Bacteriology-2013

OMICS Group Conferences
Accelerating Scientific Discovery

International Congress on
Bacteriology & Infectious Diseases

November 20-22, 2013 DoubleTree by Hilton Baltimore-BWI Airport, USA

Genome characteristics of a *Campylobacter jejuni* 63A isolated from california gull excreta

Jingrang Lu
U.S. EPA National Exposure Research Laboratory, USA

Campylobacter jejuni is not only a major cause of human gastroenteritis in western countries due to food and water contamination, but it is also associated some outbreaks of Guillain-Barre´syndrome (GBS). *C. jejuni* 63A was isolated from California gull excreta, which was in the meanwhile found to dominate in Sandhill crane (a migratory bird) excreta as well. The novel isolate is 99% identical to *C. jejuni* strain ICDCCJ07001, which was isolated from a GBS patient according to several gene sequences of *mapA*, *aspA, atpA, glnA, glyA* and *tkt*. The genome of 63A was sequenced with an Illumina HiSeq sequencing platform, assembled and compared with the strain ICDCCJ07001. It revealed that the 6A genome consisted of 1,697,260 base pairs (bp) with the GC content 30.47%. The virulence loci and virulence-associated genes evaluated were found to be 98-99% identical to the equivalent genes in ICDCCJ07001. Some sequence differences were found in 6A compared to ICDCCJ07001. For example, eight differences were observed in Invasion Antigen B, 22 were observed in *cadF*, and 12 were observed in surface-exposed lipoprotein (*jlp A*). Strain-specific assays of the 63A based on prophage similar sequences were designed, which could be used for some water fowl *C. jejuni* source tracking and further pathogenic animal model experiment.