

# cause: How fundamental ecological research in natural systems can inform and advance plant pathology

## C4.4-1

### FROM BOOTS ON THE GROUND TO NUCLEOTIDES IN THE SEQUENCER: ADVANCES IN THE STUDY OF PLANT VIRUS ECOLOGY USING PLANT VIRUS METAGENOMICS

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#### Text

Plant virus ecology began to be explored at the end of the 19th century. Since then, major advances have revealed complex virus–host–vector interactions in a variety of environments. These advances have been accelerated by development of new technologies for virus detection and characterization, the latest of which being high-throughput sequencing (HTS). HTS technologies have proved to be effective for non-targeted characterization of all or nearly all viruses present in a sample without requiring prior information about virus identity, as would be needed for virus-targeted tests. Plant virus metagenomics studies have thus made important advances, including characterization of the complex interactions between phytovirus dynamics and the structure of multi-species host communities, and documentation of the effects of anthropogenic ecosystem simplification on plant virus emergence and diversity. However, such studies must overcome challenges at every stage, from plant sampling to bioinformatics analysis. Results of two recent studies will be presented. While the first study aimed at systematically evaluate plant-associated viromes across broad agro-ecological interfaces, the second study aimed at using a predator-enabled metagenomics strategy to sample the virome of a remote and difficult to access densely forested African tropical region.

## C4.4-2

### ALTERATION OF PLANT SPECIES MIXTURES BY VIRUS INFECTION