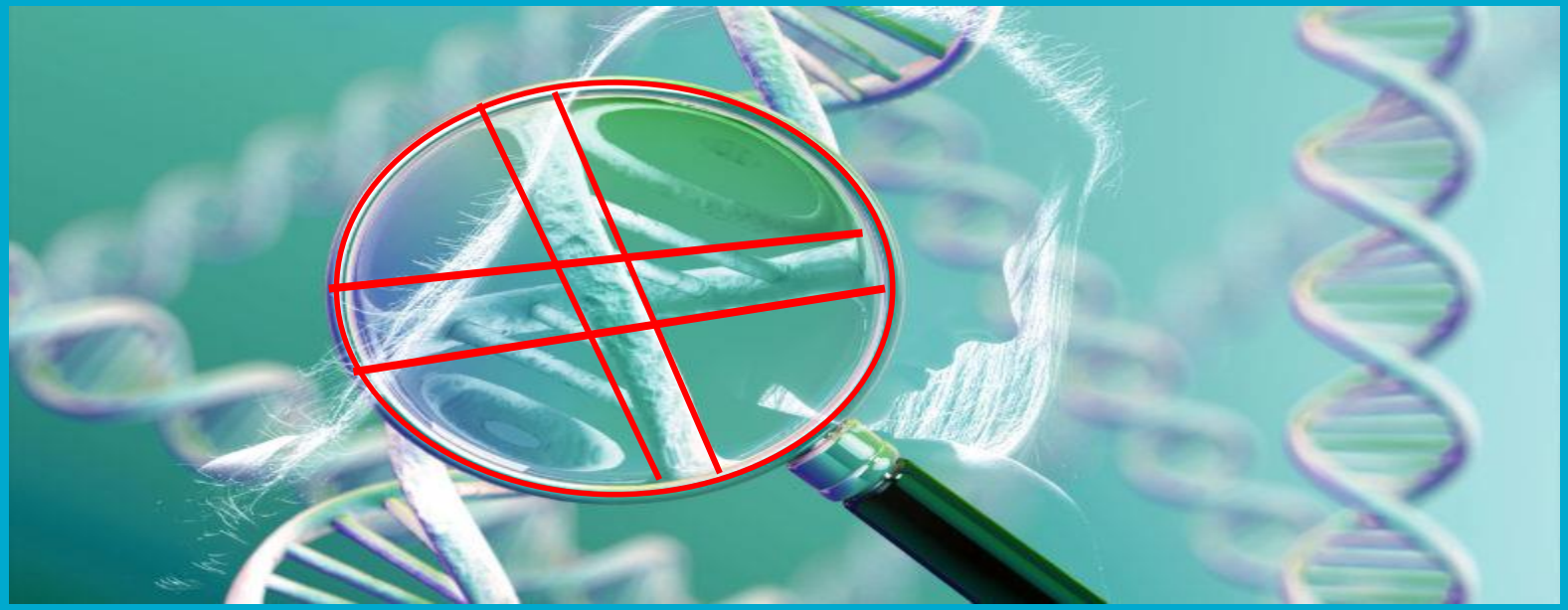

Understanding the Barriers to Genomic Healthcare in Queensland

Through an Information Management Lens

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Introduction

The biggest challenges in implementing genomic healthcare are:

- incorporating it into existing infrastructure and
- establishing its place in future investments.

The Queensland Genomics Health Alliance (Queensland Health, Queensland Universities and research organisations) seeks to understand and begin to address these challenges through a series of Clinical Demonstration Projects (CDPs) and capability building workstreams.

Queensland Genomics 2017

- Clinical Demonstration Projects designed to test use cases of genomics in healthcare:
  - melanoma (MEL),
  - lung cancer (LC),
  - infectious diseases (ID) and
  - maturity onset diabetes of the young (MODY).

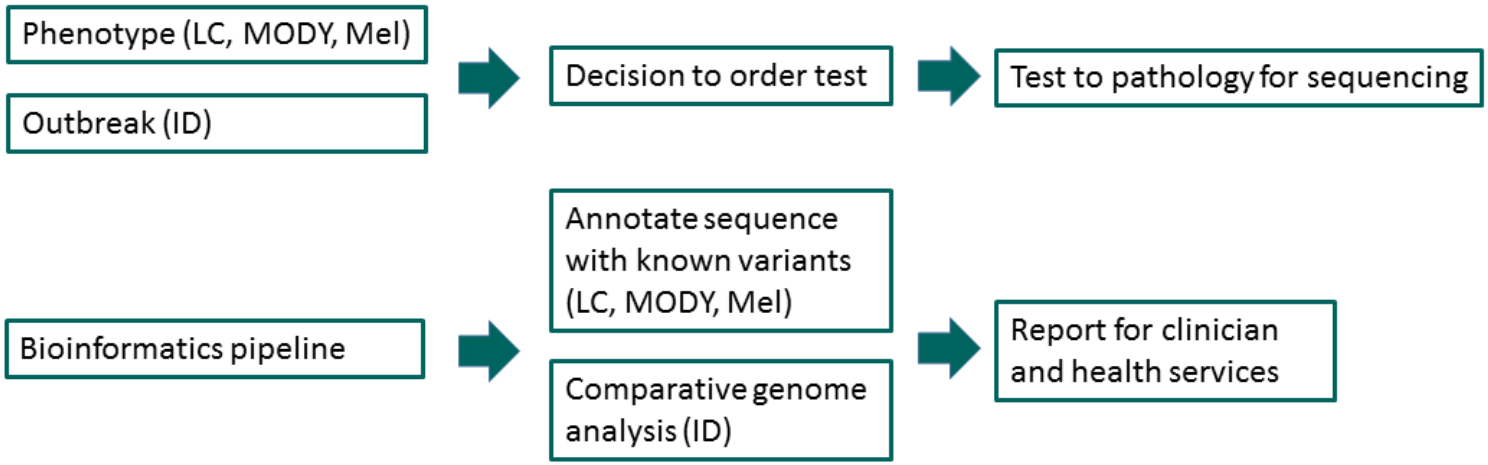
- Capability building workstreams
  - Workforce Development,
  - Evaluation of Clinical Genomics,
  - Genomic Testing Innovation,
  - Genomic Information Management (GIM) and
  - Ethics, Legal and Social Implications of Genomics.

GIM Workstream

- Workshops with key researchers from each of the CDPs were held throughout February and March 2018
  - to understand the flow and use of information for each CDP.
  - Inform the initial work through the development of a Genomics Information Pipeline prototype and
  - Inform the future development of a Genomics Information Architecture for Queensland.

- Factors that have the potential to impact the implementation of genomic healthcare in Queensland and across Australia, and
- Challenges faced in the current environment.

Genomic testing information flow



Lung Cancer (LC), maturity-onset diabetes of the young (MODY), Melanoma (MEL), and Infectious Diseases (ID).

Drivers of Queensland Genomics CDPs

- Prevalence
  - Outbreaks of IDs are on the increase; need to minimize their severity and duration, and to underpin future initiatives around outbreak prevention.
  - MEL - Queensland skin cancer rates 60% higher than the national average.
  - LC is the most common cancer-related cause of death in Queensland, and the leading cancer-related cause of death in Indigenous people across Australia.
  - MODY prevalence has increased significantly over the last 10 years, partly due to improved screening and partly due to immigration
    - Indigenous Australians

Clinical demonstration project platforms

CDP	Target population	Scope	Sequencing	Amount of data generated*
ID	Multi-resistant organisms	MRSA, VRE, CRABs, ESBLs, CPEs	Illumina NextSeq	100TB capacity
LC	Indigenous and non-Indigenous adults Somatic/ germline	N=60	Whole exome + cancer panel spike (PAH) LC panel of 300 genes (PCH)	Currently at 50TB
MEL	Melanoma diagnosis (dx)	N=383	whole exome	
MODY	Women with gestational diabetes	N=480	13 gene Illumina panel (sub panel of a Nextera 66 gene panel)	5GB/patient 100TB capacity

* Supporting data ID: Taxonomic profiling, parallel SNP calling, MLST profiling, antibiotic resistance and de-novo assembly; LC: Metro South samples go to Melbourne for Fox panel paid for through AGHA lung cancer project. Tumour and matched normal. Copy number chips - cytogenetic arrays (Mater); MEL: Extensive clinical metadata including phenotype, pedigree, imaging (2D) and telemetry (3D).

Limiting factors

1. ***There is a Need for Streamlined Consent and Ethics Processes***

2. ***Standards Need to be Developed for Curation***

3. ***New Methods for Ordering, Reporting and Dissemination for Clinical Integration***

4. ***Large Scale Implementation will be Dependent on Good Collaboration***

Streamlined Consent and Ethics Processes

- Improvements to current consent process
  - consent to cover both somatic and germline sequencing,
  - better information tools for patients (e.g. the use of videos to improve cultural applicability of the process), and
  - allowing for almost unrestricted access for researchers once they have appropriate ethics.

Queensland Genomics is undertaking a review and recommendation for consistent, fit for purpose statewide consent and ethics approvals.

Standards Need to be Developed for Curation

- Current limits on curation include
  - logistical difficulties around holding MDT meetings for variant classification,
  - whether clinical grade assertions can be made from project data,
  - a need to transfer data for annotation and interpretation,
  - scope limited to genes currently being tested by Pathology Queensland,
  - lack of clinical information passed to pathologists in the test ordering process.
- Standards development should involve training workshops
- Queensland database of both pathogenic and non-pathogenic variants that could feed into a national or international database

This is being instigated through a collaboration between AGHA and Queensland Genomics with input from Melbourne Genomics and aligned with international work through the GA4GH.

Methods for Ordering, Reporting and Dissemination

- The ID project was keen to have reports at different levels of complexity to provide to different stakeholders in the management of ID.
- The LC project was keen on synoptic reporting.
- For the MEL project, participants are only informed of outcomes if they request information and as this can sometimes include secondary findings, it is important that the research report is structured similarly to a clinical report.

Collaboration for Large Scale Implementation

- Projects were keen to further collaborate:
  - existing partnerships, similar service providers, Aboriginal Medical Services,
  - genomic community such as Melbourne Genomics or the Queensland Genomics Community Working Group, or the wider community.

- National surveillance program for ID that would require national collaboration.

Challenges

- Each project is implemented within an existing network of clinical processes, and needed to work within existing arrangements for
  - NATA accreditation,
  - MDTs,
  - bioinformatics pipelines,
  - curation, reporting and data sharing.

- Indigenous genomics
  - LC and MODY projects faced difficulties around a lack of knowledge, absence of a common catalogue of variations and little or no data in gnomAD.
  - The ID project focussed on urban hospitals; culturally appropriate handling of pathogen genome sequence data obtained from Indigenous communities remains a challenge and a potential barrier to implementation.

Challenges identified for demonstration projects

Challenge	ID	Lung	Melanoma	MODY
Collaboration	✓	✓		
Consent	✓	✓		
Curation	X	✓	✓	
Data security	✓	✓	✓	✓
Data sharing	✓			✓
Data storage		X	✓	X
Ethics	✓	✓		✓
Indigenous genetic knowledge	X	✓		✓
NATA Accreditation	✓	✓		X
Recruitment	X	✓	X	✓
Reporting	✓	✓		✓
Timeframes	✓			

✓ specified by project as a challenge; X specified as not a challenge; blank not mentioned.

Conclusion

- By working closely with CDPs and associated workstreams in Queensland and across Australia, the barriers to the implementation of genomic healthcare can be understood and overcome.

- This will involve
  - building capacity and effecting behavioral change, embracing new methods of data collection, curation and dissemination, and
  - embedding the lessons from clinical practice into policy and regulation.

Thank you

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