

Abstract

The aim of this study was to carry out an analysis of a protein composition of different crop species using the method of peptide mass mapping. The samples were analysed using analytical method LC/ESI-Q-TOF and the acquired spectra were compared with the plant protein databases. The origin of the found plants was discussed in the aspect of the reliability of the used method considering the taxonomical relationships in the taxonomical group. The results of the analysis were compared with the food composition specified by the producer, and it was evaluated, if it is possible to verify the protein composition by using the applied method.

In case of maize (*Zea mays*) this method is considered as reliable, because all of the found proteins were identified as maize proteins. In case of rice (*Oryza sativa*) and pea (*Pisum sativum*), only one, respectively, two proteins of different plants species were found in the number of the relevant plant proteins. This method was evaluated as not so reliable for samples made of cereals (*Poaceae*). It is possible to conclude, whether the product comes from *Poaceae* or not, but it is impossible to verify the taxon of genus or the inferior taxons. This fact was in a great extent discussed in this thesis – the reason is probably the resemblance of *Poaceae*, and the identification of the protein from common part of proteome is limited by the scopes of the used method.

key words: method of peptide mass mapping, flour, bakery products, wheat, rye, maize, rice