B/D-HPP Newsletter

Biology/Disease- Human Proteome Project Newsletter | September 2016

In This Issue

Welcome

Welcome to the first BD-HPP newsletter.

This communication is design to inform and encourage collaborative efforts within the HUPO community, within B/D-HPP initiatives as well as across B/D-HPP and C-HPP. In each issue, we aim to highlight the activities and achievements of two B/D-HPP initiatives, and celebrate a success story. The newsletter editor is Michelle Hill, a new HUPO council member from Brisbane, Australia.

Jennifer Van Eyk – B/D-HPP Chair

Michelle Hill – Newsletter Editor

HUPO 2016

Thanks to the leadership of the various projects, a number of HPP sessions are planned during the upcoming HUPO Congress 2016 in Taipei. The post-congress workshop will be held at the beautiful Sun Moon Lake.

HPP Program at-a-glance

	Sunday Sept 18	Monday Sept 19	Tuesday Sept 20	Wednesday Sept 21	Thursday Sept 22
	HPP General Investigators Meeting	**HUPO Congress Sessions**			**HPP Post-Congress Day (Sun Moon Lake)**
AM	•Overview •Plenary lectures, •B/D HPP and C-HPP planning sessions #1	•Cluster groups: membrane, neurodegenerative disease •Brain & EyeOME	Liver & toxicopro-teomics	Food, nutrition & immuno-peptidome	•HPP update & open strategy discussion •Bioinformatics hub, 2016 JPR issue, HUPO MS standards •Plenary Lecture •Reports on Cluster meetings
PM	•Joint cluster group meeting with lunch. •Cluster groups: cancer, IVTT, repdroduction	Diabetes & Cardio-vascular	Protein standards & model organisms	Kidney, urine & plasma	•SSAB feedback •Operations & communication matters •Strategic plan, publications & future workshops •Boat Tour

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Connecting with C-HPP through cluster groups

The concept of cluster group collaborations between HPP initiatives was first developed during the 12th C-HPP workshop at Milano in 2015, with goals of simulating collaborations, strengthening research focus and outcomes.

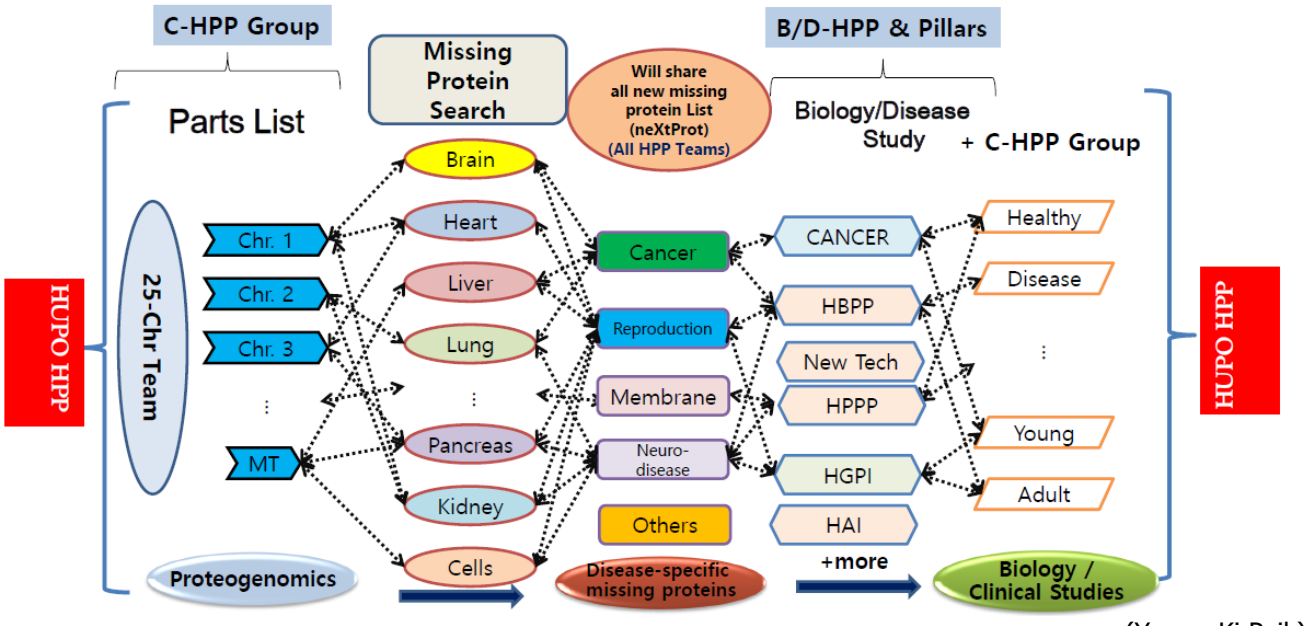
Interactions across the technology and biology/disease focused HPP investigators are expected to produced synergistic outcomes. For example, once missing proteins are identified and annotated by neXtProt (C-HPP), with indicative biological function, there may be investigators in the relevant B/D-HPP or cluster group with the required cell/tissues samples, reagents and biological understanding to start characterising the new proteins. By connecting newly verified novel proteins/proteoforms with highly relevant expertise, the HPP clusters will generate high impact biological research outputs, which may lead to disease-relevant translational outcomes.

The term "cluster" can be defined as an informal grouping to facilitate communications between the formal groups (B/D-HPP, C-HPP, Pillars) that the HUPO membership and general public see it as a way to organize sessions and workshops rather than setting up a parallel set of groups. (Chris Overall)

Hence, cluster group meetings should act as catalysts to link C-HPP information with the biological and disease knowledge of B/D-HPP, and the technological tools of the HPP Pillars.

The cluster strategy plan was accepted unanimously during the C-HPP Principal Investigators Council meeting at the Vancouver 2015 Congress, during which IVTT (*in vitro* transcription/translation), cancer and membrane proteins cluter groups held pilot meetings. An expanded cluster group meeting is on the agenda for Taipei, with the addition of reproductive disease and neurodegenerative disease cluster groups.

A Big Picture: Concept of HPP Cluster Collaboration



(Young-Ki Paik)

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Translational Success Story – Bruker MALDI Biotyper

..... Contributed by Winfred Busch, Bruker

Bruker Daltonics pioneered MALDI-TOF as an early inventor of this technology and was the first to introduce a commercially available system. Scientists welcomed this new analytical technology immediately. The process has the great advantage that the soft ionization process causes no or only little fragmentation to biomolecules and the mass spectrometric analysis is sensitive and rapid.

One area of focus became evident as we discovered that protein profiling provided simplified and highly reliable identification of microorganisms. This led to the birth of the MALDI Biotyper, a groundbreaking new approach for the identification of microorganisms like bacteria, yeast and filamentous fungi.

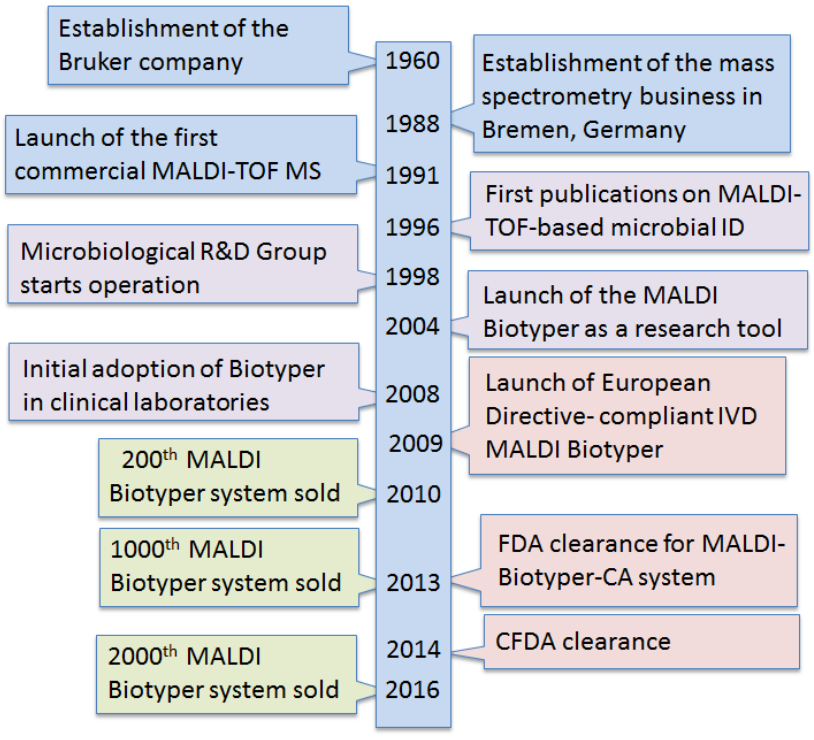
The identification of these organisms is based on pattern matching of highly abundant ribosomal proteins present in every cell, enabling the identification of individual species by this fingerprint. Pre-requisite for this pattern matching approach are spectra libraries and specific bioinformatics. Bruker spent significant efforts over the last decade to develop and expand software tools and reference libraries which are integrative parts of the MALDI Biotyper system.

The fast and reliable identification of microorganisms is of great importance in public healthcare, enabling appropriate treatment of bacterial infections in a fast and appropriate manner. MALDI Biotyper is therefore IVD-CE certified since 2010 and achieved FDA clearance in 2013 with a first expansion of the claim in 2015.

But microorganisms are not only of great importance for public healthcare. Pharmaceutical companies must reassure that their products are safe. It's the same for food and beverages industries because many microorganisms play a major role in food production - just think about the important role of yeast in the brewing process. Also of great importance is the control of drinking water where for example Legionella can be a major threat.

Further applications include taxonomical research, environmental analysis and veterinary microbiology. For this reason the reference libraries of the system cover a broad range of species important for many different applications. Bruker continuously expands the species coverage and the libraries contain, currently, spectra of for more than 2,300 species – a doubling in number compared to five years ago.

Timeline of the MALDI-Biotyper



The ease-of-use, speed, reliability and significant cost savings for the identification are so convincing that already more than 2,000 Biotyper systems have been sold worldwide. The widespread use of Biotyper, is further reflected by the cooperation of Bruker with the U.S. Centers for Disease Control to add a Biotyper module to MicrobeNet to facilitate infectious disease surveillance by U.S. health labs and hospitals.

There is more to come. A major threat for human society is the ever emerging resistance of bacteria to antibiotics and analysis of such resistances is in high demand. Bruker introduced this year for the MALDI Biotyper a specific subtyping software tool for research use to combine fast microorganism identification with instant resistant marker detection. Watch this space!

MALDI Biotyper in the community…….

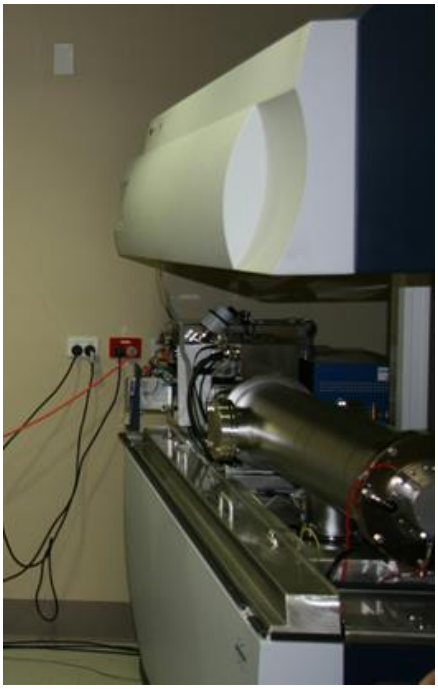
An early adopter of the technology is Deon Venter, Director of Mater Pathology in Brisbane, Australia

Prof Deon Venter was in Bremen, Germany in 2007, evaluating the Bruker Ultraflex MALDI-TOF system for imaging when, Sjoren a Bruker employee, demonstrated the potential of using MALDI for biotyping.

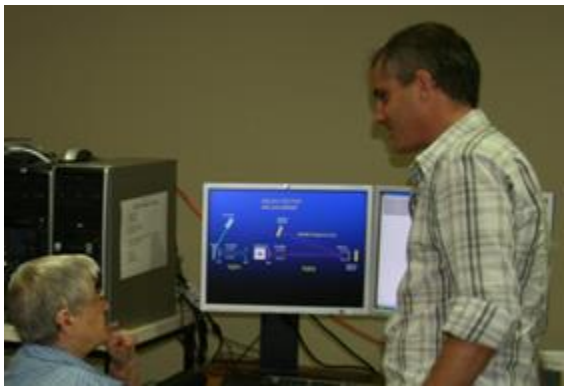
The Mater Hospital received its own Ultraflex MALDI TOF in 2008. Dr Gareth Price and Dr Sanmarie Schlebusch developed techniques for spectral acquisition from organisms seen at Mater Pathology.

Mater Pathology used MALDI TOF MS in the MRSA outbreak and have presented posters on using MALDI Biotypers in identification of difficult and resistant organisms in 2011. This laid the foundation for validation using culture collections, leading to its routine use at Mater Hospital Microbiology Department.

Bruker's innovative vision worldwide coupled with proteomic researcher's efforts have revolutionized certain areas of pathogen diagnostics and speed of analysis.



The first Ultraflex at the Mater Hospital in Brisbane, Australia.



Dr Tristan Wallis (right) of the Mater Hospital, Brisbane, Australia explaining the new technology to Sister Regus Mary Dunne (left), who had in fact started the cytogenetics lab at Mater Pathology many years before. Sister Regus Mary Dunne retained a keen interest in novel diagnostic technologies, despite being in her late 70s at the time the picture was taken. Dr Wallis demonstrated the use by putting an E.coli through the Ultraflex pictured above.

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Human Brain Proteome Project ... by Daniel Martins-de-Souza

The **Human Brain Proteome Project (HBPP)** was launched in 2003 by Prof. Helmut Meyer, who promoted the renewal of its directorship in 2015. Now, the HBPP is formed by a steering committee of eight researchers from four continents.

Focusing on unveiling the human brain and nervous system proteome, HBPP is defining new tasks for its future, including the promotion of large-scale and targeted state-of-the-art proteome studies on human brain, brain-related body fluids such as cerebrospinal fluid (CSF) and blood plasma/serum, pre-clinical models, and follow-up projects to decipher the role of proteins in brain development, health and disease.

The 25th Spring HBPP Workshop took place in Stockholm on May 3-4, 2016 and was the first organized by the new steering committee. The workshop welcomed researchers from all parts of the world, including Australia, USA, Brazil, Canada, Spain, Ireland, Germany, Netherlands, Luxembourg and Sweden.

A smorgasbord of 44 talks over 7 sessions covered diverse aspects of the human brain research as neurodegeneration, dementia, psychiatry, biomarkers and technological advances.

In a relaxed pub environment, we had an update on the Human Protein Atlas by Prof. Mathias Uhlen (SciLifeLab/KTH) and discussed MRM applications with Prof. Christoph Borchers (Genome British Columbia Proteomics Centre, Canada).

We encourage every researcher interested in brain proteomics, especially junior scientists, to get in contact and join the initiative. Join us at the exciting HUPO 2016 Brain HPP session or email: contact@hbpp.org).

HBPP Steering Committee

- **Katrin Marcus, Medizinisches Proteom-Center, Bochum, Germany.**
- **Lea Grinberg, UCSF, USA & University of Säao Paulo, Brazil.**
- **Oliver Schubert, University of Adelaide, Australia.**
- **Charlotte Teunissen, VU University Medical Center Amsterdam, Netherlands.**
- **Helmut E. Meyer, Leibniz Institute for Analytical Sciences, Dortmund, Germany.**
- **Young Mok Park, Korean Basic Science Institute, Daejeon, South Korea**
- **Daniel Martins-de-Souza, University of Campinas, Campinas, Brazil.**
- **Peter Nilsson, SciLifeLab, KTH, Stockholm, Sweden.**

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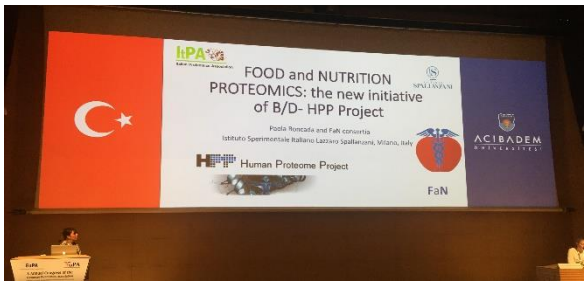
Food and Nutrition Proteomics – a new kid on the block

A new B/D-HPP initiative launched in January 2016 is **Food and Nutrition Proteomics (FaN).**

Chaired by Dr Paola Roncada of Istituto Sperimentale Italiano L. Spallanzani, Milano, Italy, FaN has ambitious translational objectives of linking proteomics to food and veterinary industries, clinical stakeholders and regulatory bodies. To achieve this, the FaN team includes an industrial advisory board in addition to a scientific advisory board.



From its conception at a morning workshop at HUPO 2015 Congress in Vancouver, the FaN team has been actively promoting the initiative at several meetings in 2016:
March - World Allergen Food Fair, Padova, Italy.
May - Italian Proteomics Organization, Perugia, Italy.
May - CN-HUPO congress, Xiamen, China.
June - EuPA Congress, Istanbul, Turkey (photo left).

The fantastic FaN proteomics ……. by Paola Roncada

We eat at least three times a day. Food and nutrition undoubtedly is central to many modern health problems from obesity, diabetes, cardiovascular disease and cancer to fetal intrauterine growth retardation and so on. Proteomics holds great promise for discoveries in nutrition research which can provide solutions that may lead to major improvements in global health.

Starting from nutrition science, we have to consider that protein components of food are subject to modifications driven by the human organism (eg. digestion) and/or food processing technologies. Moreover, the interaction of food proteins with the microbiota, present in either the food itself or inhabiting the organism, could change the entire history of adsorption, distribution, metabolism and excretion of any nutrient. Hence, the FaN initiative covers proteomics of a broad range of species, as well as their interactions with the host organism.

The first official session of the initiative will be held at the Taipei HUPO 2016 congress, together with the Immunopeptidome Initiative lead by Etienne Caron. The focus will be on food allergies which is an increasingly significant health and medical issue worldwide. Strategies of rapid identification of new food allergens, will be addressed during the session.

The **FaN proteomics** paradigm