



Draft Genome Sequence of *Janthinobacterium lividum* ID1246, Isolated from a Rainbow Trout Hatchery Biofilm

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ABSTRACT We present a draft genome sequence of *Janthinobacterium lividum* strain ID1246, isolated from within a rainbow trout hatchery raceway. *Janthinobacterium* spp. are well-known producers of antimicrobial compounds. Due to the unique isolation source, this genome may yield novel biosynthetic gene clusters.

Janthinobacterium lividum is a Gram-negative, aerobic bacterium commonly found in a broad range of soil (1), aquatic (2–4), and host-associated (5–7) biomes. Species within the genus *Janthinobacterium* have been of particular interest due to their production of bioactive secondary metabolites (6, 8). One of the best characterized of these compounds is violacein, which has antifungal (5, 6, 9), antiviral (10), antibacterial (9), and antitumoral (9, 11, 12) effects, along with imparting the quintessential violet color associated with this species (8). Interestingly, this species has been recently implicated as a potential opportunistic pathogen of rainbow trout (*Oncorhynchus mykiss*) (7). Here, we present a draft genome sequence of *Janthinobacterium lividum* ID1246, isolated from the wall of a rainbow trout hatchery raceway.

During a large-scale bacterial culturing experiment, *J. lividum* ID1246 was isolated from a surface swab sample of a hatchery raceway wall on R2A agar (13) incubated at 19°C. A single colony was streaked for isolation two consecutive times onto R2A agar to obtain a pure culture before being stocked at –80°C in a glycerol solution. For genome sequencing, this stock was streaked onto R2A agar, and a single colony was then inoculated into R2A broth for DNA extraction following 24 h of growth. Genomic DNA was extracted using the MasterPure DNA and RNA purification kit (Lucigen, Middleton, WI). DNA for all steps was quantified using the Qubit 1X double-stranded DNA (dsDNA) high-sensitivity (HS) assay kit (Invitrogen, Waltham, MA). A genome library was constructed using a DNA prep kit (Illumina, San Diego, CA) followed by 2 × 250-bp paired-end sequencing on a MiSeq device using a MiSeq reagent kit V2 (500 cycles) (Illumina). Following sequencing, raw reads were demultiplexed on BaseSpace and then downloaded for further processing.

CLC Genomics Workbench version 20.0.4 (Qiagen, Hilden, Germany) was used for read trimming (maximum ambiguities, 2; minimum accuracy, 95%; minimum read length, 60 bp) and *de novo* genome assembly (minimum contig length, 200; word size, 21; bubble size, 242) with default parameters. The draft genome sequence of *J. lividum* ID1246 was 6.35 Mb in size and was assembled into 20 contigs with an N_{50} value of 986 kbp. The G+C content was 62.9%, and the average genome coverage was 76× (Table 1).

The genome was annotated using the NCBI Prokaryotic Genome Annotation Pipeline version 5.1 (14). A total of 5,708 coding sequences were identified. Secondary metabolite gene detection was performed using antiSMASH version 5.1.2 with relaxed detection strictness (15–19). An approximately 23-kbp region was identified as containing the violacein operon. Additionally, four putative bacteriocin genes were identified along with terpene, homoserine lactone, arylpolyene, and acyl amino acid gene clusters.

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TABLE 1 Genome summary and database accession information

Characteristic	Data for <i>Janthinobacterium lividum</i> ID1246
No. of raw reads	2,000,748
No. of reads in assembly	1,992,868
Genome size (Mbp)	6.35
Genome coverage (×)	76
No. of contigs	20
N_{50} (bp)	985,652
G+C content (%)	62.9
No. of coding sequences	5,708
No. of protein-coding sequences	5,596
No. of tRNAs	74
No. of rRNAs	6
Closest neighbor, whole genome (% dDDH)	<i>Janthinobacterium lividum</i> DSM 1522 (80.4)
BioProject accession no.	PRJNA720898
BioSample accession no.	SAMN18681507
SRA accession no.	SRR14245518
WGS/GenBank accession no.	JAGRZK000000000

Species-level identification was performed using digital DNA-DNA hybridization (dDDH) using TYGS version 267 (20). The closest genome to the subject strain was *Janthinobacterium lividum* DSM 1522, with a dDDH of 80.4% when using the recommended d_4 formula.

Data availability. The genome of *J. lividum* ID1246 has been deposited in DDBJ/ENA/GenBank under accession number [JAGRZK000000000](https://doi.org/10.1128/genomeA.00689-15). The version described in this paper is the first version, [JAGRZK010000000](https://doi.org/10.1128/genomeA.00582-17). The BioProject, BioSample, SRA, and whole-genome sequencing (WGS) accession numbers are provided in Table 1.

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REFERENCES

- Shoemaker WR, Muscarella ME, Lennon JT. 2015. Genome sequence of the soil bacterium *Janthinobacterium* sp. KBS0711. *Genome Announc* 3:e00689-15. <https://doi.org/10.1128/genomeA.00689-15>.
- Wu X, Deutschbauer AM, Kazakov AE, Wetmore KM, Cwick BA, Walker RM, Novichkov PS, Arkin AP, Chakraborty R. 2017. Draft genome sequences of two *Janthinobacterium lividum* strains, isolated from pristine groundwater collected from the Oak Ridge Field Research Center. *Genome Announc* 5:e00582-17. <https://doi.org/10.1128/genomeA.00582-17>.
- McTaggart TL, Shapiro N, Woyke T, Chistoserdova L. 2015. Draft genome of *Janthinobacterium* sp. RA13 isolated from Lake Washington sediment. *Genome Announc* 3:e01588-14. <https://doi.org/10.1128/genomeA.01588-14>.
- Sharma P, Gupta S, Sourirajan A, Dev K. 2015. A novel psychrophilic *Janthinobacterium lividum* MMPP4 isolated from Manimahesh Lake of Chamba District of Himachal Pradesh, India. *J Biochem Tech* 6:846-851.
- Harris RN, Brucker RM, Walke JB, Becker MH, Schwantes CR, Flaherty DC, Lam BA, Woodhams DC, Briggs CJ, Vredenburg VT, Minbiole KPC. 2009. Skin microbes on frogs prevent morbidity and mortality caused by a lethal skin fungus. *ISME J* 3:818-824. <https://doi.org/10.1038/ismej.2009.27>.
- Brucker RM, Harris RN, Schwantes CR, Gallaher TN, Flaherty DC, Lam BA, Minbiole KPC. 2008. Amphibian chemical defense: antifungal metabolites of the microsymbiont *Janthinobacterium lividum* on the salamander *Plethodon cinereus*. *J Chem Ecol* 34:1422-1429. <https://doi.org/10.1007/s10886-008-9555-7>.
- Oh WT, Giri SS, Yun S, Kim HJ, Kim SG, Kim SW, Kang JW, Han SJ, Kwon J, Jun JW, Park SC. 2019. *Janthinobacterium lividum* as an emerging pathogenic bacterium affecting rainbow trout (*Oncorhynchus mykiss*) fisheries in Korea. *Pathogens* 8:146. <https://doi.org/10.3390/pathogens8030146>.
- Pantanello F, Berlutti F, Passariello C, Sarli S, Morea C, Schippa S. 2006. Violacein and biofilm production in *Janthinobacterium lividum*. *J Appl Microbiol* 4:992-999. <https://doi.org/10.1111/j.1365-2672.2006.03155.x>.
- Choi SY, Lim S, Yoon K, Lee JI, Mitchell RJ. 2021. Biotechnological activities and applications of bacterial pigments violacein and prodigiosin. *J Biol Eng* 15:10. <https://doi.org/10.1186/s13036-021-00262-9>.
- Andrighetti-Fröhner CR, Antonio RV, Creczynski-Pasa TB, Barardi CRM, Simões CMO. 2003. Cytotoxicity and potential antiviral evaluation of violacein produced by *Chromobacterium violaceum*. *Mem Inst Oswaldo Cruz* 98:843-848. <https://doi.org/10.1590/s0074-02762003000600023>.
- Bromberg N, Dreyfuss JL, Regatieri CV, Palladino MV, Durán N, Nader HB, Haun M, Justo GZ. 2010. Growth inhibition and pro-apoptotic activity of violacein in Ehrlich ascites tumor. *Chem Biol Interact* 186:43-52. <https://doi.org/10.1016/j.cbi.2010.04.016>.
- Venegas FA, Köllisch G, Mark K, Diederich WE, Kaufmann A, Bauer S, Chavarría M, Araya JJ, García-Piñeres AJ. 2019. The bacterial product violacein exerts an immunostimulatory effect via TLR8. *Sci Rep* 9:1-17. <https://doi.org/10.1038/s41598-019-50038-x>.
- Reasoner DJ, Geldreich EE. 1985. A new medium for the enumeration and subculture of bacteria from potable water. *Appl Environ Microbiol* 49:1-7. <https://doi.org/10.1128/aem.49.1.1-7.1985>.
- Tatusova T, DiCuccio M, Badretdin A, Chetvernin V, Nawrocki EP, Zaslavsky L, Lomsadze A, Pruitt KD, Borodovsky M, Ostell J. 2016. NCBI Prokaryotic Genome Annotation Pipeline. *Nucleic Acids Res* 44:6614-6624. <https://doi.org/10.1093/nar/gkw569>.
- Medema MH, Blin K, Cimermancic P, De Jager V, Zakrzewski P, Fischbach MA, Weber T, Takano E, Breitling R. 2011. AntiSMASH: rapid identification, annotation and analysis of secondary metabolite biosynthesis gene

- clusters in bacterial and fungal genome sequences. *Nucleic Acids Res* 39: W339–W346. <https://doi.org/10.1093/nar/gkr466>.
16. Blin K, Medema MH, Kazempour D, Fischbach MA, Breitling R, Takano E, Weber T. 2013. antiSMASH 2.0: a versatile platform for genome mining of secondary metabolite producers. *Nucleic Acids Res* 41:W204–W212. <https://doi.org/10.1093/nar/gkt449>.
 17. Weber T, Blin K, Duddela S, Krug D, Kim HU, Brucoleri R, Lee SY, Fischbach MA, Müller R, Wohlleben W, Breitling R, Takano E, Medema MH. 2015. AntiSMASH 3.0: a comprehensive resource for the genome mining of biosynthetic gene clusters. *Nucleic Acids Res* 43:W237–W243. <https://doi.org/10.1093/nar/gkv437>.
 18. Blin K, Wolf T, Chevrette MG, Lu X, Schwalen CJ, Kautsar SA, Suarez Duran HG, De Los Santos ELC, Kim HU, Nave M, Dickschat JS, Mitchell DA, Shelest E, Breitling R, Takano E, Lee SY, Weber T, Medema MH. 2017. AntiSMASH 4.0: improvements in chemistry prediction and gene cluster boundary identification. *Nucleic Acids Res* 45:W36–W41. <https://doi.org/10.1093/nar/gkx319>.
 19. Blin K, Shaw S, Steinke K, Villebro R, Ziemert N, Lee SY, Medema MH, Weber T. 2019. AntiSMASH 5.0: updates to the secondary metabolite genome mining pipeline. *Nucleic Acids Res* 47:W81–W87. <https://doi.org/10.1093/nar/gkz310>.
 20. Meier-Kolthoff JP, Göker M. 2019. TYGS is an automated high-throughput platform for state-of-the-art genome-based taxonomy. *Nat Commun* 10:2182. <https://doi.org/10.1038/s41467-019-10210-3>.