



IV Simpozijum srpskog udruženja za proteomiku – SePA

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

www.facebook.com/SerbianProteomicsAssociation

25. maj 2018. Beograd, Srbija

Knjiga abstrakata



IV simpozijum Srpskog udruženja za proteomiku - SePA

"Interaktomika i glikoproteomika:

Novi pristupi u analizi proteina na velikoj skali"

25. maj 2018

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" a sa ATIMAAFTGNTEGR (423-436)

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 6: Deep and quantitative profiling of PTMs in ecologically preserved and polluted pollen proteomes of timothy grass reveals predominant source of contamination

<u>Katarina Smiljanić</u>¹, Ivana Prodić², Ivana Aleksić³, Djordje Veljović⁴, Jelena Mutić^{1,5}, Lidija Burazer³, and Tanja Ćirković Veličković^{1,4,5*}

¹University of Belgrade – Faculty of Chemistry, Centre of Excellence for Molecular Food Sciences, Serbia

²Innovation Center Ltd, University of Belgrade - Faculty of Chemistry, Serbia
³Institute of Immunology, Virology and Sera Production, Torlak, Belgrade, Serbia
⁴University of Belgrade – Faculty of Technology and Metallurgy, Serbia
⁵Ghent University Global Campus, Incheon, South Korea 6Ghent University, Faculty of Bioscience Engineering, Belgium

Objective: to create method for unrestrictive deep, relative quantification of post translational modifications (PTMs) within different proteomes. Pollution field studies of bio indicators such as pollen are valuable because of realistic situation of target contamination, however they carry the great extent of uncertainty in attributing and delineating the polluting effect from multiple sources. Holistic research platform focusing on comprehensively characterized and quantified PTMs of comparable bio-indicator proteomes could help and overcome these obstacles of field pollution studies.

Material and Methods: Scanning electron and light microscopy assessed surface and sub pollen particle (SPP) releasing features of timothy grass (TG) pollen. Inductively coupled atomic emission spectrometry revealed metal elemental content in pollen while in solution trypsin digested pollen proteomes analysed with high resolution Orbitrap mass tandem spectrometry and PEAKS Suite 8.5 brought quantitative information on protein expression level and its PTM profiling.

Results: TG polluted pollen samples (P2) collected along regional road and chemical plant, exposed to air contaminants from road traffics and chemical plants showed 4.5 times higher SPP releasing capacity, with notable surface changes, as well as significantly higher contents of Mn, Hg and Cd. Antioxidative enzymes (oxidoreductases, superoxide dismutases and peroxidases), including actin, were upregulated several times in polluted sample compared to ecologically preserved pollen (P1). While the level of spontaneous and physiological PTMs including methylation, acetylation, deamidation and formylation, was similar without significant changes in P1 and P2 pollens, oxidative PTMs including oxidation of Met, Lys, His, Pro and HNE and hexose adducts showed several times higher and significant increase in abundancy of P2 compared to P1. PTMs connected to road traffic such as tyrosine nitration were very rare and low abundant.

Conclusion: Results suggest prominent role of chemical pollution compared to effect of road traffic pollution, with primary consequences from oxidative properties of mercury (Hg) and cadmium (Cd).

Acknowledgement: This research was carried out with the support from the Ministry of Education and Science of the Republic of Serbia, project no. 172024, and by the European Commission, under the Framework 7, project RegPot FCUBERA, GA no.256716.