Understanding the role of mycoviruses in vine fungal communities

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1- Contexte

The SARS-CoV-2 pandemic shows that viruses are infectious and are expected to be transmitted among a population. However, in the fungal endophytic population, viruses called mycoviruses are not easily transmitted to one another, even among fungi of the same species.
In this project, we seek to **understand why a virus can be present in one isolate but not in other isolates from the same species and same environment**. We will evaluate if a longer adaptation period has an influence on the prevalence of mycovirus among isolates of a fungal species.

3- Results

- Two mycovirus identified in one fungal isolates (Fig. 2).
- 1/21 isolate contained a viral segment identical to the previously identified segment (Fig. 3).
- Among the 583 fungi isolated, 268 were different isolates, of 47 different species (Fig. 4).

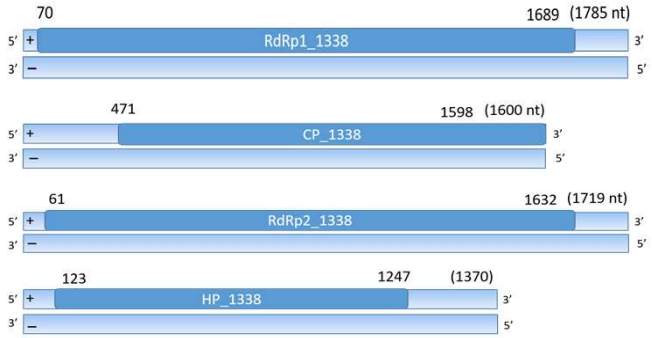

Figure 2: Four mycoviral genomic segments of 2 partitivirus identified in one isolate of *C. Cladospiroides*

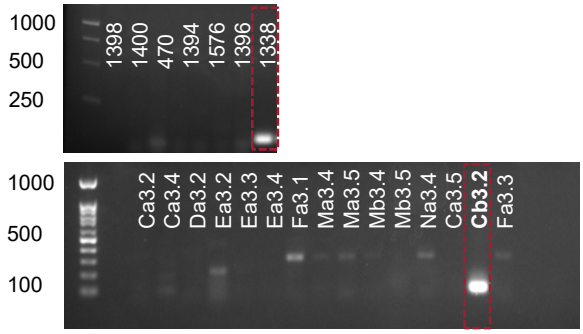

Figure 3: Screen for RdRp1_1338 among endophytic *Cladosporium sp.* isolated from vines of the same parcel same cultivar (1398,1394,1396,1400), and different parcels same cultivar (bottom), different cultivar (1576) and other plant species (470, 1576)

2- Material and method

- Fungal endophytes were obtained from **vine wood** samples deposited on growth medium. The species of fungal isolates were identified by **ITS amplification** and **sanger sequencing**.
- **Illumina sequencing** was performed for the initial identification of mycoviruses from a cultured fungal isolate of *Cladosporium Cladospiroides*. The full sequence was reconstructed with **RACE PCR**.
- The identified mycoviruses were screened in isolates of the same fungal species with **RT-PCR**.
- The fungal community was obtained from fungi living in non-grafted vine for a long time compared to fungi living more recently in grafted vines. Plants were growing in the **same pedoclimatic area** and were from the **same cultivar**.

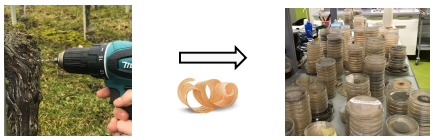

Figure 1: isolation of fungal endophytes from vine wood samples

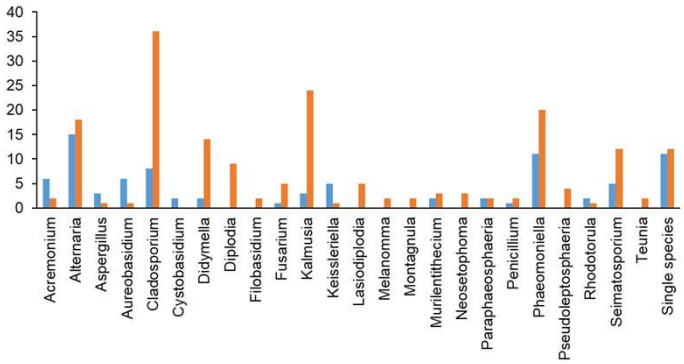

Figure 4: Number of fungal isolates from old (blue) and young (orange) vines per OTU.

4- Conclusion and ongoing work

- The presence of mycovirus in the grapevine was confirmed from the identification of **four mycoviral segments** in one isolates. It shows that mycoviruses can **be numerous in a single fungal isolate**. However, the screen of the 21 fungal isolates stresses that although the presence of a similar mycoviral segment in isolates from different origines has been found, it is a **rare situation**.
- The constructed fungal community from old and young plants presents **similar species**, permitting to identify the **prevalence of mycovirus** in a same host species among the two variables.
- **dsRNA** will be extracted from all isolates and sequenced with **Illumina sequencing** technology, for a mycovirome identification.

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