2.21 doi: 10.15789/2220-7619-2018-4-2.21

ISLAND RND FOUND IN A STRAIN OF *VIBRIO CHOLERAE* ISOLATED IN THE RUSSIAN FEDERATION

S.O. Vodop'ianov, A.S. Vodop'ianov, R.V. Pisanov, T.N. Borodina, I.P. Oleynikov, S.V. Titova

Rostov-on-Don Antiplague Institute, Rostov-on-Don, Russia

Genetic islands, VPI-I, VPI-II, VSP-I, VSP-II, ICE, VcB played an important role in *Vibrio cholerae*, providing virulence and pathogen survival. However, the authors' efforts are primarily aimed at the analysis of genetic islands in toxigenic *(ctx$^+$)* strains. Meanwhile, in the Russian Federation for many years, non-toxic *(ctx$^-$)* strains of *Vibrio cholerae* have been consistently isolated from the objects of the environment. The causes of stable residence *(ctx$^-$)* strains are unknown, and the possible role of genetic elements in this process has not been investigated.

The aim of this work is to analyze a new genetic element identified by us as the island of RND detected in a nontoxigenic strain *V. cholerae* O1 El Tor 278 isolated in August 2017 from the Temernik river.

To achieve this task, we have conducted whole genome sequencing of strain 278 using sequencers MySeq and MinION.

The RND island is localized to the second chromosome, has a size of 43.596 base pairs and contains 51 open reading frames. On two sides it is limited by the genes of glycine cleavage system aminomethyltransferase T and threonine-tRNA ligase. Four genes VCA0281, VCA0284, VCA0285 and VCA0286, described earlier in the composition of the island VcB in *tcpA*$^+$ strains, are also included in the island of RND.

In strains presented in GenBank, RND island was detected in three non-toxic strains of *V. cholerae* (1154–74, Env-390, 2012Env-9). Given that the first strain of 1154–74 with the island of RND belonged to the serogroup O49 and was isolated in India in 1974, and two other strains of serogroup O1 found in Haiti in 2012, it can be assumed that the island of RND is capable of horizontal transport, which may partly explain the global spread of this genetic structure. In our opinion, additional research is needed to study the prevalence of the island of RND and the possible function of genes in its composition.

2.22 doi: 10.15789/2220-7619-2018-4-2.22

APPLICATION OF A COMPLEX OF METHODS IN LABORATORY DIAGNOSTICS OF WEST NILE FEVER

T.V. Zamarina[1,2], N.P. Khrapova[1,2], G.A. Tkachenko[1,2], A.A. Baturin[1,2], M.L. Ledeneva[1], L.V. Lemasova[1], T.N. Sharov[1], Y.A. Kuzyutina[1,2], A.M. Markin[1,2], N.N. Teteryatnikova[1]

[1]Volgograd Research Anti-Plague Institute, Volgograd, Russia; [2]Volgograd State Medical University, Volgograd, Russia

The aim of the study was to assess the feasibility of two methods, commonly used in laboratory diagnostics of West Nile fever (WNF). We used 148 blood samples obtained from presumably WNV-infected patients to identify WNV markers (IgG, IgM, RNA WNV). All samples were tested by a reference laboratory for WNF between 2015–2017. Based on MUK 4.2.3009-12 normative guidelines numerous laboratory tests, including RT-PCR ("AmpliSens WNV-FL", Central Research Institute of Epidemiology, Russia), ELISA ("Anti-West Nile Virus ELISA (IgM)", "Anti-West Nile Virus ELISA (IgG)", Euroimmun Ltd., Germany), were carried out to confirm the diagnosis of WNF. WNV-specific antibodies were detected in 65 (44%) samples. Immune responses to WNV without a specific viral RNA were identified in 63 (42.5%) samples. Specific IgM were identified in 23 (15.5%) samples, while IgG — in 10 (6.7%) samples. Viral RNA was detected in 2 (1.3%) samples. There were no cases of identifying WNV RNA without immune response in all blood samples. Our findings indicate that ELISA has more diagnostic utility than RT-PCR in WNF laboratory diagnostics. Conversely, a low percentage of positive PCR results can be explained by untimely examination of patients and a short period of viremia. The reliability of WNF diagnosis can be enhanced by simultaneous identification of several specific markers, therefore at any stage of the disease it is necessary to use a set of basic immuno- and genodiagnostic methods.

2.23 doi: 10.15789/2220-7619-2018-4-2.23

THE USE OF MOLECULAR GENETIC METHOD TO DETERMINE THE ETIOLOGY OF COMMUNITY-ACQUIRED PNEUMONIA IN SERVICEMEN

S.D. Zhogolev, P.V. Kulikov, K.D. Zhogolev, R.M. Aminev, S.R. Roubova, A.A. Kuzin

S.M. Kirov Military Medical Academy, St. Petersburg, Russia

Community-acquired pneumonia is extremely relevant for conscripts because of the high level of morbidity of military personnel, the severity of the clinical course with the threat of deaths, the danger of serious complications such as exudative pleurisy and myocarditis, an increase in the frequency of protracted forms and repeated diseases, the tendency to epidemic spread in the troops with coverage in a short time (December-February) a significant proportion of the recruits. For the use of adequate means of prevention and treatment of pneumonia in servicemen it is important to take into account their etiology.

The aim of the work was to study the etiology of community-acquired pneumonia in military conscripts by polymerase chain reaction (PCR diagnosis).

The results of PCR diagnostics of sputum and swabs from the throat of patients with pneumonia of conscripts admitted for treatment at the Military medical academy and the district clinical military hospital in St. Petersburg in 2014–2017 are analyzed.

The frequency of determining DNA *S. pneumoniae* in patients with pneumonia was the highest — 56.3%. *Haemophilus influenzae* DNA was detected in 16.2% of cases. DNA *Mycoplasma pneumoniae* and DNA *Chlamydophila pneumoniae* were found in 13.4 and 8.1% of cases, respectively. Among agents of the viral nature adenoviruses were the leaders. The detection rate of *adenovirus* DNA was 35.9%. RNA of *rhinoviruses* was found in 23.5% of patients with pneumonia. RNA of *influenza A and B viruses* were detected in 7.6 and 4.0% of cases, respectively. RNA of *RS*-virus were detected in 3.0%, RNA *virus parainfluenza* — in 2.1%, RNA *metapneumovirus* — in 3.4%, DNA *bocavirus* — in 1.9%, *Legionella pneumophila* DNA — in 1.6%, RNA of *enteroviruses* — in 9.3% of patients with pneumonia. Most of the pneumonia — 56.1% — was of mixed, mainly of viral-bacterial etiology, more often — of adenovirus-pneumococcal etiology.

During the PCR diagnosis in the period from 2014 to 2017 the preservation of the leading role of pneumococci and adenoviruses in the etiology of pneumonia in conscripts was revealed. Mixed viral-bacterial infection was dominated.