# Role of Flagellin Methylation in *Salmonella enterica*

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*Salmonella enterica* is the leading cause of hospitalizations due to foodborne illnesses in the United States. It is an important environmental health issue that can lead to costly multistate outbreaks. Lettuce is part of a healthy diet however these leafy greens have increasingly been associated with a higher risk of food poisoning. The bacterial flagellum has been implicated in motility, adhesion to surfaces and invasion of host cells. Flagellin methylation has been detected in *S.* Typhimurium, but the biological role of this post translational modification is unknown.

The goal of this study is to determine the role flagellin methylation plays in a range of serovars. It is expected that methylation levels will correlate with surface hydrophobicity, flagellin methyl-transferase (fliB) expression levels and enhanced interactions with plant and host cells. Flagellins were purified and subjected to Western blotting with an anti-methyl-lysine antibody, while Microbial Adhesion to Hydrocarbon (MATH) assays were performed to measure surface hydrophobicity of the cells. Western blotting revealed that flagellin methylation occurs in serovars Agona, Enteriditis, Montevido and Senftenberg and is not confined to *S.* Typhimurium. Serovar Agona expressed the highest methylation levels per mg of protein while serovar Montevido expressed the lowest methylation levels. This correlates with low surface hydrophobicity in *S.* Montevido, but does not correlate with surface hydrophobicity in *S.* Agona. Future research will focus on comparing methylation levels under a range of growth conditions such as Lennox and Low Salt plates, and using qPCR to determine levels of fliB expression under these conditions.

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