

Complete Genome Sequence of *Streptococcus pneumoniae* Serotype 19A, a Blood Clinical Isolate from Northeast Mexico

Antonio Ali Perez-Maya,^a Rosa Maria Hinojosa-Robles,^b Jose Ramon Barcenas-Walls,^c Armando Vignau-Cantu,^a Hugo A. Barrera-Saldaña,^a Rocio Ortiz-Lopez^{a,c}

Departamento de Bioquímica y Medicina Molecular, Facultad de Medicina, Universidad Autónoma de Nuevo León, Monterrey, Nuevo León, Mexico^a; Hospital Universitario Jose Eleuterio Gonzalez, Universidad Autónoma de Nuevo León, Monterrey, Nuevo León, Mexico^b; Unidad de Genómica; Universidad Autónoma de Nuevo León, Centro de Investigación y Desarrollo en Ciencias de la Salud, Monterrey, Nuevo León, Mexico^c

We report here the draft genome sequence of a *Streptococcus pneumoniae* strain isolated in Monterrey, Mexico, MTY1662SN214, from a man with purpura fulminans. The strain belongs to the invasive and multidrug-resistant serogroup 19A, sequence type 320 (ST320). The draft genome sequence consists of 60 large contigs, a total of 2,069,474 bp, and has a G+C content of 39.7%.

Received 12 February 2016 Accepted 18 February 2016 Published 31 March 2016

Citation Perez-Maya AA, Hinojosa-Robles RM, Barcenas-Walls JR, Vignau-Cantu A, Barrera-Saldaña HA, Ortiz-Lopez R. 2016. Complete genome sequence of *Streptococcus pneumoniae* serotype 19A, a blood clinical isolate from Northeast Mexico. *Genome Announc* 4(2):e00195-16. doi:10.1128/genomeA.00195-16.

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Address correspondence to Rocio Ortiz-Lopez, rortizlopez@gmail.com.

After the introduction of the 7-valent pneumococcal conjugate vaccine (PCV7) in the United States and other western countries, there was a significant reduction in the incidence of invasive pneumococcal disease (IPD) (1, 2). However, the number of cases of IPD, caused by *Streptococcus pneumoniae* serotypes not included in PCV7 (2, 3), increased. Particularly, the serotype 19A-sequence type 320 (ST320) has emerged worldwide as an important pathogen associated with IPD and multidrug resistance (MDR), but the causal factors remain unclear (4–6).

S. pneumoniae 19A ST320 has been implicated in both IPD and noninvasive pneumococcal disease (6). ST320 19A is a double-locus variant of the originally described Taiwan19F-14 (ST236) clone with high antibiotic resistance, which was isolated from a Taiwanese hospital in 1997. This strain underwent capsular modification, likely through recombination that altered the *wzy* polymerase gene and gave rise the serotype 19A-ST320 (7, 8).

S. pneumoniae strain MTY1662SN214 was isolated from a blood sample in 2014 at the Dr. José Eleuterio González University Hospital, Universidad Autónoma de Nuevo León (UANL), in Northeast Mexico. The patient was a 43-year-old male with purpura fulminans. The strain belonged to serotype 19A and ST320. Strain MTY1662SN214 was multidrug resistant, with resistance to penicillin, erythromycin, trimethoprim-sulfamethoxazole, tetracycline, quinolone, clindamycin, and cefotaxime (9).

The genome sequence was determined using Illumina MiSeq platform, which generated 487,316 total reads (483,492 reads after trimming) with an average length of 250 × 2 nucleotides (nt), providing about 25-fold genome coverage. *De novo* assemblies were performed by the SPAdes Genome Assembler version 3.5.0 software (10). The unclosed draft genome of MTY1662SN214 was assembled into 60 contigs (≥500 bp), with a total length of 2,069,474 bp and a G+C content of 39.7%.

In order to obtain a functional annotation of the genome, all the assembled contigs were annotated by NCBI Prokaryotic Genome Annotation Pipeline (11). The genome possesses a total of

2,221 genes, including 2,073 coding sequences (CDSs), 5 rRNAs (three copies of 5S, one copy of 16S, and one copy of 23S rRNA genes), 47 tRNAs, and 95 pseudogenes.

Nucleotide sequence accession numbers. This whole-genome shotgun project has been deposited at DDBJ/EMBL/GenBank under the accession no. [LKAA00000000](https://www.ncbi.nlm.nih.gov/nuclink/LKAA00000000). The version described in this paper is version LKAA01000000.

FUNDING INFORMATION

This research received no specific grant from any funding agency in the public, commercial, or not-for-profit sectors.

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