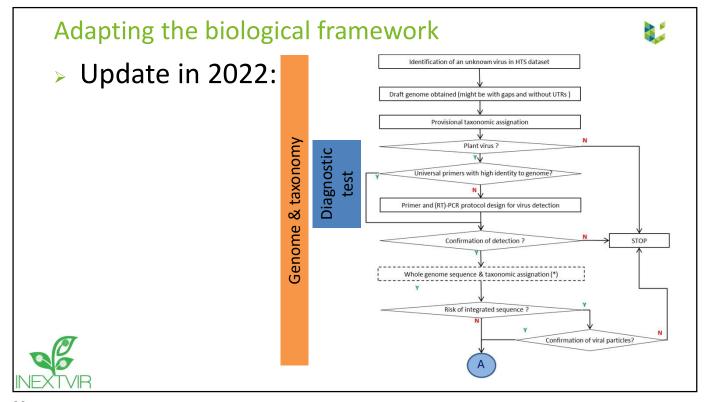
- > ToBRFV as example
- In a few years, huge effort and resistant cultivar ongoing

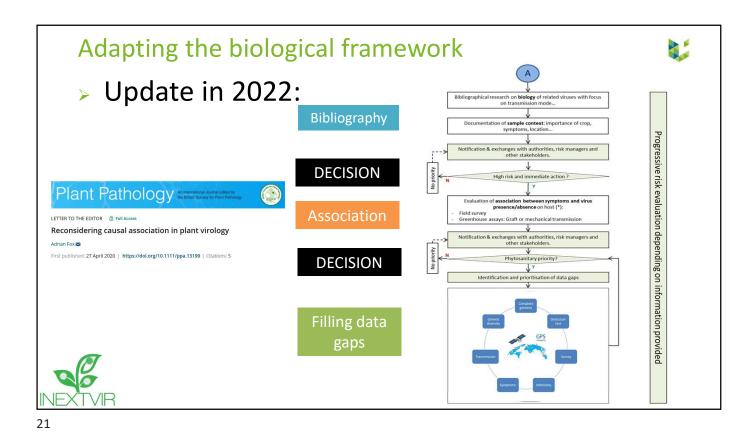


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# Darwinism creates oasis in the desert Scientific knowledge Phytosanitary risk







LIÈGE université
Gembloux
Agro-Bio Tech
GENOPREDICT:

Genome based prediction of biological features
of the newly characterized viruses

Rachid Tahzima

Federal public service
HEALTH, FOOD CHAIN SAFETY
AND ENVIRONMENT

### Predicting biological properties?



An example on animal viruses:

### **EPIDEMIOLOGY**

**Predicting reservoir hosts and** arthropod vectors from evolutionary signatures in RNA virus genomes

Simon A. Babayan<sup>1,2</sup>, Richard J. Orton<sup>3</sup>, Daniel G. Streicker<sup>1,3</sup>\*

~500 known viruses:

Dinucleotide, codon pairs, codon and amino acids



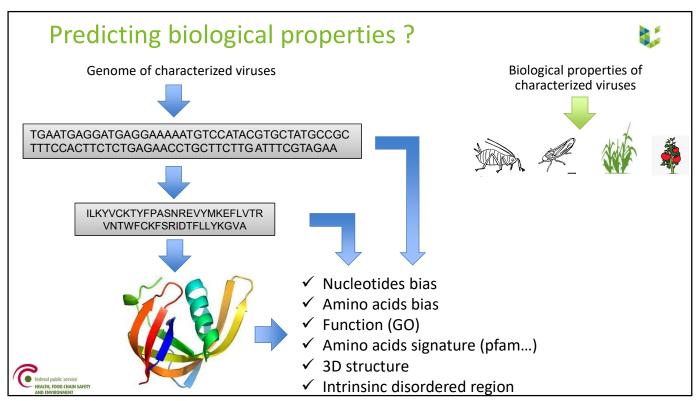
Reservoir hosts and vectors





Prediction accuracy:

- 72 % for reservoir host
- 99 % for vector group





Predicting biological properties: transmission

> At plant virome scale

\*\*Module\*\*

\*\*Module\*\*

\*\*Proteome Length\* (as)

## Predicting biological properties: vector? At family scale -> hypothesis generator! Closterovirus (Aphid)\* Crinivirus (Whilefly) Ampelovirus (Mealybug) Velarivirus Undassified Ampelovirus (Mealybug) Velarivirus Undassified To be a second of the second

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