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Proteome Society Meeting

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The October Meeting of the Proteome Society was the last of a series of five meetings held by the Society in the United States and Canada in 2005. The Society currently has nearly 2000 members from 37 countries. The meeting was attended by 64 delegates, many of whom are based in the Massachusetts biotechnology corridor, but the meeting also attracted participants from Hong Kong and Australia. Corporate Sponsors for the meeting were GE Healthcare, Bio-Rad, Beckman Coulter and Waters Corp. Event day sponsors were Pressure Biosciences, Pall Life Sciences, Eksigent, Anatek and GenoLogics.

Much of the meeting focused on biomarker identification and clinical applications of proteomics. The day's agenda consisted of nine oral presentations with interim session of seven poster presentations. Joshua LaBauer (Harvard Medical School) began the morning session with a talk on *Functional proteomics for biomarker and target discovery*. Genetic screens using FLEXGene technology, establishment of candidate biomarkers for cancer diagnosis and antigen libraries, protein microarrays and ideas on membrane protein arrays and interactome discovery were discussed in this presentation. Michael Lyristis of Fluorotechnics, an Australian company that developed the fluorescent Deep Purple protein stain for GE Healthcare, presented data on the pH-dependent, reversible binding of fluorescent epicocconone and its use for protein detection and quantitation. The FLUORO Profile Protein Assay was demonstrated to have sensitivity comparable to the Lowry assay and was able to tolerate high levels of detergents and reducing agents.

John M Luk (University of Hong Kong) discussed combination use of genomic and proteomic tools, such as DNA microarray technology, 2D gel electrophoresis, matrix-assisted laser desorption/ionization- and surface-enhanced laser desorption/ionization time-of-flight mass spectrometry (MS) profilings of biomarkers, such as the human α-fetoprotein for the early detection and diagnosis of hepatocellular carcinoma, the second leading cause of cancer death in Asia. Another contributor from the University of Hong Kong, Nikki PY Lee, described 2D electrophoresis and tandem MS profiling of protein expression in mouse liver development from embryo to adult. In another poster, Rosa Jimenez (Brown University, RI, USA) provided insights into carcinogenesis in liver by assessing the effects of rapamycin in rat liver cell lines. Towia Libermann (Beth Israel Deaconess Medical Center) discussed biomarkers for clinical significant diseases, such as hepatocellular carcinoma, and the challenges of profiling body fluids due to the extensive dynamic range of protein concentrations, which complicates the analysis of low-abundance proteins of clinical significance.

Billy Wu (Northeastern University, MA, USA) discussed extended range proteomic analysis and its application to the kinetics phosphorylation of epidermal growth factor receptor upon simulation. Reuben Gobezie (Harvard Medical School) and Jaelong Park (Harvard Medical School) presented talks on biomarker profiles in osteoarthritis and on antihormone-resistant breast cancer growth, respectively.

Sau-Mei Leung (GenoLogics) presented an application-driven laboratory information management system for clinical proteomics. Ellis Gitlin (GE Healthcare) presented a poster on software for automated differential expression analysis using 2D and 3D representations of liquid chromatography MS data for interactive confirmation of results.

In the poster session, Douglas Hinerfeld and Sunny Tam (University of Massachusetts Proteomics Consortium Protein Fractionation Group) presented data on the application of Pressure BioSciences' Pressure Cycling Technology for extraction of total protein from rat liver. This emerging new technology, which uses alternating cycles of high and low pressure to release proteins, nucleic acids and small molecules from cells and tissues, revealed several proteins in 2D gels that were not exhibited by conventional tissue-homogenization methods.

Gordon Murphy (Phillips Academy and Children's Hospital Oakland Research Institute) presented a poster on the clinical proteomics analysis of plasma from the REACH project, which focused on the molecular species associated with vitamin D deficiency. Michael Simonian (Beckman Coulter) described human plasma proteome fractionation using immunoglobulin Y antibodies to abundant proteins, coupled with multidimensional chromatography.

In other posters, TVS Murthy (Harvard Institute of Proteomics) described an automated high-throughput protein production pipeline for proteomic protein assays. Ericka Lawson (Brown University and Rhode Island Hospital) introduced a novel system for analyzing signaling pathways.

The Proteome Society has planned four US meetings for 2006, with venues to be announced.

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