The bacterial disease Huanglongbing (HLB) is one of the most serious threats to citrus production worldwide. Development of HLB-resistant or tolerant citrus cultivars is the most effective approach for long-term management of HLB. Recent studies showed that constitutive disease resistance (CDR) genes and miraculin genes have a potential role in citrus against HLB disease based on microarray, iTRAQ and meta-analysis of published reports. Based on Hidden Markov Model and BLAST searches, we have identified a total of 17 copies of CDR gene family members in two citrus genomes (nine in *Citrus clementina* and eight in *Citrus sinensis*). Similarly, we retrieved 66 miraculin gene related sequences from citrus genomes (33 in *C. clementina*, 17 in *C. sinensis* (USA) and 16 in *C. sinensis* (China). All the identified CDR and miraculin genes were further validated by conserved domain searching using CDD and Pfam databases and bootstrap neighbor-joining phylogenetic trees were created based on multiple alignments with Clustal X 2.0 and PHYML. Real-time PCR validation was done for selected CDR and miraculin genes on citrus varieties classified as HLB-susceptible ('Valencia', 'Cleopatra', 'Duncan' and 'Ruby Red') and HLB-tolerant (sour orange, 'US-897', 'US-802', 'US-812' and 'US-942'). Results showed up-regulation of some CDR (CDR-14 and CDR-15) and miraculin related (mir-3 and mir-6) genes in 'US-812', 'US-897', 'US-942', 'Cleopatra' and 'Duncan'. Down-regulation of most of these genes was noted in sour orange, 'Valencia', 'Ruby Red' and 'US-802'. These data bring new insight to the control of CDR and miraculin gene expression at the transcriptional level, which may provide clues for further functional characterization of these genes and genetic improvement of citrus for HLB resistance.
Where:
San Diego, CA

Abstract: Genome-wide Identification, Characterization and Expression...