Draft Genome Sequences of Two Ralstonia pickettii Strains with Different Aminoglycoside Resistance Phenotypes

Ivone Vaz-Moreira, Javier Tamames, José Luis Martinez, Célia M. Manaia

Universidade Católica Portuguesa, CBQF–Centro de Biotecnologia e Química Fina, Laboratório Associado, Escola Superior de Biotecnologia, Porto, Portugal; LEPABE–Laboratório de Engenharia de Processos, Ambiente, Biotecnologia e Energia, Faculdade de Engenharia, Universidade do Porto, Porto, Portugal; Centro Nacional de Biotecnologia, Conselho Superior de Investigaciones Científicas (CSIC), Cantablanco, Madrid, Spain

The genomes of two Ralstonia pickettii strains (H2Cu2 and H2Cu5), isolated from hospital effluent in a selective medium containing CuSO4, were sequenced. They presented MICs of >256 and 6 μg/ml for the aminoglycoside gentamicin, respectively. The 5.2-Mb draft genomes have 40 contigs for strain H2Cu2 and 113 for H2Cu5.

Received 14 September 2016 Accepted 21 September 2016 Published 10 November 2016

Copyright © 2016 Vaz-Moreira et al. This is an open-access article distributed under the terms of the Creative Commons Attribution 4.0 International license. Address correspondence to Javier Tamames, jtamames@cbqf.unican.es, or Célia M. Manaia, cmanaia@porto.ucp.pt.

FUNDING INFORMATION

This research was partially funded by the Fundação para a Ciência e a Tecnologia (FCT) through projects UID/Multi/50016/2013 and NanoDiaBac ENMed/0001/2014 and by FCT and MINCO through the project WaterPI/0001/2013 STARE (Stopping Antibiotic Resistance Evolution). I.V.-M. was supported by FCT grant SFRH/BPD/87360/2012, and international cooperation was funded by COST-European Cooperation in Science and Technology under COST Action ES1403: New and Emerging Challenges and Opportunities in Wastewater Reuse (NEREUS).

REFERENCES


