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Draft Genome Sequence of Erythromycin-Resistant *Streptococcus gallolyticus* subsp. *gallolyticus* NTS 31106099 Isolated from a Patient with Infective Endocarditis and Colorectal Cancer

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***Streptococcus gallolyticus* subsp. *gallolyticus* is known for its close association with infective endocarditis and colorectal cancer in humans. Here, we report the draft genome sequence of highly erythromycin-resistant strain NTS 31106099 isolated from a patient with infective endocarditis and colorectal cancer.**

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Streptococcus gallolyticus subsp. *gallolyticus* (formerly *Streptococcus bovis* biotype I) is a common gut commensal in various animals and humans. However, the species is known for its ability to cause different diseases in birds and mammals as well as for its close association with infective endocarditis and colorectal cancer in humans (1–3). Despite the extensive research on this relationship, the underlying virulence features and pathomechanisms remain unclear (4, 5). Recommended antibiotic therapy for streptococcal endocarditis is a combination of penicillin and aminoglycoside. Although penicillin-resistant strains have not yet been isolated, resistances to kanamycin, streptomycin, and erythromycin have been reported and attributed to the presence of the genes *aph*(3′)-III, *ant*(6)-Ia, and *ermB*, respectively (6–8). Nevertheless, such resistance determinants were not identified in the available genomes of *S. gallolyticus* subsp. *gallolyticus* (9–13). We report the draft genome of highly erythromycin-resistant *S. gallolyticus* subsp. *gallolyticus* NTS 31106099 isolated from a patient with infective endocarditis and colorectal cancer.

S. gallolyticus subsp. *gallolyticus* NTS 31106099 was grown overnight at 37°C on Columbia agar supplemented with 5% horse blood (Oxoid, United Kingdom) in an atmosphere of 5% CO₂. Genomic DNA extraction was accomplished using a DNeasy blood and tissue kit (Qiagen GmbH, Germany) according to the manufacturer's recommendation. A sequencing library was prepared using Nextera XT (Illumina, USA) and sequenced using Illumina MiSeq (2 × 300 bp, pair-ends). A total of 10,190, 802 pair-end reads, corresponding to 2.1 Gb was used for *de novo* assembly in SPAdes 2.5.1 (14). Short and low-coverage contigs were filtered out, resulting in a set of 17 contigs between 857 and 583,716 bp with an average coverage of 235×. Annotation was performed by the NCBI Prokaryotic Genome Automatic Annotation Pipeline (PGAAP) (15). Reordering and comparisons were done using Mauve 2.3.1 (16), ACT 8 (17), and BLAST. Acquired

antibiotic resistance genes were identified using ResFinder 2.1 (18).

The final assembly has a total length of 2,311,421 bp, an N₅₀ of 226 kb, and a G+C content of 37.5%. Annotation revealed 2,198 coding sequences (CDS), 59 tRNAs, 38 pseudo genes, 6 rRNAs, and 1 noncoding RNA. Preliminary comparative analysis uncovered a 44.6-kb strain-specific island (JYKU01000013, UG96_07020-UG96_07300) inserted in a putative RNA methyltransferase gene (Gallo_1429 in UCN34 genome [10]). The element was predicted as a putative Tn916-like conjugative transposon and designated Tn6263, according to Roberts et al. (19). It contains about 50 CDS (involved in conjugal transfer, regulation, antibiotic resistance [*aph*(3′)-III (UG96_07105), *ant*(6)-Ia (UG96_07115), and *ermB* (UG96_07135)], and virulence. About 33% of Tn6263 shows 85% identity to CTn7 of *Clostridium difficile* (20). Interestingly, about 76% of the element is 99% identical to contig 36 of recently released draft genome of vancomycin-resistant *Enterococcus faecium* VRE3 (JSET01000036.1). Future studies will shed light on the functionality and prevalence of Tn6263.

The draft genome of *S. gallolyticus* subsp. *gallolyticus* NTS 31106099 will be used for identification of virulence features associated with colorectal cancer and infective endocarditis.

Nucleotide sequence accession numbers. The draft sequence of *S. gallolyticus* subsp. *gallolyticus* NTS 31106099 studied in this project has been deposited at DDBJ/EMBL/GenBank under the accession no. [JYKU00000000](https://www.ncbi.nlm.nih.gov/nuclseq/JYKU00000000/). The version described in this paper is JYKU01000000.

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REFERENCES

- Schlegel L, Grimont F, Ageron E, Grimont PA, Bouvet A, Grimont PAD, Bouvet A. 2003. Reappraisal of the taxonomy of the *Streptococcus bovis*/*Streptococcus equinus* complex and related species: description of *Streptococcus gallolyticus* subsp. *gallolyticus* subsp. nov., *S. gallolyticus* subsp. *macedonicus* subsp. nov. and *S. gallolyticus* subsp. *pasteurianus* subsp. nov. *Int J Syst Evol Microbiol* 53:631–645. <http://dx.doi.org/10.1099/ijs.0.02361-0>.
- Shibata Y, Tien LHT, Nomoto R, Osawa R. 2014. Development of a multilocus sequence typing scheme for *Streptococcus gallolyticus*. *Microbiology* 160:113–122. <http://dx.doi.org/10.1099/mic.0.071605-0>.
- Dumke J, Hinse D, Vollmer T, Knabbe C, Dreier J. 2014. Development and application of a multilocus sequence typing scheme for *Streptococcus gallolyticus* subsp. *gallolyticus*. *J Clin Microbiol* 52:2472–2478. <http://dx.doi.org/10.1128/JCM.03329-13>.
- Abdulmir AS, Hafidh RR, Abu Bakar F. 2011. The association of *Streptococcus bovis*/*gallolyticus* with colorectal tumors: the nature and the underlying mechanisms of its etiological role. *J Exp Clin Cancer Res* 30:11. <http://dx.doi.org/10.1186/1756-9966-30-11>.
- Boleij A, van Gelder MMHJ, Swinkels DW, Tjalsma H. 2011. Clinical importance of *Streptococcus gallolyticus* infection among colorectal cancer patients: systematic review and meta-analysis. *Clin Infect Dis* 53:870–878. <http://dx.doi.org/10.1093/cid/cir609>.
- Teng LJ, Hsueh PR, Ho SW, Luh KT. 2001. High prevalence of inducible erythromycin resistance among *Streptococcus bovis* isolates in Taiwan. *Antimicrob Agents Chemother* 45:3362–3365. <http://dx.doi.org/10.1128/AAC.45.12.3362-3365.2001>.
- Kimpe A, Decostere A, Martel A, Devriese LA, Haesebrouck F. 2003. Phenotypic and genetic characterization of resistance against macrolides and lincosamides in *Streptococcus gallolyticus* strains isolated from pigeons and humans. *Microb Drug Resist* 9(Suppl 1):S35–S38. <http://dx.doi.org/10.1089/107662903322541874>.
- Leclercq R, Huet C, Picherot M, Trieu-Cuot P, Poyart C. 2005. Genetic basis of antibiotic resistance in clinical isolates of *Streptococcus gallolyticus* (*Streptococcus bovis*). *Antimicrob Agents Chemother* 49:1646–1648. <http://dx.doi.org/10.1128/AAC.49.4.1646-1648.2005>.
- Sillanpää J, Nallapareddy SR, Qin X, Singh KV, Muzny DM, Kovar CL, Nazareth LV, Gibbs RA, Ferraro MJ, Steckelberg JM, Weinstock GM, Murray BE. 2009. A collagen-binding adhesion, Acb, and ten other putative MSCRAMM and pilus family proteins of *Streptococcus gallolyticus* subsp. *gallolyticus* (*Streptococcus bovis* group, biotype I). *J Bacteriol* 191:6643–6653. <http://dx.doi.org/10.1128/JB.00909-09>.
- Rusniok C, Couvé E, Da Cunha V, El Gana R, Zidane N, Bouchier C, Poyart C, Leclercq R, Trieu-Cuot P, Glaser P. 2010. Genome sequence of *Streptococcus gallolyticus*: insights into its adaptation to the bovine rumen and its ability to cause endocarditis. *J Bacteriol* 192:2266–2276. <http://dx.doi.org/10.1128/JB.01659-09>.
- Hinse D, Vollmer T, Rückert C, Blom J, Kalinowski J, Knabbe C, Dreier J. 2011. Complete genome and comparative analysis of *Streptococcus gallolyticus* subsp. *gallolyticus*, an emerging pathogen of infective endocarditis. *BMC Genomics* 12:400. <http://dx.doi.org/10.1186/1471-2164-12-400>.
- Lin IH, Liu TT, Teng YT, Wu HL, Liu YM, Wu KM, Chang CH, Hsu MT. 2011. Sequencing and comparative genome analysis of two pathogenic *Streptococcus gallolyticus* subspecies: genome plasticity, adaptation and virulence. *PLoS One* 6:e20519. <http://dx.doi.org/10.1371/journal.pone.0020519>.
- Romero-Hernández B, Tedim AP, Sánchez-Herrero JF, Librado P, Rozas J, Muñoz G, Baquero F, Cantón R, Del CR. 2015. *Streptococcus gallolyticus* subsp. *gallolyticus* from human and animal origins: genetic diversity, antimicrobial susceptibility, and characterization of a vancomycin-resistant calf isolate carrying a *vanA*-Tn1546-like element. *Antimicrob Agents Chemother* 59:2006–2015. <http://dx.doi.org/10.1128/AAC.04083-14>.
- Bankevich A, Nurk S, Antipov D, Gurevich AA, Dvorkin M, Kulikov AS, Lesin VM, Nikolenko SI, Pham S, Pribelski AD, Pyshkin AV, Sirotkin AV, Vyahhi N, Tesler G, Alekseyev MA, Pevzner PA. 2012. SPAdes: a new genome assembly algorithm and its applications to single-cell sequencing. *J Comput Biol* 19:455–477. <http://dx.doi.org/10.1089/cmb.2012.0021>.
- Angiuoli SV, Gussman A, Klimke W, Cochrane G, Field D, Garrity G, Kodira CD, Kyrpides N, Madupu R, Markowitz V, Tatusova T, Thomson N, White O. 2008. Toward an online repository of standard operating procedures (SOPs) for (meta)genomic annotation. *Omic* 12:137–141. <http://dx.doi.org/10.1089/omi.2008.0017>.
- Darling AE, Mau B, Perna NT. 2010. progressiveMauve: multiple genome alignment with gene gain, loss and rearrangement. *PLoS One* 5:e11147. <http://dx.doi.org/10.1371/journal.pone.0011147>.
- Carver TJ, Rutherford KM, Berriman M, Rajandream MA, Barrell BG, Parkhill J. 2005. ACT: the Artemis comparison tool. *Bioinformatics* 21:3422–3423. <http://dx.doi.org/10.1093/bioinformatics/bti553>.
- Zankari E, Hasman H, Cosentino S, Vestergaard M, Rasmussen S, Lund O, Aarestrup FM, Larsen MV. 2012. Identification of acquired antimicrobial resistance genes. *J Antimicrob Chemother* 67:2640–2644. <http://dx.doi.org/10.1093/jac/dks261>.
- Roberts AP, Chandler M, Courvalin P, Guédon G, Mullany P, Pembroke T, Rood JI, Smith CJ, Summers AO, Tsuda M, Berg DE. 2008. Revised nomenclature for transposable genetic elements. *Plasmid* 60:167–173. <http://dx.doi.org/10.1016/j.plasmid.2008.08.001>.
- Sebahia M, Wren BW, Mullany P, Fairweather NF, Minton N, Stabler R, Thomson NR, Roberts AP, Cerdeño-Tárraga AM, Wang H, Holden MTG, Wright A, Churcher C, Quail MA, Baker S, Bason N, Brooks K, Chillingworth T, Cronin A, Davis P, Dowd L, Fraser A, Feltwell T, Hance Z, Holroyd S, Jagels K, Moule S, Mungall K, Price C, Rabinowitsch E, Sharp S, Simmonds M, Stevens K, Unwin L, Whithead S, Dupuy B, Dougan G, Barrell B, Parkhill J. 2006. The multidrug-resistant human pathogen *Clostridium difficile* has a highly mobile, mosaic genome. *Nat Genet* 38:779–786. <http://dx.doi.org/10.1038/ng1830>.