Draft Genome Sequence of the Photoheterotrophic
Chloracidobacterium thermophilum Strain OC1 Found in a Mat at Ojo Caliente

Patrick C. Hallenbeck, Melanie Grogger, Megan Mraz, Donald Veverka
Department of Biology, Life Sciences Research Center, U.S. Air Force Academy, Colorado Springs, Colorado, USA

Metagenomics of an enrichment culture from a New Mexico hot spring allowed the description of a draft genome of a Chloracidobacterium thermophilum strain for the first time outside Yellowstone National Park with a surprisingly high degree of identity with the type strain.

Received 12 November 2015  Accepted 4 January 2016  Published 18 February 2016

Citation Hallenbeck PC, Grogger M, Mraz M, Veverka D. 2016. Draft genome sequence of the photoheterotrophic Chloracidobacterium thermophilum strain OC1 found in a mat at Ojo Caliente Genome Announc 4(1):e01570-15. doi:10.1128/genomeA.01570-15.

Copyright © 2016 Hallenbeck et al. This is an open-access article distributed under the terms of the Creative Commons Attribution 3.0 Unported license.

Address correspondence to Patrick C. Hallenbeck, Patrick.hallenbeck.ctr@usafa.edu.

Relatively recently, a novel photoheterotroph found in Octopus Hot Springs, Yellowstone National Park (YNP), Chloracidobacterium thermophilum, was described (1, 2). This finding extended chlorophyll-dependent phototrophy to a sixth, little known bacterial phylum, Acidobacter, and showed that the organization of bacterial photosynthesis in chlorosomes, supramolecular photosynthetic structures allowing for very efficient photosynthesis at low light intensities, extends to a third bacterial group (3, 4). A wealth of information concerning molecular details of its photosynthetic system have been obtained, including its homodimeric type I reaction center (RCI) (5–8). A detailed molecular understanding of the photosynthetic system of this organism has helped inform the ongoing debate on the evolution and origin of oxygenic photosynthesis (9, 10).

Interesting insights were gained 3 years ago when the complete genome sequence of C. thermophilum was determined, even though it was still growing in a mixed culture (11). Among other things, this information helped to define the medium supplement necessary to permit complete strain characterization and taxonomic acceptance (12). Although until now this organism has been described in genomic detail from samples obtained at Octopus Hot Springs, YNP, an ecological study showed that, based on 16S rRNA analysis, C. thermophilum is abundant and widespread among mats at different YNP hot springs (13).

However, until now the presence of C. thermophilum outside YNP has not been reported even though it may represent a widespread organism of ecological importance in hot springs mats. Thus, it would be important to describe in detail strains of this organism that might be found elsewhere. Here we report on the draft genome of strain OC1, found at a thermal source in New Mexico. The OC1 draft genome was 3,600,358 bp. Surprisingly, OC1 shows a great deal of similarity with the genome of the C. thermophilum type strain, with a high degree of identity with both SSU RNA (1404/1424, 99%) and LSU RNA (2853/2900, 98%). The draft genome consisted of 3,062 coding sequences and 49 RNAs, as determined by RAST and SEED (15, 16). Strikingly, 1,215 of the predicted OC1 coding sequences shared 95% or greater identity with those of the type strain.

Genomic DNA was isolated from an enrichment culture of a sample obtained at a thermal source at Ojo Caliente, New Mexico. The library was prepared using a Nextera DNA sample preparation kit (Illumina) following the manufacturer’s user guide, with subsequent simultaneous fragmentation and addition of adapter sequences by a limited-cycle (5 cycles) PCR. The final library concentration (2.28 ng/μL) was measured using the Qubit dsDNA HS assay kit (Life Technologies), and the average library size (887 bp) was determined using the Agilent 2100 Bioanalyzer (Agilent Technologies). The library was sequenced by using a 600 Cycles v3 reagent kit (Illumina) in MiSeq (Illumina). Assembly was performed by MR DNA (Shallowater, TX) using NGEN (DNAstar) as the primary assembly method, followed by manual optimization.

Nucleotide sequence accession numbers. This whole-genome shotgun project has been deposited at DDBJ/EMBL/GenBank under the accession number LMXM00000000. The version described in this paper is version LMXM01000000.

ACKNOWLEDGMENTS

The views expressed here are those of the authors and do not reflect the official policy or position of the United States Air Force, the Department of Defense, or the U.S. Government.

This research was supported by the Air Force Office of Scientific Research (grant AFOSR 9550-14-1-0147). This research was performed while P.C.H. held an NRC Research Associateship award at LSRC-USAFA.

FUNDING INFORMATION

DOD | Air Force Office of Scientific Research (AFOSR) provided funding to Donald Veverka under grant number AFOSR 9550-14-1-0147. National Academy of Sciences (NAS) provided funding to Patrick C. Hallenbeck under grant number NRC-Hallenbeck.

REFERENCES

1. Bryant D, Costas AG, Heidelberg J, Ward D. 2007. Candidatus Chloracidobacterium thermophilum: an aerobic phototrophic acidobacterium
with chlorosomes and type 1 reaction centers. Photosynth Res 91: 269–270.

2. Bryant DA, Costas AMG, Maresca JA, Chew AGM, Klatt CG, Bateson MM, Tallon LJ, Hostetler J, Nelson WC, Heidelberg JF, Ward DM. 2007. Candidatus Chloracidobacterium thermophilum: an aerobic phototrophic Acidobacterium. Science 317:523–526. http://dx.doi.org/10.1126/science.1143236.

3. Gert T, Oostergetel GT, van Amerongen H, Boekema EJ. 2010. The chlorosome: a prototype for efficient light harvesting in photosynthesis. Photosynth Res 104:245–255. http://dx.doi.org/10.1007/s11120-010-9533-0.

4. Costas AMG, Tsukatani Y, Romberger SP, Oostergetel GT, Boekema EJ, Golbeck JH, Bryant DA. 2011. Ultrastructural analysis and identification of envelope proteins of “Candidatus Chloracidobacterium thermophilum” chlorosomes. J Bacteriol 193:6701–6711.

5. Costas AMG, Tsukatani Y, Rijpstra WIC, Schouten S, Welander PV, Summers RE, Bryant DA. 2012. Identification of the bacteriochlorophylls, carotenoids, Quinones, lipids, and hopanoids of “Candidatus Chloracidobacterium thermophilum.” J Bacteriol 194:1158–1168.

6. Tsukatani Y, Romberger SP, Golbeck JH, Bryant DA. 2012. Isolation and characterization of homodimeric type-I reaction center complex from Candidatus Chloracidobacterium thermophilum, an aerobic chlorophototroph. J Biol Chem 287:5720–5732. http://dx.doi.org/10.1074/jbc.M111.323329.

7. Tsukatani Y, Wen J, Blankenship RE, Bryant DA. 2010. Characterization of the FMO protein from the aerobic chlorophototroph, Candidatus Chloracidobacterium thermophilum. Photosynth Res 104:201–209. http://dx.doi.org/10.1007/s11120-009-9517-0.

8. Wen J, Tsukatani Y, Cui W, Zhang H, Gross ML, Bryant DA, Blankenship RE. 2011. Structural model and spectroscopic characteristics of the FMO antenna protein from the aerobic chlorophototroph, Candidatus Chloracidobacterium thermophilum. Biochim Biophys Acta 1807: 157–164. http://dx.doi.org/10.1016/j.bbabio.2010.09.008.

9. Sousa FL, Shavit-Grievink L, Allen JF, Martin WF. 2013. Chlorophyll biosynthesis ω+ gene evolution indicates photosystem gene duplication, not photosystem merger, at the origin of oxygenic photosynthesis. Genome Biol Evol 5:200–216. http://dx.doi.org/10.1093/gbe/evs127.

10. Cardona T. 2015. A fresh look at the evolution and diversification of photochemical reaction centers. Photosynth Res 126:111–134. http://dx.doi.org/10.1007/s11120-014-0065-x.

11. Costas AMG, Liu Z, Tomsho LP, Schuster SC, Ward DM, Bryant DA. 2012. Complete genome of Candidatus Chloracidobacterium thermophilum, a chlorophyll-based phototrophic troph belonging to the phylum Acidobacteria. Environ Microbiol 14:177–190. http://dx.doi.org/10.1111/j.1462-2920.2011.02592.x.

12. Tank M, Bryant DA. 2015. Nutrient requirements and growth physiology of the phototrophic acidobacterium, Chloracidobacterium thermophilum. Front Microbiol 6:226. http://dx.doi.org/10.3389/fmicb.2015.00226.

13. Tank M, Bryant DA. 2015. Chloracidobacterium thermophilum gen. nov., sp. nov.: an anoxygenic microaerophilic chlorophototrophic acidobacterium. Int J Syst Evol Microbiol 65:1426–1430. http://dx.doi.org/10.1099/ijs.0.000113.

14. Ross KA, Feazel LM, Robertson CE, Fathepure BZ, Wright KE, Turk-Macleod RM, Chan MM, Held NL, Spear JR, Pace NR. 2012. Phototrophic phylotypes dominate mesothermal microbial mats associated with hot springs in Yellowstone National Park. Microb Ecol 64:162–170. http://dx.doi.org/10.1007/s00248-012-0012-3.

15. 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. http://dx.doi.org/10.1186/1471-2164-9-75.

16. Overbeek R, Begley T, Butler RM, Choudhuri JV, Chuang HY, Cohoon M, de Crécy-Lagard V, Diaz N, Disz T, Edwards R, Fennost M, Frank ED, Gerdes S, Glass EM, Goessmann A, Hanso A, Iwata-Reuyd D, Jensen R, Jamshidi N, Krause I, Kubal M, Larsen N, Linke B, McHardy AC, Meyer F, Neuweger H, Olsen G, Olson R, Osterman A, Portnoy V, Pusch GD, Rodionov DA, Rückert 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. http://dx.doi.org/10.1093/nar/gki866.