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Molecular characterization of enterohemorrhagic *Escherichia coli* O157:H7 in dairy foods and environments

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The entry route of foodborne pathogens including EHEC O157:H7 from the dairy farm environment into raw milk and dairy foods may come from several different vectors, and influence on the human health. Here, we employed HT-29 intestine epithelial cells (IECs; *in vitro*) and *C. elegans* (*in vivo*) as host model systems and compared the specific host responses during EHEC O157:H7 infections using whole transcriptome analysis. To elucidate the immune pathways stimulated by EHEC O157, we employed quantitative real time-polymerase chain reaction (qRT-PCR), transgenic worms, and RNAi. After EHEC O157:H7 infections, the regulation of gene encoding detoxification process, stress response, immune response and oxidative stress-associated proteins were immediately remodeled. Among them, we showed that the genes encoding cytochrome P450 (*CYP450*) family were dramatically induced by >10-fold during infection of EHEC O157:H7 is common in both host models. Importantly, *C. elegans* mutants lacking *CYP450* genes were highly susceptible to EHEC O157:H7 infections comparing to wild-type N2. Consistent with susceptibility tests, qRT-PCR results showed that *CYP450* loss of function mutations significantly affected the transcriptional induction of antimicrobial peptide genes such as *clec-60*. Taken in their totality our results provide critical insights for host strategy to exclude EHEC O157:H7 pathogenesis in gastrointestinal (GI) tracts through cytochrome P450 family.

Biography

Sang Don Ryu has great experience on detection and characterization of foodborne pathogens in food microbiology research. In recent, he focused on the prevalence and molecular pathway of various foodborne pathogens including *Listeria monocytogenes*, *Staphylococcus aureus*, *Camphylobacter jejuni*, *Salmonella typhumurium*, and pathogenic *E. coli* isolated from dairy foods and environments. Especially, his outstanding results may help monitor and control the spread of bacterial species through the farm environment, which is a natural reservoir for these organisms.

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