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GENOME ANNOUNCEMENT

Genome Sequence of *Edwardsiella ictaluri* 93-146, a Strain Associated with a Natural Channel Catfish Outbreak of Enteric Septicemia of Catfish

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***Edwardsiella ictaluri* is the cause of extensive mortalities and economic losses to the channel catfish industry of the southeast United States. Here we report the complete genome of *Edwardsiella ictaluri* 93-146. Whole-genome sequence analysis of *E. ictaluri* provides a tool for understanding the genomic regions specific to the species and the *Edwardsiella* genus.**

Edwardsiella ictaluri, the causative agent of enteric septicemia of catfish (ESC), is a Gram-negative bacillus in the family *Enterobacteriaceae*. It was first reported from an epizootic in channel catfish on an Alabama farm in 1978 (3, 4) and has since become a major pathogen affecting the catfish industry. Two forms of ESC occur: acute disease that is characterized by hemorrhagic enteritis and septicemia and chronic disease that is characterized by meningoencephalitis (5, 6). Here we announce the availability of the complete genome of *E. ictaluri* 93-146, a wild-type isolate from a natural outbreak in Louisiana in 1993.

Two sets of *E. ictaluri* genomic DNA libraries were used for high-throughput shotgun sequencing: a random small-insert library (1 to 2 kb) constructed in pSmart (Lucigen Corporation, Middleton, WI) and a large-insert fosmid library constructed in pCC1FOS (Copy Control fosmid library construction kit; Epicentre Biotechnologies, Madison, WI). Clones were end sequenced to 8× coverage using fluorescent terminators (BigDye v3.1; Applied Biosystems, Foster City, CA) and universal primers (M13 forward and reverse). Reaction mixtures were analyzed on an ABI 3700 capillary sequencer (Applied Biosystems). Phred and Phrap were used for sequence processing and assembly (1, 2). A round of GS-20 454 pyrosequencing (454 Life Sciences, Roche, Branford, CT) was conducted (711,603 reads with an average length of 99 bp; approximately 19× coverage) at the Center for Comparative Genomics and Bioinformatics at Pennsylvania State University. 454 reads were assembled using Newbler (454 Life Sciences) and added to the Phrap assembly. Additional scaffolding was provided by paired-end GS-FLX 454 pyrosequencing (539,666 reads with an average length of 245 bp). Gap closure was accomplished through primer-walking plasmid and fosmid templates and direct sequencing of PCR amplicons. Assembled bases had Phred-equivalent quality scores of 40 or above, meaning that the level of accuracy was 99.99%. Automated gene predictions were made using the JCVI Annotation Engine pipeline (http://www.jcvi.org/cms/research/projects/annotation-service/overview/) followed by manual editing and curation in Manatee (http://manatee.sourceforge.net/).

The completed genome of *E. ictaluri* strain 93-146 is 3,812,315 bp in length and has a total of 3,783 predicted protein coding genes. Of these, 2,007 protein coding genes have functional predictions. Of the protein coding genes with no function predictions, 1,543 encode proteins with similarity to other bacterial proteins and 233 are unique. The sequence has an average G+C content of 57.4%, and it is approximately 84% coding. Strain 93-146 has eight ribosomal operons (7) and 94 tRNA genes. Analysis of the *E. ictaluri* genome sequence reveals many virulence mechanisms similar to those of other pathogens in the *Enterobacteriaceae*, including type III and probable type VI secretion systems, a twin-arginine translocation system, type 1 fimbriae, and multiple flagellins. Notably missing are siderophore biosynthesis genes, even though the genome possesses heme binding/transport genes. The genome contains >100 transposon/insertion sequence genes, which is surprising for a species with a single serotype and biochemical homogeneity.

Nucleotide sequence accession numbers. The complete manually annotated genome sequence of strain 93-146 is available as RefSeq NC_012779.1. The original draft genome sequence is available in GenBank under accession number CP001600.1.

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