IV Simpozijum srpskog udruženja za proteomiku – SePA

Interaktomika i glikoproteomika: novi pristupi u analizi proteina na velikoj skali

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25. maj 2018.
Beograd, Srbija

Knjiga abstrakata

Institut za biološka istraživanja "Siniša Stanković" (IBISS)
Univerzitet u Beogradu

СРПСКО УДРУЖЕЊЕ ЗА ПРОТЕОМИКУ-SePA

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Biblioteka IBISS-a

PROGRAM

14.00 Dr Melita Vidaković i dr Svetlana Dinić: Otvaranje SePA Simpozijuma

14:10 Prof. dr Đuro Josić, Odjel za biotehnoligiju, Sveučilište u Rijeci, Hrvatska; Warren Alpert, Medical School, Brown University, Providence, RI, USA
"Upotreba monolitnih stacionarnih faza za visokoprotočnu pripremu uzoraka u proteomici i glikoproteomici"

14:40 Prof. dr Marija Gavrović Jankulović, Hemijski fakultet, Univerzitet u Beogradu, Srbija
"Primena biblioteka peptidnih liganada za detekciju nisko zastupljenih alergena u proteinskim ekstraktima hrane"

15:05 Pauza za kafu

15:25 Ivana Prodić, Hemijski fakultet, Univerzitet u Beogradu, Srbija
"Gastrični digestom celog zrna kikirikija sa aspekta proteomike: karakterizacija digestovanih alergena u realnom matriksu hrane"

15:45 Aleksandra Tomov i Svetlana Jovanović
"Savremene metode u analizi proteina: western blot i gel fotodokumentacija, kvantitativna i kvalitativna obrada podataka"

16:00 Pauza za ručak

16:30 Ana Medić, Medicinski fakultet, Univerzitet u Beogradu, Institut za hemiju u medicini, Srbija
"Proteom Pseudomonas aeruginose san ai pri biodegradciji 2,6-di-terc-butilfenola"

16:40 Prof. dr Tanja Ćirković-Veličković, Hemijski fakultet, Univerzitet u Beogradu, Srbija
"Omiks u hrani, ishrani i životnoj sredini"

16:50 Dr Nebojša Dovezenski
„Od imidžinga živih ćelija do kvantitativnog Western blota radi otkrivanja novih lekova"

17:05 Diskusija

17:15 Zatvaranje

17:20 Godišnja skupština SePA

Ulaz na simpozijum je slobodan

Naučni odbor: prof. dr Tanja Ćirković Veličković, prof. dr Tatjana Simić, prof. dr Ivanka Karadžić, prof dr Marija Gavrović-Jankulović, dr Melita Vidaković, dr Svetlana Dinić, prof. dr Marija Plješa Ercegovac, dr Marko Radulović, prof dr Ivana Borišev, prof. dr Nevena Đukic, dr Romana Masnikosa

Organizacioni odbor: dr Melita Vidaković, dr Mirjana Mihailović, dr Nevena Grdović, dr Aleksandra Uskoković, dr Katarina Smiljanić, dr Svetlana Dinić, Ivana Prodić

P 3: Digestomics of Japanese abalone in real food matrix

Ivana Prodić[1], Urmila Khulal[2], Jelena Mutić[1,2], Jelena Mihailović[1], Katarina Smiljanić[1], Tanja Ćirković Veličković[1,2,3]

[1]*University of Belgrade-Faculty of Chemistry, Serbia*
[2]*Ghent University Global Campus, Korea*
[3]*Faculty of Bio-Science Engineering, Ghent University, Belgium*

Objective: Haliotis discus (Japanese abalone), mollusks among various shellfish, is a highly nutritive food resource in the world, but also among the eight allergic food groups accounting for approximately 90% of all immunoglobulin E food allergies worldwide. The general objective of our research is to comprehensively investigate stability and structures of pepsin-resistant allergens, of their larger fragments, and of short digestion resistant peptides (SDRPs) released by pepsin digestion of whole raw and extract of shellfish, under standardized and physiologically relevant gastric conditions.

Materials and Methods: Extract of raw whole shellfish (eRSS) and whole raw shellfish (wRSS), were pepsin digested according to standardized static digestion protocol. Controls were treated in a same manner without adding pepsin. Supernatant of samples and its counterpart controls were precipitated with TCA/acetone. Obtained proteins were assessed by 2D SDS PAGE and 1D SDS-PAGE, under reducing and non-reducing conditions. 1D SDS-PAGE of RSS were analyzed by ncLC-MS/MS (Orbitrap LTQ) shot-gun proteomics. Relative quantification was performed by LFQ algorithm within Peaks 8.5 software package Bioinformatics Solutions Inc. (BSI), Waterloo, Canada.

Results and Conclusion: 1D SDS-PAGE analysis of eRSS and wRSS, and its controls showed a range of proteins in varied concentrations between 10-250 kDa. In extracted and whole raw shellfish, approximately 22 prominent protein bands were observed including the distinct bands corresponding with the molecular weights of recognized shellfish allergen, tropomyosin (37-39kDa). Fewer high molecular weight proteins were observed followed by protein smearing, specifically around the low molecular weight protein bands. The smearing could possibly be due to the breakdown products and the glycation. There were slight differences between the protein profiles under reducing and non-reducing conditions as well. Nevertheless, there was the retention of a band in the 37kDa molecular weight marker in all 4 samples, likely consistent with heat stable tropomyosin (TM). Mass spectrometry showed allergens that are characterized (Hal d 1 and Hal di 1), with 90% of sequence homology with main tropomyosin allergens from seafood.

Scientific impact and relevance: The results will highlight effects of food matrix on shellfish allergens digestibility proving its relevancy in molecular allergology. Moreover, an insight will be obtained on the differences in digestibility of allergenic versus non-allergenic tropomyosins in the real food matrix.