

Aarthi Shankar

Senior Division Medicine & Health

Proteomic Characterization of ECM to Identify Tumor Associated Biomolecules Part 2

The proteomic composition of the extracellular matrix (ECM) influences the growth and motility of cancer cells. The identification of differences between healthy and cancerous ECM can provide a list of candidate biomolecules that can be validated as tumor suppressors or promoters. The proteomic composition of a sample is obtained using an optimized protein digestion protocol followed by chromatographic separation and analysis of the individual fractions using tandem mass spectrometry. The number of peptides for a given protein sequence are used to determine the proteomic composition and estimate protein abundances. Three ECM samples from rat mammary were characterized using the above procedure: virgin, involution, and involution with ibuprofen. Virgin mammary matrix supports normal mammary epithelial growth and was used as a control. Involution is the pro-inflammatory ECM that occurs following pregnancy and promotes tumor cell dissemination. Involution matrix from animals treated with ibuprofen appears to behave functionally closer to the virgin ECM. Analysis of experimental data identified ECM proteins with biological significance (e.g., decorin, agrin, biglycan). Two-way Anova showed statistically significant differences in the abundances of proteins between the samples. The proteins were ranked based on the magnitude of the difference and their biological significance, thereby providing a prioritized list of candidate tumor promoters and suppressors. Independent research has confirmed that one of the proteins identified (MMP-2) plays a critical role in the metastasis of the tumor. This research has applications to the development of new methods based on protein imbalances to detect breast cancer and drugs to treat the tumor.