

1.5 Genotyping of *Sugarcane yellow leaf virus* in Colombia, Guadeloupe and Reunion

Abu Ahmad Y¹., Royer M¹., Costet L²., Daugrois J-H³., Lett J-M²., Victoria J.I.⁴ and Rott P¹.

¹UMR 385 AGRO.M-CIRAD-INRA, Biologie et Génétique des Interactions Plante-Parasite, TA 41/K, Campus International de Baillarguet, 34398 Montpellier Cedex 5, France; ²UMR CIRAD-Université de La Réunion, Peuplements Végétaux et Bioagresseurs en Milieu Tropical, Ligne Paradis, 97410 Saint-Pierre, La Réunion; ³CIRAD-CA, Station de Roujol, 97170 Petit Bourg, Guadeloupe; ⁴CENICAÑA, Calle 58 Norte No. 3BN-110, Cali, Valle, Colombia.

Recent genetic diversity studies suggested the existence of several genotypes of Sugarcane yellow leaf virus (SCYLV), the causal agent of yellow leaf of sugarcane. In order to identify and more precisely describe the genotypes of SCYLV, we sequenced the entire genome (six ORFs) of eight virus isolates from six geographical locations (Brazil, China, Colombia, Cuba, Peru, and Reunion). Four genotypes of SCYLV (BRA for Brazil, CUB for Cuba, PER for Peru and REU for Reunion) were identified based on phylogenetic analyses with the genome sequence of these eight isolates. Specific primer pairs were designed to identify the SCYLV genotypes by RT-PCR. A unique genome fragment was amplified from each genotype, with the exception of genotypes BRA and PER which are relatively close. The RT-PCR primers were then used to identify genotypes of SCYLV present in three different sugarcane growing locations: Colombia, Guadeloupe and Reunion. Out of 41 sugarcane leaf samples from Colombia, 15 were infected by genotype BRA/PER, 19 by genotype CUB and 7 by genotypes BRA/PER and CUB. Both genotypes were found in locally bred CC varieties and in foreign varieties, but incidence of genotype CUB (84%) was higher than incidence of genotype BRA/PER (44%) in the 10 CC varieties. Out of 64 samples from Guadeloupe, 12 were infected by genotype BRA/PER, 13 by genotype CUB, 37 by genotype REU and 2 by genotypes CUB and REU. The three genotypes were found in locally bred FR varieties and in foreign varieties. In the 15 FR varieties, incidence of genotypes BRA/PER, CUB and REU was 16%, 37% and 47%, respectively. Out of 51 samples from Reunion, 2 were infected by genotype BRA/PER, 29 by genotype REU and 20 by genotypes BRA/PER and REU. Only genotype REU was found in the 29 samples from the 4 locally bred R varieties. All samples infected by genotypes BRA/PER and REU (or only BRA/PER) were obtained from variety SP-716163. Several genotypes of SCYLV can therefore co-exist in a geographical location or within a plant. Genotypes REU and CUB were, however, not found in Colombia and Reunion, respectively. Genotypes BRA/PER and REU are both present in Reunion, but genotype BRA/PER (most likely imported from Brazil with variety SP71-6163 in 1987) has not, as of yet, spread on this island. Because sugarcane is the only known natural host of SCYLV, and because this plant species did not originate from Colombia, Guadeloupe or Reunion, the virus was imported into these locations from other contaminated sugarcane growing locations. The presence of several genotypes of SCYLV suggests different virus introductions and/or an evolution of the virus after its introduction into a new environment. The biological significance of these SCYLV genotypes remains to be determined.