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Draft Genome Sequence of Strain X47-2AL, a Feline *Helicobacter pylori* Isolate

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***Helicobacter pylori* is a human-specific pathogen that exclusively inhabits the human gastric mucosa. However, occasionally, humans transmit *H. pylori* to susceptible animal hosts bred in colonies. Here, we report the genome sequence of strain X47-2AL, isolated from a domestic cat and used in anti-*H. pylori* immunization studies.**

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Helicobacter pylori strain X47-2AL was first isolated in 1995 from a colony of domestic cats which presented clinical signs of gastritis (1). The natural isolation of *H. pylori* strains in domestic cats but not from wild cats indicated that these were acquired by transmission from humans to cats. This is reminiscent of the recent emergence of *Helicobacter acinonyx* in big wild cats, probably from an ancestral *Helicobacter pylori* human hpAfrica2 strain (2). The first vaccination trials against *H. pylori* using recombinant urease were challenged with strain X47-2AL (3, 4). In fact, the strain is able to colonize the mouse model with a clear tropism for the corpus, in striking contrast to the mouse-adapted strain SS1, which preferentially colonizes the antrum. This work showed experimentally for the first time that two distinct strains can co-colonize the same stomach by occupying distinct microniches (5). In addition, X47-2AL is highly transformable, with DNA fragments allowing for efficient mutagenesis, although this strain does not take plasmid DNA. The strain has a resident plasmid incompatible with the shuttle vectors derived from pHeL2 and pHeL3 (6, 7). Additionally, the strain is naturally resistant to metronidazole, precluding the use of the *rdxA* locus for complementation studies.

Here, we announce the draft genome of the *H. pylori* strain X47-2AL. Genomic DNA was extracted using a QIAamp DNA minikit (Qiagen) from an overnight culture grown on blood agar plates. Whole-genome sequencing was performed using an Illumina HiSeq 2000 sequencer, which generated 50-bp paired reads. Furthermore, a large insert library was also sequenced (3-kb mate pair). The sequencing was done by GATC Biotech using standard protocols per the manufacturer's instructions, which were followed during the sequencing process. The sequences (two million reads) were *de novo* assembled using the CLC Bio genomic suite with 78 contigs with an average length of 20 kb. The resulting contigs were subsequently scaffolded using a 3-kb mate pair library, to result in 63 contigs with an N_{50} of 53 kb and an average length of 25 kb. Contigs were submitted to the NCBI WGS submission portal and sequences were annotated using the NCBI Prokaryotic Genomes Automatic Annotation Pipeline (PGAAP) (http://www.ncbi.nlm.nih.gov/genomes/static/Pipeline.html). The genome comprises 1,495 coding sequences as well as a complete set of 36 tRNA and 3 rRNA (5S, 16S and 23S) coding loci. The average GC content of all contigs was 38.9%, which is identical to that of strain 26695 and very similar to the J99 (39.2%) and N6 (38.7%) genomes.

Nucleotide sequence accession numbers. This whole-genome shotgun project has been deposited at DDBJ/EMBL/GenBank under the accession number AWNG00000000. The version described in this paper is version AWNG01000000.

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