

Discovery of viruses in New Zealand native plants

Dr Ana Podolyan

Collaborators:

A. Blouin, PFR Auckland

M. Dhami, MWLR Lincoln

S. Veerakone, MPI Auckland

R. MacDiarmid, PFR Auckland



A generic RT-PCR assay for the detection of *Luteoviridae*

A. Chomič^{a,*}, M. N. Pearson^b, G. R. G. Clover^c, K. Farreyrol^b, D. Saul^d,
J. G. Hampton^a and K. F. Armstrong^a

Journal of Virological Methods 171 (2011) 46–52



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Journal of Virological Methods

journal homepage: www.elsevier.com/locate/jviomet



Protocol

Detection and discrimination of members of the family *Luteoviridae* by real-time PCR and SYBR[®] GreenER[™] melting curve analysis

Anastasija Chomič^{a,*}, Louise Winder^b, Karen F. Armstrong^{a,*}, Michael N. Pearson^c, John G. Hampton^a

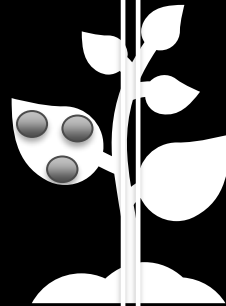


Agricultural
crops

Wild plants

Pathogenic
viruses

Asymptomatic



Tolerance

Drought

Cold

Hot soil



Virus infection improves drought tolerance

Ping Xu, Fang Chen, Jonathan P. Mannas, Tracy Feldman, Lloyd W. Sumner and Marilyn J. Roossinck

The S. R. Noble Foundation, Ardmore, OK 73401, USA

2008

nature reviews
microbiology

Review Article | Published: 04 January 2011

The good viruses: viral mutualistic symbioses

Marilyn J. Roossinck

2011



Plant Virus Metagenomics: Advances in Virus Discovery

Marilyn J. Roossinck, Darren P. Martin, and Philippe Roumagnac

2015



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Virus Research

Volume 246, 15 February 2018, Pages A1-A3



Metaviromics: a tectonic shift in understanding virus evolution

Eugene V. Koonin  , Valerian V. Dolja  

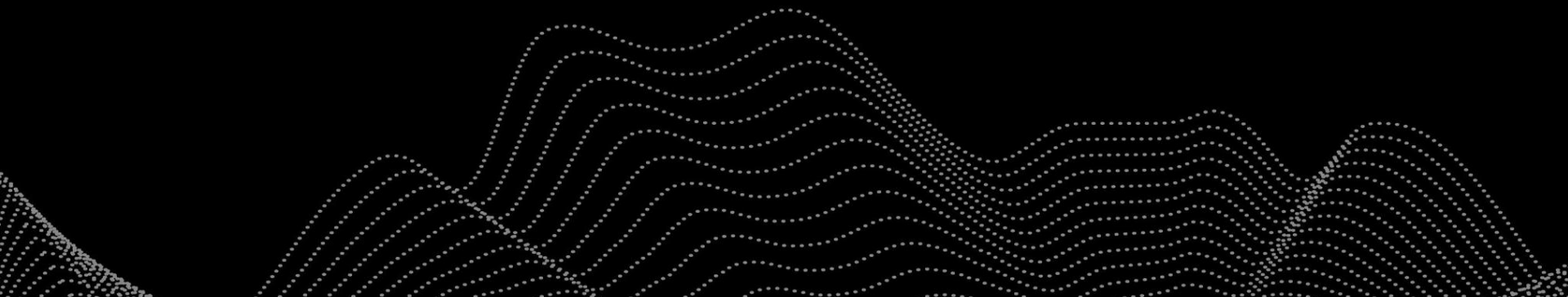
2018



Diverse and variable virus communities in wild plant populations revealed by metagenomic tools

Hanna Susi¹, Denis Filloux^{2,3}, Mikko J. Frilander⁴, Philippe Roumagnac^{2,3} and Anna-Liisa Laine¹

2019





**MOLECULAR ECOLOGY
RESOURCES**

Molecular Ecology Resources (2016) 16, 1255–1263

doi: 10.1111/1755-0998.12525

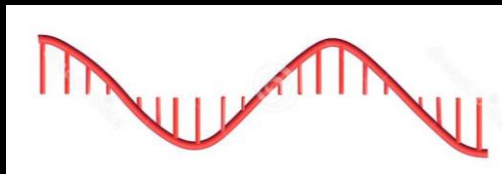
SPECIAL ISSUE: SEQUENCE CAPTURE

A new virus discovered by immunocapture of double-stranded RNA, a rapid method for virus enrichment in metagenomic studies

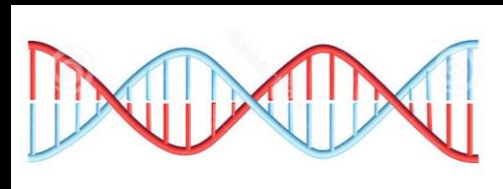
ARNAUD G. BLOUIN,*† HOWARD A. ROSS,† JODY HOBSON-PETERS,‡ CAITLIN A. O'BRIEN,‡ BEN WARREN* and ROBIN MACDIARMID*†

2016

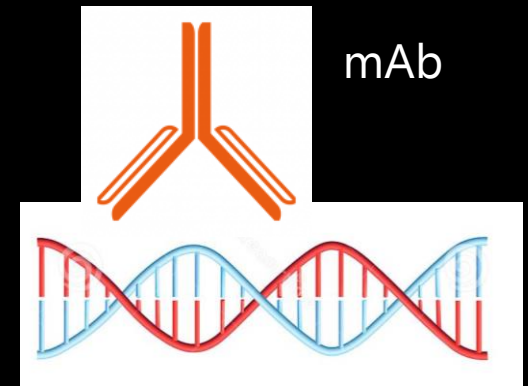
RNA



dsRNA



mAb





Brachyglottis greyi



Lophomyrtus bullata



Leptospermum scoparium (manuka)



Veronica bollonsii

Ageratum Latent Virus in New Zealand



Veronica bollonsii



Ageratum houstonianum



Gomphocarpus physocarpus

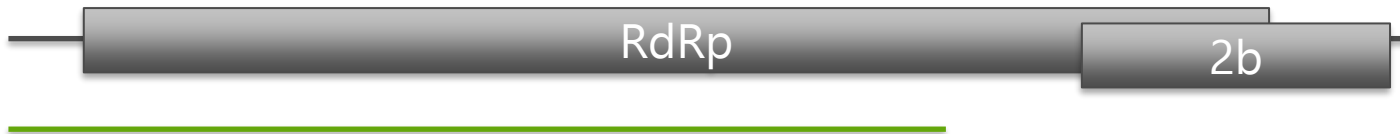


Ageratum latent virus (Iilarvirus, ssRNA)

RNA1 - 3481 bp



RNA2 - 2872 bp



RNA3 - 2224 bp





	AgLV-NZ	AgLV-Aus
RNA-1		
Replicase recovered	914 aa (out of 1097)	86.8% aa similarity
RNA-2		
RdRp	594 aa (out of 790)	85.9% aa similarity
2b	NA	NA
RNA-3		
MP	294 aa (out of 294)	89.1% aa similarity
CP	237 aa (out of 237)	87.4% aa similarity

What does it mean for the *Veronica* sp?

- Largely endemic
- Largest plant genus in New Zealand
- 90-100 species, complex taxonomy



Veronica bollonsii

To be determined:

- What is AgLV potential to cause disease in *Veronica* sp?
- What other plant species AgLV infects?
- Is it mutualistic virus? Why no symptoms?



What does it mean for the biosecurity?

OPEN ACCESS Freely available online

2013 PLOS PATHOGENS

Opinion

Biosecurity Implications of New Technology and Discovery in Plant Virus Research

Robin MacDiarmid^{1,2*}, Brendan Rodoni³, Ulrich Melcher⁴, Francisco Ochoa-Corona⁵, Marilyn Roossinck^{6,7}

OPEN ACCESS Freely available online

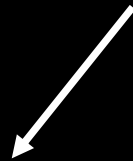
2014 PLOS ONE

Appearances Can Be Deceptive: Revealing a Hidden Viral Infection with Deep Sequencing in a Plant Quarantine Context

Thierry Candresse^{1,2}, Denis Filloux³, Brejnev Muhire⁴, Charlotte Julian³, Serge Galzi³, Guillaume Fort³, Pauline Bernardo³, Jean-Heindrich Daugrois³, Emmanuel Fernandez³, Darren P. Martin⁴, Arvind Varsani^{5,6,7}, Philippe Roumagnac^{3*}



Countries should identify what pests already exist in, and which pests pose a risk to, their native flora.



- Is virus already in the country?
- Is it a new organism?
- What is its host range?
- What is its biology under normal/extreme conditions?



Invest in basic research to determine the ecology of known and new viruses with existing and potential new plant hosts and vectors and develop host-virus pathogenicity prediction tools



Manaaki Whenua
Landcare Research

Thank you!

