

Do yams (*Dioscorea* spp.) host endogenous viral sequences ?

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Yams (*Dioscoreae* sp) are important food commodities in tropical and subtropical areas of Africa, the Caribbean, South America and the Pacific where they play a key role in food security. Yams are vegetatively propagated crops. The use of infected vegetative propagules and uncontrolled introductions of infected germplasm promotes the spread of viruses in yam-growing areas, causing significant reduction in tuber yield and quality. Control strategies rely primarily on diagnostic and the use of virus-free germplasm, but their implementation is currently hampered by the high prevalence level of potyviruses and badnaviruses in yam germplasm and the overall partial knowledge of virus species infecting yams. Moreover, the presence of endogenous pararetrovirus sequences (EPRVs) in *Dioscorea* spp, which is suspected [1] but has not yet been formally demonstrated, could also hamper the implementation of reliable indexing tests and control strategies, especially if yams host infectious EPRVs.

The presence of EPRVs in cultivated and wild yams was investigated in the yam germplasm collection of the Tropical Plant Biological Resource Center (CRB-PT) managed by INRA in Guadeloupe. This collection currently hosts 500 accessions representing 15 distinct species. PCR-based screenings were performed on *Dioscorea alata*, *D. trifida*, *D. rotundata-cayenensis* and wild yam accessions using badnavirus-specific primers [2], caulimovirus-specific primer [3] and primers specific of a newly described genus within the family *Caulimoviridae* tentatively named dionyvirus (Geering *et al.*, unpublished). Phylogenetic analyses were performed, allowing a study of the diversity of yam badnavirus, caulimovirus and dionyvirus sequences. Southern blot experiments were also performed in order to explore the nature (endogenous vs episomal) of these sequences.

Keywords : endogenous pararetrovirus; caulimovirus; badnavirus; dionyvirus; yam

References

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