

APPENDIX H.5

2010 Report from the

Human Kidney and Urine Proteome Project (HKUPP) Initiative

to the HUPO Initiatives Committee (submitted by Tadashi Yamamoto, 10 August 2010)

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Vision

The vision of the Human Kidney and Urine Proteome Project (HKUPP) is to disclose all proteins in the human kidney and urine and to elucidate functional interaction of the proteins for understanding the kidney function and pathology, and to contribute to develop new therapeutics for prevention or complete cure of human kidney diseases.

Missions

- 1) To facilitate kidney and urine proteome analysis and to disclose all proteins present in the kidney and urine,
- 2) To understand kidney functions and molecular interactions in kidney diseases,
- 3) To construct databases of the human kidney and urine proteomes in normal and diseased states,
- 4) To identify novel biomarkers and new drug targets for kidney diseases, the data and information obtained by the project are planned to be opened for the public access through the HKUPP website (<http://www.hkupp.org>) to encourage the spread of

proteomic technologies applied to the nephrology field and to disseminate knowledge pertaining to the human kidney and urine proteomes.

Major activities:

1. The 4th Human Kidney and Urine Proteome Project (HKUPP) Workshop “

Proteomics for Discovery of Urine Biomarkers during the HUPO2009 Annual Congress in Toronto on September 26, 2009.

- 1) Visith Thongboonkerd (Mahidol University, Bangkok, Thailand) overview:
"Current status of renal and urinary proteomics"
- 2) Barbara Seliger (Martin-Luther-University, Halle, Germany):
" Identification of novel biomarkers in renal cell carcinoma lesions"
- 3) Bruno Domon (Institute of Molecular Systems Biology, Zurich, Switzerland):
“Targeted mass spectrometry analysis of urine proteome using selected reaction monitoring”
- 4) Christophe Messelson (Laboratoire d'Etude de la Dynamique des Proteomes, INSERM, Grenoble, France):"AMT tag strategy for bladder cancer biomarker candidate discovery in urine"
- 5) Satish P RamachandraRao (University of California San Diego, USA):
"Proteomics to interactomics: a streamlined approach to identify high-yield hits”,
- 6) Yutaka Yoshida (Niigata University, Japan):
"Final standard protocol for non-proteinuric urine proteomics"

The proposed protocol was shown in Table.

		Practical Recommendation
1	Timing	Collect mid-stream of random-catch urine or the 2nd morning urine
2	Addition of Preservatives	Not necessary when frozen within 4 hrs (<2 or <4 hrs to be distinct) or add 10mM NaN2 (or 0.2M Boric acid) if frozen more than 4 hrs after keeping at room temperature
3	Addition of Protease inhibitor	Not necessary for non-proteinuric urine (Further evaluations may need for proteinuric urine)
4	Pretreatment & Storage	Centrifuge at 1000g for 10 min to remove cells and debris and store aliquots of 10 ml (or 50 or 1.5 ml) at -20 or -80C (to be distinct)
5	Freezing & thawing	Avoid as possible and thaw at 37C water bath (if necessary, adjust pH to 8.0 by 1M Tris buffer)

2. Human kidney glomerulus proteome database obtained by a nanoLC-MS/MS after 2D separation (solution IEF and SDS-PAGE) has been up-dated at the **HKUPP web**

site (<http://www.hkupp.org/>) by adding immunohistochemistry images provided from the Human Protein Atlas in collaboration with the Human Antibody Initiative.

3. European Kidney and Urine Proteomics (EuroKUP, European HKUPP members), a COST Action (European Cooperation in the field of Scientific and Technical Research), focusing on facilitating translational proteomic research in kidney diseases by bringing together and promoting interactions between basic scientists and clinicians working in the broader areas of kidney and urine proteomics. EuroKUP currently fosters a multi-disciplinary network of more than 120 members from 26 countries.
4. Collaborations with other HUPO initiatives: HKUPP started to analyze origins of urine proteins in collaboration with HUPO Human Plasma Project Initiative.

Plans for 2010:

1. Standard protocols and Guidelines for proteomic analysis of proteinuric urine.
2. Updating of Human Urine Proteome at the HKUPP website and proposing a prototype of inter-initiative database
3. Collection of Human Kidney and Urine Proteome Data from members

Publications in 2009

1. 2nd Combined Working Group and Management Committee Meeting of Urine and Kidney Proteomics COST Action
Vlahou A, Allmaier G, Attwood T, Bongcam-Rudloff E, Charonis A, Frokiaer J, Mischak H, Schanstra J, Spasovski G on behalf of EuroKUP
Proteomics Clin. Appl. 2009;3:1017-1022.
2. Report on the first combined working group and management committee meeting of EuroKUP (Urine and Kidney Proteomics cost action).
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3. Identification and characterization of major proteins carrying ABO blood group antigens in the human kidney.
Tasaki M, Yoshida Y, Miyamoto M, Nameta M, Cuellar LM, Xu B, Zhang Y, Yaoita E, Nakagawa Y, Saito K, Yamamoto T, Takahashi K.
Transplantation. 2009;87(8):1125-33.
4. Characterizations of urinary sediments precipitated after freezing and their effects on urinary protein and chemical analyses.
Saetun P, Semangoen T, Thongboonkerd V.
Am J Physiol Renal Physiol. 2009;296(6):F1346-54.
5. Specific adsorption of some complement activation proteins to polysulfone dialysis membranes during hemodialysis.
Mares J, Thongboonkerd V, Tuma Z, Moravec J, Matejovic M.
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6. Are protease inhibitors required for gel-based proteomics of kidney and urine?
Havanapan PO, Thongboonkerd V.
J Proteome Res. 2009;8(6):3109-17.
7. Should urine pH be adjusted prior to gel-based proteome analysis?
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8. Prediction of muscle-invasive bladder cancer using urinary proteomics.
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10. Adapting mass spectrometry-based platforms for clinical proteomics applications: The capillary electrophoresis coupled mass spectrometry paradigm.
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Diabetes Technol Ther. 2009;11(1):1-9.
12. Capillary electrophoresis-mass spectrometry as a powerful tool in biomarker discovery and clinical diagnosis: an update of recent developments.
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Mass Spectrom Rev. 2009;28(5):703-24.
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Clin Cancer Res. 2009;15(15):4935-43.
14. Brukin2D': a 2D visualization and comparison tool for LC-MS data.
Tsagkrasoulis D, Zerefos P, Loudos G, Vlahou A, Baumann M, Kossida S.
BMC Bioinformatics. 2009;10 Suppl 6:S12
15. Chromosomal and proteome analysis of a new T24-based cell line model for aggressive bladder cancer.
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17. Combined analysis of transcriptome and proteome data as a tool for the identification of candidate biomarkers in renal cell carcinoma.
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19. Systematic comparative protein expression profiling of clear cell renal cell carcinoma: a pilot study based on the separation of tissue specimens by two-dimensional gel electrophoresis.
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Mol Cell Proteomics. 2009;8(12):2827-42.
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Kiessling A, Hogrefe C, Erb S, Bobach C, Fuessel S, Wessjohann L, Seliger B.
Oncogene. 2009;28(28):2606-20.
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