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Paper Poster Session

Influenza - clinical epidemiology

Reassortment events and pandemic risk assessment of avian influenza viruses in Central Asia

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Background: Recent outbreaks of an avian-origin H5N8, H6N1, H7N9, H10N8 influenza viruses raise concern of the emergence of novel reassortant viruses in Eurasia and the potential threat to the human population. Central Asian Region covering a large part of Eurasia is of special interest for influenza virus ecology and evolution. The importance of this region has been confirmed by the previous outbreaks of HPAI H5N1 among wild birds in 2009 and 2010. Avian and Human influenza virus (AIV; HIV) surveillance is an important task prior the fundamental study and introduction these data in practice. The study was aimed for collecting specific data on different influenza strains distribution and phylogenetics, comparing this data to the data from other part of the world and filling the gap in the research of influenza A viruses evolution trend in Russia.

Material/methods: The specimens were tested for AIV and HIV by standard methods. Viruses were isolated and studied by standard virological and molecular-biological methods according to WHO and OIE manuals.

Results: During surveillance study in last decade more than 20500 samples from different animal species and humans were collected in Russia, Mongolia and Kazakhstan . The report focuses on some pathogenic, epidemiological and evolutionary aspects of animal-origin influenza and human viruses including H5N1 isolated in Northern Eurasia. During surveillance for AIV more than 300 AIVs were isolated and 25 different subtypes were detected. Moreover, we isolated some rare subtypes including H1N2, H8N8, H13N8, H10N7, H15N4, H16N3, LPAI H5N1. Some of them have not been detected in Russia earlier or elsewhere. Phylogenetic analysis of the M gene of isolated viruses revealed different lineages of influenza viruses isolated and some evolutionary trends are discussed.

Conclusions: Thus, in this study we have shown circulation of different Avian Influenza viruses in Russia in last decade. We conducted the pathogenic potential assessment of the viruses with molecular-biological analysis and animal models. We found some viruses to be reassortant containing the segments of the different genetic lineages. We studied all basic genetic markers of biological characteristics. The report contains more detailed comparative virological, molecular, pathogenic characteristics of viruses. Some molecular-epidemiological aspects are discussed. This study demonstrates the need for ongoing surveillance to detect new variants of influenza viruses and facilitate prevention of outbreaks.

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