



# Complete Genome Sequence of the *Streptococcus gallolyticus* subsp. *gallolyticus* Strain DSM 16831

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**ABSTRACT** *Streptococcus gallolyticus* subsp. *gallolyticus* DSM 16831 is an intriguing strain because of its low virulent phenotype compared to other isolates. We present here the complete genome sequence for this strain isolated from koala feces.

*Streptococcus gallolyticus* subsp. *gallolyticus* (formerly *S. bovis* biotype I) is a commensal of the human or animal gastrointestinal tract. In addition, it is a pathogen causing different diseases, especially infective endocarditis, septicemia, and meningitis (1–4). The *S. gallolyticus* subsp. *gallolyticus* strain DSM 16831, isolated from koala feces, is characterized by low virulence and shows additional strain-dependent features in different assays. This strain is the only one of 23 tested strains which is unable to invade endothelial cells, is more rapidly killed in macrophages, adheres just marginally to collagen, leads to fast cytokine expression in whole blood, and is more susceptible to lysozyme compared to other tested strains of this species (5) (I. Grimm, M. Weinstock, I. Birschmann, J. Dreier, C. Knabbe, T. Vollmer, submitted for publication; I. Grimm, N. Garben, J. Dreier, C. Knabbe, T. Vollmer, submitted for publication). To distinguish better between infection-associated *S. gallolyticus* subsp. *gallolyticus* strains [e.g., BAA-2069 (6)] and this low virulent strain, the genome of DSM 16831 was sequenced and analyzed.

The *S. gallolyticus* subsp. *gallolyticus* strain DSM 16831 grew overnight in 30 mL BHI (Oxoid, United Kingdom) and genomic DNA was extracted by the phenol-chloroform method. The genomic DNA was sequenced with Nextera technology and 2 × 250 nt long reads on a MiSeq machine (Illumina, USA). The genome was sequenced to a 113-fold coverage and assembled using Newbler v2.6. Genome finishing was performed using the software Consed (7) and Sanger reads were used to generate a complete genome sequence. Annotation was performed by GenDB v2.4 (8). Phage regions were identified by PHAST, inserting elements by ICEberg, virulence genes by VFDB (virulence factors of pathogenic bacteria), and resistance genes by RGI (resistance gene identifier) (9–12).

The genome has a length of 2,492,900 bp with a G+C content of 37.7%. Annotation disclosed 2,396 coding sequences, 12 tRNAs, and 18 rRNAs. Interestingly, the genome of DSM 16831 contains many integrative and conjugative elements with a total of 13 transposases. Additionally, three regions in the chromosomal DNA of DSM 16831 consist of phage-associated genes. Thereby, one of these regions is complete (integrase *BTR42\_02375*, terminase *BTR42\_02525*, phage structure proteins, and proteases) and has high similarity with the streptococcal phage P9 (NC\_009819). In addition, sequence analysis revealed 11 possible genes involved in antibiotic resistance. Six of these genes code for efflux pumps, two for beta-lactam resistance or mupirocin, aminocoumarin, and fluoroquinolone resistance proteins. Possible virulence genes code for agglutinin

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receptors (e.g., *BTR42\_07910*), trigger factors (e.g., *tig*), different secretion systems (e.g., *essC*), or fibronectin-binding proteins (e.g., *fbpA*). In contrast, DSM 16831 lacks the virulence-associated genes *pil1* and *pil3*, which explains to some extent the low virulent phenotype of this strain (13, 14).

The complete sequence of the genome of DSM 16831 is a valuable tool for analyzing genetic principles of the pathogen *S. gallolyticus* subsp. *gallolyticus* in future studies.

**Accession number(s).** The complete genome sequences of the chromosome have been deposited in DDBJ/EMBL/GenBank under the accession no. [CP018822](https://doi.org/10.1093/nar/gkg312).

## REFERENCES

- Jans C, Meile L, Lacroix C, Stevens MJ. 2015. Genomics, evolution, and molecular epidemiology of the *Streptococcus bovis*/*Streptococcus equinus* complex (SBSEC). *Infect Genet Evol* 33:419–436. <https://doi.org/10.1016/j.meegid.2014.09.017>.
- Sekizaki T, Nishiyama H, Nakajima S, Nishizono M, Kawano M, Okura M, Takamatsu D, Nishino H, Ishiji T, Osawa R. 2008. Endocarditis in chickens caused by subclinical infection of *Streptococcus gallolyticus* subsp. *gallolyticus*. *Avian Dis* 52:183–186. <https://doi.org/10.1637/8048-070307-Case>.
- Abeni C, Rota L, Oglioni C, Bertocchi P, Centurini PB, Zaniboni A. 2013. Correlation among *Streptococcus bovis*, endocarditis and septicemia in a patient with advanced colon cancer: a case report. *J Med Case Rep* 7:185. <https://doi.org/10.1186/1752-1947-7-185>.
- Chirouze C, Patry I, Duval X, Baty V, Tattevin P, Aparicio T, Pagenault M, Carbonnel F, Couetdic G, Hoen B. 2013. *Streptococcus bovis*/*Streptococcus equinus* complex fecal carriage, colorectal carcinoma, and infective endocarditis: a new appraisal of a complex connection. *Infect Dis* 32:1171–1176. <https://doi.org/10.1007/s10096-013-1863-3>.
- Vollmer T, Hinse D, Kleesiek K, Dreier J. 2010. Interactions between endocarditis-derived *Streptococcus gallolyticus* subsp. *gallolyticus* isolates and human endothelial cells. *BMC Microbiol* 10:78. <https://doi.org/10.1186/1471-2180-10-78>.
- 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. <https://doi.org/10.1186/1471-2164-12-400>.
- Gordon D. 2003. Viewing and editing assembled sequences using Consed. *Curr Protoc Bioinformatics* 2:11.2.1–11.2.43. <https://doi.org/10.1002/0471250953.b11102s02>.
- Meyer F, Goesmann A, McHardy AC, Bartels D, Bekel T, Clausen J, Kalinowski J, Linke B, Rupp O, Giegerich R, Pühler A. 2003. GenDB—an open source genome annotation system for prokaryote genomes. *Nucleic Acids Res* 31:2187–2195. <https://doi.org/10.1093/nar/gkg312>.
- Altschul SF, Madden TL, Schäffer AA, Zhang J, Zhang Z, Miller W, Lipman DJ. 1997. Gapped BLAST and PSI-BLAST: a new generation of protein database search programs. *Nucleic Acids Res* 25:3389–3402. <https://doi.org/10.1093/nar/25.17.3389>.
- Bi D, Xu Z, Harrison EM, Tai C, Wei Y, He X, Jia S, Deng Z, Rajakumar K, Ou HY. 2012. ICEberg: a web-based resource for integrative and conjugative elements found in Bacteria. *Nucleic Acids Res* 40:D621–D626. <https://doi.org/10.1093/nar/gkr846>.
- Zhou Y, Liang Y, Lynch KH, Dennis JJ, Wishart DS. 2011. PHAST: a fast phage search tool. *Nucleic Acids Res* 39:W347–W352. <https://doi.org/10.1093/nar/gkr485>.
- Jia B, Raphenya AR, Alcock B, Wagglechner N, Guo P, Tsang KK, Lago BA, Dave BM, Pereira S, Sharma AN, Doshi S, Courtot M, Lo R, Williams LE, Frye JG, Elsayegh T, Sardar D, Westman EL, Pawlowski AC, Johnson TA, Brinkman FS, Wright GD, McArthur AG. 2017. CARD 2017: expansion and model-centric curation of the comprehensive antibiotic resistance database. *Nucleic Acids Res* 45:D566–D573.
- Danne C, Dubrac S, Trieu-Cuot P, Dramsi S. 2014. Single cell stochastic regulation of pilus phase variation by an attenuation-like mechanism. *PLoS Pathog* 10:e1003860. <https://doi.org/10.1371/journal.ppat.1003860>.
- Martins M, Aymeric L, Du Merle L, Danne C, Robbe-Masselot C, Trieu-Cuot P, Sansonetti P, Dramsi S. 2015. *Streptococcus gallolyticus* Pil3 pilus is required for adhesion to colonic mucus and for colonization of mouse distal colon. *J Infect Dis* 212:1646–1655. <https://doi.org/10.1093/infdis/jiv307>.