



## AB070. 59. Investigating how the extracellular matrix directs gene expression in breast cancer metastasis

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**Background:** Metastasis is the number one cause of death in breast cancer patients. Understanding how and why cancer cells migrate is of significant clinical interest. Accumulating evidence suggests that the spread of breast cancer is influenced by the extracellular matrix (ECM). The ECM refers to the area around the tumour containing various proteins and cells; influencing tumour structure and behaviour.

**Methods:** We examined a panel of 40 genes that code for several categories of proteins that regulate the composition of the ECM. We selected this panel as they are known to be active at the leading edge of the cell or secreted into the

ECM. We used STRING an online tool to examine the relationship between the genes based on the experimental determination of protein homology and protein co-expression.

**Results:** Using quantitative real-time polymerase chain reaction (qRT-PCR), we examined gene dysregulation in different cell lines that represent various models of breast cancers. Cells were cultured in 2D and 3D models. Models will be used to validate our approach on matched tissue reflecting subtypes of breast cancer patients. By investigating how the cell interacts with its environment we aim to identify the first genetic changes happening in the cell as it becomes invasive.

**Conclusions:** This work could provide opportunity to generate a novel gene signature that may be used to predict invasive cancers, the primary step in cancer metastasis. It may also provide information on the design of novel treatment therapies for patients with metastatic cancers.

**Keywords:** Breast cancer; extracellular matrix; metastasis

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