Canadian Human Proteome Project

We write as executives of the Canadian National Proteomics Network (CNPN), a not-for-profit federally incorporated organization created to provide a cooperative mechanism for building the proteomics research infrastructure in Canada to further a better understanding of proteomics in the Canadian life sciences community and to sponsor scientific conferences, seminars and forums to create a national focus for scientific collaboration and education.

At this year’s annual conference of the Human Proteome Organization (HUPO) in Sydney, Australia, September 18-23, the Human Proteome Project (HPP) was officially launched. To tackle the challenging mission of “mapping” all human proteins in the most comprehensive manner, the international proteomics community has decided to divide the workload according to the organization of the genome in chromosomes. The first chromosome-centric projects have already been launched – for example, the US is mapping and studying the proteins encoded in chromosome 17; Sweden has claimed chromosome 21; Japan chromosome 3, etc. Canada, however, is not yet officially involved in the HPP.

Continues page 2 See Chromosome

Joint CNPN / ETP Symposium May 8—11 Banff Alberta

CNPN 2011 and ETP 2011 is pleased to bring together an elite panel of scientific leaders to present their latest results on cutting-edge technologies in proteomics.

Students and the first 100 registrants are eligible for reduced room rates ($149/night based on double occupancy) at the Fairmont Banff Springs Hotel. Competitive travel awards ($500) will also be available for students who submit a poster.

Registration opens Dec 1, 2010

CNPN 2011 is organized by Drs. Liang Li, University of Alberta, David Schriemer, University of Calgary and Joel Weiner of University of Alberta.

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Upcoming Meetings:

- Canadian Human Proteome Project, (CHPP) Interest Group Workshops (Page 2)
- Bellairs, Institute Barbados Week of Jan 16-18 / Vancouver or Toronto Jan 31
- Joint CNPN/ETP Symposium May 8-11 2011, Banff,
- ABETP Atlantic Conference, Oct 7 2011, Boston MA
HUPO: Chromosome based global project (Cont)

In response to this, and to explore funding possibilities for Canadian chromosome-centric projects, the Canadian National Proteomics Network (CNPN) has written a two-page letter entitled, “The Human Proteome Project: A Critical Investment in Canada's Future” (see attached document) to Genome Canada, the Genome Science Centres, and CIHR. Several weeks ago, representatives of the CNPN had a follow-up discussion, organized by Genome Quebec, with representatives of these funding agencies. In short, all of these agencies are very positive about the concept of specific Canadian chromosome-centric projects. However, the funding agencies would like to learn more about possible projects before concrete plans to support the best of these projects can be made. Genome Quebec has agreed to organize a meeting in Montreal in February 2011 to further discuss a possible Canadian HPP initiative. In the meantime, we have been asked to get organized and to develop a "road map" towards achieving this goal. Dr. John Bergeron, former HUPO President, has kindly offered to dedicate a part of next year's Barbados meeting (January 16-18, 2011) to allow the Canadian proteomic community to prepare and come up with a plan for the February meeting with the funding agencies.

The CNPN would like to invite all Canadian scientists who have an interest in being part of a chromosome-centric project to join the Canadian Human Proteome Project (CHPP) Interest Group. If you are interested and would like to know details about the Barbados meeting, please email Janette Champ, Secretary of the CNPN, at jchamp@cnpn.ca. Please also alert faculty and colleagues who would be interested in participating in CHPP.

We are looking forward to welcoming all of you to the CHPP interest group, and we hope to see you in Barbados.

Christoph Borchers, PhD, CNPN President; Professor and Facility Director, UVic / Genome BC Proteomics Centre

Juergen Kast, PhD, CHPP Chair of CNPN; Associate Professor, University of British Columbia

K.W. Michael Siu, PhD, FCIC, FRSC,CNPN Chair, Board of Directors; Distinguished Research Professor and Associate Vice-President Research, Science & Technology, York University

Canadian Proposed Organizational Meetings / Workshops

Canadian Proteome Projects Committee

7th International Barbados Proteomics Conference

Chromosome-Based Human Proteome Project (Jan 16—18), followed by a Cell Biology Proteomics Application Workshop, (Jan 18—20)

Bellairs Research Institute, Holetown, Barbados.

Contact the organizing committee and Sylvie Ouellette if you are interested. Room rates start at $35 / night, shared occupancy. (sylvie.ouellette@mcgill.ca)

Alternate Meeting proposed for Vancouver or Toronto

Not everyone can secure funding to attend Barbados in January. In order to interface with the maximum number of interested parties, a second meeting is being considered for January 31. Final venue to be determined. Please contact any of the organizational committee if you would like to attend.

http://www.mcgill.ca/bellairs/facilities/
Hydra for Structural Mass Spectrometry

Dr David Schriemer, University of Calgary

The proteomics community is no stranger to the challenges presented by large datasets. Whether applied to discovery or quantitation, proteomics generates quantities of data in need of automated solutions. The emerging field of structural mass spectrometry is faced with similar challenges. What is structural mass spectrometry? It is simply the application of mass spectrometry techniques to the determination of protein structure. This may seem an unconventional use for a mass spectrometer, and it is, but when combined with chemical labeling methods a mass spectrum “codes” for spatial information, to the resolution provided by the labeling. It can be used to orient protein binding partners, map binding domains and (in the limit) guide protein structure-building exercises.

To get a good picture of the analysis requirements for structural mass spectrometry, consider one of the more powerful methods available. The backbone amide hydrogens in a protein are “sensors” of structure and dynamics. Monitoring the hydrogen exchange rates at these sites simply requires the addition of heavy water to a sample and a mass spectrometer to measure deuteration. Deuteration is typically measured in a bottom-up fashion, from enzymatic digests of the labeled protein. That is, the deuterium content of individual peptides or their fragments is the quantity to be measured. For the method to really shine, we need sequence coverage to approach 100%, which means a lot of peptides! Together with the short chromatographic runtimes required for exchange experiments, we have a complex mixture with the same detection issues found in discovery proteomics. On top of this, each isotopic envelope requires careful analysis for deuteration states.

The Hydra software package was developed to provide a proteomics-grade solution to the problem of deuteration data extraction. The current version is built to extract data in up to three dimensions, from LC-MS or LC-MS/MS. It accepts large numbers of acquisitions, requiring only a standard output from a database search tool to get started. This output provides the “index file” to identify where peptides elute and what fragments are seen. Specific algorithms are applied to extract exchange-driven mass shifts from each feature, along with other useful information such as deuterium distribution. Automated reporting and statistical metrics offer the user an output ready for structural interpretation. Supporting MS/MS data is a particularly powerful feature, enabling the use of new fragmentation methods for localizing chemical label with greater structural resolution. Because we all feel a level of discomfort in accepting the output of high-throughput engines, a manual validation tool provides a streamlined opportunity to test the output, make adjustments, and then apply those adjustments quickly and easily to all files in the dataset. With Hydra on the scene, the bottleneck has been returned to data collection, not data analysis.

Since the field of structural mass spectrometry is in its growth phase, Hydra is built on a modular concept to support the easy inclusion of innovations as they occur. All the “grunt-like” activities of Hydra’s core are separated from the interesting pluggable features, such as data extraction algorithms. This allows the community to plug in new features without having to rebuild the core, and will be available in the next release. This will support an extension to other structural mass spectrometry labeling methods, involving oxidative labeling, carbene labeling and the like. For the current download of Hydra (v1.5) see http://people.ucalgary.ca/~dschriem/.

CNPN Membership

It is important to be aware of CNPN membership. It is through member numbers that we develop a credible voice. I urge everyone to get your colleagues and students to sign up. We are actively seeking to expand proteomics to include plant and agricultural as well as microbiology and environmental applications. The tools we have developed have many applications throughout life science research.

Current Canadian Membership as of Oct 27, 2010

Total Members: 118 with 6 of those from the US, 75 General Members, 43 Students

Regional distribution

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Joint CNPN / ETP Symposium May 8—11 Banff Alberta

Symposium Chair: Dr. Randal Johnston, University of Calgary
Keynote Speaker: Dr. Daniel W. Chan, Johns Hopkins Medical Institutions

Sessions:
Proteomics in Biology John Wilkins (University of Manitoba)
Proteomics for Clinical Applications Michael Siu (York University)
Proteomics at the Interface of Biology and Medicine Dave Schriemer (U Calgary)

Invited Speakers:

Dr. N. Leigh Anderson, Plasma Proteome Institute
Dr. Alison Ashcroft, University of Leeds
Dr. Catherine Costello, Boston University School of Medicine
Dr. Daniel Figeys, University of Ottawa
Dr. Lars Konermann, University of Western Ontario
Dr. Bin Ma, University of Waterloo
Dr. Alan Marshall, Florida State University
Dr. Jochen Schwenk, School of Biotechnology, KTH
Dr. Richard D. Smith, Pacific Northwest National Laboratory
Dr. John Yates, The Scripps Research Institute

Student Workshop & Job Fair - NEW FEATURE  Sunday, May 8, 2011.

Complete Details at  http://www.cnpn.ca/events/events/symposium.html

Symposium Sponsors:  (as of Dec 1 2010)

Platinum Sponsor

Gold Sponsor

Ken Standing Award

Media Sponsor

Membership Input

Suggestions or ideas for this news letter or any other CNPN topic, please forward to the newsletter editor at: mikemcd@cnpn.ca
The eating quality of fresh fruit is a combination of many aspects, including appearance, color, texture, flavor (taste and aroma) and nutritional value, which play an important role in consumer satisfaction and enjoyment. Despite recognition of the challenges associated with the maintenance of fruit eating quality, information regarding the biology of fruit quality is limited. Fundamental questions regarding which metabolic pathways contribute to fruit ripening and its associated secondary metabolisms, especially flavor/aroma biosynthesis and how they are regulated remain. Proteomics is a relatively new analytical approach that is complementary to genomic technologies by en masse interrogation of biological phenomena on the protein level. The ability to reliably identify and accurately quantify a set of proteins of interest in a proteome is an essential task in any biology research and will determine metabolic pathways responsible for eating quality of fruit. In a series of studies, we have developed and modified fruit protein sample preparation procedure and applied both 2-D gel and quantitative proteomic methodologies on apple and strawberry fruit, linked chemical and genomic findings with alterations in the fruit protein complement. We have also modified and improved quantitative proteomic methods by employing multiplex N-terminal dimethylation of apple fruit proteins in collaboration with Dr. Pinto, NRC Halifax. In total, we have identified over 1,000 proteins and collected 36,000 peptides from apple and strawberry fruit during ripening.

Our goal is to understand the key biochemical pathways that regulate fruit ripening and flavor biosynthesis through the application of quantitative proteomic techniques. To address this objective, state-of-the-art technologies, including quantitative proteomic, genomics and underlying the eating quality of fresh fruit during ripening and postharvest handling. By characterizing the molecular changes at both the transcript and protein levels, these studies will provide new insights into the molecular framework of fruit ripening, reveal new pathways or processes affecting fruit eating quality, and provide avenues for product improvement in the future. Findings of these studies can be used in breeding programs to select or create plant material with the potential for better quality and higher in flavor. In addition, new approaches to prevent flavor loss and alteration associated with fruit aging and postharvest handling may be identified. Ultimately, results from our research will help to improve product appeal and consumption.

Agriculture and Agri-Food Canada. AFHRC, Kentville, Nova Scotia, Canada. B4N 1J5. E-mail: jun.song@agr.gc.ca
**CNPN Awards**

(* Student and Young Investigator Awards available for CNPN Members *)

**Student Travel Awards:** $500 will be awarded to 20 students for travel to the attend the joint CNPN/ETP 2011 Symposium

**Young Investigator Awards** A total of 20 travel grants of $750 each are provided to allow postdoctoral fellows and research associates of Canadian Universities to attend and present poster abstracts at the Canadian National Proteomics Network (CNPN) annual symposium. The Awards Committee will select 6 of those abstracts to present a 10 min oral presentation. No more than one postdoctoral fellow or research associate from a research group may apply. The CNPN Awards Committee will review the submissions received and will notify the award winners by April 1.

**AWARDS: Call for Nominations**

**CNPN Distinguished Researcher Award**

The CNPN established this Award in 2009 to recognize a Canadian researcher who made outstanding contributions to the field of proteomics. This award recognizes singular or lifetime achievement that has had a significant impact on the fundamental understanding and/or practice of proteomics in biological sciences. Nomination is not restricted to members of the CNPN. The award is announced at the CNPN Annual meeting. The recipient of the Distinguished Contribution in Proteomics will give a 50-minute lecture, will receive a commemorative plaque, and includes a $2500 cash award. To nominate candidates please review the Award Guidelines and Nomination Form

**The Ken Standing Award**

The Ken Standing Award is presented by the sponsors of the Enabling Technologies for Proteomics (ETP) Symposium to honor a young scientist who has made a significant contribution to technology development in support of research in the life sciences. Nominees are expected to be 45 years or younger at the time of the nomination. The award is presented at the ETP Symposium and includes a $5000 cash award and a commemorative sculpture. The award winner will be a featured speaker at the symposium. The award honors the career of Ken Standing, Professor Emeritus at the University of Manitoba, who was a major figure in the development of time-of-flight mass spectrometry for bio-analytical applications. The selection committee will include peer scientists and the ETP Scientific Advisory Committee.

**CNPN Web Site Improvements and Members Section**

We urge members to check out the newly revised website. We have created a Forum and Members area that includes job postings

**2011 Membership now open**

Anyone considering joining CNPN for 2011 can now join. We would encourage all P.I.’s to sign up their labs. Students must be CNPN members to be eligible for travel awards for the Banff symposium.

**CNPN Board of Directors**

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