

First Report of a Phytoplasma-Associated Leaf Yellowing Syndrome of Palma Jipi Plants in Southern México. I. Cordova and C. Oropeza, Centro de Investigación Científica de Yucatán, Apdo. Postal 87, 97310, Cordemex, Yuc. México; H. Almeyda, INIFAP/Universidad Autónoma de Nuevo León; N. A. Harrison, University of Florida, Fort Lauderdale Research and Education Center, Fort Lauderdale 33314-7799. Partial funding provided by CONACYT and CONACYT-SISIERRA. Plant Dis. 84:807, 2000; published on-line as D-2000-0503-03N, 2000. Accepted for publication 26 April 2000.

The palm-like monocot Palma Jipi (*Carludovica palmata*, Cyclanthaceae), from which Panama hats are traditionally made, is important to the rural economy of southern Mexico and other Latin American countries. A lethal decline of *C. palmata* plants was first recognized by farmers at Kalkini in the state of Campeche, Mexico, during 1994. Characterized by a progressive yellowing of successively younger leaves, affected plants died within a few weeks after the onset of this primary symptom. Annual losses estimated at 10% of the naturalized *C. palmata* population have since occurred in the vicinity of Kalkini, an area in which coconut lethal yellowing (LY) disease is also prevalent. The close proximity and superficially similar symptomatology of these two diseases suggested that both might share a common etiology. DNA samples were obtained from five diseased and five healthy *C. palmata* plants by small scale extraction of immature leaf bases and assessed for phytoplasma DNA by use of the polymerase chain reaction (PCR) at laboratories in Mérida, INIFAP/Universidad Autónoma de Nuevo León (Nuevo León) and the University of Florida (Fort Lauderdale). Samples from symptomatic plants consistently tested positive by PCR employing universal rRNA primers (P1/P7), which amplify a 1.8-kb phytoplasma rDNA product (4), and negative when LY-specific primers LYF1/LYR1 (1) or MMF/MMR (3) were used. No PCR products were evident when DNAs of symptomless plants were evaluated with these primer combinations. Fragment patterns resolved by 8% polyacrylamide gel electrophoresis of rDNA digested separately with either *AluI*, *BamHI*, *BstUI*, *DdeI*, *DraI*, *EcoRI*, *HaeIII*, *HhaI*, *HinfI*, *MspI*, *RsaI*, *Sau3AI*, *TaqI*, or *Tru9I* endonucleases revealed no differences between phytoplasma isolates associated with five *C. palmata* plants. Collectively, restriction fragment length polymorphism (RFLP) patterns generated with key enzymes *AluI*, *BamHI*, *DraI*, and *HaeIII* clearly differentiated the *C. palmata* yellows (CPY) phytoplasma from LY and other known phytoplasmas previously characterized by this means (2). A sequence homology of 99.21% between 16S rDNA of CPY (1,537 bp; GenBank accession, AF237615) and LY (1,524 bp; accession, U18747) indicated that these strains were very similar. This relationship was confirmed by phylogenetic analysis of 16S rDNA sequence, which placed both strains into the same phytoplasma subclade.

References: (1) N. A. Harrison et al. Plant Pathol. 43:998, 1994. (2) I.-M. Lee et al. Int. J. Syst. Bacteriol. 48:1153, 1998. (3) J. P. Martínez-Soriano et al. Rev. Mex. Fitopat. 12:75, 1994. (4) C. D. Smart et al. Appl. Environ. Microbiol. 62: 2988, 1996.