AMERICAN SOCIETY FOR MICROBIOLOGY | genomeAnnouncements™

PROKARYOTES

Draft Genome Sequences of Two Unclassified *Chitinophagaceae* Bacteria, IBVUCB1 and IBVUCB2, Isolated from Environmental Samples

Russell J. S. Orr,[a]* Stephane Rombauts,[b,c] Yves Van de Peer,[b,c] Kamran Shalchian-Tabrizi[a]

Section for Genetics and Evolutionary Biology (EVOGENE), Department of Biosciences, University of Oslo, Oslo, Norway[a]; Department of Plant Biotechnology and Bioinformatics, Ghent University, Ghent, Belgium[b]; VIB Center for Plant Systems Biology, Ghent, Belgium[c]

ABSTRACT We report here the draft genome sequences of two *Chitinophagaceae* bacteria, IBVUCB1 and IBVUCB2, assembled from metagenomes of surface samples from freshwater lakes. The genomes are >99% complete and may represent new genera within the *Chitinophagaceae* family, indicating a larger diversity than currently identified.

Received 27 June 2017 **Accepted** 29 June 2017 **Published** 17 August 2017

Citation Orr RJS, Rombauts S, Van de Peer Y, Shalchian-Tabrizi K. 2017. Draft genome sequences of two unclassified *Chitinophagaceae* bacteria, IBVUCB1 and IBVUCB2, isolated from environmental samples. Genome Announc 5:e00787-17. https://doi.org/10.1128/genomeA.00787-17.

Address correspondence to Russell J. S. Orr, russell_orr@hotmail.com.

* Present address: Russell J. S. Orr, Kristine Bonnevies hus, Oslo, Norway.

Advances in high-throughput sequencing, coupled with decreasing costs, have increased the number of available bacterial genomes almost exponentially. Genome sequencing, however, has traditionally been limited to species that can be held and grown in culture due to the high DNA volumes needed. A predominant focus on cultivable species has led to a genome bias, and, as a result, true bacterial diversity is poorly represented. Metagenomic studies are rectifying this bias and have already revealed a large novel diversity (1). However, metagenomics remains limited, with many ecosystems yet to be sampled. We aim to expand species richness by identifying novel bacteria from varied environmental samples. Here, we present the draft genomes of two unclassified *Chitinophagaceae* bacteria, which were surface-isolated from freshwater lakes in Norway (Årungen, Ås) and Japan (Tsukuba, Ibaraki).

DNA was isolated using the standard phenol-chloroform protocol with ethanol precipitation and subsequent cleaning using Zymo genomic cleaner and concentrator. DNA was prepared and sequenced on an Illumina HiSeq 2500 (150-bp paired-end reads; 350-bp insert size) and PacBio RS2 with P6-C4 chemistry (20 kb) at the Norwegian Sequencing Centre. Metagenome drafts were assembled using SPAdes version 3.9.0 (2); single genomes were separated with MetaBAT (3); and quality was assessed with CheckM (4). Separate genomes were scaffolded using LINKS (5), and gaps were closed with Sealer (6). Genome assemblies were evaluated with PROmer (7) and REAPER (8) before being improved with Pilon (9). Genomes were annotated using the NCBI Prokaryotic Genome Annotation Pipeline (10). Taxonomical rank was established upon evaluation of CheckM (4), PhyloSift (11), and a megaBLAST search against the NCBInr database.

Chitinophagaceae bacterium IBVUCB1 was assembled into two scaffolds constituting six contigs with a sequence length of 3.41 Mb and a GC content of 42.64%. Scaffold N_{50} was 1.92 Mb with an Illumina coverage of 143× and a PacBio coverage of 9×. CheckM estimated genome completeness at 99.01% with no contamination or strain heterogeneity. The genome constitutes 3,056 genes, 43 RNAs, 36 tRNAs, 3 noncoding RNAs (ncRNAs), and 5 pseudogenes.

Chitinophagaceae bacterium IBVUCB2 was assembled into three scaffolds constituting four contigs with a total sequence length of 3.99 Mb and a GC content of 38.42%.

The scaffold N_{50} was 2.26 Mb with an Illumina coverage of 32× and a PacBio coverage of 8×. CheckM estimated genome completeness at 99.51% with no contamination or strain heterogeneity. The genome constitutes 3,527 genes, 42 RNAs, 36 tRNAs, 3 ncRNAs, and 25 pseudogenes.

The genomes were confirmed as novel *Chitinophagaceae* bacteria according to a BLASTn search of 16S queries against the NCBInr database: IBVUCB1 had a 93% identity to *Sediminibacterium salmoneum* 16S (NR_044197), and IBVUCB2 had a 96% identity to the 16S of the same species. IBVUCB1 and IBVUCB2 had a 94% 16S identity to each other. The low identity to known *Chitinophagaceae* spp. may suggest IBVUCB1 and IBVUCB2 as new genera, indicating a larger diversity than currently identified.

Accession number(s). The draft genomes of *Chitinophagaceae* bacteria IBVUCB1 and IBVUCB2 sequenced under this project have been deposited at DDBJ/EMBL/GenBank under the accession numbers NFUW00000000 and NFUV00000000, respectively. These biosamples (SAMN06840505 and SAMN06840506, respectively) are part of BioProject PRJNA384425.

ACKNOWLEDGMENTS

We thank Abel (UiO), in particular projects nn9244k and nn9404k, for providing computing resources. We also thank the Midas cluster at VIB for providing additional computing resources. We are grateful to the Norwegian Sequencing Centre (NSC) for providing sequencing support and analysis for both Illumina and PacBio. We thank Thomas Haverkamp (IBV, UiO) for discussions related to the assembly and analysis of prokaryote genomes.

This work has been supported by research grants from the Norwegian Research Council to R.J.S.O. (project 230868).

REFERENCES

1. Nayfach S, Pollard KS. 2016. Toward accurate and quantitative comparative metagenomics. Cell 166:1103–1116. https://doi.org/10.1016/j.cell.2016.08.007.
2. Bankevich A, Nurk S, Antipov D, Gurevich AA, Dvorkin M, Kulikov AS, Lesin VM, Nikolenko SI, Pham S, Prjibelski AD, Pyshkin AV, Sirotkin AV, Vyahhi N, Tesler G, Alekseyev MA, Pevzner PA. 2012. SPAdes: a new genome assembly algorithm and its applications to single-cell sequencing. J Comput Biol 19:455–477. https://doi.org/10.1089/cmb.2012.0021.
3. Kang DD, Froula J, Egan R, Wang Z. 2015. MetaBAT, an efficient tool for accurately reconstructing single genomes from complex microbial communities. PeerJ 3:e1165. https://doi.org/10.7717/peerj.1165.
4. Parks DH, Imelfort M, Skennerton CT, Hugenholtz P, Tyson GW. 2015. CheckM: assessing the quality of microbial genomes recovered from isolates, single cells, and metagenomes. Genome Res 25:1043–1055. https://doi.org/10.1101/gr.186072.114.
5. Warren RL, Vandervalk BP, Jones SJ, Birol I. 2015. LINKS: scaffolding genome assemblies with kilobase-long nanopore reads. bioRxiv https://doi.org/10.1101/016519.
6. Paulino D, Warren RL, Vandervalk BP, Raymond A, Jackman SD, Birol I. 2015. Sealer: a scalable gap-closing application for finishing draft genomes. BMC Bioinformatics 16:230. https://doi.org/10.1186/s12859-015-0663-4.
7. Delcher AL, Phillippy A, Carlton J, Salzberg SL. 2002. Fast algorithms for large-scale genome alignment and comparison. Nucleic Acids Res 30:2478–2483. https://doi.org/10.1093/nar/30.11.2478.
8. Hunt M, Newbold C, Berriman M, Otto TD. 2014. A comprehensive evaluation of assembly scaffolding tools. Genome Biol 15:R42. https://doi.org/10.1186/gb-2014-15-3-r42.
9. Walker BJ, Abeel T, Shea T, Priest M, Abouelliel A, Sakthikumar S, Cuomo CA, Zeng Q, Wortman J, Young SK, Earl AM. 2014. Pilon: an integrated tool for comprehensive microbial variant detection and genome assembly improvement. PLoS One 9:e112963. https://doi.org/10.1371/journal.pone.0112963.
10. Angiuoli SV, Gussman A, Klimke W, Cochrane G, Field D, Garrity GM, Kodira CD, Kyrpides N, Madupu R, Markowitz V, Tatusova T, Thomson N, White O. 2008. Toward an online repository of standard operating procedures (SOPs) for (meta) genomic annotation. OMICS 12:137–141. https://doi.org/10.1089/omi.2008.0017.
11. Darling AE, Jospin G, Lowe E, Matsen FA, Bik HM, Eisen JA. 2014. PhyloSift: phylogenetic analysis of genomes and metagenomes. PeerJ 2:e243. https://doi.org/10.7717/peerj.243.

AMERICAN SOCIETY FOR MICROBIOLOGY | genomeAnnouncements™

ERRATUM

Erratum for Orr et al., "Draft Genome Sequences of Two Unclassified *Chitinophagaceae* Bacteria, IBVUCB1 and IBVUCB2, Isolated from Environmental Samples"

Russell J. S. Orr,[a] Stephane Rombauts,[b,c] Yves Van de Peer,[b,c] Kamran Shalchian-Tabrizi[a]

Section for Genetics and Evolutionary Biology (EVOGENE), Department of Biosciences, University of Oslo, Oslo, Norway[a]; Department of Plant Biotechnology and Bioinformatics, Ghent University, Ghent, Belgium[b]; VIB Center for Plant Systems Biology, Ghent, Belgium[c]

Volume 5, no. 33, e00787-17, 2017, https://doi.org/10.1128/genomeA.00787-17.

Page 2: Reference 5 should read as follows.

5. Warren RL, Yang C, Vandervalk BP, Behsaz B, Lagman A, Jones SJ, Birol I. 2015. LINKS: scalable, alignment-free scaffolding of draft genomes with long reads. Gigascience 4:35. https://doi.org/10.1186/s13742-015-0076-3.

Published 12 October 2017

Citation Orr RJS, Rombauts S, Van de Peer Y, Shalchian-Tabrizi K. 2017. Erratum for Orr et al., "Draft genome sequences of two unclassified *Chitinophagaceae* bacteria, IBVUCB1 and IBVUCB2, isolated from environmental samples." Genome Announc 5:e01152-17. https://doi.org/10.1128/genomeA.01152-17.