MOHCCN Gold Cohort Standards Policy_V1

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1. Introduction

The Marathon of Hope Canadian Cancer Network (MOHCCN) aims to create a "gold-standard" cohort of clinical cancer specimens with a well-annotated, uniformly generated, and consistently quality-controlled dataset (clinical and genomic) from 15,000 (15k) cases collected from across Canada over 5 years. Not only does the MOHCCN aim to build a pan-Canadian Cancer Network and to produce immediate clinical impact by identifying actionable targets through molecular profiling, but it also proposes to generate in-depth molecular profiling data from cancer patient cohorts to address important scientific questions. This richly clinically annotated molecular dataset (starting with standardized clinical information, treatment response data, and whole-genome and transcriptome profiles (WGTS) will serve as an invaluable resource for cancer biology discovery (Figure 1).

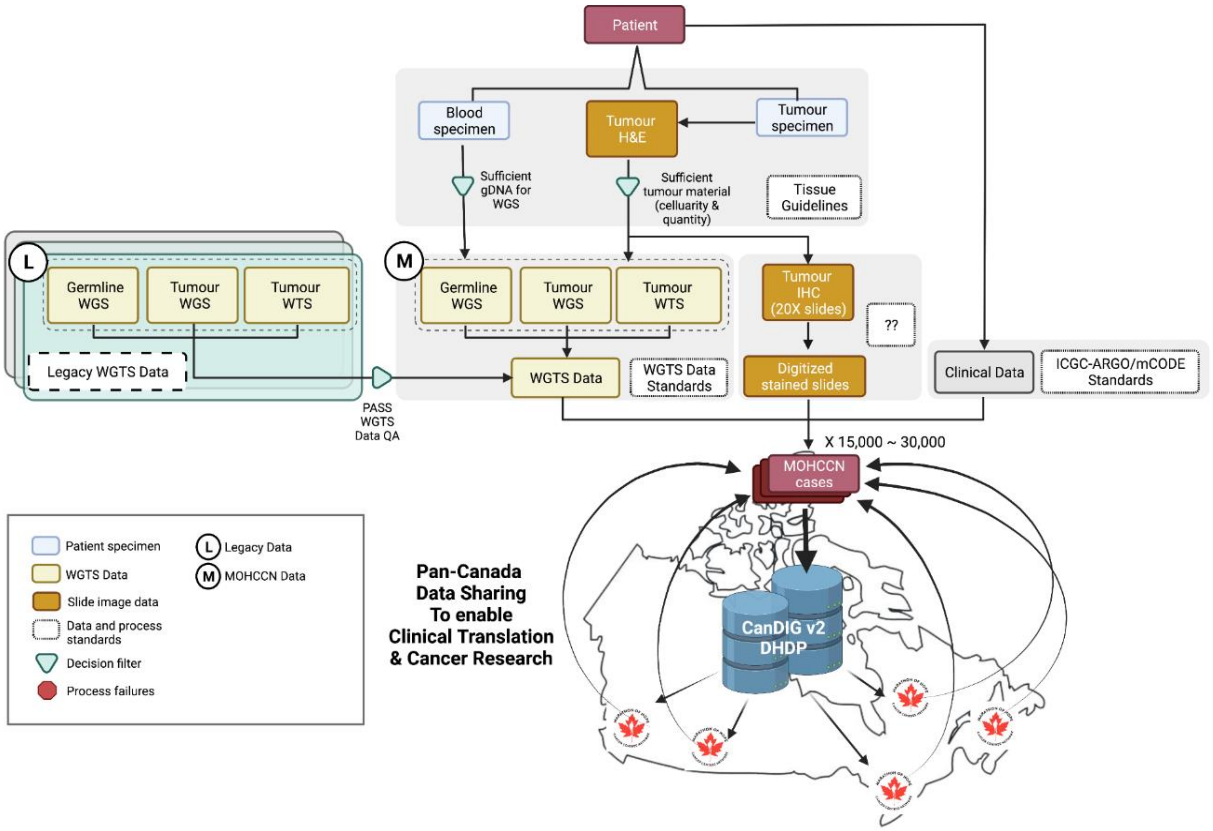


Figure 1. MOHCCN data roadmap to 15k gold standard cases.

2. MOHCCN Case definition and Data Requirements for the 15k Gold Standard

A MOHCCN case is defined as a unique patient. The table below provides the patient specimen requirements (Tumour samples and non-tumour samples, like blood or non-neoplastic tissue) to meet the Minimum (Gold Standard) data standards (Table 1). Guidelines to support collections of samples will be developed through the following MOHCCN working groups:

Complete case components	Responsible MOHCCN Working Group
Clinical information	Clinical Data Standards Subgroup
Specimen/non-neoplastic materials (whole blood, buffy-coat, PBMC, extracted genomic DNA)	Biospecimens Working Group
Tumor materials (FFPE, FF, viably frozen, extracted genomic DNA and RNA). Digitized image of the pathology reviewed H&E	Biospecimens Working Group
WGTS Data Guidelines	Technology Working Group

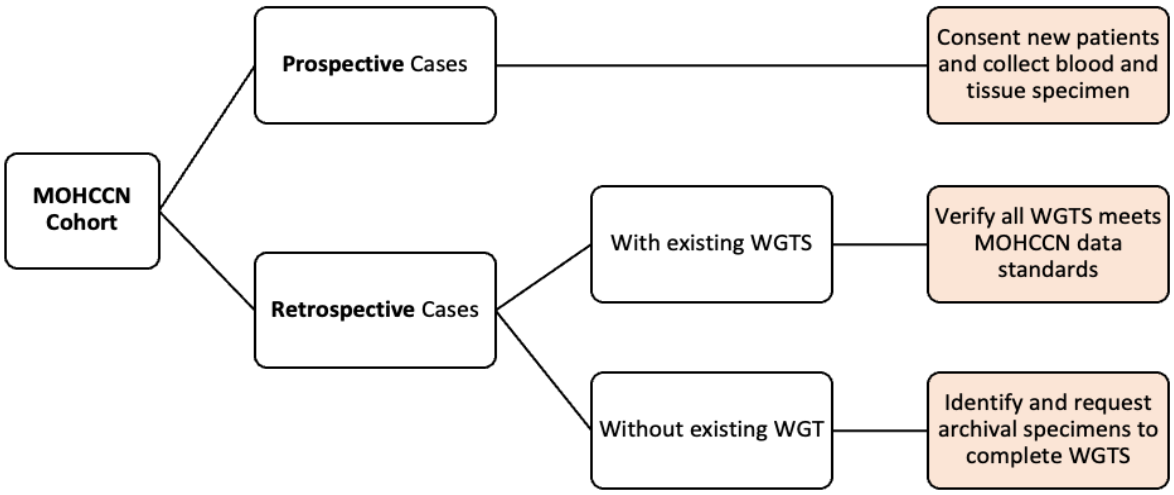
Data Requirements for the 15k Gold Standard Case

	Required* (MOHCCN standards available)	Preferred** (MOHCCN standards needed)
Clinical data		
Cross-sectional imaging (CT/MRI/PET)		✓
MOHCCN Clinical Fields (v1)	✓	✓
Health technology assessment		✓
Disease-specific		✓
Tumor Tissue		
Pathology-reviewed cellularity (Digital H&E slide or clinical flow-cytometry)	✓	✓
Whole Genome (FFPE & frozen)	✓	✓
Whole Transcriptome (FFPE & frozen)	✓	✓
Multiplexed IHC (FFPE & frozen) [*Solid tumors only*]		✓
ATAC-seq (frozen)		✓
ChIP-seq (frozen)		✓
Bisulphite Whole Genome (frozen)		✓
Proteomic Assay (FFPE & frozen)		✓
Flow cytometry or CyTOF (frozen)		✓
Single cell RNAseq (viable/frozen)		✓
Spatial transcriptomics/proteomics profiling (FFPE/frozen)		✓
Blood		
PBMC Flow Cytometry (viable)		✓
Plasma cfMeDIP-seq		✓
Plasma cytokines/metabolites		✓
Others (stool, urine, pleural fluid, etc.)		
Microbiome analysis (stool)		✓

*Required: MOHCCN standards are available to support data collection.
**Preferred: MOHCCN standards to support data collection are in development.

3. Case collection: prospective and/or retrospective.

Patient specimens for WGTS and molecular profiling can be obtained via one of or a mixture of two methods: Prospective and/or Retrospective, as in Figure below.



Prospective specimen procurement is the set of procedures to collect and store new (since the time of study approval) patient specimens for WGTS. Solid tumor tissues can be collected via surgical resection or biopsies at baseline. If possible, prospective specimen handling protocols should be followed to ensure quality of specimens for WGTS success. By adhering to best-practices guidelines for specimen collection and processing for WGTS, prospective cases have the highest probability of success in meeting MOHCCN case standards. We recommend focusing the majority of efforts towards acquiring and enrolling patients/cases prospectively for the MOHCCN 15k gold cohort in Years 3 to 5.

Retrospective specimen procurement is the set of procedures to identify the most optimal available/archival (previously collected) patient specimen for WGTS. This procedure may also involve identifying and obtaining available partial germline WGS and or tumor WGTS data. As the specimens may originate from multiple biobanks and storage facilities, this is a labor-intensive and nuanced process. Cohorts relying on retrospective specimen procurement encounter many unique challenges prohibiting successful WGTS data generation. To complete the MOHCCN 15k gold cohort, we recommend minimizing the number of retrospectively procured specimens or cases where possible.

Document revision history

Developed by	Reviewed by	Endorsed by	Effective Date	Policy Version	Summary of revisions
TWG	Steering Committee	Network Council	October 6, 2022	V1	n/a