

Detection of plant viruses by next-generation sequencing (NGS)

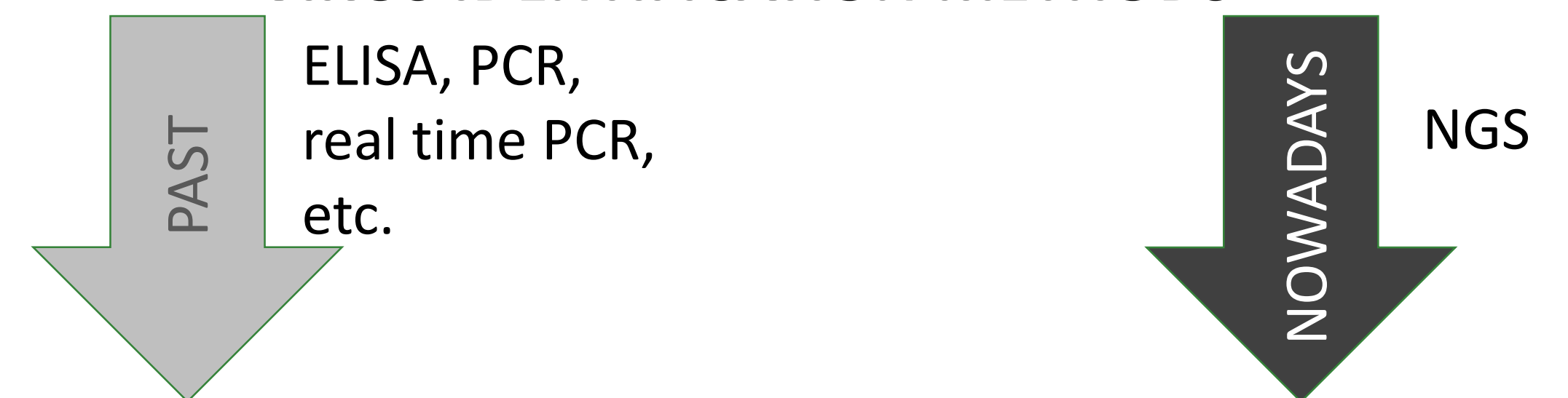
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INTRODUCTION

Climate changes around the globe and increased international trade are pushing plant pathogens and their vectors into unexpected new areas, raising many new risks for agriculture. These not only increase the chance of introduction of new pathogens into the new area, but also increase the chance of the pathogen persisting in a new host species. The accurate identification of plant pathogens, e.g., virus species, is crucial for planning an effective prevention of new disease spreading and its eradication.

VIRUS IDENTIFICATION METHODS



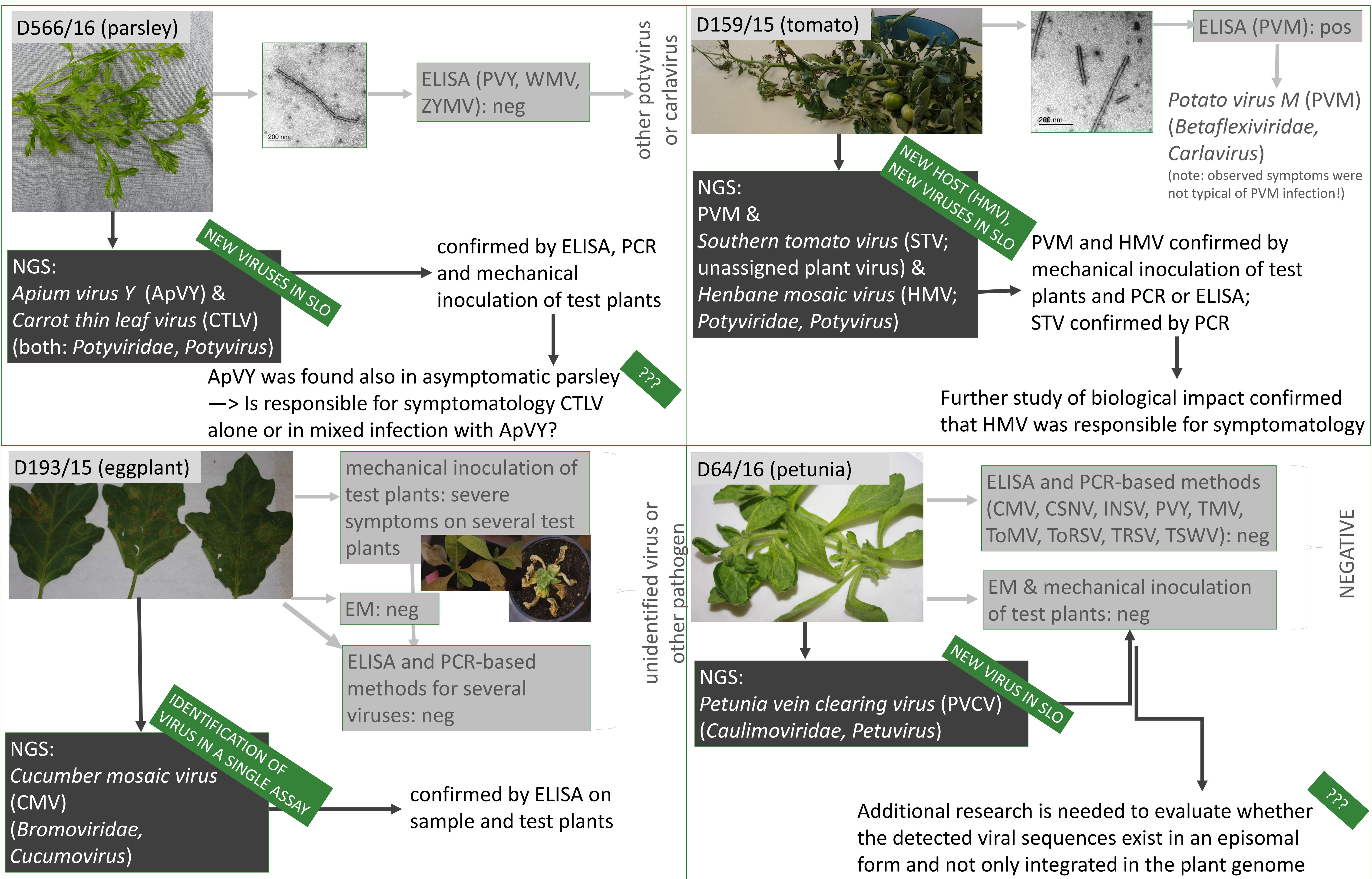
Methods designed to identify one or few viruses at the same time

Universal technology for virus identification

WETLAB & AUTOMATIC TECHNICAL WORKFLOW OF NGS ANALYSIS

Sample → RNA isolation → small RNA deep sequencing → user-friendly automatic bioinformatics pipeline in CLC Genomics Workbench developed at NIB → confirmation (e.g., by electron microscopy (EM), ELISA, PCR-based methods) and study of biological impact

EXAMPLES:



CONCLUSIONS

- With NGS analyses of ornamental and vegetable samples we discovered new plant viruses and new hosts in Slovenia
- Automatic bioinformatics pipeline in CLC Genomics Workbench developed at NIB was shown to be fast and reliable tool for the official detection of plant pathogens, as a support for the Phytosanitary Administration of the Republic of Slovenia and the Phytosanitary Inspection Service
- NGS was introduced as regular diagnostic method at NIB

ACKNOWLEDGEMENT

This study was supported by the Slovenian Research Agency (grant number L4-5525), by the Ministry of Agriculture, Forestry and Food of the Republic of Slovenia and by the COST FA 1407. EM analyses were carried out by dr. Magda Tušek Žnidaršič. The authors thank Larisa Gregur for excellent technical help.