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**Abstract No: 1503****Presentation at ESCV 2015: Poster 1  
Influenza in Russia in the season 2014–2015:  
Epidemiology and antigenic properties of  
viruses**

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**Background:** variability of influenza strains, especially A(H3N2) during the season 2014–2015 and incomplete fitness with the H3N2 and B vaccine strains.

**Methods:** virus isolation, identification, antigenic analysis in HI-test, MUNANA-test of sensitivity to neuraminidase inhibitors.

**Results:** Data of Federal Influenza Center of Russia on epidemic indexes in the season 2014–2015 are presented, such as morbidity, intensity, geographic spread and laboratory confirmed lethal cases. The epidemic in the current season was more intensive according to the most parameters comparing to the previous season. Epidemic started on the week, ending December 18, 2014. The peak of epidemic in general population was registered on the week 7 ending February 15, 2015 and in adults on the week 8. Morbidity in general population on the epidemic peak reached 1% and exceeded epidemic threshold on 77.4% in adults and 66.4% in children. Antigenic analysis of virus isolates (about 350) demonstrated that the predominant etiologic agent was influenza B – 63% of isolates. Influenza A(H3N2) was responsible for 30% of isolates and pandemic influenza 2009 was isolated in only 7% of studied clinical samples. All analyzed strains of influenza A(H1N1)pdm09 obtained by WHO NIC were A/California/07/09-like and reacted in HI at 1–1/2-fold of homological titre. Influenza A(H3N2) viruses formed two antigenic and genetic groups: strains similar to A/Switzerland/9715293/13 (clade 3C.3a) and those similar to A/Hong Kong/5738/14 (clade 3C.2a). The former circulated in the Far East and Eastern Siberia though the later on the European part of Russia and Western Siberia. At the end of season we also discovered in Saint Petersburg several strains of the clade 3C.2b. Most of the strains of influenza B belonged to Yamagata lineage (B/Phuket/3073/14-like). Strains of Victorian lineage were isolated in 3 cities and composed only 4.5% of all isolates of influenza B viruses and were B/Brisbane/60/08-like. All analyzed strains proved to be sensitive to the neuraminidase inhibitors according the results of the fluorescent MUNANA-test.

**Conclusion:** Pronounced antigenic drift of influenza A(H3N2) and B viruses was one of the reasons of low effectiveness of influenza vaccines which was registered in the season 2014–2015 in many countries. Investigation of peculiarities of further evolution of viruses stress the urgency of expansion of the epidemiological surveillance, virus isolation and characterization with the modern techniques in different time periods and geographic regions. Only in these conditions we can assure high efficiency of flu seasonal vaccines.

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**Abstract No: 1504****Presentation at ESCV 2015: Poster 1  
Virus etiology of SARI cases and protective role  
of influenza vaccination determined in sentinel  
surveillance system**

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**Background:** During the seasons 2013–2014 and 2014–2015 10 cities of Russia were involved into sentinel surveillance (SS). SS hospitals and laboratories were located in 6 Federal Districts (FDs) of Russia.

**Methods:** The investigations were conducted at 19 hospitals reporting weekly data on severe acute respiratory infections (SARI) according to case definition. PCR was used for determination of etiological structure of SARI.

**Results:** Data on 2685 SARI patients was entered into RII/SS database in 2013–2015 seasons. According to PCR data influenza SARI cases accounted on the average for 17.9% in 2013–14 and 24.5% in 2014–15. With that, in the season 2013–14 and 2014–15 total impact of influenza A (H1N1)pdm09 virus was estimated as 49.8%, and 2.7% of SARI cases, influenza A (H3N2) virus in 36.6% and 64.5% cases and influenza B cases were revealed in 13.2% and 32.5% of cases, correspondingly. Geography of different influenza viruses spread was different. In 2013–14 in cities of Siberian and Far-Eastern FDs most part of SARI cases was associated with influenza A(H1N1)pdm09 virus, the most number of influenza A(H3N2) associated SARI cases was detected in Central, North-Western, Volga and South FDs. Influenza B viruses caused most SARI cases in cities of Siberian and Far-Eastern FDs. In 2014–15 season influenza A(H3N2) virus was detected in most SARI cases in Central, North-Western, Volga and Siberian FDs. Influenza B virus was detected in all FDs. Influenza A(H1N1)pdm09 SARI cases were diagnosed in single cases only. Extended research of etiological structure of SARI including influenza, parainfluenza, adenoviruses, RSV, coronaviruses, metapneumoviruses, bocaviruses and rhinoviruses was determined in 10 hospitals. Etiological structure was recognized in 34% and 35.1% of SARI cases in 2013–2014 and 2014–2015 season, correspondingly, and was associated mostly with influenza, RSV, parainfluenza and rhinoviruses. Analysis of previous vaccination data showed that low percent of SARI patients both with influenza and non-influenza etiology was immunized with influenza vaccine. A total of 57% and 44.5% of SARI patients had underlying somatic pathology or pregnancy in these seasons.

**Conclusion:** Etiological structure of SARI cases was associated mostly with influenza, RSV, parainfluenza and rhinoviruses. Significant role of underlying diseases and especially pregnancy was revealed in SARI development. Low percent of SARI patients was immunized with influenza vaccine.

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