

2nd International Metaproteomics Symposium

What can we learn about microbial communities and their functions?

Alghero (Sardinia, Italy) - June 14-16, 2017
Porto Conte Ricerche

Final programme

Wednesday, June 14

13:30 Arrival and Registration

14:15 Opening and Welcome address

Session 1: New methods and trends in metaproteomics

*Chair: **Paul Wilmes** - University of Luxembourg, Luxembourg, Luxembourg*

14:30 Recent advances in experimental and informatics aspects of mass spectrometry-based metaproteomics approaches for characterizing human gut microbiome development
***Robert Hettich** - Oak Ridge National Lab, Oak Ridge, TN, USA*

14:50 Metaproteogenomics of human, rodent and ruminant gut microbiota enables in-depth characterization of active metabolic pathways
***Alessandro Tanca** - Porto Conte Ricerche, Alghero, Italy*

15:10 Integrated meta-omics in digestive ecosystems: from biogas reactors to marine host-associated microbiomes
***Magnus Ø. Arntzen** - Norwegian University of Life Sciences, Ås, Norway*

15:20 Ultra-deep metaproteomics for human gut microbiome study
***Xu Zhang** - University of Ottawa, Ottawa, ON, Canada*

15:30 Metagenomics and metaproteomics provide insights into the roles of Bacteroidetes and Firmicutes in lignocellulose deconstruction by wheat straw-enriched microbial consortia
***Emeline Flajollet** - INRA/INSA/CNRS/Université de Toulouse, Toulouse, France*

15:40 Discussion - Q&A

16:00 Coffee and tea break

Workshop 1: Metaproteome biodiversity analysis with Unipept

16:30 *Coordinator: **Bart Mesuere** - Ghent University, Ghent, Belgium*
The Unipept workshop will give an overview of the different functionalities of the Unipept application; from exploring the biodiversity of a single sample to setting up a high-throughput data-analysis pipeline.

18:30 Q&A and hors d'oeuvres

Thursday, June 15

Session 2: Metaproteomics in health and disease

Chair: Sergio Uzzau - Porto Conte Ricerche, Alghero, Italy

09:20 Integrated multi-omics for identifying discriminant features in the human microbiome

Paul Wilmes - University of Luxembourg, Luxembourg, Luxembourg

09:40 Chemical-probe enrichment with mass spectrometry proteomics identifies aberrant proteins in IBD-related gut microbiomes

Dennis Wolan - The Scripps Research Institute, La Jolla, CA, USA

10:00 Gastric Bypass surgery clearly perturbs the community structure and the functional composition of the intestinal microbiota

Nico Jehmlich - Helmholtz-Centre for Environmental Research-UFZ, Leipzig, Germany

10:10 Reconstruction of medieval oral microbiomes by metaproteomics analysis of archaeological human dental calculus

Rosa R. Jersie-Christensen - University of Copenhagen, Copenhagen, Denmark

10:20 Stratified FDR results in an increased identification rate of proteins in a metaproteomic analysis of Viking dental calculus

David Lyon - University of Copenhagen, Copenhagen, Denmark

10:30 The ObOmics program: search for metaproteomic predictors of the outcome of a nutritional intervention in overweight patients

Catherine Juste - Université Paris-Saclay, Jouy-en-Josas, France

10:40 Discussion - Q&A

11:00 Coffee and tea break

Session 3: Metaproteomics in environmental biotechnology and animal science

Chair: Dirk Benndorf - Otto von Guericke University, Magdeburg, Germany

11:30 The gut microbiome of livestock – influences of feeding and interactions with the host

Jana Seifert - University of Hohenheim, Stuttgart, Germany

11:50 Differential sensitivity of total and active microbial communities to forest management and drought

Felipe Bastida - CEBAS-CSIC, Murcia, Spain

12:00 Multi-omic characterization of a commercial-scale, food-waste biogas reactor

John Christian Gaby - Norwegian University of Life Sciences, Ås, Norway

12:10 Dietary changes in pig nutritional studies shape the structural and functional composition of the pig's fecal microbiota – from days to weeks

Bruno Tilocca - University of Hohenheim, Stuttgart, Germany

12:20 Metaproteomic analysis of environmental microbiome dynamics

Jacob Kuruvilla - Linköping University, Linköping, Sweden

Combination of metagenomics and quantitative metaproteomics to unravel microbial interactions during cellulose deconstruction

Benoît J. Kunath - Norwegian University of Life Sciences, Ås, Norway

12:40 Discussion - Q&A

13:00 Lunch break

Workshop 2: Quantitative mass spectrometry and its potential for metaproteomics

Coordinator: Daniela Pagnozzi - Porto Conte Ricerche, Alghero, Italy

14:30 The workshop will give an overview on quantitative mass spectrometry-based applications covering untargeted relative quantification methods for discovery studies and targeted methods for validation studies, as well as label-free and label-based approaches. Case studies and applications in the field of metaproteomics will be then presented.

High resolution accurate mass-based quantitative strategies for both discovery studies and validation studies

Lars Kristensen - Thermo Fisher Scientific

16:30 Coffee and tea break

17:00 Comparison of spectral counting with matched ion intensities for quantification in metaproteome research

Robert Hettich - Oak Ridge National Lab, Oak Ridge, TN, USA

17:10 Evaluation of the SWATH-MS potential for comparative metaproteomic of complex ecosystems

Mélanie Beraud - Université de Mons, Mons, Belgium

17:20 Mix24X, a complex lab-assembled microbiota reference resource for evaluating data acquisition and processing procedures for metaproteomics

Jean Armengaud - CEA, Bagnols-sur-Cèze, France

17:30 Discussion - Q&A

17:45 Poster session and hors d'oeuvres

Friday, June 16

Session 4: Bioinformatics for metaproteomics

Chair: Lennart Martens - Ghent University, Ghent, Belgium

09:15 Galaxy-P for Metaproteomics: Advancing functional microbiome research via community-based informatics development and dissemination

Pratik Jagtap - University of Minnesota, Minneapolis, MN, USA

09:35 A graph-centric approach for metagenome-guided protein identification in metaproteomics

Haixu Tang - Indiana University, Bloomington, IN, USA

09:55 Improving the quality of genome, protein sequence, and taxonomy databases: a metaproteomics prerequisite

Olivier Pible - CEA, Bagnols-sur-Cèze, France

10:05 Metaproteomic data analysis and evaluation of a large data set from biogas plants

Kay Schallert - Otto von Guericke University, Magdeburg, Germany

10:15 Discussion - Q&A

Demonstration of Galaxy platform for metaproteomics

Pratik Jagtap - University of Minnesota, Minneapolis, MN, USA

10:30 This session will demonstrate the use of Galaxy platform (<https://usegalaxy.org/>) for metaproteomics studies. This will include workflows for database generation, database search strategies, taxonomy and functional characterization. It will be also discussed the ongoing work on setting up a metaproteomics gateway so that tools can be developed and tested and workflows can be developed and used by researchers.

11:00 Coffee and tea break

Workshop 3: The MetaProteome Analyzer software - part I

Coordinator: Dirk Benndorf - Otto von Guericke University, Magdeburg, Germany

11:30 The MetaProteomeAnalyzer (MPA) is a software pipeline to analyze and visualize metaproteomics data. The workshop will demonstrate the use of the MPA software as follows: using multiple database search engines; grouping of protein identifications to metaproteins; metagenome annotation by BLAST; taxonomic and functional data analysis; comparison of multiple datasets.

13:00 Lunch break

Workshop 3: The MetaProteome Analyzer software - part II

Coordinator: Dirk Benndorf - Otto von Guericke University, Magdeburg, Germany

14:30 Up to ten registered users can process own data within the MPA workshop using their own computers. The accounts for the MPA web service will be also available after symposium and offer full access to the software.

16:00 Conclusions and farewell