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# Circulation patterns of seasonal influenza virus, 2017-2018, Romania

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**Background**. Seasonal influenza causes substantial illness and death. Influenza viruses undergo constant mutation, which plays an important role in virus escape from host immune defense. The evolving nature of influenza viruses mandates that the composition of seasonal influenza vaccines is adjusted annually in order to remain effective. We aimed to investigate the characteristics of influenza viruses circulating in Romania during the 2017-2018 influenza season witch indicates an unpredictable circulation pattern.

**Methods**. As part of virological surveillance of influenza in Romania respiratory specimens were collected from patients with influenza-like illness during the 2017/18 influenza season. Sequencing and phylogenetic analysis using maximum-likelihood method of the HA gene amino acid sequences (1650 nt) were performed to characterize the circulating strains.

**Results**. First influenza virus from sentinel system was detected in week 49/2017, but constantly detection of the virus started with week 2/2018. HA genes from selected cases (n=142) were sequenced for genetic characterization: 67.6% B (Yamagata lineage), 21.8 A(H1N1), 10.5% A(H3N2).

Genetic analyses revealed a number of variations at the HA sequences of Romanian circulating strains. All influenza B viruses tested fall in clade 3, the **B/Phuket/3073/2013 clade**, with all falling into a genetic group defined by HA1 amino acid substitutions: L172Q, M251V, D196N and D198T. Influenza A(H1N1)pdm09 virus analyses shows that all viruses fell into clade 6B.1 defined by the substitutions S84N, S162N (+CHO) and I216T in HA1 (compared with **A/Michigan/45/2015**). The analysis of HA sequences of Influenza A(H3N2) virus reveals that fall within genetic group 3C, subgroup 3C.2a with the characteristic amino acid substitutions: N145S, L3I, N144S, F159Y, K160T, N225D and Q311H, like **A/Hong Kong/5738/2014** and 3C.2a1 subclade which encodes N121K, N171K in HA1.

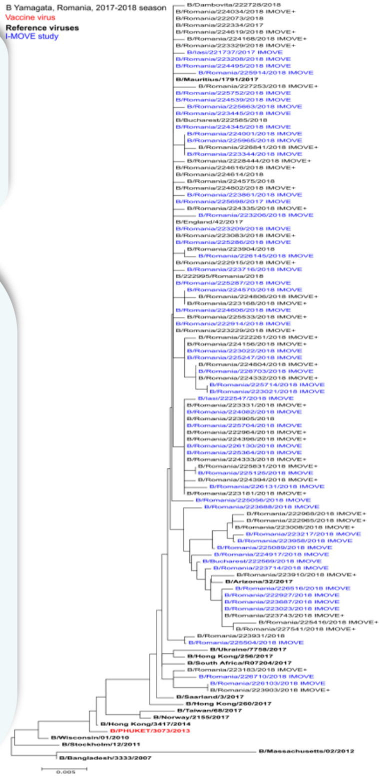

Fig.1. Analysis of the molecular evolution of seasonal influenza B Yamagata strains.

Fig.2. Analysis of the molecular evolution of seasonal influenza A(H1N1)pdm09 strains.

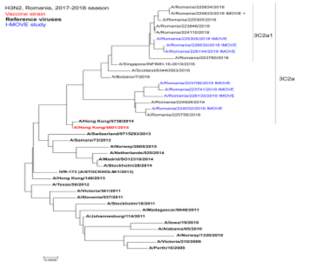

Fig.3. Phylogenetic analysis of seasonal influenza A(H3N2) strains.

**Conclusions**. The influenza activity was higher than in the previous season, characterised by co-circulation of influenza A(H3N2), A(H1N1)pdm09 viruses with B influenza virus (Yamagata lineage) being dominant. The circulation patterns of seasonal influenza viruses vary with antigenic drift. Genetic and antigenic data along with epidemiological surveillance are able to early capture the molecular changes of the circulating influenza viruses and can support vaccination programs. A wide knowledge of the seasonality patterns is important but it is a challenge due to the unpredictable circulation of influenza viruses. A careful surveillance of genetic changes in the HA gene during seasonal influenza epidemics in comparison to the vaccine virus may provide early information on newly emerging strains.

**References**.

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