Genome Sequences of Three Pseudoalteromonas Strains (P1-8, P1-11, and P1-30), Isolated from the Marine Hydroid Hydractinia echinata

The Harvard community has made this article openly available. Please share how this access benefits you. Your story matters

Citation


Published Version
doi:10.1128/genomeA.01380-15

Citable link
http://nrs.harvard.edu/urn-3:HUL.InstRepos:23993623

Terms of Use
This article was downloaded from Harvard University’s DASH repository, and is made available under the terms and conditions applicable to Other Posted Material, as set forth at http://nrs.harvard.edu/urn-3:HUL.InstRepos:dash.current.terms-of-use#LAA
M}arine pseudoalteromonads are commonly associated with diverse marine eukaryotic hosts (1, 2) and exhibit a remarkable ability to produce small molecules with a broad range of bioactivities, including antibacterial (3), (anti)biofouling (4, 5), and algicidal (6) activities. We isolated three Pseudoalteromonas strains from the tissue of Hydractinia echinata, a colonial marine hydroid growing on gastropod shells inhabited by hermit crabs (Pagurus pollicaris). Sequencing these strains’ genomes will assist the manipulation of Pseudoalteromonas genomes, facilitate the discovery and production of new and biologically active molecules (7), and might provide insights into the molecular cues and mechanisms involved in the recruitment and settlement of H. echinata larvae (8).

Freshly collected H. echinata were purchased from the Marine Biological Laboratory (Woods Hole, MA, USA), and the tissue surface of feeding polyps were investigated for the presence of bacteria from the Pseudoalteromonas genus. Clean isolates were cultured in marine broth (Difco 2216) for 3 days at 30°C (150 rpm), and metabolites were extracted using standard solid-phase extraction methods. The resulting organic extracts were tested for antimicrobial activity against a broad range of human pathogenic bacteria and fungi, and showed weak to moderate antimicrobial activity against Gram-positive bacteria (e.g., Staphylococcus aureus). Genomic DNA was extracted using the GenElute blood genomic DNA kit (Sigma-Aldrich) according to the manufacturer’s protocol. Sequencing was performed at the Harvard Medical School Biopolymers Facility using Illumina TruSeq 50-bp paired-end libraries and a HiSeq2000 instrument (Illumina CASAVA version 1.8.2). A fraction of these reads representing ~50× coverage were assembled using the A5 pipeline version 201401013 (9) and screened for potential contaminations using bologyd (10). Genomes were annotated using Prokka version 1.10 (11), and statistics were calculated using scripts from the Assemblathon 2 project (12).

The draft genome of strain P1-8 was sequenced to 50× coverage and comprises 37 contigs in 29 scaffolds, totaling 4,488,653 bases in length and having a G+C content of 41.2%. Its annotation includes 3,992 coding sequences (CDSs), 36 tRNAs, and 3 rRNAs.

The draft genome of strain P1-11 was sequenced to 51× coverage and comprises 44 contigs in 31 scaffolds, totaling 4,377,754 bases in length and having a G+C content of 41.0%. Its annotation includes 3,885 CDSs, 39 tRNAs, and 3 rRNAs.

The draft genome of strain P1-30 was sequenced to 51× coverage and comprises 51 contigs in 35 scaffolds, totaling 4,337,278 bases in length and having a G+C content of 40.9%. Its annotation includes 3,824 CDSs, 36 tRNAs, and 3 rRNAs.

Genes associated with biofilm formation and surface attachments, including genes encoding for curli, type II secretion system, type IV pili, and capsular polysaccharide (O-antigen) were identified, reflecting the adaptation to successful persistence and competition on marine surfaces (13). Genes encoding for secondary metabolite production (e.g., alterochromides), bacteriocins, and siderophore function (e.g., desferrioxamines) were detected using antiSMASH (14) and SMIPS (15). These genomes will promote the genetic analysis of the Pseudoalteromonas genus and will provide insights into secondary metabolite production and the molecular cues and mechanisms involved in the recruitment and settlement of H. echinata larvae (8).

Nucleotide sequence accession numbers. The whole-genome shotgun projects for strains P1-8, P1-11, and P1-30 have been deposited in DDBJ/EMBL/GenBank under the accession numbers LJSO00000000, LJSP00000000, and LKBC00000000, respectively. The versions described in this paper are the first versions, LJSO01000000, LJSP01000000, and LKBC01000000.

ACKNOWLEDGMENTS

We are grateful for financial support from the NIH to J.C. (GM086258) and the German National Academy of Sciences Leopoldina for a postdoctoral fellowship to C.B. (LPDS 2011-2). J.L.K. was supported by funds from the University of Connecticut. M.R. was supported by the graduate school Jena School for Microbial Communication (JSMC), financed by the Deutsche Forschungsgemeinschaft, and T.W. was supported by the...
Klassen et al.

International Leibniz Research School for Microbial and Molecular Interactions (ILRS), as part of the JSMC.

REFERENCES


