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Analyses of proteomic expression profiles and nutrient status of citrus plants in response to Huanglongbing

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Huanglongbing (HLB) is a highly devastating citrus disease and represents a major threat to the citrus industries in US. The etiology of HLB worldwide is associated with three insect-transmissible phloem-limited members of the bacterial group '*Candidatus Liberibacter spp.*', prevalently '*Candidatus Liberibacter asiaticus*' (Las). All citrus cultivars are susceptible to HLB. To better understand the physiological and molecular processes involved in host responses to Las, proteomic analyses via 2-DE and mass spectrometry as well as ICP spectroscopy analysis were employed to elucidate protein expression profiles in leaves of Las-infected grapefruit and lemon plants at presymptomatic and symptomatic stages of the disease. Las-mediated down-regulation of 56 proteins including those associated with photosynthesis, protein synthesis, and metabolism was correlated with significant reductions in the concentrations of Ca, Mg, Fe, Zn, Mn, and Cu, especially in symptomatic plants. Interestingly, Las-mediated up-regulation of 13 proteins including those associated with pathogen response, redox-homeostasis, and starch anabolism was correlated with an increase in K concentration in pre-symptomatic and symptomatic plants. Since starch synthase requires K for activation, this result highlights a coordinated accumulation of granule-bound starch synthase and K in Las-infected plants. Analysis of host responses to HLB provides new information concerning physiological and biochemical processes of citrus to HLB. Those proteins that are up regulated specifically in response to Las infection could be useful biomarkers to develop a host-based diagnostic tool for early detection of HLB-affected citrus plants.