



UNIVERSITÀ
CATTOLICA
del Sacro Cuore

Dipartimento di scienze biotecnologiche di base, cliniche intensivologiche e perioperatorie



Proteomics and Metabolomics for Personalized Medicine

XV ITALIAN PROTEOMICS ASSOCIATION ANNUAL
MEETING



Italian Proteomics Association

IN PARTNERSHIP WITH
HELLENIC PROTEOMICS SOCIETY

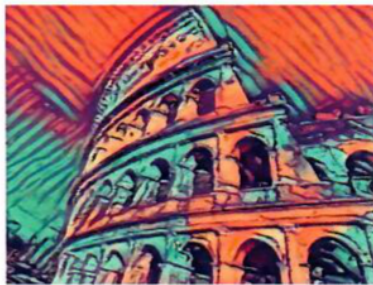


Hellenic Proteomics Society

SERBIAN PROTEOMICS ASSOCIATION
AND



СРПСКО УДРУЖЕЊЕ ЗА ПРОТЕОМИКУ-SePA



CATHOLIC UNIVERSITY OF THE SACRED HEART
ROMA, ITALY
AUDITORIUM

2021
September
8th-10th

P-28

Effects of lysine's and arginine's modifications on trypsin proteolytic efficacy imposed before and after the peanut roasting

Katarina Smiljanić^{a*}, Ivana Prodić^b, Teodora Đukić^a, Tamara Vasović^a,
Vesna Jovanović^a and Tanja Ćirković Veličković^{a,c,e}

^aUniversity of Belgrade – Faculty of Chemistry, Center of Excellence for Molecular Food Sciences & Department of Biochemistry, Serbia;

^bUniversity of Belgrade – Faculty of Chemistry, Innovation Center Ltd, Serbia;

^cGhent University Global Campus, Incheon, South Korea;

^dGhent University, Faculty of Bioscience Engineering, Belgium;

^eAcademy of Sciences and Arts, Belgrade, Serbia

Porcine-derived trypsin generated proteomic data of the major peanut allergen Ara h 1 from the raw and roasted peanut, were reassessed for possible facilitating/hindrance effects on trypsin digestion efficacy caused by post-translational and chemical modifications (PTMs) positioned on arginine or lysine (K/R) residues. If the potential hindrance effects caused by PTMs are observed with porcine trypsin, then they can be just augmented and more pronounced within human intestinal digestion [1]. The reasoning is in inferior performance of human trypsin compared to porcine-derived used in proteomic digestion protocols, also in the lower trypsin-to-sample ratio and much shorter digestion times, even though gastric digestion precedes and trypsin is not the sole digestive enzyme [1].

Novel method was developed to decipher cleavage or miscleavage outcomes at scissile bonds using PEAKS Studio-X+ in reassessment of high-resolution tandem mass spectrometry data on 18h-long trypsin digestion protocol. In general, eight modified K/R residues with methylation, dihydroxy and formylation, showed significantly higher content of miscleaved bonds (at least >10%) compared to its unmodified counterpart peptides. Roasting caused dihydroxylation and formylation PTMs with hindrance effects to trypsin efficacy, while methylation on several K/R showed opposite effects. It is important to elucidate general impact of modifications on trypsin digestion performance, but also if there are additional effects generated by food processing, which could influence digestion outcomes and consequently, allergenicity of food proteins/peptides.

Funding: Ministry of Education, Science and Technological Development of Republic of Serbia No. 451-03-9/2021-14/200168 and Horizon2020, FoodEnTwin project, GA No.810752

* *Corresponding author:* Katarina Smiljanić
University of Belgrade – Faculty of Chemistry, Serbia
Tel.: +381 11 3336676;
fax: +381112184330
E-mail address: katarinas@chem.bg.ac.rs (K. Smiljanić)

References:

- [1] Katarina Smiljanić, Jelena Mihailović, Ivana Prodić, Teodora Đukić, Tamara Vasović, Vesna Jovanović and Tanja Ćirković Veličković, *Trypsin as a proteomic probe for assessment of food protein digestibility in relation to chemical and post-translational modifications in a closer look at proteolysis*, J. Radosavljević, Editor. 2020, Nova Science Publishers, Inc. p. 157-183.