

P013 Application of mass spectrometry for identification of oxidative modifications in muscle proteins in *in vivo* model of X-ray irradiation

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Oxidative stress caused by reactive oxygen species (ROS) has been implicated in the pathogenesis of a number of human diseases, including Alzheimer's disease, Parkinson's disease and diabetes mellitus. ROS can oxidatively modify major groups of biomolecules, especially proteins due to their high intra- and extracellular concentration. Oxidative modifications of amino residues can alter the protein structure and result in a loss of functional activity.

As an *in vivo* model of oxidative stress, rats were irradiated by X-rays (5 Gy dose). Proteins were isolated from skeletal muscle tissues 0, 3, 9 or 24 hours after irradiation. The extracts were separated by two-dimensional PAGE and the proteins were visualized with Coomassie Brilliant blue. Protein spots of interest were excised, digested with trypsin, and identified by MALDI-TOF mass spectrometry. Peptides with oxidized residues were analyzed by tandem mass spectrometry. Several types of modifications were identified, such as different stages of tryptophan oxidation (kynurenine, hydroxytryptophan, N-formylkynurenine, hydroxyN-formylkynurenine), hydroxyleucine, hydroxyisoleucine, oxidized methionine and cysteic acid.