



ABSTRACT BOOK



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**INTERNATIONAL SCIENTIFIC
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INFECTIOUS DISEASES



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ANALYSIS OF THE EFFECT OF GENE POLYMORPHISM ON THE COURSE OF EPSTEIN-BARR VIRUS INFECTION

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Introduction. Currently, infectious diseases occupy a dominant place in human pathology. The relevance of the Epstein-Barr virus infection (VEB) is due to a high degree of infection of the population around the world, as well as specific antibodies to this virus, detected in almost 95% of the adult population.

Materials and methods. We have examined 96 patients with chronic VEB infection, the main clinical manifestations of which were various immunopathological and immunodeficiency states, as well as 10 patients who had undergone a history of VEB without any complaints at the moment. The comparison group consisted of 10 clinically healthy people who had no record of infectious mononucleosis. Polymorphism of the genes was determined using the RFLP method (polymorphism of the length of restriction fragments) and the real-time PCR method using the Corbett Research Rotor-Gene-3000 and the DNA-detecting DT-96 amplifier. To detect the polymorphisms under study, amplification of certain sections of the corresponding genes was carried out. To determine the allelic variation of the IL28B gene, a commercial DNA-technology test system was used. SNP 39743165T> G (rs8099917) and SNP 39738787C> T (rs2979860) of the IL-28B gene were used to detect point mutations using polymerase chain reaction and polymorphism of restriction fragment lengths. As a material for the study, DNA obtained from leukocytes was used with commercial reagents to extract DNA from the clinical material "Cytolysin" by AmpliSens (Russia). Statistical processing of the results of the study was carried out in accordance with the recommendations for statistical processing of biomedical data. The statistical software package STATISTICA 10.0 was used.

Results of research. A group of patients with a record of VEB who do not currently have any complaints, and also in the comparison group for the IL-28B gene, found the CC genotype at the locus rs12979860, and the TT genotype at the locus rs8099917. This suggests that in patients with chronic VEB infection, when the genotype of the CC genotype in the locus rs12979860 and the TT genotype at the locus rs8099917 are detected in the IL-28B gene, a more favorable course. In the analysis of single nucleotide substitutions in the regulatory regions rs8099917 and rs12979860 of the gene IL28B, statistically significant evidence was obtained of a non-random combination of allele pairs CC and TT in individuals with a more favorable course of EBV infection was also obtained, and the number of episodes of exacerbation during the year is significantly less.

Conclusions. The data suggest that the IL-28B genotype is a significant factor influencing the favorable course of the VEB infection, the frequency and severity of episodes of exacerbation throughout the year, and even the probability of transition or non-transition of the disease to a chronic form, and is an important factor in the

prognosis. A more favorable course of EBV infection was noted in patients with CC genotype at the locus rs12979860 and TT genotype at the locus rs8099917 compared with the genotypes of CT and TT in the locus rs12979860 and the genotypes GT and GG at the locus rs8099917. Thus, the study of the genotype of IL-28B is an urgent issue and requires further study.

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PREVENTION OF CHOLERA

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Introduction. Cholera is an acute epidemic infectious disease of the small intestine characterized by watery diarrhoea, extreme loss of fluid and electrolytes, and severe dehydration. It can be fatal. It is caused by eating food or drinking water which is contaminated with a bacteria called *Vibrio cholerae* (*V. Cholerae*). Some common sources of contaminated food and water include: municipal water supplies, ice made from municipal water, foods and drinks sold by street vendors, vegetables grown with water containing human wastes, raw or undercooked fish and seafood caught in waters polluted with sewage.

Materials and methods. When a person takes the contaminated food or water, the bacteria release a toxin in the intestine that produces severe diarrhoea. Although cholera may be life-threatening, prevention of the disease is normally straightforward if proper sanitation practices are followed. In developed countries, due to nearly universal advanced water treatment and sanitation practices, cholera is no longer a major health threat. For example, the last major outbreak of cholera in the United States occurred in 1910–1911. Effective sanitation practices, if put in place and adhered to in time, are usually sufficient to stop an epidemic. There are several ways to stop the transmission of cholera, some of which are as follows: sterilization, sources, sewage, water purification. Sterilization: This includes proper disposal and treatment of infected faecal waste water produced by cholera patients and all contaminated materials (e.g. clothing, bedding, etc.) are essential. All materials that comes in contact with cholera patients should be sanitized well by washing them in hot water, using chlorine bleach if available. Hands should be thoroughly cleansed and disinfected with chlorinated water or other effective antimicrobial agents, when there is a touch of patients clothing, bed linens and so on. The WHO recommends rubbing a wet soapy hands together, for at least 15 seconds before rinsing, after visiting the wash-room, before eating or handling any food. Sources: Warnings posters should be posted with directions on how to decontaminate the water (boiling, chlorination etc.) for possible use, at contaminated water sources. General public education on the sources of infection and transmission should be given as well.

Sewage: Antibacterial treatment of general sewage by chlorine, ozone, ultraviolet light or other effective treatment before it enters the waterways or underground water supplies helps us to prevent undiagnosed patients from spreading the disease.

Salawu K., Raliat A.....	66
Sameja Majida.....	222
Schebetenko V.....	195
Sendeha O.....	223
Sesay-Tlahyoni A.	158
Shafranetskaya V., Sukhonosov R.	20
Shaikh A.	159
Shapoval V.	194
Sharlai K., Volkova J.	121
Shpylenko O.	122
Shubina M.	224
Shubina M.	67
Skopenko A.,Krasun O.....	160
Skoryi D.....	21
Skoryi D.....	68
Sokolnikova N., Kumar Ravi	69
Sokur O.....	124
Sokur O., Masalitina E.	225
Sorokina O. ¹ , Liadova T. ¹ , Kolesnik Y. ²	226
Srinath S.	125
Sukhina I. ¹ , Splyukhina O. ²	260
Sukhodolska O., Spuzyak A., Gavrylenko N.....	126
Sukhonos N., Diasamidze M.....	70
Sukhonos N., Hrechukha A.....	71
Sultan M.	161
Sultan M.	162
Sultan M.	176
Sultan Mohamad.....	72
Surendran Arun, Kucherenko O., Freeman Elvera, Clio Jis Francis	227
Sushetska D., Zatoloka D.	196
Sushetskaya D., Zatoloka D., Matowe C.	72
Svetlichnaya K.....	197
Symkina V., Kauk O.	198
Sypalo A.	74