Abstract

Proteomics is a booming field with application in many areas of medicine, including dentistry. Nevertheless, proteomic characterization of bone tissues in oral surgery is not still commonly used. The main reason is involvement of demanding analytical approaches due to insoluble chatacter of bone tissues. The goal of this work was to develop and apply straightforward methodology that could lead to the routine use of proteomics in this area as well.

Using porcine jawbones as a model samples, a technique was developed allowing identifying about hundreds of proteins thanks to their trypsin digestion directly in bone tissues ("in-bone digestion") followed by analysis using liquid chromatography coupled with tandem mass spectrometry (LC-MS/MS). This technique was subsequently applied to the analysis of human maxillary and mandibular bone tissues obtained during surgical procedures. In both maxillary and mandibular bone samples, it was possible to identify a considerable amount of proteins using the "in-bone digestion" technique. Additionaly, the mathematical analysis of the obtained data was able to distinguish between the inflammatory and healthy tissues. The approach based on direct cleavage was subsequently successfully extended to the analysis of *in vitro* models of human bone tissues. Direct cleavage followed by analysis of the released peptide fragments using LC-MS/MS and subsequent mathematical analysis of the obtained data was able not only to distinguish the samples of models with induced pathological conditions from the control ones, but also allowed distinguishing between two different pathological conditions. The possibility of using a technique of "in-bone digestion" followed by different analysis than LC-MS/MS was verified. Namely capillary electrophoresis with ultraviolet detection (CE-UV) was tested. After evaluating of the obtained CE-UV profiles by mathematical analysis, it was possible to distinguish between inflammatory and healthy bone tissue samples.

The use of the above-mentioned non-traditional and very straightforward methodological approaches makes it possible to introduce routine insight at the molecular level into the field of oral surgery. For example, it should be possible to monitor the proteomic reflections of certain pathological conditions, which should help to understand the mechanism of their occurrence and the choice of appropriate treatment. Proteomic analyzes of jaw bones after surgical procedures could also serve as a suitable supplement, or even an alternative, to their traditional histological evaluation.