Medical University of Graz

# The role of the microbiome and archaeome in chronic rhinosinusitis and sinubronchial syndrome

## Summary

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| Supervisors: | Prof. Dr. Christine Moissl-Eichinger<br>Dr. Vasile Foris |
| Availability: | This position is available. |
| Offered by: | Medical University of Graz |
| Application deadline: | Applications are accepted between March 24, 2021 00:00 and May 05, 2021 23:59 (Europe/Zurich) |

## Description

Background: The respiratory tract harbors numerous microorganisms. Also the lung, which was originally considered to be largely sterile, contains an endogenous microbial community. As e.g. asthma and lung cancer, but also oropharyngeal squamous cell carcinoma [1] and olfactory capacity [2] correlate with the relative abundance of certain bacterial and archaeal taxa [3], we consider the microbiome as a potential target for future therapeutic approaches in the human respiratory tract.

Chronic rhinosinusitis (CRS) is an inflammatory disease of the nose and paranasal sinuses affecting up to 11-12% of the human population in developed countries. The sinubronchial syndrome, however, is known as one of the most severe forms of the second form, which appears as a combination of sinusitis and resulting lower respiratory tract symptoms such as bronchitis or asthma. Despite the lack of knowledge with respect to the interplay of the microbiome and the sinubronchial syndrome, it has been shown that CRS is accompanied by a higher level of anaerobic microorganisms, including *E. coli*, a typical gut-associated microbe.

Hypothesis and Objectives: We hypothesize that **chronic rhinosinusitis and the sinubronchial syndrome is associated with a dysbiotic microbiome (bacterial and archaeal) profile and function in the respiratory tract and that the gastrointestinal tract could serve as a potential source of infection (gut-lung axis).** In this project, we will analyze the microbial community and its function (metagenome/transcriptome) from upper to lower respiratory and gastrointestinal tract. In order to decipher the interplay of the microbiome and the human body, we will analyze the mucus and bronchoalveolar lavage (BAL) with respect to the proteome/metabolome. We will correlate our findings with the clinical information derived from the samples and corresponding patients in order to obtain insights into the diversity, activity, function, dispersal and distribution of archaea and bacteria in CRS patients, the CRS sub-groups (with/without polyps) and patients with sinubronchial syndrome.

Methodology: We will use different methods in state-of-the-art microbiome research, including 16S rRNA gene-based next-generation sequencing, shot-gun metagenomics/transcriptomics, metabolomics/proteomics fluorescence, as well as *in situ* hybridization (FISH)/scanning electron microscopy to visualize the microorganisms. Microbiome data will be exploited by using a variety of bioinformatics tools, including genomic binning and comparative genomics methodology, with a particular focus on archaeal signatures. Furthermore, data will be correlated with clinical metadata and the functional interaction of respiratory tract and gastrointestinal tract microbiome will be analyzed. The PhD student will specifically be trained in Archaea microbiology. In **the 1$^{st}$ year**, the student will perform extensive datamining of already available datasets. Beyond, he/she will be involved in patient recruitment, sampling and sample processing, including DNA extraction, amplicon/metagenomic-sequencing, FISH. In **the 2$^{nd}$-3$^{rd}$ year**, the student will be trained to process, analyze and interpret the microbiome data and to perform profound statistical analyses. Information derived from metabolomics/proteomics will be integrated. Genomes of key-species will be assembled and comparative genomics will be performed, comparing the capacities of respiratory tract-associated microbiome vs gut microorganisms in health and disease. **The 3$^{rd}$ year** will be dedicated to data analysis and publication of the results.

References:

1. Wolf A, Moissl-Eichinger C, Perras A, *et al.* The salivary microbiome as an indicator of carcinogenesis in patients with oropharyngeal squamous cell carcinoma: A pilot study. *Sci Rep* 2017;**7**:5867.

2. Koskinen K, Reichert JLJL, Hoier S, *et al.* The nasal microbiome mirrors and potentially shapes olfactory function. *Sci Rep* 2018;**8**:1296. doi:10.1038/s41598-018-19438-3
3. Borrel G, Brugere J-F, Gribaldo S, *et al.* The host-associated archaeome. *Nat Rev Microbiol* 2020;**18**:622–36.