Title Metabolomics for rapid identification of huanglongbing in orange trees and rapid detection of *Escherichia coli* o157:h7, *Salmonella typhimurium*, *Salmonella hartford*, and *Salmonella muenchen* in ground beef and chicken

Author Juan Manuel Cevallos-Cevallo

Citation Thesis, Doctor of Philosophy (Food Science and Human Nutrition), University of California. 148 pages. 2010.

Keywords beef; chicken

Abstract

Rapid and reliable detection methods are of critical importance in preventing the spread of both plant diseases and foodborne pathogens. Citrus Huanglongbing (HLB) is the most destructive disease of citrus worldwide. Metabolomic techniques based on extraction, separation, and quantification methods were developed to find potential HLB biomarkers in leaves from „Valenc ia" orange trees from commerc ial groves. Flavonoids and the ir derivatives such as naringenin, hesperidin, and quercetin, as well as the amino acid L-proline were significantly ($P < 0.05$) up-regulated in HLB-infected trees. Conversely, sesquiterpenes β-elemene, (-)transcaryophyllene , and α-humulene were significantly down-regulated in HLB samples when compared to healthy and zinc deficient trees. Foodborne pathogens were also studied using metabolomic techniques. *Escherichia coli* O157:H7, *Salmonella* Hartford, *Salmonella* Typhimurium, and *Salmonella* Muenchen were grown in tryptic soy broth (TSB) at 37 °C followed by metabolite quantification at two-hour intervals for 24 h. Results were compared to the metabolite profile similarly obtained with *E. coli* K12, *Pseudomonas aeruginosa, Staphylococcus aureus, Saccharomyces cerevisiae,* and *Aspergillus oryzae* grown individually and as a cocktail under the same conditions described. Principal component analysis (PCA) achieved sample discrimination of the microorganisms grown in TSB. Metabolites responsible for PCA classification were dextrose, cadaverine, the aminoacids L-histidine, glycine, and L-tyrosine, as well as the volatiles 1-octanol, 1-propanol, 1butanol, 2-ethyl-1-hexanol, and 2,5-dimethyl-pyrazine. Partial least square (PLS) models based on the overall metabolite profile of each bacteria group were created to predict the presence of *E. coli* O157:H7 and *Salmonella* spp. in food samples. The models were tested in ground beef and chicken and were able to detect the presence of the pathogens at levels as low as 1 CFU/ g within 18 h.