SUMMARY

The goal of this bachelor work was to find out if it is possible to recognize mammal species by analyzing the proteins extracted from their hairs. This information could be of use, for example, in forensic science as evidence in cases of exotic animal species smuggling or it could be helpful for solving some specific criminal cases.

Fur is a characteristic sign of mammals which is forming their body surface. It mainly consists of keratin, which is a fibrous protein. This bachelor thesis deals with proteomic analysis of animal hair using mass spectrometry working on MALDI-TOF (Matrix-Assisted Laser Desorption/Ionization – Time of Flight) principle.

Analyzed animal hairs were collected from ten local domestic and wild animals, such as dog, goat, cat, fallow deer, sika deer, degu, horse, rabbit, roe deer and Belgian blue calf breed.

For the analyses of samples that are rich in proteins a specific enzyme cleavage by trypsin was used. The proteins were cleaved into peptides, from which mass spectra were obtained by MALDI-TOF mass spectrometry. Then these spectra were evaluated by the Principal Component Analysis (PCA) method.

Then the obtained aminoacid sequences of the keratins found in the individual animal hair were searched through publicly available protein database – UniProt. The aminoacid sequences were processed with mMass software where also a model cleavage with trypsin was done. The sequences obtained by the model cleavage were compared to experimentally obtained data.

By these mentioned techniques it was possible to distinguish between all ten animal species types of animal hairs.

KEYWORDS

Animal hair, enzyme digestion, peptides, mass spektrometry, Principal Component Analysis