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The genome sequence of a new strain of *Mycobacterium ulcerans* ecovar Liflandii, emerging as a sturgeon pathogen

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ABSTRACT

Mycobacterium ulcerans ecovar Liflandii (*Mu*Liflandii) is emerging as a non-mycobacterial pathogen in amphibians. Here, we make the first report on the prevalence of a new strain of *Mu*Liflandii infection in Chinese sturgeon. All the diseased fish showed the classic clinical symptoms of ascites and/or muscle ulceration. A new slow-growing and acid-fast bacillus ASM001 strain was obtained from the ascites of infected fish; this strain demonstrated pathogenicity when tested in hybrid sturgeon. The complete genome sequence of *Mu*Liflandii ASM001 is a circular chromosome of 6,167,296 bp, with a G+C content of 65.57%, containing 4,518 predicted coding DNA sequences and 999 pseudo-genes, 3 rRNA operons, and 47 transfer RNA sequences. In addition, we found 245 copies of IS2404, 34 microsatellites, and 36 CRISPR sequences in the whole *Mu*Liflandii ASM001 genome. Among the predicted genes of *Mu*Liflandii ASM001, we found orthologs of 203 virulence factors of clinical *Mu*Liflandii 128FXT operating in host cell invasion, modulation of phagocyte function, and survival inside the macrophages. These virulence factor candidates provide a key basis for understanding their pathogenic mechanisms at the molecular level. A comparative analysis that used complete, existing genomes showed that *Mu*Liflandii ASM001 has high synteny with

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