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EDITED AND REVIEWED BY

Jeremy R. Thompson,
Plant Health & Environment Laboratories
(MPI), New Zealand

*CORRESPONDENCE

Ioly Kotta-Loizou
✉ i.kotta-loizou2@herts.ac.uk

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Editorial: Women in fundamental virology

Ioly Kotta-Loizou^{1,2*}, Izabela Mauricio De Rezende³,
Livia Sacchetto⁴ and Judith Kay Brown⁵

¹Department of Clinical, Pharmaceutical and Biological Science, School of Health, Medicine and Life Sciences, University of Hertfordshire, Hatfield, United Kingdom, ²Department of Life Sciences, Faculty of Natural Sciences, Imperial College London, London, United Kingdom, ³Department of Paediatrics Infectious Diseases, Stanford University School of Medicine, Stanford, CA, United States, ⁴Faculdade de Medicina de São José do Rio Preto, São José do Rio Preto, São Paulo, Brazil, ⁵School of Plant Sciences, University of Arizona, Tucson, AZ, United States

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Editorial on the Research Topic

Women In fundamental virology

The Frontiers Research Topic on “*Women in fundamental virology*” was initiated in the context of *Frontiers in Virology*, covering the section *Fundamental Virology*. Our Research Topic accommodates an interesting Brief Research Report, two high-quality Original Research articles, and a detailed Review. Although limited in number, these articles highlight the diversity of research performed across the field of virology, presenting advances in human, plant, and fungal viruses.

In the Brief Research Report “Analysis of parvovirus B19 persistence and reactivation in human heart layers”, [Badrinath et al.](#) investigate heart disease, which is the leading cause of death worldwide, with viral infections often implicated in myocarditis. The research focuses on parvovirus B19 (B19V), commonly found in endomyocardial biopsies, and its potential role in heart disease. B19V causes a variety of symptoms, such as a rash that initially appears on the face and later spreads to the trunk and extremities, fever, headache, nausea, or joint pain. Interestingly, B19V is commonly found in the human heart while performing endomyocardial biopsies, suggesting it can persist in the cardiac tissue after the initial infection. To assess the presence of B19V, a polymerase chain reaction-based assay was used to detect its genome and mRNA in epicardium, endocardium, and myocardium samples from individuals with and without heart conditions. The results showed variability in the presence of the B19V genome across different heart layers, suggesting localized infection sites. B19V transcriptional activity, indicated by mRNA presence, was also detected in samples derived from the inflamed hearts and not in the control patients with no cardiac inflammation. In conclusion, the study suggests that localized sites of B19V infection exist within individual heart layers, which may have implications for cardiac muscle inflammation.

In the Original Research article “First waikavirus infectious clones and vascular expression of green fluorescent protein from maize chlorotic dwarf virus”, [Stewart et al.](#) constructed complete genome clones for two strains of maize chlorotic dwarf virus (MCDV), mild (M) and severe (S), respectively, and a green fluorescent protein (GFP) tagged MCDV-S clone, all infectious in maize. Further, the infectious clones were delivered by the vascular

puncture method, previously developed to inoculate maize seeds with wild-type, purified virions, collectively, circumventing the use of *Agrobacterium* spp. plasmid transfection systems, often less than optimal or incompatible with cytoplasmic-replicating large RNA virus genomes. The MCDV is a positive-sense, single-stranded RNA virus with a genome size of ~12,000 nucleotides, classified in the genus *Waikavirus*. MCDV emerged in the 1960s and prevails as a destructive pathogen in the midwestern U.S., causing stunting and yield loss in maize plants. It has been particularly recalcitrant to study due to low virus accumulation, phloem tissue tropism, and reliance on the leafhopper vector for experimental transmission. This report describes an approach for infectious clone construction that involves the use of an improved plasmid backbone, high-efficiency *in vitro* transcription of full-length virus, and vascular puncture delivery of the plasmid vector-virus construct to maize phloem cells. Both the M and S strain clones were infectious, yielding characteristic symptoms in inoculated maize seedlings, and MCDV phloem-tropism was recapitulated by visualization of the GFP-tagged MCDV-S infectious clone in maize phloem cells. The availability of these infectious clones will facilitate studies aimed at better understanding the biology of MCDV host-virus interactions and accelerate efforts to screen germplasm for disease tolerance/resistance.

In the Original Research article “Sorting motifs target the movement protein of ourmia melon virus to the *trans*-Golgi network and plasmodesmata”, [Ozber et al.](#) investigate how a plant virus spreads across plant cells. Ourmia melon virus (OuMV) infection leads to mosaic and chlorotic spots and smaller fruit production in melon plants. However, the molecular mechanisms underpinning its transmission and movement have yet to be fully elucidated. Here, the OuMV movement protein (MP) was shown to be localized at the *trans*-Golgi network using fluorescence microscopy. Two sorting motifs located close to its N-terminus are required to target the OuMV MP to plasmodesmata, leading to efficient systemic infection. Mutations altering the amino acid sequence of these two sorting motifs result in the loss of OuMV infectivity in two model plants, *Nicotiana benthamiana* and *Arabidopsis thaliana*. The OuMV MP was also shown to be associated with vesicle trafficking and lipid-binding proteins through co-immunoprecipitation. In the future, these findings may form the basis for approaches that will be used to combat OuMV infection in melon plants.

In their Review titled “A comprehensive review of mycoviruses infecting the plant pathogenic fungus *Rosellinia necatrix*”, [Hassan et al.](#) focus on an important plant pathogenic ascomycete and its mycovirome. *R. necatrix* has a worldwide distribution and is the causative agent of white root rot disease in a wide range of species, including ornamental and fruit plants. Over 50 mycoviruses have been reported to infect *R. necatrix*, belonging to families accommodating double-stranded (ds) or positive-sense single-

stranded (+ss) RNA genomes. In particular, the families *Megabirnaviridae* and *Quadriviridae* were established based on mycoviruses discovered in *R. necatrix*. In addition to their genetic organization and structure, numerous reported studies investigated the effects of exemplar mycoviruses on their natural host *R. necatrix* or a heterologous host *Cryphonectria parasitica*. Mycovirus infection was shown to change the host transcriptome and small RNA profile and interfere with the host antiviral RNA silencing mechanisms. Observed alterations in morphology and pigmentation, together with reduced growth and virulence, indicate that mycoviruses in *R. necatrix* appear to be promising agents for biological control applications against white root rot.

As Associate Editors, we would like to take this opportunity to acknowledge all contributing women scientists who chose our Research Topic on “*Women in fundamental virology*” as a vehicle for sharing their stimulating work.

Author contributions

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Conflict of interest

The authors declare that the research was conducted in the absence of any commercial or financial relationships that could be construed as a potential conflict of interest.

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