Sanjeeva Srivastava et al., J Chromatogr Sep Tech 2017, 8:3(Suppl)
DOI: 10.4172/2157-7064-C1-025

Discovery and validation of biomarkers for gliomas using mass spectrometry based quantitative and targeted proteomics

Sanjeeva Srivastava[1], **Kishore Gollapalli**[1], **Nikita Gahoi**[1], **Saicharan Ghantasala**[1], **Aliasgar Moiyadi**[2] and **Sridhar Epari**[2]
[1]Indian Institute of Technology Bombay, India
[2]Tata Memorial Centre-Advanced Centre for Treatment, India

Glioma brain tumors arise from glial cells. Glioblastoma multiforme (GBM) is the most common and most malignant of the glial tumors. We have performed a comprehensive iTRAQ-based quantitative tissue proteomic analysis of gliomas and compared it with different controls, including other cancer samples as disease control to identify differentially expressed proteins in different groups of brain tumors. The iTRAQ-labeled peptides were fractionated using off-gel fractionation followed by LC-MS/MS analysis. Various metabolic pathways including fructose & mannose metabolism, spliceosome and amino acid metabolism were found to be altered in GBM, medulloblastoma and meningiomas respectively. Proteins like CRYAB, GFAP, BASP1 and SNCA were found to be significantly altered in gliomas, whereas VIM, RABP1, ANXA2 and SBP1 showed differential expression in meningiomas. Protein biomarkers identified from discovery-phase were further validated using MRM-based quantitative approach. Targeted proteomics data was analyzed using Skyline and for each protein a minimum of three peptides with at least three corresponding transitions were used for quantification. The in-solution digested peptides from the tissue lysates were run on triple quadrupole mass spectrometry. This comprehensive mass spectrometry based quantitative and targeted proteomic profiling of brain tumors identified few potential markers and provided insights into tumor pathophysiology.

Biography

Sanjeeva Srivastava is an Associate Professor and group leader of proteomics laboratory at Indian Institute of Technology, Bombay. He completed his PhD at University of Alberta and Post-doc at Harvard Medical School in the area of Proteomics, Stress Physiology and has expertise in “Applications of data enabled sciences in global health, developing country and resource limited settings”. He is an active contributor to global proteomics science and innovation. He serves on the Council of Human Proteome Organization (HUPO) and Executive Committee of Proteomics Society, India (PSI). He has organized two successful conferences – PSI-2014 and Targeted Proteomics International Symposium in 2015. He has extensive teaching experience at IIT-Bombay and experience of conducting proteomics courses at Cold Spring Harbor Laboratory (CSHL). He continues to develop proteomics & omics science and innovation together with and for the next generation of keen students, researchers and the research and education commons in Asia and global OMICS community.

sanjeeva@iitb.ac.in

Notes: