Scientists find new breast cancer genes, rewrite rulebook

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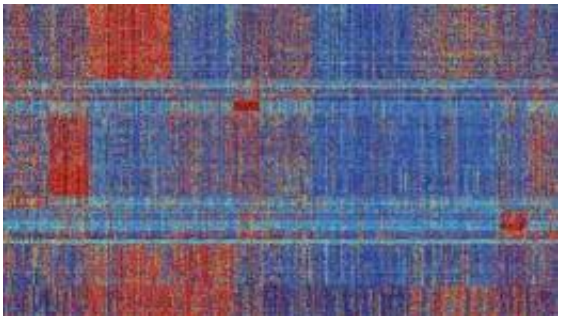

Partial view of genetic analysis. Image by Prof Carlos Caldas

Scientists at the BC Cancer Agency and University of British Columbia have identified new breast cancer genes that could change the way the disease is diagnosed and form the basis of next-generation treatments.

Researchers have reclassified the disease into 10 completely new categories based on the genetic fingerprint of a tumour. Many of these genes could offer much-needed insight into breast cancer biology, allowing doctors to predict whether a tumour will respond to a particular treatment. Whether the tumour is likely to spread to other parts of the body or if it is likely to return following treatment.

The study, published online today in the international journal *Nature*, is the largest global study of breast cancer tissue ever performed and the culmination of decades of research into the disease.

In the future, this information could be used by doctors to better tailor treatment to the individual patient.

"This is a major step forward in building the genetic encyclopedia of breast cancer and in the process we've learned there are many more subtypes of breast cancer than we imagined. The new molecular map of breast cancer points us to new drug targets for treating breast cancer and also defines the groups of patients who would benefit most." said Dr. Sam Aparicio, study co-lead author. "The size of this study is unprecedented and provides insights into the disease such as the role of immune response, which will stimulate other avenues of research.

The team at the BC Cancer Agency, in collaboration with Cancer Research UK's Cambridge Research Institute and Manitoba Institute of Cell Biology at University of Manitoba, analyzed the DNA and RNA of 2,000 tumour samples taken from women diagnosed with breast cancer between five and 10 years ago. The sheer number of tumours mapped allowed researchers to spot new patterns in the data.

Study milestones include:

- Classified breast cancer into 10 subtypes grouped by common genetic features, which correlate with survival. This new classification could change the way drugs are tailored to treat women with breast cancer.
- Discovered several completely new genes that had never before been linked to breast cancer. These genes that drive the disease are all targets for new drugs that may be developed. This information will be available to scientists worldwide to boost drug discovery and development.
- Revealed the relationship between these genes and known cell signaling pathways – networks that control cell growth and

division. This could pinpoint how these gene faults cause cancer, by disrupting important cell processes.

This is the second major breakthrough announced by BC Cancer Agency scientists in as many weeks. On April 4, a team led by Dr. Sam Aparicio celebrated the decoding of the genetic makeup of the most-deadly of breast cancers, triple-negative breast cancer, which until then was defined by what it was missing, not what it was. Similar to that announcement, today's new discovery identifies genes that were previously unknown to be linked to breast cancer and makes it clear that breast cancer is an umbrella term for what really is a number of unique diseases.

While the research is unlikely to benefit women who currently have breast cancer, it substantially advances how scientists approach further research and clinical trials by providing them with a springboard to develop new treatment options and drugs targeted to specific genes.

More information: "The integrative genomic and transcriptomic architecture of 2000 breast tumours." Curtis et al. *Nature*. DOI: 10.1038/nature10983

Provided by University of British Columbia