PHSA Laboratories

BCCDC Public Health Laboratory

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For the attention of British Columbia laboratories and public health partners

Respiratory Virus Typing and Sequencing Guidelines

Background: Provincial influenza A NAT-based subtyping strategies have been in place in past years, with random sampling from each region performed during the height of the respiratory season, annually. Surveillance of respiratory virus types has expanded beyond influenza A in recent years. Currently, BCCDC Public Health Laboratory (PHL) performs genomic surveillance for respiratory viruses, including Influenza A and SARS CoV-2. As we enter the 2024/2025 respiratory virus season, the following guidelines provide information on the current sampling and surveillance strategies and the process for requesting typing for enhanced or targeted surveillance for outbreaks and other public health responses.

ROUTINE SURVEILLANCE

Influenza A

Low influenza season (currently):

During low influenza A season, the lower volume of testing allows for characterization of a larger proportion of samples to help predict the strains that will be circulating during the upcoming season, and to monitor for infections due to highly pathogenic avian influenza circulating in birds.

We ask testing laboratories to ensure that **all positive influenza A respiratory samples with a NAT detection cycle threshold signal (Ct) of 30 or less are subtyped for H1 and H3**, either at the local hospital lab or at the PHL. Samples that are untypeable as H1 or H3 should be forwarded to the PHL for typing by H5 PCR.

High influenza season:

During the height of influenza A season (~January each year, with specific date notified to frontline microbiology laboratories in BC), only a portion of influenza A positive samples require subtyping for surveillance purposes.

During this period, we recommend samples from **one pre-determined day each week be typed**, either at the local hospital lab or at the PHL, be typed by H1, H3 NAT (labs choice of day; e.g. all samples testing positive on Wednesday typed or sent for typing the next day). Additional samples from cases with **known high-risk exposures for avian influenza** (including visiting a region where avian influenza continues to circulate) should also be typed.

Where Ct values are available and typing is to be performed at the PHL, please only forward samples that have a Ct less than 30. Samples that are untypeable as H1 or H3 by NAT should be forwarded to the PHL for typing by H5 PCR or sequencing.

Please note, during low and high influenza season a subset of H1 and H3 subtyped samples will be sequenced to identify the viral clade for surveillance purposes.

SARS-CoV-2

Starting this season, we are moving toward sequencing only a select portion of the SARS-CoV-2 positive samples to monitor for circulating variants.

We ask testing laboratories **to forward all samples testing positive for SARS-CoV-2 (Ct ≤ 30) on one pre-determined day of the week** (labs choice of day e.g. all samples testing positive on Wednesday, sent every week).

RSV

Genomic surveillance for RSV is still under development. However, to facilitate the investigation of monoclonal antibodies (i.e. nirsevimab and palivizumab) breakthrough infections, **we ask all testing laboratories to forward RSV positive samples (Ct ≤ 30) from patients aged 30 months or less.** These will be stored at the PHL for future investigation.

SPECIAL INQUIRIES

In addition to sequencing for routine surveillance, targeted sequencing will be performed for the following situations:

Severe cases: We encourage testing laboratories to send specimens from severe cases of influenza A and SARS-CoV-2 whenever possible and to flag them by adding the mention "Severe case" on the requisition. These specimens will be prioritized for sequencing as they will be helpful to monitor if some genotypes/variants are associated with severity.

Outbreaks: For influenza A or SARS-CoV-2 cluster investigations request, please email BCCDCWGSRequest@bccdc.ca and mention "Outbreak" on the requisition when forwarding samples.

Complex cases: When helpful to guide clinical management, sequencing can be performed for samples from complex cases of influenza A or SARS-CoV-2 (e.g. suspicion of resistance to antivirals, immunocompromised host with persistent infection). For these special inquiries, please contact BCCDCWGSRequest@bccdc.ca.

Atypical diagnostic results: We can assist laboratories by sequencing indeterminate or negative results for influenza A or SARS-CoV-2 that are deemed atypical by a microbiologist. For these special inquiries, please contact BCCDCWGSRequest@bccdc.ca.

ORDERING PROCESS

Please use the **Virology requisition** and indicate the information below. For those interfaced sites, please include the following information in the appropriate **"Comment fields"** for the order**:**

a) name of the virus (e.g. influenza A, SARS-CoV-2, RSV);
b) Ct value (specify N/A if not available);
c) FOR SPECIAL INQUIRIES: indication for sequencing (e.g. severe case, outbreak).

Sincerely,

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