

agrobacterium into the crown region of young rice plants. This opens the way for precise mutations to be introduced in RTBV genes to study their effects on pathogenesis. ORF IV-encoded P4 functions as a suppressor of RNA silencing in an isolate from Philippines. Interestingly, the 5' UTR gives rise to a large population of small RNAs, a potential decoy against RNA silencing. Emerging evidence indicates that PRT of an Indian isolate interacts with a component of RNA silencing machinery, revealing a surprising diversity of function. Rice plants show global changes in gene expression patterns, including hormonal pathways and membrane transport, among others. Using a transgenic approach, an ORF IV-derived dsRNA generating construct gives rise to tolerance against RTBV and reduces the viral levels 103-fold, simultaneously dampening the RTD symptoms.

C9.7-6

UNRAVELLING THE STRUCTURE OF ENDOGENOUS BADNAVIRUSES OF AFRICAN YAM SHED LIGHT ON THE ORIGIN AND DIVERSITY OF YAM CAULIMOVIRIDAE INSERTIONS

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Text

Endogenous viral elements (EVEs) of four distinct badnavirus species were previously partially characterized in the genome of African yam (*Dioscorea cayenensis* and *D. rotundata*), using molecular approaches. In order to fully elucidate the structure of badnaviral EVEs in African yams, the genomes of accessions 'Ti Guinée' (*D. cayenensis*) and 'Msg 5' (*D. rotundata*) were sequenced using HiFi PacBio high-throughput sequencing (HTS) and searched for badnavirus EVEs.

Large contigs of up to 50 Mbp were assembled and combined with optical maps produced by Saphyr system (Bionano), resulting in two high-quality reference sequences for *Dioscorea*. Twelve and six contigs originating from the genomes of 'Ti Guinée' and 'Mgs 5', respectively, contained badnaviral EVEs ranging in size between 124.4 and 17.7 kbp. All badnaviral EVEs were highly rearranged, especially those of *D. cayenensis*, which were also larger, and most contained interspersed sequences originating from distinct badnavirus species or from viruses in different *Caulimoviridae* genera. One EVE from accession 'Ti Guinée' contained badnaviral sequences surrounded by putative *Geminiviridae* sequences. Several EVEs from 'Ti Guinée' contained sequences of a yet unreported *Caulimoviridae* closely related to but distinct from *Dioscorea nummularia*-associated virus (DNUaV; *Dioscovirus*). Several EVEs originating from either species contained more-than-length copies of badnaviral genomes that may be replication competent and infectious.