SI “Kyiv City Center for Diseases Control and Prevention of the Ministry of Health of Ukraine”

The Results of Virological Respiratory Pathogen Monitoring among Kyiv Population in 2025-2026 season

A.Mironenko, S.Chumak, I.Holoviienko, N.Teteriuk, L.Radchenko, Y.Kuiarova, I. Zakharchuk

Introduction

For today the world exists in the condition of a post pandemic period. Influenza viruses in the pandemic period caused by coronavirus SARS-CoV-2 showed minimal activity, but didn’t disappear. After the end of the COVID-19 pandemic influenza viruses continue to cause epidemic raises of morbidity.

The aim

of our work was to conduct the virological monitoring for the circulation of pathogens of respiratory infections in Kyiv in the season of 2025-2026.

Materials and methods

Samples for testing (nasopharyngeal swabs), were collected from patients with respiratory symptoms and tested by a real time PCR method. The testing was conducted for influenza A and B viruses, SARS-CoV-2, RSV, parainfluenza viruses, adenoviruses, metapneumoviruses, rhinoviruses, bocaviruses and seasonal coronaviruses. 1752 respiratory samples were tested by the PCR method and 74 of influenza viruses were sequenced.

The evolutionary history was inferred using the Neighbor-Joining method.

The optimal tree with the sum of branch length = 0.05961491 is shown. The tree is drawn to scale, with branch lengths in the same units as those of the evolutionary distances used to infer the phylogenetic tree. The evolutionary distances were computed using the Maximum Composite Likelihood method and are in the units of the number of base substitutions per site. The analysis involved 36 nucleotide sequences. Codon positions included were 1st+2nd+3rd+Noncoding. All positions containing gaps and missing data were eliminated. There were a total of 1713 positions in the final dataset. Evolutionary analyses were conducted in MEGA 7.

Results

Influenza viruses caused an epidemic in Kyiv and amounted to 30% from all tested samples. The biggest quantity of tested samples was collected during 2-8 weeks 2026 (37.8%) the same as the majority of samples (26%). The main pathogen of epidemic was subtype A(H3N2) of influenza viruses: strains A/Singapore/GP20238/2024 and A/Darwin/1454/2025. Influenza viruses subtype A(H1N1) was in the minority - the strain A/Missouri/11/2025.

Among all of the tested samples only 7.5% were positive for SARS-CoV-2. Another 11.5% were positive for other respiratory viruses.

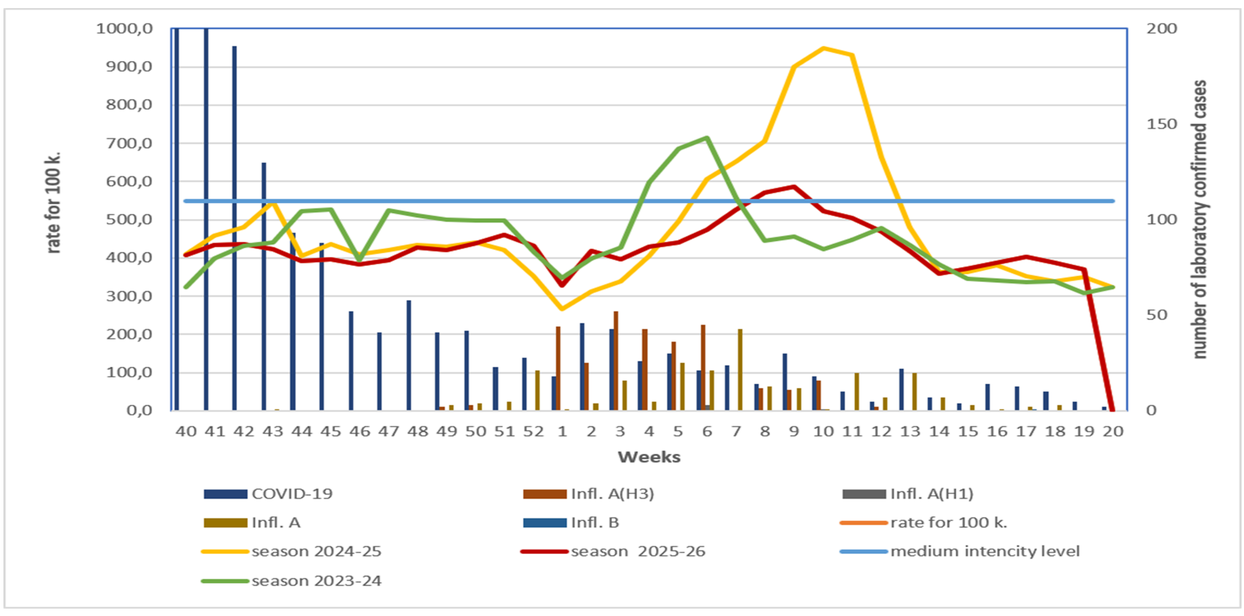


Fig. 1. The level of influenza and ILI & SARI morbidity in Kyiv city and number of laboratory confirmed influenza and COVID-19 cases in season 2025-2026

As we can see on figure 1, the level of influenza and ILI & SARI morbidity in Kyiv city was lower in 2025-2026 season than two previous.
The proportion of different respiratory viruses among the patients in Kyiv city in 2025-2026 season (fig.2) demonstrate the domination of influenza A viruses among all others respiratory viruses.

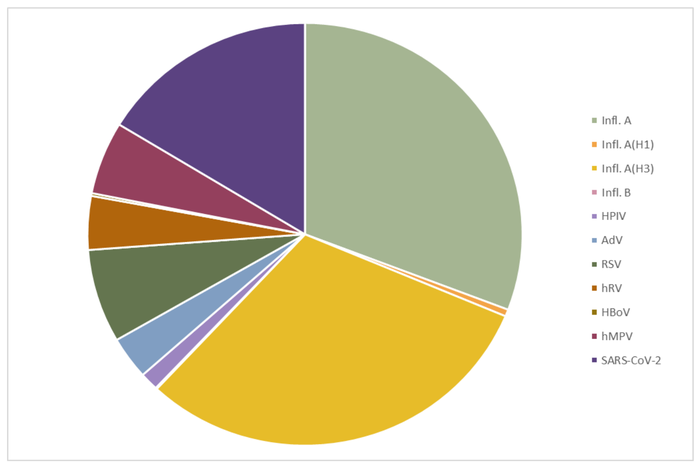


Fig. 2. The proportion of different respiratory viruses among the patients in Kyiv city in 2025-2026 season

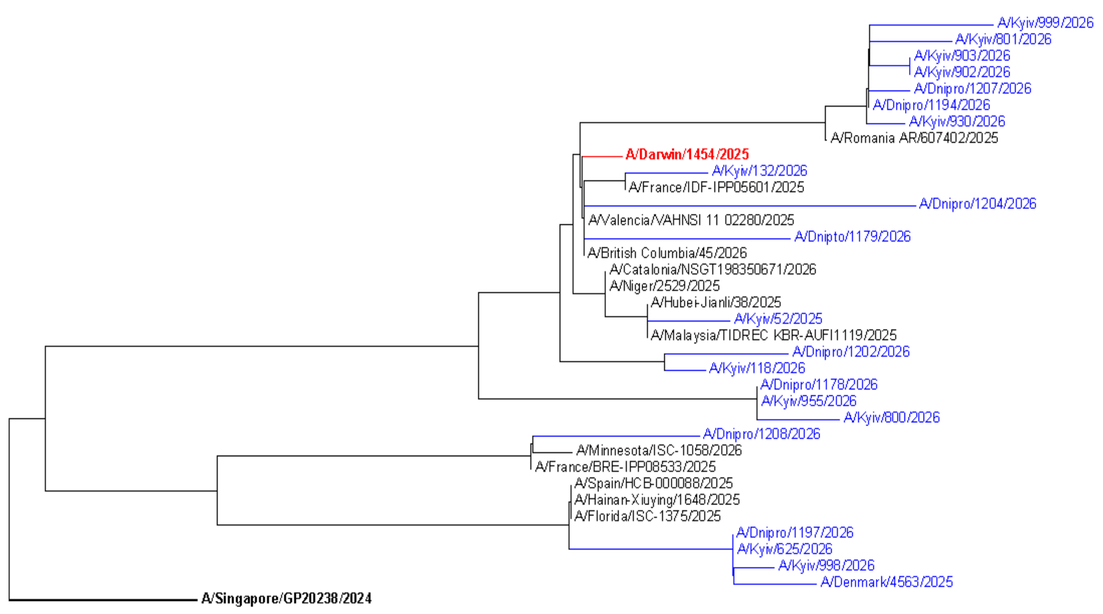
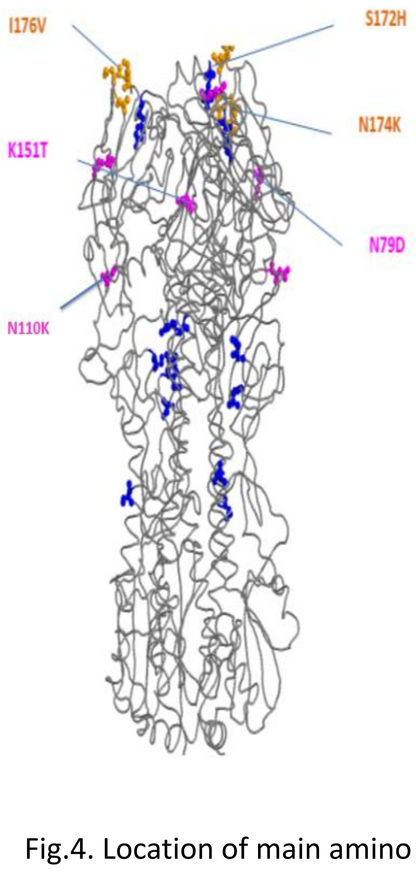


Fig.3 Phylogenetic tree of the HA gene of some influenza A(H3N2) viruses 2025-2026 season



Among all influenza viruses 74 of them were sequenced in 2025-2026 season: 50 (67,6%) of all sequenced viruses belonged to subtype A(H3N2) and 24 (32,4%) – to subtype A(H1N1)pdm09. The viruses A(H3N2) belonged to strain A/Darwin/1454/2025 and A/Singapore/GP20238/2024.
Mutational analyses of A(H3N2) influenza viruses hemagglutinin revealed no critical mutations (amino acid substitutions) that fundamentally altered the virus’s properties. For example, an amino acid substitution K151T was responsible for the creation of a new potential N-glycosylation site; another one N110K – for the removal of a potential N-glycosylation site. The amino acid substitutions S172H, N174K and I176V are associated with antigenic drift, escape mutant and host cell receptor binding.
3D model of hemagglutinin of A(H3N2) virus with some mutations is illustrated in Fig.4.

Fig.4. Location of main amino acid substitutions (a) in HA of A(H3N2) influenza viruses of 2025-2026 season.

Conclusions

Today the etiological factor of epidemics are influenza viruses. SARS-CoV-2 viruses cause seasonal growths of morbidity in the periods when influenza viruses almost don’t circulate. There is a necessity of respiratory pathogen monitoring, including genetic monitoring and because of their constant variability and easy way of transmission.

Acknowledgments

The authors would like to acknowledge Foundation de France for the funding of these investigations and Global Influenza Hospital Surveillance Network for cooperation; Prof. Bruno Lina and his team (Lyon, France) for the sequencing of Ukrainian viruses, all physicians who take part in SARI surveillance in Ukraine.