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GENOME ANNOUNCEMENT

Draft Genome Sequence of *Actinobacillus pleuropneumoniae* Serotype 7 Strain S-8

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The Gram-negative bacterium *Actinobacillus pleuropneumoniae* is the etiological agent of porcine pleuropneumonia, a respiratory disease that leads to severe economic losses in the swine industry. For years, scientists working with it have lacked a reliable genome sequence for comparison with other *Actinobacillus* species. Here, we report the draft genome sequence of *A. pleuropneumoniae* serotype 7 (strain S-8), isolated from swine lung in China in 1992.

Actinobacillus pleuropneumoniae is the major cause of porcine pleuropneumonia, a highly contagious respiratory disease that causes important economic losses to the swine industry worldwide (3). To date, 2 biotypes and 15 serotypes have been described (1). Although all serotypes can cause disease, differences in virulence exist (4). The virulence of the bacterium is mediated by the coordinated action of several virulence factors, namely, the capsule polysaccharides (CPS), outer membrane proteins (OMPs) involved in iron uptake, Apx toxins (ApxI to -IV), and lipopolysaccharide (LPS) (2).

Animals that survive natural or experimental infection with *A. pleuropneumoniae* develop immunity that protects them from future infections with homologous and heterologous serotypes; however, the antigens that confer such protection are still unknown (9). To date, a fully cross-protective, safe vaccine against all *A. pleuropneumoniae* serotypes has not been developed (4). Multiple genome sequences from different strains of a single species can offer comprehensive information to explore the relationship between genotypes and phenotypes and to discover additional genetic markers and universal vaccines for clinical purposes (12).

Here we report the draft genome sequence of *A. pleuropneumoniae* serotype 7 strain S-8, isolated from swine lung in China, 1992, and obtained using the Illumina HiSeq 2000 system with a paired-end library. The reads were assembled with the SOAPdenovo v1.05 software program. The draft genome sequence of *A. pleuropneumoniae* S-8 was annotated with the Prokaryotic Genomes Automatic Annotation pipeline (PGAAP) (8). In addition, the contigs were searched against the KEGG (7), UniProt (10), and Clusters of Orthologous Groups (COG) databases (11) to annotate the gene descriptions. The G+C mole percent values were calculated for the genome sequence.

In total, the draft genome includes 2,263,722 bases, with a G+C content of 41.18%, similar to values reported for other serotypes (12), and more than 100-fold genome coverage, consisting of 83 large contigs (>300 bp in size) and 2,157 predicted coding sequences (CDSs; 921 bp, average length) in the genome sequence. The coding percentage was 87.78%. With the tRNAscan-SE serve (6), 60 tRNA-encoding genes were predicted. rRNA genes were identified by RNAmmer (5), and four rRNA gene operons (16S-23S-5S) were predicted in the draft genome.

According to KEGG pathway analysis, most genes encoding proteins for carbohydrate or amino acid metabolism and environmental or and genetic information processing were successfully annotated. Compared to three other complete genomic sequences available online (for CP000569, CP000687, and CP001091), the pan-genome included 2,413 gene clusters; 1,826 core gene clusters were shared by all strains, and 104 unique genes were exclusive to S-8. Some reported and potential virulence factor genes were annotated from the draft genome sequence, which will allow a good chance to explore the mechanism of the pathogenesis of *A. pleuropneumoniae*. The genomic information will provide crucial clues for the development of genomic typing of *A. pleuropneumoniae* and new universal vaccines against the severe swine disease caused by this pathogen.

Nucleotide sequence accession numbers. The results of this whole-genome shotgun project have been deposited at DDBJ/EMBL/GenBank under the accession number ALYN00000000. The version described in this paper is the first version, ALYN01000000.

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REFERENCES

1. **Blackall PJ, Klaasen HL, van den Bosch H, Kuhnert P, Frey J.** 2002. Proposal of a new serovar of Actinobacillus pleuropneumoniae: serovar 15. Vet. Microbiol. **84**:47–52.
2. **Chiers K, De Waele T, Pasmans F, Ducatelle R, Haesebrouck F.** 2010. Virulence factors of Actinobacillus pleuropneumoniae involved in colonization, persistence and induction of lesions in its porcine host. Vet. Res. **41**:65.
3. **Dubreuil JD, Jacques M, Mittal KR, Gottschalk M.** 2000. Actinobacillus pleuropneumoniae surface polysaccharides: their role in diagnosis and immunogenicity. Anim. Health Res. Rev. **1**:73–93.
4. **Haesebrouck F, et al.** 2004. Efficacy of vaccines against bacterial diseases in swine: what can we expect? Vet. Microbiol. **100**:255–268.
5. **Lagesen K, et al.** 2007. RNAmmer: consistent and rapid annotation of ribosomal RNA genes. Nucleic Acids Res. **35**:3100–3108.
6. **Lowe TM, Eddy SR.** 1997. tRNAscan-SE: a program for improved detection of transfer RNA genes in genomic sequence. Nucleic Acids Res. **25**: 955–964.
7. **Ogata H, et al.** 1999. KEGG: Kyoto Encyclopedia of Genes and Genomes. Nucleic Acids Res. **27**:29–34.

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8. **Pruitt KD, Tatusova T, Klimke W, Maglott DR.** 2009. NCBI reference sequences: current status, policy and new initiatives. Nucleic Acids Res. **37**:D32–D36.
9. **Rycroft AN, Garside LH.** 2000. Actinobacillus species and their role in animal disease. Vet. J. **159**:18–36.
10. **Suzek BE, Huang H, McGarvey P, Mazumder R, Wu CH.** 2007. UniRef: comprehensive and non-redundant UniProt reference clusters. Bioinformatics **23**:1282–1288.
11. **Tatusov RL, et al.** 2003. The COG database: an updated version includes eukaryotes. BMC Bioinformatics **4**:41. doi:10.1186/1471-2105-3-41.
12. **Xu Z, et al.** 2010. Comparative genomic characterization of Actinobacillus pleuropneumoniae. J. Bacteriol. **192**:5625–5636.