1.1 Genomic Comparisons of the Ca. Liberibacter asiaticus Chromosome with Other Members of the Rhizobiales

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Ca. Liberibacter asiaticus is a member of the Rhizobiales, as are the nitrogen fixing Sinorhizobium meliloti and Bradyrhizobium japonicum, the plant pathogen Agrobacterium tumefaciens, and the facultative intracellular mammalian pathogen Bartonella henselae. Comparisons of chromosomal gene content identified 52 clusters of conserved orthologous genes found in all five metabolically diverse species. The intracellular pathogens, Ca. Liberibacter asiaticus and Bartonella henselae, have drastically reduced genomes with low content of guanine and cytosine. The Ca. Liberibacter asiaticus genome has 319 coding sequences not found on the chromosomes of the other members of the Rhizobiales from a total of 1136 coding sequences. Ca. Liberibacter asiaticus has all 100 COGs previously found in all bacteria to support basic physiological functions, but also has representatives of 10 COGs that have been lost in other intracellular pathogens (Merhej et al., 2009) including a hemolysin, an ATP dependent Clp protease, an ABC transport permease, and a flagellar motor component. These COGS, as well as six proteins uniquely shared by Ca. Liberibacter asiaticus and Bartonella henselae, may condition host cells for intracellular colonization or facilitate transmission by insects. InvA, shared with Bartonella henselae and believed to prevent apoptosis of cells infected by Rickettsia prowazekii (Gaywee et al., 2002), is also present. Only two chromosomal protein encoding genes were uniquely shared by Ca. Liberibacter asiaticus and Agrobacterium tumefaciens, the other plant pathogen in the study. These genes may also be important to the host-pathogen interaction. Five and twelve chromosomal genes were uniquely shared between Ca. Liberibacter asiaticus and Sinorhizobium meliloti and Bradyrhizobium japonicum, respectively.

References
