Important Considerations When Establishing the Influenza B Lineage Genotyping Assay

Background

CDC has recently released the CDC Influenza B Lineage Genotyping Kit (IVD) to be used in conjunction with the other CDC Flu rRT-PCR DX Panel assays. Adoption of the assay is voluntary and each laboratory is encouraged by CDC to incorporate the influenza B genotyping assay into their testing algorithms to improve domestic influenza B surveillance data.

The data from the influenza B lineage genotyping assay are a valuable source of information for state and national influenza situational awareness. Some public health laboratories have indicated that adding genotyping information to submitter reports may help to promote the value of the influenza vaccine (particularly the quadrivalent vaccine), encourage and maintain specimen submissions and promote submitters’ role in influenza surveillance.

To assist PHLs with establishing the assay in their laboratories, the APHL Influenza Subcommittee has developed the following guidance for PHLs regarding verification of the assay, testing algorithms and other items to consider as PHLs implement the assay.

Important Considerations for Using the Assay

PHLs are encouraged to communicate with their state epidemiologists and influenza coordinators when adopting this assay. The APHL Influenza Subcommittee has provided a list of questions below for use when considering the assay and when determining an appropriate testing algorithm (see below for example testing algorithms). This list is intended to generate, not limit, discussion; some questions may not be applicable to all jurisdictions. Each jurisdiction is encouraged to determine additional questions and areas for further discussion.

- Do surveillance and/or clinical partners want this information and why? How will you explain the new information to clinical partners?
- How will the information/data be used?
  - By the PHL?
  - By the state epidemiologists and influenza coordinators?
- Should every influenza B virus detected by the laboratory be genotyped?
- Will genotyping be performed on influenza B viruses as they are identified or will they be batched?
  - Does it depend on the severity, what is circulating and the time of season? If so, how will those factors impact this decision?
  - Does the laboratory have the capacity to perform the additional testing on the expected number of specimens?
- How will an influenza outbreak impact the laboratory’s testing algorithm?
  - How will an influenza B outbreak impact the laboratory’s testing algorithm?
- How will genotyping influenza B viruses affect sampling strategies?
  - How will the laboratory ensure that sufficient sampling strategies are in place across temporal and geographical parameters, age and clinical presentations and other demographic variables to appropriately capture representative samples of circulating lineages?
- How, to whom and why will these results be reported within the state? To CDC?
- How will the assay be verified? See next page for an example practice.
**Verification Practices**

CDC is not providing a verification panel for the influenza B genotyping assay. Laboratories are encouraged to use their own specimen repositories for verification. Previously characterized influenza B positive specimens submitted to the CDC as part of national surveillance can be used for verification. In some cases, it may be necessary to partner with another laboratory to receive characterized influenza B specimens if sufficient pre-identified influenza B viruses are not available in the laboratory’s own repository. Another alternative to requesting specimens from another PHL is to ask a PHL, who has verified the assay, to test the specimens as a reference test. If assistance is needed in connecting with another state for verification assistance, please contact Sarah Muir-Paulik (sarah.muir-paulik@aphl.org).

**Example Verification Practice:**

- Include 10-20 influenza B positive specimens (depending on availability and internal laboratory verification protocols) of each lineage (characterized by CDC, the laboratory or by another PHL) using the assay. Compare results with virus characterization by CDC, the laboratory or by another PHL.

**Example Testing Algorithms**

**New Hampshire Public Health Laboratories**

- Influenza B specimens are genotyped as they are identified. Samples are not being batched at this time but the approach may be re-evaluated as the influenza season progresses. Genotyping results are reported to the provider with the following comments to aid providers in interpreting results and to encourage immunization education:
  - “Influenza B/Yamagata lineage virus detected. An influenza B/Yamagata lineage virus has been included in the 2014-2015 northern hemisphere trivalent and quadrivalent vaccines.”
  - “Influenza B/Victoria lineage virus detected. An influenza B/Victoria lineage virus has been included in the 2014-2015 northern hemisphere quadrivalent vaccine, but not the trivalent vaccine.”

**New York State Department of Health-Wadsworth Center**

- Influenza B specimens are currently genotyped as they are identified. Genotyping may be batched or lineage testing reduced to a representative sampling of influenza B-positive specimens, depending on how the influenza season progresses.

**Wisconsin State Laboratory of Hygiene**

- Influenza B specimens are batched and genotyping is performed one or two times a week. Specimens may be batched and genotyped less frequently (bi-weekly or monthly) depending on how the season progresses.

**National Surveillance Value**

In addition to informing state and national influenza situational awareness, genotyped influenza B specimens submitted for national surveillance (either to CDC and/or designated contract laboratory) improves CDC testing efficiency for antigenic characterization. When establishing testing algorithms and determining the utility of the influenza B genotyping assay, consider testing those specimens submitted for national surveillance. If the lineage is known prior to submission to CDC and/or your designated contract laboratory, please include this information in the type/subtype field on Influenza Specimen Submission form. If testing is completed later, it will be updated in reports to CDC (see data reporting information below).

**Sampling Strategies**

Please refer to the Influenza Virologic Surveillance Right Size Roadmap Sampling Implementation Guidance for more information on sampling strategies for your jurisdiction.
Data Reporting

The CDC Influenza B Lineage Genotyping Kit (IVD) package insert has a link to the PHLIP coding guidance to map these results accordingly. If you have questions about mapping, contact CDC (Desiree Mustaquim, dwc6@cdc.gov) or the PHLIP technical assistance team.

Questions about the assay?

Contact CDC at https://partner.cdc.gov/Sites/NCIRD/FS/default.aspx or at flusupport@cdc.gov.

Questions for APHL and/or other PHLs?

Contact Sarah Muir-Paulik at sarah.muir-paulik@aphl.org.