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ISOLATION AND COMPARATIVE ANALYSIS OF PotC GENE OF THE ABC-TRANSPORT SYSTEM FROM COCONUT ROOT WILT AND SUGARCANE GRASSY SHOOT (16SrXI GROUP) PHYTOPLASMAS

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Abstract

Root wilt disease of coconut and grassy shoot diseases of sugarcane are diseases associated with phytoplasmas of the 16SrXI group. The present study aimed at characterizing and comparing the potC gene of the coconut root wilt (RWD) and sugarcane grassy shoot (SCGS) phytoplasmas with that of aster yellows (AY) phytoplasma. We isolated the full length potC gene of ATP-Binding Cassette (ABC) transport system from RWD, SCGS, AY phytoplasmas and a partial gene segment of Brinjal little leaf (BLL) phytoplasma using PCR. The full length potC gene, partial sequence of potB and potD genes were sequenced and characterized. Comparative molecular analysis of the potC gene from RWD, SCGS showed that both sequences had 99% nucleotide identity with each other and 70% with AY phytoplasma. Phylogenetic analysis revealed that the potC gene of coconut and sugarcane phytoplasmas clustered together and that AY phytoplasma clustered with 16SrI group phytoplasmas. The phylogeny of potC genes followed the 16S rRNA-based taxonomic classification of phytoplasmas so that it can be considered as a potential candidate for phylogenetic studies. Bioinformatics analysis of putative PotC proteins revealed that phytoplasmas have conserved motifs which are absent in other bacteria. However, the PotC proteins of phytoplasma and bacteria have one common domain (ABC transporter intergral membrane type-1 domain) and six transmembrane helices.

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