

Predicting breast cancer patient outcome: Researchers identify new genes

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Not a day goes by without a new story about the environment. Although we often consider the environment on a global scale, cells in our body also have to contend with environmental factors. New studies from a team of researchers from the Research Institute of the MUHC and McGill University show that the environment surrounding breast cancer cells plays a crucial role in determining whether tumor cells grow and migrate or whether they fade away. Their study is the first to identify the genes behind this environmental control and correlate them with patient outcome. Their findings are published in this week's issue of *Nature Medicine*.

“A tumour can not exist on its own. It has to be supported and nourished by the cell types around it, the microenvironment,” says senior author Dr Morag Park, Director of the molecular oncology group at the Research institute of the MUHC. “When we began this study there was little known about the importance of this microenvironment on cancer initiation and progression. We now know that this environment is pivotal; different patients have distinct tumour microenvironments at a gene level. Our findings show that the gene profile of these distinct microenvironments can be used to determine clinical outcome – who will fare well and who will not.”

Dr Park, a professor of oncology, biochemistry, and medicine at McGill University, and her team analyzed tissue from 53 breast cancer patients. They used a unique technique, laser capture microdissection (LCM), to separate tumour cells from microenvironment tissue. They compared the

gene expression between the microenvironment tissue and controls using micro-array analysis. From thousands of genes they identified 163, which correlated with patient outcome. A good outcome was defined as having no tumour metastasis and tumour migration and non-responsiveness to therapy was considered poor outcome.

From the original 163 genes, the team further identified a panel of 26 specific genes that could be used to accurately predict clinical outcome. This 26 gene-profile, called the stromal derived prognostic predictor (SDPP), was used to predict outcome from a second set of breast cancer patients.

“We were able to show that the SDPP effectively predicts outcome in a second group of patients,” says Dr Park, “This panel accurately forecasted patient status, suggesting that this may be a promising diagnostic tool.

“Our next steps are to develop this 26-gene predictor into a functional test. We are currently working on this and we anticipate a product for clinical trials within a year,” adds Park.

“This work takes tremendous dedication and collaboration from a number of people including pathologists, surgeons, oncologists as well as researchers. I would like to thank the outstanding work done by G. Finak from the laboratory of Dr M. Hallett of McGill’s Computer Science Department, the breast surgeons of the MUHC, including Dr S. Meterissian, and by the Department of Pathology at McGill, where Dr A. Omeroglu works.”

Source: McGill University

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