Virus diseases are one of the most important problems in yam (Dioscorea spp.) culture by reducing yield and tuber quality, and by causing the lost of sensitive varieties. Until now, different viruses such as poty-, potex-, badnav- and cucumovirus, have been reported to infect yams (Brunt et al., 1989). Among them, Dioscorea latent virus (DLV) was the only potexvirus found in medicinal yams D. floribunda and D. composita at Porto Rico (Phillips et al., 1996). But, until now, no molecular characterization was done on this potexvirus and specific detection tools were not available.

In order to detect DLV during quarantine procedures at CIRAD, Filloux and Girard (2006) used potexvirus-specific PCR test and then reported the detection of several putative potexviruses on edible yams. We describe here the first partial biological and molecular characterization of two new putative potexviruses infecting yams detected by this way.

**Results**

Four positive plants were detected, including 1 D. rotundata from Guadeloupe Island (FWI) and 3 D. nummularia from Vanuatu (Fig. 2).

The 3 D. nummularia isolates were each other very similar at the nucleotide level (88.5-89.6% identity) (Fig. 3).

The D. rotundata isolate showed only 62.6-63.8% identity at the nucleotide level with the 3 D. nummularia isolates.

The partial RNA-dependent RNA polymerase (RdRp) amplified from the D. rotundata isolate (215 aa) was related to the PepMV homolog gene (68.4% identity).

The partial RdRp sequence obtained for the 3 D. nummularia isolates (217 aa) were associated with the PepMV (68.7% identity) and the CymMV (68.2% identity).

No obvious symptoms were observed on the positive plants which were also infected with DBV (D. nummularia) and YMV (D. rotundata) respectively.

Very few filamentous particles (400-600 nm long) were observed by electron microscopy in the semi-purified virus preparation (Photos 1, 2 and 3).

No serological relation (Elisa tests) was found with 6 other potexviruses (CymMV, HVX, PAMV, PapMV, PepMV and PVX).

Mechanical transmission to *Nicotiana benthamiana*, *N. bigelovii* and *D. trifida* was unsuccessful (but YMV was transmitted on *D. trifida*).

**Perspectives**

- Sequencing of the complete genomes of these two putative members of Potexvirus genus.
- Design of primers for the specific and sensitive detection of each potexvirus.
- Screening of new germplasm for prevalence studies.
- Monitoring virus elimination (by thermotherapy and/or meristem culture, for example) of infected plants in order to recover potexvirus-free material.

**Materials and methods**

- One hundred and ninety three worldwide yam accessions (Caribbean islands, South America, Madagascar, Pacific islands, Central and West Africa), including 122 Dioscorea alata, 55 D. rotundata, 13 D. nummularia and 3 D. trifida were screened for potexviruses.

- One step RT-PCR tests using potexvirus-specific degenerate primers (Potex1RC/Potex5) amplifying the C-terminal region of the viral replicase (van der Vlugt and Berendsen, 2002) were carried out (Fig. 1).

- The 737 bp amplified products were single-pass double stranded sequenced and were BLAST searched against the GenBank database.

**References**


