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The complete genome sequence of *Candidatus Liberibacter americanus*, a bacterium associated with Citrus Huanglongbing in Brazil

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We used PFGE followed by CsCl bisbenzamide centrifugation to obtain sufficient DNA for pyrosequencing of the *Ca. Liberibacter americanus* (Lam) strain “São Paulo” genome. The complete circular genomic DNA sequence of Lam is 1,195,201 bp, with an average GC content of 31.12%, somewhat lower than other *Liberibacter*s. There are 1,056 predicted Lam genes, with 1,002 encoding proteins, 9 encoding rRNA genes and 45 encoding tRNAs. The overall gene organization and structure of the Lam genome is more similar to Lso than to Las. There are 951 genes common to Lam, Lso and Las, 27 genes found in Lam and Lso but not Las, and only 8 genes common to Lam and Las but not found in Lso. Many pseudogenes or truncated genes were found among the unique genes of all 3 species. As with Las, two prophage were confirmed in Lam, with SP2 being 39,941 bp and SP1 being 16,398 bp in size; as in Las, the one that appears to replicate as an excision plasmid prophage carries putative lysogenic conversion genes, specifically peroxidases and a Type Vc secreted adhesin. These predicted peroxidases and adhesin were found in both Las and Lam, but appeared fragmentary or degenerated in Lso, indicating their potential for citrus host range determination. *Liberibacter* genomes seem to be under selective pressure to reduce GC% content and to lose unimportant genes. Although Lam have an outer membrane, most of the genes required for biosynthesis of lipopolysaccharide, which can trigger ROS production, are missing from the Lam genome.

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