Developments of the global influenza hospital surveillance network to support better monitoring of influenza virus genetic evolution: The GIHSN-SevVIR network

Bruno LINA1, John Page1, Melissa K Andrew2, Luzhao Feng3, Justin R Ortiz5, Daria Donilenko6, Xavier Lopez-Labrador7, Robert C Reiner Jr8,
Marta C Nunes9, Catherine Commaille-Chapus10, Clotilde El Guerche-Seblain11

1Université de Lyon / Lab virology, National Influenza Centre, HCL & CSF Saint Vincent, Inserm U1111, CNRS 5308, ENS, UCBL, France; 2IDepartmental Epidemiology, NVB, Netherlands; 3Pathouise University / Canadian Center for Vaccinology, Canada; 4Chinese Center for Disease Control and Prevention, Branch of Respiratory Infectious Disease Division of Infectious Diseases, China; 5University of Maryland / School of Medicine, United States; 6National Institutes of Health, National Institute of Allergy and Infectious Diseases, National Institute of Diabetes and Digestive and Kidney Diseases, United States, 7FISABIO-Public Health, Virology Laboratory, Genomics and Health Area, Spain; 8University of Washington, Institute for Systems Biology, Seattle, United States; 9Chinese Center for Disease Control and Prevention, Branch of Respiratory Infectious Diseases, China; 10University of the Witwatersrand, Johannesburg, South Africa; 11Foundation for Influenza Epidemiology, France.

INTRODUCTION

After seven seasons of active influenza surveillance, the Global Influenza Hospital Surveillance Network (GIHSN) is leveraging capacities to link clinical and virological data.

OBJECTIVE

The main objective is to analyze and monitor Influenza viruses’ characteristics from hospitalized cases, and to provide this information to WHO for vaccine strain composition decisions.

RESULTS

Countries mapping
Sixteen laboratories participated in the sequencing data survey, eleven (including nine national reference laboratories) perform strain sequencing and share their sequence data with WHO’s GISRS network via the GISAID platform.

Three laboratories (Valencia, St. Petersburg, Lyon) shared reports with the WHO ahead of the February Vaccine composition meeting.

Strain sequencing results
- 6 GIHSN sites provided viruses for sequencing.
- 73 A(H3N2),105 A(H1N1)pdm09 and 4 B Yam were sequenced by these laboratories.
- 70 A(H3N2) belonged to clade 3C.2a1b while only 2 viruses were from clade 3C.2a and 1 from clade 3C.2a1a (Figure 2).
- All 105 A(H1N1)pdm09 belonged to the 6B.1A clade, and 100/105 had the S183P substitution as described in the A/Brisbane/2/2018 reference strain. (Figure 3)
- Only B Yamagata viruses have been sequenced by the GIHSN lab, close to the B/Phuket/3073/2013 virus.

Figure 1. Map of GIHSN laboratory capacities

Figure 2. Phylogenetic tree of the GIHSN A(H3N2) strains detected during the 2018-2019 season

Figure 3. Phylogenetic tree of the GIHSN A(H1N1)pdm09 strains detected during the 2018-2019 season. Strains with a X are S183

CONCLUSIONS

- The development of a coordinated approach to link clinical and virological information is key to get a better picture of influenza strain circulation and associated clinical characteristics of patients.
- The first year of the GIHSN sequencing platform development has been promising in terms of capacity building and partnerships developments with GISAID and the WHO GISRS and Vaccine composition meeting.
- As compared to the GISRS data, GIHSN reports similar distribution of the viruses, with limited B viruses. However, as a result of the lack of recent strains, the GIHSN failed to detect the recent A (H3N2) 3C.3a viruses.
- An improved sampling strategy for sequencing (timeliness of sequencing, geographic diversity, time of collection) and further comparison of the sequencing viruses (severe vs non severe, etc…) will provide more valuable data for the influenza surveillance and strain selection.

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CONTACT AUTHOR

bruno.lina@univ-lyon1.fr