IMS2021 Luxembourg

Programme



4th International Metaproteomics Symposium

Neumünster Abbey Cultural Exchange Center, Luxembourg September 27-29 2021

The 4th International Metaproteomics Symposium

Luxembourg

27-29 September 2021





Metaproteomics is the large-scale characterisation of the entire protein complement of a microbiota directly from an environment at a given point in time. Research examining environmental and human-associated microbiomes via multiomics is expending rapidly. Especially, functional meta-omic approaches such as metaproteomics are currently employed intensively and provide a more comprehensive picture of multiple environments and their associated microbial communities than what could be done previously.

The International Metaproteomics Symposium is the leading event in the field of metaproteomics and related microbiome studies. The aim of the symposium is to provide a platform for the participants to share their latest results in their respective fields using metaproteomic methods as well as discussing recent technologic innovations and presenting newly developed bioinformatic tools.

The Metaproteomics Symposium welcomes international scientists from every career stage and is characterised by its human dimension and promotion of high-quality interactions.

We hope you will find everything you are looking for during our symposium.

Funding and Supports

The organisation of the 4th International Metaproteomics Symposium is mainly and strongly supported by the **Luxembourg National Research Fund** (FNR).



The Symposium is also supported by the Federation of European Microbiological Societies (FEMS) as well as the Luxembourg Society for Microbiology (LSfM). They are both supporting us and you, by offering travel grants and awards for Early Career Researchers.





Federation of European Microbiological Societies

Monday 27th September

| 8:45 | Arrival And Registration |
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| 9:30 | Welcome Speeches and Introduction |
| | Benoît Kunath & Paul Wilmes - University of Luxembourg |
| | Session 1: Metaproteomics of complex/technical habitats and Eukaryotes |
| 10:00 | Keynote Presentation Using proteins to study the structure and function of soil microbial communities Dr. Robert Starke - Czech Academy of Sciences, Czech Republic |
| 10:30 | 3 Selected Abstracts Challenges and solutions for exploring taxonomical and functional changes of microbiota along a soil core Virginie Jouffret - Technological Innovations for Detection and Diagnosis Laboratory, France |
| | Exploring protozoal function and their greater metabolic influence in the rumen microbiome using (meta)-genome resolved metaproteomics Thea Os Andersen - Norwegian University of Life Sciences, Norway |
| | The bacterial microbiome of <i>Lobaria L. Hoffm</i> .: Composition and variability Grimm Maria - University of Greifswald, Germany |
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Monday 27th September

| | Session 2: Metaproteomics in Health and Diseases - Covid19 |
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| 11:30 | 2 Selected Abstracts Preliminary functional insights into the gut microbiota of Covid-19 patients probed by metaproteomics Lucia Grenga - Technological Innovations for Detection and Diagnosis Laboratory, France |
| | Comprehensive metaproteomic analysis of nasopharyngeal swabs to investigate co-infection status in Covid-19 patients Surbhi Bihani - Indian Institute of Technology, India |
| 12:00 | LUNCH |
| | Session 2: Metaproteomics in Health and Diseases |
| 13:00 | Keynote Presentation Functional metaproteomics from bench to clinics Prof. Daniel Figeys - University of Ottawa, Canada |
| 13:30 | 4 Selected Abstracts Metaproteomic features related to intestinal bowel diseases Catherine Juste -Institut national de la recherche agronomique, France |
| | Characterization of time-dependent signatures of antibiotic administration and resistance-related microbial modulation of host immune response in preterm infants Samantha Peters - Oak Ridge National Laboratory, USA |
| | Metaproteomic analysis of colonic luminal content microbiota from colon cancer patients Alessandro Tanca - University of Sassari, Italy |
| | Quantitative metaproteomic analysis of a mouse model for Parkinson's disease Jinqiu Xiao - Max Planck Institute of Psychiatry, Germany |

Monday 27th September

| | Poster Session |
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| 14:45 | Poster Pitch |
| 15:00 | COFFEE BREAK |
| 15:15 | Poster Session |
| | A hybrid nanopore-metaproteomics approach for the characterization of raw cow milk resistome Alessio Soggiu - University of Milan, Italy |
| | Activity of microbial communities living in carbonate rocks at seafloor methane seeps Magdalena Mayr - California Institute of Technology, USA |
| | Integrative meta-omics in Galaxy Valerie Schiml - Norwegian University of Life Sciences, Norway |
| | PEPGM: A probalistic graphical model for taxonomic profiling of viral proteomes and metaproteomic datasets Tanja Holstein - Bundesanstalt für Materialforschung und Prüfung, Germany |
| | Metaproteomic investigation of marine sediment to evaluate the metabolic potential for hydrocarbon degradation Anne Ostrzinski - University of Greifswald, Germany |
| | Critical Assessment of metaproteome investigation (CAMPI): A multi-lab comparison of established workflows Tim Van Den Bossche - Ghent University, Belgium |
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Monday 27th September

Poster Session

Metaproteomic profiling of the lung microbiota from cystic fibrosis patient

Pauline Hardouin - Technical Innovations for Detection and Diagnosis Laboratory, France

A metaproteomic approach to prove functional stability within the intestinal microbiome of piglets after challenge with chlorotonil A Madita Brauer - University of Greifswald, Germany

Tackling challenges in clinical metaproteomic analysis of bronchoalveolar lavage fluid to characterize microbial contributors to cystic fibrosis

Monica Kruk - University of Minnesota, USA

Sewage treatment plants can increase prevalence of antimicrobial resistances in aquatic environments Tjorven Hinzke - University of Greifswald, Germany

Metaproteomic investigation on the role of the gut microbiota in type 1 diabetes onset

Stefano Levi Mortera - Bambino Gesù Children's Hospital IRCCS, Italy

17:00 End of Day 1

Tuesday 28th September

| 8:45 | Arrival And Coffee |
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| | Session 3: Identification and Annotation of (Novel) Proteins |
| 9:30 | Keynote Presentation Large-scale analyses of Human Microbiomes reveal thousands of small, novel genes Prof. Ami Bhatt - Stanford University, USA |
| 10:15 | 2 Selected Abstracts Discovery of novel community-relevant small proteins in a simplified human intestinal microbiome Nico Jehmlich - Helmholtz Centre for Environmental Research, Germany |
| | Mantis: Flexible and consensus-driven genome annotation Pedro Teixeira Queiros - University of Luxembourg, Luxembourg |
| 11:00 | COFFEE BREAK |
| 11:15 | Session 4: Integrative Multi-Omics Keynote Presentation Critical Assessment of Metagenome Interpretation Prof. Alice McHardy - Helmholtz Centre for Infectious |
| 11:45 | Research, Germany <i>3 Selected Abstracts</i> Can we predict a microbial ecosystem? Francesco Delogu - University of Luxembourg, Luxembourg |
| | Transkingdom network analysis across the host-microbiome nexus in the bovine rumen reveals association to host fitness Ianina Altshuler - Norwegian University of Life Sciences, Norway |

Tuesday 28th September

| | Diet drives host and microbial changes in the gastrointestinal tract of rainbow trout (<i>Oncorhynchus mykiss</i>) Arturo Vera Ponce De Leon - Norwegian University of Life Sciences, Norway |
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| 12:45 | LUNCH |
| | Session 5: Bioinformatics for Metaproteomics |
| 13:45 | 5 Selected Abstracts Promoting metaproteomics: Empowering researchers through online, on-demand metaproteomics educational resources and training materials via the Galaxy platform Pratik Jagtap - University of Minnesota, USA |
| | Mapping metaproteomic data on metabolic pathways and prototyping metabolic modeling Robert Heyer - Otto-von-Guericke University, Germany |
| | Unipept desktop: Getting Unipept ready for proteogenomics Pieter Verschaffelt - Ghent University, Belgium |
| | Novolign: Peptide annotation of DeNovo metaproteomics by diamond alignment Hugo Kleikamp- Technical University Delft, The Netherlands |
| | MS2Rescore: Using predicted fragment ion intensities and retention time to increase identification rates in metaproteomics Tim Van Den Bossche - Ghent University, Belgium |
| 15:15 | COFFEE BREAK |
| 15:30 | Metaproteomics Initiative - General Assembly |

Wednesday 29th September

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Wednesday 29th September

| | Session 7: Environmental Metaproteomics |
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| 12:45 | Keynote Presentation Applying metaproteomics to Ocean Environments: Progress and Challenges Dr. Mak Saito - Woods Hole Oceanographic Institution, USA |
| 13:15 | 5 Selected Abstracts Metaproteomic characterization of the particle-associated microbial community of a north sea spring phytoplankton bloom Robin Siebers - University of Greifswald, Germany |
| | Combined metagenomics and metaproteomics of a two-stage bio gas plant questions the benefit of the hydrolysis fermenter for process performance Patrick Hellwig - Otto-von-Guericke University, Germany |
| | Adaptation of a methanogenic community to demand-oriented biological methanation Dirk Benndorf - Otto-von-Guericke University, Germany |
| | Metaproteomics reveals alteration of the gut microbiome in weaners by the ingestion of the mycotoxins deoxynivalenol and zearalenone Johan Saenz - Hohenheim University, Germany |
| | Functional response of a lignocellulolytic microbial consortium derived from cow rumen to substrate modifications induced by pretreatment Guillermina Hernandez Raquet - Toulouse Biotechnology Institute, France |
| 15:00 | Concluding Remarks Dr. Robert Hettich - Oak Ridge National Laboratory, USA |

Abstracts Selected for Oral and Poster Presentations

All the selected abstracts can be downloaded as a PDF version on the IMS2021 website or by following this QR-Code:

https://ims2021.uni.lu/programme/



Metaproteomics Initiative

For more information and interactions with the metaproteomics community, join the newly launched Metaproteomics Initiative

