

## BEEF INDUSTRY SAFETY SUMMIT

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**Project Title:** Prevalence and Identification of *Salmonella* Bacteriophages in the Beef Feedlot Environment

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**Objective:** Identify and isolate bacteriophages against *Salmonella* from beef cattle feedlots that have varying *Salmonella* prevalence and perform characterization of the recovered phages. This will help determine what role phages may play in the ecology of *Salmonella* in the feedlot environment.

### **Experimental Design & Analysis:**

Thirty-six pooled samples representing feed, soil, water and feces were collected from south Texas beef feedlots and enriched for phage recovery using a mixed-host method with two sets of five *Salmonella* strains of varying serotypes. Enrichments were plated to each strain individually to determine the presence or absence of phage. The initial enrichment set included previously-isolated *Salmonella* strains, while the second set was conducted using *Salmonella* strains isolated from the same feedlot samples used for enrichment. These enrichments were pooled by pen to create 12 samples that were re-enriched as above, and individual phages were isolated on the enrichment host strains. Restriction digestion was performed on phage genomic DNA to determine the relatedness of the phages in the collection. Unique phages were tested for their host range against a diverse panel of 20 *Salmonella* strains representing 12 serotypes.

### **Key Results:**

In the initial 36-sample enrichment, all samples containing phages active against the well-characterized laboratory *S. Typhimurium* strain LT2, and 34 of 36 (94%) contained phages active against a MDR *S. Newport* strain. *S. Montevideo* and *S. Anatum* representatives were least sensitive to phages in feedlot samples (16 and 10 samples, respectively). Phage-positive samples were distributed evenly over the three sampled feedlot sites, suggesting that phage prevalence is not strongly correlated with the presence of culturable *Salmonella*. In the second round of phage detection, which used *Salmonella* isolates obtained from feedlot samples, phages were detected far less frequently, with only 12 of 36 samples yielding detectable phages upon enrichment. Phages active against *S. Montevideo* and *S. Anatum* were found most frequently (six samples each), with five samples positive for *S. Muenchen*, four for *S. Newport* and three for *S. Kentucky*. Twenty-nine phage isolates were collected from feedlot environmental samples; following restriction analysis, 18 unique bacteriophages, comprised of 14 distinct types and 4 sub-types, were identified. Host ranges of the phages were highly variable, with the broadest host range phage infecting 16 of the 20 *Salmonella* strains tested. Phages with broadest

host ranges were able to infect beef cattle feedlot-related *Salmonella* strains *S. Anatum*, *S. Muenchen* and *S. Montevideo* as well as human disease-related serotypes including *S. Heidelberg*, *S. Dublin*, *S. Typhimurium*, *S. Kentucky*, *S. Enteritidis* and *S. Newport*. No single phage was able to infect all 20 *Salmonella* strains that were used in this host range experiment.

**Industry Application:**

Asymptomatic *Salmonella* carriage in beef cattle is a significant food safety concern and the beef feedlot environment is a reservoir of this pathogen. Bacteriophages found in the *Salmonella*-free feedlot suggests that phages might play a role in suppressing the *Salmonella* population in a feedlot environment; it could also indicate that endogenous phages may contribute to false-negative results in culture-based *Salmonella* detection. Some phages were able to infect a broad range of *Salmonella* serovars, giving them possible function as an intervention against *Salmonella* in feedlots.