Characterizing phage encoded DNA methyltransferases of enterohemorrhagic *Escherichia coli* (EHEC)

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Enterohemorrhagic *Escherichia coli* (EHEC) are a subset of diarrheagenic *E. coli* that are often associated with severe bloody diarrhea or hemorrhagic colitis, which can also result in the potentially life-threatening sequelae hemolytic uremic syndrome (HUS) particularly in young children. Many of the critical virulence factors of EHECs, including Shiga toxin, are encoded by genes within prophages in the *E. coli* genome. Numerous other important genes are commonly encoded within prophages in *E. coli* genomes including DNA methyltransferases. These enzymes methylate the DNA of the host bacteria at specific sites or DNA sequences and are often part of restriction-modification systems that protect the host against bacteriophages. However, DNA methylation in bacteria has also been shown to be an important regulatory factor for numerous different types of genes, and in pathogenic *E. coli* that has included regulating the expression of certain virulence genes. In this study, we aim to assess the effects of various bacteriophage encoded methyltransferases on the methylome of EHEC strains. We will also assess any resulting phenotype changes to better understand the role bacteriophage encoded methylases have on EHEC pathogenesis, environmental adaptation, and overall physiology. We have induced lysogenic bacteriophages out of *E. coli* O157:H7 strain EDL933, which is computationally predicted to have at least eleven intact prophages in its genome and at least seven that may be intact. We are currently classifying those that are released and capable of transducing into other strains of *E. coli* including other serotypes of EHEC. Upon confirmation of transduction into additional *E. coli* strains with bacteriophages that encode DNA methylases, we will assess alterations to the methylome, transcriptome, and overall phenotype of the recipient *E. coli* strains.