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## Development and Validation of Comparative Genomic Hybridization Arrays for Clinical Use in Cancer

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| <b>Status</b>          | Current  |
| <b>Competition</b>     | Applied Genomics and Proteomics Research in Human Health |
| <b>Sector</b>          | Health   |
| <b>Genome Centre</b>   | Genome British Columbia                                  |
| <b>Project Leaders</b> | Douglas Horsman & Wan Lam                                |

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### Project Description

#### *Managing cancer by detecting genetic changes*

Cancer in humans results from acquired changes in our DNA, which is subject to damage over time. Often, this damage is repaired or the affected cell is prevented from further division by an organized process called 'cell death.' But some types of DNA damage allow damaged cells to continue to live and proliferate—and these genetically damaged cells eventually give rise to cancer, with uncontrolled cell growth and invasion of other body sites.

Cancer research is currently focused on detecting the genetic changes associated with cancer development and progression. New technologies, fuelled by the Human Genome Project, allow researchers to examine thousands of genes at once, in order to identify alterations that may be associated with cancer. "These genetic alterations may be quite specific for certain types of cancer," explains Douglas Horsman of the B.C. Cancer Agency, "We use them to assist in cancer diagnosis, to determine if a cancer is benign or aggressive, and to understand whether it will respond to certain types of therapy. In the future, as these technologies evolve, they will lead to the development of gene-based cancer therapies."

Led by Dr. Horsman and Dr. Wan Lam, the Development and Validation of Comparative Genomic Hybridization Arrays for Clinical Use in Cancer project aims to develop and evaluate a new technology called whole genome array comparative genomic hybridization (aCGH). This technology allows cancer researchers to scan the total DNA in cancer cells to identify sites where there has been a change in the amount of DNA. Regions of DNA with an abnormal gain or loss may point to the location of genes responsible for cancer development or progression. The project will involve a collaboration between the BC Cancer Research Centre, the BC Cancer Agency and cancer centres in Edmonton and Toronto.

“This technique springs from an innovative genome-based process that applies small fragments of DNA representing the whole human genome onto ordinary glass microscope slides using a special printer, and then using coloured-light emitting dyes, to identify complementary DNA sequences from cancer specimens,” explains Dr. Horsman. “Using special cameras, the intensity of the coloured light emitted from each spot on the glass slide indicates whether there are gains or losses of the number of copies of specific DNA fragments in the tumour cells.” Using computer programs, the researchers then compare the identities of the altered fragments directly to the human genome sequence to determine which gene is contained within those fragments.

To date, the prototype whole genome aCGH technology (called a SMRT array) has been assembled at the BC Cancer Research Center and Genome Sciences Centre, with the ongoing support of the Genome Canada investment in the project “Cancer Genomics: A multidisciplinary high throughput approach to identify genes involved in early stage cancers’. Moving forward, the project will now further develop and validate aCGH for research use and routine clinical application. Whole genome aCGH technology will integrate with other research techniques now under development, ultimately transforming the investigation and management of cancer patients. In the near future, it will enable the introduction of high-resolution, partially automated and competitively priced technology to assess DNA copy number changes in cancer.