Proteogenomics insights into the biology and treatment of HPV-negative head and neck cancer

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Abstract

Precision oncology has largely been driven by genomic profiling, but success so far has been limited. By combining next generation-based genomics and transcriptomics and mass spectrometry-based proteomics, proteogenomic profiling of human tumors holds promise in providing deeper mechanistic insights and generating therapeutic hypotheses to better match patients to targeted treatments than analyzing each ‘ome in isolation. Using data generated by the National Cancer Institute’s Clinical Proteomic Tumor Analysis Consortium (CPTAC) on HPV-negative head and neck squamous cell carcinoma (HNSCC) as an example, I will present a few strategies on using proteogenomics data to drive therapeutic hypothesis generation for precision oncology. Predictive biomarkers identified through integrated proteogenomic characterization of the target proteins and pathways of existing drugs enable matching tumors to the most effective drugs. Meanwhile, new targets identified through unbiased exploratory analysis of proteogenomic data provide rationale for new drug development.

Biosketch

Dr. Bing Zhang is a Professor of Molecular and Human Genetics at Baylor. He is a CPRIT Scholar in Cancer Research and a McNair Medical Institute Scholar. Before joining Baylor, he was at Vanderbilt in the Department of Biomedical Informatics for ten years. Dr. Zhang’s research program focuses on integrating genomic and proteomic data to better understand cancer biology and to improve cancer diagnosis and treatment. He has more than 130 papers in key journals in the areas of bioinformatics, proteomics, and cancer systems biology. He is an associate editor of Clinical Proteomics and a member of the editorial board of Molecular & Cellular Proteomics. His scientific reputation has led to frequent invitations to give talks at national and international institutions and conferences.