



Omics-based tracking of *Pseudomonas aeruginosa* persistence in “eradicated” cystic fibrosis patients

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For 80 cystic fibrosis patients, this study used omics and positive culture history of *P. aeruginosa* infections to show that strains routinely persist over lengthy *Pseudomonas*-free periods. The authors recommend using genomic data in “eradication” metrics. <https://bit.ly/2H318Ca>

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ABSTRACT Whenever *Pseudomonas aeruginosa* is cultured from cystic fibrosis (CF) patient airways, the primary goal is eradication by antibiotic therapy. Success is defined by ≥ 6 months of negative bacterial airway cultures. However, we suspect that *P. aeruginosa* persists in airways without clinical detection for long periods.

Out of 298 *P. aeruginosa*-infected Copenhagen CF patients, we identified 80 with complete *P. aeruginosa* monitoring records and measured their maximum *P. aeruginosa*-free eradication periods (MEP). Isolates from 72 patients were whole-genome sequenced (n=567) and clone typed. Select isolate relatedness was examined through phylogenetic analysis and phenotypic multivariate modelling.

69 (86%) patients exhibited eradication in the monitoring period (2002–2018). Sequenced isolates bridged the MEP of 42 patients, and the same clone type persisted over the MEP in 18 (43%) patients. Patients with failed eradication were on average treated more intensively with antibiotics, but this may be linked to their more severe pre-MEP infection trajectories. Of the 42 patients, 26 also had sinus surgery; the majority (n=15) showed MEPs adjacent to surgery, and only five had persisting clone types. Importantly, combined phylogenetic–phenomic evaluation suggests that persisting clone types are a result of re-emergence of the same strain rather than re-infection from the environment, and similar relatedness is exhibited by paired lower and upper airway samples and in transmission cases.

In conclusion, nearly half of CF patients with supposed eradication may not truly be cleared of their original bacteria according to omics-based monitoring. This distinct cohort that is persistently infected would probably benefit from tailored antibiotic therapy.