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GENOME ANNOUNCEMENTS

Genome Sequence of the Vertebrate Gut Symbiont *Lactobacillus reuteri* ATCC 53608▽

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***Lactobacillus reuteri*, inhabiting the gastrointestinal tracts of a range of vertebrates, is a true symbiont with effects established as beneficial to the host. Here we describe the draft genome of *L. reuteri* ATCC 53608, isolated from a pig. The genome sequence provides important insights into the evolutionary changes underlying host specialization.**

The Gram-positive bacterium *Lactobacillus reuteri* is an excellent model organism to study the evolutionary strategy of a vertebrate gut symbiont, as this species inhabits the gastrointestinal tracts of mammals as diverse as humans, pigs, mice, and rats, as well as different species of birds (11). Population genetics, using amplified fragment length polymorphism and multilocus sequence analysis; genomic; and experimental approaches using lactobacillus-free and germfree mouse models revealed that host-specific subpopulations exist among members of the species *L. reuteri* (9). Furthermore, several trials have shown that *L. reuteri* confers health benefits on humans and animals, and strains of this species have been shown to modulate the host immune system (11). Efforts to understand the mechanism by which *L. reuteri* strains have remained restricted to particular hosts are ongoing (5).

To further investigate the genomic basis for host adaptation of *L. reuteri* to the gut, we have determined the genome sequence of the pig isolate *L. reuteri* ATCC 53608 (8). Genomic DNA was isolated using a modified form of the method of Oh and colleagues (9) and used to generate in excess of 365 Mbp of sequence from a combination of shotgun and 3-kbp paired-end libraries (220 Mbp and 145 Mbp, respectively) on the 454 GS FLX sequencer (Roche) using the Titanium Chemistry. Reads passing the default filter settings were assembled using gsAssembly V2.3 software (Roche) and generated 13 scaffolds containing 99 large contigs (>500 bp) and spanning 1.96 Mbp of sequence. The genome of *L. reuteri* ATCC 53608 is 1,969,869 bp in length and has an average G+C content of 38.4%. Automatic gene prediction was performed using Glimmer3 and GeneMark software (2, 3). Annotation was transferred from the related strain *L. reuteri* JCM 1112^T. Unique regions were manually annotated using Artemis (10), augmented with InterPro (6), TMHMM (transmembrane prediction using hidden Markov models) (7), and SignalP domains (4). A total of 2,024 protein-coding sequences were predicted, with a coding percentage of 88.7%. The coding density was 1.03 genes per kb, with an average gene length of 863 bp. The genome contains six predicted copies of the rRNA genes. Comparative genomics of ATCC 53608 with genome sequence available for the *L. reuteri* 100-23 and DSM 20016^T/JCM 1112^T strains isolated from rats and humans (5), respectively, revealed approximately 500 ATCC 53608-specific genes, whereas 1,335 genes are present in all four strains. Genome analysis also revealed the presence of a putative prophage or plasmid of 137,391 bp with flanking resolvase/integrase and transposase genes. ATCC 53608 lacks the 10.2-kb native plasmid pLUL631 described in original isolate 1063 (1) but harbors one small plasmid of 9,003 bp. Detailed analysis of the assembled ATCC 53608 genome will help to predict the competitiveness of *L. reuteri* strains *in vivo* and to provide a context for the rational selection of probiotic strains.

Nucleotide sequence accession numbers. This genome sequencing project has been deposited at DDBJ/EMBL/GenBank under accession number CACS00000000. The version described in this paper is CACS02000000. The 138 contigs contained in the genome have been deposited under accession numbers CACS02000001 to CACS02000138. The 13 fully annotated scaffolds built from the contigs have been deposited under accession numbers FR854361 to FR854373.

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