Evolutionary insight from whole-genome sequencing of Pseudomonas aeruginosa from cystic fibrosis patients - DTU Orbit (28/12/2018)

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The opportunistic pathogen Pseudomonas aeruginosa causes chronic airway infections in patients with cystic fibrosis (CF), and it is directly associated with the morbidity and mortality connected with this disease. The ability of P. aeruginosa to establish chronic infections in CF patients is suggested to be due to the large genetic repertoire of P. aeruginosa and its ability to genetically adapt to the host environment. Here, we review the recent work that has applied whole-genome sequencing to understand P. aeruginosa population genomics, within-host microevolution and diversity, mutational mechanisms, genetic adaptation and transmission events. Finally, we summarize the advances in relation to medical applications and laboratory evolution experiments.

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