

## Technical Note

# Influenza Virus Nomenclature

22 November 2022

Influenza viruses are among the most important agents of acute respiratory infection in the human population, presenting high rates of morbidity and mortality, constituting an important burden on health services with about 3 to 5 million cases of severe disease and about 290,000 to 650,000 annual deaths<sup>1</sup>.

### Influenza genetic characterization

Several influenza virus gene sequences are available on public databases, including more than 1,777,000 sequences available to date at the Global Initiative on Sharing Avian Influenza Data (GISAID). Sequences deposited into these databases allow comparing the genes of currently circulating influenza viruses with the genomic information from older influenza viruses and those composing the vaccines.

Genetic characterization is important to monitor the influenza virus's evolution; to identify genetic changes that could be associated with influenza viruses spreading, severity, or antiviral resistance; to assess the genetic similarity between virus circulating and vaccine strains; to monitor for genetic changes in influenza viruses circulating in animal populations<sup>2</sup>.

Considering the constant evolution of influenza viruses, real-time, high-quality surveillance data, specifically genetic sequence data, are needed to allow public health decision makers to generate informed decisions about prevention and control strategies, such as influenza vaccine composition<sup>3</sup>.

### Influenza virus classification

Influenza viruses belong to the *Orthomyxoviridae* family, which are characterized by single-stranded segmented RNA of negative polarity. There are four types of influenza viruses designated as A, B, C, and D. Influenza A and B viruses circulate in humans causing seasonal epidemics and eventually pandemics<sup>1</sup>.

<sup>1</sup> WHO. Influenza (Seasonal). 2018 [updated 6 November 2018]. Available from: [https://www.who.int/en/news-room/fact-sheets/detail/influenza-\(seasonal\)](https://www.who.int/en/news-room/fact-sheets/detail/influenza-(seasonal))

<sup>2</sup> CDC. Influenza Virus Genome Sequencing and Genetic Characterization. 2021 [updated 2 November 2021]. Available from: <https://www.cdc.gov/flu/about/professionals/genetic-characterization.htm>

<sup>3</sup> Leite JA, et al. (2020) Genetic evolution of influenza viruses among selected countries in Latin America, 2017–2018. PLOS ONE 15(3): e0227962. <https://doi.org/10.1371/journal.pone.0227962>.



## Global Initiative on Sharing Avian Influenza Data (GISAID)

The GISAID platform was launched in 2008 as an alternative to the public domain sharing model, to improve the sharing of influenza data. Since its launch GISAID plays an essential role in the sharing of data among the WHO Collaborating Centers and National Influenza Centers for the influenza vaccine virus recommendations by the WHO Global Influenza Surveillance and Response System (GISRS)<sup>7</sup>.

Publishing sequences on GISAID require using the nomenclature recommended for WHO. For that, there are two naming conventions for the mandatory field, the isolate name, one for human hosts and another for all other hosts.

The format for humans is:

[influenza type]/[region]/[internal reference number]/[year of collection]  
A/Wisconsin/2145/2001

and for all other hosts:

[influenza type]/[host]/[region]/[internal reference number]/[year of collection].  
A/chicken/Rostov/864/2007

### Guidance for national authorities

PAHO/WHO reiterates to Member States the need to maintain standardized influenza virus nomenclature when uploading influenza virus genomic sequences to GISAID or other existing database in order to avoid rejection of the sequences in the platforms and for maintaining the informative and critical information associated to influenza virus nomination.

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<sup>7</sup> GISAID. Global Initiative on Sharing Avian Influenza Data (GISAID). 2022. <https://gisaid.org/>.