



Draft Genome Sequences of Three β -Lactam-Catabolizing Soil *Proteobacteria*

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ABSTRACT Most antibiotics are derived from the soil, but their catabolism there, which is necessary to close the antibiotic carbon cycle, remains uncharacterized. We report the first draft genome sequences of soil *Proteobacteria* identified for subsisting solely on β -lactams as their carbon sources. The genomes encode multiple β -lactamases, although their antibiotic catabolic pathways remain enigmatic.

Antibiotic synthesis and antibiotic resistance are both ancient and well-studied features of the soil microbiome (1). Missing from our understanding of antibiotic ecology is the ultimate environmental fate of these potential carbon sources. While antibiotic catabolism has been recognized since the discovery of the first compounds (2–4), including in multiple *Proteobacteria* species (5–10), the cellular machinery underlying these phenotypes has eluded discovery. In order to facilitate the study of this phenomenon, we have undertaken the whole-genome sequencing of three soil isolates termed ABC07 (*Pseudomonas* sp. strain PE-S1G-1), ABC08 (*Pandoraea* sp. strain PE-S2R-1), and ABC10 (*Pandoraea* sp. strain PE-S2T-3). These strains were previously described as being capable of utilizing penicillin as their sole source of carbon for growth in minimal medium (9).

Each ABC strain was inoculated into 5 ml of LB from -80°C glycerol stocks (15% in LB) and grown aerobically at room temperature. ABC strain genomic DNA was extracted from cell pellets using the Mo Bio PowerMax soil kit (catalog no. 12988-10) and dissolved in Tris-EDTA (TE) buffer. Genomes were sequenced at the Edgewood Chemical Biological Center Genomics Laboratory using a 454-GS FLX sequencer, and raw .sff files were assembled *de novo* using Newbler version 2.0.01.14 (454 Life Sciences) with the following parameters: SeedStep, 12; SeedLength, 16; MinSeedCount, 1; SeedHitLimit, 10,000; HitPositionLimit, 200; MinMatchLength, 40; MinMatchIdentity, 90; MatchIdentScore, 2; MatchDiffScore, -3 ; and MatchUniqThresh, 12. Each sequenced genome resulted in ca. 500,000 reads encompassing $\sim 10^8$ bp. ABC07, ABC08, and ABC10 were assembled into 137, 38, and 25 large contigs, respectively, with contig N_{50} metrics of 98,867, 1,179,846, and 601,724 bp, respectively.

To identify features of the genomes potentially pertinent to antibiotic catabolism, genomes were uploaded to the online KBase server (11) for annotation using RAST (12). RAST predicted 6,594, 5,771, and 5,569 total features, and 10, 8, and 8 β -lactamases or

Received 26 May 2017 Accepted 13 June 2017 Published 10 August 2017

Citation Crofts TS, Wang B, Spivak A, Gianoulis TA, Forsberg KJ, Gibson MK, Johnsky LA, Broomall SM, Rosenzweig CN, Skowronski EW, Gibbons HS, Sommer MOA, Dantas G. 2017. Draft genome sequences of three β -lactam-catabolizing soil *Proteobacteria*. *Genome Announc* 5:e00653-17. <https://doi.org/10.1128/genomeA.00653-17>.

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β -lactamase-like features in the genomes of ABC07, ABC08, and ABC10, respectively. The top three functional categories identified for each strain were carbohydrates, amino acids and derivatives, cofactors, vitamins, prosthetic groups, and pigments for ABC07; carbohydrates, metabolism of aromatic compounds, and amino acids and derivatives for ABC08; and carbohydrates, metabolism of aromatic compounds, and amino acids and derivatives for ABC10.

Analysis of genomes from three antibiotic-catabolizing bacteria has revealed the presence of multiple β -lactamase genes in each organism and suggests a conserved role for the metabolism of aromatic carbon sources and amino acids. Antibiotic inactivation is confirmed in these strains phenotypically (9) and, here, by genotype, and it may represent the first step in β -lactam catabolism. The release of these genomes should significantly aid in the identification of antibiotic catabolism pathways.

Accession number(s). This whole-genome shotgun project has been deposited at DDBJ/ENA/GenBank under the accession numbers [NGUS00000000](#), [NGUR00000000](#), and [NGUQ00000000](#) for strains ABC07, ABC08, and ABC10, respectively. The versions described in this paper are the first versions, NGUS01000000, NGUR01000000, and NGUQ01000000, respectively.

ACKNOWLEDGMENTS

This work is supported in part by awards to G.D. through the Edward Mallinckrodt, Jr Foundation (Scholar Award) and from the NIH Director's New Innovator Award (<http://commonfund.nih.gov/newinnovator/>), the National Institute of Diabetes and Digestive and Kidney Diseases (NIDDK [<http://www.niddk.nih.gov/>]), the National Institute of General Medical Sciences (NIGMS [<http://www.nigms.nih.gov/>]), and the National Institute of Allergy and Infectious Diseases (NIAID [<https://www.niaid.nih.gov/>]) of the National Institutes of Health (NIH) under award numbers DP2DK098089, R01GM099538, and R01AI123394, respectively. T.S.C. received support from a National Institute of Child Health and Development training grant through award no. T32 HD049305 (Kelle H. Moley, principal investigator). K.J.F. received support from the NIGMS Cell and Molecular Biology Training Grant (GM 007067), the NHGRI Genome Analysis Training Program (T32 HG000045), and the NSF as a graduate research fellow (award number DGE-1143954). M.K.G. received support as a Spencer T. Olin Fellow at Washington University and from the NSF as a graduate research fellow (DGE-1143954). Sequencing through the U.S. Army Edgewood Chemical Biological Center was supported in part through funding provided by the Transformational Medical Technologies Initiative of the Defense Threat Reduction Agency, U.S. Department of Defense.

The content is solely the responsibility of the authors and does not necessarily represent the official views of the funding agencies.

We are thankful to Robert Potter of the Dantas lab for general helpful discussions regarding the manuscript.

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