

The nose and the sinuses, just like the mouth, even in health are inhabited by various microbes. Twenty years ago it was assumed that there were no bacteria in healthy sinuses and invasion of bacteria into the sinuses caused sinusitis and required antibiotic treatment.

In recent years, new and much more accurate methods have been introduced to study the microbial communities in various niches of the human body. Previously, it was only possible to detect bacteria that could be grown in the laboratory. New molecular methods that are available nowadays do not require the cultivation of bacteria. The genetic material in a sample (for example in a swab) is examined to determine what microbes are present in the sample. This way, it is possible to identify ten times more bacteria than using traditional methods. The sinuses of a healthy person may harbor even several dozen types of bacteria. Many of them are beneficial for the physiological functions of the organism, produce necessary substances and protect from the invasion of pathogenic bacteria.

The microbiome of the nose and the sinuses has been the subject of research for the last two decades but many questions remain unanswered. One of the issues stems from the fact that the samples from a patient are taken only once or alternatively before and after treatment. It is not clear whether the bacteria detected in a sample taken at a single time point are characteristic of the individual and whether they will be still present after a week, a month or a year.

Moreover, the microbial communities in the nose and the sinuses can be damaged during antibiotic therapy. Whenever we take antibiotics (for example for an inflammation of a tooth) we usually remember that it can have a negative effect on the gut bacteria and cause diarrhea. We tend to forget that the antibiotic is present in the whole system and affects also the bacteria in the nose and the sinuses. It is not known, how significant and how long-lasting the disturbance can be. Most studies on the influence of antibiotic therapy on the sinus microbiome to date were conducted in patients with rhinosinusitis who probably already had disturbance of the microbiome before treatment. Meanwhile, it was shown that frequent exposure to antibiotics increases the risk of chronic rhinosinusitis in the future. Besides, it is probable that after taking antibiotics more antibiotic-resistant bacteria may emerge in the nose and the sinuses. It poses a risk for the person who is the carrier of such bacteria and for the people who contact them because antibiotic-resistant strains may be passed from person to person.

In our project, we are planning to find out whether the microbiome of the nose and the sinuses remains the same in an individual or changes significantly over time. We also want to answer the question if short courses of antibiotics frequently prescribed by doctors are dangerous for the sinonasal microbiome, result in aberrations in its composition and may promote the spread of antibiotic resistance in this niche of the organism that is frequently overlooked during antibiotic therapy prescribed for other diseases.

In the project, we will take samples several times over a year from healthy people, patients with chronic rhinosinusitis and patients receiving antibiotics for other diseases than sinusitis. We will use both traditional culture and antibiotic susceptibility testing and a more novel sequencing technique than the one used in previous research on the sinonasal microbiome. Sequencing of longer fragments of the bacterial genome we will be able to identify the bacterial species with much greater resolution.

If our study shows that the sinonasal microbiome is significantly disturbed during antibiotic therapy, it will be reasonable to search for strategies that rebuild a “healthy” microbial community, such as the application of probiotics, to prevent chronic dysfunction of the sinuses and prevent the spread of antibiotic resistance.