

**Human Proteome Project
Working Group
News - June 1st, 2010**

The second meeting of the working group took place on May 10, 2010, at the Queen Elizabeth Hotel in Montreal, one day ahead of the Canadian workshop on the HPP. In the opening remarks, strong emphasis was placed on:

- Definition of terms with respect to HPP, Gene Centric HPP, Protein Centric HPP and Disease Centric HPP
- The need for standards and references for protein identification and characterization, using mass spectrometry as well as affinity-based technologies (mostly antibodies).
- Databases systems, utilization, applications and interoperability. The role of a putative HPP portal.
- The link between HPP, on going large scale scientific initiatives and coordination of national efforts.

Proteomics standards for mass spectrometry specificities and antibody characterization.

It was suggested to combine MS and Ab approaches. Establishing standards in MS should be part of the work plan (reference tissue, body fluid, etc.). In addition, the validation of MS processes through institutional recommendation was discussed. The HPP group will commit to standardized protocols. Prof. Steve Carr (The Broad Institute) presented present CPTAC, an international initiative for characterization and quantitation of human proteins. It was agreed on the need for coordination of all initiatives in the frame of HPP to avoid any duplication of efforts.

Novel affinity capture reagents technologies are needed or alternatively, access to well-defined reagents should be organised. Polyclonal Abs are often provided without clear description of interacting epitopes on proteins; monoclonal Ab (MAbs) technology remains expensive but seems a valuable investment for the long term. Already 500-1000 MAbs are probably available, but without a standardized description of reactivity. The HPP WG should perhaps pursue the idea of a MAbs repository, with a formalized description of MAbs including the antigen.

Ideally HPP should start with the “normal-ome”, ie an accurate description of human proteins in their normal production and localisation profile.

Databases and informatics tools

ProteomExchange was proposed as a very good starting point, with connection with biology oriented databases. The aim for HPP is to create a portal, not a whole HPP database. This portal should provide the scientific community with a standardized “minimal knowledge” on all proteins. This would define the needs and provide criteria on deliverables. It might be necessary to narrow the focus to get deliverables.

HPP and other major initiatives in Biology and Medicine.

HPP cannot be envisioned without taking into account environment (microbiomes) or medical issues. Proteomics has a better entry point for clinics, compared with other large scale approaches. HPP could have specific programmes to deal with relatively abundant proteins. “Normal-ome” must be connected with well documented clinical samples, and access to normal clinical samples. Biobanking will therefore be critical.

Three countries have committed on chromosome-based HPP. In those cases, linkage to disease or specific biological issues will be critical. The challenge for HPP is to identify specific “anchor projects” that go across diseases and that are feasible. Europe and Canada are strongly supportive of initiatives linked to personalized medicine. Other research agencies also look for applied programs. The HPP might be closer to medical applications than other “omics”, which might turn out to be more challenging because explicit deliverables will be required.

HPP and HUPO initiatives should be thought carefully alongside each other. Cross-fertilisation is expected, especially when the initiative has already raised significant publications and collaborations.

Preparation of next steps

It is crucial first to issue the HPP report to scientific stakeholders before trying to connect with other worldwide or international initiatives. Industry will be relied upon to bring the push for technology advancement and possible breakthroughs. At some point in the near future a meeting between funders will be needed, once a good scientific case can be presented.

At the present stage, HPP is envisioned as a coordinated effort which will be implemented as smaller focused projects that can go to research funding agencies to get support and expand on specific areas.

The next step for the working group is to prepare the report due for HUPO2010. Several subgroups have been constituted to address the different parts: Experimental design for protein signatures; Antibody description ; Data formats ; HPP Pilot projects.

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