Title of the tentative project: Interaction of commensal bacteria with *P. aeruginosa* during airway infections in cystic fibrosis

*Research Area*: Microbiology&Immunology

*Duration*: at least 8 weeks

*Background*: undergraduate in life sciences

*Pseudomonas aeruginosa* is one of the primary pathogens causing chronic airway infections in patients suffering from Cystic Fibrosis (CF). Infections caused by *P. aeruginosa* are characterized by increased inflammation, which ultimately leads to the destruction of the CF patients’ lung tissue, limiting the life span of these patients. However, it has now been recognized that airway infections in CF patients most often are of polymicrobial nature and that the mucus from the airways contains a rich microbiome. The microbiome typically contains a number of commensal bacteria and two opposing roles for these bacteria have been suggested: Whereas some commensal bacteria might worsen the outcome of concomitant *P. aeruginosa* infection, others might have a protective role. Arguing in favor of the latter we observed in a longitudinal study that lung function remains better in patients with a microbiome rich in commensal bacteria. Within an internship project in 2019 we cultivated and grew 96 strains of oral commensal bacteria from samples of patients with CF, followed by in-vitro stimulation of airway epithelial cell lines with commensal bacteria alone, or in co-culture with *P. aeruginosa*. We hypothesized that the commensal bacteria including *Neisseria*, *Veillonella*, *Prevotella*, and *Streptococcus* spp. would reduce pro-inflammatory responses and exert protective effects against a subsequent infection with *P. aeruginosa*. Indeed a few strains could be identified that had inhibitory functions in co-infections. Embedded in a PhD project the proposed internship will follow-up these observations by doing co-infections within precision-cut lung slices, an organoid model to study airway infections. Experiments will also be done in lung slices from mice showing a “CF-like” defect. Besides bacterial growth analysis, various immune readouts will be done to analyze the interplay of commensals with pathogens.