

Complete Genome Sequence of *Streptococcus suis* Serotype 14 Strain JS14[∇]

Pan Hu,^{1†} Ming Yang,^{2,3†} Anding Zhang,¹ Jiayan Wu,² Bo Chen,¹ Yafeng Hua,¹
Jun Yu,² Jingfa Xiao,^{2*} and Meilin Jin^{1*}

Division of Animal Infectious Disease in the State Key Laboratory of Agricultural Microbiology, College of Veterinary Medicine, Huazhong Agricultural University, Wuhan 430070, People's Republic of China¹; CAS Key Laboratory of Genome Sciences and Information, Beijing Institute of Genomics, Chinese Academy of Sciences, Beijing 100029, People's Republic of China²; and Graduate University of Chinese Academy of Sciences, 100049 Beijing, People's Republic of China³

Received 17 January 2011/Accepted 28 February 2011

***Streptococcus suis* is an important zoonotic agent leading to a variety of diseases in swine and can be transmitted to human beings upon close contact. Here, we report the complete genome sequence of *S. suis* serotype 14 strain JS14 which was isolated from a diseased pig in Jiangsu Province, China.**

Streptococcus suis infections have been considered a major problem worldwide in the swine industry (10, 21). Thirty-three serotypes of *S. suis* have been described (types 1 to 31, 33, and 1/2), and in addition to serotype 2, serotype 14 has also been associated with severe infections in pigs and humans (11, 16). However, almost all studies have been conducted with serotype 2 strains and little is known about serotype 14. Thus, a pathogenic serotype 14 strain, JS14, which was isolated from articulation of a diseased pig in Jiangsu Province, China, was chosen for sequencing.

The complete genome sequence of *S. suis* strain JS14 was determined by Solexa pyrosequencing (653,741,120 Mb of 75-bp paired-end reads with an insertion size of 500 bp) at Beijing Institute of Genomics. Assembly was performed using SOAPdenovo. Gaps were closed by primer walking and sequencing of PCR products. Coding sequences (CDSs) were predicted using Glimmer 3.02 (7) and GeneMarkS (2) and compared with a nonredundant protein database to obtain descriptions. tRNAs and rRNAs were identified using tRNAscan-SE (14) and RNAmmer (13), respectively.

The genome of strain JS14 consists of a single circular chromosome which is 2,137,435 bp in length, with a GC content of 41.22%. There are 2,106 CDSs that account for 88.4% of the genome, 62 tRNAs, 4 rRNA loci, and 26 IS elements. Seventeen putative genome islands (GIs) were identified in the genome, two of which harbored a tetracycline resistance gene and a macrolide efflux gene, respectively, and resulted in resistance to tetracycline, erythromycin, and azithromycin. In addition, one prophage region was found and was specific to *S. suis* JS14 compared to serotype 2 strains. Besides those phage-

related genes, many other JS14-specific genes were found, and most of them were annotated as hypothetical proteins.

CPS has been considered to be essential for the virulence of the bacterium and to serve as an antigen to identify the serotype (5). Homologues of Cps2A, Cps2B, Cps2C, and Cps2D genes were also found in the *cps* locus of the JS14 genome, which indicated that these genes may play a common role in different serotypes (17). Overall, the *cps* locus in the JS14 genome showed strong similarity to that in serotype 1 strain identified earlier, which may explain why serotype-specific PCR method could not differentiate serotype 1 and serotype 14 (18). CDSs for a few virulence-associated factors, such as suislysin, extracellular protein factor, fibronectin/fibrinogen-binding protein (6), serum opacity-like factor (1), sortase A (15, 19, 20), peptidoglycan GlcNAc deacetylase (8), D-alanylated lipoteichoic acid (9), and subtilisin-like serine protease (3, 4, 12), which were confirmed to contribute to the virulence of serotype 2, were also found in the genome of JS14. Learning more about these factors would strengthen our understanding on the virulence of *S. suis* serotype 14. This determination of the complete genome sequence will promote the study of the pathogenesis of the infection and mechanisms of protection of *S. suis* serotype 14.

Nucleotide sequence accession number. The complete genome sequence of *S. suis* serotype 14 has been assigned GenBank accession number CP002465.

This study was supported by the National Major Program of Science & Technology (2008ZX10004-013, 2009ZX10602-14), the National Transgenic Major Program (2009ZX08009-141B), the Special Fund for Public Welfare Industry of Chinese Ministry of Agriculture (200803016), and the Innovative Research Team in University (IRT0726).

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* Corresponding author. Mailing address for Meilin Jin: Division of Animal Infectious Disease, State Key Laboratory of Agricultural Microbiology, Huazhong Agricultural University, Wuhan 430070, People's Republic of China. Phone: 86-27-87286905. Fax: 86-27-87282608. E-mail: jml8328@126.com. Mailing address for Jingfa Xiao: CAS Key Laboratory of Genome Sciences and Information, Beijing Institute of Genomics, Chinese Academy of Sciences, Beijing 100029, People's Republic of China. Phone: 86-10-82995384. Fax: 86-10-82995401. E-mail: xiaojingfa@big.ac.cn.

† The first two authors contributed equally to this work.

∇ Published ahead of print on 11 March 2011.

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