

Invasion, adaptation and evolution of bacteria moving from the environment to human airways

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One major aim of our research is to understand the mechanisms and routes by which bacteria change their life-style when moving from one environment to another. In particular we have investigated shifts between highly complex environments with mixtures of environmental cues. Our model system has been *Pseudomonas aeruginosa* moving from the environment to human airways of patients suffering from cystic fibrosis (CF). The current investigation platform is a strain collection composed of more than 600 clinical isolates of *P. aeruginosa* obtained from children and young adults suffering from CF. This collection covers longitudinal sampling of close to 60 different clone types isolated from 40 patients with *P. aeruginosa* airway infections from 1-10 years. Additionally, about 100 bacterial isolates from older chronically infected patients have been genome sequenced and phenotypically investigated.

In the presentation I will summarize our findings covering 40 years of adaptation of the bacteria to the airways. Although no common adaptation pattern has been identified, there are interesting examples illustrating what may be important for optimal fitness development.