Description for the general public:

Changes in the oral microbiome as an early cancer marker

Despite much progress in the diagnosis and treatment of cancer, tumour diseases constitute one of the main reasons for deaths worldwide. Oral squamous cell carcinoma (OSCC) is one of the most common malignancies. In the last few years, oral cancers increased and the survival rate remains low. OSCC is diagnosed mainly in advanced stages (III and IV) which correlates with an unfavorable prognosis and a high risk of death. Therefore there is an urgent need for rapid, non-invasive and screening methods for the prognosis and early detection of OSCC. Oral bacterial biomarkers seem to be promising new diagnostic approach. There is an increasing interest in the human oral microbiome (HMO) which consist of a large and diverse microbial community and has a tremendous impact on human health and disease. The composition of the oral microbiome and the changes within have been associated with diagnosis, pathogenesis and treatment of cancer. Oral microbiome-based diagnostics and therapeutics may benefit from easy accessibility to the oral cavity and saliva. Saliva is a body fluid that comprises bacteria shed from diverse oral surfaces and has been shown as an individualized, temporally stable diagnostic material. The composition of the salivary microbiome can thereby mirror oral and general health status. Recent studies showed that changes in the composition of the oral microbiome, detected in saliva, can be used not only in the local prognosis and early detection of oral squamous cell carcinomas but also in other types of cancers in distant places of the body.

Although the topic of the oral microbiome and its relationship to cancer, has been hot in recent years, there is still little scientific evidence based on experimental data. There are many review articles that highlight the advantages and disadvantages of several sequencing methods, sample collection, and potential disease impact. However, each of these articles shows a key need for other research and standardization of their methods. This project plans to compare the composition of the oral microbiome of healthy people and those with early diagnosis of OSSC, and to determine potential bacterial biomarkers in oral squamous cell carcinoma. For such analysis of microbiome, metagenomics is used – method based on characterization of whole bacterial genetic material of given clinical / environmental niche. Within this project, a new metagenomic approach based on next generation sequencing (NGS) of the 16S-23S rRNA region will be used to describe the species composition of bacteria with very high accuracy. When we will know the bacterial species content within the saliva samples, then we will perform another high-throughput technique - metatranscriptomics to detect not only bacterial species but also virulence factors and antibiotic resistance genes for active members of the microbial community. Metatranscriptome describes the actual active transcripts from bacteria within a sample. Finding significant differences in the composition of the oral microbiome as saliva biomarkers will provide an opportunity to increase early prognosis and cancer detection. The study will include 200 patients, 100 patients with OSCC and 100 healthy individuals. Unstimulated saliva samples will be collected, then will undergo routine microbiological diagnostics and metagenomic analysis of the microbiome using NGS of the 16S-23S rRNA region. Metatranscriptome (RNASeq) analysis will be performed for selected representative oral samples. The analysis of bioinformatics data will include: preparation of appropriate reference sequences, quality control of reads and filtering, optional pre-classification of reads into types / species, reading mapping, qualitative and quantitative determination of species composition, differential expression analysis for selected genes, analysis of unmapped reads. The presented research methodology will result in the identification of significant, discriminatory differences in the composition of the oral microbiome as salivary biomarkers, which will translate into progress in early prognosis and cancer detection.