Isolation of wild-type *Salmonella* and *Escherichia coli* bacteriophage

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Salmonella enterica is a leading cause of bacterial food borne illnesses in humans, and cattle are an important reservoir for these organisms. *S. enterica* includes over 2,200 defined serovars, but within cattle populations we usually find that a single serovar is overrepresented at a regional scale. Over time this dominant serovar changes but the mechanism driving this change has not been identified. We hypothesize that bacteriophage play an important role in structuring the distribution of *S. enterica* serovars. If correct, then we predict that at a smaller spatial and temporal scale bacteriophage play a role in limiting salmonellosis outbreaks on dairies. To test this hypothesis we adapted published protocols for plaque assays with and without overnight bacteriophage "amplification" with their respective host strains. We had good success detecting *E. coli* bacteriophage from farm fecal and water samples without phage amplification, but *Salmonella* bacteriophage were only detected when amplified overnight with their corresponding host serovar. The next step in this study is to determine the presence and quantity of *Salmonella* bacteriophage during a *Salmonella* epizootic. For this application, pooled fecal samples are recommended. Quantification may be possible by using dilutions of fecal samples prior to overnight amplification.