

Draft Genome Sequences of Marine Flavobacterium *Algibacter lectus* Strains SS8 and NR4

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Here, we present the draft genome sequences of a zeaxanthin-producing flavobacterium, *Algibacter lectus* strains SS8 and NR4, isolated from coastal sediment and rock surfaces in Hakodate, Japan, respectively. This genomic information represents the first *Algibacter* genome sequences, which will help us to elucidate the biology and evolution of *Flavobacteriaceae* bacteria.

Received 30 September 2014 Accepted 6 October 2014 Published 13 November 2014

Citation Takatani N, Nakanishi M, Meirelles P, Mino S, Suda W, Oshima K, Hattori M, Ohkuma M, Hosokawa M, Miyashita K, Thompson FL, Niwa A, Sawabe T, Sawabe T. 2014. Draft genome sequences of marine flavobacterium *Algibacter lectus* strains SS8 and NR4. *Genome Announc.* 2(6):e01168-14. doi:10.1128/genomeA.01168-14.

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Flavobacteriaceae is a group of bacteria containing a diverse array of Gram-negative, aerobic, nonmotile, pigmented bacteria that show yellow to orange colonies (1) and includes >114 genera (see <http://www.bacterio.net/>). One genus, *Algibacter*, was proposed in 2004 for gliding, orange-pigmented, facultatively anaerobic heterotrophs and currently consists of 10 species (2–4). *Algibacter lectus* is the type species of the genus *Algibacter* and in the proposal of the genus and species that produce orange nondiffusible pigments (2). We recently isolated the yellow agarolytic *A. lectus* strains SS8 and NR4. Strain SS8 produced zeaxanthin, which occupied up to 97% of the total carotenoids. However, as the genome structures of the strains have never been reported until now, the genomic plasticities of the *A. lectus* strains are still presently unknown.

The genome sequences of *A. lectus* strains SS8 and NR4 were sequenced with the Ion PGM system (Life Technologies, Carlsbad, CA). The genome sequences were *de novo* assembled using Newbler version 2.8. The annotation and genome analysis were performed by Rapid Annotations using Subsystems Technology (RAST) (5). The sizes of the draft genome of *A. lectus* strains SS8 and NR4 are 4,692,319 bp and 4,815,979 bp, comprising 56 and 72 contigs, respectively. Both have G+C contents of 33.3%. The redundancies are 18 and 17, and the N_{50} contig lengths are 194,285 bp and 205,911 bp, respectively. The numbers of putative coding sequences (CDSs) are 4,609 and 5,640, the numbers of rRNA sequences are 3 and 2, and the numbers of tRNA sequences are 38 and 37, respectively. Both strains possess a carotenoid biosynthesis gene cluster (encoding phytoene dehydrogenase, phytoene synthase, and β -carotene hydroxylase), as is the case with other *Flavobacteriaceae* bacteria. In addition, the lycopene cyclase was located downstream of the gene cluster. These genes are essential for zeaxanthin production (6). The orange-pigmented colony was reported in the *A. lectus* type strain

(2). However, both *A. lectus* strains in this study formed yellow colonies. It is interesting to compare the genome to phenotype plasticity in carotenoid synthesis. This genome report will help reveal this difference. Strains SS8 and NR4 have been deposited in the Japan Collection of Microorganisms as JCM 19300 and JCM 19274.

Nucleotide sequence accession numbers. The genome data have been deposited in DDBJ/EMBL/GenBank under the accession numbers BBNQ01000001 to BBNQ01000056 and BBNU01000001 to BBNU01000072 for *A. lectus* strains SS8 and NR4, respectively.

ACKNOWLEDGMENTS

This work was supported by the Genome Information Upgrading Program of National BioResource Project from the Ministry of Education, Culture, Sports, Science and Technology (MEXT) (to M. Hattori and M. Ohkuma) of Japan, Strategic Japanese-Brazilian Cooperative Program, Biomass & Bioenergy (to Tomoo Sawabe), and Kaken (26660168) to Tomoo Sawabe. P. Meirelles thanks CAPES for the PhD scholarship (4848-14-9 CAPES/JSPS).

REFERENCES

- Holmes B, Owen RJ, McMeekin TA. 1984. Genus *Flavobacterium* Bergey, Harrison, Breed, Hammer and Huntton. 1923:97^{AL}, p 353–361. In Krieg NR, Holt JG (ed), *Bergey's manual of systematic bacteriology*, vol 1. Williams & Wilkins, Baltimore, MD.
- Nedashkovskaya OI, Kim SB, Han SK, Rhee MS, Lysenko AM, Rohde M, Zhukova NV, Frolova GM, Mikhailov VV, Bae KS. 2004. *Algibacter lectus* gen. nov., sp. nov., a novel member of the family *Flavobacteriaceae* isolated from green algae. *Int. J. Syst. Evol. Microbiol.* 54:1257–1261. <http://dx.doi.org/10.1099/ijs.0.02949-0>.
- Park SC, Hwang YM, Choe HN, Baik KS, Kim H, Seong CN. 2013. *Algibacter aquimarinus* sp. nov., isolated from a marine environment, and reclassification of *Pontirhabdus pectinivorans* as *Algibacter pectinivorans* comb. nov. *Int. J. Syst. Evol. Microbiol.* 63:2038–2042. <http://dx.doi.org/10.1099/ijs.0.045815-0>.
- Park S, Jung YT, Yoon JH. 2013. *Algibacter miyuki* sp. nov., a member of

- the family *Flavobacteriaceae* isolated from leachate of a brown algae reservoir. *Antonie Van Leeuwenhoek* 104:253–260. <http://dx.doi.org/10.1007/s10482-013-9944-y>.
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* 9:75–89. <http://dx.doi.org/10.1186/1471-2164-9-75>.
 6. Misawa N, Nakagawa M, Kobayashi K, Yamano S, Izawa Y, Nakamura K, Harashima K. 1990. Elucidation of the *Erwinia uredovora* carotenoid biosynthetic pathway by functional analysis of gene products expressed in *Escherichia coli*. *J. Bacteriol.* 172:6704–6712.