Dan L Crimmins, J Proteomics Bioinform 2014, 7:8
http://dx.doi.org/10.4172/0974-276X.S1.074

OMICS Group Conferences
Accelerating Scientific Discovery

4th International Conference on
Proteomics & Bioinformatics
August 04-06, 2014 Hilton-Chicago/Northbrook, Chicago, USA

Mining mouse ASS genes-successes to date

Dan L Crimmins
Washington University School of Medicine, USA

We used an Abundance and Specificity Strategy in 2006 to identify mouse genes via gene array analysis with the ultimate goal of identifying human homologues. The criteria for inclusion was that tissue array data had an absolute value of at least 10,000 array units (Abundance) and the candidate gene was present in the target tissue by at least 10-fold over the other tissues (Specificity). Eight tissues from three normal mice, 2 male and 1 female C57BL/6 4-6 week old, were carefully dissected to provide: Brain, Liver, Spleen, Kidney, Skeletal Muscle, Lung, Pancreas, Heart, and Small Intestine. Note that our experimental mining approach is unlike other typically used methodologies where analysis rests on a differential (increase/decrease) of a specific biomarker from a normal vs. a diseased state analyzed by gene array, 2D electrophoresis, or mass spectrometry. Over 200 mouse genes were ASS positive. Interestingly, the seven genes identified in cardiac tissue are either in use or proposed as respective cardiac injury biomarkers, thus providing confidence in our mining process. Brain VILIP-1, calcium-myristoyl switch protein, has shown potential utility in stroke and in a cohort of cognitively normal individuals who may develop AD in the future. Kidney FXYD2, a type III membrane protein of the trimeric Na+,K+-ATPase complex, has shown excellent sensitivity and specificity for chromophobe renal cell carcinoma. Recently we identified renal MIOX as a promising biomarker for AKI. Thus, our ASS mining can provide clinically relevant biomarkers.

Biography

Dan L Crimmins received his PhD at Washington University (WU) in Saint Louis in 1980. He trained in physical chemistry. Post-doctoral work (WU School of Medicine) investigated viral membrane glycoprotein structure and endocytosis via clatherin-coated pits. Crimmins then worked at Mallinckrodt developing radio-labeled antibodies. Next he directed the HHMI Core Protein/Peptide Facility at WU for 10 years; later joining the Department of Pathology & Immunology in the Division of Laboratory & Genomic Medicine at WUSM. His expertise and research interests are: Bioanalytical protein/peptide characterization, immunogen design/antibody selection, biomarker discovery/evaluation, clinical/biological implications of post-translationally modified pro forms of diagnostic protein analytes.

crimmins@pathology.wustl.edu