LABORATORY TRENDS

A Report from the BCCDC Public Health Laboratory

Inside this Issue

LABORATORY NEWS 2
Welcome new staff
Stat malaria testing changes

SPOTLIGHT 3
Wastewater testing and surveillance

SURVEILLANCE 4
Invasive Group A Streptococcus
Norovirus

OUTBREAKS 7
GI outbreaks and norovirus sequencing

Issues: www.bccdc.ca/publichealthlab
Welcome to new staff

Dr. Jonathan Gubbay is a Medical Microbiologist, currently at BC Children’s and Women’s Hospitals. Prior to that he oversaw the virus detection, arboviruses and respiratory bacteriology laboratories at the Public Health Ontario laboratory and had a pediatric infectious diseases practice with the Hospital for Sick Children. Dr. Gubbay will be working with our Virology laboratory on a part-time basis (on Fridays), focusing on select projects on different aspects of laboratory emergency preparedness and of public health importance.

We also welcome Carissa Juson who joined the Pre-Analytical/Call Centre as Team Lead in March. Carissa graduated from BCIT in 2007 and then started as a Medical Laboratory Technologist at Surrey Memorial Hospital. Since then she has worked at multiple sites within Fraser Health in different capacities including as an LIS Analyst and most recently, the interim Pre & Post Analytic Team Lead at Burnaby Hospital. Through her years of experience she became the subject matter expert for various testing platforms and was instrumental in setting up the Seegene platform at Surrey Memorial Hospital in response to COVID.

Finally, Dr. Adriana Airo is our new Locum Clinical Microbiologist. She is a Fellow of the Canadian College of Microbiologists who completed her post-graduate training at the University of Toronto. Prior to that, Dr. Airo completed her doctoral studies in virology in the Department of Medical Microbiology & Immunology at the

STAT malaria testing changes

We recently changed our STAT (urgent) malaria testing protocol at the BCCDC Public Health Laboratory (PHL). After gathering information on the current status of malaria testing in BC, we recognized that the availability of malaria diagnostics has expanded significantly across the province in recent years. Current malaria testing protocols across all BC Health Authorities and Yukon include microscopy and/or rapid diagnostic testing (RDT) before sending to BCCDC PHL. In addition, most Health Authorities also screen with loop-mediated isothermal amplification (LAMP) and perform microscopy and/or RDT on positive samples prior to submitting to BCCDC PHL.

The BCCDC PHL previously provided off-hour STAT malaria testing for all malaria requests via an on-call technologist. However, given the wider availability of malaria testing highlighted above, the BCCDC PHL has now changed its reference laboratory malaria diagnostic strategy as follows:

• Off-hour malaria STAT testing will only be performed when requested by a BCCDC Medical Microbiologist. As such if STAT malaria testing is required, please consult the BCCDC Medical Microbiologist on-call at 604-661-7033.
• Providers need to consider that routine testing will be performed on weekdays 8:00AM-4:30PM. Any testing outside of these hours including weekends and holidays will require BCCDC Medical Microbiologist approval as above.
• Off-hour malaria STAT testing will include rapid diagnostic test, microscopy +/- parasitemia. If the parasitemia has already been performed and reported at the referring hospital, it will not be performed as part of the BCCDC PHL STAT testing.

In the future, the BCCDC PHL also plans to incorporate malaria qPCR for species confirmation as part of the STAT testing offer when needed. We will send a separate update when this is available. For the time being, the BCCDC PHL malaria qPCR is routinely performed twice a week, and testing can be expedited on request. Please share this with your interested colleagues.
Wastewater testing and surveillance program

As part of the pan-Canadian wastewater surveillance network the BCCDC Public Health Laboratory (PHL) partners with Metro Vancouver and other regional treatment plants for this community-level surveillance program. Wastewater samples are collected 2-3 times a week from 12 sites across the province and transported for SARS-CoV-2 testing by the Environmental Microbiology Laboratory of the BCCDC PHL. Wastewater samples are concentrated by ultracentrifugal filtration, nucleic acids extracted and SARS-CoV-2 envelope gene (E gene) is detected by real-time quantitative polymerase chain reaction (RT-qPCR). To account for changes in wastewater contributions, data are normalized by the daily flow rate from the treatment plant before a daily viral load estimate is generated. Environmental Health Services and Data Analytics Services programs at the BCCDC also contribute to this program by supporting analytics and maintaining the BCCDC Wastewater Surveillance Dashboard. Efforts are also made to integrate the signals provided by the wastewater data with the clinical testing and hospitalization data to inform temporal models between the two datasets.

Wastewater monitoring can provide an early warning if COVID-19 is increasing in a community. This is particularly important given the reduction in testing when the focus is more on acute or clinical cases or in regions with greater test availability. Beyond molecular detection and quantification the BCCDC PHL is also able to apply sequencing technologies to inform SARS-CoV-2 variant tracking, with the wastewater samples showing concordance with the clinical data. As wastewater can contain a multitude of other organisms this provides an opportunity to also detect and monitor other pathogens such as influenza and respiratory syncytial virus. Underlying this new direction are the efforts made by the Molecular Microbiology & Genomics program of the BCCDC PHL to develop and validate new assays with the complex matrix that is wastewater.

The wastewater surveillance program will continue to expand into other regions for increased coverage of the province. The program also informs the national picture by reporting regularly to the Public Health Agency of Canada where the data are consolidated into a national dashboard.

Figure 1. Viral Load Summary from the Wastewater Surveillance Dashboard.
Invasive Group A Streptococcus

Between 2017-2023 (to date) there have been 2302 isolates from 2187 cases confirmed positive for *Streptococcus pyogenes* (Group A Streptococcus) and submitted for serotyping. Submissions in the years of 2017-2019 were consistent until 2020 when they plummeted to a third of the previous years’ submissions (Figure 2). In 2021, the number of cases of Group A *Streptococcus* increased to nearing pre-pandemic levels again while in 2022 the number surpassed these previous volumes. Cases this year will likely be comparable or surpass the numbers seen in previous years.

Molecular characterization of *S. pyogenes* is through *emm* typing of the M protein virulence factor and is performed by the the National Microbiology Laboratory. There are over 250 *emm* types classified by genetic sequencing. From 2017-2019, *emm*1 (9%-20% of all cases yearly; avg. 15%) followed by *emm*76 (8%-18% of all cases yearly; avg. 13%) were the most frequently seen subtypes. From 2021 to present, the dominant subtype has been *emm*49 (14%-28% of all cases; avg. 21%) with very few cases with *emm*1 until 2023 when it was detected in 11% of all cases to date (Figure 3).

So far in 2023, *emm*12 has been the dominant serotype detected in 20% (n=61) of the Group A *Streptococcus* cases. Sixty percent of *emm*12 cases are over the age of 40 years with 43% (n=16) of these from cases 70 years and older. Within the 40 years and older group, the top subtypes are *emm*12 (17%; n=37) and *emm*49 (13%; n=29).

As *emm*1 strains are considered highly virulent and associated with invasive infections, further M-typing is performed to assess if the M1<sub>UK</sub> sublineage is detected compared to the previously contemporary M<sub>global</sub> strain. This sublineage of *emm*1 was first detected in BC in 2016. Of the cases with *emm*1 detected so far in 2023 (n=33), 36% (n=14) have M1<sub>UK</sub> identified so far.

![Figure 2. Cases of Streptococcus pyogenes (Group A Streptococcus) from 2017 to date.](image1)

![Figure 3. Top emm types detected from 2017 to date.](image2)
### Gastrointestinal outbreaks

From January to August there were 164 gastrointestinal (GI) outbreaks investigated by the BCCDC PHL (*Figure 4*). The number of outbreaks investigated in February, March and May were on the upper end of the number of outbreaks investigated in previous years. Outbreaks were investigated from 74 (45%) longterm care facilities (LTCF), 71 (43%) daycares/schools, 10 (6%) hospitals, six restaurants (4%) and three other facility/event types (2%). Samples were received from 55% of these outbreaks with norovirus detected in 73 (81%) (from 54 LTC facilities, eight hospitals/acute care facilities, six daycares/schools, and five restaurants). Astrovirus was also detected from two daycares/schools in May while rotavirus was detected in a daycare/school in July.

### Norovirus sequencing

The Environmental Microbiology Program of BCCDC PHL provides norovirus genotyping by sequencing the norovirus polymerase gene (region B) and Capside gene (region C). From 2012 to 2017 genotype GII.4 predominated as the genotype most detected in the samples submitted for sequencing. In 2018, the dominate genotype switched to GII.4_GII.P16 which has been the trend for 2023 so far as well (*Figure 5*).
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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