

First Report of the Causal Agent of Huanglongbing (“*Candidatus Liberibacter asiaticus*”) in Brazil. H. D. Coletta-Filho, M. L. P. N. Targon, M. A. Takita, J. D. De Negri, J. Pompeu, Jr., and M. A. Machado, Centro APTA Citros ‘Sylvio Moreira’, IAC, CP 04, 13490-970, Cordeiropolis, Sao Paulo, Brazil; A. M. do Amaral, Embrapa Recursos Geneticos e Biotecnologia, 70770-900, Brasilia, Brazil; and G. W. Muller, Universidade Estadual de Maringa, 87020-900, Parana, Brazil. Plant Dis. 88:1382, 2004; published on-line as D-2004-0922-01N, 2004. Accepted for publication 31 August 2004.

Huanglongbing (ex-greening) disease is one of the most serious diseases of citrus. It is caused by the phloem-limited, gram-negative bacterium “*Candidatus Liberibacter* spp.”. This bacterium is not well characterized mainly because it is still uncultured. There are two known strains, Asian (“*Candidatus Liberibacter asiaticus*”) and African (“*Candidatus Liberibacter africanus*”) that cause severe damage to citrus plants including twig dieback, decline, and death. Symptoms first appear as leaf mottling and chlorosis occurring in one shoot or sector of trees. Later, leaf symptoms resemble nutritional deficiencies (Zn, Ca, and N) that vary depending on the strains, with more severe symptoms caused by “*Ca. L. asiaticus*”. The Asian strains are transmitted by the Asian citrus psyllid (AsCP), *Diaphorina citri*, which is present in Brazil. The bacterium has been detected in citrus plants in many geographic locations including China, Japan, Thailand, India, the Philippines, the Arabian Peninsula, and Africa. In 2004, plants showing Huanglongbing symptoms were observed in the Araraquara County, a central region of the State of Sao Paulo, the largest citrus-producing area in Brazil. To verify the presence of “*Ca. L. spp.*” in these plants, leaf samples of sweet orange cvs. Hamlin and Valencia were used for DNA extraction and polymerase chain reaction amplification using the specific OI1 and Oi2c primers (1). Amplification of the 16S rDNA was positive for 2 (cvs. Hamlin and Valencia) of 10 analyzed plants. The amplified fragments were cloned and sequenced. The amplicons obtained from both plants showed the same sequence, which differed from “*Ca. L. africanus*”, utilized as the positive control in the amplification experiment (27 divergent bases in 1,160). The sequences were used for BLAST searches, and the results showed identities ranging from 94.71 to 100% with “*Ca. L. spp.*” sequences available at the National Center for Biotechnology Information database (on-line publication). The highest scores were obtained with “*Ca. L. asiaticus*” sequences. These analyses confirmed the presence of such agent in the State

of Sao Paulo. To our knowledge, this is the first report of “*Ca. L. asiaticus*” in Brazil as well as elsewhere in the Americas. The significance of this report relates to the potential damage that this pathogen could cause to the citrus industry in the largest citrus-producing country in the world. It remains unclear how and when the pathogen entered Brazil.

Reference: (1) S. Jagoueix et al. Mol. Cell Probes 10:43, 1996.