

Surveillance Advances
Progrès dans le domaine de la surveillance

Genomics for Public Health Surveillance

La génomique pour renforcer la surveillance de la santé publique

May 28, 2024

12:00 – 1:00pm CT / 1:00 – 2:00pm ET

Speakers

Dr. Jennifer Gardy

Bill & Melinda Gates Foundation

Dr. Linda Hoang

British Columbia Centre for Disease Control



National Collaborating Centre
for Infectious Diseases
Centre de collaboration nationale
des maladies infectieuses



Public Health
Agency of Canada

Agence de la santé
publique du Canada



Land Acknowledgment: NCCID



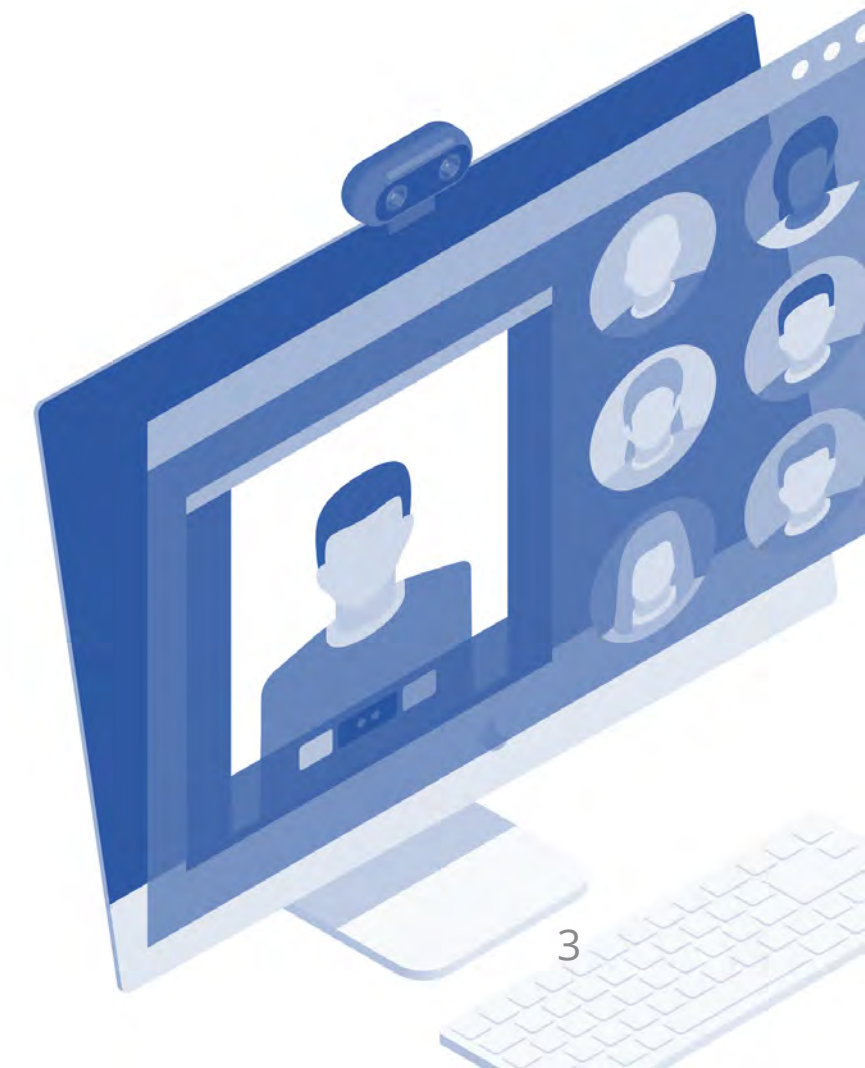
The National Collaborating Centre for Infectious Diseases is hosted by the University of Manitoba. Both the University of Manitoba and I are situated on Treaty 1 Territory, the original lands of the Anishinaabe, Cree, Oji-Cree, Dakota, and Dene peoples, and homeland of the Métis Nation. I am thankful for these lands that I live and work upon as a descendant of settlers with European ancestry and with inherited responsibilities for the lands' protection.

As an organization, NCCID recognizes the systemic inequities and treaties that have been implemented as part of the process of colonization intended to benefit some while harming others. We are committed to working with our partners towards reconciliation and we strive to honour the lands and their original caretakers in our work.

Housekeeping



- Seminar recording and presentation slides will be available shortly after the seminar at the NCCID website: <https://nccid.ca/>
- If you have technical problems with Zoom, please email us at nccid@umanitoba.ca
- The chat box for participants has been disabled for this session. We will use the chat box to share additional information.
- Please use the Q&A tab to submit your questions for our speakers. You can “like” other people’s questions to push them up in priority



Accreditation



Surveillance Advances is a self-approved group learning activity (Section 1) as defined by the Maintenance of Certification Program of the **Royal College of Physicians and Surgeons of Canada**.

The seminar series is also approved by the Council of Professional Experience for professional development hours for members of the **Canadian Institute of Public Health Inspectors**.

If you would like a letter of participation, please complete the survey which will be shared after the seminar.



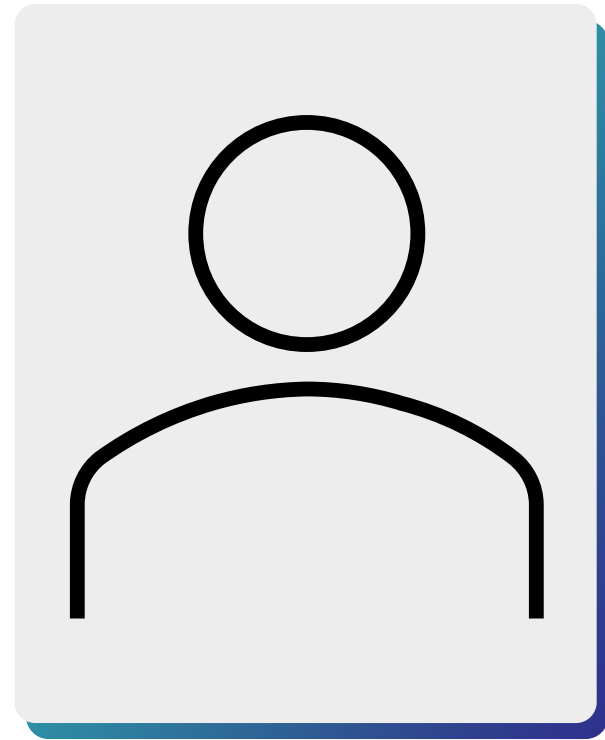
Land Acknowledgment: PHAC



I would like to take this time to acknowledge the land that I live and work on is the traditional territory of the Wendat, the Anishnaabeg, Haudenosaunee, Métis, and the Mississaugas of the Credit First Nation.

It is home to many First Nations, Métis, and Inuit peoples. I am grateful for the opportunity to share their home.

Today's speakers



Dr. Jennifer Gardy

PhD, Bioinformatics

Deputy Director,
Surveillance, Data, and Epidemiology (Malaria),
Bill & Melinda Gates Foundation

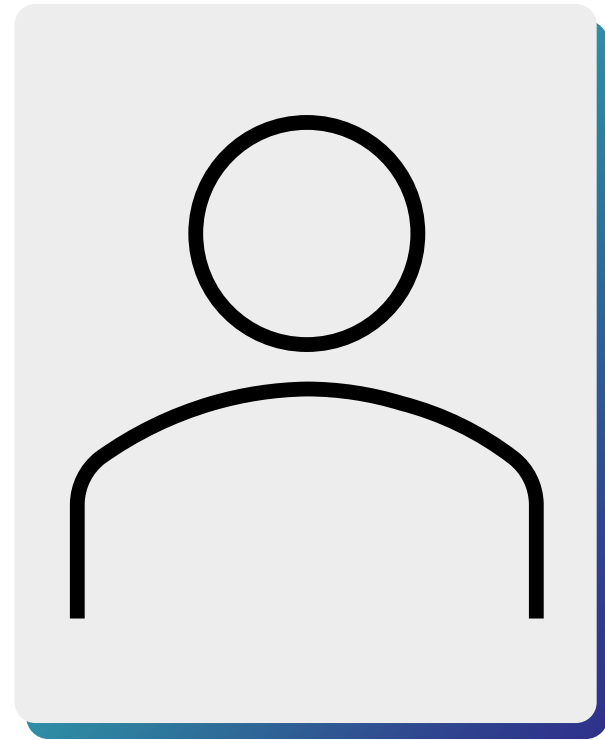


Dr. Linda Hoang

MD, MSc, DTM&H, FRCPC

Medical Director,
British Columbia Centre for Disease Control

Today's speakers



Dr. Jennifer Gardy

PhD, Bioinformatics

- Deputy Director, Surveillance, Data, and Epidemiology (Malaria), Bill & Melinda Gates Foundation
- Leadership team and recent Interim Director, Institute for Disease Modeling (IDM), Bill & Melinda Gates Foundation
- Canada Research Chair in Public Health Genomics, British Columbia Centre for Disease Control and the University of British Columbia's School of Population and Public Health
- 2018 – One of BC's Most Influential Women in STEM by BC Business Magazine and one of the Government of Canada's 20 Women of Impact in STEM
- 2021 – Elected to the National Academy of Medicine (pathogen genomic epidemiology)
- Award-winning science communicator (The Nature of Things, Daily Planet, children's science books)

Today's speakers



Dr. Linda Hoang
MD, MSc, DTM&H, FRCPC

- Medical Microbiologist, Clinical Professor, and Medication Director, British Columbia Centre for Disease Control (BCCDC) Public Health Laboratory (PHL)
 - Pathogen genomics program for COVID-19 pandemic response measures
- Recent Medical Co-Director, Provincial Infection Control Network (PICNet), BC
 - Carbapenamase producing organism (CPO) surveillance program
- Passionate about operationalization of pathogen genomics methods to provide a standardized tool informing infection prevention and public health responses in BC and Canada

Strengthening Genomic Surveillance for Malaria Across sub-Saharan Africa

Jennifer Gardy

PhD

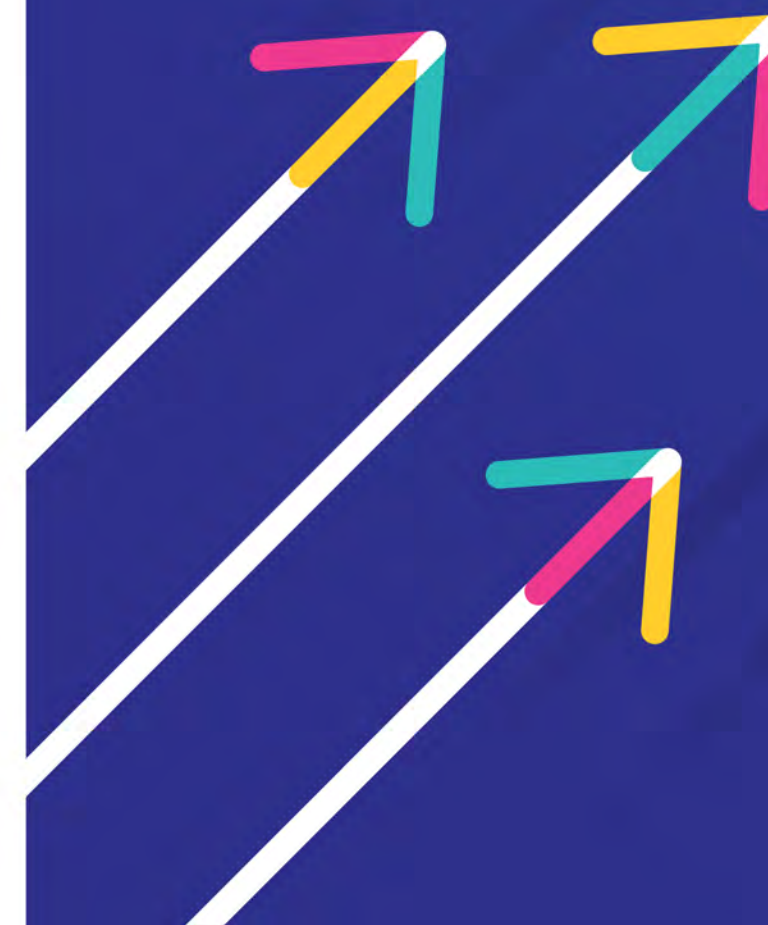
Deputy Director, Surveillance, Data, & Epidemiology

Bill & Melinda Gates Foundation



Conflicts of interest

None to declare



Learning Objectives



- Describe the role genomics can play in surveillance, strategic planning, and commodity procurement in malaria-endemic countries
- Understand the Bill & Melinda Gates Foundation's strategic priorities for malaria genomic surveillance
- Articulate some of the challenges associated with establishing genomic surveillance capacity in sub-Saharan Africa



Polling Question








How many SARS CoV-2 genomes have African labs sequenced and shared globally?

- A. <1,000**
- B. 1,000-10,000**
- C. 10,000-50,000**
- D. 50,000-100,000**
- E. >100,000**



Malaria genomic surveillance (parasites & vectors) can inform country planning & resource procurement/allocation



Assay	Microscopy 	PCR 	Serology 	Amplicon Sequencing 	Whole Genome Sequencing 
Description	<ul style="list-style-type: none"> Manual visual examination of blood smears using a microscope 	<ul style="list-style-type: none"> Molecular laboratory assay used to amplify and detect parasite DNA 	<ul style="list-style-type: none"> Protein-based laboratory assay used to detect anti-malaria antibodies 	<ul style="list-style-type: none"> Targeted sequencing of the parasite or vector genome in specific genetic regions 	<ul style="list-style-type: none"> Broad sequencing of the parasite or vector genome to identify novel markers
Data Generated	<ul style="list-style-type: none"> Presence of malaria parasite 	<ul style="list-style-type: none"> Presence of malaria parasite Emergence of resistance 	<ul style="list-style-type: none"> Past exposure to malaria parasite Population-level surveillance 	<ul style="list-style-type: none"> Resistance in known, susceptible regions of the genome 	<ul style="list-style-type: none"> Novel drug resistance markers and population genetics structures

Malaria genomics addresses multiple use cases

Resistance

- Detect/track antimalarial drug resistance
- Detect/track pfhrp2/3 gene deletions
- Detect/track insecticide resistance
- Monitor changes over time in antimalarial and insecticide resistance

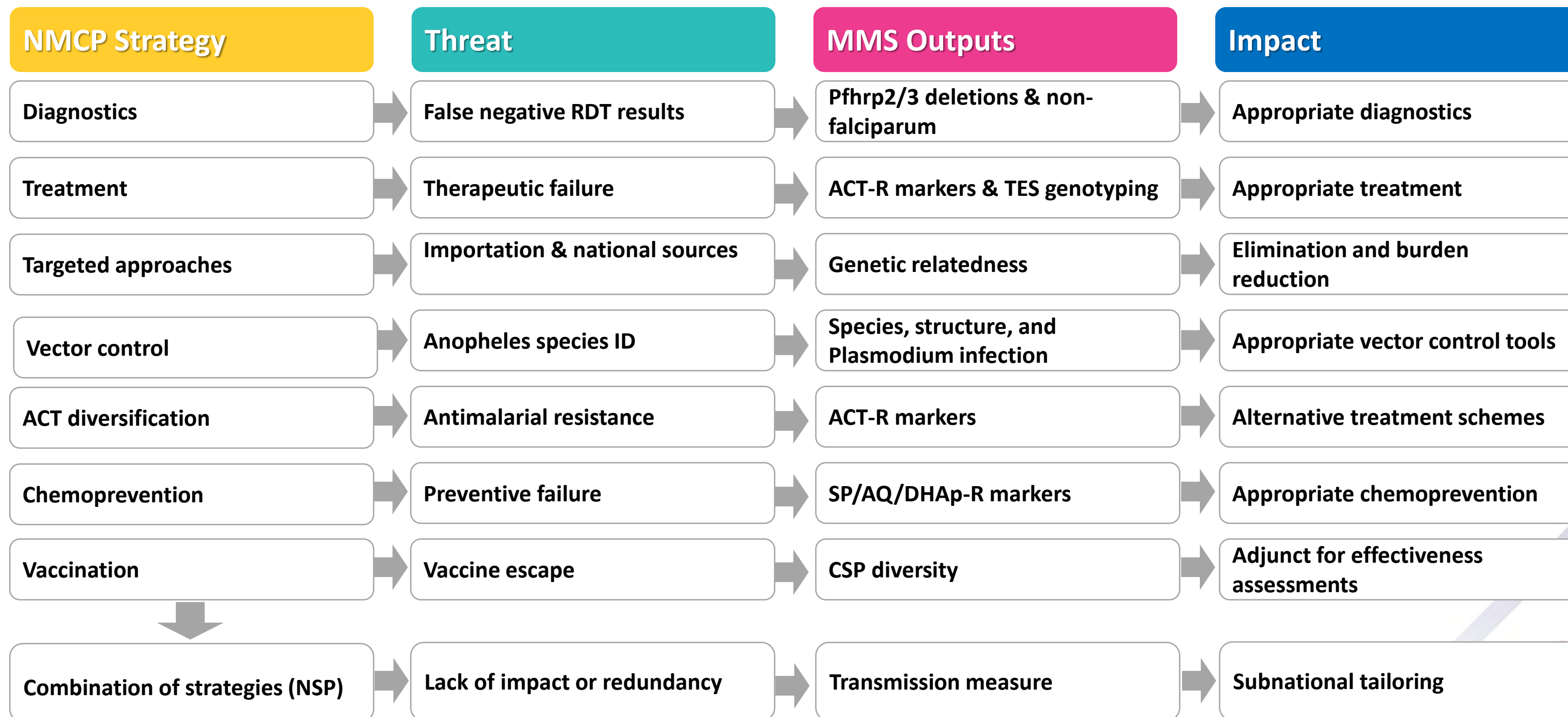
Transmission:

- Identify local transmission
- Distinguish local from imported cases
- Identify outbreaks
- Quantify transmission intensity and changes over time
- Determine connectivity of parasite populations

Population dynamics:

- Monitor parasite populations and changes over time
- Monitor vector populations and changes over time, including *A. stephensi* and gene drive releases
- Survey for variation in vaccine, monoclonal Ab, and gene drive target sites

Malaria genomic surveillance (parasites & vectors) can inform country planning & resource procurement/allocation



Getting to an ideal future state requires investment across multiple thematic areas

MMS today:

- Nascent / catalytic state
- Academic partner led
- Single disease focus
- Largely BMGF-funded



MMS in the future:

- Mature / steady-state
- Public health/gov't partner led
- Multi-disease focus
- Funded through a variety of sources (domestic & development)



Genomics In the Time of COVID

Public Health Laboratory

BC Centre for Disease Control

Linda M. N. Hoang, MSc, MD, DTM&H, FRCPC

Medical Director

BCCDC Public Health Laboratory

BC Centre for Disease Control

Provincial Health Services Authority

Clinical Professor

Department of Pathology and Laboratory Medicine

Faculty of Medicine

The University of British Columbia



BC Centre for Disease Control



Provincial Health
Services Authority

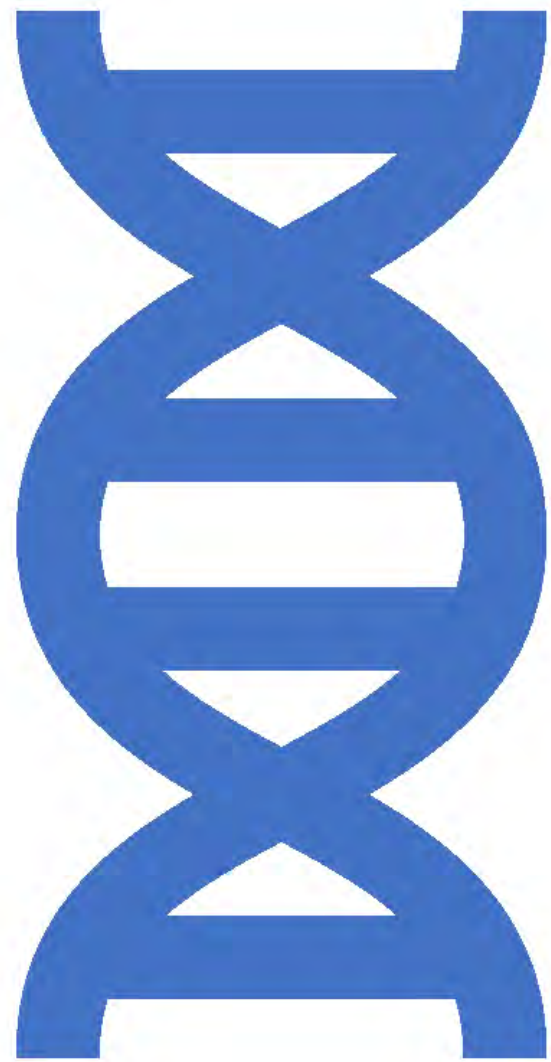
Inherent Rights of Indigenous Peoples



- First Nations territories stretch to every inch of this province, and across Canada
- Inherent rights, rooted in connection to lands and waters, have never been ceded or surrendered.
- Inherent rights are upheld in international, national and provincial law.
- Long-standing Indigenous laws and systems are integrally tied to the lands and waters of these territories.
- Generations of Indigenous rights holders who are First Nations, Métis, and Inuit from elsewhere in “Canada” also call these lands and waters home.

We gratefully acknowledge that we live and work on the traditional unceded territory of the Coast Salish Peoples, including the Squamish, Musqueam and Tsleil-Waututh First Nations

Objectives



- Describe advances in microbiology tools for surveillance, an important core function of a public health laboratory
- Outline the key applications of pathogen genomics for patient care and public health response
- Describe the development of a pathogen genomics program at the BC Centre for Disease Control
- Outline features of a genomics infrastructure, to inform patient care, public health and One Health

Subtyping and Fingerprinting

Information:

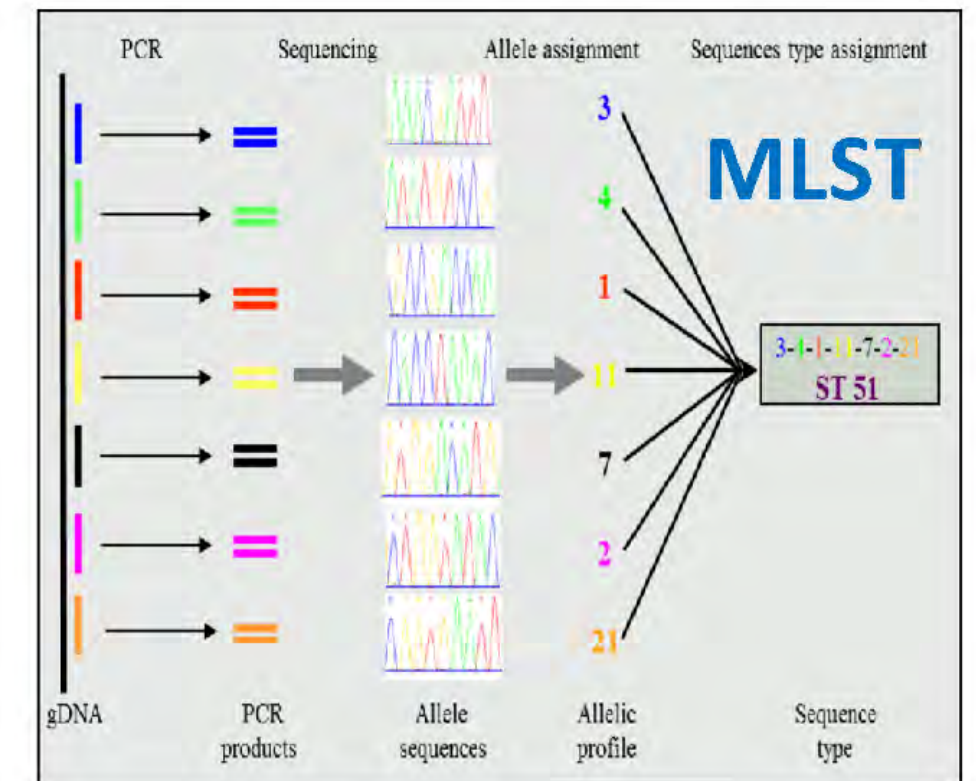
- Strain typing
- Cluster identification
- Virulence characterization
- Strain evolution
- Resistance profiling

Limitations:

- Can be subjective
- Low sample throughput
- Slow turn around time, serial testing
- Poorly discriminative



E.g. Common tools



Whole Genome Sequencing

PFGE

MLST

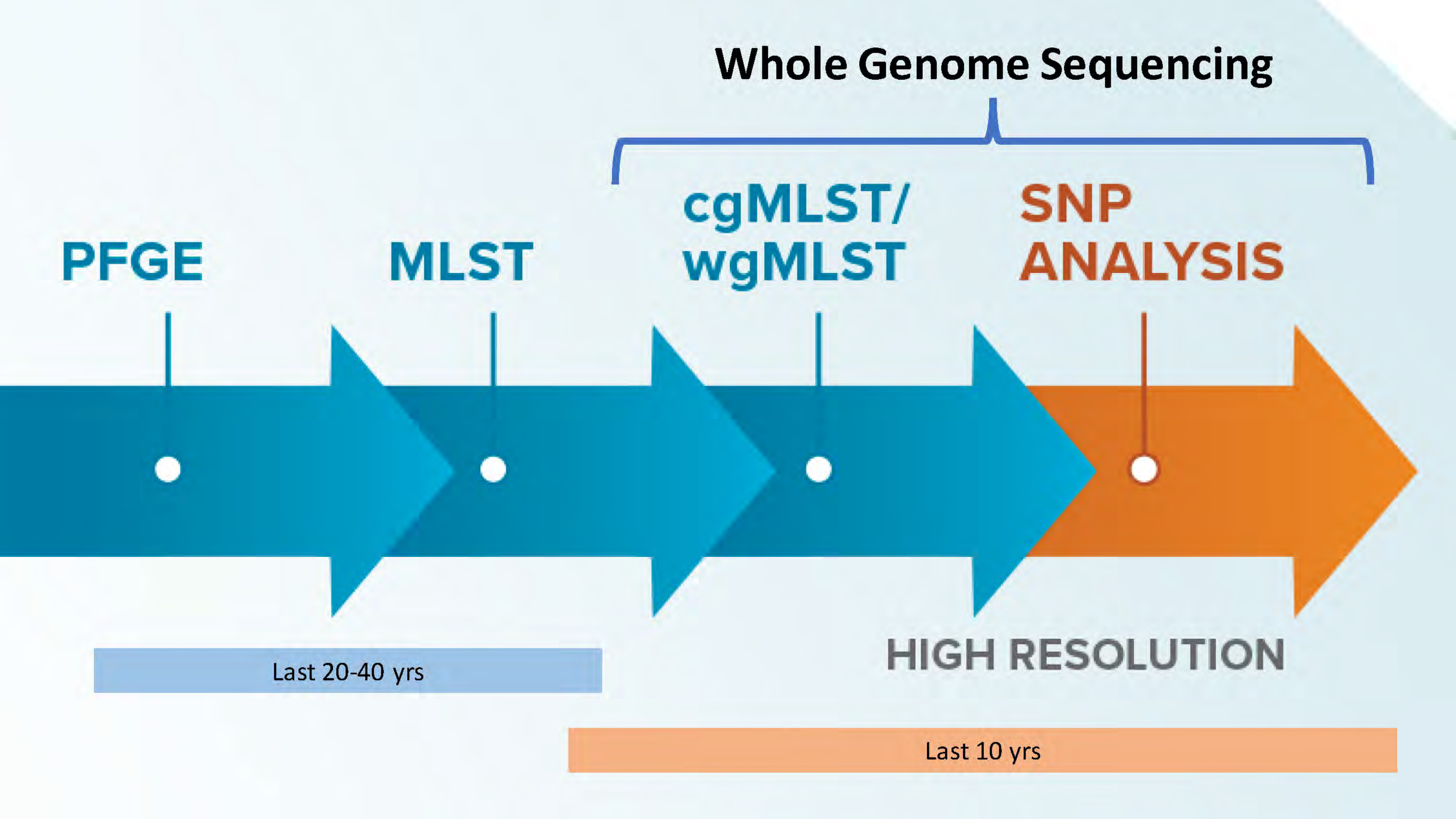
**cgMLST/
wgMLST**

**SNP
ANALYSIS**

Last 20-40 yrs

HIGH RESOLUTION

Last 10 yrs



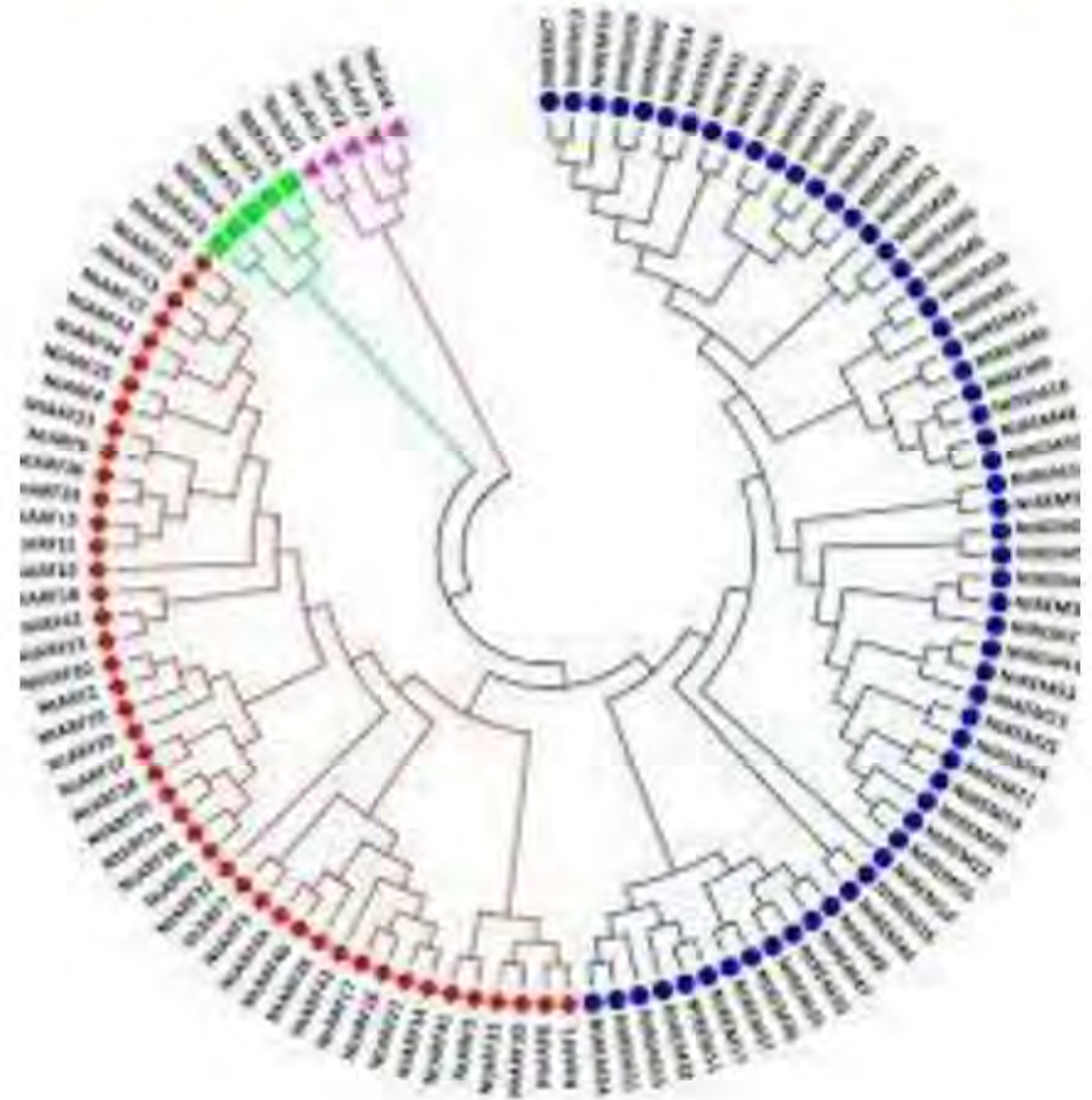


Advances in genomics over the past 10 yrs allows direct access to entire genetic makeup of microbes

- Technical advances
- Cost reduction
- Turn-around time
- Computational capacity
- Mechanism for linking meta-data
- Information is clear and actionable
- Available accreditation standards

Genomics superpower is in its database!!!

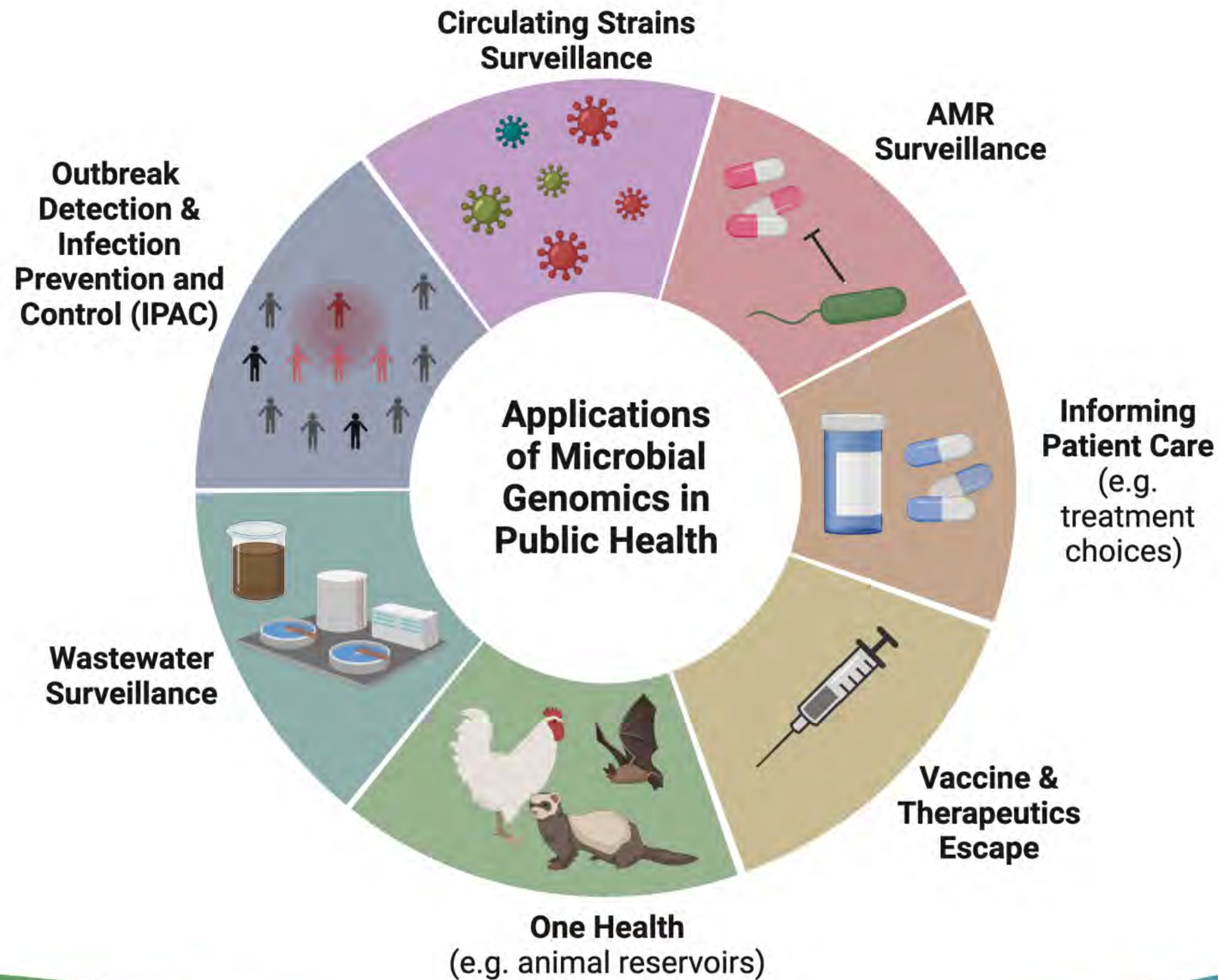
- Standardized and quality assured sequences
- Curated, robust
- Unbiased representation
 - Time
 - Person
 - Place
- Improves discriminatory power
- Confidence in results
- Needs regular maintenance for circulating strains



"Pathogen genomics is one of the most powerful tool we have against infectious diseases and environmental hazards"

*Professor Susan Hopkins
Chief Medical Advisor, UK Health Security Agency*





Genomics Program Informs Public Health & Patient Care

Early Genomics Adoption at BCCDC Public Health Lab

External/grant funded (CIHR, Genome BC, Genome Canada, NML, etc)

- PulseNet Canada Foodborne Bacterial Pathogen Surveillance
- Carbapenemase Producing Organisms Genomics Surveillance
- Tuberculosis
- Avian Influenza

Pre-pandemic (2019) State of Genomics at BCCDC



	Pathogen	Wet Lab	Bioinformatics	Reporting/ Data Viz
RESPIRATORY	SARS-CoV-2			
	Human influenza A			
	Human influenza B			
	RSV			
	TB			
WASTEWATER	SARS-CoV-2			
AMR	CPO	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>
	<i>Shigella</i>			
	TB	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>
HCAI*	Various bacteria			
ENTERIC	<i>Salmonella</i>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>
	<i>E. coli</i>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>
	<i>Listeria</i>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>
STBBI	Hepatitis C			
	<i>N. gonorrhoeae</i>			
	Syphilis			
EMERGING THREATS	Avian influenza			
	Mpxv			
	<i>H. influenzae</i> D			
	Enteroviruses			
	Group A Strep			
PARASITES	<i>Leishmania</i>			
METAGENOMICS	Various bacteria			

- Operational
- In Development
- Prioritized

Resources:

- Shoe-string resources
- Operationalized as part of PulseNet
- CPO genomics, PICNet provincial surveillance
- No dedicated scientific staff (PhD)

Throughput:

- Up to 3-4 weeks to generate a WGS result - months to generate an outbreak report
- Up to 24 samples per week

*Healthcare-associated infections (e.g. MRSA, *C. difficile*, *Pseudomonas*, *Serratia*)

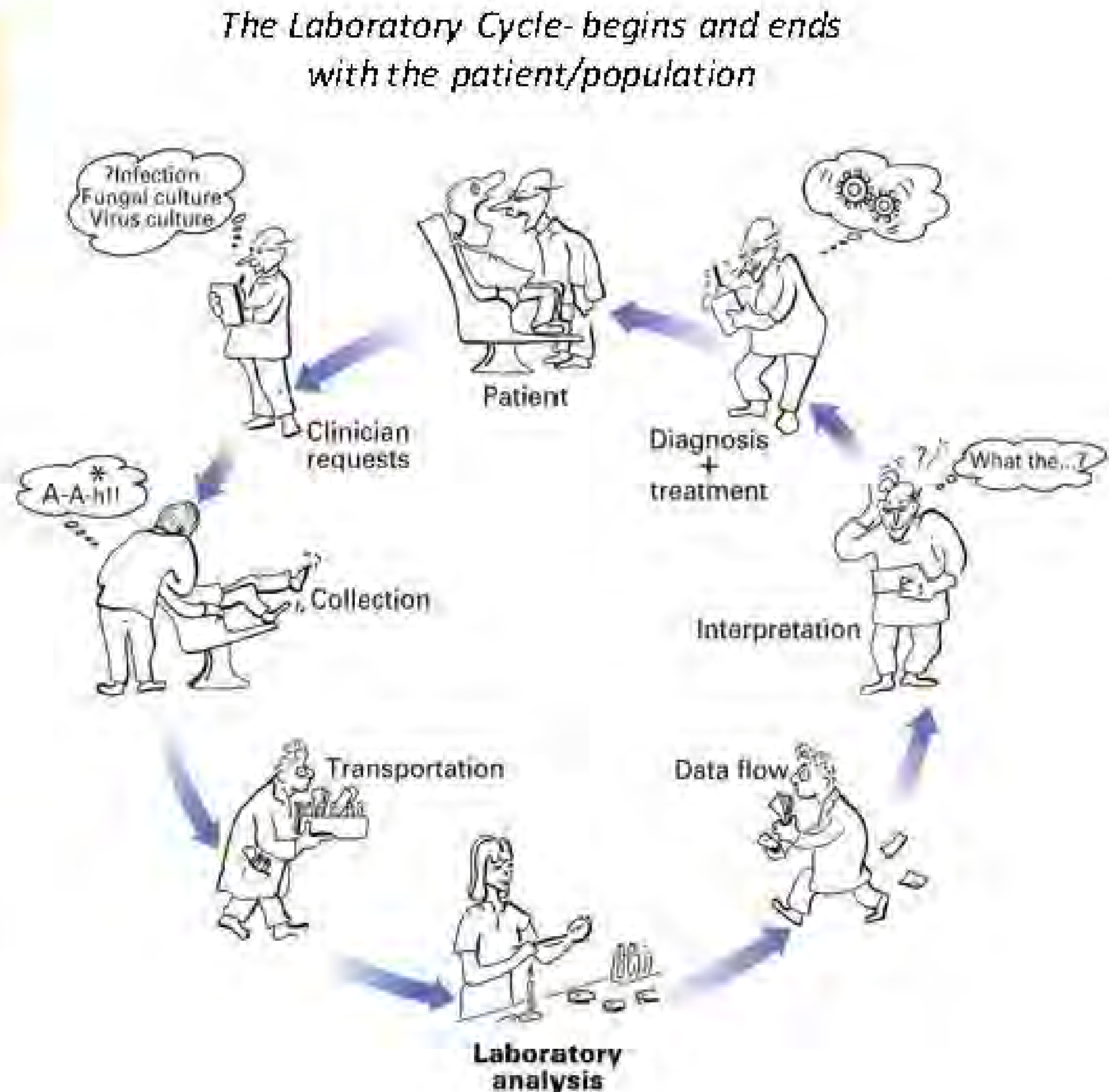
COVID-19 happened.....

To stand up a SARS-CoV2 genomics testing program:

Need high volume sequencing capacity

Need process improvement and automation

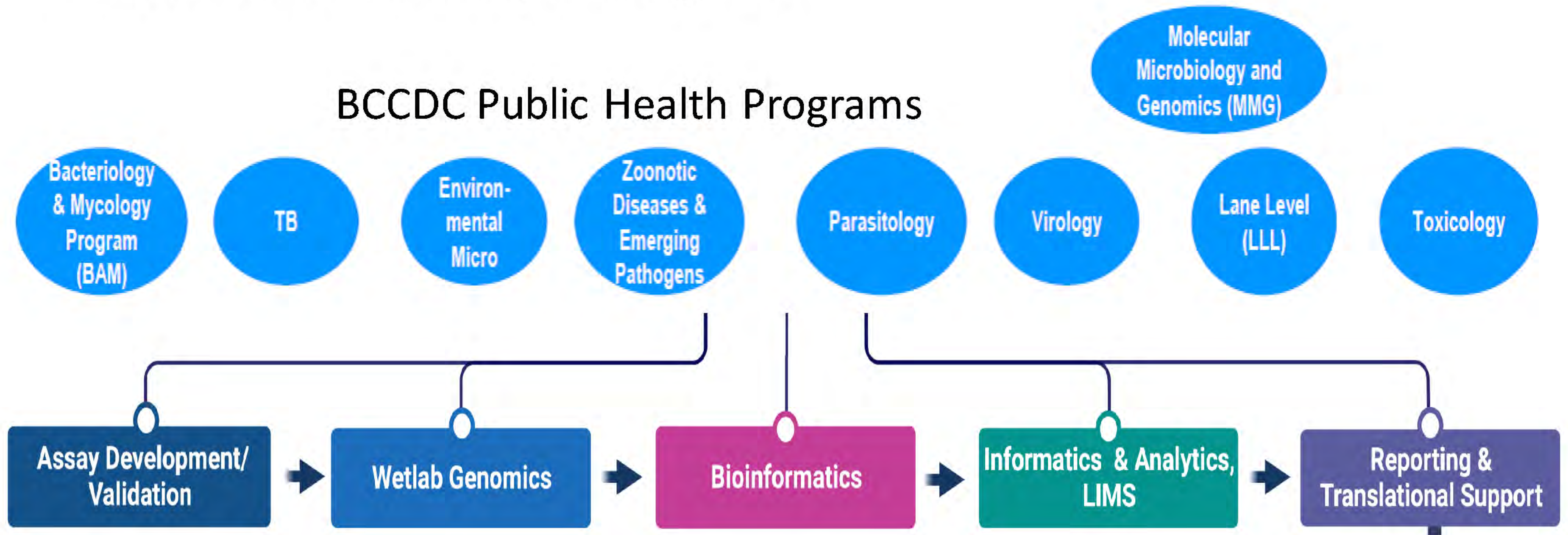
Affects all stages from patient sample to interpreted results





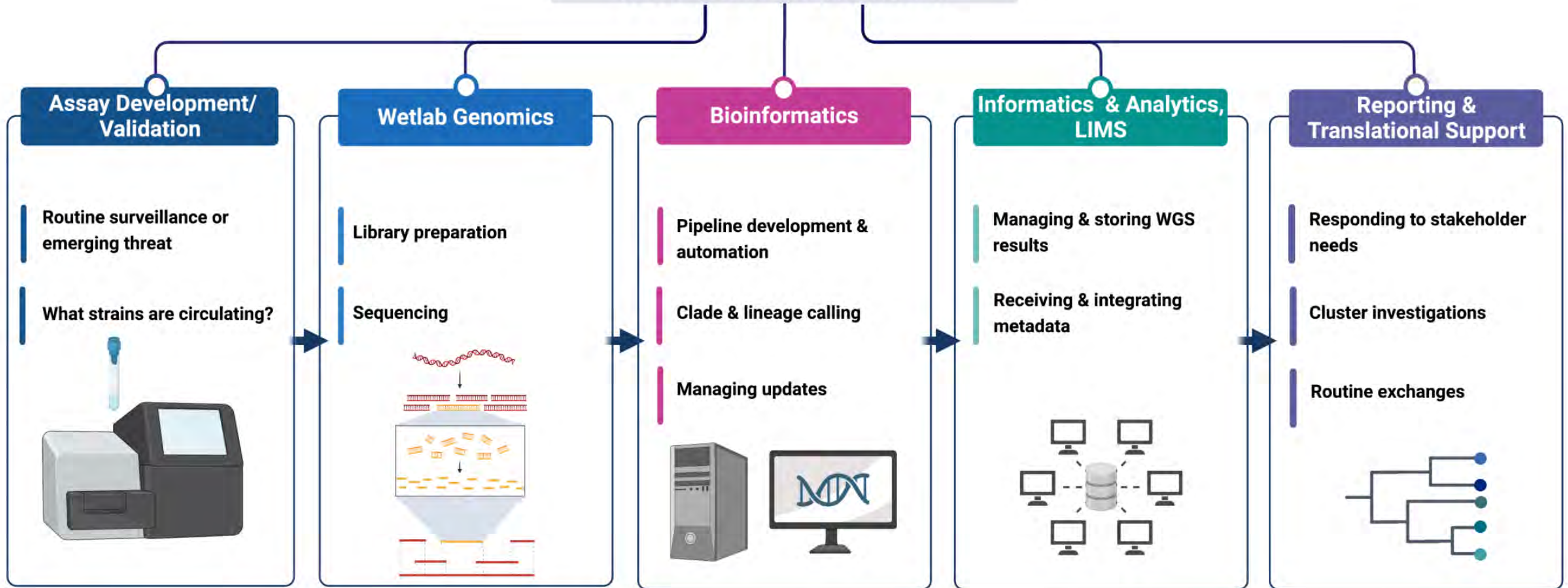
Need an agnostic genomics workflow for COVID and other pathogens

BCCDC Public Health Programs



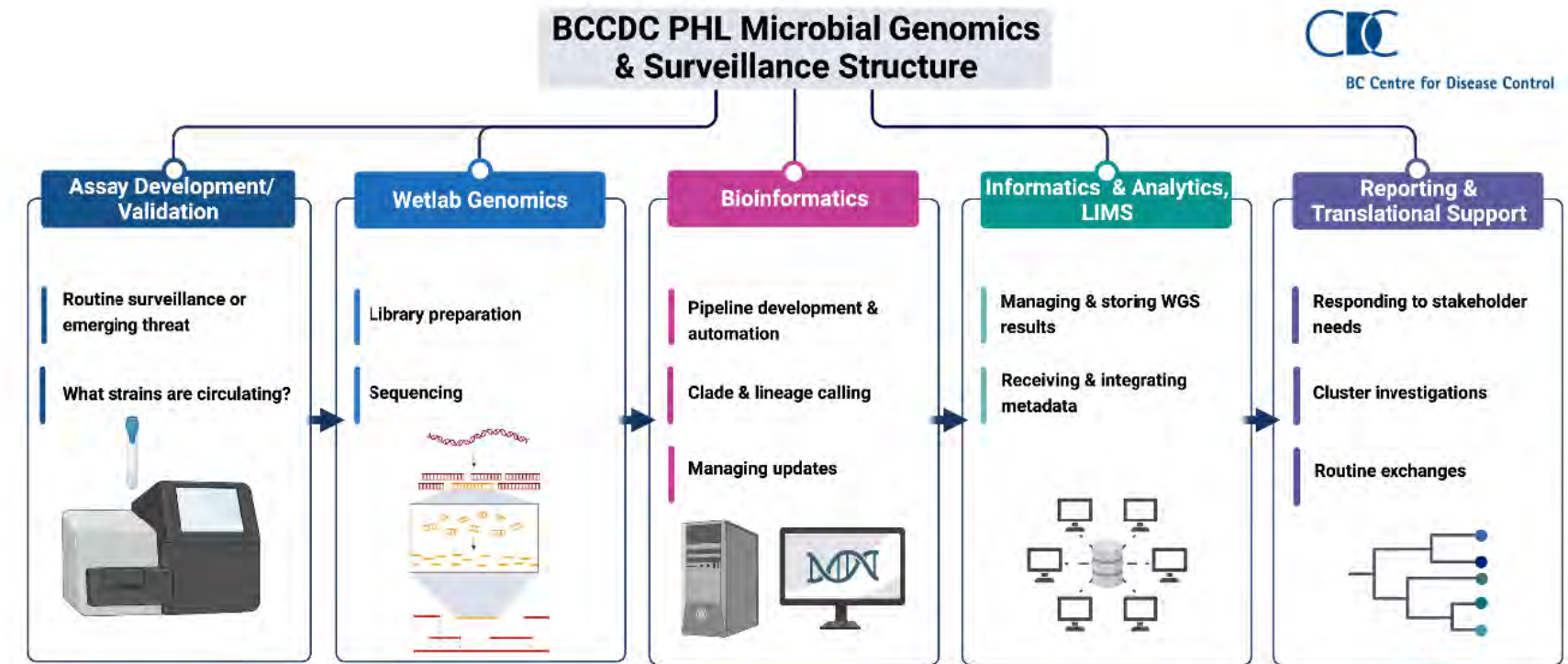
Genomics Core Established: 5 Functional Modules

BCCDC PHL Microbial Genomics & Surveillance Structure



Modular work flow

- Organism agnostic
- Easy to pivot
- Respond to priority pathogens
- Centralize skillsets and expertise
- Integrated
- Meets needs of end users



External End Users



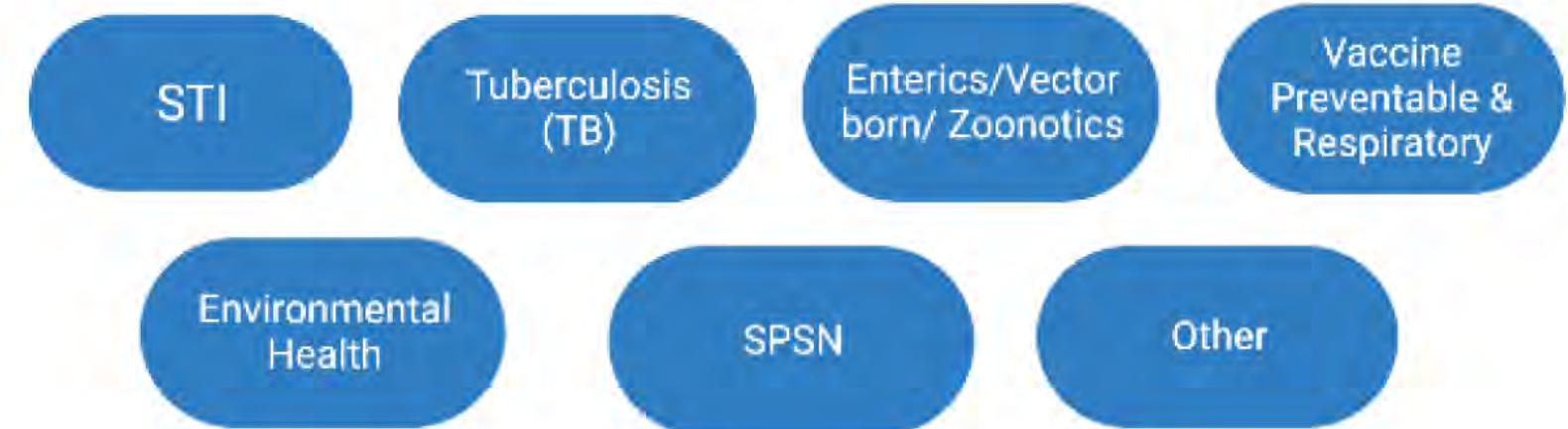
Government of Canada / Gouvernement du Canada
NML
 Ministry of Health
 Ministry of Agriculture and Food
PICNet
 PROVINCIAL INFECTION CONTROL NETWORK OF BRITISH COLUMBIA
 A program of the Provincial Health Services Authority
 Wastewater
 Remote, Rural, Indigenous
 Other Provincial Ref Labs

HA IPAC and Outbreak Epids



island health
 Interior Health
 Vancouver Coastal Health
 First Nations Health Authority
 Health through wellness
fraserhealth
 Better health. Best in health care.
 Provincial Health Services Authority
 Proven. wise solutions. Better health.

BCCDC Internal End Users



STI
 Tuberculosis (TB)
 Enterics/Vector born/ Zoonotics
 Vaccine Preventable & Respiratory
 Environmental Health
 SPSN
 Other

✓ | Clinical Microbiology | Research Article | 5 February 2024



Rapid, high-throughput, cost-effective whole-genome sequencing of SARS-CoV-2 using a condensed library preparation of the Illumina DNA Prep kit

Authors: [Rebecca Hickman](#), [Jason Nguyen](#), [Tracy D. Lee](#), [John R. Tyson](#), [Robert Azana](#), [Frankie Tsang](#), [Linda Hoang](#), [Natalie A.](#)

[Prystajcky](#)   | [AUTHORS INFO & AFFILIATIONS](#)

BCCDC Method minimizes cost, hands-on time, and complexity while maintaining high-quality and robust sequence data.

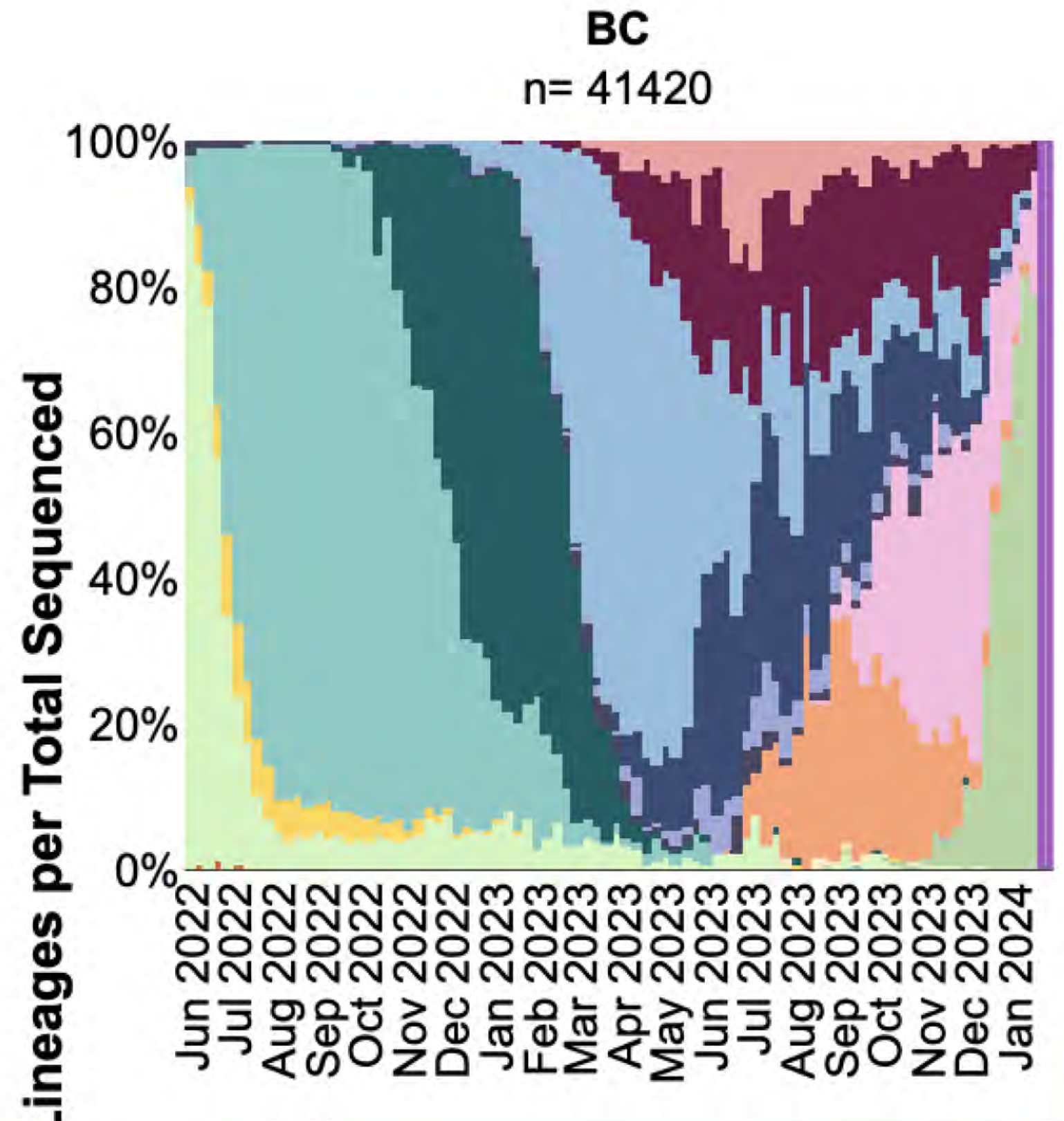
- 1 tech in 1 x 8 hr shift
 - 1 x 96 well plate --> 576 library prep
 - 600-800% improvement in throughput

BCCDC COVID-19 Genomics Surveillance



- COVID-19 genomics knowledge contributes to the understanding of the changing nature of circulating COVID-19 variants.
- Data system integration a legacy for BCCDC/PHSA/BC
 - BCCDC Public Health Lab (PHL)
 - BCCDC Data and Analytics Services (DAS)
 - Public Health Reporting Data Warehouse (PHRDW)
 - Data, Analytics, Evaluation and Reporting (DARE)
 - Public health Lab Operations Data ViEwer and Reporter (PLOVER)

https://bccdc.shinyapps.io/genomic_surveillance/



Genomics clusters – going beyond samples to provide insights into local outbreaks

Sobkowiak et al. BMC Genomics (2022) 23:710
https://doi.org/10.1186/s12864-022-06936-4

BMC Genomics

RESEARCH

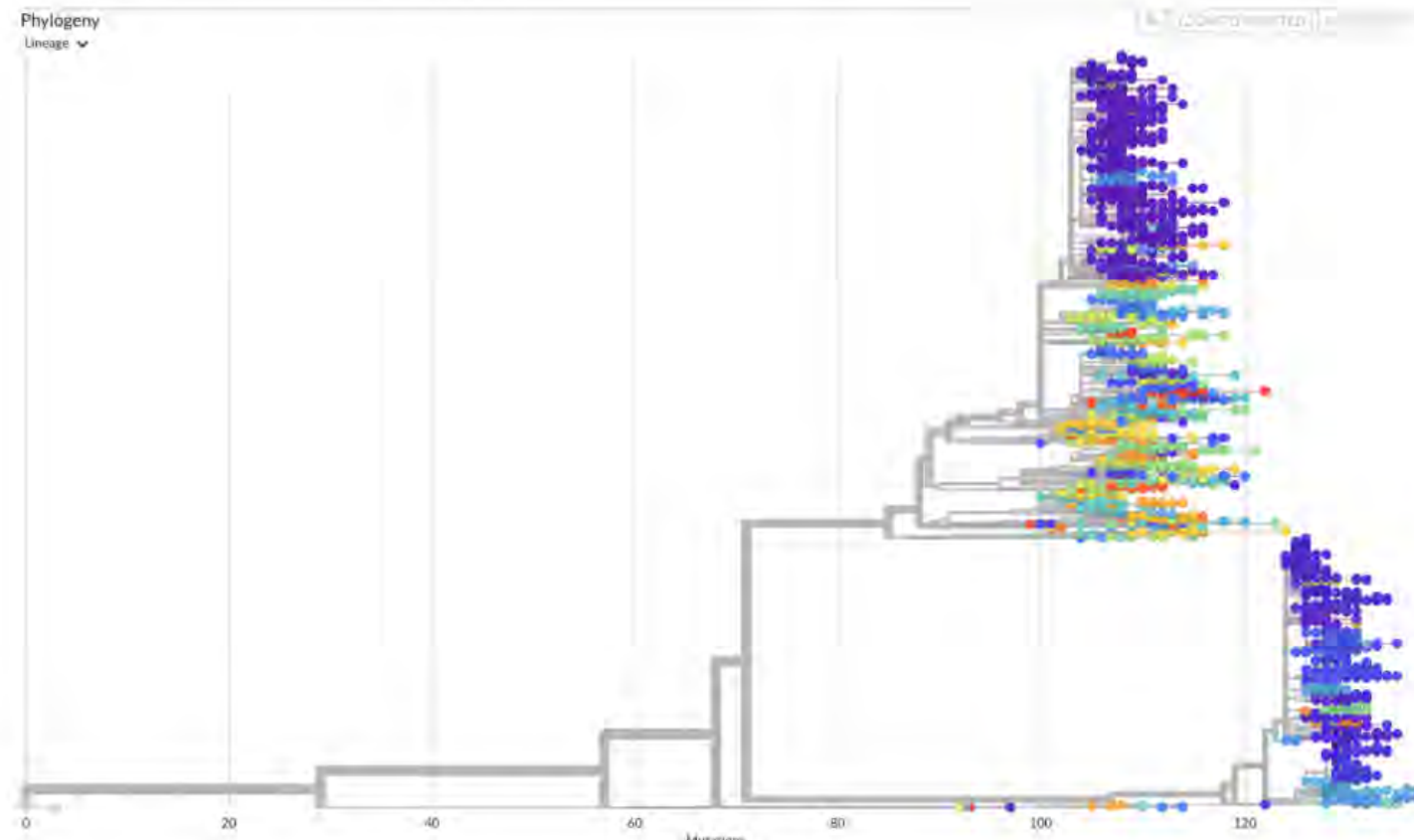
Open Access

Cov2clusters: genomic clustering of SARS-CoV-2 sequences

Benjamin Sobkowiak^{1*}, Kiria Kamiellari², James E. A. Zlosnik³, John Tyson⁴, Anders Gonçalves da Silva⁵, Linda M. N. Hoang^{2,3}, Natalie Prystajecky^{2,3} and Caroline Colijn⁷

Nextstrain build for SARS-CoV-2 - Displaying Illumina Run-1-2824_Tree (September-January)

Data updated 2024-01-29.
Showing 3484 of 3454 genomes sampled between Dec 2019 and Jan 2024.



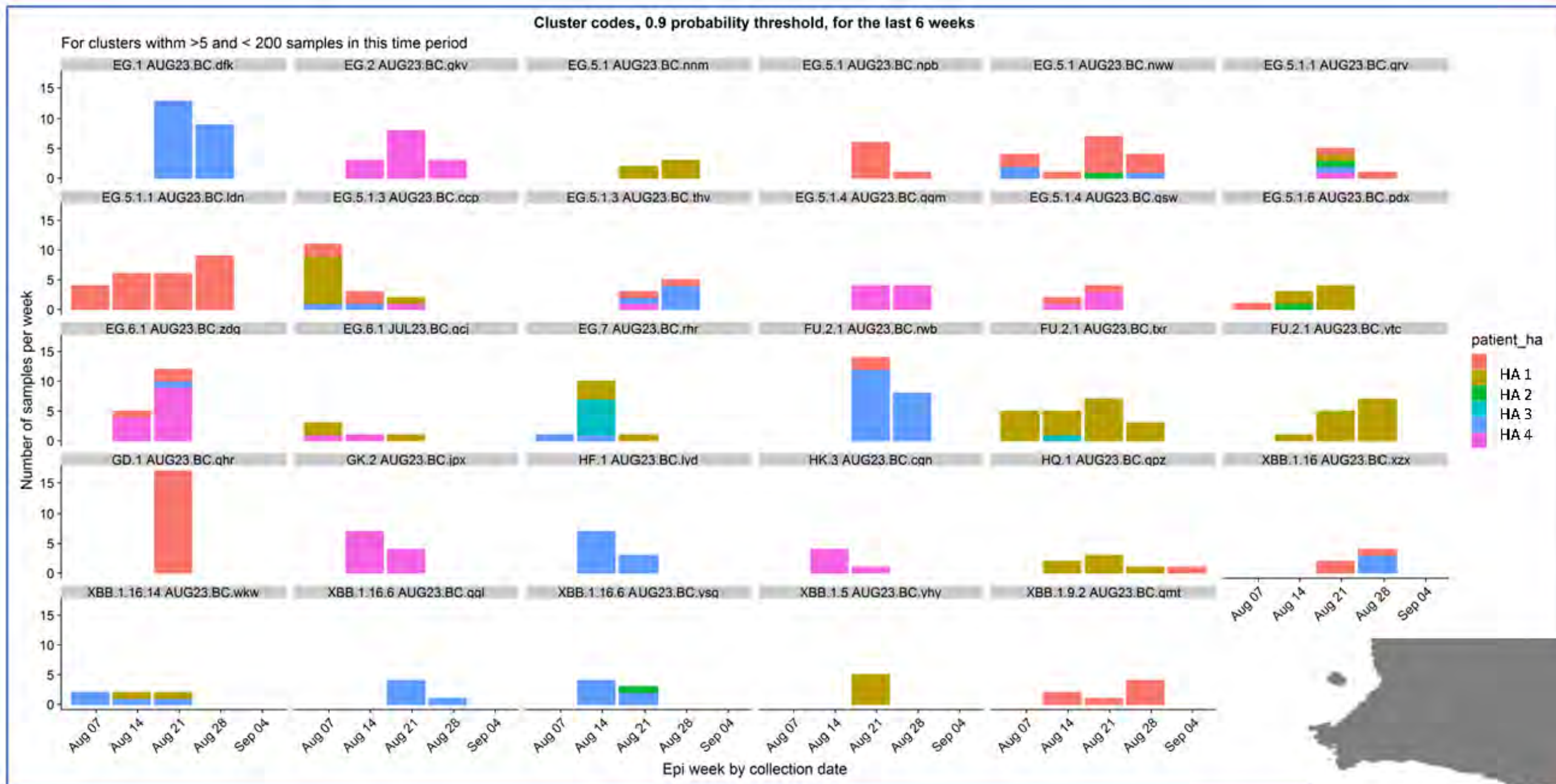
• Problem:

- We needed an automated way of detecting samples that cluster with each other on a phylogenetic tree.
- Tools existed that met academic needs (typically a single tree for publication)
- None suitable for public health needs because the cluster code changes as soon as new samples were added (new tree built).
- Additionally, phylogenetics is very challenging!

• Solution:

- Cov2Clusters tool built.
- We run on ever tree we build and has been stable for over 2 years.

Genomics clusters – going beyond samples to provide insights into local outbreaks



Samples assigned unique code

We can see geographic clustering around outbreaks

Useful to identify unknown outbreaks.



Lineage - Cluster(nxtstr 0.9)

EG.1 - AUG23.BC.dfk

EG.1.7 - JUL23.BC.zrb

FU.2.1 - AUG23.BC.rwb

XBB.1.5.44 - JUL23.BC.jfp

NA

Sobkowiak et al. BMC Genomics (2023) 24:710
<https://doi.org/10.1186/s12864-023-08930-4>

BMC Genomics

RESEARCH

Open Access

Cov2clusters: genomic clustering of SARS-CoV-2 sequences

Benjamin Sobkowiak^{1*}, Kimia Kamelian¹, James E. A. Dixon¹, John Tyson¹, Anders Gonçalves da Silva¹, Lorea M. W. Huang^{1†}, Natalie Prysanicay^{1†} and Caroline Collin¹

BCCDC PHL Surveillance Services for End-Users



Respiratory Surveillance
Genomic Surveillance

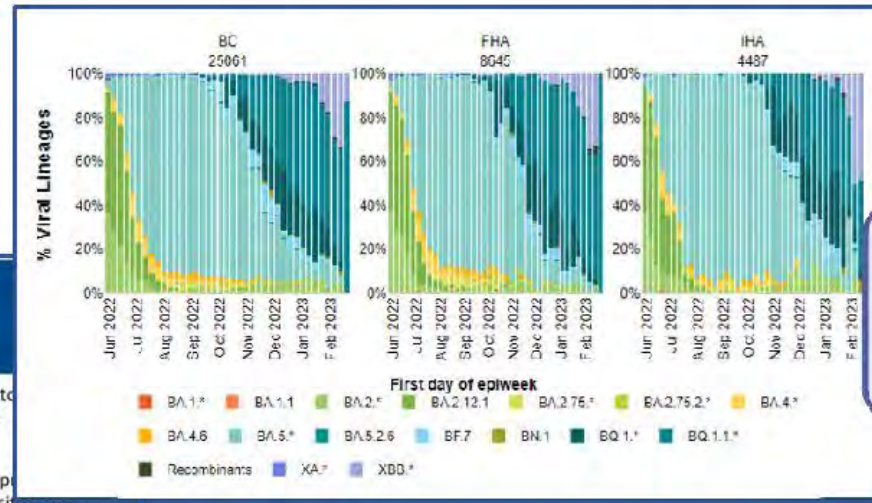
Whole genome sequencing (Illumina only) was performed on 185,737 specimens up to week 2 (January 08 - January 14) in BC. Figure 4 above illustrates BC's whole genome sequencing strategy of COVID cases.

The VOCs represent a cumulative 85.5% of all the variants that were detected in the province since the start of the pandemic (see [WGS frequency of lineages table](#) on BCCDC website). The Delta (n = 57,837) and Omicron (n = 73,915) variants account for largest proportion of the VOCs. Omicron includes B.1.1.529, the parent lineage, and BA sub-lineages (Figure 5 and appendix Table).

Figure 5. Distribution of Omicron**

Panel A: three most prevalent lineages cumulatively; Panel B: sublineages in the past 6 weeks

** These counts represent the total number of samples (not cases) sequenced.



Surveillance Reports

Cluster/Outbreak Reports

Public Health Laboratory
WGS Summary Report: [redacted] Mar 28, 2023

To: Dr. Smith, MD
From: BCCDC Public Health Laboratory
Test: COVID-19 Whole Genome Sequencing

Organization: SARS-CoV-2 (COVID-19) viral
Outbreak Name: Public Hospital Surgical Ward (Cluster 1-100)

Executive Summary

- Of those that have been sequenced (677), 4 cases generated high-quality data, 1 case generated partial data and 1 case failed.
- The majority of the cases in this cluster investigation belong to 1 distinct genetic clade within the SARS-CoV-2 lineage B.1.1.2.2.1.
- There is 1 case that appears to be an outlier. This case is different from the other cases identified in this outbreak and different from each other.
- The cases in this investigation are considered genetically related to cases identified in another outbreak in HA, as well as community cases in HA. Details of these cases can be found in the appendix.
- No variants of current concern detected in successfully sequenced samples.

Table 1. Summary of cases in the Public Hospital Surgical Ward Cluster investigation

Case	Reporting ID	Name	DOB	DOB (YYMMDD)	Collection Date (YYMMDD)	HA	Site (City/Region)	Case Source	Genetic Clade	Outbreak
1	PHL000001	John Doe	1980-01-01	2022-11-15	2022-11-15	HA	BC	Community	B.1.1.2.2.1	Cluster 1-100
2	PHL000002	Jane Smith	1985-03-03	2022-11-16	2022-11-16	HA	BC	Community	B.1.1.2.2.1	Cluster 1-100
3	PHL000003	John Doe	1980-01-01	2022-11-15	2022-11-15	HA	BC	Community	B.1.1.2.2.1	Cluster 1-100
4	PHL000004	Jane Smith	1985-03-03	2022-11-16	2022-11-16	HA	BC	Community	B.1.1.2.2.1	Cluster 1-100
5	PHL000005	John Doe	1980-01-01	2022-11-15	2022-11-15	HA	BC	Community	B.1.1.2.2.1	Cluster 1-100
6	PHL000006	Jane Smith	1985-03-03	2022-11-16	2022-11-16	HA	BC	Community	B.1.1.2.2.1	Cluster 1-100
7	PHL000007	John Doe	1980-01-01	2022-11-15	2022-11-15	HA	BC	Community	B.1.1.2.2.1	Cluster 1-100
8	PHL000008	Jane Smith	1985-03-03	2022-11-16	2022-11-16	HA	BC	Community	B.1.1.2.2.1	Cluster 1-100
9	PHL000009	John Doe	1980-01-01	2022-11-15	2022-11-15	HA	BC	Community	B.1.1.2.2.1	Cluster 1-100
10	PHL000010	Jane Smith	1985-03-03	2022-11-16	2022-11-16	HA	BC	Community	B.1.1.2.2.1	Cluster 1-100

The image alignment generated using the Phylogenetic Alignment of SARS-CoV-2 Outbreak Lineage (PAL) tool, a software for analyzing SARS-CoV-2 genomic sequences in global lineage reference. Version 1.0.0. A dynamic nomenclature protocol for SARS-CoV-2 to assist genomic epidemiology. Nature Microbiology 11:1407-1417. Images updated August 2022.

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Version 3

Public Health Laboratory
WGS Summary Report: [redacted] Mar 28, 2023

To: Dr. Smith, MD
From: BCCDC Public Health Laboratory
Test: COVID-19 Whole Genome Sequencing

Organization: SARS-CoV-2 (COVID-19) viral
Outbreak Name: Public Hospital Surgical Ward (Cluster 1-100)

Executive Summary

- This cluster name is generated chronologically by the BCCDC PHL, and reflects other laboratory genetically identified clusters of epidemiologically identified clusters. These cluster designations are subject to change following availability of information.
- A clade refers to a group of SARS-CoV-2 sequences that are genetically related by 2 mutations or less. Cases that belong to a clade during a Clade 1.1.2.2.1 are considered genetically related. Note: the clade designations (e.g. Clade 1.1.2.2.1) are arbitrary numbers assigned to different genetic clusters containing identical sequences. The clade names may change. We are in the process of formulating the nomenclature for SARS-CoV-2 genetic clades.
- **NAC names are based on the lineage and are as designated by the World Health Organization (<https://www.who.int/en/activities/tracking-SARS-CoV-2-variants/>).
- Sequence positions that differ by 0 mutations are "identical", 1 mutation are "single" and 2 mutations "double", as well as others. In cases that differ from all the other cases in this clade (e.g. differ by 13 mutations).

Figure 1. SARS-CoV-2 genetic diversity for a subset of samples sequenced by the BCCDC PHL. This tree is rooted to the original Wuhan reference strain (MN082047.3), and displays sequences based on the number of mutations that differ from this reference strain (green). Cases belonging to the Public Hospital Surgical Ward cluster investigation (Cluster 1-100) are clustered in purple and blue dots on the tree tips.

Please do not hesitate to contact us if you require any further clarification.

Li Huang
Debra Huang MSc, MD, DTMH, FRCPC

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Version 3



“Genome sequencing is a powerful tool in Canada’s public health response to COVID-19, allowing decision makers to respond rapidly to new outbreaks and variants of concern.”

CanCOGeN 



Sr. Stephen Lucas, Deputy Minister of Health Canada (April 2021)



COVID-19 Sequencing on Illumina (Aug 2020 – present)

Genomes passed QC: 205,586

Sequences in GISAID: 179,458

Outbreaks Investigated: ~1000

VOC Sequenced.



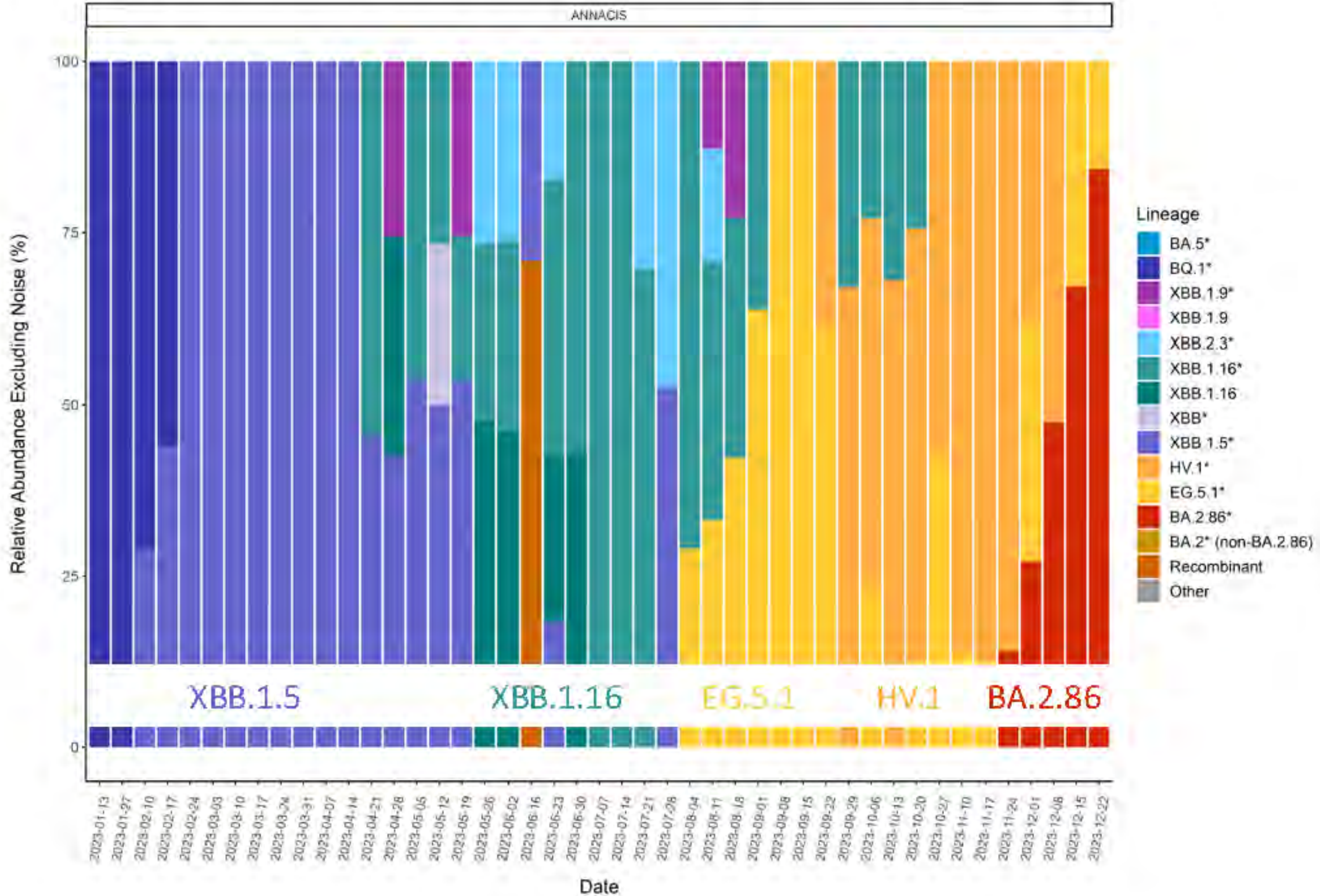
Alpha: 15,034

Gamma: 11,918

Delta: 58,557

Omicron: 93,928

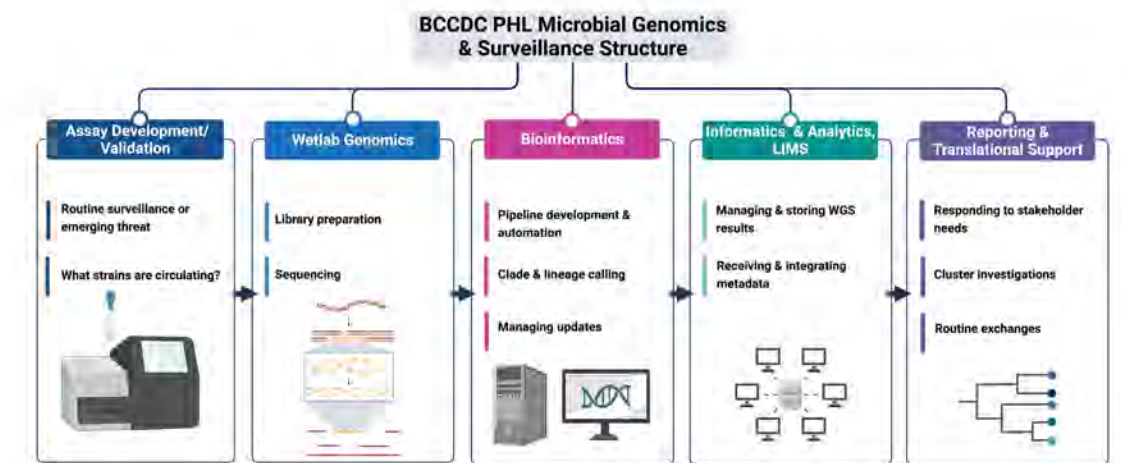
Transitioning COVID-19 Sequencing Know-How to Wastewater Sequencing of SARS-CoV-2



Other recent applications

Mpox: COVID genomics experience applied

- Developed detection assay
- Genomic mutational tracking for
 - epidemiological introductions,
 - outbreak investigations
 - monitoring for vaccine effectiveness drift



TB antibiotic resistance testing now routine

- Faster detection of resistance for early appropriate treatment (TB takes weeks/months to grow)
- Supports TB elimination goal

Current State of Genomics Capacity

	Pathogen	Wet Lab	Bioinformatics	Reporting/ Data Viz
RESPIRATORY	SARS-CoV-2	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>
	Human influenza A	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input type="checkbox"/>
	Human influenza B	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>
	RSV	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>
	TB	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input type="checkbox"/>
WASTEWATER	SARS-CoV-2	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>
AMR	CPO	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>
	<i>Shigella</i>	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>
	TB	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>
HCAI*	Various bacteria	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>
ENTERIC	<i>Salmonella</i>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>
	<i>E. coli</i>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>
	<i>Listeria</i>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>
STBBI	Hepatitis C	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>
	<i>N. gonorrhoeae</i>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>
	Syphilis	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>
EMERGING THREATS	Avian influenza	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input type="checkbox"/>
	Mpox	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input type="checkbox"/>
	<i>H. influenzae b</i>	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>
	Enteroviruses	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>
	Group A Strep	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>
PARASITES	<i>Leishmania</i>	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>
METAGENOMICS	Various bacteria	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>

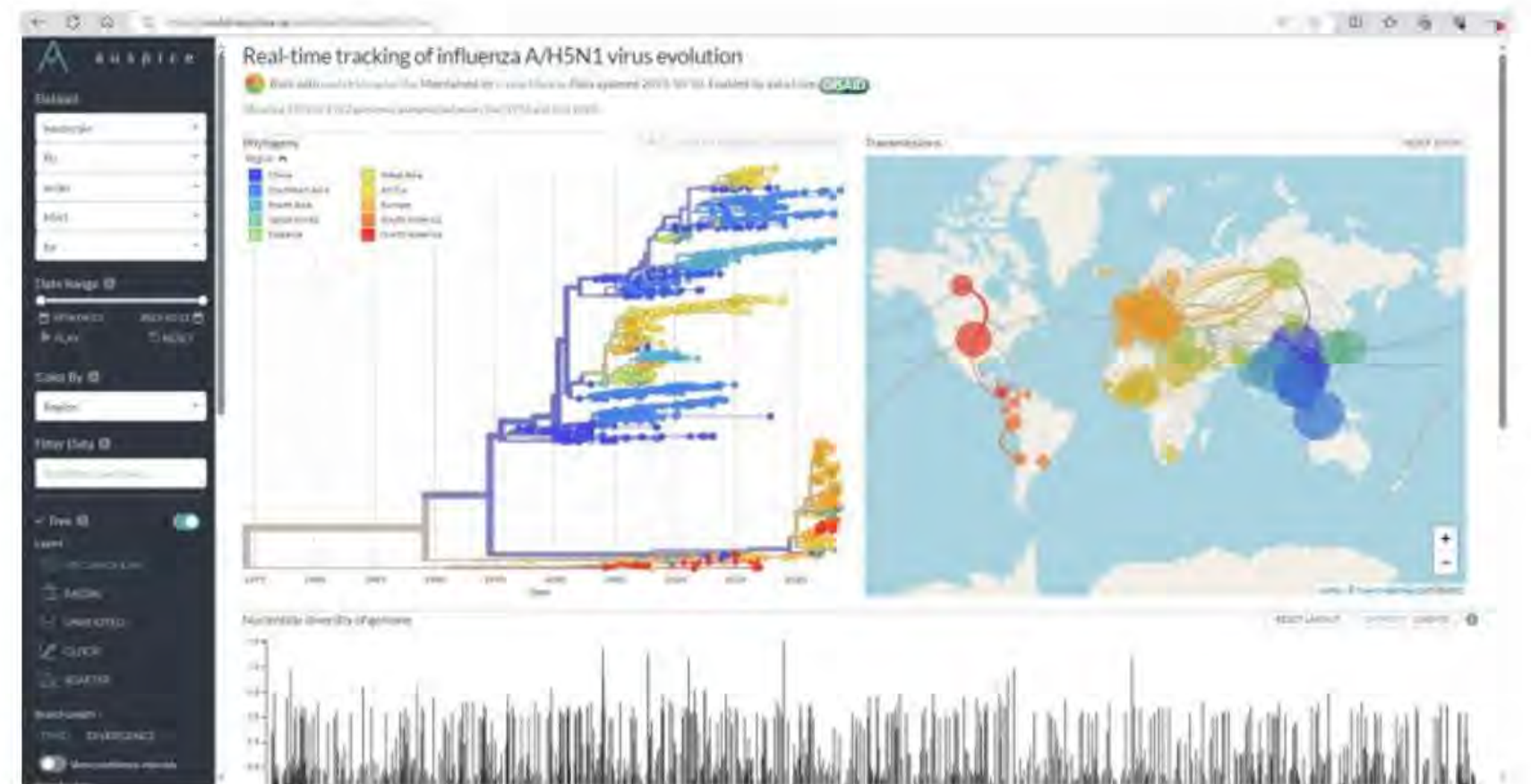
Operational
 In Development
 Prioritized

- Staff additions
- Senior scientists: support genomics
- Bioinformaticians: PHL + NML resources
- Technical staff (COVID Contingency funding)
- Capital additions: liquid handlers, 2 high-throughput sequencers
- 3-7 days to generate a WGS result - 1 week to generate an outbreak report
- ~4K samples per week during peak COVID activity

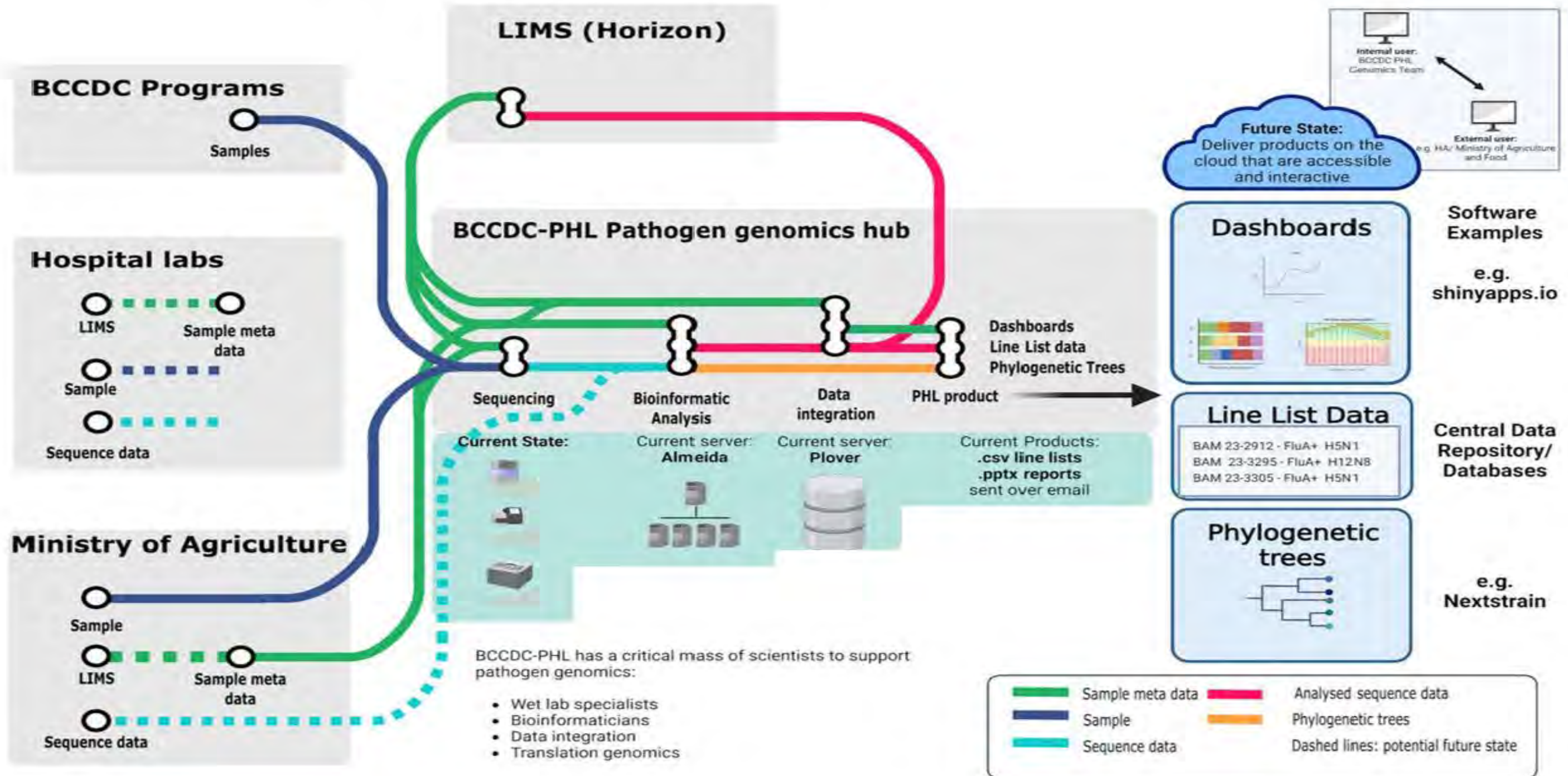
*Healthcare-associated infections (e.g. MRSA, *C. difficile*, *Pseudomonas*, *Serratia*)

One Health Proof-of-Concept

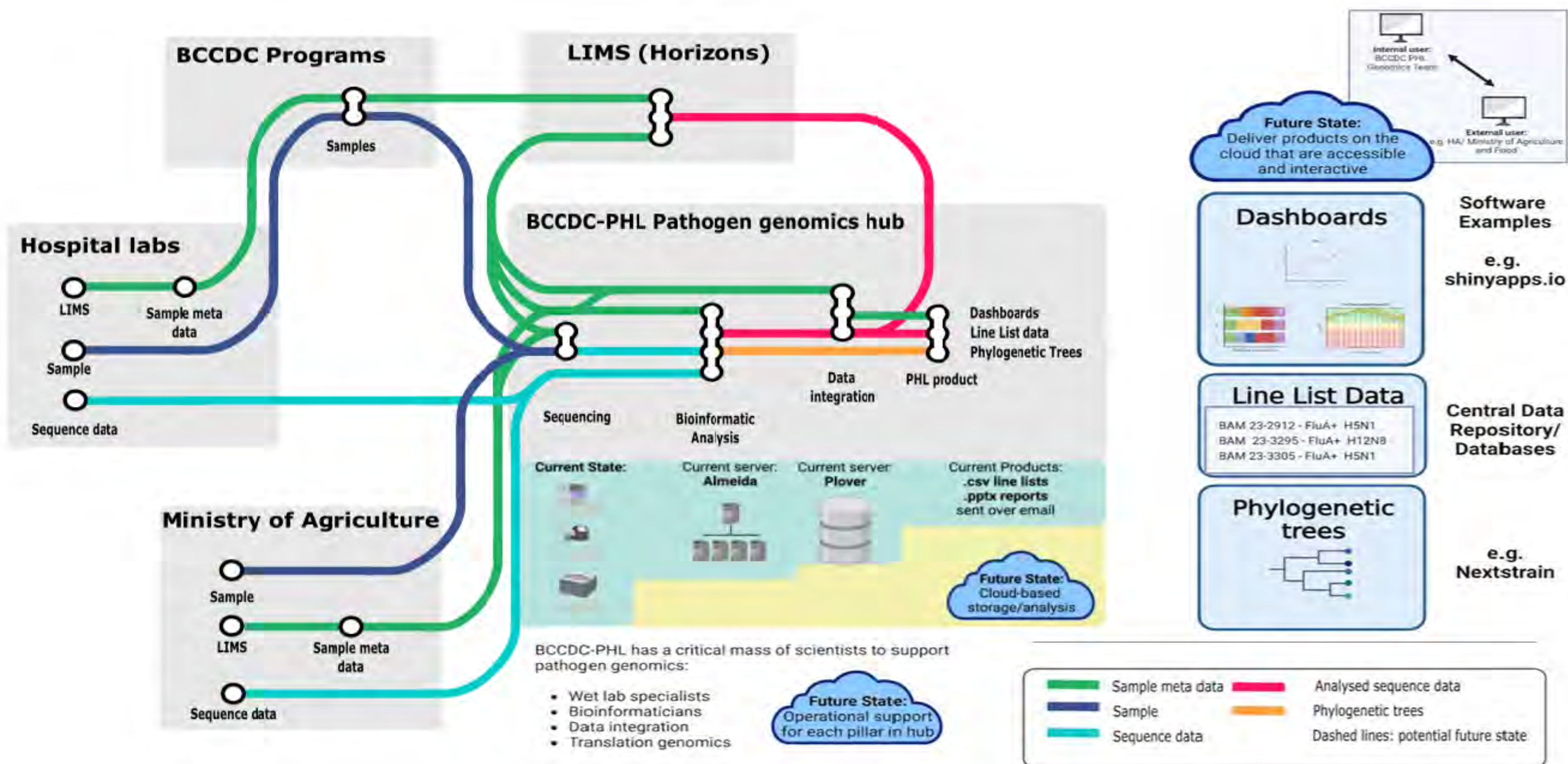
- BCCDC PHL sequencing highly pathogenic avian influenza for Animal Health Centre (Ministry of Agriculture and Forestry)
- Results are in PDF or in Powerpoint format, not user friendly
- > provide genomics dashboard, and software access to AHC via PHSA Cloud
- > automate reports and dashboards



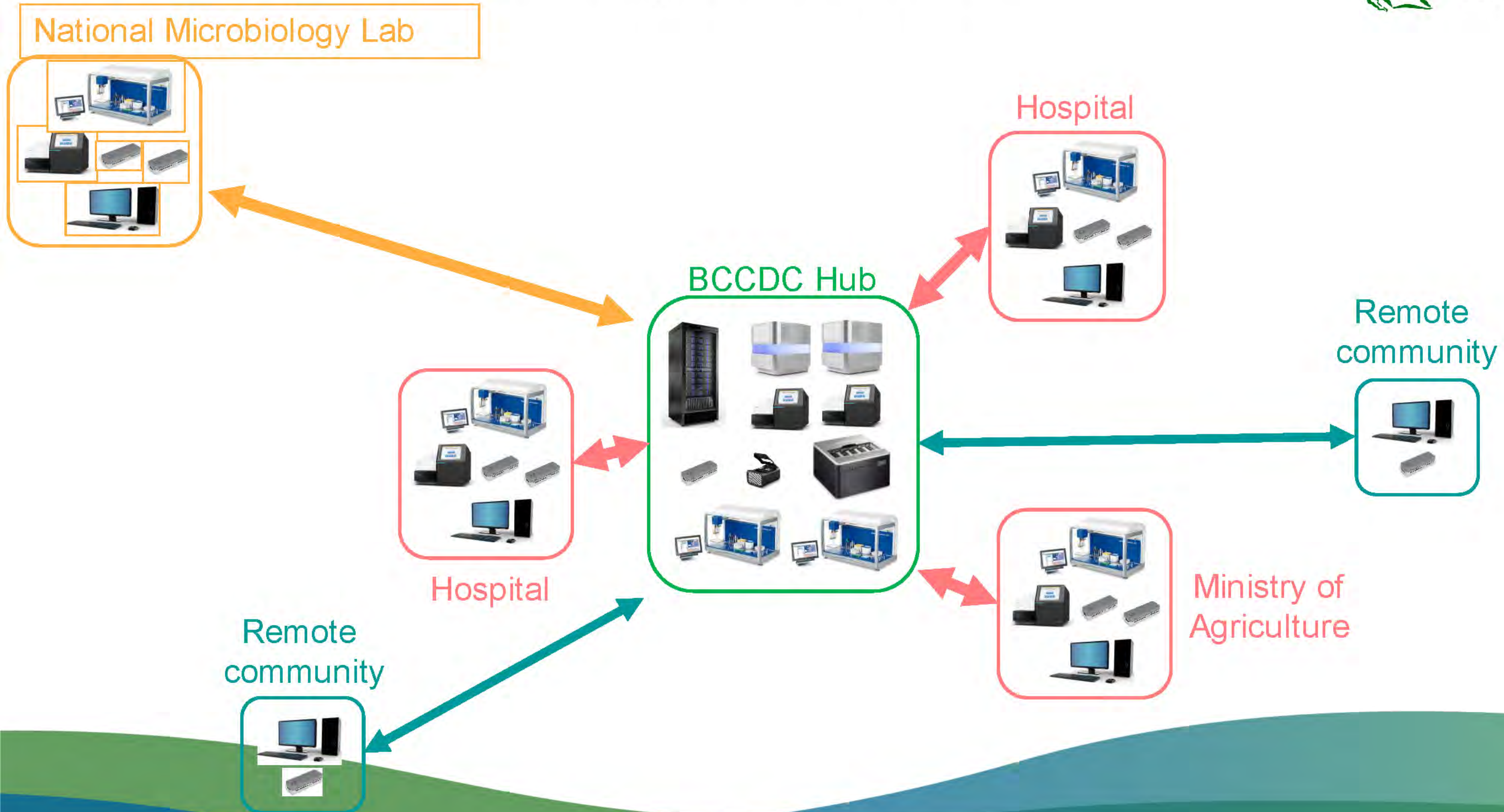
BCCDC PHL Pathogen Genomics Hub – Near Future



BCCDC PHL Pathogen Genomics Hub: Future State, an integrated pathogen genomics platform for BC

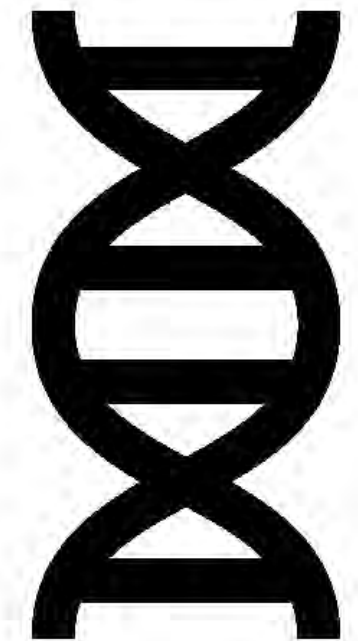


Genomics Hub and Spoke Model



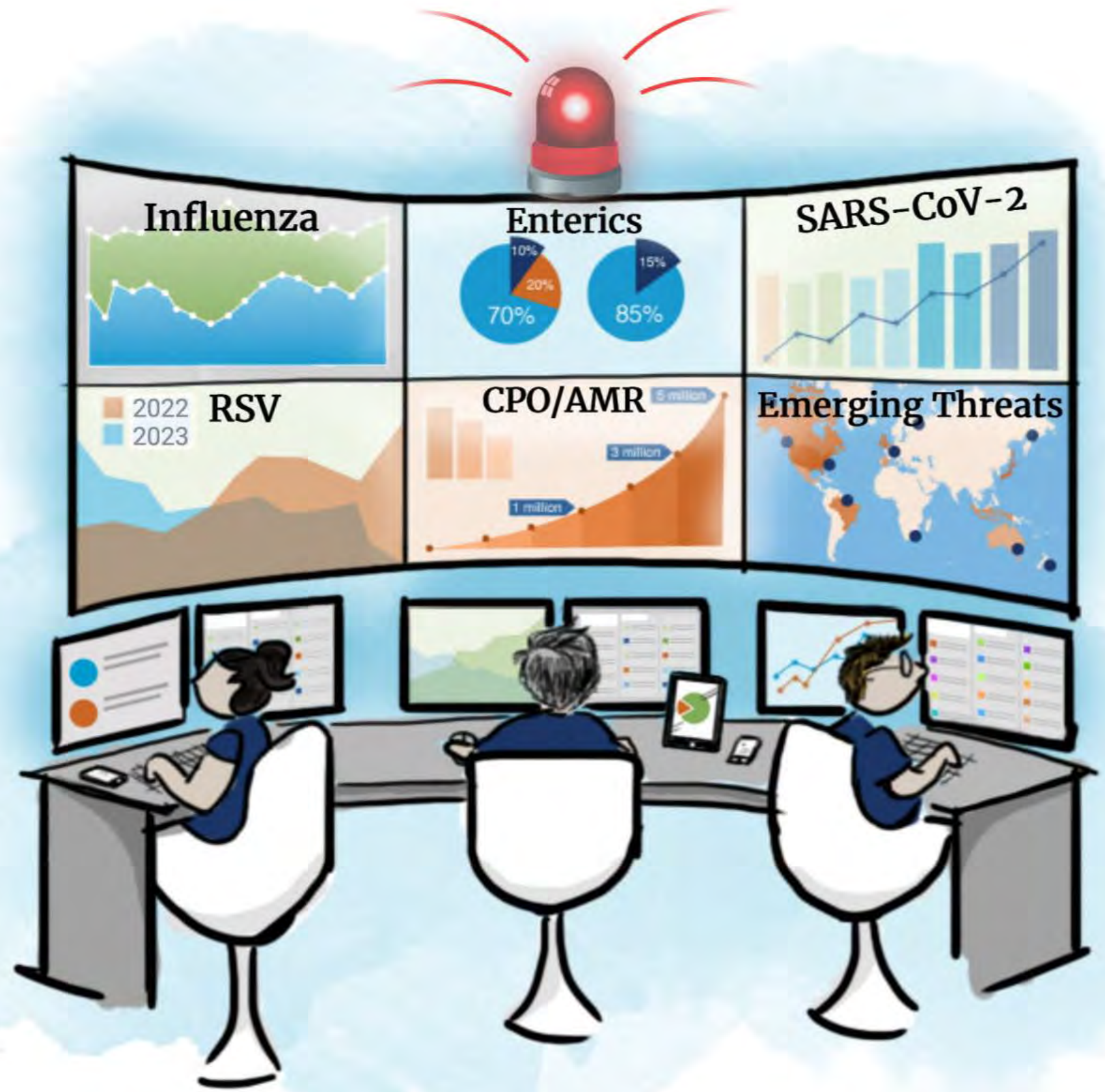
Role of Pathogen Genomics in BC

- Drive improvement in diagnostics, therapeutics and vaccines
- Inform clinical, public health, policy decision making
 - Based on provincial/national/international databases
 - Core "brain trust"
 - Innovation capacity
 - Response ready
- Build cost-effective, integrated capacity and services
- Equitable access to advanced genomics tools across RHAs
- Optimize connectivity
- One Health



The vision:

Provincial hub-spoke
microbial genomics
infrastructure and tools
to support patient care,
public health and One
Health



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- Dr. John Tyson (Wetlab)
- Dr. Shannon Russell (Translational Genomics)
- Dr. Chris Fjell (Data Informatics)

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- Jessica Caleta
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- Adriana CarbreraDelgado
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- Mycobacteriology
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- Informatics
 - Kelvin Lam, King Choi, Harris Kim, Omid Ghahramani
 - Kevin Yang (NML LLTO)
- Outbreak coordinator
 - Yin Chang

BCCDC Data and Analytics Services

- Dr. Hind Sbihi
- Yayuk Joffres
- And team!!!!

AND SO MANY OTHERS!!!



DARE/PANDA

THANK YOU!



Discussion Period

Any questions?

Please use the **Q&A tab** to submit your questions for our speaker. You can “**like**” other people’s questions to push them up in priority.



Closing Remarks



Thank You!

Join us on Tuesday, June 25, 2024 (1:00-2:00pm ET) for the next seminar!

Please complete our **survey** that will be shared shortly after the seminar. Scan the QR code.

Seminar recording and presentation slides will be posted on <https://nccid.ca/> within two weeks.

Visit <https://nccid.ca/surveillance-advances-seminar-series/> for more information about the Surveillance Advances seminar series.

