METAGENOMICS-BASED EXPLORATION OF THE GENETIC DIVERSITY OF SCYLV IN THE SUGARCANE COLLECTION OF GUADELOUPE.

Fernandez E(1), Filloux D(1), Julian C(1), Lubin-Adjanoh N(2), Pavie C(3), Teycheney PY(4), Candresse T(5), Roumagnac P(1) and Daugrois JH (1)

(1) CIRAD-BIOS-UMR BGPI TA A-54 / K Campus international de Baillarguet - 34398 Montpellier Cedex5 France (jean-heinrich.daugrois@cirad.fr),
(2) CIRAD-BIOS-UMR BGPI (GLP),
(3) INRA (FRA),
(4) INRA (GLP),
(5) CIRAD-BIOS-UMR AGAP (GLP)

BACKGROUND and OBJECTIVES

Sugarcane yellow leaf virus (SCYLV) is a phloem-restricted RNA virus species in the genus *Polerovirus* of the family *Luteoviridae*, which is either transmitted by aphids or propagated through plantation of sugarcane infected cuttings. Yellow leaf disease had emerged two decades ago in Guadeloupe where it was firmly identified for the first time in 1996. Since its introduction in Guadeloupe, the virus incidence has continuously increased throughout the island and has reached in 2010 levels of 20% in the commercial fields and 50 % in the sugarcane variety collection. While the genotype (REU) was initially over-dominant at the commercial field level (2005, 98%) two other genotypes (BRA-PER and CUB) were subsequently identified throughout the island. Interestingly, the incidence of the genotype CUB, which is the most aggressive SCYLV genotype, has tremendously increased the last decade (>85% in 2010). Additionally genotypes mixed infections were frequently observed at the variety level. However, intra-plant SCLYV population structure remains widely unknown, which hampers straightforward analyses of SCYLV microevolution.

MATERIAL and METHODS

We here use the virion-associated nucleic acids (VANA) metagenomics-based approach for estimating the genetic diversity of SCYLV in the sugarcane variety collection context in 2012. Leaf samples were randomly collected from 300 sugarcane varieties (1). The VANA-based 454 pyrosequencing approach was used to analyse individually the virome of each of the 300 sugarcane samples.

RESULTS

SCYLV-related reads were identified from 134 samples out of the 300 processed plant samples, which suggest an overall SCYLV prevalence of 45%, which is in full agreement with recent SCYLV prevalence studies. We focus on thirty-three sugarcane samples for which more than 400 SCYLV-related reads were obtained. For the thirty-three samples, based on the reads mapping into ORF1 and ORF3, we show that 12 varieties are infected by the SCYLV genotype REU, 11 varieties by genotype BRA-PER and 4 varieties by the genotype CUB. We also find that 4 varieties are co-infected by two genotypes (CUB/REU) and, unexpectedly, that 2 varieties, namely ROC7 and PR1059 are infected by SCYLV chimeric variants that are assigned to CUB (ORF1) / REU (ORF3) genotypes and BRA-PER (ORF1) / REU (ORF3) genotypes, respectively. This result suggests the occurrence of recombination events between SCYLV genotypes. We further show that the chimeric variant obtained from the variety ROC7 results from a recombinant event, which may involve the transfer of the CP-RDT zone from a SCYLV REU isolate (minor parent) to a SCYLV CUB genome (major parent). We could also assembled scaffolds covering at least 80% of publicly available SCYLV genomes from 21 of the 33 varieties. Those 21 varieties are infected by a single genotype (3 CUB; 11 REU; 7 BRA-PER) and phylogenetic analyses reveal that all 21 SCYLV isolates unambiguously group within the SCYLV REU, BRA-PER and CUB phylogenetic clusters. Interestingly, the 3 CUB isolates are forming a subgroup within the CUB phylogenetic cluster.

CONCLUSIONS

Our results suggest that SCYLV has been locally evolving the last two decades, suggesting that the virus virulence can quickly evolve enabling SCYLV adaptation to local varieties and vector complex.

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