



Complete Genome Sequence of *Lacinutrix venerupis* DOK2-8 Isolated from Marine Sediment from the East Sea, Republic of Korea

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ABSTRACT *Lacinutrix venerupis* has recently been considered a potential fish pathogen. Here, we report the complete genome sequence of *L. venerupis* DOK2-8, which possesses several virulence-related genes. This strain may be potentially virulent to other marine organisms, and its genomic information will provide important insights into the biodiversity of the genus *Lacinutrix*.

The genus *Lacinutrix*, which is a member of the family *Flavobacteriaceae* (*Proteobacteria*: *Gammaproteobacteria*) was created in 2005 and comprises 10 valid marine species, including *L. algicola*, *L. cladophorae*, *L. copepodicola*, *L. gracilariae*, *L. himadriensis*, *L. iliipiscaria*, *L. jangbogonensis*, *L. mariniflava*, *L. undariae*, and *L. venerupis* (1, 2). Although all of these species were considered nonpathogenic (2), *L. venerupis* was recently found to be associated with disease outbreak among marine fish (3). Four draft genomes (*L. algicola*, *L. himadriensis*, *L. jangbogonensis*, and *L. mariniflava*) are currently available in the GenBank database; however, the genome of *L. venerupis* has not yet been sequenced. Since 2015, we have screened several indigenous bacterial strains with advantageous characteristics for biotechnological applications. Here, we present the first complete genome sequence of an *L. venerupis* strain isolated from the Republic of Korea.

The DOK2-8 strain was isolated from marine sediment collected from Dokdo, East Sea, Republic of Korea (37°14'25.9"N 131°52'02.6"E), using the standard dilution plating technique on marine agar 2216 (Difco) followed by incubation at 28°C. The 16S rRNA of the isolate (GenBank accession number MG493235) showed >99.9% similarity to *L. venerupis* Cmf 20.8^T (HG970752); hence, it was finally classified as *L. venerupis* DOK2-8. The isolate showed strong extracellular proteolytic activity, as determined with the method of Amoozegar et al. (4). Genomic DNA of DOK2-8 was extracted and sequenced at Macrogen, Inc. (Seoul, Republic of Korea), with a PacBio RS II system (Pacific Biosciences) by constructing a 20-kb SMRTbell template library. The PacBio long-read data (1,055,787,767 bp, 122,792 reads) were assembled *de novo* with the Hierarchical Genome Assembly Process (HGAP) version 3.0 and annotated using the NCBI Prokaryotic Genome Annotation Pipeline (PGAP) (<http://www.ncbi.nlm.nih.gov/books/NBK174280>).

The final assembled circular chromosome of DOK2-8 comprised 3,192,399 bp, with a 30.6% G+C content (92.5% coding region percentage), and encoded 2,857 genes, 2,811 coding sequences, 6 rRNAs (5S, 16S, and 23S), 36 tRNAs, and 4 noncoding RNAs. Overall genome similarities among DOK2-8 and the other four *Lacinutrix* species strains were assessed using the orthologous average nucleotide identity algorithm (5). The highest genome similarity (80.7%) was with *L. algicola* (GenBank accession number LIQH00000000), and the lowest (75.5%) was with *L. himadriensis* (LIQI00000000).

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Potential virulence genes in DOK2-8 were identified by searching the Virulence Factor Database (6, 7); consequently, several putative genes involved in capsule biosynthesis, metalloprotease, and *htpB* chaperonin, which were homologous to those of other Gram-negative species, were detected. Moreover, three putative hemolysin genes were detected in the DOK2-8 genome. These results indicate that *L. venerupis* DOK2-8 may have potential virulence to other marine organisms, similar to other species in the family *Flavobacteriaceae* (2), and information regarding its genome will provide important insights into the biodiversity of the genus *Lacinutrix* in the marine niche. To our knowledge, this is the first study to reveal a complete genome sequence in the genus *Lacinutrix*.

Accession number(s). *L. venerupis* DOK2-8 was deposited in the Korean Agricultural Culture Collection (KACC) as KACC 19202. The 16S rRNA and complete genome (chromosome) of *L. venerupis* DOK2-8 have been deposited at DDBJ/ENA/GenBank under the accession numbers [MG493235](https://www.ncbi.nlm.nih.gov/nuccore/MG493235) and [CP019352](https://www.ncbi.nlm.nih.gov/nuccore/CP019352), respectively.

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REFERENCES

- Bowman JP, Nichols DS. 2005. Novel members of the family *Flavobacteriaceae* from Antarctic maritime habitats including *Subsaximicrobium wynnwilliamsii* gen. nov., sp. nov., *Subsaximicrobium saxinquilinus* sp. nov., *Subsaximicrobium broadyi* gen. nov., sp. nov., *Lacinutrix copepodicola* gen. nov., sp. nov., and novel species of the genera *Bizionia*, *Gelidibacter* and *Gillisia*. *Int J Syst Evol Microbiol* 55:1471–1486. <https://doi.org/10.1099/ijs.0.63527-0>.
- Lasa A, Diéguez AL, Romalde JL. 2015. Description of *Lacinutrix venerupis* sp. nov.: a novel bacterium associated with reared clams. *Syst Appl Microbiol* 38:115–119. <https://doi.org/10.1016/j.syapm.2014.10.012>.
- López JR, Alcantara R, Lorenzo L, Navas JI. 2017. Isolation of *Lacinutrix venerupis* strains associated with disease outbreaks in sea bream *Sparus aurata* and European sea bass *Dicentrarchus labrax*. *Dis Aquat Organ* 124:85–90. <https://doi.org/10.3354/dao03103>.
- Amoozegar MA, Schumann P, Hajighasemi M, Fatemi AZ, Karbalaie-Heidari HR. 2008. *Salinivibrio proteolyticus* sp. nov. a moderately halophilic and proteolytic species from a hypersaline lake in Iran. *Int J Syst Evol Microbiol* 58:1159–1163. <https://doi.org/10.1099/ijs.0.65423-0>.
- Lee I, Ouk Kim Y, Park SC, Chun J. 2016. OrthoANI: an improved algorithm and software for calculating average nucleotide identity. *Int J Syst Evol Microbiol* 66:1100–1103. <https://doi.org/10.1099/ijsem.0.000760>.
- Chen L, Yang J, Yu J, Yao Z, Sun L, Shen Y, Jin Q. 2005. VFDB: a reference database for bacterial virulence factors. *Nucleic Acids Res* 33:D325–D328. <https://doi.org/10.1093/nar/gki008>.
- Chen L, Zheng D, Liu B, Yang J, Jin Q. 2016. VFDB 2016: hierarchical and refined dataset for big data analysis—10 years on. *Nucleic Acids Res* 44:D694–D697. <https://doi.org/10.1093/nar/gkv1239>.