

Characterization of a putative periplasmic cystine binding protein from *Candidatus Liberibacter asiaticus*

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The *Candidatus Liberibacter asiaticus* (CLAs), an unculturable Gram-negative α -proteobacterium, causes citrus greening or Huanglongbing disease which causes severe economic losses to citrus industries worldwide. One of the potential strategies to control this devastating disease could be to identify critical proteins and develop potential inhibitor molecules. ATP-binding cassette (ABC) transporters are known drug targets. The genome analysis of CLAs revealed the presence of two putative amino acid binding periplasmic receptors belonging to ABC transporter family. Among them, one is specific for cationic amino acid binding while the other resembles putative cystine binding protein. The present work reports the characterization of a putative periplasmic cystine-binding protein from *Candidatus Liberibacter asiaticus* (CLasTcyA). The sequence and crystal structures analysis, in ligand-bound states, revealed unique features of CLasTcyA as compared to related proteins. The analysis of substrate-binding pocket of CLasTcyA suggested a broad specificity and a completely different orientation of the bound substrates as compared to related structures. The open conformation for one of the two chains in asymmetric unit in Arg-bound structure revealed a limited open state (18.4°) for CLasTcyA as compared to open state of other related proteins (~60°). The dissociation constant of 1.26 μ M by SPR and 3.7 μ M by MST exhibited low affinity for the cystine. Our results suggested that CLasTcyA may have evolved to cater to specific needs for its survival in the host.