



Public Lecture Evaluation

Masaryk University

Faculty

Procedure field

Applicant

Lecture date

Lecture topic

Persons present

(number)

Designated evaluators

(board members)

Faculty of Science

Genomics and Proteomics

doc. RNDr. Zbyněk Zdráhal, Dr.

October 16, 2018

Deciphering of proteome complexity

..... (see attached list of attendees)

Prof. RNDr. Jiří Fajkus, CSc.

Assoc. Prof. Gerda Egger, Ph.D.

Prof. Ing. Vladimír Havlíček, Dr.

Prof. RNDr. Jozef Nosek, DrSc.

Prof. Mgr. Marek Šebela, Dr.

Doc. Zdráhal presented his public lecture with the title *Deciphering of proteome complexity* on October 16, 2018 at 3 pm, in the University campus Brno-Bohunice (room 305, building A11) in the frame of Mendel Centre seminars.

At the beginning, he introduced specific terms used in the lecture and briefly recapitulated his proteomic career. He continued with outlining of analytical aspects of proteome characterization. He summed up capabilities of mass spectrometry in proteome analysis and he documented progress of proteomic approaches in last twenty years. In the second part of his lecture, he presented results of his research activities in the field of MALDI-MS profiling method development and characterization of histone posttranslational modifications. He presented also examples of application of the proteomic expertise of his laboratory in collaborative studies. The first two example projects done in cooperation with the group of Doc. David Honys from the Institute of Experimental Botany, CAS, Prague, were focused on pollen biology. In these studies they characterized tobacco pollen tube secretome which resulted in identification of hundreds of novel pollen tube-secreted proteins with potential functions in pollen tube guidance towards ovules. Quantitative analysis has been performed of three types of ribonucleoprotein particles during tobacco male gametophyte development and the subsequent functional progamic phase. As the next examples, Doc. Zdráhal presented studies done in cooperation with Vítězslav Bryja group at the Faculty of Science, MU. Here they performed the detailed characterization of phosphorylations of Dishevelled proteins and applied a two-dimensional separation technique to whole proteome and phosphoproteome analysis of changes in HEK293 cells induced by Wnt3a activation. The results contributed considerably to elucidation of the processes related to Wnt signaling.

The lecture of 50 minutes duration was clearly presented and well prepared. Doc. Zdráhal proved a deep knowledge of his field in the follow-up discussion, answering questions from the committee members and from the audience.

Specific questions: prof. Havlíček – what is the usual false discovery rate in your experiments? What were the usual concentration ranges in which “important” proteins were



found? Prof. Nosek – How to distinguish pervasive translation from false results, artifacts? Assoc. Prof. Egger – Does it make sense to examine archived samples – is the dynamics of PTM maintained there? Prof. Šebela – Have you seen other physiologically important PTM than those presented here? Prof. Fajkus – is there a way to analyse PTM in chromatin and chromosome subdomains? Audience – How do you discriminate among phosphorylation sites? Doc. Bryja – How much is left as unidentified from the whole peptide spectra after processing? What is the current status of clinical proteomics? Are there any benchtop instruments for a simplified use? Is the labelling of samples still necessary for quantitative proteomics?

Conclusion

The lecture delivered by Zbyněk Zdráhal, entitled *Deciphering of proteome complexity* and delivered as part of the professor appointment procedure, **demonstrated** sufficient scholarly qualifications and pedagogical capabilities expected of applicants participating in a professor appointment procedure in the field of Genomics and Proteomics.

In Brno on October 16, 2018

Jiří Fajkus

Gerda Egger

Vladimír Havlíček

Jozef Nosek

Marek Šebela