A new genus-level geminivirus lineage isolated from the South African fynbos

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The state of the art on the diversity of plant viruses mainly concerns those causing symptoms affecting plants of economic interest. However, wild plants have the potential to be reservoirs of viral biodiversity which contribute to the emergence of virus without necessarily showing symptoms. It is very important to study the viral diversity in natural environments in order to predict future outbreaks and know how to manage them. Among the virus-DNA plants, the family Geminiviridae is known for being responsible for many plant diseases of economic interest, including tomato, cotton and cassava. Africa is a continent particularly affected by the impact of geminiviruses that threaten its main crops.

Here, we describe a new genus-level geminivirus lineage isolated from the fynbos wild ecosystem (South Africa): *Euphorbia caput-medusae Virus* (EucmV)

### Methodological approach

- **Study area:**
  - *Euphorbia caput-medusae*

- **Host plant:** *Euphorbia caput-medusae*

- **Total DNA extraction, RCA, EcoR1 restriction:**

- **Cloning and sequencing:**

- **Operating sequence of EucmV**
  - **Genome map and ORFs:**
    - Organization similar to mastrevirus:
      - a spliced rep in the complementary sense (ORF a and c)
      - a cp on the virion sense (ORF b)
      - But a lack of mp
      - 3 unknown ORFs
  - **Phylogenetic tree (Maximum likelihood):**

- **Recombination analysis:**
  - Weak signal of recombination (15 aa)
  - But the significance of this signal remains unclear because the sequence alignment was not optimal (because of the diversity of sequences in the *Geminiviridae* family)
  - EucmV is probably not recombinant

- **Prospects**
  - Study the infectivity of EucmV
  - Study the « genera concept » by finding EucmV vector and host range investigation
  - Study the function of each ORF
  - Confirm the phylogenetic position of EucmV within the *Geminiviridae* family