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LETTER TO THE EDITOR

Adjusted Molecular Epidemiology Pattern of Influenza A Virus: Effects of Isolation Rate due to Cell Culture Type

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Dear Editor, influenza is an important respiratory infection. The influenza A viruses have a high rate of mutation and are a significant global health issue. For future pandemic and epidemic outbreak preparedness, molecular laboratory research to gather epidemiological data and genetic characterization of influenza viruses in circulation is essential. The influenza A virus is initially discovered in the clinical sample from a suspected case in order to obtain the molecular epidemiology data. Reverse transcription-quantitative polymerase chain reaction is typically used for the detection, followed by subsequent isolation. The cell culture method is typically employed for isolation. Then, the viral genomes are amplified and sequenced, and whole genome sequences can be used to characterize, build phylogenies, analyze mutations, and determine the nucleotide diversity of the viruses.

A crucial stage in determining the final molecular epidemiology pattern is the virus's isolation. Mammalian influenza A viruses are frequently isolated using Madin-Darby canine kidney (MDCK) cells. Varied cell lines have different rates of isolation, which can further change the final molecular epidemiology pattern that is observed. False negative results are conceivable and must be corrected in order to address the issue with the isolation capabilities of various MDCK cell lines. The authors here report the influenza A virus's modified molecular epidemiology pattern in a tropical environment. The most recent data indicated that, in this situation, on-

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Table 1. Adjustment to correct for false positivity in monitoring rotavirus epidemiology pattern based on immunochromatography test surveillance.

	Influenza A pattern (% of the possible least frequency)	
	A/H1N1	A/H3N2
Background data among studied isolatable positive samples before adjustment *	70.59	29.41
Converting to represent overall isolatable positive samples	27.91	11.63
Converting to represent overall positive samples	13.33	5.56
Adjustment to correct the non-isolation limitation **	22.04	14.27

*** - Background data from the previous clinical investigation in the setting [1].**
**** - adjusted data is based on correction for adding additional isolatable rate if the best cell lines are used (8.71%).**

ly 43 of 90 positive samples could be isolated using MDCK cells [2]. Seventeen of those isolated samples were ultimately amplified and whole genome sequenced. In 12 samples, A/H1N1 was detected, and in 5 samples, A/H3N2 [2]. The important concern is on the isolation ability of the MDCK cells. According to a recent study, the best cells, the MDCK-SIAT1 cells, had an isolation ability of 36.21 percent, compared to the classical MDCK cell's 27.5 percent. As a result, 8.71 percent of non-isolatable samples are falsely negative as a result of MDCK use [2]. It is necessary to adjust the laboratory limitation, and Table 1 shows the step-by-step modification. After adjustment, it can show that not using the best cell lines can result in incorrect data on molecular epidemiology pattern. Furthermore, a possible underestimation of an important emerging mutation can result in an unsuccessful further implementation for disease control and influenza vaccination plan. According to the analysis of Mackay et al. of the external quality evaluation studies [3], there is a problem with accurate genotyping and identification of the influenza A virus in many laboratories. The molecular identification of influenza viruses and influenza virus A hemagglutinin subtyping both need to be improved, according to Mackay et al. [3]. The only way to guarantee that the most amount of time is available for intervention is by swift and accurate identification of the pandemic influenza virus in circulation [3].

Declaration of Interest:
None.

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