Draft Genome Sequence of *Endozoicomonas acroporae* Strain Acr-14^T, Isolated from *Acropora* Coral

Kshitij Tandon,[a,b,c] Pei-Wen Chiang,[a] Wen-Ming Chen,[d] Sen-Lin Tang[a]

[a]Biodiversity Research Center, Academia Sinica, Taipei, Taiwan

[b]Bioinformatics Program, Institute of Information Science, Taiwan International Graduate Program, Academia Sinica, Taipei, Taiwan

[c]Institute of Bioinformatics and Structural Biology, National Tsing Hua University, Hsinchu, Taiwan

[d]Laboratory of Microbiology, Department of Seafood Science, National Kaohsiung Marine University, Nantzu, Kaohsiung City, Taiwan

ABSTRACT A lacuna exists in our understanding of the genetic makeup of *Endozoicomonas* bacteria, due to scarcity of genome sequences. We report here the first draft genome sequence of *Endozoicomonas acroporae* Acr-14, a type strain isolated from the coral *Acropora*. This sequence will foster an understanding of the genetic makeup and role of hosts in shaping gene repertoires.

The genus *Endozoicomonas* belongs to the phylum *Proteobacteria*, class *Gammaproteobacteria*, with the type species being *Endozoicomonas elysicola* (1). Members of this genus form a significant proportion of the bacterial community in diverse marine hosts, including sponges (2), mollusks (1, 3–5) tubeworms (6), gorgonians (7, 8), and corals (9–14). Currently, there are only two whole-genome sequences of *Endozoicomonas montiporae* strains isolated from the Scleractinia coral *Montipora aequituberculata* (15, 16). Here, we report the first draft genome sequence of strain Acr-14^T from the novel species *Endozoicomonas acroporae*, isolated from *Acropora* coral off the coast of southern Taiwan. The type strain and taxonomic information have been reported previously (17).

Strain Acr-14^T was purified and cultivated as described previously (17), genomic DNA was isolated with the cetyltrimethylammonium bromide (CTAB) method, and the purity of DNA was checked with NanoDrop 1000 (Thermo Scientific, USA). Whole-genome sequencing was performed at the Biodiversity Research Center Academia Sinica (BRCAS) core sequencing facility with a paired-end MiSeq library generated to achieve a 500-bp insert size with an Illumina MiSeq platform. The obtained reads were quality filtered and trimmed (at a Phred score of ≥30) with the NGS QC toolkit (18). Quality-filtered and trimmed reads were *de novo* assembled using CLC Genomics Workbench version 1.10.1 (Qiagen), with a bubble size of 40, automatic detection of word size enabled, and a minimum contig length of 500 bp (no scaffolding was performed). A total of 309 contigs yielded a genome sequence 6,048,850 bp long, with 448× coverage and a G+C content of 49.16%. The largest contig and N_{50} value were 161,511 bp and 47,658 bp, respectively. The genome was estimated to be 98.56% complete using CheckM (19).

Open reading frame (ORF) prediction and automatic annotation were performed using the Prokka software (20), with default parameters, obtaining the outputs in GenBank format. The genome contains 5,104 genes, 5,018 coding sequences (CDSs), 79 tRNAs, 5 rRNAs (16S and 5S), and 4 repeat regions.

Furthermore, 5 prophages (2 intact, 2 incomplete, and 1 questionable) were detected in the genome using PHAST (21), and 4 typical clustered regularly interspaced short palindromic repeat (CRISPR) structures were also detected with Prokka (20).

A BLASTn (22) comparison of 16S rRNA obtained after assembly with the NR database gave an identical (100%) match with the already-deposited type strain 16S rRNA (GenBank accession no. LN875493). According to phylogenetic analysis based on 16S rRNA, the closest relative of Acr-14^T is *Endozoicomonas atrinae* WP70^T (sequence similarity, 96.7%) (17).

Accession number(s). This whole-genome shotgun project has been deposited at DDBJ/ENA/GenBank under the accession no. PJPV00000000. The version described in this paper is version PJPV01000000.

ACKNOWLEDGMENTS

REFERENCES

1. Kurahashi M, Yokota A. 2007. *Endozoicomonas elysicola* gen. nov., sp. nov., a γ-proteobacterium isolated from the sea slug *Elysia ornata*. Syst Appl Microbiol 30:202–206. https://doi.org/10.1016/j.syapm.2006.07.003.
2. Nishijima M, Adachi K, Katsuta A, Shizuri Y, Yamasato K. 2013. *Endozoicomonas numazuensis* sp. nov., a gammaproteobacterium isolated from marine sponges, and emended description of the genus *Endozoicomonas* Kurahashi and Yokota 2007. Int J Syst Evol Microbiol 63:709–714. https://doi.org/10.1099/ijs.0.042077-0.
3. Hyun DW, Shin NR, Kim MS, Oh SJ, Kim PS, Whon TW, Bae JW. 2014. *Endozoicomonas atrinae* sp. nov., isolated from the intestine of a comb pen shell *Atrina pectinata*. Int J Syst Evol Microbiol 64:2312–2318. https://doi.org/10.1099/ijs.0.060780-0.
4. Jensen S, Duperron S, Birkeland NK, Hovland M. 2010. Intracellular *Oceanospirillales* bacteria inhabit gills of *Acesta* bivalves. FEMS Microbiol Ecol 74:523–533. https://doi.org/10.1111/j.1574-6941.2010.00981.x.
5. Zielinski FU, Pernthaler A, Duperron S, Raggi L, Giere O, Borowski C, Dubilier N. 2009. Widespread occurrence of an intranuclear bacterial parasite in vent and seep bathymodiolin mussels. Environ Microbiol 11:1150–1167. https://doi.org/10.1111/j.1462-2920.2008.01847.x.
6. Forget NL, Kim Juniper S. 2013. Free-living bacterial communities associated with tubeworm (*Ridgeia piscesae*) aggregations in contrasting diffuse flow hydrothermal vent habitats at the Main Endeavour Field, Juan de Fuca Ridge. Microbiologyopen 2:259–275. https://doi.org/10.1002/mbo3.70.
7. Bayer T, Arif C, Ferrier-Pagès C, Zoccola D, Aranda M, Voolstra CR. 2013. Bacteria of the genus *Endozoicomonas* dominate the microbiome of the Mediterranean gorgonian coral *Eunicella cavolini*. Mar Ecol Prog Ser 479:75–84. https://doi.org/10.3354/meps10197.
8. Correa H, Haltli B, Duque C, Kerr R. 2013. Bacterial communities of the gorgonian octocoral *Pseudopterogorgia elisabethae*. Microb Ecol 66:972–985. https://doi.org/10.1007/s00248-013-0267-3.
9. Lema KA, Willis BL, Bourne DG. 2014. Amplicon pyrosequencing reveals spatial and temporal consistency in diazotroph assemblages of the *Acropora millepora* microbiome. Environ Microbiol 16:3345–3359. https://doi.org/10.1111/1462-2920.12366.
10. Apprill A, Hughen K, Mincer T. 2013. Major similarities in the bacterial communities associated with lesioned and healthy Fungiidae corals. Environ Microbiol 15:2063–2072. https://doi.org/10.1111/1462-2920.12107.
11. Speck MD, Donachie SP. 2012. Widespread *Oceanospirillaceae* bacteria in *Porites* spp. J Mar Biol 2012:1–7.
12. Lesser MP, Jarett JK. 2014. Culture-dependent and culture-independent analyses reveal no prokaryotic community shifts or recovery of *Serratia marcescens* in *Acropora palmata* with white pox disease. FEMS Microbiol Ecol 88:457–467. https://doi.org/10.1111/1574-6941.12311.
13. Bayer T, Neave MJ, Alsheikh-Hussain A, Aranda M, Yum LK, Mincer T, Hughen K, Apprill A, Voolstra CR. 2013. The microbiome of the Red Sea coral *Stylophora pistillata* is dominated by tissue-associated *Endozoicomonas* bacteria. Appl Environ Microbiol 79:4759–4762. https://doi.org/10.1128/AEM.00695-13.
14. Jessen C, Villa Lizcano JF, Bayer T, Roder C, Aranda M, Wild C, Voolstra CR. 2013. *In-situ* effects of eutrophication and overfishing on physiology and bacterial diversity of the Red Sea coral *Acropora hemprichii*. PLoS One 8:e62091. https://doi.org/10.1371/journal.pone.0062091.
15. Neave MJ, Michell CT, Apprill A, Voolstra CR. 2014. Whole-genome sequences of three symbiotic *Endozoicomonas* strains. Genome Announc 2:e00802-14. https://doi.org/10.1128/genomeA.00802-14.
16. Ding JY, Shiu JH, Chen WM, Chiang YR, Tang SL. 2016. Genomic insight into the host-endosymbiont relationship of *Endozoicomonas montiporae* CL-33^T with its coral host. Front Microbiol 7:251. https://doi.org/10.3389/fmicb.2016.00251.
17. Sheu SY, Lin KR, Hsu MY, Sheu DS, Tang SL, Chen WM. 2017. *Endozoicomonas acroporae* sp. nov., isolated from *Acropora* coral. Int J Syst Evol Microbiol 67:3791–3797. https://doi.org/10.1099/ijsem.0.002194.
18. Patel RK, Jain M. 2012. NGS QC toolkit: a toolkit for quality control of next generation sequencing data. PLoS One 7:e30619. https://doi.org/10.1371/journal.pone.0030619.
19. 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.
20. Seemann T. 2014. Prokka: Rapid prokaryotic genome annotation. Bioinformatics 30:2068–2069. https://doi.org/10.1093/bioinformatics/btu153.
21. Zhou Y, Liang Y, Lynch KH, Dennis JJ, Wishart DS. 2011. PHAST: a fast phage search tool. Nucleic Acids Res 39:W347–W352. https://doi.org/10.1093/nar/gkr485.
22. Altschul SF, Gish W, Miller W, Myers EW, Lipman DJ. 1990. Basic local alignment search tool. J Mol Biol 215:403–410. https://doi.org/10.1016/S0022-2836(05)80360-2.