Abstract ID: 93520

Student: Waked Pamela

Area of Research: Immunology, microbiome research and respiratory diseases

PhD Programme: PhD Immune Modulation in Respiratory Diseases (RESPImmun)

Semester: 3

## Endotyping of Chronic Rhinosinusitis using proteomics approach

Pamela Waked; Peter Valentin Tomazic; Valentina Biasin

Chronic Rhinosinusitis (CRS) is an inflammatory disease of the nose and paranasal sinuses and may affect the upper airways in severe cases. In the EPOS guidelines, CRS is diagnosed by at least two of the following major symptoms present for at least 12 weeks: nasal congestion, nasal discharge, pain or facial pressure or impaired sense of smell. There are two major types of CRS: presence of nasal polyps (CRSwNP) or without nasal polyps (CRSwNP). However, clinical classification by those two phenotypes does not reflect the variety of CRS endotypes which are related to different cytokine profiles and inflammatory responses and often lead to varying therapeutic response, surgical failures and recurrence, indicating that CRS is a hetegenous disease and proper pathophysiologic endotyping is necessary for advancement in patient management and treatments.

The aim of this project is to endotype CRS based on the proteomic analysis of the nasal mucus, Bronchoalveolar Lavage (BAL) and serum by profiling of inflammatory cytokines and immune cells and cluster analysis of CRS patients through untargeted proteomic analysis and targeted immunoassays and flow cytometry.

Difference in proteome of nasal mucus, BAL and peripheral blood of 200 samples will be studied and analysed. First, Proteomic analysis will be performed on TimsTOF mass spectrometry and protein abundances will be calculated as mean and standard deviation and statistically analysed. Second, FACS analysis will be performed and immune cell profile will be established. All these data from patient samples will be analysed and compared with clinical tests and data to cluster our patient cohort into relevant pathophysiologic subgroups.

This study gives us an insight into the different pathophysiological mechanisms that are involved in the disease and how it differs between individuals in the hopes of finding endotypes within this heterogeneous disease through analysing the protein profile and immune cells in CRS patients.