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## **Program and Abstracts**

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## Diversity and structure of Poaceae-infecting mastreviruses communities on Reunion Island using a viral metagenomics-based approach

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### Abstract

The *Mastrevirus* genus (*Geminiviridae* family) contains circular single-stranded DNA viruses transmitted by leafhoppers (in the Cicadellidae family) to a wide range of either monocotyledonous or dicotyledonous host species. Most of the known monocot-infecting mastreviruses have been identified either in Africa or surrounding islands. This group of mastreviruses have collectively been called the “African streak viruses” (AfSV). Of the 13 AfSV species infecting cultivated and wild *Poaceae* species, six have been identified on Reunion Island. Interestingly, these species were probably introduced at different time and they present with putatively distinct host ranges. Understanding how this virus community operates remains an essential question in the understanding of virus ecology, evolution and emergence. Therefore, to elucidate the diversity, host ranges and structure of mastrevirus communities on Reunion Island, we undertook an extensive survey in a single sampling site of one acre including crop fields, orchards and uncultivated areas. After four sampling campaigns, 2917 samples of 30 cultivated and uncultivated *Poaceae* species were randomly collected, regardless of their health status. Total plant DNA was isolated and circular viral genomes were amplified by a sequence-independent amplification procedure combining rolling circle amplification, a random amplification tagging (RCA-RA) and high-throughput sequencing (Illumina HiSeq). For every sample, mastrevirus reads were classified using phylogenetic placement within species and strains. Mastrevirus species were confirmed by cloning and Sanger sequencing. Besides uncovering previously undescribed mastrevirus species, our results provide an exhaustive view of the mastrevirus-host association network within an agroecosystem. The topology of this network suggests (1) the co-existence of viruses ranging from generalist to specialist and (2) that certain hosts may act as hubs of virus infection and transmission.