The International Consortium of the Chromosome-Centric Human Proteome Project

9th C-HPP Workshop in Haeundae Ocean Beach

Busan, Korea

(Final Printed Version: Updated on March 10, 2014)

□Date: Wednesday, March 26, 2014, 08:00-18:00
□Venue: Novotel Ambassador Busan Hotel, Haeundae Ocean Beach, Busan, Korea
□Organized by Young-Ki Paik, Bill Hancock and György Marko-Varga
□Hosted by Young-Ki Paik, Yonsei Proteome Research Center, Yonsei Univ., Seoul, Korea
□Sponsored by AB SCIEX Korea and the Korean Ministry of Health and Welfare
□Theme: Integration of the Proteome Parts List with Transcriptomic Information
□Goals: To set up the goals for completion of missing protein mapping

AGENDA

08:00-09:30 **Session 1: Discussion on the Revised C-HPP Long-term Plans**

Moderated By
Young-Ki Paik, Chair, YPRC, Seoul, Korea
Bill Hancock, Co-chair, Northeastern Univ., Boston, USA (call-in)
György Marko-Varga, Co-chair, Lund Univ. Sweden

Update on the C-HPP Long-term Plans (2012.9-2022.9)

●Highlights of the C-HPP Progress (Sept 10, 2012-March 26, 2014)
●Update on the Goals and Deliverables of the C-HPP (C-HPP 10 Year Plans)

09:30-10:10 **Session 2: Discussion on the MRM Standardization for the C-HPP**

Chair: Mark Baker, HUPO President-elect
Macquarie Univ., Sydney, Australia

Large-scale Inter-lab MRM Initiative for the C-HPP and Plans for the Big paper publication plans
Christoph Borchers (Chr 6 group)
Genome British Columbia Proteomics Centre, University of Victoria, Canada.

●Overview of the standardization kit developments and its application to quantitative plasma proteomic studies
●Strategy and update of the large-scale, inter-lab MRM study toward global standardization.
●Outline of publication plans for the large-scale study and discussion on future standardization initiatives.

10:10-10:50 **Session 3**: **Plenary Lecture 1- MRM & Glycoprotein Analysis**

Chair: Christoph Borchers
Genome British Columbia Proteomics Centre, University of Victoria, Canada.

MRM-based analysis of protein isoforms and automatic analysis of site-specific N-linked glycoproteins
Jong Shin Yoo (Chr 11 group)
Korea Basic Science Institute, Ochang, Korea

10:50-11:10 **Coffee Breaks**

11:10-12:00 **Session 4: Discussion on the C-HPP Milestone Papers**

Presented and Moderated by
Young-Ki Paik and György Marko-Varga

Next Big Paper: Contribution of each chromosome team to the major milestones in discovering missing proteins and parts list per chromosome

●C-HPP Co-chairs will present the overall strategy, timeline and contents for this landmark paper that targets **Sept 9, 2016, end of Phase I (2012.9.10-2016.9.9).**
●Supportive Roles for neXtProt, GPMDB, PeptideAtals and HPA to catalogue the missing proteins in coordination with each chromosome team
●A strategy for the actual cross-links with B/D-HPP teams

12:00-13:30 **Luncheon Seminar: Quantitative Proteomics & Tips on the C-HPP Grant Applications (Grand Ballroom)**

Chairs:
Lydie Lane, SIB, Geneva, Switzerland
Young-Ki Paik, YPRC, Seoul, Korea

New LCMS Data Acquisition and Processing Strategies for Quantitative Proteomics ***(40 min)***
Jason Neo, AB SCIEX

Sharing Tips for the C-HPP Funding Strategy: Chr 1, 8, 9, 11, 13, 16 and 20 ***(30 min)***

-Chinese Grant Awards on Chr 1, 8 and 20: Pengyuan Yang (Fudan Univ.)
-Korean Grant Awards on Chr 9, 11, 13 and HQ: Young-Ki Paik (YPRC)
-Spanish Grant Awards on Chr 16: Juan Pablo Albar (CNB-CSIC)

13:30-14:10 **Session 5**: **Plenary Lecture 2 – Genomics and Transcriptomics**

Chair: Siqi Liu, BGI, Beijing, China

Discovery of Druggable Targets from Liver Cancer Genome*
Hyun Goo Woo
Dept. of Physiology, Ajou University School of Medicine, Suwon, Korea

14:10-14:50 **Session 5**: **Plenary Lecture 3 – Use of ENCODE Data**

Chair: Carol Nilsson, UTMB, TX, USA

Introduction of ENCODE data for potential linkage with Proteomics Research**
Sung-Min Ahn
Department of Oncology, University of Ulsan College of Medicine

● This talk will focus on the use of ENCODE in the proteomics research which fits well to our working scheme. He has been working on both genomics and proteomics and will give us a vision as to how we can merge two disciplines into the C-HPP.

14:50-15:30 **Session 6: Transcriptomics & ENCODE: Invited Short Talks and Discussion**

Chairs:
Tadashi Yamamoto, Chair of HUPO Initiative Comm., Niigata Univ., Niigata, Japan
Gerome Garin, CEA, France

Integrated chromosome 19 transcriptomic and proteomic data sets derived from glioma cancer stem-cell lines. ***(20 min)***
Carol Nilsson (C-HPP EC)
UTMB, Galveston, Texas, USA

Transcriptomic maps for all chromosomes using RNA-Seq data from ENCODE ***(20 min)***
Alberto Pascual-Montano (Chr 16 Group)
Centro Nacional de Biotecnología - CSIC, UAM Campus Cantoblanco, Madrid, Spain

15:30-15:50 **Coffee Breaks with Photo**

15:50-17:30 **Session 7**: **C-HPP Bioinformatics Forum: Invited Short Talks and Discussion**

Chairs
Juan Pablo Albar, CNB-CSIC, Spain
Pengyuan Yang, Fudan Univ., Shanghai, China

Update on the neXtProt ***(15 min)***
Lydie Lane, SIB, Switzerland

Update on the Major Genome-wide ProteomeDBs, Chromosome 1, 8, 20: CAPER 2.0 ***(15 min)***
Ping Xu, BPRC, Beijing, China

Session 8: **Progress Reports from Individual Chromosome Teams/Discussion**

Part A: Chr 8 and 14

Chairs:
Ravi Sirdeshmukh, CSIR, Hyderabad, India
Andrea Urbani, Univ. of Rome, Italy

Chromosome 8: Looking for missing protein further with cell function (12 min)
Pengyuan Yang, Fudan Univ., Shanghai, China

Bioinformatics pipelines and methodology for the discovery of missing proteins (12 min)
Jerome Garin, CEA, France

Part B: **Chromosomes 18 and 20**

Chairs
Visith Thongboonkerd, Mahidol University, Bangkok, Thailand
Jerome Garin, CEA, France

Chromosome 18 TranscriptoProteome: update 2013 (12 min)

Andrey Lisitsa, Russian Academy of Medical Science, Moscow, Russia

Translating evidence and chromosome-centric human proteome investigations (12 min)

Qingyu He, Jinan University, Guangzhou, China

Part C: **Mitochondria and KC-HPP Group Activities (Chr 9, 11, 13)**

Chairs:
Toshihide Nishimura, Tokyo Medical Univ., Tokyo, Japan
Daniel Figeys, Ottawa Univ., Ottawa, Canada

Progress on the Studies of the Subunit 4 of Complex (MT-ND4L) (12 min)

Andrea Urbani, Univ. of Rome, Italy

17:30-17:55 **Session 9**: **Future Plans on the C-HPP Workshops in 2014/2015**

Chairs: Young-Ki Paik and György Marko-Varga

- 10th C-HPP Workshop: Bioinformatics Janboree in Bangkok, Thailand (August 9 after AOHUPO Congress)
  Visith Thongboonkerd, Bangkok, Thailand

- 11th C-HPP Workshop during the Madrid Congress, Spain, Oct 5-8, 2014
  Juan Pablo Alba
  Centro Nacional de Biotecnología - CSIC, UAM Campus Cantoblanco, Madrid, Spain

- 12th C-HPP Workshop during the Milan EXPO in conjunction with the EuPA Congress 2015, June 23-28th 2015, Milan, Italy
  Paola Roncada, Università degli Studi di Milano, Italy

17:55-18:00 **Closing Remarks**
- Summary on the Action Plans

18:30-20:30 **C-HPP Dinner (Sponsored by AB SCIEX Korea)**

----------The end of the C-HPP Workshop----------

Note:

* *References*
1): Kwon SM et al., Woo HG. Genomic copy number alterations with transcriptional deregulation at 6p identify an aggressive HCC phenotype. Carcinogenesis 2013 Jul;34(7):1543-50.
2): Woo HG, et al., Exploring genomic profiles of hepatocellular carcinoma. Mol Carcinog. 2011 Apr;50(4):235-43.
3): Woo HG et al., Association of TP53 mutations with stem cell-like gene expression and survival of patients with hepatocellular carcinoma. Gastroenterology. 2011 Mar;140(3):1063-70.

**References*
1): Ahn SM et al., The first Korean genome sequence and analysis: full genome sequencing for a socio-ethnic group. Genome Res. 2009 Sep;19(9):1622-9.
2): Kim D et al., and Ahn SM. Revising a personal genome by comparing and combining data from two different sequencing platforms. PLoS One. 2013 Apr 8;8(4):e60585.
3): Ahn SM, Simpson R, Lee B. Genomics and proteomics in stem cell research: the road ahead. Anat Cell Biol. 2010 Mar;43(1):1-14.

Acknowledgement

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Appendix 1

Travel Information: How to get Novotel from the Airport

Transportation [Gimhae International Airport -> Novotel Ambassador Busan]

Novotel Ambassador Busan 292, Haeundaehaebyun-ro, Haeundae-gu, Busan, Korea Tel: 82 51 743-1234/Fax:82-51743-1250 https://novotel.ambatelen.com/busan/main.amb

Check-in 14:00, Check-out 12:00

Novotel Ambassador Busan: Novotel Ambassador Busan is a luxurious 4-star hotel conveniently located near the centre of Haeundae. Local tourist attractions such as Gwangan Grand Bridge, Haeundae Beach and Gwangalli Beach are not far from the hotel. Also easily within reach are Busan Aquarium, City Centre Haeundae and City Centre Busan. The preferred airport for Novotel Ambassador Busan is Busan (PUS-Gimhae) - 19.4 km / 12.1 mi. In Busan Haeundae). **Hotel facilities**: Room service (24 hours) - Dry cleaning/laundry service - Secure parking - Restaurant - ***Free*** guest parking during stay - Health club - ***Free*** parking - Breakfast available (surcharge) - Safe-deposit box at front desk - Swimming pool - indoor - Bar/lounge - Airport transportation - 24-hour business center - 24-hour front desk - Medical assistance available - Luggage storage - Air-conditioned public areas - Babysitting or childcare - Sauna - Express check-in

From Gimhae International Airport
- Airport Limousine Bus: 80 minute,
- Cost: Adult-KRW 7000, Kid-KRW 4500
- Operation Hours :
  To Hotel 6:50~22:00, To airport 05:10~20:00 / every 25~30 minute

Category	Bus Name	BusStop
Limousine	Haeundae line no.1	Airport(International Terminal) - Domestic Terminal - Namcheondong - Crossing the Gwang-an bridge - Centum hotel - Bexco - Olympic yacht stadium - Park Hyatt Busan - Hanwha resort – Hyundai Hyperion - The Westin Chonsun Hotel – **Novotel Ambassador Hotel** – Paradise Hotel - Seacloud hotel – Grand Hotel - Hyundai Hyperion - Hanwha resort - Park Hyatt Busan – Gyeongnam Marina apt – Centurm Homeplus –Centurm Hotel - Crossing the Gwang-an bridge - Namcheondong - Airport(International Terminal, Departure) - Domestic Terminal, Arrival

-Taxi : 1 hour, Fee : About KRW 30000

From Busan Train Station
Subway : Get off at 'Haeundae Station' line 2 and use exit 3
Taxi : 45 minutes, Fee : About KRW 17000
Exchange rate: 1 USD=KRW1080 (variable every day)

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Appendix 2 Abstracts and additional information

PL1:

MRM-based analysis of protein isoforms and automatic analysis of site-specific N-linked glycoproteins

Jong Shin Yoo

Korea Basic Science Institute, Ochang, Korea

MRM approach is a targeted MS technique in which the researcher optimizes the assay for the confirmation and quantification of specific peptides that are representative of the unique proteins in C-HPP. MRM-based analysis of protein isoforms will be suggested as an alternative to antibody-based verification due to its high throughput, selectivity, and sensitivity. Next, glycoproteins have enormously complex heterogeneities in glycan structures at different aminoacid sites but few studies characterize their site-specific glycoforms in major biological processes. High-throughput analysis of site-specific glycoforms of N-glycoproteins in human plasma, rather than a single glycoprotein purified in advance, is challenging because of extremely high sample complexity, wide dynamic ranges in abundance of analytes. The automatic mapping of N-glycoproteins in human plasma by high resolution mass spectrometry with Glycoprotein Analysis (GPA) algorithm will be presented

PL2:

Discovery of druggable targets from liver cancer genome

Hyun Goo Woo

Ajou University School of Medicine

During the last decade, mounting evidences have shown the heterogeneity of cancer genome at genomic and epigenomic levels. Recently, unbiased and genome-wide analyses of multiple genomic profile data could unveil the underlying mechanisms of the tumor heterogeneity and complexity. Functional processes including cell fate, survival, and differential signaling pathways play critical roles in the heterogeneous progression of cancers. Thus, the tumor heterogeneity is thought as one of primary huddles in the discovery of druggable cancer targets. Here, by performing multi-layered integration of liver cancer genome data with clinicopathological features, we could obtain a precise map of the tumor heterogeneity. In addition, our approach could reveal new candidate targets which are specific to a certain tumor type. Undoubtedly, our approach will accelerate the opening of the new era of personalized medicine.

PL3:

Introduction of ENCODE data for potential linkage with Proteomics Research

Sung-Min Ahn

Department of Oncology
Department of Biomedical Informatics
Asan Medical Center, Seoul, Korea

The Encyclopedia of DNA Elements (ENCODE) project has generated extensive datasets designed to annotate functional elements in the genome, which encode defined products or display reproducible biochemical signatures. The Chromosome-Centric Human Proteome Project (C-HPP) aims to define the full set of proteins encoded in each chromosome. One of the key challenges of C-HPP will be to establish intellectual infrastructure by which C-HPP can generate and position vast amount of proteomics data in the right context of pre-existing, complementary datasets such as ENCODE. The aim of this workshop is to provide potential solutions for bridging ENCODE and C-HPP which will be a continuous challenge to C-HPP group till the end of its journey. In this workshop, ENCODE datasets and proteomic viewpoints on them will be introduced.

Invited short talk 1

Integrated chromosome 19 transcriptomic and proteomic data sets derived from glioma cancer stem-cell lines.

Carol Nilsson

Department of Pharmacology and Toxicology, UTMB Cancer Center, University of Texas Medical Branch, Galveston, Texas 77555, United States

One subproject within the global Chromosome 19 Consortium is to define chromosome 19 gene and protein expression in glioma-derived cancer stem cells (GSCs). Chromosome 19 is notoriously linked to glioma by 1p/19q codeletions, and clinical tests are established to detect that specific aberration. GSCs are tumor-initiating cells and are hypothesized to provide a repository of cells in tumors that can self-replicate and be refractory to radiation and chemotherapeutic agents developed for the treatment of tumors. In this pilot study, we performed RNA-Seq, label-free quantitative protein measurements in six GSC lines, and targeted transcriptomic analysis using a chromosome 19-specific microarray in an additional six GSC lines. The data have been deposited to the ProteomeXchange with identifier PXD000563. Here we present insights into differences in GSC gene and protein expression, including the identification of proteins listed as having no or low evidence at the protein level in the Human Protein Atlas, as correlated to chromosome 19 and GSC subtype. Furthermore, the upregulation of proteins downstream of adenovirus-associated viral integration site 1 (AAVS1) in GSC11 in response to oncolytic adenovirus treatment was demonstrated. Taken together, our results may indicate new roles for chromosome 19, beyond the 1p/19q codeletion, in the future of personalized medicine for glioma patients.

Invited short talk 2

Transcriptomic maps for all chromosomes using RNA-Seq data from ENCODE

Alberto Pascual-Montano
Spanish Consortium (Chr-16) Centro Nacional de Biotecnología - CSIC, UAM Campus Cantoblanco,
Madrid, Spain Spain

The Encyclopedia of DNA Elements (ENCODE) provides a vast amount of data on experiments of different human cell lines, including RNA-Seq assays. A first logic approximation to integrate data from ENCODE in the Human Proteome Project (C-HPP) is the identification of those cell lines with a high level of expression values for protein coding genes, especially those classified as “missing” where no strong proteomic expression evidences are available. Even if there is a high degree of overlapping, there are some unique expressed genes that encode missing proteins differentially among the cell lines. This transcriptomic map allows, among other things, the selection of the best cell lines to conduct proteomic studies. This is the first initial step to have a transcriptomics dashboard where each cell line and tissues can be explored for expression evidences and supplement it with protein expression data produced in the C-HPP project.

Progress Reports: Session 7 & 8

Translating evidence and chromosome-centric human proteome investigations

Tong Wang, Gong Zhang and Qing-Yu He*

Key Laboratory of Functional Protein Research of Guangdong Higher Education Institutes, Institute of Life and Health Engineering, College of Life Science and Technology, Jinan University, Guangzhou 510632, China.

C-HPP raised an importantly scientific question to resolve human proteome in a chromosome-by-chromosome manner, both qualitatively and quantitatively. As co-investigators of this community, we are also facing the known challenges to address C-HPP goals, including unidentifiable proteins by mass spectrometry (MS), the data integration across different laboratories as well as the identification and quantification of single-nucleotide variations (SNVs) and alternative splicing transcripts (ASTs). To meet these demands, we have proposed to introduce the next generation sequencing on translating mRNA to serve as the fourth pillar of C-HPP, in addition to SRM/MRM MS and antibody-based verifications as well as bioinformatics. As it is known that about 5% of total transcripts cannot be translated, translating mRNA sequencing provides accurate translating evidence for most protein products, with high sequence coverage. This is useful information for directing subsequent verifications of “missing proteins” as well as new proteins that could have wrong annotations based on our current knowledge of human genome. In addition, translating mRNA sequencing can provide a comprehensive list of SNVs in translating mRNA, which potentially alter the protein sequence. We have also found that translating mRNA can serve as a standard reference for proteomic data integration and predicting protein abundances. This can be applied to characterize the differentially expressed genes and proteins in various tissues and cell types. In the next phase of CHPP, we will try to find translating and protein evidence in the resources of ribosome-bound “non-coding” mRNA and epigentically modified cell lines.

Appendix 3

List of Participants

Total ~60 (C-HPP PIs and their co-workers/guests)

The following is the current list of participants to this workshop. We would like to encourage you to make update on the list of each chromosome team ASAP by contacting at cprc@proteomix.org

Chr 01: Ping Xu (for Fuchu He); (1)
Chr 02: Lydie Lane (SIB) (1)
Chr 03: Toshihide Nishimura (Tokyo Medical University, Japan) (1)
Chr 06: Christoph Borchers (for Paul Kweon, University of Victoria-Genome British Columbia) (1)
Chr 07: Mark Baker (Macquarie Univ., Australia)(1)
Chr 08: Pengyuan Yang (Fudan Univ., China), Fan Zhong (Fudan Univ., China) (2)
Chr 09: Je Yoel Cho (Seoul National Univ, Korea), Soo-Youn Lee (Samsung Hospital Seoul, Korea) Jeong-Mo Ahn (Seoul National Univ., Korea) and a few post-doc fellows (6)
Chr 10: Jin Park (for Joshua LaBaer, Arizona State Univ., USA) (1)
Chr 11: Jong Shin Yoo (KBSI, Korea), Kyung-Hoon Kwon (KBSI, Korea), Jin-Young Kim, Young-Hye Kim et al. (8)
Chr 12: Visith Thongboonkerd (Mahidol University, Thailand); Ravi Serdeshmukh (2)
Chr 13: Young-Ki Paik (YPRC, Korea), Seul-Ki Jeong (YPRC), Jin Han (Inje Univ., Korea), Heui-Soo Kim (Pusan National Univ.), Keun Na, Ju-Wan Kim, Jin-Young Cho, Han-Ho Lee, Jong-Sun Lim (YPRC)(9)
Chr 14: Jerome Garin (CEA, France), Yves Vandenbrouck (CEA, France) (2)
Chr 16: Juan Pablo Alba (CNB-CSIC, Spain, C-HPP EC Member); Alberto Pascual-Montano (2)
Chr 17: Bill Hancock (Northeastern Univ., USA, Co-Chair) (call in), Gil Omenn (HPP Chair)(call in)
Chr 18: Andrey Lisitsa (RAMS), Victor Zgoda RAMS) (2)
Chr 19: Gyorgy Marko-Varga (Lund Univ, Co-Chair), Carol Nilsson (Univ. Texas Medical Branch, USA, C-HPP EC Member) (2)
Chr 20: Seqi Liu (BGI, China), Liang Lin (BGI, China), Quanhui Wang (BGI); Qing Yu He, Jinan University, Tong Wang, Jinan University, Gong Zhang, Jinan University (7)
Chr 21: Daniel Figeys (Ottawa Univ., Canada) (1)
Chr 22: Jun Zhong (for Akhilesh Pandey; Johns Hopkins Univ., USA) (1)
Chr X: Tadashi Yamamoto (Niigata Univ., Japan) (1)
Mito: Andrea Urbani (University of Rome, Italy); Paola Roncada (2)

Invited speakers (2) and KHUPO leadership (Bonghee Lee, KHUPO President, Gachon Univ.)(1)

Contacts

●Administrative Assistance for the C-HPP Workshop: Ms. Sun Hee Choi cprc@proteomix.org

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●Administrative Assistance for the KHUPO Meeting: Ms. Hee Ja Lee admin@khupo.org