

Characterizing Proteases In Triple Negative Breast Cancer By Proteomic Mass Spectrometry

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10AM - 11AM

MD10 LEVEL 2
SEMINAR ROOM
DEPT OF ANATOMY

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Functional proteolytic processing plays vital roles in cancer initiation, progression and metastatic pathways. Characterizing these roles in a given cancer type provide important insights into disease pathology and therapeutics intervention. This proposal focuses on understanding proteolytic functions in triple-negative breast cancer subtype (TNBC). This breast cancer (BC) subtype does not express estrogen receptor (ER), progesterone receptor(ER) and human epidermal growth factor receptor 2 (HER2), and is highly aggressive and with limited treatment options as compared to other subtypes, despite the fact that there are several studies in this area. Recent studies suggest that various proteolytic activities are associated with TNBC tumorigenesis. Thus, it is hypothesized that characterization of such activities through analysis of TNBC-specific patterns of protease expression, activity and substrates will allow better understanding of the aggressive nature of this subtype, leading to potentials in uncovering therapeutic targets. This comprehensive analysis will be executed by employing a strategic pipeline based mainly on advanced proteomics mass spectrometry (MS) as an unbiased integrated approach for systematically studying proteases. First, system-wide profiling of the proteome of representative cells from all breast cancer subtypes will be carried out for extraction of differentially-expressed proteases in TNBC or its subcategory, followed by MS-based assays to evaluate their enzymatic activities. Detailed characterization of a selected protease, whose activity has the most prominent effect on TNCB metastasis, will be carried out through MS-based substrate tracking strategies and relevant biological assays. In all, this study will widen our view for exploiting novel diagnostic and therapeutic potential for TNBC.