

Improved diagnostic tools for the detection badnaviruses in yams unveil the existence of endogenous sequences of extant badnavirus species in yams

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French West Indies Biological Resources Centre for Tropical Plants (CRB-PT) maintains several germplasm collections of tropical crops and wild relatives, including a collection of more than 450 yam accessions (*Dioscorea* spp). The purpose of this Centre is to conserve and distribute virus-free germplasm to end users. To this aim, virus populations infecting conserved accessions are characterized and appropriate detection tools are created or optimized, then implemented for the sanitation of infected germplasm.

Several badnavirus species have been reported in yams. Recently, endogenous *Dioscorea* badnaviral sequences (eDBVs) were described in the genome of African yams of the *D. cayenensis-rotundata* complex [1, 2]. These sequences interfere with badnavirus PCR-based detection methods and are therefore a constraint for the accurate diagnostic of badnaviruses in yams. To address this problem, an analysis of the diversity of eDBVs was carried out in *D. rotundata*, using virus-free seedlings. It showed that sequences from at least four distinct *Badnavirus* species are integrated in yam genomes, and that these viral species belong to the groups 5, 8, 9 and 12 defined by Kenyon *et al.* [3].

This finding enabled the development and implementation of a reliable technique for the specific detection of badnavirus episomal forms in yams. Using this method, we showed that the CRB-PT yam collection hosts different strains of *Dioscorea bacilliform AL virus* (DBALV; group 8) and yet unreported episomal forms of one badnavirus species of group 9, for which only endogenous forms were known so far. The genome of this new yam badnavirus species was amplified from an infected *Dioscorea trifida* accession, cloned and sequenced. Its organization is similar to that of DBALV and *Dioscorea bacilliform SN virus* (DBSNV; group 4). However, phylogenetic analyses showed that it is a novel and distinct badnavirus species, for which the name *Dioscorea bacilliform TR virus* (DBTRV) is proposed.

This first report of the occurrence of endogenous sequences (eDBV8 and eDBV9) from extant badnavirus species in yams should suggest that some eDBVs could be infectious. Conversely, molecular evidence supporting the role of these eDBVs in antiviral defense will also be presented.

Mots-clés : Yams, *Badnavirus*, endogenous viral sequence, diagnosis.

Références :

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