World Congress on

MASS SPECTROMETRY AND ANALYTICAL TECHNIQUES September 19-20, 2018 Singapore

Metabolic analysis and transcriptomic response of *Escherichia coli* O157:H7 treated with electrolyzed water and mild heat

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Metabolite levels and gene expression in bacteria offer significant insights into the response of bacteria to disinfection intervention. The purpose of this study was to explore the possible mechanisms underlying the metabolic and transcriptomic changes of *Escherichia coli* O157:H7 in the response to Electrolyzed Water (EW) and mild heat treatments. The oxidant-sensitive probe 2', 7-Dichlorodihydrofluorescein Diacetate (H_2DCFDA) was used to assess the intracellular reactive oxidative species. The metabolomic changes were investigated by UPLC-QToF-MS coupled with multivariate analysis. EW (4 mg/L free available chlorine) combined with heat treatment at 50 °C resulted in 2.31 log CFU/mL reductions of *E. coli* O157:H7. The fluorescence intensity of EW at 50 °C showed the greatest and was 10 times greater than the control group. The decreased ribose-5-phosphate level strongly indicated affected nucleotide biosynthesis, which was consistent with nucleotide level in the E. coli O157:H7 cells in response to EW and heat treatments. A 50 fold increase in heat shock regulatory gene rpoH expression remained unchanged. However, when treated with EW at 50 °C almost all the gene expressions (except *rpoH*) were dampened with about 0.024-, 0.286- fold decrease for *udk* (encoding uridine kinase) and *gadA* (encoding glutamate decarboxylase alpha), respectively, as compared to control group. The results demonstrate a synergistic effect of EW and heat treatment on inactivating *E. coli* O157:H7.

Biography

Hongshun Yang has completed his PhD from the University of Minnesota and Postdoctoral studies from University of Maryland College Park. He has published more than 90 papers in reputed journals and has been serving as an Editorial Board Member of LWT-Food Science and Technology.

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