

# CNHUPO

PIONEER AND VIGOROUS ROLES FOR PROTEOMICS INVESTIGATION IN CHINA

Fuchu He<sup>‡</sup> and Siqi Liu<sup>§</sup>

Proteomics investigation in China has been almost paced with international movement of proteomics. The kickoff of China Human Proteome Organization (CNHUPO)<sup>1</sup> could be backdated to October 2002. CNHUPO was formally established in 2003. Dr. Fuchu He from Beijing Proteome Research Center and Beijing Institute of Radiation Medicine was elected as its inaugural president.

CNHUPO is a unique academic organization of proteomics in China, and it has effectively united with most scientists working in this area. Since participating in Human Proteome Organization (HUPO) and Human Proteome Initiatives (HPIs), CNHUPO has made great contributions for launching and developing several initiative projects, especially Human Liver Proteome Project (HLPP). On behalf of the embryonic CNHUPO, Dr. He proposed the HLPP blueprint in Second Workshop of HUPO in Washington (April, 2002) and First World Congress of HUPO in Versailles (November, 2002) (1). The HLPP strategies and goals were widely accepted and supported by the international colleagues of HUPO. Since then, China has become one of the leading countries in the studies of human liver proteome. The CNHUPO members are also playing active roles in many committees of HUPO. Most importantly, CNHUPO successfully hosted the HUPO 3<sup>rd</sup> World Congress in Beijing (October, 2004) and the HUPO 2<sup>nd</sup> Initiatives Roundtable (October, 2005). Except for international meetings, CNHUPO has annually organized national conferences since 2003 and regularly held different kinds of training courses of proteomics. For a better education in this field, CNHUPO has contributed much to advocating sponsored many young talents to attend international and domestic proteomics conferences. Furthermore, CNHUPO has implemented several program project grants related to proteomics in China during the last six years and advocated to establish the Chinese National Medium- and Long-term

Program for Scientific and Technological Development on Protein Science Investigation (2006–2020). Due to a full collaboration of CNHUPO and the journal editors, the research achievements of Chinese proteomics were published in the special issue of “Proteomics in China” (2). With the efforts of CNHUPO, in recent years, several research centers focusing on proteomics sciences have been successively founded throughout major academic institutions and universities in China, including Beijing, Shanghai, Changsha, Guangzhou, Xian, Tianjin, Xiamen, and HongKong (Fig. 1). These centers have steadily become the core facilities of proteomics nationwide and firm stood the frontier of proteomic research worldwide. In last three years, the scientists from CNHUPO have made great contributions to the published papers in the peer journals of proteomics.

There have been three major proteomics projects carried out by CNHUPO in the last five years, Chinese Human Liver Proteome Project (CNHLPP), Human Disease Proteomics (HDP), and Development of Proteomic Technology (DPT). With the efforts of more than 80 laboratories in China, the pilot phase of CNHLPP was accomplished in 2005, resulting in the first protein profiling of Chinese normal human liver with 6788 unique proteins, which is the largest proteomic database of human liver so far. HDP, aiming at the proteomic characterizations in cancer and other life-threatening diseases, was first funded by the National Basic Research Program from big proteome project of Chinese Ministry of Science & Technology (MOST) at the beginning of this century. During the period of HDP implementation, the outbreak of severe acute respiratory syndrome (SARS) appeared in China in spring, 2003. Chinese proteomic scientists have made important contributions to control the infectious disease, including the first SARS-CoV proteome that was identified using two-dimensional LC-MS/MS; the differential proteomes of Vero E6 cells with/without infection of SARS-CoV were quantitatively resolved, and the immune assay for SARS diagnosis was developed within a short period based upon the proteomic database (3). Seeking cancer biomarkers is an important frontier of HDP. A group of Chinese scientists invented a new approach to screen the lung cancer biomarkers from the conditioned medium for culturing the primary cell or tissues of lung cancer through proteins resolved by SDS-PAGE and identified by nano-ESI-MS/MS (4). A combination of CD98, fascin, polymeric immunoglobulin receptor/secretory component and 14–3–3  $\eta$  was first proposed for evaluation of the risk of lung cancer development. Additionally, during screening

From the <sup>‡</sup>State Key Laboratory of Proteomics, Beijing Proteome Research Center, Beijing Institute of Radiation Medicine, Beijing 102206 and <sup>§</sup>Beijing Genomics Institute, Chinese Academy of Sciences, Beijing 100318, China

<sup>‡</sup> To whom correspondence may be addressed. E-mail: hefc@nic.bmi.ac.cn.

<sup>§</sup> To whom correspondence may be addressed. E-mail: siqiliu@genomics.org.cn.

<sup>1</sup> The abbreviations used are: CNHUPO, China Human Proteome Organization; HLPP, Human Liver Proteome Project; SARS, severe acute respiratory syndrome; HDP, human disease proteomics; DPT, development of proteomic technology.



FIG. 1. A glance at outdoor and indoor view of Beijing Proteome Research Center (BPRC)

and validation of disease biomarkers, the proteomic techniques have emerged in their importance. Chinese scientists have strategically acknowledged the fact and initiated the technology development projects at the early stage of proteomics movement. With the DPT support, many new proteomic techniques, especially in global quantitation, affinity chromatography, auto-analysis and nano-techniques, have been developed, optimized and widely applied in the related fields in China (5).

In the next phase of proteomics movement, the focus of CNHUPO on proteomic projects is being gradually transferred from establishment of proteomic technique platforms for profiling protein expression to settlement of applicatory strategy of proteomics for addressing the critical physiological and pathophysiological issues of Chinese population. CNHUPO will tirelessly strengthen the international collaborations in proteomics and revolutionarily explore proteomic theory and technology. Being beyond question, CNHUPO is always a

vigorous and constructive member of proteomics society in this globe.

REFERENCES

1. He, F. (2005) Human liver proteome project: Plan, progress, and perspectives. *Mol. Cell. Proteomics* **4**, 1841–1848
2. He, F. (2006) Proteomics in China. *Proteomics* **6**, 397–403
3. Wang, J., Wen, J., Li, J., Yin, J., Zhu, Q., Wang, H., Yang, Y., Qin, E., You, B., Li, W., Li, X., Huang, S., Yang, R., Zhang, X., Yang, L., Zhang, T., Yin, Y., Cui, X., Tang, X., Wang, L., He, B., Ma, L., Lei, T., Zeng, C., Fang, J., Yu, J., Wang, J., Yang, H., West, M. B., Bhatnagar, A., Lu, Y., Xu, N., and Liu, S. (2003) Assessment of immunoreactive synthetic peptides from the structural proteins of severe acute respiratory syndrome coronavirus. *Clin. Chem.* **49**, 1989–1996
4. Xiao, T., Ying, W., Li, L., Hu, Z., Ma, Y., Jiao, L., Ma, J., Cai, Y., Lin, D., Guo, S., Han, N., Di, X., Li, M., Zhang, D., Su, K., Yuan, J., Zheng, H., Gao, M., He, J., Shi, S., Li, W., Xu, N., Zhang, H., Liu, Y., Zhang, K., Gao, Y., Qian, X., and Cheng, S. (2005) An approach to studying lung cancer-related proteins in human blood. *Mol. Cell. Proteomics* **4**, 1480–1486
5. Jia, W., Chen, X., Lu, H., and Yang, P. (2006) CaCO<sub>3</sub>-poly(methyl methacrylate) nanoparticles for fast enrichment of low-abundance peptides followed by CaCO<sub>3</sub>-core removal for MALDI-TOF MS analysis. *Angew Chem. Int. Ed. Engl.* **45**, 3345–3349