Multi-Omic Approaches for Liver Cancer Biomarker Discovery

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Abstract:
Omic technologies offer the opportunity to characterize liver cancer at various molecular levels. In particular, characterizing the association of biomolecules such as metabolites and glycoproteins with liver cancer is a promising strategy to discover clinically relevant biomarkers. Metabolites are molecular fingerprints of what cells do at a particular point in time; they can reveal early signs of cancers when the chances for cure are highest. Also, the analysis of protein glycosylation is relevant to liver pathology because of the major influence of this organ on the homeostasis of blood glycoproteins. This talk will focus on the application of multi-omic approaches to identify biomarkers for early detection of liver cancer in patients with liver cirrhosis. Specifically, I will present transcriptomic, proteomic, glycomic/glycoproteomic, and metabolomic (TPGM) studies we conducted by analysis of samples from HCC cases and cirrhotic controls using multiple omic platforms such as next generation sequencing, liquid chromatography-mass spectrometry (LC-MS), and gas chromatography-mass spectrometry (GC-MS). In addition to candidate biomarkers discovered by evaluating the changes in the levels of transcripts, proteins, glycans, and metabolites between HCC cases and cirrhotic controls, I will present network-based methods we developed for integrative analysis of multi-omic data to identify aberrant pathways/network activities and biomarkers for early detection of liver cancer.

Short Bio:
Dr. Ressom is a Professor of Oncology at Georgetown University Medical Center (GUMC). His research focuses on using multi-omic approaches for liver cancer biomarker discovery. His laboratory collects biospecimens from human research participants, designs workflows for multi-omic studies, and develops computational methods for omic data analysis. Dr. Ressom is the Director of GUMC’s Genomics and Epigenomics Shared Resource (GESR), which provides various services including next generation sequencing, SNP genotyping, copy number variation analysis, DNA methylation analysis, and mRNA/miRNA expression analysis.