



Draft Genome Sequences of *Pseudomonas aeruginosa* B3 Strains Isolated from a Cystic Fibrosis Patient Undergoing Antibiotic Chemotherapy

Marvig, Rasmus Lykke; Jochumsen, Nicholas; Johansen, Helle Krogh; Høiby, Niels; Molin, Søren; Sommer, Morten; Jelsbak, Lars; Folkesson, Anders

Published in:
Genome Announcements

Link to article, DOI:
[10.1128/genomeA.00804-13](https://doi.org/10.1128/genomeA.00804-13)

Publication date:
2013

Document Version
Publisher's PDF, also known as Version of record

[Link back to DTU Orbit](#)

Citation (APA):
Marvig, R. L., Jochumsen, N., Johansen, H. K., Høiby, N., Molin, S., Sommer, M., Jelsbak, L., & Folkesson, A. (2013). Draft Genome Sequences of *Pseudomonas aeruginosa* B3 Strains Isolated from a Cystic Fibrosis Patient Undergoing Antibiotic Chemotherapy. *Genome Announcements*, 1(5), [e00804-13]. <https://doi.org/10.1128/genomeA.00804-13>

General rights

Copyright and moral rights for the publications made accessible in the public portal are retained by the authors and/or other copyright owners and it is a condition of accessing publications that users recognise and abide by the legal requirements associated with these rights.

- Users may download and print one copy of any publication from the public portal for the purpose of private study or research.
- You may not further distribute the material or use it for any profit-making activity or commercial gain
- You may freely distribute the URL identifying the publication in the public portal

If you believe that this document breaches copyright please contact us providing details, and we will remove access to the work immediately and investigate your claim.

Draft Genome Sequences of *Pseudomonas aeruginosa* B3 Strains Isolated from a Cystic Fibrosis Patient Undergoing Antibiotic Chemotherapy

Rasmus Lykke Marvig,^a Nicholas Jochumsen,^a Helle Krogh Johansen,^b Niels Høiby,^b Søren Molin,^a Morten O. Sommer,^a Lars Jelsbak,^a Anders Folkesson^a

Department of Systems Biology, Technical University of Denmark, Lyngby, Denmark^a; Department of Clinical Microbiology, Rigshospitalet, Copenhagen, Denmark^b

***Pseudomonas aeruginosa* frequently establishes chronic infections in the airways of patients suffering from cystic fibrosis (CF). Here, we report the draft genome sequences of four *P. aeruginosa* B3 strains isolated from a chronically infected CF patient undergoing antibiotic chemotherapy.**

Received 6 September 2013 Accepted 27 September 2013 Published 17 October 2013

Citation Marvig RL, Jochumsen N, Johansen HK, Høiby N, Molin S, Sommer MO, Jelsbak L, Folkesson A. 2013. Draft genome sequences of *Pseudomonas aeruginosa* B3 strains isolated from a cystic fibrosis patient undergoing antibiotic chemotherapy. *Genome Announc.* 1(5):e00804-13. doi:10.1128/genomeA.00804-13.

Copyright © 2013 Marvig et al. This is an open-access article distributed under the terms of the [Creative Commons Attribution 3.0 Unported license](https://creativecommons.org/licenses/by/3.0/).

Address correspondence to Anders Folkesson, afol@vet.dtu.dk.

Cystic fibrosis (CF) patients are subjected to intensive antibiotic therapy, and it is evident that this crucially affects the process of bacterial adaptation to the CF lung environment (1, 2). To further investigate the effects of antimicrobial chemotherapy on the adaptation of *Pseudomonas aeruginosa* to the CF lung, we sequenced the genomes of four strains of the *P. aeruginosa* B3 clone type isolated from consecutive sputum samples from a patient with long-term chronic *P. aeruginosa* infection undergoing 3 months of combination chemotherapy with oral ciprofloxacin and inhaled colistin due to recurrent isolation of *P. aeruginosa*. The sputum samples were collected and the strains were isolated as part of a longitudinal study where the first and subsequent samples were stored from the beginning of 2005 until July 2009 (1). The first sample was collected before chemotherapy was initiated and is represented by *P. aeruginosa* B3-1811, a mucoid isolate that was determined at the clinic to be colistin and ciprofloxacin sensitive. A sputum sample collected 2 months after the initiation of therapy contained *P. aeruginosa* with two different bacterial colony morphologies: a mucoid and colistin-sensitive strain (*P. aeruginosa* B3-208) and a nonmucoid and colistin-resistant strain (*P. aeruginosa* B3-20M). The last strain (*P. aeruginosa* B3-CFI), also colistin resistant, was isolated from a sputum sample obtained at the end of the 3-month treatment regime. Genomic DNA from the B3-1811, B3-208, B3-20M, and B3-CFI strains was prepared and sequenced as described previously (3) to generate 3,077,857, 2,445,795, 3,026,144, and 3,881,715 75-bp reads, respectively.

Using Velvet version 1.0.16, the reads were assembled into the draft genomes of strain B3-1811, with 6,657,892 bp, 285 contigs, and an N_{50} of 82,268 bp; strain B3-208, with 6,701,506 bp, 344 contigs, and an N_{50} of 66,611 bp; strain B3-20M, with 6,704,349 bp, 278 contigs, and an N_{50} of 77,595 bp; and strain B3-CFI, with 6,727,794 bp, 252 contigs, and an N_{50} of 87,472 bp. The optimal assembly settings were estimated using Velvet-Optimiser (the Victorian Bioinformatics Consortium [VBC],

Monash University; see <http://www.vicbioinformatics.com/software/velvetoptimiser.shtml>), with only contigs of ≥ 500 bp retained, and the assembly was assisted by initial mapping of the reads against the reference genome sequences of *P. aeruginosa* PAO1 (4) using the Velvet Columbus module.

A comparison of the genomes using MUMmer3 (5) revealed the four isolates to be closely related, sharing at least 99.6% of their genomic contents. The sequences of the four strains reported here will help to elucidate the genetic diversity that exists within clonal populations of *P. aeruginosa* sampled from a single CF patient and how the genetic composition can change quickly due to new selection pressures, such as antibiotic therapy.

Nucleotide sequence accession numbers. These genome sequences have been deposited in EMBL under the following accession no. (BioProject no.): [CBMP010000001](https://www.ebi.ac.uk/ena/browser/view/CBMP010000001) to [CBMP010000341](https://www.ebi.ac.uk/ena/browser/view/CBMP010000341) (PRJEB4309) for strain B3-1811, [CBMT010000001](https://www.ebi.ac.uk/ena/browser/view/CBMT010000001) to [CBMT010000418](https://www.ebi.ac.uk/ena/browser/view/CBMT010000418) (PRJEB4310) for strain B3-208, [CBMU010000001](https://www.ebi.ac.uk/ena/browser/view/CBMU010000001) to [CBMU010000338](https://www.ebi.ac.uk/ena/browser/view/CBMU010000338) (PRJEB4311) for strain B3-20M, and [CBMS010000001](https://www.ebi.ac.uk/ena/browser/view/CBMS010000001) to [CBMS010000314](https://www.ebi.ac.uk/ena/browser/view/CBMS010000314) (PRJEB4312) for strain B3-CFI.

ACKNOWLEDGMENTS

This work was supported by grants from the Danish Research Agency and the Lundbeck Foundation to S.M.

REFERENCES

- Hansen SK, Rau MH, Johansen HK, Ciofu O, Jelsbak L, Yang L, Folkesson A, Jarmer HØ, Aanaes K, von Buchwald C, Høiby N, Molin S. 2012. Evolution and diversification of *Pseudomonas aeruginosa* in the paranasal sinuses of cystic fibrosis children have implications for chronic lung infection. *ISME J.* 6:31–45.
- Folkesson A, Jelsbak L, Yang L, Johansen HK, Ciofu O, Høiby N, Molin S. 2012. Adaptation of *Pseudomonas aeruginosa* to the cystic fibrosis airway: an evolutionary perspective. *Nat. Rev. Microbiol.* 10:841–851.
- Yang L, Jelsbak L, Marvig RL, Damkiaer S, Workman CT, Rau MH, Hansen SK, Folkesson A, Johansen HK, Ciofu O, Høiby N, Sommer MO,

- Molin S. 2011. Evolutionary dynamics of bacteria in a human host environment. *Proc. Natl. Acad. Sci. U. S. A.* **108**:7481–7486.
4. Stover CK, Pham XQ, Erwin AL, Mizoguchi SD, Warrener P, Hickey MJ, Brinkman FS, Hufnagle WO, Kowalik DJ, Lagrou M, Garber RL, Goltry L, Tolentino E, Westbrook-Wadman S, Yuan Y, Brody LL, Coulter SN, Folger KR, Kas A, Larbig K, Lim R, Smith K, Spencer D, Wong GK, Wu Z, Paulsen IT, Reizer J, Saier MH, Hancock RE, Lory S, Olson MV. 2000. Complete genome sequence of *Pseudomonas aeruginosa* PAO1, an opportunistic pathogen. *Nature* **406**:959–964.
 5. Kurtz S, Phillippy A, Delcher AL, Smoot M, Shumway M, Antonescu C, Salzberg SL. 2004. Versatile and open software for comparing large genomes. *Genome Biol.* **5**:R12. doi:[10.1186/gb-2004-5-2-r12](https://doi.org/10.1186/gb-2004-5-2-r12).