1.3 Comparison of the *Ca. Liberibacter asiaticus* Genome with a Draft *Ca. L. americanus* Genome Reveals Similar Prophage with Likely Pathogenicity Factors

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Huanglongbing is a lethal disease of citrus caused by psyllid transmitted, phloem limited, \(\alpha\)-Proteobacteria: *Ca. L. asiaticus* (Las), *Ca. L. americanus* (Lam), and *Ca. L. africanus* (Laf). Genomic sequencing of curated Las strain UF506 revealed two largely homologous, circular phage genomes, SC1 and SC2, which were found tandemly integrated in the UF506 chromosome as prophages in all hosts tested. SC1 carried suspected lytic cycle genes, was found in lytic cycle DNA forms only *in planta*, and its genes were highly induced only *in planta* and particularly in periwinkle. Phage particles associated with Las were found in the phloem of infected periwinkles by transmission electron microscopy. SC2 appeared to lack lytic cycle genes and replicated as an excision plasmid in psyllids and *in planta*. SC2 encoded putative adhesin and peroxidase genes that had not previously been identified in Las and which may be involved in lysogenic conversion (pathogenicity). Shotgun sequencing of Lam strain São Paulo is ca. 98% complete, with a total of 1,203,790 bps of sequence in 355 contigs with average length of 3.4 kb to date. Lam has a high level of synteny with Las, including 80% of the likely proteins encoded by SC1 and SC2. Overall, DNA sequence similarity is surprisingly low. SC1 encodes one putative colicin and SC2 encodes a putative colicin immunity protein; neither has been found in Lam, which is being supplanted by Las as the predominant HLB species in Brazil. It is possible that Las colicin kills Lam, indicating a potential control strategy.

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