

Worldwide genetic diversity of *Sugarcane white streak virus*

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Sugarcane white streak virus (SWSV), a novel mastrevirus, was recently discovered using virion-associated nucleic acids (VANA) metagenomics approach from two sugarcane cultivars originating from Egypt (Candresse et al, PLoS ONE 9(7): e102945). Systematic diagnosis of plants grown at the CIRAD's sugarcane quarantine station further revealed that SWSV was also infecting sugarcane cultivars originating from Sudan (KN variety) and Réunion Island (R variety). Nine genomes amplified from plants originating from these two locations were cloned and sequenced. The genome organization of these nine genomes was most similar to that of SWSV-B/C strains. Genome-wide pairwise comparisons using Mega6 indicated that the nine isolates share 91.1% pairwise identity. This analysis also showed that each of the three coding region of the genome, movement protein (*mp*), coat protein (*cp*) and replication associated protein (*rep*), contains polymorphic parts. We designed specific primers for amplifying the polymorphic region of each coding region and sequenced them from 40 isolates, including 12 isolates from Réunion Island issued from KN varieties, 7 isolates from Guadeloupe Island issued from KN varieties and 21 isolates from CIRAD's quarantine, including 11 and 10 isolates issued from R and KN varieties, respectively. Phylogenetic analyses based on *mp*, *cp* and *rep* partial genes reveal that the isolates are split into two polymorphic groups that correspond to SWSV-B and SWSV-C strains. However, phylogenetic trees issued from the three genomic regions were not congruent, suggesting recombination events. Interestingly, SWSV-C isolates are more prevalent in R varieties (64%) than in KN varieties (24%). They are also more frequent in KN varieties sampled from Reunion Island (31%) than from KN varieties collected from the two other locations (17%). Reunion Island is the only location sampled where the putative vector of the virus *Cicadulina mbila* is present, which may account for the strongest prevalence of SWSV-C in this region and for R cultivar contamination. This assumption will need to be confirmed. This new virus already stresses the need to set up efficient diagnostic and sanitation tools in order to detect and clean the infected cultivars for quarantine purposes.