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Utilizing plants defensive mechanism to detect viruses – from theory to practice

Johanna Santala

Senior reseacher

Plant pest and grain section, Plant Analytics, Finnish Food Authority

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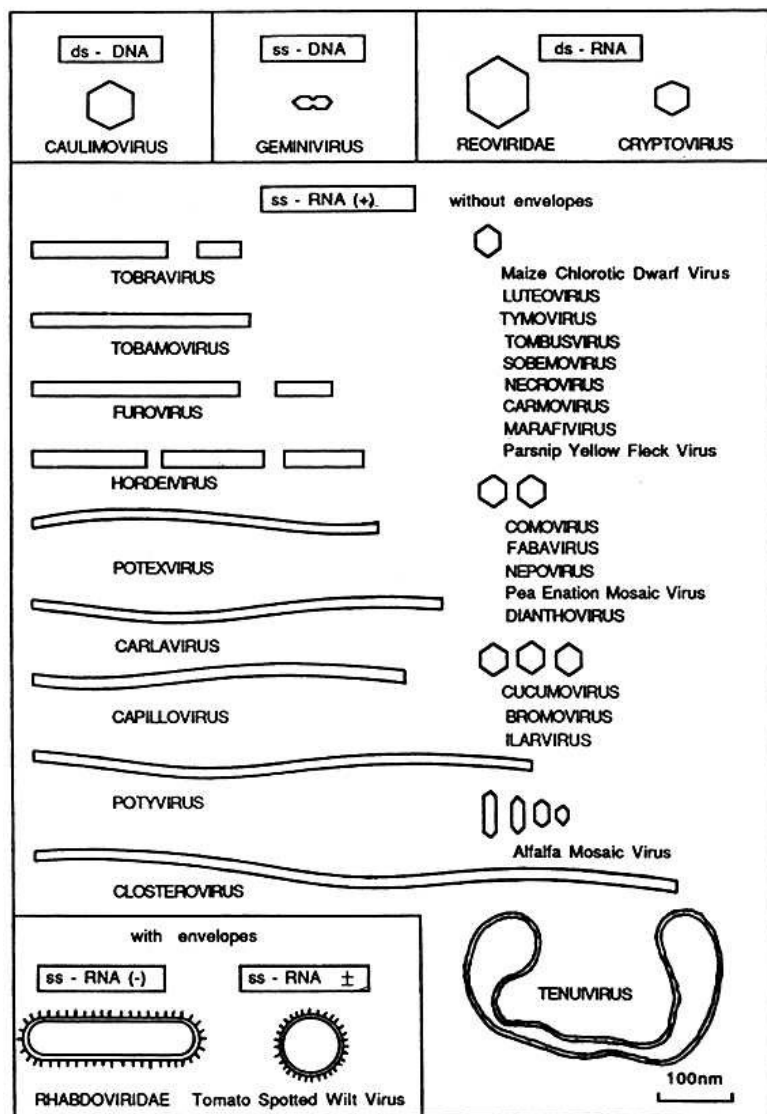


Figure 5.1 The families and groups of viruses infecting plants. Outline diagrams are drawn approximately to scale. (Courtesy R. I. B. Francki.) One additional group, the commelina yellow mottle virus group with dsDNA and bacilliform particles, was approved by the I.C.T.V. in August 1990.

Potato viruses

Alfalfa mosaic virus (AMV), *Alfavirus*, *Bromoviridae*
Andean potato latent virus (APLV), *Tymovirus*, *Tymoviridae*
Andean potato mottle virus (APMV), *Comovirus*, *Comoviridae*
Arracacha virus B (AVB), tentative *Cheravirus*, *Sequiviridae*
Beet curly top virus (BCTV), *Curtovirus*, *Geminiviridae*
Cucumber mosaic virus (CMV), *Cucumovirus*, *Bromoviridae*
Eggplant mottled dwarf virus (EMDV), *Nucleorhabdovirus*, *Rhabdoviridae*
Potato aucuba mosaic virus (PAMV), *Potexvirus*, *Flexiviridae*
Potato black ringspot virus (PBRSV), *Nepovirus*, *Comoviridae*
Potato deforming mosaic virus = Tomato yellow vein streak virus (ToYVSV), *Begomovirus*, *Geminiviridae*^d
Potato latent virus (PotLV), *Carlavirus*, *Flexiviridae*
Potato leafroll virus (PLRV), *Polerovirus*, *Luteoviridae*
Potato mop-top virus (PMTV), *Pomovirus*, -
Potato rough dwarf virus = Potato virus P, tentative *Carlavirus* ^e
Potato virus A (PVA), *Potyvirus*, *Potyviridae*
Potato virus M (PVM), *Carlavirus*, *Flexiviridae*
Potato virus S (PVS), *Carlavirus*, *Flexiviridae*
Potato virus T (PVT), *Trichovirus*, *Flexiviridae*
Potato virus U (PVU), *Nepovirus*, *Comoviridae*
Potato virus V (PVV), *Potyvirus*, *Potyviridae*
Potato virus X (PVX), *Potexvirus*, *Flexiviridae*
Potato virus Y (PVY), *Potyvirus*, *Potyviridae*
Potato yellow dwarf virus (PYDV) *Nucleorhabdovirus*, *Rhabdoviridae*
Potato yellow mosaic virus (PYMV), *Begomovirus*, *Geminiviridae*
Potato yellow vein virus (PYVV), tentative *Crimivirus*, *Closteroviridae*
Potato yellowing virus (PYV), tentative *Alfavirus*^f
Solanum apical leaf curl virus (SALCV), tentative *Begomovirus*
Sowbane mosaic virus (SoMV), *Sobemovirus*, -
Tobacco mosaic virus (TMV), *Tobamovirus*, -
Tobacco necrosis virus (TNV), *Necrovirus*, *Tombusviridae*
Tobacco rattle virus (TRV), *Tobravirus*, -
Tobacco ringspot virus (TRSV), *Nepovirus*, *Comoviridae*
Tobacco streak virus (TSV), *Ilarvirus*, *Bromoviridae*
Tomato black ring virus (TBRV), *Nepovirus*, *Comoviridae*
Tomato mosaic virus (ToMV), *Tobamovirus*, -
Tomato mottle Taino virus (ToMoTV), *Begomovirus*, *Geminiviridae*
Tomato spotted wilt virus (TSWV), *Tospovirus*, *Bunyaviridae*



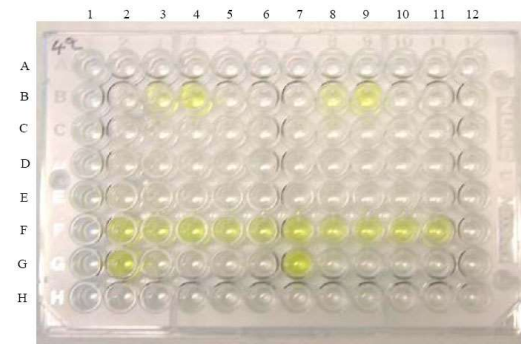
Currently used methods: test selected based on symptoms or legislation



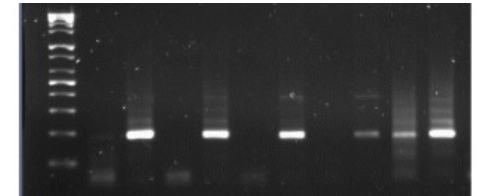
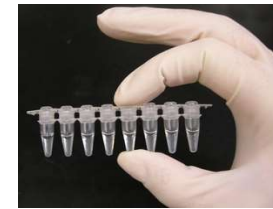
Symptoms + host =
Virus present?



Selection of test plants



Selection of antibodies
(ELISA)



Selection of primers (PCR)
and probe (real time PCR)

Tests are maintained for the most common viruses and for the viruses mentioned in legislation.

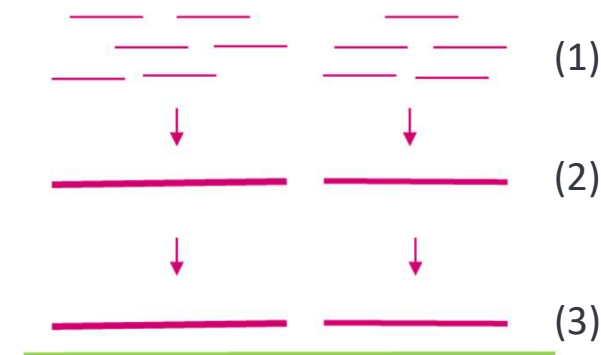
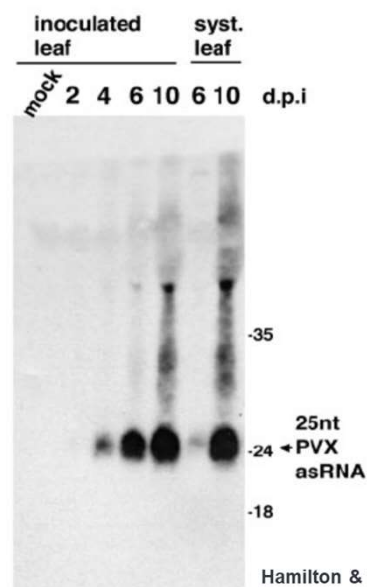


Small RNA sequencing

- All plants use RNA silencing to defend against viruses

- RNA silencing causes accumulation of (viral) small RNA in the plant

- These small RNAs can be sequenced (1) and contiguous sequences (contigs) can be built using bioinformatics (2). Contigs can be aligned to viral sequences in databases (3).



Hamilton & Baulcombe, 1999
Science 286:950-952


Small RNA sequencing (and other HTS methods)



- Detection of known, unexpected and 'new-to-science' viruses
 - No need to decide which viruses are tested
- Already in wide use in research purposes

DISEASE NOTES

First Report of *Tobacco rattle virus* Infecting *Lysimachia nummularia* in Finland

J. Santala , J. Jukkala, J. Tuomola, and J. P. T. Valkonen

Affiliations 

Published Online: 9 Dec 2019 | <https://doi.org/10.1094/PDIS-03-19-0464-PDN>

DISEASE NOTE



First Report of Soybean Dwarf Virus Infecting White Clover (*Trifolium repens*) in Finland

A. Luoto, M. Lehtonen, J. P. T. Valkonen, and J. Santala 

Affiliations 

Published Online: 3 Dec 2021 | <https://doi.org/10.1094/PDIS-04-21-0822-PDN>



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Research project: Viruses in Finnish potato production

Samples



Pre-basic and basic seed

172 samples obtained from official seed samples arriving to Finnish Food Authority

Other seed classes

64 samples from field inspections

Ware potato

94 samples obtained from official plant health samples arriving to Finnish Food Authority

Wild plants

241 samples belonging to 52 plant species collected from HG zone and other potato production areas



Samples analyzed using small RNA sequencing



Viruses threatening Finnish potato production. Assessment of the national seed potato legislation.



Results

- From seed potato only PVY was found
 - PVY was found from the same samples as in official tests (ELISA)
- From ware potato also PMTV, PVS and PVM were found
 - PVS was found from 6 potato samples and PVM from 1 sample
 - PVS and PVM confirmed by real-time-PCR

Year of harvest	Number of samples	Proportion of individual samples containing viruses (estimated using Seedcalc 8 –software)			
		PVY	PMTV	PVS	PVM
2017	48	11,4 %	25,5 %	0 %	0 %
2018	46	45,1 %	4,9 %	10,7 %	2,4 %



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Routine use in plant health

COST-DIVAS: Deep Investigation of Virus Associated Sequences

- Application of deep sequencing methods in plant health
- Best practices and limits for the use of deep sequencing in routine diagnostics
- E.g. proficiency test for the bioinformatics pipelines used in different laboratories (detection of viruses from ready-made data sets)
- Co-operation with EPPO to design quality assurance policy for small RNA sequencing

High-throughput sequencing technologies for plant pest diagnosis: challenges and opportunities

A. Olmos¹, N. Boonham², T. Candresse³, P. Genti⁴, B. Giovani⁵, D. Kutnjak⁶, L. Liefing⁷, H.J. Maree⁸, A. Minafra⁹, A. Moreira¹⁰, M.K. Nakhla¹¹, F. Petter⁵, M. Ravnikar⁶, B. Rodoni¹², J.W. Roenhorst¹³, M. Rott¹⁴, A.B. Ruiz-García¹⁴, J. Santala¹⁵, G. Stancanelli¹⁶, R. van der Vlugt¹⁷, C. Varveri¹⁸, M. Westenberg¹³, T. Wetzell¹⁹, H. Ziebell²⁰ and S. Massart²¹

¹Instituto Valenciano de Investigaciones Agrarias, Ctra Moncada a Nàquera km 4.5, 46113, Moncada, Valencia (Spain); e-mail: aolmos@ivia.es

²Newcastle University, Newcastle upon Tyne, NE1 7RU (UK)

³Equipe de Virologie, UMR 1332 Biologie du Fruit et Pathologie, INRA, University of Bordeaux, 71 avenue E. Bourlaux, CS 20032, 33882, Villenave d'Ornon Cedex (France)

⁴French Agency for Food, Environmental and Occupational Health and Safety-Plant Health Laboratory, Unité de Bactériologie, Virologie et détection des OGM, 7 rue Jean Dismèzes, 49004, Angers Cedex 01 (France)

⁵European and Mediterranean Plant Protection Organization, 21 boulevard Richard Lenoir, 75011, Paris (France)

⁶National Institute of Biology, Večna pot 111, 1000, Ljubljana (Slovenia)

⁷Ministry for Primary Industries, PO Box 2095, Auckland, 1140 (New Zealand)

⁸Stellenbosch University, Private Bag XI, Matieland, 7602 (South Africa)

⁹Institute for Sustainable Plant Protection, CNR, Via Amendola, 122/D, I-70126, Bari (Italy)

¹⁰Secretariat of the International Plant Protection Convention, Viale delle Terme di Caracalla, 00153, Rome (Italy)

¹¹Beltsville Laboratory, USDA APHIS PPQ, Science and Technology, Building 580, BARC-East, Beltsville, MD, 20705 (USA)

¹²AgriBio, La Trobe University Bundoora, Vic, 3083 (Australia)

¹³National Reference Centre, National Plant Protection Organization, Geertjesweg 15, 6706 EA, Wageningen (The Netherlands)

¹⁴Canadian Food Inspection Agency, 8801 East Saanich Road, Sidney, BC, V8L 1H3 (Canada)

¹⁵Research Department, Plant Analysis Laboratory Unit, Finnish Food Safety Authority Evira, Mustialankatu 3, FI-00790, Helsinki (Finland)

¹⁶Animal and Plant Health Unit, European Food Safety Authority, Via Carlo Magno 1A, 43126, Parma (Italy)

¹⁷Wageningen Plant Research, P.O. Box 16, 6700 AA, Wageningen (The Netherlands)

¹⁸Benaki Phytopathological Institute, 8 Stefanou Delta Street, Kifissia, Athens, 14561 (Greece)

¹⁹DLR Rheinpfalz, Institute of Plant Protection, 67455, Neustadt an der Weinstrasse (Germany)

²⁰Institute for Epidemiology and Pathogen Diagnostics, Julius Kühn-Institute, Messeweg 11/12, 38104, Braunschweig (Germany)

²¹Gembloux Agro-Bio Tech, TERRA, Laboratory of Plant Pathology, University of Liège, Passage des déportés, 2 - 5030, Gembloux (Belgium)

High-throughput sequencing (HTS) technologies have revolutionized plant pest research and are now raising interest for plant pest diagnostics, with plant virus diagnostics at the forefront of development. However, the application of HTS in plant pest diagnostics raises important challenges that plant health regulators will have to address. Adapted infrastructures, technical guidelines and training are pivotal for further use and adoption of the HTS technologies in the phytosanitary framework.

1. Introduction

Early diagnosis and a rapid response are crucial to reduce the risk of entry and spread of plant pests into an area. In 2016, the Commission on Phytosanitary Measures adopted a recommendation recognizing that 'pest diagnosis is a cross cutting issue that underpins most International Plant Protection Convention (IPPC) activities. In order to take action against a pest, it must be accurately identified. To enable safe trade, pest diagnosis must further be completed quickly and to a high level of confidence' (FAO, 2016). National Plant Protection Organizations (NPPOs) routinely perform pest diagnosis to support export certification, import inspections, pest surveillance and

eradication programmes. Plant pests can be managed most effectively when control measures are implemented at an early stage of infestation. Plant pest diagnostics is based on the use of a range of methods underpinned by different biological principles (e.g. bioassay, biochemical, isolation/extraction methods, molecular methods, morphological and morphometric and serological methods), some of them being highly specific and others more generic. The ability to detect plant pests varies with the sensitivity and specificity of the detection tools used. The recent development of high-throughput sequencing (HTS) technologies, also called next-generation sequencing (NGS) or deep sequencing, has revolutionized the research on plant-associated organisms. These techniques are beginning to be



Routine use requires harmonization

- To be used in routine testing, characteristics of a test have to be evaluated
 - Sensitivity
 - Specificity (inclusivity and exclusivity)
 - Repeatability
 - Reproducibility
- EPPO standard almost ready
 - How to set up a HTS test
 - How to evaluate test characteristics
 - How to ensure traceability
 - When is additional testing required
 - How to report findings

European and Mediterranean Plant Protection Organization
Organisation Européenne et Méditerranéenne pour la Protection des Plantes

22-XXXXX

PM 7/XX

Diagnostics

PM 7/NEW Considerations for the use of High Throughput Sequencing in plant health diagnostics

Specific scope

This Standard describes elements to take into consideration for the use of High Throughput Sequencing



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Thank you!

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