Data sharing in Canada through the Canadian Open Genetics Repository



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opengenetics.ca

This work was funded by the Government of Canada through Genome Canada and the Ontario Genomics Institute (OGI-070)

GenomeCanada



Objectives

- To create Canada's unified, open-access, clinical-grade genetic database using a commonly shared platform
- Standardize variant assessment procedures
- Data extraction and variant classification consensus building
- Data Access and Disseminate results to a large public repository

Workflow Overview





COGR - BRCA Participating Institutions



- A. Alberta Children's Hospital (Calgary, AB)
- B. Atlantic Cancer Research Institute (Moncton, NB)
- C. British Columbia Cancer Agency (Vancouver BC)
- D. Children's & Women's Health Centre of BC (Vancouver BC)
- E. Children's Hospital of Eastern Ontario (Ottawa ON)
- F. Credit Valley Hospital, Trillium Health Centre (Mississauga ON)
- G. Dept of Medical Genetics, University of Alberta (Edmonton, AB)
- H. Hamilton Health Sciences, McMaster University (Hamilton, ON)
- I. Impact Genetics Inc. (Bowmanville, ON)
- J. Izaak Walton Killam Health Centre (Halifax, NS)
- K. Kingston General Hospital, Queen's University (Kingston, ON)

- L. McGill University Health Complex (Montréal, QC)
- M. Memorial Health University Medical Center (St. John's, NL)
- N. Mount Sinai Hospital, University of Toronto (Toronto, ON)
- O. North York General Hospital (Toronto ON)
- P. Ontario Institute of Cancer Research (OICR) (Toronto, ON)
- Q. Regional Health Authority, University of Manitoba (Winnipeg, MB)
- R. Sainte-Justine Hospital, University of Montreal (Montréal, QC)
- S. SickKids Hospital and McLaughlin Centre (Toronto, ON)
- T. University Hospital, Western University (London, ON)
- U. Women's College Hospital, University of Toronto (Toronto, ON)
- V. Jewish General Hospital, Montreal (Montréal, QC)



Discrepancy Report Results Overview

- **11** participating labs across 4 provinces
 ON, BC, AB, MB
- Received total of **5,554** *BRCA1/2* variants
 - 3014 unique variants
 - 1,148 seen in >2 labs
 - 110 to 1072 variants per lab (505 on average)

Tiered Discrepancy Models





5-tiered

Initially implemented

3-tiered

 Recommended by participants

2-tiered

- Clinical management

Data Received

5-tier

- 900 variants had 2 or more classifications
- 350 (38.9%) were discordant
 - 1410 observations of these variants

3-tier

- 240 (26.7%) discordant

2-tier

- 45 (5%) discordant

After analysis

330 (23.8%) discordant variant observations changed classification after analysis

5-tier

Number of discordant variants decreased from 38.9% to 30.7%

3-tier

- Decrease from 26.7% to 12.45%

2-tier

- Decrease of from 5% to 1%

Classification Changes



Direction of Classification Changes



Reason for Reclassification





Typographical error

- Based on new evidence provided
- Revised classification criteria

Other (Please specify)

Methods for Reassessment





- We used our own methodology or tools to reassess
- We used the COGR variant assessment tool (VAT)
- We used the ACMG reclassification tool provided

Take Home

- A Canadian inter-institutional quality improvement program
- Importance of periodic review, tracking and maintaining versioned variant information including for variant classification
- mandatory data submission proficiency testing, laboratory accreditation
- Real-time reporting of variant data quality assessment program
- We encourage individual institutions to share their data holdings generate, maintain and preserve knowledge
- Clinicians using genetic data for risk assessment, diagnosis, prognosis or management of patients should be aware of the variability in variant interpretations

opengenetics.ca Collaborating Organizations

COGR Canadian Open Genetics Repository



American College of Medical Genetics and Genomics





ClinVar Clinically relevant variation

AGGTACGGCTGGCATCACCTAGA AGGGCTGGGATAAAGTCAGG CATGGTGCATCAGACCCCTGAG CAGGTTGGTATCAAGGTTACAAG GCACTGACTCTCTCTGCCTATTC



Can(SHARE



HUMAN VARIOME PROJECT



Beacon Network

DNASTACK

VARIANTWIRE

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