

Characterization of novel, highly divergent geminiviruses and insights into the evolutionary history of geminiviruses

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In 2010 and 2012 we undertook large scale “*non a priori*” geometagenomics sampling surveys within two agro-ecosystems: Camargue (France) and Western Cape region (South Africa) aiming at determining the influence of agricultural activities on the diversity of plant viruses associated with species rich natural ecosystems that are threatened by human encroachment. Besides determining the spatial and host distributions of various groups of both known and previously unknown plant viruses, we focus primarily on geminiviruses because of their rapid evolution rates (they are among the most rapidly evolving viruses) and because of the fact that many of the most important emergent crop pathogens of the past century in Africa and Europe (e.g. pandemic Tomato yellow leaf curl virus in Europe and maize streak and cassava mosaic viruses in Africa) have belonged to this family. Both of these features make geminiviruses an excellent and highly relevant model for studying evolutionary aspects of viral emergence. We used a hierarchical procedure, including a first stage sequence-independent NGS step followed by a second step yielding complete genome sequences. New geminivirus species have been discovered, and we have recently undertaken a detailed characterization of one of these: a highly divergent geminivirus found infecting the fynbos species *Euphorbia caput-medusae*: *Euphorbia caput-medusae latent virus* (EcmlV). Although clearly a geminivirus, EcmlV is so divergent that we have proposed its placement within a new genus that we have tentatively named Capulavirus. In addition to being infectious in *Euphorbia caput-medusae*, the cloned viral genome was also infectious in tomato and *Nicotiana benthamiana*. Importantly, two new geminiviruses belonging to this new genus have been recently discovered from French bean in India and from alfalfa in France through the analysis of a 2010 metagenomics survey of the Camargue region, which raises questions about whether this sudden worldwide discovery of crop-infecting capulaviruses might indicate the first stages in the emergence of these viruses as agricultural pathogens.

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