Breast cancer: Reducing the risk of unnecessary chemo

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Published in *Nature Communications*, NRC researchers have developed a tool to determine which breast cancer patients have little risk of their disease recurring. The tool -- an algorithm that identifies "gene expression signatures" or biomarkers that can predict low risk tumors with 87-100 percent accuracy in different groups of patients -- has the potential to virtually eliminate unnecessary chemotherapy.

A fundamental principle of medicine is: "first, do no harm." However, for doctors who treat breast cancer, this is easier said than done. Every year, almost 22,000 Canadian women are diagnosed with breast cancer — their treatment usually involves surgery to remove a tumour and then chemotherapy to reduce the risk of cancer returning. But studies show that for most patients with early stage breast cancer, chemotherapy following surgery is totally unnecessary and therefore does more harm than good.

Identifying whether a patient's cancer is at low or high risk of recurring would help doctors reduce unnecessary treatments for low risk patients. This could have a huge impact on a patient's quality of life and also significantly reduce the cost of health care.

Did you know?

Chemotherapy can be devastating both physically and emotionally. Side effects of breast cancer chemotherapy range from nausea, vomiting and hair loss to mouth sores, menopause, infertility, numbness and aching of

the joints, hands and feet.

Currently, most doctors assess a patient's prognosis using their age and "tumour grade," but this approach doesn't work very well. Now, NRC researchers have developed a tool to determine which breast cancer patients have little risk of their disease recurring. The tool — an algorithm that identifies "gene expression signatures" or biomarkers that can predict low risk tumours with 87-100 percent accuracy in different groups of patients — has the potential to virtually eliminate unnecessary chemotherapy.

To conduct their study, which appeared in a recent issue of *Nature Communications*, Dr. Edwin Wang and his colleagues at the NRC Biotechnology Research Institute in Montreal (NRC-BRI) used published data on gene expression profiles from more than 1000 breast cancer samples. "Every tumour has a gene expression profile, which indicates how the patient's genes have changed," he explains. "We combined this data with information on the patient's outcome — such as whether the original tumour spread and how long the person survived — to develop our algorithm."

The NRC team now hopes to see its algorithm applied in a clinical setting. "We have a provisional patent on the intellectual property and we would like to get a Canadian company to license it and turn it into a kit format," says Dr. Maureen O'Connor of NRC-BRI, who co-authored the study. "We've had interest expressed from more than one company so far."

Dr. O'Connor adds that the NRC algorithm could be adapted to other types of cancer where over-treatment is common, such as prostate cancer. "Prostate cancer in particular is usually not an aggressive disease, but the treatment can be extreme," she says. "We would like to develop a test that can predict with 99 percent accuracy whether a patient's cancer

is not aggressive, so they can make the best decision about whether to proceed with treatment right away."

In future, the algorithm may also help pave the way toward personalized therapy for cancer patients. "On average, every cancer patient has 14-16 mutated genes," says Dr. Wang. "Based on their unique genetic signature, we hope to figure out which mutations to target to block the cancer process in each patient."

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