JOURNAL OF BACTERIOLOGY, Jan. 2011, p. 583 Vol. 193, No. 2
0021-9193/11/$12.00 doi:10.1128/JB.01290-10

GENOME ANNOUNCEMENTS

Complete Genome Sequence of Adherent Invasive *Escherichia coli* UM146 Isolated from Ileal Crohn's Disease Biopsy Tissue▽

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Received 25 October 2010/Accepted 4 November 2010

***Escherichia coli* UM146 was isolated from the ileum of a Crohn's disease patient. It adheres to and invades enterocytes and can replicate inside macrophages. Its complete genome sequence reveals that it is most closely related to the human urinary tract pathogen *E. coli* CFT073, but it has a host of genes that are novel and to which no function has been ascribed.**

Adherent invasive *Escherichia coli* (AIEC) is associated with Crohn's disease (5, 6). It invades epithelial cells, survives in macrophages, occurs in 25 to 35% of patients, is present at first diagnosis and in pediatric patients, and is most closely related to the genome of the urinary tract pathogenic *E. coli* CFT073 (5, 6). These bacteria are distinct from other pathogenic *E. coli* strains because they do not produce the genes that are typically associated with pathogens like enterotoxigenic, enterohemorrhagic, enteroinvasive, enteroaggregative, and enteropathogenic *E. coli* (2). A distinguishing phenotype is that they do not cause diarrhea. The bacteria appear to adhere specifically to carcinoembryonic antigen-related cell adhesion molecules in humans via FimH, the terminal subunit of the type I pilus (4, 6, 7). These bacteria are not only found in humans but appear to be very similar to the same types of bacteria in cattle, mice, dogs (8), and poultry (1, 3).

We report the full genome sequence of AIEC strain UM146, the first being *E. coli* strain LF82 (5). *E. coli* UM146 is a highly invasive strain that was isolated from a Crohn's disease patient (4). Utilizing the Roche genome sequencer and titanium chemistry, a shotgun sequencing run on a 70-by-75 picotiter plate was conducted. Based upon initial assembly in DNAstar NGen, 66 final contigs representing an estimated 99.9% of the full genome were resolved. Annotation in RAST revealed 223 virulence factors, including 31 genes involved in adhesion, 43 genes involved in iron scavenging, 25 genes associated with type VI secretion systems, 31 genes involved in type IV secretion and conjugative transfer systems, 2 genes with a relationship to *Yersinia*-like quorum sensing, 4 biofilm poly-β-1,6-*N*-acetyl-D-glucosamine synthase biosynthesis genes, one accessory colonization factor, and 20 genes associated with Ton and Tol transport systems. Overall, this new *E. coli* isolate (UM146) had 39 predicted virulence factors not identified within the CFT073 genome, including a full complement of type IV secretion/conjugation systems, four resistance genes, several TonB and adhesion accessory proteins, heavy metal resistance factors, and a macrolide resistance factor. Conversely *E. coli* CFT0173 possesses nine virulence factors not found in the draft genome of UM146, including six genes involved in aerobactin siderophore biosynthesis. An abundance of phage genetic information, including what we hypothesize to be an intact lysogenic phage and large populations of mobile elements, suggests that this genome is highly plastic. *E. coli* CFT073 contains 73 genes not encoded by *E. coli* UM146, while the new genome encodes 118 genes not encoded by *E. coli* CFT073. Although UM146 and CFT073 are closely related, there are many genetic elements that distinguish these two bacteria. A significant observation is that UM146 has a range of resistance determinants that may help to explain the varied effectiveness in treating inflammatory bowel disease patients with antimicrobials. The resistance genotype also provided clues to potential therapies.

Nucleotide sequence submission numbers. The draft genome accession number for this organisms is available at GenBank with accession number CP002167. The accession number for the plasmid is CP002167.

This study was funded partly by the Natural Science and Engineering Council of Canada and the Crohn's and Colitis Foundation of Canada.

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▽ Published ahead of print on 12 November 2010.