Over the last several years, we have been observing a growing knowledge about the fundamental role of the human microbiome in the initiation, adaptation and functioning of the human immune system. Mainly, the role of gastrointestinal microbiota and its impact on host health has been extensively studied for many years. Recently, the microbiome of respiratory system has attracted more attention. It is now becoming clear that the microbiota of lung may also contribute to local homeostasis and that persistent imbalance of microbial community of lung may be associated with asthma. Furthermore, the concept of gut-lung axis has emphasized the role of both gut and lung microbiota in the pathology of asthma. Our knowledge of how the nasopharyngeal microbiota shapes lung homeostasis and how nasopharyngeal dysbiosis affects respiratory health is still incipient. Both the nasopharyngeal microbiome and the gut microbiome change during our live. Focusing only on sinonasal microbiomes it has been shown that during the first two years of life they are more dense and less diverse in comparison to adult years. Shortly after birth the early colonization of *Moraxella*, *Corynebacterium* in combination with *Dolosigranulum* ensures the stability in the microbiota profile14. The microbiota of sinonasal passage of adults contains a rich, complex microbiome and is distinctive with similar phyla between individuals. The majority of bacteria in healthy individuals is derived from four bacterial phyla: *Actinobacteria* such as *Corynebacterium*, *Bifidobacterium*, *Rothia*, or *Propionibacterium*; *Firmicutes* such as *Dolosigranulum*, *Staphylococcus*, *Streptococcus*; *Bacteroides* such as *Sphingobacterium* and *Prevotella* and *Proteobacteria* with representatives of *Moraxella* and *Haemophilu*s.

Research so far has indicated that there are significant changes in bacterial diversity of nasopharyngeal cavity between healthy and diseased individuals. For example, the nasal microbiome of patients with chronic rhinosinusitis (CRS) has been shown to most commonly include coagulase-negative *Staphylococcus, Pseudomonas aeruginosa*, *Haemophilus*, *Fusobacterium* spp, *Alloiococcus,* and *Corynebacterium* spp. Interestingly, it has been observed that patients suffering from CRS very often develop airway asthma. However, we still do not know the exact nature of the relationship between the incidence of nasopharyngeal microflora dysbiosis in patients with CRS and the occurrence of allergic diseases. Despite the lack of a clearly confirmed relationship between specific bacteria and occurance of allergic airway inflammation in CRS patients, there are reasonable premises to assign microbiome dysbiosis the role of factors initiating the disease, as well as modifying its activity and course. Differences in the composition of the nasopharyngeal microbiome in patients with CRS may be one of the factors influencing the individual differentiation of the development of the disease and the effect of the therapies used in it.

As part of this project, the influence of the commensal microbiota of the nasopharynx in people suffering from CRS will be investigated in the context of its influence on the functioning of the respiratory system, as well as its potential influence on the development of inhalation allergies in *in vitro* and *in vivo* experiments.