Draft Genome Sequence of *Pseudoalteromonas* sp. Strain PAB 2.2 Isolated from Abrolhos Bank (Brazil)

Bruno S. O. Silva, Maria S. Nobrega, Luciana Leomil, Diogo A. Tschoeke, Gizele D. Garcia, Graciela Dias, Cristiane C. Thompson, Fabiano L. Thompson

Instituto de Biologia, Universidade Federal do Rio de Janeiro, Rio de Janeiro, Brazil; Núcleo em Ecologia e Desenvolvimento Sócio-Ambiental de Macaé (NUPEM), Universidade Federal do Rio de Janeiro, Macaé, Rio de Janeiro, Brazil; Instituto de Microbiologia, Universidade Federal do Rio de Janeiro, Macaé, Rio de Janeiro, Brazil; SAGE, COPPE, Federal University of Rio de Janeiro, Rio de Janeiro, Brazil

**ABSTRACT** We present here the draft genome sequence of *Pseudoalteromonas* sp. strain PAB 2.2, isolated from water of Parcel de Abrolhos coral reef (17°57′32.7″; 38°30′20.3″), on Abrolhos Bank, at a depth of 12 m. The assembly consists of 4,434,635 bp and contains 40 contigs, with a G+C content of 41.60%.

The genus *Pseudoalteromonas* was described in 1995, when it was separated from the genus *Alteromonas* (1) and includes Gram-negative, gammaproteobacteria, heterotrophic and aerobic with polar flagellum bacteria. *Pseudoalteromonas* spp. are involved in the production of antimicrobial metabolites that protect coral holobionts against pathogens (2) and show the ability to degrade many components of petroleum (3). *Pseudoalteromonas* spp. can be found in a variety of habitats, including deep and surface waters (4, 5), polar waters (6), and sediments (7). These distinct lifestyles are based on different sets of genes, such as those for lateral flagellum expression in sediment strains and those for reactive oxygen production in polar strains (6, 7). These ubiquitous characteristics point to expressive and diverse adaptive strategies for *Pseudoalteromonas* spp., leading to important research topics. Here, we present the genome sequence of *Pseudoalteromonas* sp. strain PAB 2.2, which was isolated from the waters of Parcel de Abrolhos coral reef, in Abrolhos Bank, at a depth of 12 m.

The DNA was extracted using an adaptation of Pitcher’s protocol (8). The genomic DNA was sequenced using a Nextera XT DNA sample preparation kit (Illumina, San Diego, CA, USA). The size distribution of the libraries was evaluated using a 2100 Bioanalyzer and a High-Sensitivity DNA kit (Agilent, Santa Clara, CA, USA). A 7500 Real Time PCR machine (Applied Biosystems, Foster City, CA, USA) and a KAPA Library Quantification kit (Kapa Biosystems, Wilmington, MA, USA) were used for the quantification of the libraries. Paired-end sequencing (2 × 300 bp) was performed on a MiSeq platform (Illumina, Rio de Janeiro, Brazil). The sequences obtained were preprocessed using PRINSEQ software to remove reads smaller than 35 bp and sequences with a Phred score lower than 30 (9). Sequence reads were assembled using A5-Miseq software (10) with default parameters. A second assembly using CAP3 software (11), based on the contigs obtained, was completed to improve the assembly, as done previously (12). The gene prediction and functional annotation were performed using the RAST server (13).

The sequencing generated 40 contigs that concatenate in 4,434,635 bp with a G+C content of 41.60%. RAST predicted 2,926 open reading frames, 3,926 coding sequences, and 115 RNA sequences (100 tRNAs and 15 rRNAs). Analyzing the genes predicted by RAST, it was possible to observe 95 genes involved in resistance to antibiotics and toxic...
compounds, such as multidrug resistance efflux pumps and copper, zinc, and arsenic resistance; 11 genes for the metabolism of aromatic compounds, especially benzoate degradation; and 126 genes for motility and chemotaxis, including operons \textit{fli}, \textit{flg}, and \textit{flh} and genes for flagellar motor rotation proteins MotA, MotX, MotB, and MotY. The absence of genes encoding for lateral flagellum indicates that even though this strain presents a great number of genes related to motility, it is incapable of surviving on sediments.

\textbf{Accession number(s).} This whole-genome shotgun project has been deposited in GenBank under the accession number \texttt{LYPI00000000}. The version described in this paper is the first version.

\textbf{ACKNOWLEDGMENTS}  
We thankfully acknowledge CNPq, CAPES, and FAPERJ for their funding and support for this project. This paper is part of the D.Sc. requirements of Bruno Sergio de O. Silva, at the Biodiversity and Evolutionary Biology Graduate Program of the Federal University of Rio de Janeiro.

\textbf{REFERENCES}  
1. Gauthier G, Gauthier M, Christen R. 1995. Phylogenetic analysis of the genera \textit{Alteromonas}, \textit{Shewanella}, and \textit{Moritella} using genes coding for small-subunit rRNA sequences and division of the genus \textit{Alteromonas} into two genera, \textit{Alteromonas} (emended) and \textit{Pseudoalteromonas} \textit{gen. nov.}, and proposal of twelve new species combinations. Int J Syst Bacteriol 45:755–761. \url{https://doi.org/10.1099/00207713-45-4-755}.

2. Offret C, Desriac F, Le Chevalier P, Mounier J, Jégou C, Fleury Y. 2016. Spotlight on antimicrobial metabolites from the marine bacteria \textit{Pseudoalteromonas}: chemodiversity and ecological significance. Mar Drugs 14:129. \url{https://doi.org/10.3390/md14070129}.

3. Harris AP, Techtmann SM, Stelling SC, Utturkar SM, Alshibli NK, Brown SD, Hazen TC. 2014. Draft genome sequence of \textit{Pseudoalteromonas} sp. strain NDE8, an oil-degrading isolate from eastern Mediterranean Sea water collected at a depth of 1,210 meters. Genome Announc 2(6):e01212-14. \url{https://doi.org/10.1128/genomeA.01212-14}.

4. Wietz M, Gram L, Jørgensen B, Schramm A. 2010. Latitudinal patterns in the abundance of major marine bacterioplankton groups. Aquat Microb Ecol 61:179 –189. \url{https://doi.org/10.3354/ame01443}.

5. Qin QL, Li Y, Zhang YJ, Zhou ZM, Zhang WX, Chen XL, Zhang XY, Zhou BC, Wang L, Zhang YZ. 2011. Comparative genomics reveals a deep-sea sediment-adapted life style of \textit{Pseudoalteromonas} \textit{sp.} SM9913. ISME J 5:274 –284. \url{https://doi.org/10.1038/ismej.2010.103}.

6. Médigue C, Krin E, Pascal G, Barbe V, Bernsel A, Bertin PN, Cheung F, Cruveller S, D’Amico S, Duillo A, Fang G, Feller G, Ho C, Mangenot S, Marino G, Nilsson J, Parrilli E, Rocha EP, Rouy Z, Sekowska A, Tutino ML, Vallenet D, von Heijne G, Danchin A. 2005. Coping with cold: the genome of the versatile marine Antarctica bacterium \textit{Pseudoalteromonas haloplanktis} TAC125. Genome Res 15:1325–1335. \url{https://doi.org/10.1101/gr.4126905}.

7. Park YD, Baik KS, Yi H, Bae KS, Chun J. 2005. \textit{Pseudoalteromonas byunsansensis} \textit{sp. nov.}, isolated from tidal flat sediment in Korea. Int J Syst Evol Microbiol 55:2519 –2523. \url{https://doi.org/10.1099/ijs.0.63750-0}.

8. Pitcher OG, Saunders NA, Owen RJ. 1989. Rapid extraction of bacterial genomic DNA with guanidium thiocyanate. Lett Appl Microbiol 8:151–156. \url{https://doi.org/10.1111/j.1472-765X.1989.tb00262.x}.

9. Schmieder R, Edwards R. 2011. Quality control and preprocessing of metagenomic datasets. Bioinformatics 27:863–864. \url{https://doi.org/10.1093/bioinformatics/btr026}.

10. Coil D, Jospin G, Darling AE. 2015. AS-miseq: an updated pipeline to assemble microbial genomes from Illumina MiSeq data. Bioinformatics 31:587–589. \url{https://doi.org/10.1093/bioinformatics/btu661}.

11. Huang X, Madan A. 1999. CAP3: a DNA sequence assembly program. Genome Res 9:868 –877. \url{https://doi.org/10.1101/gr.9.9.868}.

12. Tschoeke DA, Moreira APB, Chimetto Tonon LA, de Mesquita MMA, Gregoracci GB, Gomes-Gil B, Valle R, Thompson CC, Thompson FL. 2014. Exploring the genome of cheese starter lactic acid bacterium \textit{Lactococcus lactis} subsp. lactis CECT 4433. Genome Announc 2(6):e01142-14. \url{https://doi.org/10.1128/genomeA.01142-14}.

13. Overbeek R, Olson R, Pusch GD, Olsen GJ, Davis JJ, Disz T, Edwards RA, Gerdes S, Parrello B, Shukla M, Vonstein V, Wattam AR, Xia F, Stevens R. 2014. The SEED and the Rapid Annotation of microbial genomes using Subsystems Technology (RAST). Nucleic Acids Res 42:D206–D214. \url{https://doi.org/10.1093/nar/gkt1226}.