JOURNAL OF BACTERIOLOGY, Nov. 2010, p. 5846–5847 Vol. 192, No. 21
0021-9193/10/$12.00 doi:10.1128/JB.00867-10

Draft Genome Sequences of *Actinobacillus pleuropneumoniae* Serotypes 2 and 6[▽]

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Received 23 July 2010/Accepted 13 August 2010

Actinobacillus pleuropneumoniae **is a bacterial pathogen that causes highly contagious respiratory infection in pigs and has a serious impact on the production economy and animal welfare. As clear differences in virulence between serotypes have been observed, the genetic basis should be investigated at the genomic level. Here, we present the draft genome sequences of the *A. pleuropneumoniae* serotypes 2 (strain 4226) and 6 (strain Femo).**

Previous studies of different serotypes of *Actinobacillus pleuropneumoniae* showed that there are significant variations among them at the DNA sequence level, supposed to cause differences in pathogenicity and immunogenicity (2, 8). However, it is difficult to carry out more general studies of the immunity mechanisms of different serotypes, typing-based diagnosis, and multivalent genetically engineered vaccines due to the lack of complete genome sequences of the different serotypes (11).

Draft genome sequences of serotypes 2 and 6 were assembled by combining Roche 454-FLX reads with Illumina Genome Analyzer IIx paired-end reads. The final assembly (CLC-GenomicsWorkbench version 3.6, CLCbio) of the serotype 2 genome has a length of 2,314,315 bp (38 contigs), while the assembly of serotype 6 has a length of 2,375,501 bp (36 contigs). The average GC contents are 41.17% and 40.95% in serotypes 2 and 6, respectively, similar to those reported for other serotypes (1, 12). Using EasyGene (6, 9), 2,100 putative open reading frames were predicted for serotype 2 and 2,168 for serotype 6. Approximately 86% of the nucleotides were predicted to be involved in coding sequences, which is similar to results reported for other finished *A. pleuropneumoniae* genomes (1, 12). There are 86 and 136 genes found to be specific for serotypes 2 and 6, respectively, that do not have any homologue in other reported serotypes. rRNA genes were identified by RNAmmer (5). Serotype 2 harbors six rRNA operons (16S-23S-5S rRNA) and three additional 5S rRNA genes, while six rRNA operons and one additional 5S rRNA gene are present in serotype 6. Using the tRNAscan-SE server (7), 61 and 59 tRNA operons were predicted for serotypes 2 and 6, respectively.

Since porcine pleuropneumonia caused by *A. pleuropneumoniae* leads to large economic losses for the swine industry (3), it is of considerable interest to investigate the virulence factors of the different serotypes. We compiled a list of 105 known and putative virulence genes of *A. pleuropneumoniae* from published literature and performed a diversity study of these genes at the nucleotide level, comparing serotypes 2 and 6. Sixty-two conserved virulence genes (>99% identity or fewer than three mismatches) were found between these two serotypes, while 28 virulence genes showed a larger degree of dissimilarity (<95% identity or more than 20 mismatches), including candidates like the *apxIVA* gene encoding RTX toxin and the *cysI* gene encoding NADPH-sulfite reductase hemoprotein. Capsular polysaccharides (CPS) produced by *A. pleuropneumoniae* are considered to be important virulence factors (10). Investigation of CPS genes among different *A. pleuropneumoniae* serotypes, performed by Jessing et al. (4), was based mainly on partial sequences of CPS operons; here, the full-length sequences of CPS-related genes of serotypes 2 and 6 provide additional information for a better understanding of the role of this antigen.

The genomic sequences of *A. pleuropneumoniae* serotypes 2 and 6 have been included in the construction of a DNA microarray (Nimblegen, Roche) (Klitgaard et al., unpublished data), thus providing a valuable tool for transcriptional profiling studies and typing-based diagnostics.

Nucleotide sequence accession numbers. Genome sequences have been deposited in GenBank under the project identification number 49597 with accession number ADXN00000000 for *A. pleuropneumoniae* serotype 2 and under project identification number 49599 with accession number ADXO00000000 for *A. pleuropneumoniae* serotype 6.

This project was funded by the Danish Research Council for Technology 116 and Production Sciences (grant no. 274-07-0127) and, in part, by the Danish Strategic Research Council (Nabiit; grant no. 2106-07-0021).

We thank Pernille K. Andersen for managing the 454 sequencing and Kirstine K. Schou, Mette Boye, Kerstin Skovgaard, and Peter M. H. Heegaard for their comments on the manuscript.

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▽ Published ahead of print on 27 August 2010.

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