

# Badnavirus sequences identified from *Passiflora* spp. in Guadeloupe and Australia

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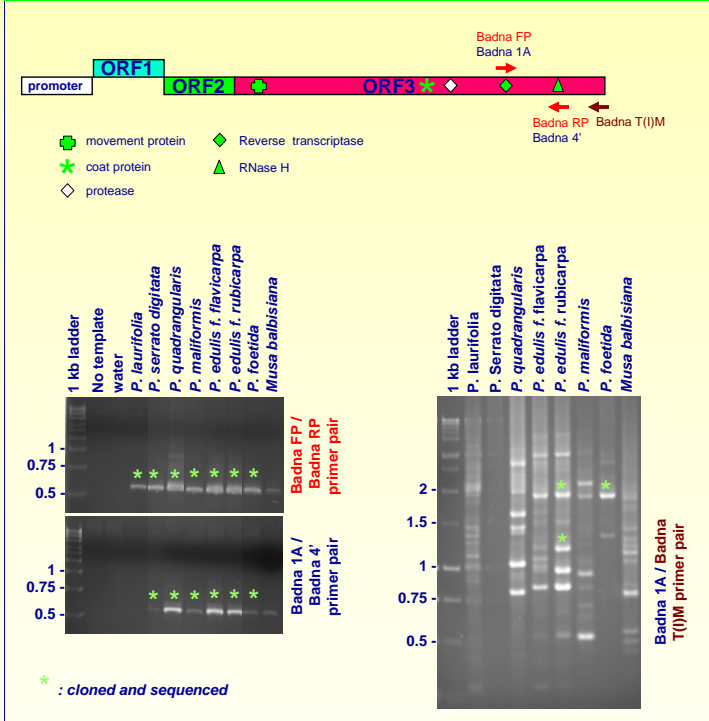
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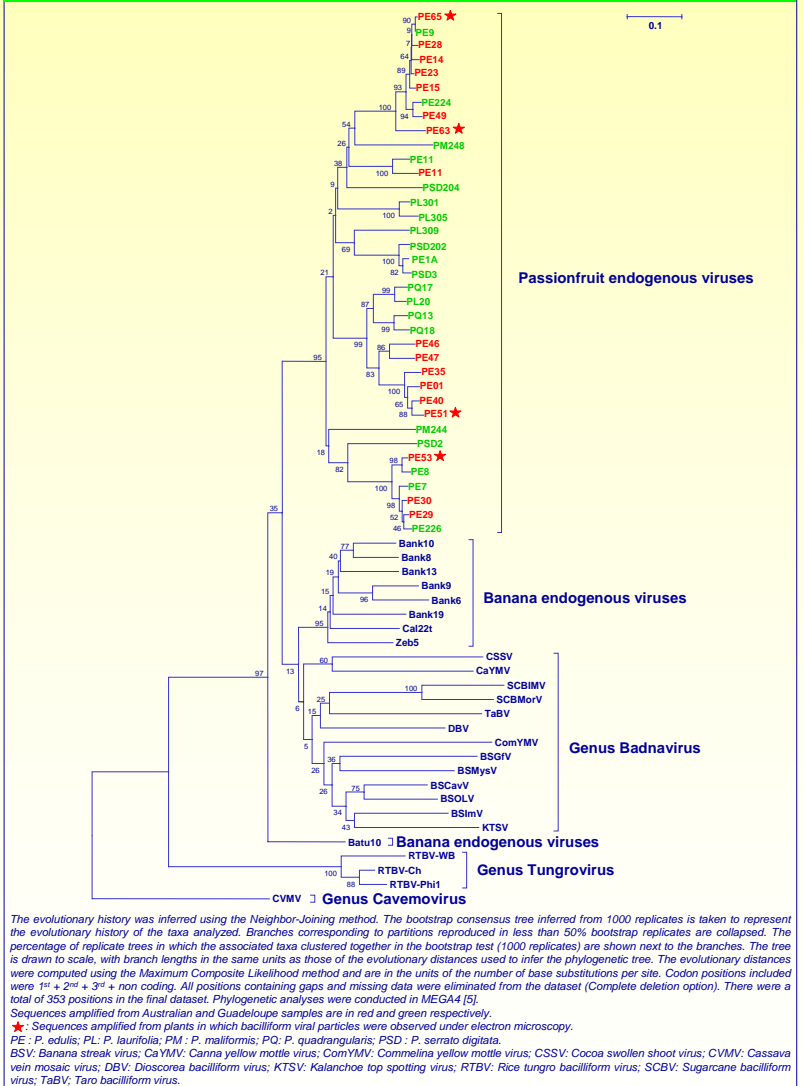
Badnaviruses (family *Caulimoviridae*, genus *Badnavirus*) have non-enveloped bacilliform particles containing a single copy of a circular dsDNA genome of c. 7.4–7.6 kbp arranged in at least three conserved open reading frames. They are transmitted in a semi-persistent mode by mealybugs and, for some species, also by aphids, scale insects or lacebugs. Several badnaviruses infect economically important tropical crops such as banana, cocoa, pineapple, sugarcane, taro and yam, and have a serious impact on yields. Over the past 10 years, endogenous viral sequences have been discovered and characterized in the genome of numerous crops, including badnavirus sequences in the genome of banana, yam and pineapple. It is expected that *in silico* analysis of plant genomic sequence data will reveal more endogenous viral sequences.

*Passiflora* spp. from Guadeloupe and Australia were screened for badnavirus sequences by PCR across the conserved reverse transcriptase/RNaseH region of the ORF 3 polyprotein. PCR was performed on purified total DNA, using degenerate primer pairs Badna 1A / Badna 4' [1] and Badna FP / Badna RP [2, 3]. Badnavirus sequences were amplified from *Passiflora edulis* f. *flavicarpa*, a yellow mutant introduced to Australia and Guadeloupe in the beginning of the XXth century, and *P. edulis* f. *rubicarpa*. Badnavirus sequences were also amplified from species *P. foetida*, *P. laurifolia*, *P. maliformis*, *P. quadrangularis* and *P. serrato-digitata*, which were introduced in Guadeloupe from South and Central America at the turn of the XXth century. On the contrary, no badnavirus sequences could be amplified from Australian native *P. aurantia* and *P. herbertiana*. In order to extend DNA sequences, amplification products obtained from total DNA purified from *P. edulis* f. *flavicarpa* and *P. foetida* using primer pair Badna 1A / Badna T(I)M [1, 4] were also cloned and sequenced.

**Figure 1 : Amplification of the reverse transcriptase/RNaseH region of the ORF 3 polyprotein**



**Figure 2 : Evolutionary relationships of 63 taxa, generated from ORF3 nucleotide sequences amplified using badnavirus degenerate primers.**



➤ **Phylogenetic analyses show that :**

- there is no host speciation of endogenous badnavirus sequences found in the *Passiflora* spp. used in this work.
- *P. edulis* samples from Guadeloupe and Australia share highly similar sequences. The nature of these sequences (episomal vs integrated) is currently being explored.

➤ Although no badnavirus has been reported yet in *Passiflora* spp., bacilliform particles could be observed in an Australian *P. edulis* f. *flavicarpa* plant (see ★ on figure 2) showing severe fruit puckering and leaf shoestring symptoms. Nevertheless, all other plants used in this study were asymptomatic.

**References**

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