Title:

Isolation and genome characterization of a novel lytic bacteriophage against non-O157 Shiga toxin-producing *Escherichia* coli

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Abstract:

Foodborne pathogens continue to burden our economy and society with illness. Pathogenic *Escherichia coli* is a global foodborne pathogen that is a threat for public health worldwide. Shiga toxin producing *E. coli* (STEC) strains account for over 2.8 million cases of acute gastrointestinal illness worldwide. In Canada, *E*. *coli* O157 strains cause an estimated 12,827 cases of foodborne illness each year. Interestingly, around 15% of these cases develop hemolytic uremic syndrome (HUS) which leads to higher mortality rates in susceptible populations. The rise of antimicrobial resistance suggests a need for novel solutions to mitigate the risk of these strains throughout the food production chain. Recently, lytic bacterial viruses (bacteriophages) have been envisioned as natural biocontrol tools to control the growth of various foodborne pathogens including pathogenic *E. coli*. Hence, the main objective of this study was to identify and characterize different lytic bacteriophages against STEC and apply these phages to enhance the food safety. Here, we present a novel phage, *Escherichia* phage vB_EcoM_4HA13 (4HA13), isolated against one of the top six non-O157 Shiga toxin producing E. coli (O111:NM) from Guelph wastewater. Transmission Electron Microscopy (TEM) imaging revealed 4HA13 to have an icosahedral head and contractile tail, characteristic of the Myoviridae family. However, genomic analyses have suggested 4HA13 to be a new species potentially belonging to a novel phage family - its closest homologue being Erwinia phage Faustus (%identity=77.7%). This was supported by phylogenetic trees using the phage's RNA polymerase and large terminase subunit. No lysogenic or virulence encoding genes were

identified in 4HA13 phage genome. Further characterization have shown this phage is able to inhibit E. coli O111:NM growth for 20 hours at MOI of around 1. Future direction of this project includes the proteomic analysis of the phage protein and biocontrol efficacy against different STEC strain for food applications.