Acute phlegmonous gastritis is an uncommon endogenous bacterial gastritis presenting with a high mortality rate. Here, we report the complete genome sequence of an emm89 Streptococcus pyogenes strain, JMUB1235, which is the causative agent of acute phlegmonous gastritis.

Acute phlegmonous gastritis (APG) is a rare and rapidly progressive endogenous bacterial infection with high mortality (1). The most frequent causative bacteria of APG are hemolytic streptococci, particularly group A streptococci (GAS) (2, 3). GAS is a group of important human pathogens that causes a wide range of infections from local skin infections to life-threatening severe systemic diseases, including streptococcal toxic shock syndrome and necrotizing fasciitis. Accordingly, there have been many studies of GAS genomes relevant to the ordinary infections but none on whole-genome sequencing of the GAS strain that causes APG. Here, we report the whole-genome sequence of Streptococcus pyogenes strain JMUB1235 isolated from an APG patient in Jichi Medical University Hospital, Japan, in 2016.

Bacterial culture and DNA extraction were performed as previously described (4, 5). A mate-pair sequencing library from whole-genome DNA was prepared using the Nextera mate-pair sample preparation kit (Illumina, Inc., San Diego, CA, USA) with out-size selection. Sequencing was performed using the Illumina MiSeq platform (2 × 301 bp) with the MiSeq reagent kit version 3 (Illumina, Inc.), which generated 1,155,944 paired-end reads. After quality trimming using the FASTQ toolkit version 2.0.0 with a quality level of 30, a total of 1,055,944 high-quality reads were assembled with the Velvet de novo assembly version 1.2.10 algorithm into contigs and a scaffold. The resulting assembly comprised 21 contigs, 10 of which were linked to a 1,733,042-bp scaffold close to the expected size of the S. pyogenes genome. Ten persisting gaps were filled by gap-spanning PCR, followed by Sanger sequencing using an ABI3130xl genetic analyzer (Applied Biosystems, Carlsbad, CA, USA) to generate a single circular genome. Gene extraction and annotation were performed using the Microbial Genome Annotation Pipeline (http://www.migap.org).

S. pyogenes strain JMUB1235 harbors a single circular genome of 1,741,982 bp (G+C content, 39.2%) and no plasmid. A total of 1,717 coding sequences, 57 tRNA genes, and 15 rRNA genes were identified. JMUB1235 is an emm89 strain; it is increasingly recognized as a leading cause of the disease worldwide and is reportedly the dominant strain in the United Kingdom (6). The JMUB1235 lost hyaluronic acid capsular synthesize gene (hasABC) was similar to the most closely related genome of the M89 epidemic strain MGAAS27061, showing an acapsular phenotype (7). On the other hand, compared with MGAAS27061, JMUB1235 had polymorphisms in two membrane proteins (SclA and M protein), with amino acid identities of 78% and 87%, respectively, and carried an intact negative gene regulator, csrSR (synonym, conSR). In addition, two clustered regularly interspaced short palindromic repeat (CRISPR) candidates were identified in JMUB1235 using the CRISPR Finder tool (http://crispr.i2bc.paris-saclay.fr/). CRISPR-1 was identical in two strains, while the number of spacers in CRISPR-2 differed, occurring five and eight times in the genomes of JMUB1235 and MGAAS27061, respectively. Overall, the genome analysis of strain JMUB1235 can provide insight into understanding the pathological process of APG caused by GAS.

Accession number(s). The complete genome sequence of strain JMUB1235 has been deposited in the DDBJ GenBank under the accession number AP017629.

FUNDING INFORMATION
This work was supported in part by JSPS KAKENHI grant no. 15H05654 (to S.W.), the Takeda Science Foundation (to S.W.), and GSK Japan Research Grant 2015. The funders had no role in the study design, data collection and analysis, decision to publish, or preparation of the manuscript.

REFERENCES
1. Schultz MJ, van der Hulst RWM, Tytgat GNJ. 1996. Acute phlegmonous gastritis. Gastrointest Endosc 44:80–83. http://dx.doi.org/10.1016/S0016-5107(96)70236-5.
2. Miller AI, Smith B, Rogers AI. 1975. Phlegmonous gastritis. Gastroenterology 68:231–238.
3. Starr A, Wilson JM. 1957. Phlegmonous gastritis. Ann Surg 145:88–93. http://dx.doi.org/10.1097/00000658-195701000-00009.
4. Watanabe S, Kirikae T, Miyoshi-Akiyama T. 2013. Complete genome sequence of Streptococcus dysgalactiae subsp. equisimilis 167 carrying Lancefield group C antigen and comparative genomics of S. dysgalactiae subsp.

Acute phlegmonous gastritis is an uncommon endogenous bacterial gastritis presenting with a high mortality rate. Here, we report the complete genome sequence of an emm89 Streptococcus pyogenes strain, JMUB1235, which is the causative agent of acute phlegmonous gastritis.
equisimilis strains. Genome Biol Evol 5:1644–1651. http://dx.doi.org/10.1093/gbe/evt117.

5. Miyoshi-Akiyama T, Watanabe S, Kirikae T. 2012. Complete genome sequence of Streptococcus pyogenes M1 476, isolated from a patient with streptococcal toxic shock syndrome. J Bacteriol 194:5466. http://dx.doi.org/10.1128/JB.01265-12.

6. Turner CE, Abbott J, Lamagni T, Holden MT, David S, Jones MD, Game I, Efstratiou A, Sriskandan S. 2015. Emergence of a new highly successful acapsular group a streptococcus clade of genotype emm89 in the United Kingdom. mBio 6:e00622-15. http://dx.doi.org/10.1128/mBio.00622-15.

7. Beres SB, Kachroo P, Nasser W, Olsen RJ, Zhu L, Flores AR, de la Riva I, Paez-Mayorga J, Jimenez FE, Cantu C, Vuopio J, Jalava J, Kristinsson KG, Gottfredsson M, Corander J, Fittipaldi N, Di Luca MC, Petrelli D, Vitali LA, Rainford A, Jenkins L, Musser JM. 2016. Transcriptome remodeling contributes to epidemic disease caused by the human pathogen Streptococcus pyogenes. mBio 7:e00403-16. http://dx.doi.org/10.1128/mBio.00403-16.