



BACKGROUND

2015 Disruptive Innovation in Genomics Competition Results for Phase 2 (Round 1)

In June 2015, Genome Canada launched the Disruptive Innovation in Genomics (DIG) Competition. The major objective of the competition is to support the development of **disruptive innovation** in the field of genomics, which is defined as *a new genomics-based technology or the application of an existing technology from another field, applied to the field of genomics, that is truly transformative in that it has the potential to either displace an existing technology, disrupt an existing market or create a new market. A disruptive innovation offers the capability to do things not previously possible and is not an incremental improvement of an existing technology.*

To maximize the benefits for the genomics community, the DIG program is being delivered in two phases:

Phase 1 supports activities to prove the feasibility of an “idea” – does this technology work and what can it do? This phase supports ideas for potential disruptive innovations from either individuals with a need (i.e. users of genomics), technology developers or others with great ideas.

Phase 2 supports the development of a prototype (e.g. process, product and/or method) to advance the “idea”. Two rounds of Phase 2 funding are available (the second Round open only to eligible Phase 1 projects.)

Five projects have been selected for funding in the first round of Phase 2, with an investment of approximately \$4.1 million from Genome Canada and \$9.2 million in co-funding from other sources, including provinces, private sector, not-for-profit organizations and others. (Phase 1 projects are listed in a separate [backgrounder](#).)

BRITISH COLUMBIA

Replacing Immunoassays with MS-based Technology: Quantitative Proteomics Kits Enabling Deep Molecular Phenotyping of the Mouse

Project Leader: Christoph Borchers, University of Victoria

Co-Leader: Albert Sickmann, Bioanalytics department, Leibniz-Institut für Analytische Wissenschaften Dortmund

Administrative Lead Genome Centre: Genome BC

Total Funding: \$3,865,231

Mice are the most commonly used mammals in health research, playing a key role in drug development and biomedical research. Determining the concentration of a wide variety of proteins in biofluids and tissues of mice is an important way of assessing mouse models. Dr. Christoph Borchers at the University of Victoria, in collaboration with partner Dr. Albert Sickmann in Germany (ISAS), will develop new mass spectrometry (MS)-based technology for rapid analysis of 3,000 mouse proteins, or about 20 per cent of the total number, in 20 different tissues. The technology will be provided as a service, as well as formatted as an easy-to-use kit. The team will also publish reference ranges to help researchers interpret the data they obtain. The new technology will be commercialized by a Canadian biotechnology company, MRM Proteomics Inc.

Next generation immune profiling technology based on microfluidic single cell analysis

Project Leader: Carl Hansen, University of British Columbia

Administrative Lead Genome Centre: Genome BC

Total Funding: \$2,993,509

Antibodies are molecules the immune system makes to fight infection and disease. There is an immense variety of different antibodies, each one binding to a specific target molecule. It is this specificity that makes antibodies highly effective as targeted therapies – that is, if you can find the best candidates out of the billions of antibodies the body produces. Current methods allow the sampling of less than 0.001 per cent of all antibodies and are time-consuming and expensive. Dr. Carl Hansen of the University of British Columbia will develop and deliver a disruptive technology that allows measuring and isolating antibodies directly from individual immune cells, with the ability to screen millions of cells in a single day to find those that may be developed into therapeutics. The outcomes of this work will be commercialized in Canada, promoting economic growth and creating new high-tech jobs in BC.

Automated Tumour Pathology

Project Leader: Marco Marra, BC Cancer Agency

Co-Leader: Robin Coope, BC Cancer Agency

Administrative Lead Genome Centre: Genome BC

Total Funding: \$409,858

DNA sequencing is increasingly used for medical applications. In cancer, it can determine inherited risk factors and inform treatment decisions. Such analysis requires DNA from the tumour itself, usually obtained by biopsy. Because biopsied tissues usually contain both tumour and normal cells, this mix can render the sample useless for DNA sequence analysis. Drs. Marco Marra and Robin Coope of the BC Cancer Agency will implement an automated method to identify and enrich tumour cells in biopsy materials, making DNA sequencing of tumour cells more practical. In addition, large-scale analysis of archived tumour cells, correlated with data on treatments and outcomes can inform current treatment decisions.

ONTARIO

Synthetic inhibitors of ubiquitin-binding cancer targets

Project Leader: Sachdev Sidhu, University of Toronto

Administrative Lead Genome Centre: Ontario Genomics

Total Funding: \$3,009,018

Our cells remove damaged or nonfunctional proteins through a small protein called ubiquitin, which attaches to target proteins and signals their destruction. In many diseases, ubiquitin does not work as it should. Dr. Sachdev Sidhu of the University of Toronto is using an innovative high-throughput molecular genetics engineering platform, which is unique in the world and has attracted intense interest from industry and academia, to enable the rapid and cost-effective development of highly specific and potent ubiquitin-like molecules. These molecules attach to key, cancer-associated enzymes of the ubiquitin system, to block or enhance their function. The project will enable the discovery of new drug targets, speed up drug development and generate effective anti-cancer drugs with fewer side effects, all of which should be of great socio-economic benefit to Canadians.

The Mammalian Membrane Two-Hybrid (MaMTH) Assay - an Advanced Proteomics Technology for Biomedical Research

Project Lead: Igor Stagljar, University of Toronto

Administrative Lead Genome Centre: Ontario Genomics

Total Funding: \$3,000,000

Integral membrane proteins have roles in many human diseases, but are notoriously difficult to study due to their unique biochemical features. Dr. Igor Stagljar and his team at the University of Toronto recently developed a powerful new technology, the Mammalian Membrane Two-Hybrid (MaMTH) assay, which can map protein-to-protein interactions (PPIs) of integral membrane proteins directly in the natural context of the cell. They now propose to further develop MaMTH technology by converting it into a platform that can map these PPIs on an extremely large scale. This work will allow researchers to develop better-targeted therapies for human disease more rapidly. The technology will be the foundation for an Ontario-based company called Protein Network Sciences that will offer easy access to this novel disruptive

MaMTH technology, advancing biomedical research and therapeutic discovery while benefiting Canadian social and economic infrastructure.