

Technical Note Influenza Virus Nomenclature

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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 deaths¹.

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 populations².

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 composition³.

Influenza virus classification

Influenza viruses belong to the *Orthomyxoviridae* family, which are characterized by singlestranded 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 pandemics¹.

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

^{2.} 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

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



Influenza virus nomenclature

The first WHO recommendation from Influenza virus nomenclature was done in 1953⁴, after some other suggestions, based on antigenic characteristics, followed. Currently, the recommended influenza virus nomenclature (Figure 1) system should state⁵:

- a) the antigenic type (A, B, C, or D)
- **b)** the non-human host (e.g., swine, equine, chicken, etc.). For human-origin viruses, no host of origin designation is given.
- c) the geographical place where the sample was collected (e.g., Denver, Taiwan, etc.)
- d) the sample number (e.g., 7, 15, 875543, etc.)
- e) the year of sample collection (e.g., 1957, 2009, 2022, etc.)
- f) the subtype for influenza A viruses (e.g., influenza A(H1N1) virus, influenza A(H5N1) virus).



Sample identifier

Figure 1: Influenza virus nomenclature. The name starts with the Influenza virus type, followed by the place where the virus was collected, the virus strain number (often a sample identifier), the year of sample collection, and finally, the Influenza virus subtype. *Source: WHO*⁵, *CDC*⁶.

The 2009 pandemic virus was assigned a distinct name: A(H1N1)pdm09 to distinguish it from the seasonal influenza A(H1N1) viruses that circulated before the pandemic. When humans are infected with influenza viruses that normally circulate in swine (pigs), these viruses are called "variant viruses", and are designated with the letter "v" (e.g., an A(H3N2)v virus)⁶.

Examples:

A/swine/South Dakota/152B/2009 (H1N2) A/equine/Texas/2/2021 (H3N8) A/duck/New York/492/2010 (H5N2) A/environment/Wisconsin/1/2021 (H3N2) A/Rio de Janeiro/62434/2021 (H3N2) A/Denver/1234/2020 A(H3N2)v A/California/04/2009 A(H1N1)pdm09 B/Santiago/29615/2020 C/Minnesota/10/2015

^{5.} WHO. A revision of the system of nomenclature for influenza viruses: a WHO Memorandum. Bulletin of the World Health Organization, 58 (4): 585-591 (1980). Available at: <u>https://apps.who.int/iris/handle/10665/262025</u>.

^{6.} CDC. Types of Influenza Viruses. 2021. [updated 2 November 2021]. Available at: <u>https://www.cdc.gov/flu/about/viruses/types.htm</u>.

^{4.} Chanock, R. H. et al. A Revised System of Influenza Virus Nomenclature: A Report of the WHO Study Group on Classification. Virology 47, Issue 3, 854-856 (1972). <u>https://doi.org/10.1016/0042-6822(72)90580-6</u>.



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)⁷.

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

<u>The format for humans is</u>: [influenza type]/[region]/[internal reference number]/[year of collection] A/Wisconsin/2145/2001

<u>and for all other hosts</u>: [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.

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