

The specificity of examined sandwich-ELISA variants was high, the sensitivity widely varied. The best result (7 ng/ml of purified AV 6 type) was obtained with capture MAbs #1 and PX conjugate of these MAbs. For AV antigens detection in infected cell the most promising is MAbs #2 FITC conjugate that allows to detect AV of epidemic types in infected cells in form of nuclear localized clear fluorescence. Usage of MAbs for development of high sensitivity and specificity test-kits for differential diagnosis of AV infection provides new possibilities for medical practice. Diagnostic properties of developed sandwich-ELISA and MAbs #2 FITC conjugate will be investigated with clinical samples.

3.48

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THE ROLE OF MOLECULAR-GENETIC RESEARCH IN THE SYSTEM OF EPIDEMIOLOGICAL SURVEILLANCE OVER ENTEROVIRUS INFECTION IN THE RUSSIAN FAR EAST AND SIBERIA

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A seasonal peak of enterovirus (EV) incidence is typical for majority of the constituent entities of the Russian Far East and Siberia. The spectrum of identified EV is diverse. Genetic variability of EV leads to emergence of new sub-subtypes.

The goal of the research was to evaluate the role of genotyping and phylogenetic analysis in epidemiological surveillance over enterovirus infection (EVI).

Epidemiological analysis was performed based on the official reporting forms. A total number of 1474 environmental samples, biomaterial from patients with EVI and exposed persons were analyzed via molecular-genetic methods. Reconstruction of genetic affinity was performed using Bayesian modeling.

Circulation of Russian and foreign EV strains was registered in the Russian Far East and Siberia. The most epidemiologically significant strains were as follows — Coxsackie B-4, B-5, ECHO-6, 9, 30. During the last four years Coxsackie A, mostly Coxsackie A-6 was also identified. The breakouts of Coxsackie A-6-infection were registered in children's ensembles in the Amur, Sakhalin and Khabarovsk Regions. Most EV had a genetic relation to reference sequences obtained from the GenBank database. This indicates the possibility of importation of EVI from different countries. Epidemiological investigations confirmed that some cases were imported. That said, during the summer season of 2017 EVI was diagnosed in patients arrived from resorts located in Turkey, Vietnam and Tunisia. The diseases were caused by Coxsackie A-6, Coxsackie A-2, EV-A71C1 variants as well as EV-C104 that was never registered in Russia before.

Molecular-genetic research not only promotes the enhancement of diagnostic subsystem of epidemiological surveillance, but also improves evaluation of epidemiological situation in the constituent entities of the country, facilitates identification of territorial peculiarities of genetically isolated and epidemiologically significant EV variants circulation, helps to identify imported cases of EVI.

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CONTROL OF INFLUENZA VIA VACCINES: CHALLENGES AND PERSPECTIVES AS VIEWED BY VARIOUS STAKEHOLDERS

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Influenza remains one of the principal challenges of modern healthcare on a global scale. Despite vaccination efforts, morbidity and mortality — especially among high-risk groups during seasonal epidemics — are high. Each year more emerging and re-emerging strains of animal origin are designated as having pandemic potential. Vaccines are the cornerstone of influenza control, including mitigation of yearly epidemics and out-of-season outbreaks, as well as prepandemic preparedness. Challenges, however, still remain, and here we explore varying views of different stakeholders (international agencies, regulators and manufacturers) as one of the reasons why.

Influenza virus is constantly evolving, thus, recommended strains for seasonal vaccines are regularly updated. Current WHO position includes 3- and 4-valent vaccines; and a nominal 25% increase in manufacturing capacities is needed for the switch to the latter. Moreover, even a single change in strain recommendation would require manufacturers to develop a new process within 6 months at most, and strain yield and HA activity for the candidate virus may be lower than had been anticipated. Separate WHO recommendations for tropical countries (similarly to northern and southern hemispheres) are still highly debatable. Until then local authorities at the country level should make the decision; however, current-season vaccines may already (or yet) be unavailable.

Though effectiveness, safety and economical feasibility for influenza vaccines has been proved numerous times, manufacturing capacities worldwide are still lacking. Current technology is classic at best and utilizes chicken embryos, whereas promising approaches (e.g. cell cultures) would require overhauling of the whole monitoring (e.g. GISRS) and manufacturing system. Academia could generate a breakthrough (e.g. next generation vaccines), but the transition from a prototype even to a preclinical setting is a very high-risk and money-intensive endeavor. Similarly, since there is no guaranteed market for prepandemic influenza vaccines, except periodic stockpiling by international or national bodies, R&D activities in this area for manufacturers are not a priority. Finally, we have lately seen a surge of support for the anti-vaccination movement.

Thus, combined efforts of all stakeholders are urgently needed to advance control of influenza via vaccines to the next stage and as part of the universal health coverage paradigm.

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CROSS-ANTIGENIC AND IMMUNOGENIC FEATURES OF CANONICAL AND NEW GENOGROUPS OF ENTEROVIRUS 71

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Enterovirus 71 (EV-A71) is a member of the *Enterovirus A* species. EV-A71 is a leading public health problem, because