Proceedings of the 11th International Plant Virus Epidemiology Symposium and 3rd Workshop of the Plant Virus Ecology Network, 20-24 June 2010, Cornell University, Ithaca, NY, USA. http://www.isppweb.org/ICPVE/

Variation in sugarcane cultivar host range of *Sugarcane yellow leaf virus* genotypes in Guadeloupe

Daugrois¹ Jean Heinrich, Debibakas¹ Sarah, Fernandez² Emmanuel, Girard² Jean-Claude and Rott² Philippe.

¹UPR 75 Amélioration génétique d'espèces à multiplication végétative, CIRAD Département BIOS, Station de Roujol, 97170 Petit-Bourg, Guadeloupe F.W.I.; ²UMR BGPI, CIRAD – TA A-54/K, Campus international de Baillarguet, 34398 Montpellier Cedex 5, France.

Corresponding author: Daugrois J. H., e-mail address: jean-heinrich.daugrois@cirad.fr

Yellow leaf is a widely spread disease of sugarcane that can cause yield losses in susceptible cultivars. This disease is caused by Sugarcane yellow leaf virus (SCYLV) which belongs to the genus Polerovirus (Luteoviridae family). Five different SCYLV genotypes have been described and three of these were found in Guadeloupe (genotypes BRA-PER, CUB and REU). Additionally, variation in infection capacity and virulence exists among SCYLV genotypes. In order to investigate the cultivar host range of SCYLV genotypes occurring in Guadeloupe, we explored the capacity of genotypes BRA-PER, CUB and REU to infect different sets of sugarcane cultivars. A first experiment was performed with 30 cultivars from a breeding plot (non-replicated design). Four leaves were sampled per cultivar, bulked and processed for identification of virus genotype by RT-PCR. A second experiment was performed with 25 cultivars from a core collection of 200 accessions (experimental design with three replications). Ten leaves were sampled per accession and per replication, bulked and processed for identification of virus genotype by RT-PCR. The breeding plot and the core collection were both located at CIRAD's research station in Guadeloupe where disease pressure was high. In both experiments, SCYLV genotypes CUB and REU were found in a larger number of cultivars than genotype BRA-PER. In the second experiment, genotype CUB was present in all SCYLV-infected cultivars and was therefore the virus genotype with the largest cultivar host range. This genotype appears to have the propensity to infect all sugarcane cultivars infected by genotypes BRA-PER and REU. Additionally, cultivar host range varied to some extent between genotypes BRA-PER and REU, suggesting the occurrence of host-ranges specific to these SCYLV genotypes. Variation in sugarcane cultivar host range between SCYLV genotypes may explain, at least in part, the variations in SCYLV incidence and epidemics reported in different sugarcane growing locations.