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

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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.

METHODS

- During the 2018-2019 season, a coordinated approach was developed by the French National Reference Laboratory for respiratory viruses (incl Influenza) in Lyon.
- GIHSN surveillance sites and associated laboratories were mapped for their sequencing capacities.
- A standardized method was proposed using Whole Genome Sequencing and the sites were invited either to share information from sequenced strains or send material for sequencing in Lyon.
- This sequencing data was linked to detailed epidemiological and clinical information on hospitalized patients collected by GIHSN.

RESULTS

Countries mapping

- All eighteen countries participating in GIHSN have laboratory capacity for influenza typing and subtyping (**Figure 1**).
- 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

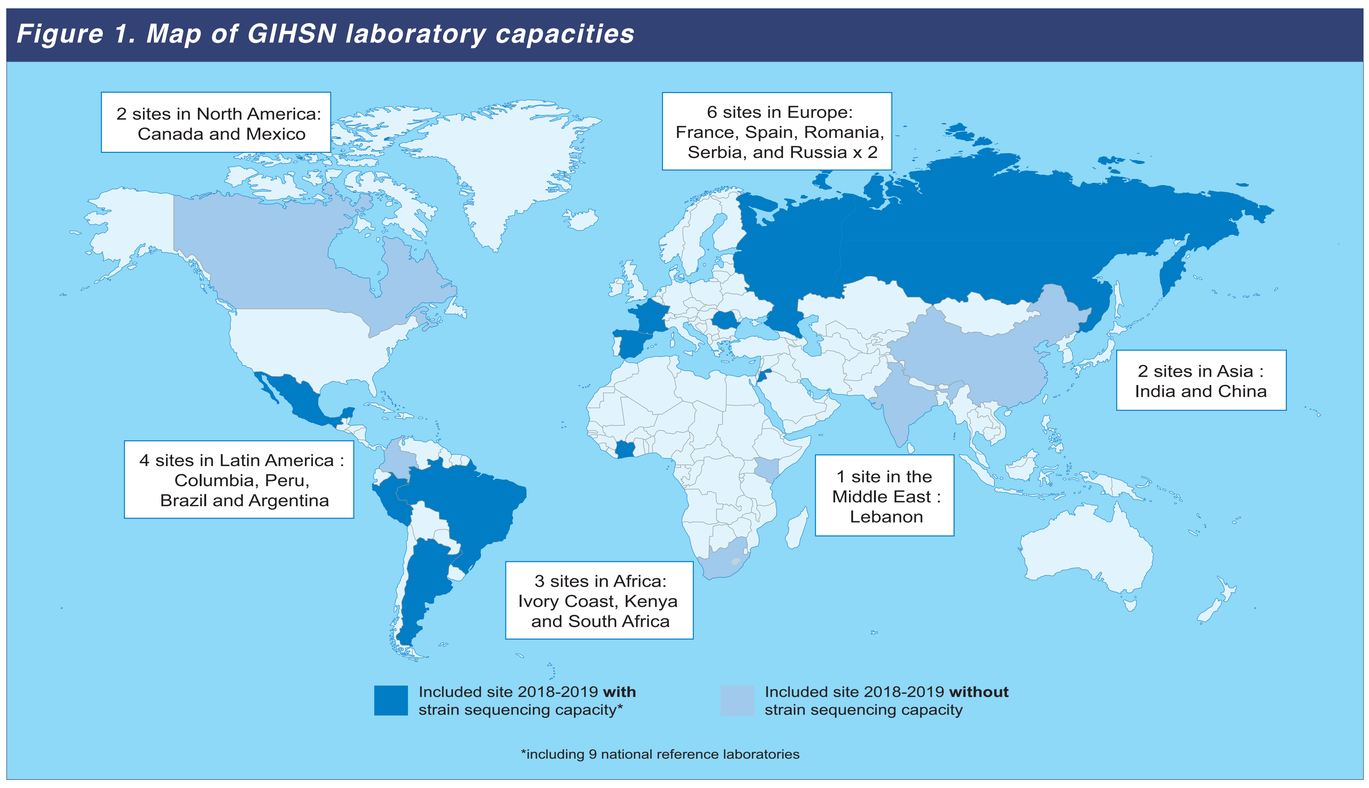


Figure 2. Phylogenetic tree of the GIHSN A(H3N2) strains detected during the 2018-2019 season

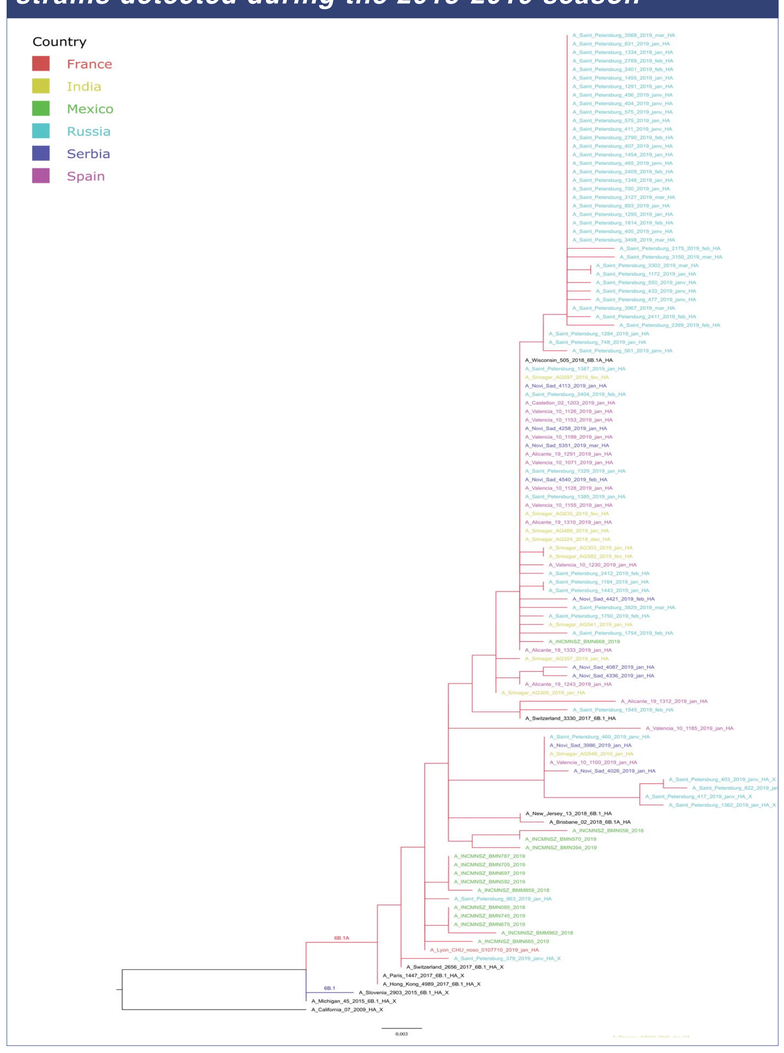
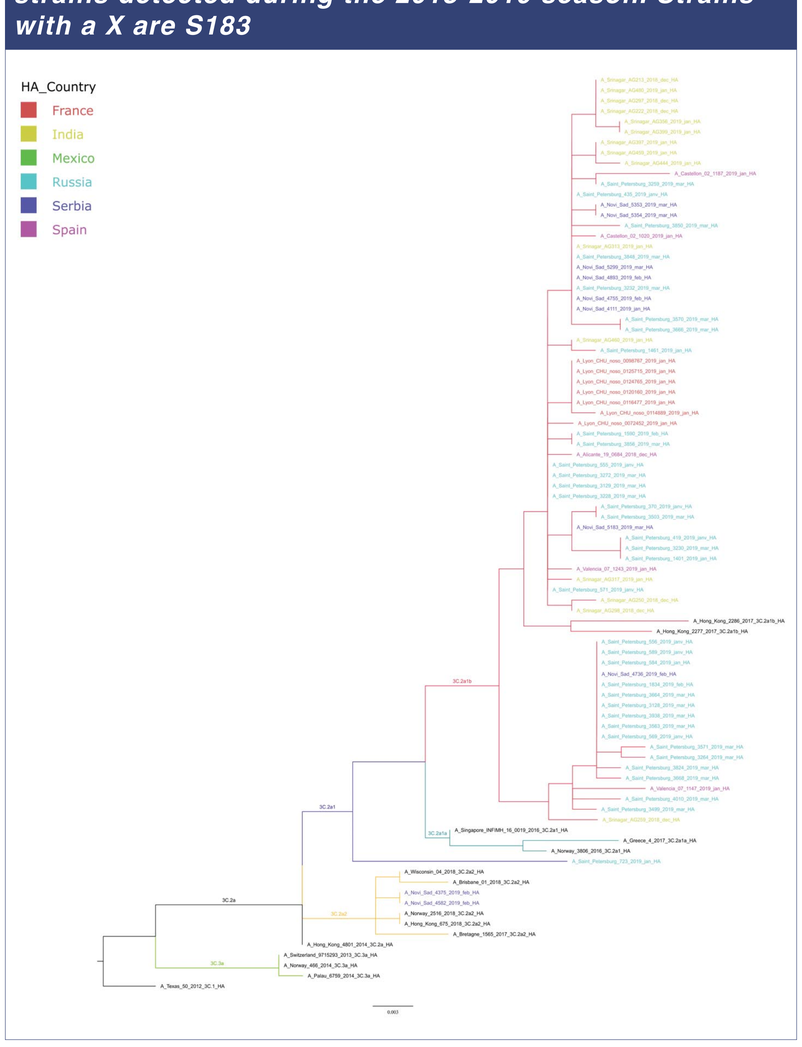


Figure 3. Phylogenetic tree of the GIHSN A(H1N1)pdm09 strains detected during the 2018-2019 season. Strains with a X are S183



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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