

C9.7-4

IDENTIFICATION AND DISTRIBUTION OF NOVEL BADNAVIRAL SEQUENCES INTEGRATED IN THE GENOME OF CACAO (THEOBROMA CACAO)

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Text

As part of an ongoing study to understand the diversity of the badnavirus complex, responsible for the cacao swollen shoot disease in West Africa, evidence was found recently of virus-like sequences in asymptomatic cacao plants. The present study exploited the wealth of genomic resources in this crop, and combined bioinformatic, molecular, and genetic approaches to report for the first time the presence of integrated badnaviral sequences in most of the cacao genetic groups. These sequences, which we propose to name eTcBV for endogenous Theobroma cacao bacilliform viruses, varied in type with each predominating in a specific cacao genetic group. Additionally to the viral insert of type VI first identified, we recently described, with the help of Oxford Nanopore technology, viral inserts of type I, II, III and V longer than 10kb. A diagnostic multiplex PCR method was developed to identify the homozygous or hemizygous condition of the specific insert of type VI, which was inherited as a single Mendelian trait.

These data suggest that these integration events occurred before or during the species diversification in Central and South America, and prior to its cultivation in other regions. Such evidence of integrated sequences is relevant to the management of cacao quarantine facilities, and may also aid novel methods to reduce the impact of such viruses in this crop.

C9.7-5

MOLECULAR BIOLOGY OF RICE TUNGRO BACILLIFORM VIRUS (TUNGROVIRUS BACILLOORYZAE): NEW LEADS TO CONTROL RICE TUNGRO DISEASE

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Text

Rice tungro bacilliform virus (RTBV), family Caulimoviridae, genus Tungrovirus, is the causative agent for the devastating rice tungro disease (RTD), a potential threat to the regional food security in Asia. The viral dsDNA has a long 5' untranslated region (5' UTR) capable of folding into strong secondary structures, and four open reading frames (ORFs), ORF IV being the most variable. ORF III-encoded protein has domains resembling coat protein, aspartate protease (PRT) and reverse transcriptase-RNaseH. Infectious clones of RTBV have been developed, which give rise to mild RTD symptoms upon delivering through