Abstract

This thesis deals with the analysis of the dentin-enamel junction layer in human third molar teeth. Three different methods of analysis were tested. In the first one teeth were demineralized in EDTA buffer to release the protein layer DEJ. In the other two cases thin slils of dental tissue were preparedand from them the DEJ layer was cut using laser microdissection. Severals methods were tested for extraction of proteins from DEJ samples (for comparsio also from dentin and enamel samples). Extracted proteins were cleavaged into peptides with trypsin. Subsequently, peptides were purified by Stage tips and analyzed by nLC MS/ MS. Using the optimal method over 40 different proteins, for example: apolipoproteins, vimentin, vitronectin, clusterin, biglycan weres found in the sample DEJ.

Keywords: proteomics, dentin-enamel junction, laser microdissection, mass spectrometry