

Current impact and future direction of High Throughput Sequencing in plant virus diagnostics

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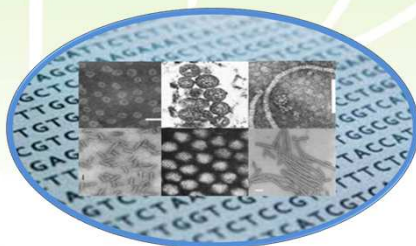
,Antonio Olmos, Haissam Jijakli and Thierry Candresse

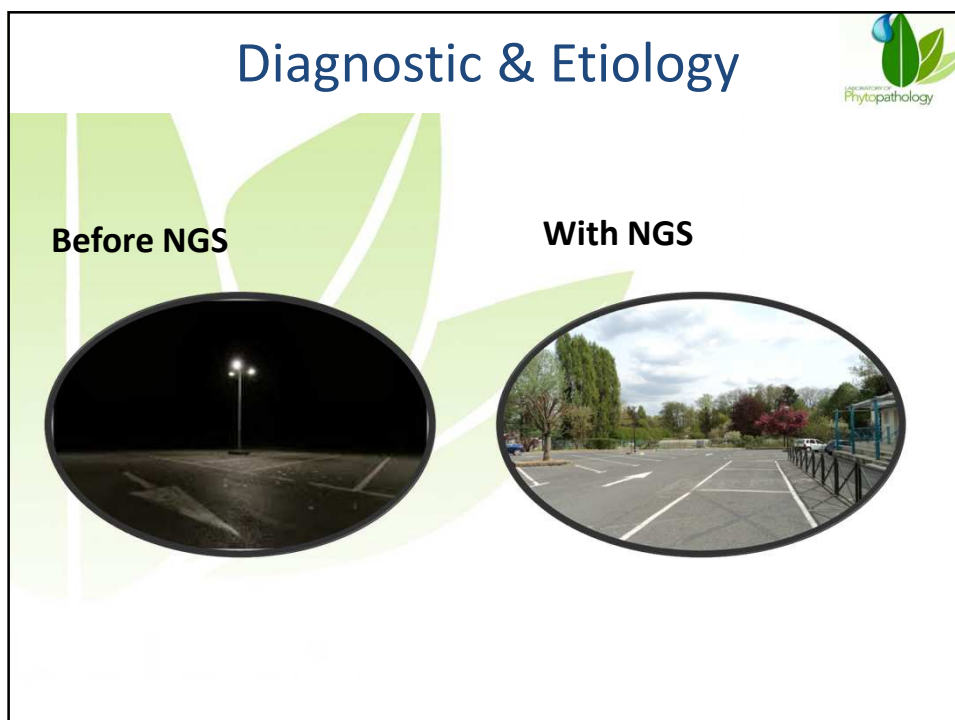
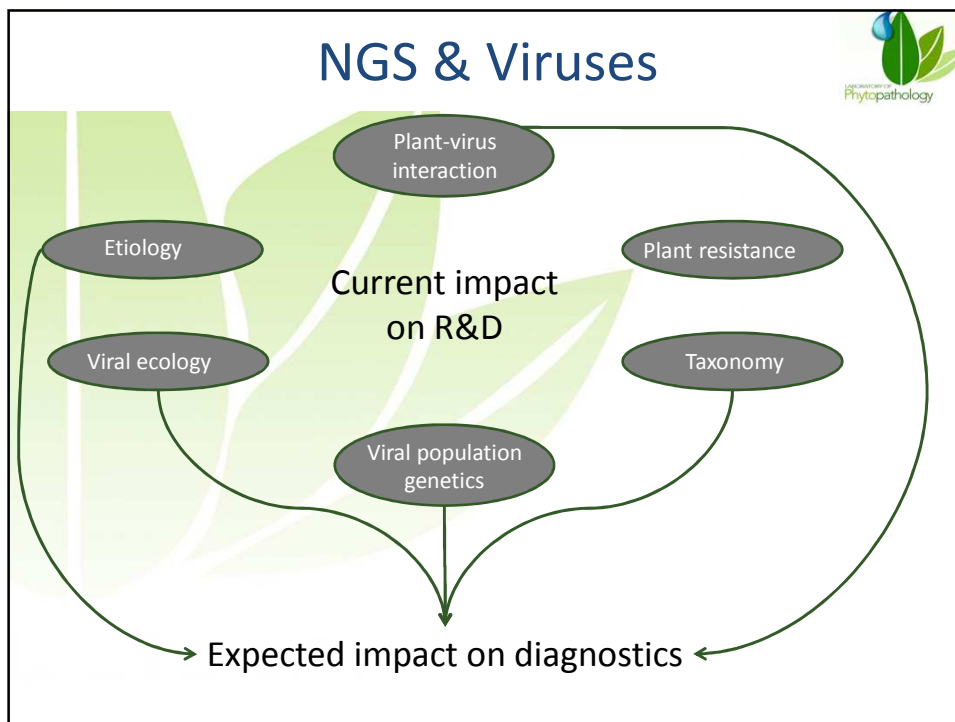


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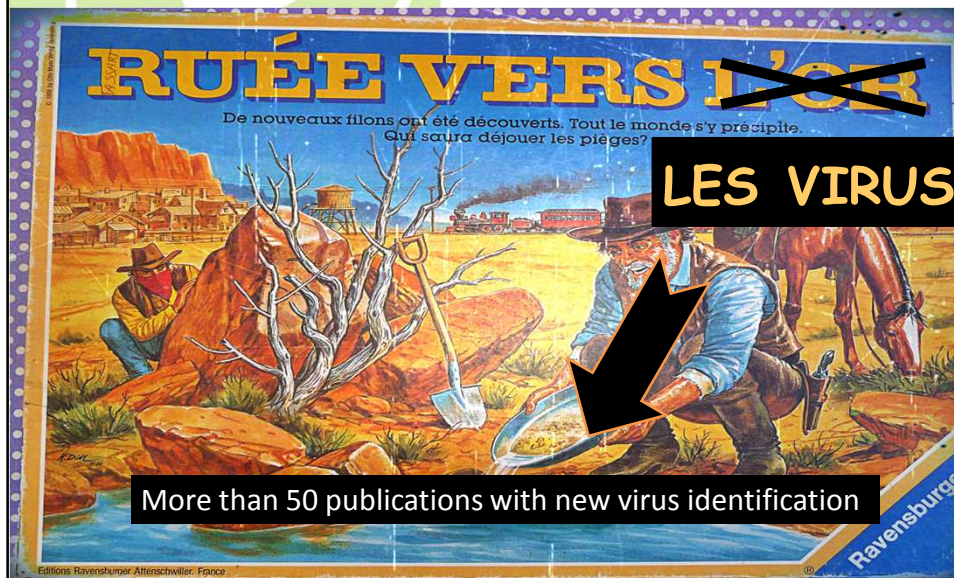


Driving factors





Diagnostic & Etiology

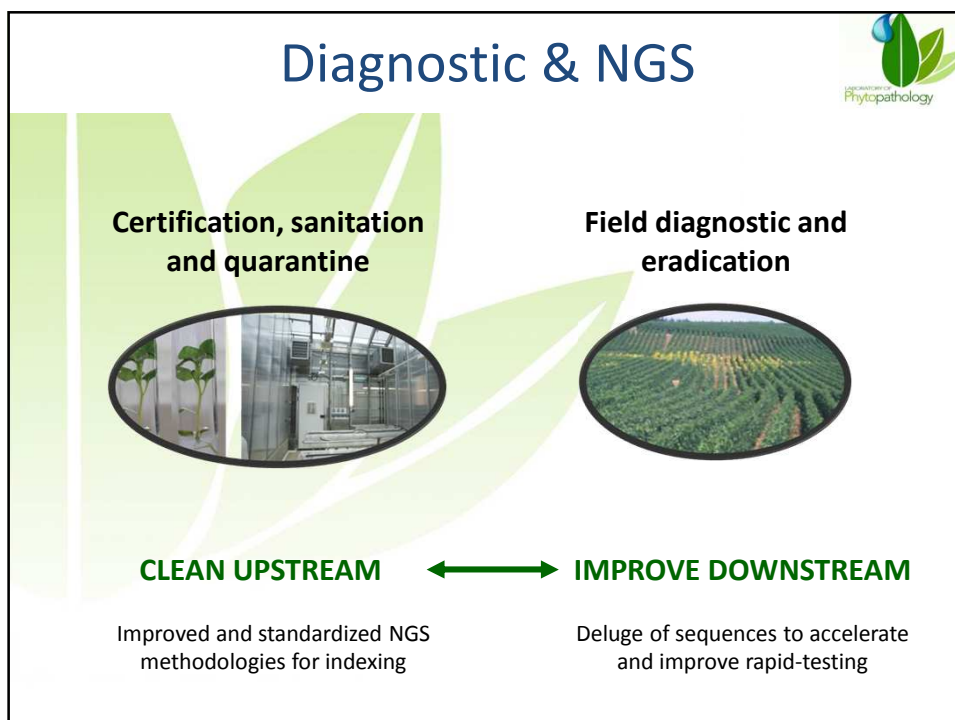
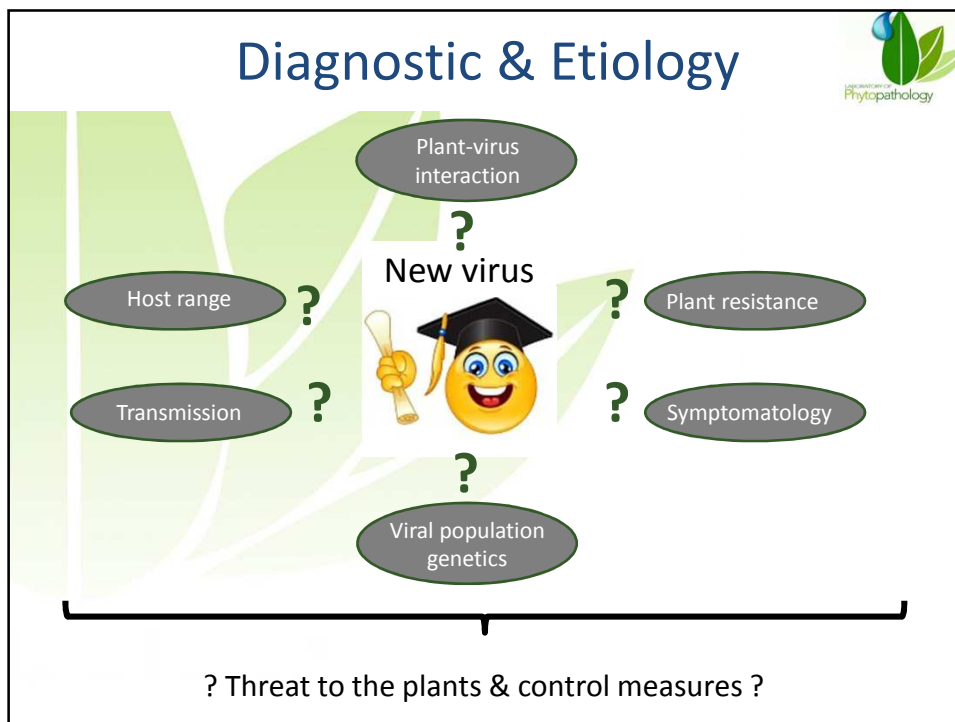


Diagnostic & Etiology



New virus





Technical Challenges



1. Preparation & sequencing strategies ?

Extraction protocol
DNA, total RNA, particle isolation, small RNA, dsRNA

2. Sensitivity ?

Dependent on sequencing depth
Similar to PCR
What about a single or a couple of viral reads ?

3. Reproducibility and repeatability ?

Intra and inter-laboratory comparison

Technical Challenges



4. Contaminations ?

Human & beef contigs -> what about viruses ?

Partial or total genome coverage

Strict confinement needed !


5. Adaptation to host species ?

Virus titre and extraction method



Practical and technical challenges requiring both fundamental and applied research

Practical impact



Identification of a new virus or a poorly characterized virus by a diagnostician ?

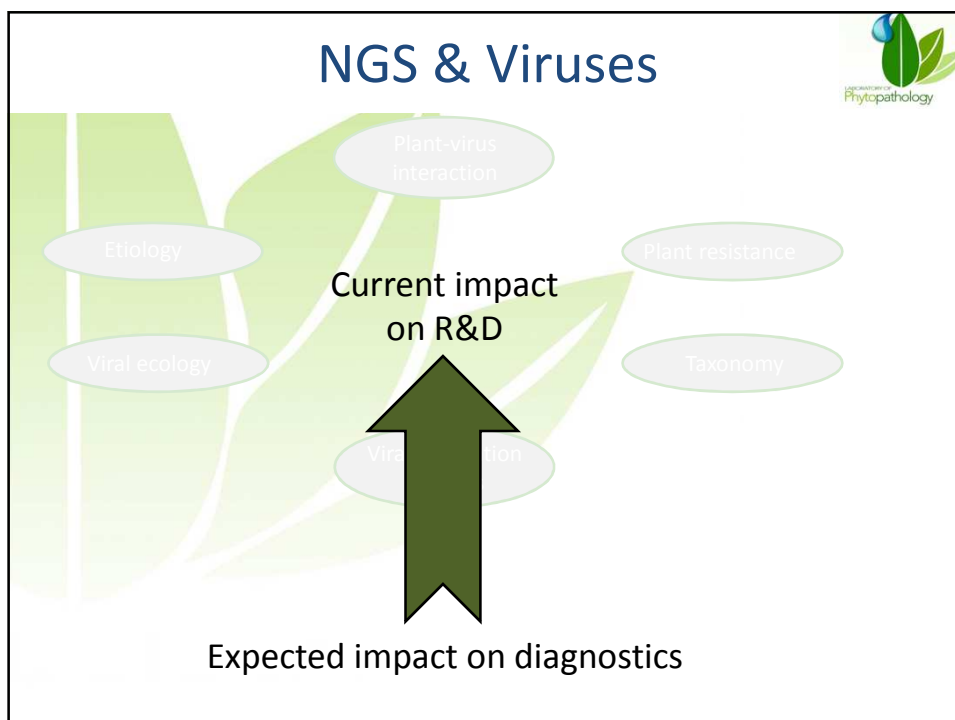
- Halt the distribution of the plant material ?
- Confirmatory assays (Molecular Koch postulate) ?
- Long-term experiment on virus biology ?

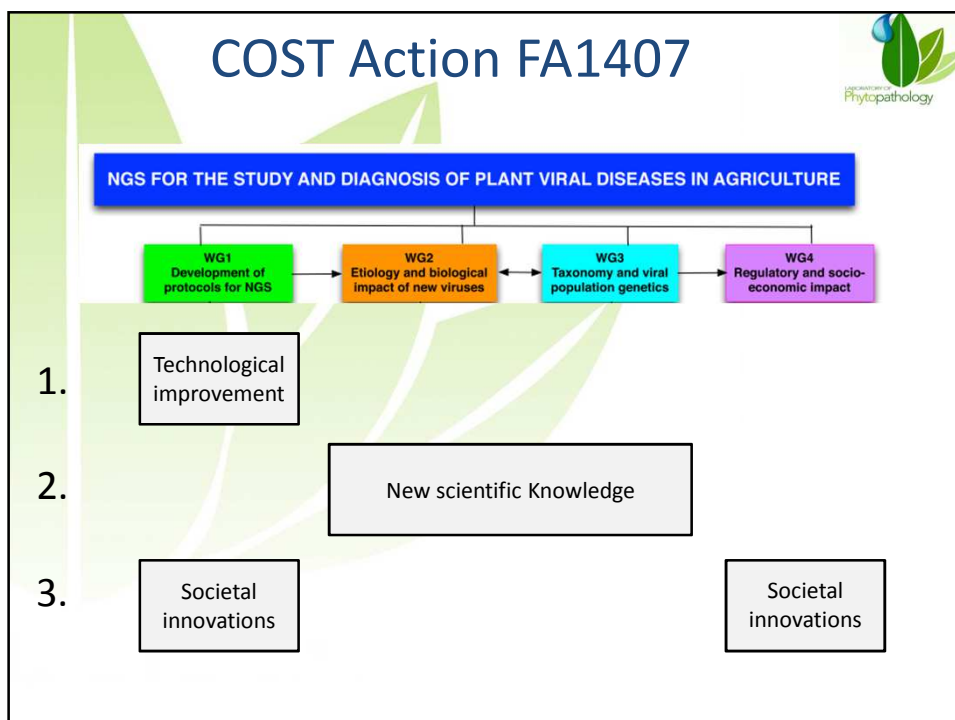
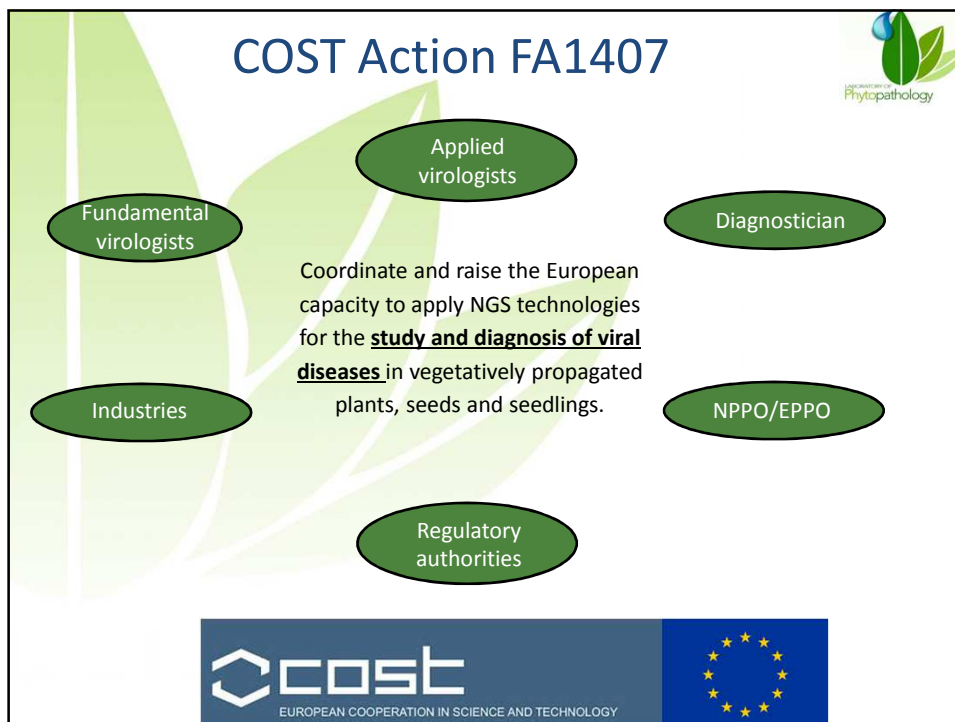
➔ Technical framework and decision schemes are needed

Latent (or symbiotic)viruses discovered ?

- Probability of discovering non pathogenic viruses is high
- Re-think trophic relationships ?

➔ Adaptation of regulatory framework ?





Conclusion



- ✓ Large impact in R&D
- ✓ Impact ongoing in diagnostic
 - ❖ Scientific & regulatory consequences
 - ❖ Feedback loop to fundamental research
- ✓ Long term :
 - ❖ Safer movement and trade
 - ❖ Better understanding of the virus threat and biology (including the Pathovirome)

Merci – Thanks



For more information:

Massart et al., 2014. *Virus Research*, 188: 90-96

Massart et al., 2014 *Virologie*, 18(5):247-250

