OMICS Group Conferences
Accelerating Scientific Discovery

2nd International Conference and Exhibition on
Metabolomics & Systems Biology
April 08-10, 2013 Hilton Chicago/Northbrook, USA

Meta-analysis of metastatic cancer transcriptomes: A new approach to uncover molecular pathological events in different cancer tissues

Aisha Naeem, Sundus Iqbal, Hira Ejaz and Muhammad Sulaman Nawaz
COMSATS Institute of Information Technology, Pakistan

To spill secrets of metastatic cancers, individual expression of true sets of respective genes must spread across the tissue. During this study, meta-analysis for transcriptional profiles of metastatic cancers was performed to explore the genes or gene regulatory elements that can possibly serve as signature elements for the initiation and progression of metastatic cancers. In the analysis, transcriptional profiles of lung, liver, spleen, colorectal, colon, breast, bladder, blood, and kidney cancerous and normal tissue were extracted from Gene Expression Omnibus (GEO; an online source). A newly developed bioinformatics approach, Dynamic Impact Analysis (DIA) was applied for enrichment analysis of transcriptional profiles using freely available online resource Database for Annotation Visualization and Integrated Discovery (DAVID). For an in-depth analysis of differentially expressed transcription factors (TFs) and regulatory gene networks, oPOSSUM and Cytoscape (v. 2.8.2) were used. An ANOVA using a MIXED model in SAS was conducted on all microarray data with a multiple comparison correction and false discovery rate (FDR) to extract lists of differentially expressed genes (DEGs P value < 0.01) in all of the samples. The DAVID analysis uncovered the most significantly enriched pathways in molecular functions. The molecular functions "Ubiquitin thiol esterase activity" and "Structural constituent of ribosome" were up regulated in bladder, colorectal, lung, spleen, and prostate cancer. "Transforming growth factor beta receptor activity" was inhibited in all cancers except colon, blood, and liver. oPOSSUM further revealed highly over-represented TFs comprising Broad-complex_3, Broad-complex_4, and Foxd3 except for blood and bladder cancer. These findings can help to identify those genes or networks that play a crucial role in the progression of cancer. Therefore, these transcription factors can be the potential candidates for the therapeutic drug targets that can hinder the deadly spread.

Biography

Aisha Naeem has completed her Ph.D. from University of Illinois at Urbana-Champaign, USA (Aug, 2009-Aug, 2011). Currently, she is serving as an assistant professor in COMSATS Institute of information Technology, Islamabad, Pakistan.

aisha_naeem@comsats.edu.pk