

New test discovered to better predict breast cancer outcomes

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(PhysOrg.com) -- Researchers from McGill University's Rosalind and Morris Goodman Cancer Research Centre (GCRC), the Research Institute of the McGill University Health Centre (RI MUHC), the Dana-Farber Cancer Institute and Harvard Medical School have discovered a gene signature that can accurately predict which breast cancer patients are at risk of relapse, thereby sparing those who are not from the burdens associated with unnecessary treatment.

For years, clinicians have been faced with the problem that breast cancer cannot be treated with a one-size-fits-all approach. Some cancers respond to specific treatments while others do not. Close to 50 per cent of [breast cancer](#) patients belong to a group – defined as "estrogen receptor positive/lymph node negative (ER+/LR-)" – that is at low risk of relapse. The majority of patients in this group may not require any treatment beyond the surgical removal of their tumour, while a small minority should receive additional treatment.

“The added information provided by our test would enable oncologists to identify those at very low risk of relapse, for whom the risk-benefit ratio might be in favour of withholding chemotherapy, and to identify patients in this low-risk group who would benefit from more aggressive treatments,” explains Dr. Alain Nepveu, GCRC and RI MUHC researcher and co-author of the study. “Since many treatments are associated with short- and long-term complications including premature menopause, cardiotoxicity and the development of secondary cancers, risks must be balanced against the potential benefit for each patient to

avoid unnecessary suffering, needless expense and added burdens on the health-care system.”

While more research is required before the test would be ready for market and incorporated into existing diagnostic procedures, Nepveu suggests it has the potential to be commercialized within five years.

More information: These findings were published in a recent issue the *Proceedings of the National Academy of Sciences* of the United States of America (PNAS). For the abstract, please visit:

www.pnas.org/content/early/2011/01/14/1008403108.short

Provided by McGill University

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