BOOK OF ABSTRACTS

11th International Symposium on RECENT ADVANCES IN FOOD ANALYSIS

November 5-8, 2024 Prague, Czech Republic

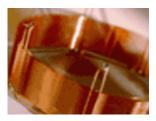
Jana Pulkrabová, Monika Tomaniová, Stefan van Leeuwen, Michele Suman, Michel Nielen and Jana Hajšlová

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IDENTIFICATION OF PROCESS-DEPENDENT MAILLARD ADDUCTS IN WHOLEMEAL DRY PASTA BY UNTARGETED HIGH RESOLUTION TANDEM MASS SPECTROMETRY: A COMPARATIVE ANALYSIS OF DIFFERENT DRYING CYCLES AND SEMOLINA COMPOSITION

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Durum wheat pasta is a common source of complex carbohydrates, which have been thoroughly investigated in terms of starch digestibility, but poorly analysed in terms of protein profile and digestibility.

In this contribution, the proteomic profile of wholemeal pasta prepared with different mixtures of semolina and using different drying cycles will be presented. Comparative investigation by highresolution mass spectrometry of process-dependent formation of Maillard adducts (MAs) and chemical modifications (deamidation and oxidation) was accomplished and correlated to semolina composition and drying cycles. Spaghetti was selected as model pasta shape and produced in a pilot-scale, using two semolina with different protein content corresponding to medium and high quality, and two different drying cycles: (i) 21h at 50°C and 6h at 85°C. First, total protein extraction was performed under strong denaturant and reducing conditions for all sample types and the extracted proteins were quantified by colorimetric assay. Three independent samples were prepared for each sample and the differences in averaged contents resulted to be not statistically significant, confirming comparable and satisfactory extraction yields for all samples. Discovery high resolution MS/MS analysis and software-based identification were tailored to disclose the presence of MAs on lysine residue, as well as chemical modifications of methionine, glutamine, asparagine and arginine. More than four thousand peptide sequences have been identified for each sample with on average half of them presenting at least one modified amino acid. Most of the modifications were accounted by MAs on lysine (about 49%), and by deamidation of glutamine (about 29%) and asparagine (14%). Specifically, advanced glycation end product MGH1 (Δm=+96,0318), carboxymethyl-lysine ($\Delta m = +58,0049$) and carboxyethyl-lysine ($\Delta m = +72,0206$) containing peptides resulted to be the most common process-dependent Maillard modifications. Detailed discussion about difference among the four types of pasta samples will be presented in the contribution in correlation with the semolina composition and the drying cycles.

Keywords: Maillard adducts, high resolution tandem mass spectrometry, pasta drying cycles, proteomic profile, protein heat damage

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