

# PHYLOGENETIC ANALYSIS OF INFLUENZA VIRUS TYPE A H1N1 NEURAMINIDASE GENE ISOLATED FROM HUMAN

Zelena L.B.<sup>1,2</sup>, Parchevska D. D.<sup>1</sup>, Tkachuk N.V.<sup>3</sup>, Zahorodnia S.D.<sup>2</sup>

<sup>1</sup>Kyiv National University of Technologies and Design

<sup>2</sup>Zabolotny Institute of Microbiology and Virology, NAS of Ukraine,  
zelenalyubov@gmail.com

<sup>3</sup>T.H. Shevchenko National University “Chernihiv Colehium”

## Abstract

*The research was devoted to the study of influenza virus H1N1 neuraminidase gene genetic variability between isolates of various geographic localization and year of collection. The analysis of nucleotide sequence variability and phylogenetic analysis were performed using data from NCBI's Influenza Virus Resource and MEGA 10. The obtained results revealed clear differentiation between isolates of 2009 and the earlier collected ones. The level of genetic polymorphism was low among the isolates of 2009 and 98,6% of nucleotide sites were conservative.*

**Keywords:** *influenza virus, neuraminidase, phylogenetic analysis*

**Introduction.** Influenza viruses are RNA viruses belonging to the *Orthomyxoviridae* family. The virus genome is composed of 8 single-stranded RNA segments and genetic variability can be caused, among other reasons, by genetic drift and genetic shift [1]. The influenza viruses are divided into three types – A, B and C, and type A are composed of several subtypes depending on antigenic and genetic properties, it is known 18 different HA (hemagglutinin) types and 11 NA (neuraminidase) types [2]. The influenza virus type A is one of the most dangerous pathogens that infect humans, mammals, birds and poultry, it caused severe illness, and it is harmful for human health. Hemagglutinin and neuraminidase are considered as the main virus glycoproteins encoded by the fourth and sixth genome segments and responsible for the virion adhesion to hosts and releasing of new viral particles [3].

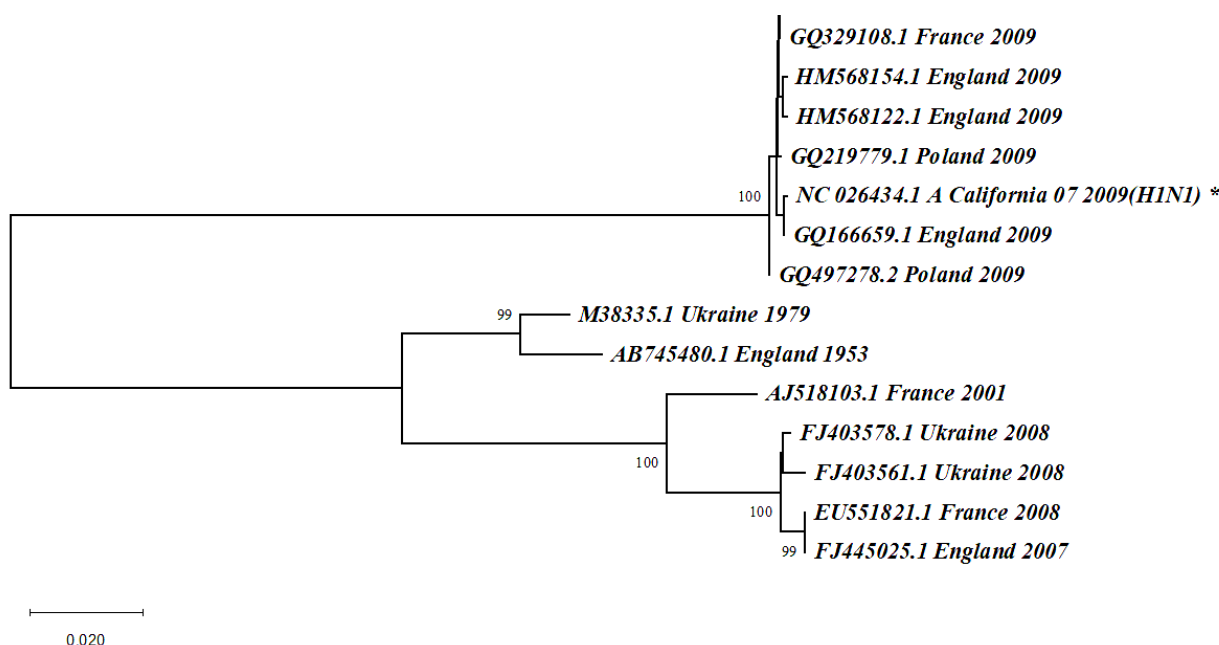
The purpose of the presented study was to compare nucleotide sequences of the neuraminidase gene of influenza virus type A H1N1 between isolates of various collection year and analyze their genetic variability.

**Materials and methods.** To perform the analysis nucleotide sequences of H1N1 neuraminidase gene were downloaded from the NCBI's Influenza Virus Resource defining search set as type – A, host – human, country – England / France / Poland / Ukraine, segment – NA, subtype – H1N1, collection date – from 1953 to 2009. Totally, 17 sequences were downloaded. As a reference strain vaccine strain A/California/07/2009 (H1N1) was used. The analysis of genetic polymorphism and phylogenetic analysis were carried out using MEGA 10 program [4].

**Results and discussion.** The analysis of neuraminidase gene nucleotide sequences showed that the most heterogeneous were isolates collected before 2009 epidemic. This group was presented by three Ukrainian, two French and two the UK isolates, from 1953 to 2008 years. There were 162 variable, 113 parsimony informative and 49 singletons out of 1318 sites. The group of isolates collected during 2009 epidemic consisted of two French, three the UK and four Polish isolates and was characterized by 15 variable, 4 parsimony informative and 11 singleton sites. The comparative analysis between two groups isolates revealed that isolates collected before 2009

epidemic differed from the last by nucleotide variations and 3-nucleotide insertion. It supposes that during the 2009 epidemic neuraminidase gene sequences were more conservative and had 3-nucleotide mutation in comparison to non-epidemic isolates.

Dendrogram constructed on the basis of neuraminidase gene sequences showed that all isolates formed two groups: one combined isolates of 2009 epidemic and the another – isolates collected before 2009 epidemic. The last group also was divided into two subgroups: comprising isolates of 1953 and 1979 (1) and isolates of 2001, 2007 and 2008 (2) (fig.1.) It is worth noticing that the geographical differentiation between isolates was not detected.



**Fig.1. The dendrogram of genetic similarities between different influenza virus type A H1N1 isolates based on nucleotide sequences of neuraminidase gene constructed using Neighbor-Joining algorithm and Kimura 2-parameter model.**

**Conclusions.** The results obtained in the presented research suggest that genetic variability of influenza viruses H1N1 depends on the epidemiological situation and to develop relevant vaccine the permanent monitoring of virus genetic heterogeneity should be done.

### References:

1. Sanjuan R., Domingo-Calap P. Genetic diversity and evolution of viral populations. Encyclopedia of virology. 2021. P. 53-61. doi: 10.1016/B978-0-12-809633-8.20958-8
2. CDC. Types of Influenza Viruses. <http://www.cdc.gov/flu/about/viruses/types.htm>. Accessed 25 April 2024
3. Webster R.G., Bean W.J., Gorman O.T., Chambers T.M., & Kawaoka Y. Evolution and ecology of influenza A viruses. Microbiological reviews.1992. Vol. 56, No. 1. P. 152-179.
4. Kumar S., Stecher G., Li M., Knyaz C., Tamura K. MEGA X: molecular evolutionary genetics analysis across computing platforms. Molecular biology and evolution. 2018. Vol. 35, No.6. P. 1547-1549. doi: 10.1093/molbev/msy096