December 2025

PROVINCIAL LABORATORY MEDICINE SERVICES
Provincial Health Services Authority
BCCDC Public Health Lab

LABORATORY TRENDS

BC Centre for Disease Control
Provincial Health Services Authority

A Report from the BCCDC Public Health Laboratory

Photo courtesy of Michael Donoghue

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Staffing Highlights

Dr. Agatha Jassem—UBC Faculty of Medicine, Clinical Faculty Award for Excellence in Research

The University of British Columbia Faculty of Medicine recently awarded Dr. Agatha Jassem with the 2025 Early Career Clinical Faculty Award for Excellence in Research. This award recognizes faculty members who are working to transform health for everyone through their research.

Dr. Jassem is a leader and collaborator on numerous research endeavors, including seroprevalence studies for mpox in Vancouver[1], the development of whole genome sequencing testing for respiratory virus genomic surveillance in Canada[2], and the design of novel diagnostic tests for emerging viral pathogens such as mpox[3] and avian influenza (H5N1).

Congratulations to Dr. Jassem in receiving this notable distinction.

(1) Unpublished. Márquez C, Cortez G, Enriquez I, Luk D, Valabeigy T, Tan D, Singal M, Jassem A. Estimating mpox seroprevalence in Vancouver metropolitan area. 2025 May 3. https://www.bccdc.ca/Health-Professionals-Site/Documents/May%202025%20Laboratory%20Trends.pdf

(2) Gao R, Buchanan C, Dust K, Van Caeseele P, Wong H, Sjaarda C, Sheth PM, Jassem AN, Minion J, Bastien N. Whole genome sequencing and phylogenetic classification accelerate the implementation of respiratory syncytial virus genomic surveillance in Canada: a pilot study. Microbiol Spectr. 2025 Sep 3:e0314224. doi: 10.1128/spectrum.03142-24. Epub ahead of print. PMID: 40899818.

(3) Jassem AN, Roberts A, Tyson J, Zlosnik JEA, Russell SL, Caleta JM, Eckbo EJ, Gao R, Chestley T, Grant J, Uyeki TM, Prystajecky NA, Himsworth CG, MacBain E, Ranadheera C, Li L, Hoang LMN, Bastien N, Goldfarb DM. Critical Illness in an Adolescent with Influenza A(H5N1) Virus Infection. N Engl J Med. 2025 Feb 27;392(9):927-929. doi: 10.1056/NEJMc2415890. Epub 2024 Dec 31. PMID: 39740022.

Dr. Muhammad Morshed—Inducted as a Fellow of the World Academy of Sciences (TWAS)

This fall, during the World of Academy Sciences (TWAS) 17th annual General Conference in Rio de Janeiro, Brazil, Dr. Muhammad Morshed, clinical microbiologist and program head of the Zoonotic and Emerging Pathogens laboratory at the BC Centre for Disease Control and Clinical Professor at UBC in the Department of Pathology & Laboratory Medicine, was inducted as a fellow of TWAS in the field of Medical Sciences.

Dr. Morshed was recognized for his countless contributions to advancing science that serves humanity. Please join us in celebrating Dr. Morshed on this outstanding recognition.

Chikungunya Virus Testing Now Performed at the BCCDC PHL

What is chikungunya virus?

Chikungunya virus (CHIKV) was first detected in 1952-1953 in Tanzania and is the pathogenic agent of chikungunya fever. CHIKV is characterized as an enveloped single-stranded RNA virus of the alphavirus genus from the Togaviridae family. It is classified as an arbovirus with its main vectors being the *Aedes aegypti* and *Ades albopictus* mosquitoes. Although these mosquito species are not present in BC, they are widespread in the Americas including the Southern US and are described as "aggressive daytime biters" with peak biting activity at dawn and dusk. The main symptoms of CHIKV infection are severe joint and muscle pain as well as headache, high fever, dermatitis, lymphadenopathy, maculopapular rash, nausea, and conjunctivitis[1].

How is chikungunya virus testing performed?

Similar to other viruses, laboratory testing can either look for the viral RNA of CHIKV in a patient sample or use serological methods to detect antibodies against CHIKV in a patient's blood. While viral RNA testing is typically used during the viremic phase, between the 5th and 10th day of symptom onset, serological testing can be used to detect CHIKV specific IgM/IgG antibodies in the viremic phase as well as up to 3 to 8 months after symptom onset, and in some cases up to one year. Currently, only serological testing results are used in the laboratory criteria for diagnosing CHIKV infections[2].

Previously, the National Microbiology Laboratory (NML) performed all chikungunya testing on behalf of British Columbia. However, the BCCDC Public Health Laboratory recently completed its evaluation of a commercial chikungunya virus testing kit (EUROIMMUN Anti-Chikungunya Virus ELISA IgG/M) that will enable chikungunya virus testing to be performed in-house. This commercial kit is the same product that is used by the NML which will minimize any continuity issues when comparing to previously assessed patient serological profiles. BCCDC Public Health Laboratory (PHL) began in-house chikungunya virus testing on September 15th, 2025.

(1) https://www.cdc.gov/chikungunya/site.html#hcp

(2) https://ndc.services.cdc.gov/case-definitions/arboviral-diseases-neuroinvasive-and-non-neuroinvasive-2015/

Developing a Molecular Method to Detect California Serogroup Viruses in Mosquitoes from British Columbia*

California Serogroup virus belongs to the Orthobunyavirus genus of viruses. This serogroup is a part of several viruses, however, Snowshoe Hare Virus (SSHV), Jamestown Canyon Virus (JCV) , and La Cross Virus (LCV) prevalent throughout North America. In the summer of 2024, a cluster of three pediatric encephalitis cases was identified in the Whistler area. All cases tested positive for mosquito-borne viruses belonging to the California serogroup, specifically JCV and SSHV, prompting the implementation of molecular surveillance of mosquito populations in the surrounding area.

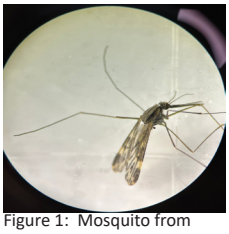

Figure 1: Mosquito from local trapping, shown under a microscope.

Sample collection and pathogen testing

Mosquito trapping was conducted during the summer of 2025 at multiple locations in Squamish, Whistler, and Pemberton. Traps were collected weekly and transported to the Matthews Lab at the University of British Columbia for species identification. Following identification, individual mosquitoes were pooled according to collection date, trapping location, and species. Pooled samples were then transported to the Parasitology and Zoonotic and Emerging Pathogens laboratories at the BCCDC PHL for detection of California serogroup viruses. Nucleic acid extractions were performed using automated KingFisher protocols, and molecular detection assays were adapted and modified from NML protocols.

Results

Over 2,500 mosquitoes representing 30 species were collected and grouped into 180 mosquito pools. These mosquito pools will first be screened using a PCR for California Serogroup Viruses. Any positive sample pools will then be further characterized and tested using Sanger sequencing and next-generation sequencing. Testing is ongoing.

A team effort

This project was completed through the collaboration of multiple teams, including the Virology, Parasitology, Zoonotic and Emerging Pathogens programs at the BCCDC PHL, the BCCDC Public Health Response team, the Matthews and King laboratories at the University of British Columbia, Vancouver Coastal Health, and the Lil'wat and Squamish First Nations.

*Prepared by Kenning Tran

Driving Innovation in Tuberculosis Diagnostics*

The start of innovation

Until 2017, the Tuberculosis (TB)/Mycobacteriology laboratory at the BCCDC PHL used traditional methods, such as culturing and phenotypic susceptibility testing, to identify and recommend treatment options for individuals infected with *Mycobacterium tuberculosis* and other non-tuberculosis mycobacteria. Then, in 2018, the TB/Mycobacteriology laboratory, lead by Dr. Inna Sekirov, began establishing a whole genome sequencing (WGS) program which placed them at the global forefront of TB diagnostic testing. The development of a WGS program began with a retrospective study of samples that allowed for the sequencing methodology and analysis pipeline to be created and tested without halting ongoing testing.

The retrospective work was carried out between 2019 and 2022 and successfully demonstrated the utility and performance of WGS in a clinical setting. As a result, in July 2023, the TB/Mycobacteriology laboratory at the BCCDC PHL became the first provincial laboratory in Canada to report TB results using WGS. However, the laboratory did not stop there—they continued to enhance the diagnostic capacity of the WGS program for TB.

Continued improvements

In January 2025, the TB/Mycobacteriology laboratory successfully transitioned to performing WGS routinely on liquid cultures (BD MGIT tubes) for *Mycobacterium tuberculosis* isolates. Previously, WGS was performed on isolates from the traditional Lowenstein-Jensen sub-culturing method which could take weeks for the *Mycobacterium tuberculosis* isolates to grow. This transition in methodology significantly reduced costs and turnaround times for genotypic speciation, cluster grouping, and predictive antimicrobial resistance profiling —enabling more timely and precise treatment guidance, which helps minimize patient harms. Even after this huge achievement, the TB/Mycobacteriology laboratory still saw opportunities to further to improve TB diagnostic testing through WGS.

The next achievement

On January 5, 2026, the TB/Mycobacteriology laboratory will reach another significant milestone by eliminating *Mycobacterium tuberculosis* phenotypic antimicrobial susceptibility testing for isolates that are determined, by WGS, to lack known genes or markers associated with resistance to a wide range of antibiotics (pan-sensitive). This change in testing is supported by extensive data and will allow the TB/Mycobacteriology laboratory to reduce the number of phenotypic antimicrobial susceptibility testing by approximately 75%, which will reduce costs, shorten turnaround times, and improve efficiency while maintaining confidence in resistance prediction.

The success of the WGS program at the TB/Mycobacteriology laboratory is the result of a large team of individuals who have and continue to contribute to its success. This team includes the laboratory personnel who work with isolates, genomic scientists who have built and optimized the analysis pipelines, the Plover team who supports knowledge dissemination, the operations and quality teams who ensure the excellence and sustainability of the program, and medical leadership who have ensured the program has maximum clinical impact.

*Prepared by Trevor Hird, TB/Mycobacteriology PHL

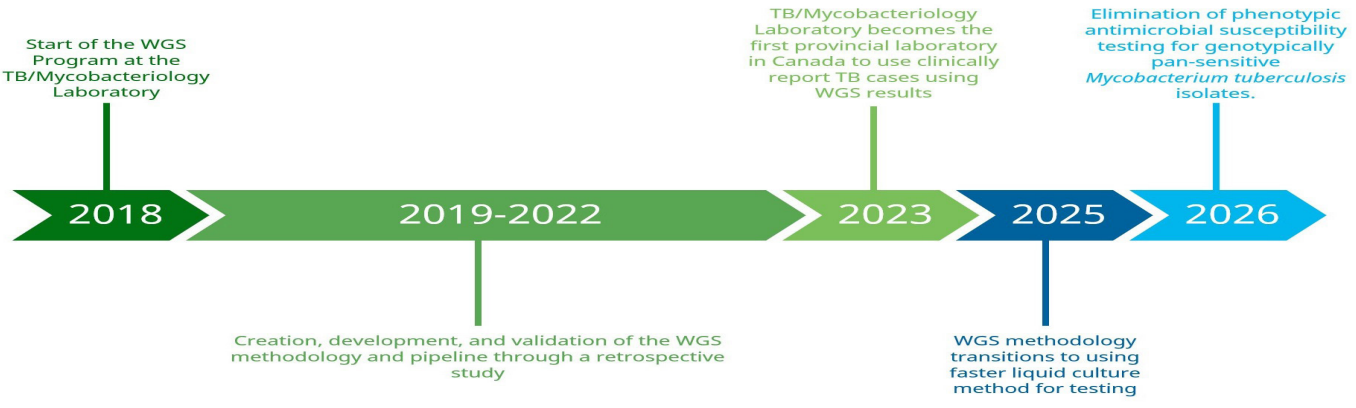

Figure 2: Timeline of major milestones for the whole genome sequencing program at the TB/Mycobacteriology laboratory.

Collaboration at the Core of Foodborne Illness Outbreak Investigations

In 2025 alone, the Bacteriology and Mycology and Environmental Microbiology laboratories at the BCCDC PHL have assisted in five major foodborne illness investigations that have led to multiple food product recalls – which protects others from infection. Identifying and investigating these foodborne illness outbreaks requires tremendous collaboration at the local, provincial, and national level between the public, the laboratories, epidemiologists, health authorities, PulseNet Canada, and the Canadian Food Inspection Agency (CFIA).

Launching an investigation

The first step in a foodborne illness outbreak investigation, is for members of the public to seek health care when experiencing foodborne illness symptoms and to submit samples for testing. Then, frontline laboratories will screen patient samples for numerous pathogens. If a patient sample is positive, it will be sent to reference laboratories, such as the BCCDC PHL, where additional testing will be performed. The additional testing determines whether the positive sample is related to other recently positive samples. Not all positive samples prompt a public health investigation, but if two or more samples are determined to be related or if there is an increase in testing positivity, the labs collaborate with epidemiologists, health authorities, PulseNet Canada, and the CFIA to launch a foodborne illness outbreak investigation.

Gathering the evidence

To begin the foodborne illness outbreak investigation, food(s) of interest are identified by engaging with affected members of the public through interviews and reviews of their recent food purchases. Then, the multidisciplinary group involved in flagging a potential foodborne illness outbreak meet to review the findings and build a hypothesis of potential foods that may be involved in the outbreak. These foods are then collected and sent to the BCCDC PHL and the CFIA for testing.

The testing of food for foodborne pathogens requires innovative methodology that is based on years of expertise at the testing laboratories. If the laboratory is successful in identifying and isolating a foodborne pathogen from a food sample, then the next step is to demonstrate whether this pathogen is related to the human cases in the investigation.

WGS and other advanced molecular techniques are performed by the BCCDC PHL to further characterize the pathogen found in both the patient sample and the food. While both samples may contain *E. coli* O1:57, it is possible that the *E. coli* O1:57 found in the food is genetically different than the *E. coli* O1:57 in the patient's sample, which means that it is unlikely that the food sample was the source of the foodborne illness. Figure 3 is an example from a foodborne illness investigation of how WGS data can be visualized, as a genomic tree, to understand the genomic similarity between pathogens sequenced from both human and food sources. The numbers shown on Figure 3 indicate the approximate number of genetic differences between isolates and the branches of the tree show how the isolates cluster together based on their genetic similarity. This figure demonstrates that the pathogen isolated from the cheese sample is very similar, genetically, to human isolates 5, 6, and 7 and may also be closely related to human isolates 1-4. Thus, WGS and advanced analyses can characterize pathogens to narrow food source(s) of interest in the investigation, demonstrate the relatedness of pathogens isolated from suspect food to human cases, and even identify additional cases related to the outbreak.

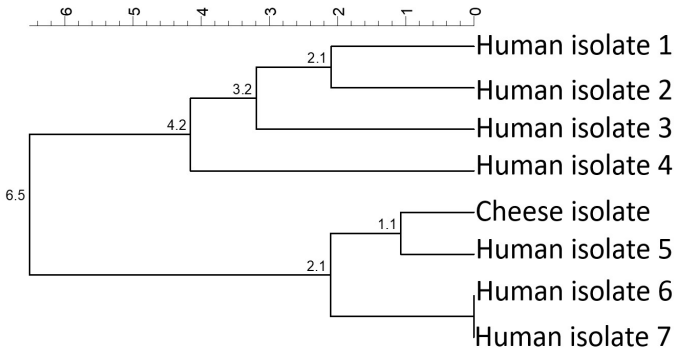

Figure 3: A genomic tree displaying the number of genetic differences and relatedness of pathogens isolated from humans and food sources in a foodborne illness invetigation which is based on whole genome sequencing data and analysis.

Putting it together

All the information collected by health authorities, epidemiologists, and laboratories during a foodborne illness investigation is shared at the local, provincial, and national level through extensive datasharing networks and infrastructure supported by the laboratories, PulseNet Canada, and the CFIA. This collaborative data-sharing infrastructure is essential for integrating the information needed to guide decisions on whether a food recall is issued.

Ultimately, food recalls and the associated foodborne illness investigations are never the work of a single expert or even institution, but the result of many teams working together towards the common goal of keeping our food and communities healthy.

For more information on current food recalls in Canda, visit the Government of Canada's website on Safety recalls and notices (https://recalls-rappels.canada.ca/en).

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The Public Health Laboratory at the BC Centre for Disease Control (BCCDC) provides consultative, interpretative testing and analyses for clinical and environmental infectious diseases in partnership with other microbiology laboratories and public health workers across the province and nationally. The BCCDC PHL is the provincial communicable disease detection, fingerprinting, and molecular epidemiology centre providing advanced and specialized services along with international defined laboratory core functions. The Provincial Toxicology Centre conducts toxicology testing and analysis for clinical patients, including therapeutic drug monitoring, drug screening tests, and forensic toxicology analyses for the BC Coroners Service.

This report may be freely distributed to your colleagues. If you would like more specific information or would like to include any figures for other reporting purposes, please contact us.

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