46-Towards a better characterization of endogenous badnavirus sequencesofyams (*Dioscorea* spp.)

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Yams, and more generallytubers, are very important crops for food security in tropical and subtropical countries.They are propagated vegetativelytherefore they accumulate viruses over long periods of time. Viruses are currently the main constraint for yam production and yam germplasm conservation and distribution.
A wide range of badnavirus sequences belonging to 13 distinct viral species were amplified from genomic DNA of severalyam species when using badnavirus degenerate primers [1; 2].However, we consistently observed that the proportion of amplification products raised by PCR performed on total genomic DNA is significantly higher than that raised by direct binding PCR, which has been designed to detect episomal forms of yam badnaviruses.Both observations have fueled suspicion that yams might host endogenous badnavirus sequences, and possibly infectious ones like bananas [3]. Therefore, search for endogenous badnavirus sequences was undertaken in yam accessions conserved in the germplasm collection of the Guadeloupe Tropical Plant Biological Ressource Center (CRB-PT) and the yam quarantine facility in Montpellier (France).

Southern blots performed on genomic DNA extracted from uninfected *Dioscoreatrifida*and using parts of yam badnavirus genomes as probes confirmed the suspicion of endogenous badnavirus sequences in yam genomes. Furthermore, PCR performed on genomic DNA extracted from healthy seedlings of *D. alata* and *D. rotundata* using badnavirus degenerate primers raised amplification products whose sequences fit in the current phylogeny of badnaviruses. Amplification products raised from several of these DNA samples by long-PCR displayedrearrangements such asduplications andreversions which are reminiscent of endogenous badnavirus sequences encountered in the genome of other crops such as banana. Similarly rearranged sequences were raised by rolling circle amplification, which is known to sometime amplify chromosomal sequences.
These results suggest that yams do host endogenous sequences of several distinct badnavirus species.

Keywords: yams; badnavirus; endogenous viral sequence;

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