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Progress on Dissecting and Controlling the Citrus Huanglongbing Complex

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Citrus huanglongbing (HLB) is a century-old and emerging disease that impedes citrus production worldwide. ‘*Candidatus Liberibacter asiaticus*’ (Las) is the globally prevalent species of HLB bacteria. Here we describe our molecular characterizations of Las, and our newly-developed control methods for citrus HLB. From a genomics standpoint, we revealed Las has a significantly reduced genome (1.26Mb) and unique features adapted to its intracellular life style. Although the genome is small, Las contains at least two prophages that make up ca. 1/16 of the entire genome. Frequent recombination and reassortment of these prophages/phages may contribute to Las’s evolving diversity and plasticity. There are at least 9 different types of Las populations that may co-exist in a single infection, but some exist preferentially in different hosts and different geographical locations. Furthermore, different Las populations may account for titer variations, such as the extreme low titer of Las bacteria (detected by our qPCR method) from seed-transmitted citrus and infected *Murraya paniculata*. From a functional genomics standpoint, we revealed Las encodes a functional ATP translocase and acts as an “energy parasite”. To modulate host energy biosyntheses and/or defense responses, Las encodes two novel autotransporter proteins that target to mitochondria. To compete for the limited zinc nutrient, Las encodes a ZuABC high affinity zinc uptake system. To avoid host defense machinery, Las encodes a functional flagellin that slowly triggers the citrus basal defense response. Although HLB is extremely difficult to manage, our newly-developed thermotherapy and chemotherapy methods provide potential components of an integrated control strategy for this devastating disease. In addition to the molecular characterization of the Las bacterium and its responses to stress, we have also revealed the dynamics of the microbial community (over 7000 OTUs-“species”) in HLB-affected citrus plants and how the microbial community responds to antibiotic treatments and seasonal variations.