The Role of Flagella in Mediating Interactions Between *Salmonella enterica* and Red Leaf Lettuce

Emily Jackson & Anne Reid

Biology & Biomedical Sciences, Salve Regina University, Newport, RI

Salmonella enterica is a gram-negative bacterium that is the causative agent of Salmonellosis, the leading cause of hospitalizations due to foodborne illnesses in the United States. The objective of this research was to determine the role of flagellar components in attachment, colonization, and persistence of *S. enterica* on red leaf lettuce. Flagellar genes fliC (flagellin, phase 1), fljB (flagellin, phase 2), flgK (flagellar hook gene), and fliB (flagellin methyltransferase) were targeted for deletion in several *S. enterica* serovars using Lambda Red homologous recombineering and the expression levels of these genes were determined using qPCR. The deletion of these genes is expected to lead to loss of flagellin expression (one or both phases) or methylation, which we hypothesize will impair attachment, colonization, and/or persistence on red leaf lettuce. Antibiotic resistance cassettes were successfully amplified for all genes and transformed into *S. enterica* serovars expressing lambda red proteins by way of electroporation and recombinants were selected on media containing antibiotics. To date, putative deletion mutants in fliB, fliC, and flgK have been obtained for *S.* Typhimurium. While we have obtained antibiotic resistant clones, suggesting recombination of the cassette onto the chromosome, PCR amplification of the target region has not yielded expected products. As a result, these mutations have not yet been confirmed. Analysis of expression levels of the target genes under a range of growth conditions is currently underway. Lettuce adherence assays show significantly higher levels of attachment when serovars are grown in media with lower salinity. By understanding the role of the flagellar components in plant-bacterium interactions, strategies can be developed to interfere with these interactions and subsequently decrease the frequency of Salmonellosis cases worldwide.

This work was supported by RI INBRE