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Project Title: Genomic Comparison of *Salmonella enterica* Serotypes Commonly Associated with Cattle and Beef – *Analysis of Variation in Virulence Potential*

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Objective: To create a *Salmonella* genomic DNA sequence resource for the purpose of characterizing differences in gene content and identification of DNA markers for rapid detection of virulent *Salmonella* strains. Further, to characterize the ability of *Salmonella* in this reference collection to grow using different kinds of nutrients, to form biofilms and to resist the action of quaternary ammonia and chlorine-based sanitizers.

Experimental Design & Analysis:

In the described study, 48 strains of *Salmonella*, 12 each of serotypes Anatum, Montevideo, Newport and Typhimurium, were characterized. These strains were isolated from various cattle sources (feces, hide, carcass surface, lymph nodes, trim and ground beef) as well as from human cases of salmonellosis. The genomes of all strains were fully sequenced using PacBio SMRT sequencing technology, *de novo* assembled, annotated and the resulting sequence data uploaded to the *Intrepid Bioinformatics* Portal. Strains in the assembled collection also were assessed for differences in nutrient utilization, sanitizer resistance and biofilm formation.

Key Results:

The results of this study demonstrate the extensive genetic diversity present among *Salmonella enterica* and support the notion that a spectrum exists within this genus, in which some strains are more able to illicit a virulence response in humans while others may be generally commensal with little impact on the human host. The sequence data collected lay the foundation for defining key genetic differences between virulent and potentially commensal *Salmonella*. These data will be instrumental in developing rapid tests for identifying *Salmonella* strains determined to be of concern.

Industry Application:

The creation of this *Salmonella* sequence data resource: 1) allows genomic differences between virulent and potentially commensal *Salmonella* strains to be determined, so that *Salmonella* strains that pose an increased risk to human health can be identified, and 2) will facilitate the identification of molecular targets for differentiating specific *Salmonella* strains, when present as contaminants of ground beef or trim.

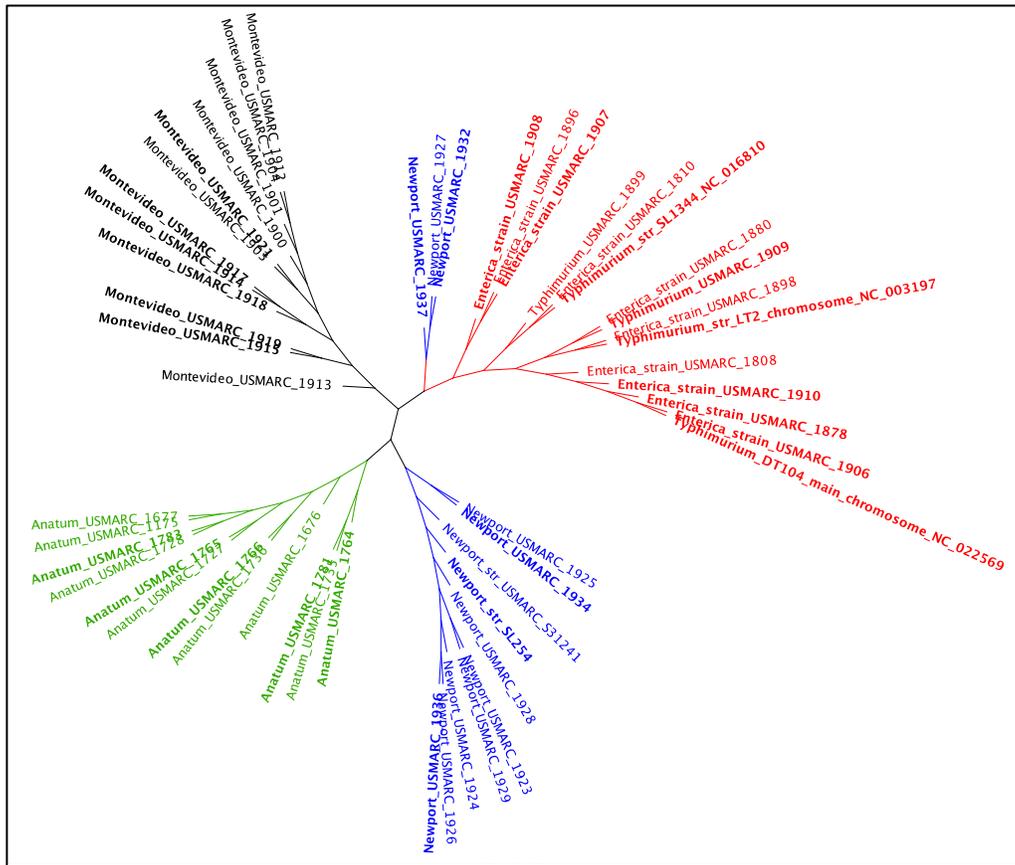


Figure 1. Phylogenetic tree based on whole genome sequence data from the 48 *Salmonella* strains characterized in this study, as well as *Salmonella* strains presently in GenBank, including *S. Newport* SL254, *S. Typhimurium* LT2, *S. Typhimurium* SL1344, and *S. Typhimurium* DT104 (NC_022569).