



# Draft Genome Sequence of a *Shewanella halifaxensis* Strain Isolated from the Intestine of Marine Red Seabream (*Pagrus major*), Which Includes an Integrative Conjugative Element with Macrolide Resistance Genes

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**ABSTRACT** *Shewanella halifaxensis* strain 6JANF4-E-4 was isolated from the intestine of a red seabream (*Pagrus major*). Here, we report the draft genome sequence of this bacterium, which includes an integrative conjugative element of the SXT/R391 family, where the macrolide resistance determinants *mef*(C) and *mph*(G) exist.

The genus *Shewanella* contains facultative anaerobic Gram-negative rod bacteria, which are often found in marine environments. *Shewanella halifaxensis* was recorded from marine sediment (1). Our strain, *S. halifaxensis* 6JANF4-E-4, was isolated from the intestine of a red seabream (*Pagrus major*), and it shows macrolide resistance and possesses the tandem gene set of *mef*(C)-*mph*(G) (2). We revealed the alignment of *mef*(C) and *mph*(G) on a chromosome and their integration within an integrative conjugative element of the SXT/R391 family (SRI).

We provide here the draft genome sequence of a gene cassette containing *mef*(C)-*mph*(G) in the SRI. SRIs were first described in *Vibrio cholerae* strains isolated from human clinical specimens and have been found in several species of *Vibrio*, *Photobacterium*, *Providencia*, *Proteus*, *Alteromonas*, *Marinomonas*, and *Shewanella* (3).

The genome sequencing of the 6JANF4-E-4 strain was performed by shotgun sequencing using the PacBio RS II system (Pacific Biosciences). The 87,318 sequence reads were pooled and *de novo* assembled using single-molecule real-time (SMRT) Portal analysis software version 2.3 (Pacific Biosciences) (4). The draft genome of the strain was 5,462,838 bp, with an average G+C content of 42.8%, and consisted of 5 contigs (average contig length, 1,092,567 bp). Rapid Annotations using Subsystems Technology (RAST) and SEED Viewer were used for gene annotation and an overview of the annotated genome, respectively (5, 6), and revealed 5,068 coding sequences and 177 RNA genes on this genome.

An SRI has the specific sequences *attL* and *attR* (3) at opposite ends. We confirmed that *mef*(C)-*mph*(G) was coded between *attL* and *attR* on the SRI. Other antibiotic resistance genes, namely *floR*, *sul2*, and a putative  $\beta$ -lactamase gene, were also coded. We assigned the nomenclature ICEShaJpn1, according to the international naming standard for the SRI (7). The length of ICEShaJpn1 was 107,133 bp and contained the functional genes for maintenance, dissemination, and regulation as an SRI (8).

**Accession number(s).** The *S. halifaxensis* strain 6JANF4-E-4 genome sequence data have been deposited in DDBJ/EMBL/GenBank under accession numbers [BFBQ01000001](https://doi.org/10.1093/nar/gkx1000001) to [BFBQ01000005](https://doi.org/10.1093/nar/gkx1000005). The released sample is available on the DDBJ BioSample listing page under sample number SAMD00112641.

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## REFERENCES

1. Zhao J-S, Manno D, Leggiadro C, O'Neil D, Hawari J. 2006. *Shewanella halifaxensis* sp. nov., a novel obligately respiratory and denitrifying psychrophile. *Int J Syst Evol Microbiol* 56:205–212. <https://doi.org/10.1099/ijs.0.63829-0>.
2. Sugimoto Y, Suzuki S, Nonaka L, Boonla C, Sukpanyatham N, Chou HY, Wu JH. 2017. The novel *mef(C)-mph(G)* macrolide resistance genes are conveyed in the environment on various vectors. *J Glob Antimicrob Resist* 10:47–53. <https://doi.org/10.1016/j.jgar.2017.03.015>.
3. Poulin-Laprade D, Carraro N, Burrus V. 2015. The extended regulatory networks of SXT/R391 integrative and conjugative elements and IncA/C conjugative plasmids. *Front Microbiol* 6:837. <https://doi.org/10.3389/fmicb.2015.00837>.
4. Chin CS, Alexander DH, Marks P, Klammer AA, Drake J, Heiner C, Clum A, Copeland A, Huddleston J, Eichler EE, Turner SW, Korlach J. 2013. Non-hybrid, finished microbial genome assemblies from long-read SMRT sequencing data. *Nat Methods* 10:563–569. <https://doi.org/10.1038/nmeth.2474>.
5. Aziz RK, Bartels D, Best AA, DeJongh M, Disz T, Edwards RA, Formsma K, Gerdes S, Glass EM, Kubal M, Meyer F, Olsen GJ, Olson R, Osterman AL, Overbeek RA, McNeil LK, Paarmann D, Paczian T, Parrello B, Pusch GD, Reich C, Stevens R, Vassieva O, Vonstein V, Wilke A, Zagnitko O. 2008. The RAST server: rapid annotations using subsystems technology. *BMC Genomics* 9:75. <https://doi.org/10.1186/1471-2164-9-75>.
6. Overbeek R, Begley T, Butler RM, Choudhuri JV, Chuang HY, Cohoon M, de Crécy-Lagard V, Diaz N, Disz T, Edwards R, Fonstein M, Frank ED, Gerdes S, Glass EM, Goesmann A, Hanson A, Iwata RD, Jensen R, Jamshidi N, Krause L, Kubal M, Larsen N, Linke B, McHardy AC, Meyer F, Neuweger H, Olsen G, Olson R, Osterman A, Portnoy V, Pusch GD, Rodionov DA, Ruckert C, Steiner J, Stevens R, Thiele I, Vassieva O, Ye Y, Zagnitko O, Vonstein V. 2005. The subsystems approach to genome annotation and its use in the project to annotate 1000 genomes. *Nucleic Acids Res* 33:5691–5702. <https://doi.org/10.1093/nar/gki866>.
7. Burrus V, Marrero J, Waldor MK. 2006. The current ICE age: Biology and evolution of SXT-related integrating conjugative elements. *Plasmid* 55: 173–183. <https://doi.org/10.1016/j.plasmid.2006.01.001>.
8. Toussaint A, Merlin C. 2002. Mobile elements as a combination of functional modules. *Plasmid* 47:26–35. <https://doi.org/10.1006/plas.2001.1552>.