Abstract

Breast cancer is the second-most common cancer and the second-leading cause of cancer-related deaths in women\textsuperscript{1}. Despite advances in cancer early detection, prevention and treatment, breast cancer is still a major health challenge due to low survival caused by breast cancer metastasis\textsuperscript{2}. This warrants critical attention and intervention. From the proteomic standpoint, a protein-based multiplex system that provides large array of informative signals for cancer identification and prognosis is still limited\textsuperscript{3}. In this dissertation work, we developed two mass spectrometry-based strategies involving chemical biology tools for rapid protein fingerprinting of breast cancer cell lines, and for probing the O-linked N-acetylglucosaminyl (O-GlcNAc) proteome in transforming growth factor-beta (TGF-β) induced epithelial-mesenchymal transition (EMT), a process that initiates metastasis. Investigation of O-GlcNAc EMT proteomics is critical in understanding how aberrant O-GlcNAc post-translational modification (PTM) promotes cancer invasion and metastasis, as well as in the identification of early stage therapeutic targets. Until now the role of O-GlcNAc PTM in TGF-β-induced EMT is unknown. Aside from demonstrating diversity of applications of mass spectrometry in breast cancer research, methodologies developed and findings entailed in this thesis, respectively, underscore the affinity enrichment of O-GlcNAc proteome, and corroborate published work showing that O-GlcNAc modification plays essential role in breast cancer metastasis\textsuperscript{4}.

References:


