

Abstract

Periodontitis is a multifactorial inflammatory disease which can result in a complete loss of teeth. Its main cause is the accumulation of bacteria from the dental plaque followed by massive reaction of the host immune system. It was proved that the composition of oral microbiome (OM) differs in periodontally healthy individuals and patients with periodontitis. This work aims to solve specific parts of the long-term project concerning the taxonomic composition of the OM of periodontally healthy individuals and patients with chronic and aggressive form of the disease. The OM was characterized based on 16s rDNA sequencing. It is evident from the results that the shift in the OM composition occurs prior the development of clinical signs of the disease and that the precise dental care can significantly postpone or even avoid the onset of the disease. When comparing the OM composition in individuals with chronic and aggressive periodontitis, no remarkable differences were detected to explain the faster progress of the aggressive form of the disease. This work also aimed to compare the results obtained by 454 pyrosequencing and Illumina. Both sequencing methods were found to provide statistically comparable results. Illumina MiSeq thus can be employed to build on the former results of the long-term study obtained by 454 pyrosequencing. Based on our results the two parameters for periodontitis prediction as well as monitoring of the treatment were proposed.

Keywords: periodontitis, oral microbiome, sequencing, red komplex bakteria, prevention, diagnosis of periodontitis