2022 – 2023 Influenza A Sequence Surveillance Assessment for BIOFIRE® FILMARRAY® and BIOFIRE® SPOTFIRE® Respiratory Solutions

Introduction

The BIOFIRE® FILMARRAY® and BIOFIRE® SPOTFIRE® Respiratory Solutions include multiplexed PCR-based in vitro diagnostic tests for the detection of nucleic acids of viruses and bacteria in upper and lower respiratory specimens and are intended to aid in the diagnosis of respiratory infections, including pneumonia.

The BIOFIRE FILMARRAY Respiratory Solutions, including the BIOFIRE® Respiratory 2.1 (RP2.1) Panel, BIOFIRE® Respiratory 2.1*plus* (RP2.1*plus*) Panel, BIOFIRE® FILMARRAY® Pneumonia (PN) Panel, and BIOFIRE® FILMARRAY® Pneumonia *plus* (PN*plus*) Panel, are intended to be used as indicated in moderate- and high-complexity laboratories. The BIOFIRE SPOTFIRE Respiratory Solutions, including BIOFIRE® SPOTFIRE® Respiratory/Sore Throat (R/ST) Panel, BIOFIRE® SPOTFIRE® Respiratory (R) Panel and BIOFIRE® SPOTFIRE® Respiratory (R) Panel Mini, are intended to be used as indicated in moderate- and high-complexity laboratories. The BIOFIRE SPOTFIRE R Panel and BIOFIRE SPOTFIRE R Panel Mini are also cleared for use in CLIA-waived settings.

Each BIOFIRE Panel includes one or more assays for the detection of influenza A viruses. The influenza A virus results reported by each panel (including haemagglutinin (HA) subtype, if applicable) are indicated in Table 1.

Table 1. Influenza A Virus Reporting for BIOFIRE FILMARRAY and BIOFIRE SPOTFIRE Respiratory Solutions Products.

System	Product	Influenza A Virus Reporting
BIOFIRE FILMARRAY	**BIOFIRE RP2.1/RP2.1*plus* Panels**	**Influenza A virus** Influenza A virus A/H1 Influenza A virus A/H1-2009 Influenza A virus A/H3
	BIOFIRE PN/PN*plus* Panels	**Influenza A virus**
BIOFIRE SPOTFIRE	**SPOTFIRE R/ST Panel**	**Influenza A virus** Influenza A virus A/H1-2009 Influenza A virus A/H3
	SPOTFIRE R Panel	**Influenza A virus** Influenza A virus A/H1-2009 Influenza A virus A/H3
	SPOTFIRE R Panel Mini	**Influenza A virus**

Influenza A viruses have a single-stranded segmented RNA genome and the low-fidelity viral RNA polymerase causes continuous genetic mutation and evolution as the virus replicates. Consequently, the genome sequence of influenza A viruses circulating and infecting humans changes over time. Seasonal or global pandemics can arise when antigenic drift (small mutations in viral genes that can lead to changes in surface proteins) and antigenic shift

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(major mutations resulting in new surface proteins in viruses that infect humans) lead to the emergence of a novel influenza A virus in a population where there is little to no immunity. Viral genetic variation and evolution can also affect the ability of sequence-based diagnostic tests to accurately identify the virus in clinical specimens. Therefore, it is important for manufacturers of influenza A virus diagnostic tests to monitor the genetic changes in the virus over time to assess whether the test continues to be safe and effective for its intended purpose.

Surveillance of 2022-2023 Influenza A Virus Sequences

To monitor for emerging variant viruses with genetic changes that may alter detection of influenza A viruses by the BIOFIRE Panels, bioMérieux regularly (at least annually) assesses newly available influenza A virus sequence data from the Global Initiative on Sharing All Influenza Data (GISAID) database and other sources where appropriate. Sequences are aligned to the influenza A virus assay primers, allowing for sequence-based predictions of reactivity with each assay and identification of potential sequence-dependent limitations on reactivity (referred to as in-silico analysis). Sequence-based assay specificity (risk of cross-reactivity with non-influenza A virus sequences) is also evaluated annually.

In silico analysis for pan-influenza A assays include all available sequences of the targeted genes from human H1N1/H1N1pdm09, H1N2, and H3N2 virus subtypes as well as sequences of influenza viruses of avian and swine origin. The most recent surveillance in silico reactivity assessment for influenza A virus was performed on >20,000 pan-influenza A virus and >10,000 haemagglutinin subtype sequences deposited to the GISAID database from October 1, 2022 to May 31, 2023. Predicted assay reactivity for each panel (percent (%) and number of total sequences predicted to be efficiently amplified by an assay) is presented in Table 2.

Table 2. Predicted Reactivity of Influenza A Virus Sequences for BIOFIRE FILMARRAY and BIOFIRE SPOTFIRE Respiratory Solutions Products.

Influenza A assay/assay group	BIOFIRE Respiratory Solutions			
	BIOFIRE FILMARRAY RP2.1/RP2.1*plus* Panels	BIOFIRE FILMARRAY PN/PN*plus* Panels	BIOFIRE SPOTFIRE R/ST and R Panels	BIOFIRE SPOTFIRE R Panel Mini
FluA	-	**99.4%** (23,582/23,722[a])	-	-
Pan-FluA assays	**99.4%** (23,582/23,722[a])	-	**99.4%** (23,582/23,722[a])	-
	99.4% (26,661/22,856[b])	-	**99.4%** (26,661/22,856[b])	-
H1 subtype	**97.7%** (127/130)	-	-	-
H1-2009 subtype	**98.4%** (10,488/10,654)	-	**98.3%** (10,598/10,784)	-
H3 subtype	**99.8%** (16,505/16,541[c])	-	**99.8%** (16,498/16,534[c])	-
Group 1 assays	-	-	-	**99.4%** (23,582/23,722[a])
	-	-	-	**99.4%** (26,661/22,856[b])
Group 2 assays	-	-	-	**98.3%** (10,598/10,784)
	-	-	-	**99.8%** (16,498/16,534[c])

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[a] 8,785 sequences of influenza A H1 subtype, 13,716 sequences of influenza A H3 subtype, 18 sequences of swine origin, 1,203 sequences of avian origin.
[b] 8,442 sequences of influenza A H1 subtype, 13,157 sequences of influenza A H3 subtype, 17 sequences of swine origin, 1,240 sequences of avian origin.
[c] 170 sequences of swine origin, 1 sequence of avian origin.

This in silico analysis reveals that all pan-influenza A virus and influenza A virus subtype assays in the BIOFIRE Respiratory Solutions panels are predicted to be efficiently reactive with approximately 98% of the influenza A virus sequences deposited to the GISAID database during the 2022 - 2023 respiratory season. The prevalence of sequences that would be predicted to have a minor (>3x) to major (≥10x) impact on amplification, detection, and/or reporting of influenza A virus or specific H1, H1-09, or H3 subtypes is 2% or less.

In future annual analyses, if a variant sequence that is predicted to impact reactivity (>10-fold) represents 5% or more of the annual deposited sequences, the potential impact on amplification, detection and reporting by each panel will be investigated. If the investigation confirms a limitation on reactivity with one or more assays that would alter panel performance, a notification about the impact on test performance will be released and distributed.

NOTE: Testing with BIOFIRE FILMARRAY and BIOFIRE SPOTFIRE Panels containing assays for the detection of influenza A virus (and viral subtype sequences) is not intended to monitor for or identify novel variant viral strains of public health concern nor potential zoonotic transmission events.

In Silico Reactivity Assessment of Influenza A Virus Strains Recommended for 2023-2024 Influenza Vaccine

The World Health Organization (WHO) Global Influenza Surveillance and Response System (GISRS) recommends the composition of influenza virus vaccines biannually based on global surveillance data. The recommended influenza A virus strains to include in vaccines for use in the 2023-2024 northern hemisphere influenza season are:

H1N1pdm09:	A/Victoria/4897/2022 (egg-based vaccines)
	A/Wisconsin/67/2022 (cell-based or recombinant vaccines)
H3N2:	A/Darwin/9/2021 (egg-based vaccines)
	A/Darwin/6/2021 (cell-based or recombinant vaccines)

bioMérieux evaluated each of the recommended influenza A virus vaccine strain sequences against respective BIOFIRE FILMARRAY and BIOFIRE SPOTFIRE Panel pan-influenza A or subtype assay(s) and no reactivity limitations for vaccine strains were predicted by in silico analysis. Consequently, the panels are predicted to detect nucleic acids from vaccines if present in the specimens being tested.

Conclusion

- Influenza A virus assays in BIOFIRE FILMARRAY and BIOFIRE SPOTFIRE Panels are predicted to react with >98% of influenza A virus sequences deposited to the GISAID database from October 1, 2022 to May 31, 2023.
- bioMérieux has a surveillance program in place to evaluate newly deposited influenza A virus sequences. This active annual sequence surveillance program, along with other post-market monitoring activities, allows bioMérieux to maintain claims of state-of-the-art performance for detection and (subtyping) of influenza A virus in upper and lower respiratory specimens with BIOFIRE FILMARRAY and BIOFIRE SPOTFIRE Panels and to notify if new deficiencies or limitations on influenza A virus detection are identified.

Customer and Technical Support

bioMérieux is dedicated to providing the best customer support available. If you have any questions or concerns about this process, please contact the Customer and Technical Support team for assistance.

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