Since January 2020 Elsevier has created a COVID-19 resource centre with free information in English and Mandarin on the novel coronavirus COVID-19. The COVID-19 resource centre is hosted on Elsevier Connect, the company's public news and information website.

Conclusion: These genomic adaptations strongly suggest that, after an initial period of adaptive evolution in response to strong selective pressures in the host, persistent *P. aeruginosa* populations may become fragmented and subject to stronger effects of genetic drift. Mutator phenotypes are enriched under these conditions and lead to early stages of degenerative genome evolution as *P. aeruginosa* persists in the respiratory tract of adults with CF. Our findings advance the literature on mechanisms driving *P. aeruginosa* evolution in this niche and underscore the relevance of CRS in overall CF respiratory health.

409

Pseudomonas aeruginosa intracellular survival in cystic fibrosis airway epithelial cells

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Background: The ubiquitous gram-negative bacteria *Pseudomonas aeruginosa* is an opportunistic pathogen causing chronic infection in adult cystic fibrosis (CF) patients, eventually leading to lung function decline [1]. Although *P. aeruginosa* is mainly described as residing in microcolonies in the sputum of larger airways of the conducting and respiratory system of CF patients, multiple in vitro studies have showed its ability to invade and survive intracellularly in different epithelium models, including airway epithelial cells (AECs) [2]. We hypothesized that the intracellular lifestyle of *P. aeruginosa* enables it to reside in the AECs of CF patients, providing a way to escape extracellular host immune defenses and drug therapy. This project aims to characterize the host–pathogen interactions occurring during the intracellular lifestyle of *P. aeruginosa* in AECs. We also propose to study the impact of CFTR mutation in this model of infection.
Methods: We used an approach based on immunohistochemistry to detect the association between *P. aeruginosa* and AECs in lungs from CF and non-CF patients. We characterized more deeply the intracellular cycle of *P. aeruginosa* using an in vitro model of AEC infection. The intracellular survival and cytotoxicity induction of different strains of *P. aeruginosa* was assessed by flow cytometry, confocal imaging, and CFU count. We finally characterize the impact of CFTR activity on *P. aeruginosa* intracellular cycle using cell lines (CF bronchial epithelial cells) and primary cells expressing functional or mutated nonfunctional forms of CFTR.
Results: Preliminary histological analysis revealed the presence of intracellular *P. aeruginosa* in AECs of CF patients. In vitro analysis of infected AECs showed that *P. aeruginosa* can be retrieved intracellularly up to 5 days after infection. We also observed longer intracellular survival of *P. aeruginosa* in polarized and nonpolarized cells expressing nonfunctional forms of CFTR (ΔF508 mutation) than in cells expressing a functional form of CFTR.
Conclusion: Our results indicate that *P. aeruginosa* can survive for a prolonged period of time in AECs and that expression of a nonfunctional form of CFTR leads to longer intracellular bacterial survival.
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410

Pseudomonas aeruginosa modulates SARS-CoV-2 infectivity in CF airway epithelial cells by increasing expression of the host protease TMPRSS2

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Background: One of the major challenges of the COVID-19 pandemic is to identify factors of susceptibility to SARS-CoV-2 infection. Doing so could allow recommendations to be adapted to populations and reduce the risk that the most vulnerable people will contract COVID-19, especially those with chronic respiratory diseases, including cystic fibrosis (CF). Until now, clinical follow-up of people with CF (PwCF) indicates that adults and children are not at higher risk of severe COVID-19 than the general population, although some factors (older age, CF-related diabetes, poor lung function, transplantation) have been shown to increase the risk of a severe clinical course. Airway epithelial cells (AECs) play a critical role in the lung immune response and in COVID-19 severity. SARS-CoV-2 infects the airways through ACE2 receptors; with 2 host proteases, TMPRSS2 and FURIN, involved in SARS-CoV-2 infectivity. We hypothesized that previous *P. aeruginosa* infection of AECs, frequent in PwCF, may affect SARS-CoV-2 infection.
Methods: Primary healthy and CF AECs were infected by *P. aeruginosa* (PAK strain). Primary AECs and Calu-3 cells (wild-type or knock-down for CFTR) were exposed to flagellin or SARS-CoV-2 (strain BetaCoV/France/IDF0571/2020). mRNA and protein expression of TMPRSS2, ACE2, and FURIN were assessed using RNAseq, RT-qPCR, and immunofluorescence and viral quantification by RT-qPCR targeting ORF1b-nsp14.
Results: We detected by RNAseq that TMPRSS2 mRNA is induced in CF primary AECs infected by *P. aeruginosa*. We further observed that the main component of *P. aeruginosa* flagella, flagellin, increases TMPRSS2 mRNA (primary AECs and Calu-3) and protein expression (Calu-3 cells) through TLR5-dependent signaling—especially in individuals deficient in CFTR. ACE2 and FURIN expression were not modified. This increase is mediated by the activation of p38 MAPK and NFkB. This increased TMPRSS2 expression is associated with an increase in the level of SARS-CoV-2 replication inside bronchial epithelial cells.
Conclusion: We observed that *P. aeruginosa* and its virulence factor flagellin are able to upregulate TMPRSS2 expression, which plays an essential role in SARS-CoV-2 infectivity. These results are of major significance for PwCF, who are frequently infected and colonized by *P. aeruginosa* during the course of their disease, and may partly explain why patients with advanced CF disease develop severe COVID-19.
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411

Pseudomonas aeruginosa sphingolipid metabolism and its role in high-ceramide environments such as the CF lung

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Background: One of the metabolic consequences of CF is age-dependent accumulation of ceramide in cells and in the airway, with concomitant loss of the epithelial antimicrobial lipid sphingosine. However, host sphingolipids are not the only source of sphingosine, as *Pseudomonas aeruginosa* expresses a sphingomyelinase PlcH and neutral ceramidase CerN, which can act to liberate sphingosine from host-derived ceramide and sphingomyelin. Thus, the context of high ceramide in the CF lung may enhance the sphingosine stress experienced by *P. aeruginosa,* as well as other bacteria in the community.