



*9<sup>th</sup> International Geminivirus Symposium*  
*7<sup>th</sup> ssDNA Comparative Virology Workshop*  
UNIVERSITY OF CALIFORNIA - DAVIS

## **Program and Abstracts**

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## **Night at the museum: Contribution of small RNA from historical herbarium specimens in the reconstruction of evolutionary histories of geminiviruses**

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### Abstract

Emerging infectious diseases of plants, almost half of which are caused by viruses, are recognized as a growing threat to global food security. However, little is known about the evolutionary processes and ecological factors that underlie the emergence and success of viruses that have caused past epidemics. With technological advances in the field of ancient DNA and RNA, it is now possible to sequence historical viral genomes, which provides us direct access to the dimension of time in evolutionary studies. Herbarium collections are an enormous source of dated, identified and well-preserved material that can be used to elucidate the emergence and evolutionary history of viral plant pathogens. Geminiviruses are responsible for many of the emerging plant diseases worldwide with a major economic impact on food crops such as cassava, which are a vital source of dietary calories in many sub-Saharan African countries. Their high potential for evolution, with high rates of mutation and recombination, makes such viruses an ideal model for understanding the epidemiological and evolutionary processes associated with viral emergence. Our proof of concept study investigated whether small interfering RNA (siRNA) can be used to reconstruct a complete geminivirus DNA genome from a herbarium sample despite the existence of post-mortem nucleic acid damage. Using a metagenomics approach based on the high-throughput sequencing of siRNA, we obtained a siRNA database from cassava leaf samples presenting typical symptoms of cassava mosaic disease that were collected in 1928 from Madagascar and 1968 from Cameroon, and then stored in the National Museum of Natural History herbarium in Paris. Our preliminary results demonstrate our ability to reconstruct the almost complete sequence of bipartite begomoviruses in particular from a 90-year-old herbarium specimen. These sequences are now used in phylogenetic, comparative genomic and phylogeographic studies to elucidate the emergence and evolutionary history of this important crop pathogen.