Ten-year anniversary of the Global Influenza Hospital Surveillance Network (GIHSN)

Foundation for Influenza Epidemiology

Global Influenza Hospital Surveillance Network
10-YEAR ANNIVERSARY

Sandra S. Chaves[1,2]*, Catherine Commaille-Chapus[3], Laurence Torcel-Pagnon[1,2], Mendel Haag[4]**, Paula Barbosa[5]**, Vanessa Moeder[6]**, Erica Dueger[2]**, Gavin Cloherty[7], Melissa Andrew[8] **, John Paget[9]* **, Justin R. Ortiz[10]*, John McCauley[11]*, Elena Burtseva[12]*, Marta Nunes[13]*, Joseph Bresee[14]*, Wenqing Zhang[15]*, Bruno Lina[16]* **, Cedric Mahe[1,2]**

[1] Foundation for Influenza Epidemiology, Fondation de France, Paris, France ; [2] Sanofi Vaccines, Lyon, France; [3] Impact Healthcare, Paris, France; [4] Center for Outcomes Research and Epidemiology, Seqirus, Amsterdam, The Netherlands; [5] International Federation of Pharmaceutical Manufacturers and Associates (IFPMA), Geneva, Switzerland; [6] Illumina, Inc., 5200 Illumina Way, San Diego, CA 92122; [7] Abbott Laboratories, Abbott Park, Illinois, USA; [8] Canadian Serious Outcomes Surveillance Network, Halifax, Canada; [9] Netherlands Institute for Health Services Research (NIVEL), Utrecht, The Netherlands; [10] Center for Vaccine Development and Global Health, University of Maryland School of Medicine, Baltimore, Maryland, USA; [11] WHO Collaborating Centre for Reference and Research on Influenza, The Francis Crick Institute, London, UK; [12] Gamaleya Federal Research Center for Epidemiology and Microbiology, Ministry of Health of Russian Federation, Moscow, Russia; [13] Vaccines and Infectious Diseases Analytics Research Unit, Faculty of Health Sciences, University of the Witwatersrand, Johannesburg, South Africa; [14] Task Force for Global Health, USA;[15]World Health Organization, Geneva, Switzerland; [16] Laboratoire de Virologie, Institut des Agents Infectieux, Hôpital de la Croix-Rousse, Hospices Civils de Lyon, Lyon, France.

*Member of the Independent Scientific Committee providing guidance to the Global Influenza Hospitalization Surveillance Network; **Member of the Executive committee supporting the Foundation for Influenza epidemiology

Background

GIHSN currently includes more than 100 hospitals in 20 countries, collecting, analyzing, and sharing epidemiologic, clinical and laboratory data on influenza and other respiratory viruses. The network operates under a public-private partnership governance: the Foundation for Influenza Epidemiology (FIE). FIE provides catalytic funding that complements other financial sources (e.g., local ministry of health, WHO, CDC etc.)
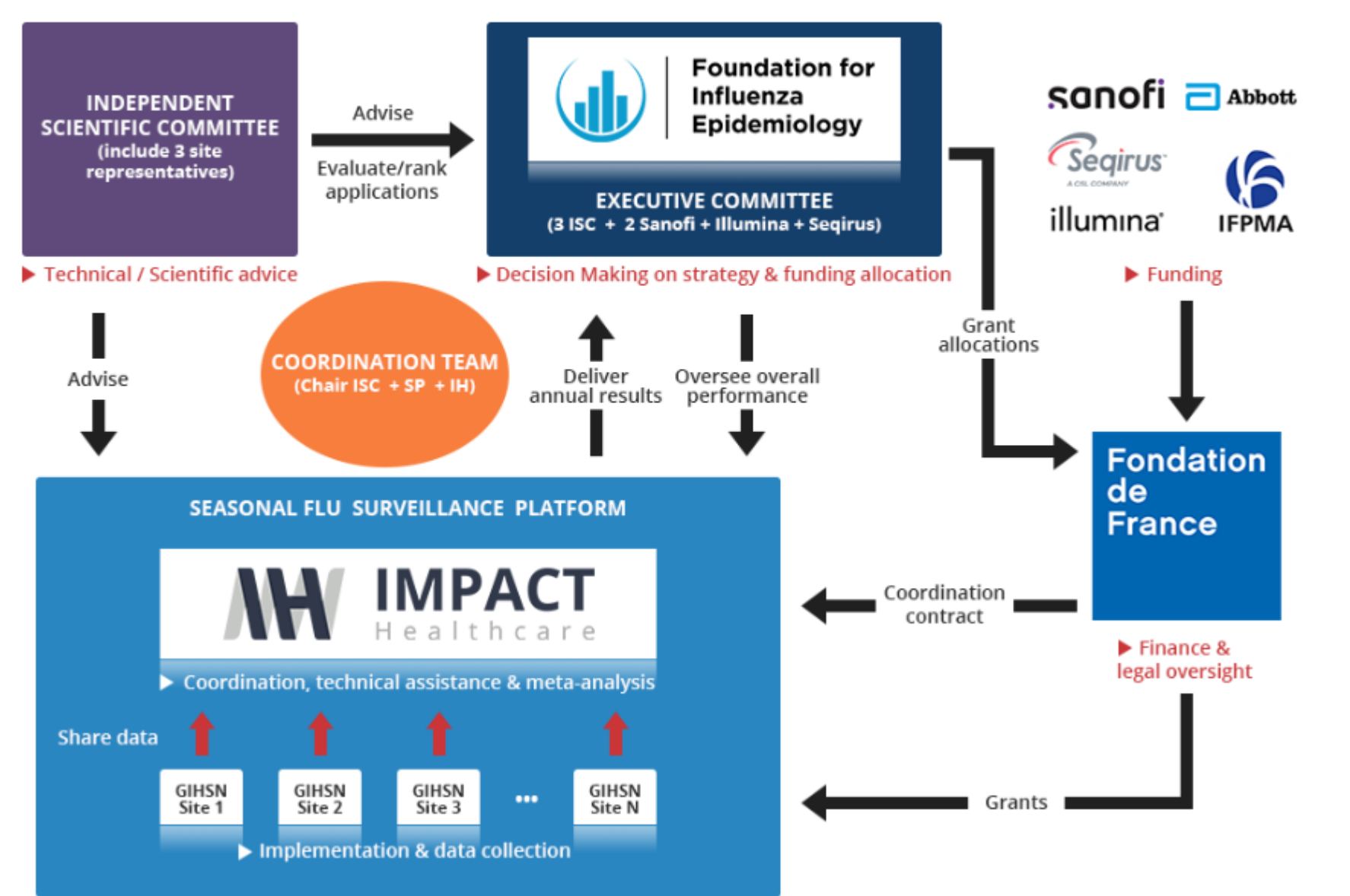
The executive Committee is the decision maker, in charge of the strategic directions related to the project

Methods

- An independent multidisciplinary scientific committee manages the scientific direction of the network, but sites remain owner of their data.
- Using standard protocols, the sites collect demographic and clinical information from patients admitted with respiratory illnesses, including clinical outcomes by discharge
- Respiratory specimens are collected to test for influenza and other respiratory virus by multiplex RT-PCR
- The GIHSN promotes sharing of surveillance data with local health authorities, WHO and the scientific community at large. The network has evolved over time to focus on linking epidemiologic and clinical data with whole genome sequencing (WGS) information to facilitate exploring viral phenotypes as they relate to severity or vaccine-breakthrough cases
- Despite the pandemic, the network has been able to pursue its activities with limited disruption and it is currently active year-round
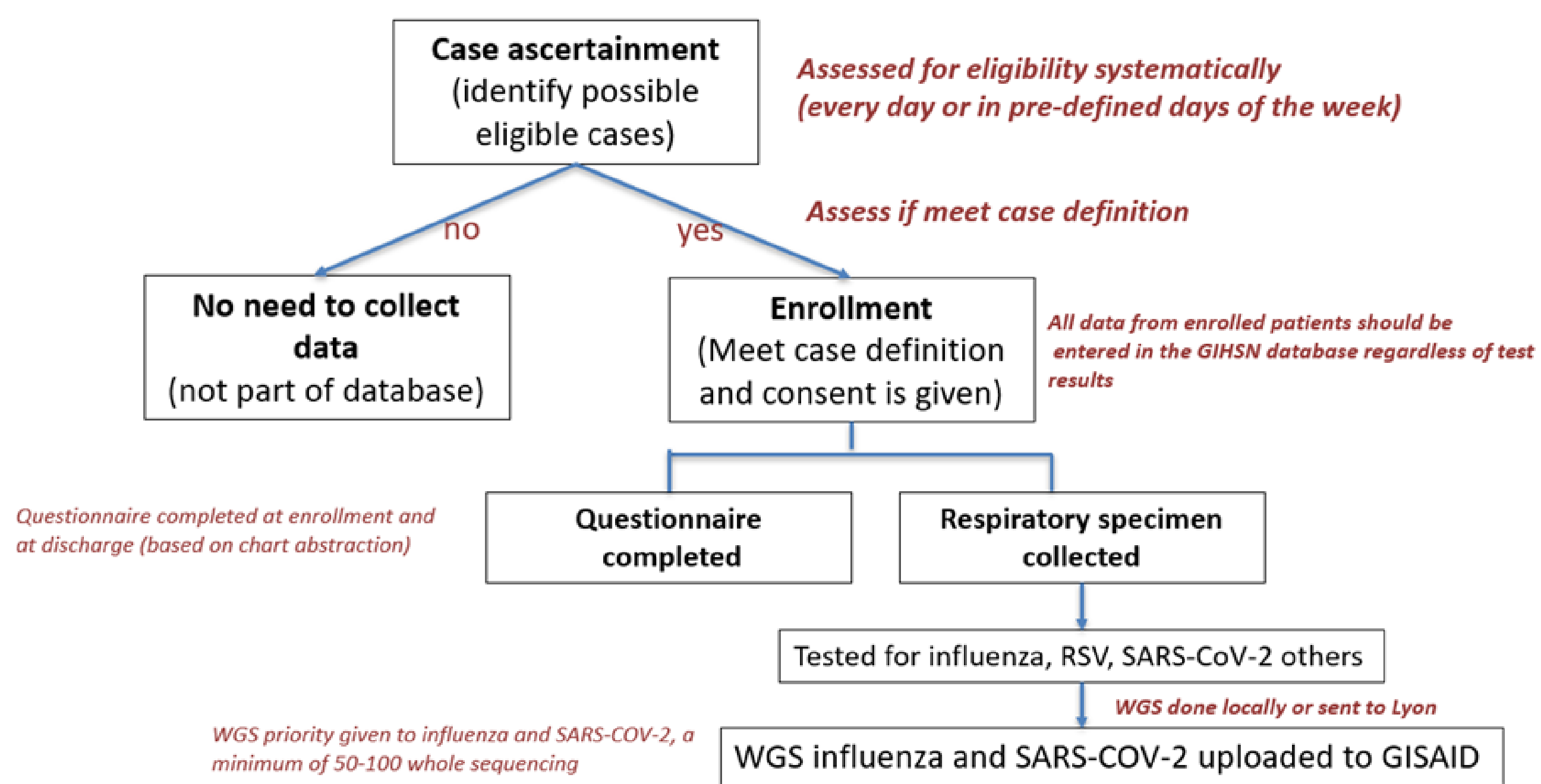

Figure 1: Case ascertainment and enrolment procedures for patients hospitalized with respiratory illness, GIHSN
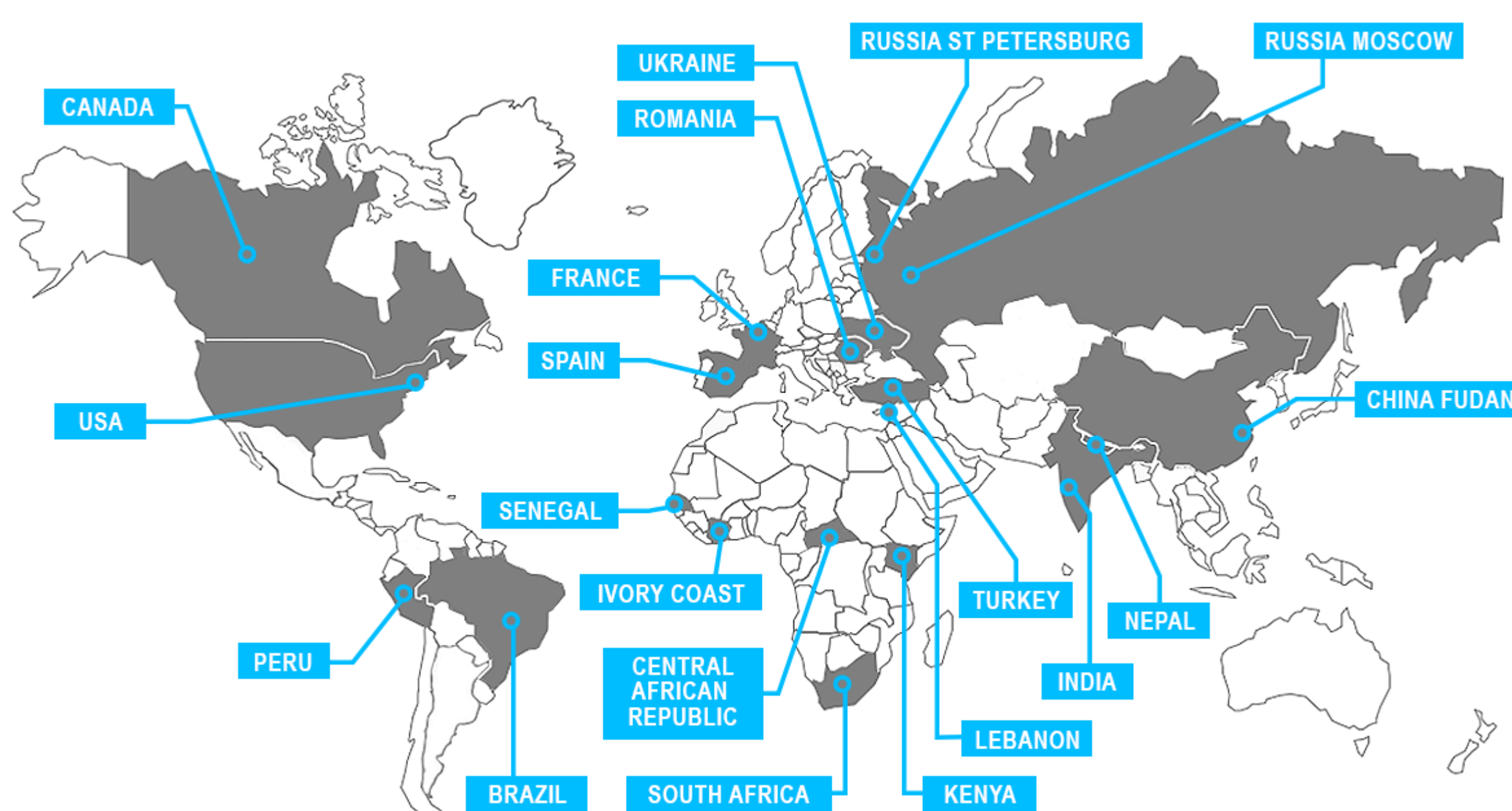

Figure 2: Participant sites during the 2021-22 surveillance cycle. The GIHSN progressively expanded since 2012 to include sites from both hemispheres and inter-tropical areas.

Results

- A total of 110,827 patients hospitalized with respiratory illness have been enrolled so far, including laboratory-confirmation of 21,159 Influenza cases and 30,125 patients with other respiratory viruses
- The annual positivity rate for influenza has ranged from 29% in 2018-19 to 2% in 2020-21 (COVID-19 pandemic period)
- The network has contributed to more than 20 published manuscripts and numerous local and international meetings and conferences since its initiation
- More recently, the FIE is also supporting research activities that leverage the community of scientists to use data gathered through the GIHSN and expanding collaborations to better understand the burden of influenza. GIHSN data are also shared with WHO to support vaccine strain selection
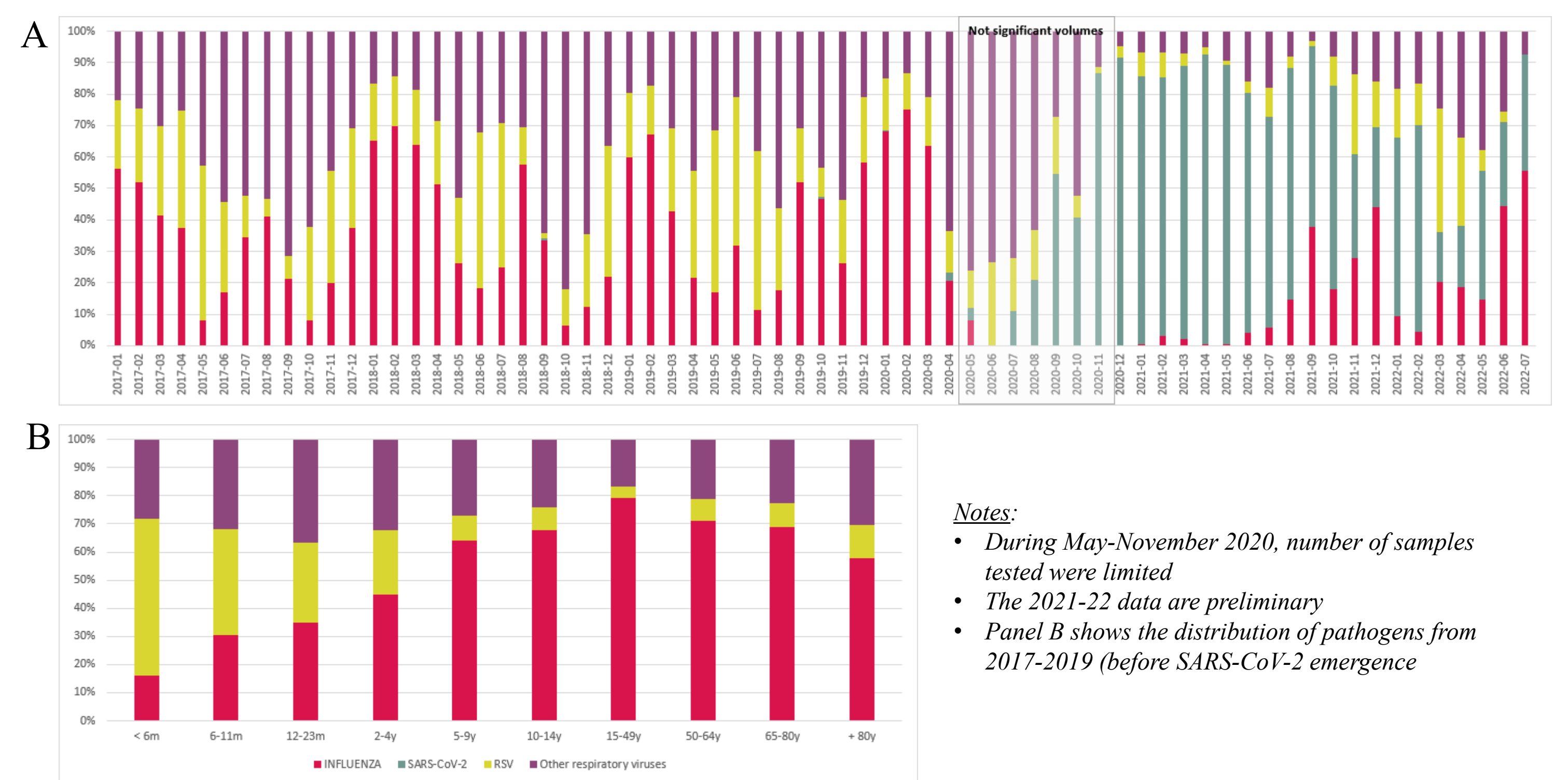
Notes:
- *During May-November 2020, number of samples tested were limited*
- *The 2021-22 data are preliminary*
- *Panel B shows the distribution of pathogens from 2017-2019 (before SARS-CoV-2 emergence)*

Figure 3: Distribution of respiratory viruses detected among hospitalized patients by year of surveillance (A) and by age group (B), GIHSN 2017-18 through 2021-22
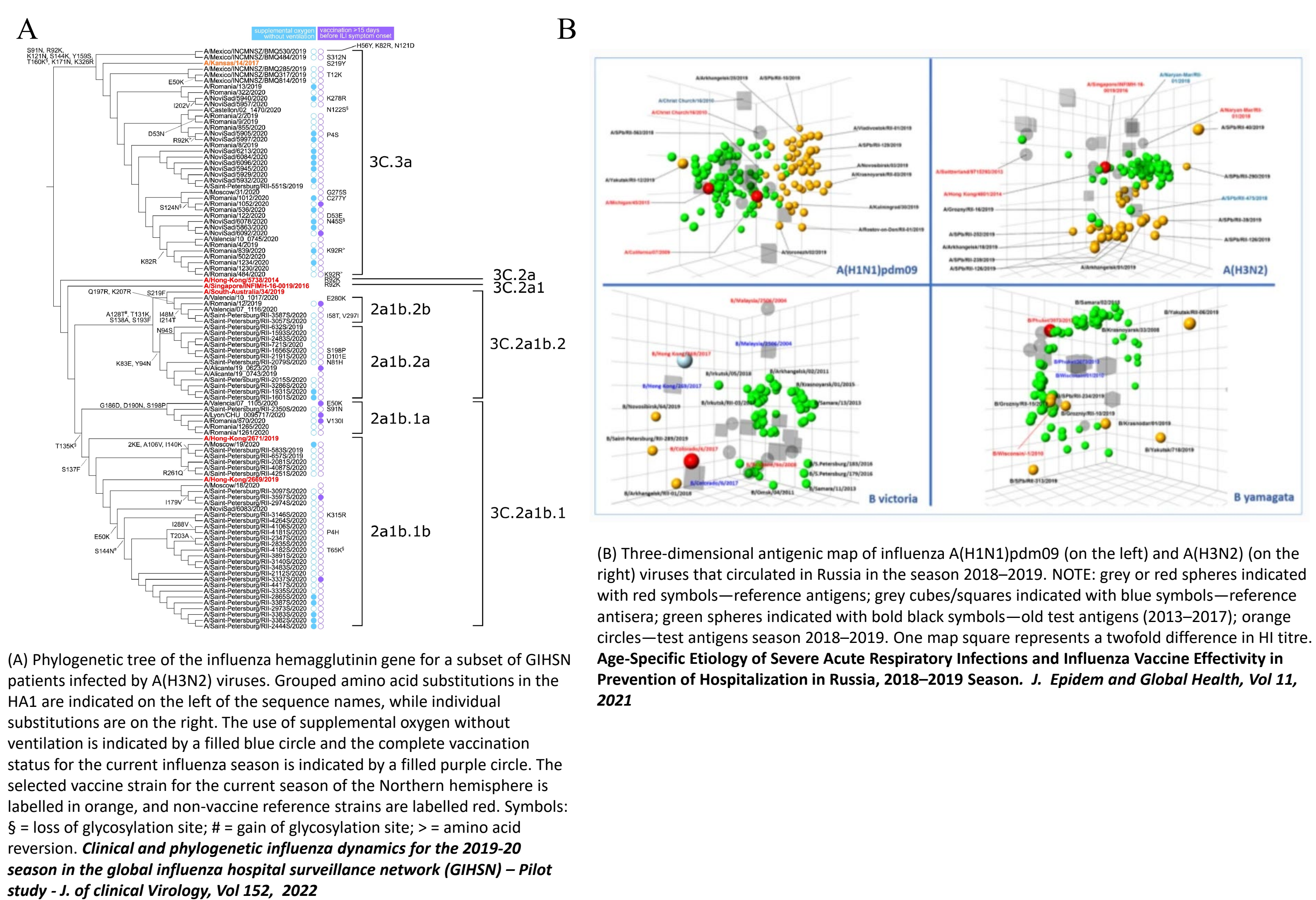
(A) Phylogenetic tree of the influenza hemagglutinin gene for a subset of GIHSN patients infected by A(H3N2) viruses. Grouped amino acid substitutions in the HA1 are indicated on the left of the sequence names, while individual substitutions are on the right. The use of supplemental oxygen without ventilation is indicated by a filled blue circle and the complete vaccination status for the current influenza season is indicated by a filled purple circle. The selected vaccine strain for the current season of the Northern hemisphere is labelled in orange, and non-vaccine reference strains are labelled red. Symbols: § = loss of glycosylation site; # = gain of glycosylation site; > = amino acid reversion. *Clinical and phylogenetic influenza dynamics for the 2019-20 season in the global influenza hospital surveillance network (GIHSN) – Pilot study - J. of clinical Virology, Vol 152, 2022*

(B) Three-dimensional antigenic map of influenza A(H1N1)pdm09 (on the left) and A(H3N2) (on the right) viruses that circulated in Russia in the season 2018–2019. NOTE: grey or red spheres indicated with red symbols—reference antigens; grey cubes/squares indicated with blue symbols—reference antisera; green spheres indicated with bold black symbols—old test antigens (2013–2017); orange circles—test antigens season 2018–2019. One map square represents a twofold difference in HI titre. *Age-Specific Etiology of Severe Acute Respiratory Infections and Influenza Vaccine Effectivity in Prevention of Hospitalization in Russia, 2018–2019 Season. J. Epidem and Global Health, Vol 11, 2021*

Figure 4: Examples of two scientific peer-reviewed papers using data collected through GIHSN

Conclusion

- The COVID-19 pandemic has highlighted the need for resilient and ready surveillance systems, targeted genetic sequencing scale up and a multi-stakeholder approach
- The pandemic has also shown the critical importance of understanding the circulation and burden of respiratory viruses to guide public health decision making and research and development initiatives
- Emerging infectious diseases represent an ongoing threat and GIHSN illustrates the feasibility and pertinence of public and private sector coming together to optimize global efforts under economy of scale approach
- GIHSN is above all a community of local researchers sharing their expertise and data, and contributing to the global public health arena

Contact :   🌐 www.gihsn.org   ✉ fie@gihsn.org