AB071. 60. Using *in vitro* models to identify and target proteins involved in the progression of breast cancer

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Background: In Ireland, almost three thousand women are diagnosed with invasive breast cancer every year. Of those diagnosed, approximately 1/5 are affected by triple negative breast cancer (TNBC), a sub-type characterised by an aggressive phenotype and poor prognosis. The lack of expression of common pharmacological targets, i.e., the estrogen receptor, progesterone receptor and human epidermal growth receptor 2, means that current treatment is limited to traditional chemotherapeutics. As a result, there is an urgent need to identify novel biomarkers and molecular targets so that we can more accurately and quickly diagnose and treat TNBC. Our study aims to investigate exactly how the progression of breast cancer is influenced by specific micro-environmental cues and identify the key proteins involved in the growth and migration of tumour cells.

Methods: We used Click-iT chemistry and mass spectrometry analysis to identify proteins that are synthesised by the cancer cells as they are stimulated to migrate towards an epidermal growth factor (EGF) chemoattractant, in both 2D and 3D *in vitro* models of cancer metastasis.

Results: We have identified a list of 97 proteins spanning a myriad of different functions such as metabolism, intracellular calcium sensing, anti-oxidation and proteins that regulate the cell structure.

Conclusions: We hypothesise that these newly synthesised proteins play a vital role in cancer cell migration and metastasis. We are currently investigating the role of several of these proteins in regulating the cells' response to the tumour microenvironment and from this, will develop novel therapeutic targets for the treatment of TNBC.

Keywords: Breast cancer; *in vitro*; newly synthesised proteins

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