

METAGENOME SEQUENCING OF LICHEN PLANUS INDICATES PERTURBATIONS IN THE HEALTHY ORAL MICROBIOME

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Introduction: Lichen planus is a chronic, inflammatory idiopathic disease of mucosal tissue or skin. The inducers are unknown, but it is thought to be the result of a severe autoimmune process with an unknown initial trigger. However, the pathomechanism is not really understood yet, the unknown trigger of immun response and the lichen as the precancerous disease could indicate the role of microbial flora in the oral cavity.

Materials and methods: Lichenoid and healthy tissue samples were collected from patients of our clinic. Total DNA was extracted from the samples and metagenomic DNA was quantified using Qubit® 2.0 Fluorometer and Ion Torrent PGM Fragment libraries of 200 nt were generated. Sequencing was performed on Ion Torrent Personal Genome Machine™ using Ion 318 chip. The MG-RAST software performs a QC (quality control) and an automatic normalization of the FASTQ sequence data with maximum e-value cut-off of 10^{-5} , minimum percent identity cut-off 90% and minimum alignment length cut-off 25 bp. For the functional and taxonomical analyses MG-RAST utilized the M5nr protein database (GO, IMG, KEGG, NCBI (RefSeq & GenBank), SEED, UniProt, eggNOG and PATRIC) and various ribosomal RNA databases (RDP, Silva and Greengenes), respectively.

Results: High-throughput, sequencing-based metagenome analysis identified 20 versus 47 bacteria species in contralateral healthy and lichenoid tissues, respectively. Although the most frequent species are the *Streptococcus mitis* and *Streptococcus pneumoniae*, the diversity of bacterial flora is markedly higher in the precancerous tissue samples. In lichen planus, the relative abundance of *S. mitis* and *S. pneumoniae* was 31% of the total bacterial community compared to that of 55% in normal samples.

Discussion: It is well known, that the microbiome of the cancerous tissue shows strong differences compared to the normal, healthy microbial flora of the oral cavity. One of the main points in the pathogenesis of oral cancer, that the alteration of bacterial flora is the cause or causative of the malignant disease. We have found clear changes in the composition of microbiome in lichenoid tissue and these alterations involved a decreased ratio of the healthy, normal bacterial flora. These microbial changes in the precancerous lichenoid tissue might induce malignant transformation of mucosal membrane in the oral cavity.

Előadást szeretnék tartani. A téma elméleti jellegű.