

First Report of a 16SrIV Group Phytoplasma Associated with Declining Coyol Palms in Honduras

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Lethal yellowing (LY) of coconut palm (*Cocos nucifera* L.) caused by a subgroup 16SrIV-A phytoplasma has been present along the northern coast and adjacent Bay Islands of Honduras since 1996. In the southern municipalities of San Esteban and Guanaco, approximately 150 km from the Atlantic coast, substantial numbers of coyol palm (*Acrocomia aculeata* (Jacq.) Lodd. ex Mart.) and several coconut palms growing nearby were either dead or in an advanced stage of decline during 2005. Declining palms of both species exhibited loss of fruit, withered inflorescences, and dried, discolored (grayish brown) leaves. Most or all leaves on declining palms had collapsed and hung downward around the stem. Samples (3 to 5 g) of tissue were excised from stems of 20 coyol and 2 coconut palms. DNA was extracted from each sample using a previously described protocol (2) and assayed for phytoplasma DNA using polymerase chain reaction (PCR) employing phytoplasma universal rRNA primer pair P1 (1) and P7 (4). A product of expected size (approximately 1.8 kb) was amplified from 12 of 20 diseased coyol palms, 2 of 2 diseased coconut palms and from DNA of a Florida-grown Chinese fan palm (*Livistona chinensis* (Jacq.) R. Br. ex Mart.) with LY symptoms included as a known positive control. Amplified P1/P7 products used in a nested PCR assay with 16SrIV-specific primer pair LY16Sf (2) and LY16Sr (5'-GCTTACGCA-GTTAGGCTGTC-3') yielded a product of approximately 1.39 kb. Neither primary nor nested PCRs generated a product from DNA of healthy coconut palm. Poor quality of tissues within stems of declining palms may have contributed to lack of amplification of any product from eight coyol samples. A reevaluation of DNA samples using PCR employing nonribosomal primer pair LYF1/LYR1, which specifically detects subgroup 16SrIV-A phytoplasmas (3), failed to amplify an expected 1-kb product from any palm

sample other than the LY positive control. Digestion of nested amplification products (1.39 kb) with AluI endonuclease and electrophoresis of digests through 8% polyacrylamide gels revealed the same three-fragment restriction pattern for all phytoplasmas detected in coyol and coconut palms. The pattern differed from the five-fragment profile of LY phytoplasma rDNA included for comparative purposes. These results indicate that coyol palm is a new phytoplasma host and that decline symptoms on coyol and adjacent coconuts were not a consequence of natural dispersion of subgroup 16SrIV-A phytoplasmas from the northern coast. The 16S rDNA sequences amplified from coyol palm decline (CPD) (GenBank Accession No. DQ321818) and coconut decline (CLDO) (GenBank Accession No. DQ321819) phytoplasmas were coidential and most similar (99.87%) to that of Yucatan coconut lethal decline (LDY), a known subgroup 16SrIV-B strain. This relationship was further supported by phylogenetic analysis of rDNA sequences. On the basis of these findings, we have tentatively concluded that strains CPD and CLDO represent new members of the coconut lethal yellows subgroup 16SrIV-B.

References:

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