

Identification and Determination of Genetic Variation of the Causal Agent of Sugarcane White Leaf Disease in Sri Lanka

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Sugarcane White Leaf (SCWL) is a highly destructive disease of sugarcane plantations in Sri Lanka and it is caused by phytoplasma. The present study was conducted to confirm the identity of SCWL and determine possible genetic variations among them. To this end, leaf samples were collected from ratoon and plant crops showing typical symptoms at Uda Walawe, Sevanagala, Siyambalanduwa, Pelwaththa and Hingurana. Genomic DNA was extracted from 42 symptomatic samples and subjected to direct PCR using SCWL specific primers, SPP1 and SPP2. PCR products were sequenced and homology search was performed. Construction of phylogenetic tree was done by Maximum Likelihood method using Mega 7.0.14 software, targeting the amplified 16S rRNA gene sequence (321 bp) of the pathogen and other reference SCWL sequences in NCBI GenBank. Homology search identified the pathogen as a member of 16Sr XI Rice yellow dwarf phytoplasma group. Eighty one percent of the samples had the highest homology with sugarcane white leaf phytoplasma isolate XM7S-China (MK028619) with a 98-100 % identity and 84-94 % query cover. Seven percent of the studied isolates gave the highest homology with sugarcane white leaf phytoplasma isolate XM7S-China (MK028618) with a 100 % identity and 91-92 % query cover. Another 5 % of the samples were best matched with Sugarcane white leaf Phytoplasma isolate XM7S-India (MH688459) with a 97 % identity and 85 % query cover. Five percent gave the best match with SCWL phytoplasma isolate XM7S Thailand (KT270948) with a 98 % identity and 93-94 % query cover. The rest, 2 percent, gave the highest homology to SCWL phytoplasma isolate XM7S-India (JN967902) with a 99 % identity and 90 % query cover. Phylogenetic tree revealed a distinct genetic divergence of two phytoplasma isolates obtained from Siyambalanduwa (SI SL 87 219 and SI SL HOSG 12 58) from the rest.

Keywords: Genomic variation, Homology, NCBI -BLAST, Phylogenetic tree

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