Salmonella enterica is an important pathogen, and serotyping has proved useful in understanding host specificity and its impact on the evolution of virulence. More than 2,500 serotypes of Salmonella enterica species have been identified using the Kauffman-White immunological classification scheme, which is based on somatic (O) and flagellar (H) antigens. The O antigen is determined by a capsular polysaccharide component, and currently 46 O serogroups of Salmonella are recognized. O antigens, which exhibit significant structural diversity due to variations in the carbohydrate backbone, are associated with the rfb gene cluster, which varies substantially between serotypes. Recently, rfb gene clusters of more than 2,500 Salmonella serogroups are available, including serogroups O:1, O:2, O:3, O:4, O:5, and O:6. To expand our knowledge of the rfb locus and to support DNA-based typing, whole-genome alignments were performed using the Mauve software to analyze the rfb region of 56 different Salmonella enterica serovars. The resulting alignments were used to identify differences in the biosynthesis of O-antigens, an important virulence factor, and to provide a framework for the development of new typing methods.

**MATERIALS AND METHODS**

Isolates: Sixteen Salmonella isolates were selected for whole genome sequencing. These isolates represent the serotypes Alph勞, Alibus, Gaminus, Giv, Hettling, Inverness, Jahnainen, Baltimore, Minnesota, Mississippi, Moscari, Rubilen, Senftenberg, Uganja, Urbana, and Windey (Table 1).

Genome sequencing and assembly: Genomes were sequenced using the Illumina (San Diego, CA) system (Applied Biosystems, Foster City). Paired-end libraries with approximate 150-bp inserts were constructed and deposited at the National Center for Biotechnology Information (NCBI). After culling errors in colorspace reads using a modified version of the CLC workbench tool (CLC bio), de novo assembly was performed using the SOAPdenovo2 de novo pipeline, which employs the Velvet assembly engine (Zerbino & Birney, 2008). scaffolds were aligned to two reference genomes (D. Typhimurium LT2 and E. Enteritidis) and consensus sequences were generated. Scaffolds that did not match the chromosome of the reference genomes considered to be putative plasmids or strain-specific transposable elements.

Whole genome alignment: Automated annotation was performed with the RAST server (Aziz et al., 2008) and whole genome alignments were performed using the Mauve Genome-Alignment Software (Darling et al., 2006).

**RESULTS AND DISCUSSION**

The rfb locus region is the primary determinant of O-antigen type, and is responsible for the development of robust, reliable typing methods. This analysis can contribute to understanding the pathogenesis of Salmonella enterica and to developing improved tools to track and characterize pathogens.

**REFERENCES**

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