the seroprevalence of hepatitis A antibodies among children in Guinea by analyzing the detection of antibodies to hepatitis A virus in the local population. Materials and methods. The study was carried out in 2017 year in the Russian-Guinea Research Center for Epidemiology and Prevention of Infectious Diseases of Rospotrebnadzor (Kindia, Republic of Guinea) laboratory by St. Petersburg Pasteur Institute researches (St. Petersburg, Russia) with the assistance of the Republic of Guinea specialists. Serum samples were obtained from 71 conditionally healthy children living in the provinces of Boke (39 samples) and Kindia (32 samples) at the age 0−18 years (mean — 7.4±5.1 year), both sexes (male — 46.5%, female — 53.5%). There are no data about hepatitis A vaccination or case of hepatitis A in the past. Antibodies of the IgG class to hepatitis a virus were determined by enzyme immunoassay with the use of the test systems Vektohep A-IgG (manufactured by Vector-Best, Russia).

Antibodies of the IgG class to the hepatitis a virus were detected in 84.5% of samples. Seropositive persons at the age 0−5 years was 72.9% (95% CI: 55.9−86.2%), at the age 0−10 years — 77.6% (95% CI: 63.38−88.23%), at the 0−15 year — 83.0% (95% CI: 71.73−91.24%). The study was conducted in 1987−1988 years by A.P. Ivanov et al. showed the presence of antibodies IgG class to hepatitis a virus in children 0−10 years in 82.0% of cases, 0−15 years in 74.0%. There is no gender difference in antibody identification at the children 0−15 years (males and females 82.1% and 85.7% respectively, p = 0.5110), and among children 0−10 years (male and female — 76.2% and 84.0% respectively, p = 0.2167). In accordance with the WHO criteria, if antibodies detected in more than 50% of cases among children 0−15 years and less than 90% among children 0−10 years, this indicates the medium seroprevalence of hepatitis A in the population.

The prevalence of hepatitis A in accordance with our data, is at the middle level and has not significantly changed over the last 30 years.

HIGH BURDEN OF HEPATITIS B IN VIETNAM: IMPACT OF A HIGHLY HETEROGENEOUS VIRAL POPULATION

O.V. Kalinina[1,2,7], L.T. Duong[3], E.V. Lichnaia[1], A.T.L. Bui[4], C.V. Vo[4], D.P. Nguyen[3], G. Pham Thi[4], T.T.N. Bui[4], V.P. Chulanov[5], A.V. Dmitriev[6,7]

[1]St. Petersburg Pasteur Institute, St. Petersburg, Russia; [2]Almazov National Medical Research Centre, St. Petersburg, Russia; [3]Joint Russian-Vietnamese Tropical Science and Technology Center, Hanoi, Vietnam, [4]Institute of Military Preventive Medicine, Hanoi, Vietnam; [5]Research Institute of Epidemiology, Moscow, Russia; [6]St. Petersburg Institute of Experimental Medicine, St. Petersburg, Russia; [7]State Technological Institute, St. Petersburg, Russia

South-East Asia is highly endemic area for hepatitis B. In Viet Nam, 8.4 million individuals were estimated to live with HBV infection that resulted in 23 300 deaths in 2005. Here, we investigated naturally occurring genetic variants of hepatitis B virus circulating in general population in Viet Nam.

A total of 3080 adults of 18−79 years old from 16 regions (An Giang, Binh Duong, Dong Nai, Ha Giang, Hoa Binh, Hue, Kien Giang, Lam Dong, Kontum, Nghe An, Ninh Binh, Quang Tri, Thai Nguyen, Hi Phon, Kanh Hoa and Thanh Hoa) were enrolled in this study in 2012−2014. All serum samples were analyzed for the presence of HBsAg with Monolisa® HBsAg detection kit (Bio-Rad, USA) or rapid test (Alere Determine™ HBsAg, USA). As a result, 309 (10.03%, 95% CI, 8.99−11.15) out of 3080 adults were positive for HBsAg. HBV DNA was extracted from HBsAg positive serum samples. HBV genotypes were determined by phylogenetic analysis based on S or P genes.

A total of 117 HBV isolates were genotyped. Six HBV subgenotypes (B2, B4, B6, C1, C5; I) and two recombinant forms (B/C; C/B) were identified. Subgenotype B2 was found in 4 (3.42%, 95% CI 1.34−8.46) isolates; B4 — in 82 (70.09%, 95% C I 61.26−77.64); B6 — in 2 (1.71%, 95% CI 0.47−6.02); C1 — in 20 (17.09%, 95% CI 11.35−24.93); C5 — in 1 (0.85%, 95% CI 0.15−4.68); I — in 3 (2.56%, 95% CI 0.88−7.27); recombinant forms B/C — in 3 (2.56%, 95% CI 0.88−7.27) and C/B — in 2 (1.71%, 95% CI 0.47−6.02). The phylogenetic analysis revealed that Vietnamese HBV strains of subgenotypes B4, B2 and C1 formed the several distinct clusters that separated from other strains isolated in Asia. HBV strains belonged to other subgenotypes were scattered among Asian variants. Subgenotype I was found only in the northern mountain region. Based on "a" determinant in S protein the HBV strains were classified into four subtypes: adr, adw2, ayw1, ayw3. No amino acid substitutions, which may alter HBsAg antigenicity or be responsible for vaccine escape were detected in preS region as well as in major hydrophilic region of the S region.

The predominance of HBV subgenotype B4 in all studied regions indicates crucial impact of this HBV variant on the persistence infection in Viet Nam. The high genetic diversity of viral population highlights the multiple sources of infection, successful spreading of a variety of viral variants and provides insight into the driving force of the HBV epidemic process in Viet Nam.

MOLECULAR-GENETIC CHARACTERISTICS OF THE HEPATITIS B IN THE NANAYSKY DISTRICT OF THE KHABAROVSK TERRITORY

V.O. Kotova[1], O.E. Trotsenko[1], L.A. Balakhontseva[1], M.F. Ryazankina[2], E.A. Bazykina[1]

[1]Khabarovsk Research Institute of Epidemiology and Microbiology, Khabarovsk, Russia; [2]Far Eastern Medical University, Khabarovsk, Russia

Hepatitis B continues to stay a pressing issue due to frequent development of chronic cases of the disease.

Aim of the research was to analyze the genetic diversity of the hepatitis B virus (HBV) circulating among the indigenous population of the Nanaysky District of the Khabarovsk Territory.

A total number of 82 samples (59 women, 23 men) of blood plasma were obtained from the Nanaysky District patients with the diagnosis of chronic hepatitis B (CHB). According to the ethnic composition, there were 62.3% of Nanai people, 32.9% of Russians, Udege and Evenks totaled by 2.4% each. The HBV DNA was detected using the PCR kits "AmpliSens®HBV-FL" and "AmpliSens®Monitor-FL" (Central research institute of epidemiology of the Rospotrebnadzor, Russia). The PCR was followed by genotyping using a two-step PCR with primers to a conservative region of overlapping S and P genes. Phylogenetic analysis was performed with the MEGA6.0 software. Neighbor-Joining method was used to build the phylogenetic trees. Nucleotide distance was estimated via Kimura method.

HBV DNA was found in 46 (56.1%) samples of the blood serum. The viral load levels in 13 (28.3%) patients was low (< 10^3 ME/ml), in 26 patients it was intermediate (10^3−10^6 ME/ml) and in 7 cases it was high (> 10^6 ME/ml). The phylogenetic analysis was performed for 43 nucleotide sequences. Genotype D was dominant and was found in 34

samples (79.1%). The phylogram showed that the strains of one genotype divided into three subgenotypes: D1 — 1 (2.9%), D2 — 15 (44.2%) and D3 — 18 (52.9%). The genotype C was detected in 7 (16.3%) patients and four of them formed a cluster with Chinese samples that were registered in the GenBank database. Genotype A was isolated in 2 (4.6%) samples and formed a cluster with strains isolated in Poland and Belgium.

HBV genotype D comprised out of subgenotypes D1, D2, D3 and prevailed among the CHB patients living in the Nanaysky District of the Khabarovsk Territory. The second prevalent strain was genotype C. Genotype A was detected in individual cases.

THE OCCURENCE OF HEPATITIS C MARKERS AMONG RESIDENTS OF THE KINDIA PREFECTURE OF THE REPUBLIC OF GUINEA AND THE KHANH HOA PROVINCE OF VIET NAM

E.V. Lichnaia[1], O.V. Kalinina[1,2], T.L.A. Bui[3], V.M. Nguyen[3], V.C. Vo[3], T.H.G. Pham[3], T.T.N. Bui[3], P.T. Ha[3], N.Q. Pham[3], E.A. Bil'ko[4], A.S. Abdrashitova[4], D.M. Gando[5], M.Y. Boiro[5], A.A. Totolian[1], A.V. Dmitriev[6]

[1]*St. Petersburg Pasteur Institute, St. Petersburg, Russia; *[2]*Almazov National Medical Research Centre, St. Petersburg, Russia; *[3]*Institute of Tropical Medicine, Hanoi, Vietnam; *[4]*Institute Microbe, Saratov, Russia; *[5]*Institute of Applied Biology in Guinea, Kindia, Guinea; *[6]*Institute of Experimental Medicine, St. Petersburg, Russia*

Hepatitis C virus (HCV) infection plays an important role in liver diseases. The burden of HCV infection continues to be significant in low- and middle-income countries, especially in Asia and Africa. The global elimination of HCV by 2030 is possible with the advent of effective diagnostic methods available to the majority of the population. The aim of the study was to estimate the prevalence of serological and molecular HCV markers among the apparently healthy people in Kindia region of the Republic of Guinea and Khanh Hoa region of Viet Nam.

Serum blood samples were obtained from apparently healthy adults of the Kindia prefecture (n = 248, the average age was 41.59±9.89) of Republic of Guinea and Khanh Hoa province (n = 256, the average age was 41.98±11.73) of Viet Nam. The presence of total anti-HCV and the specific antibodies to the core, NS3, NS4, NS5 HCV proteins were determined using ELISA-kits (Diagnostic Test Systems LLC, Russia). RNA HCV in the serum samples was detected by real-time PCR using the "AmpliSens HCV-FL" kit (FBIS "CRIE", Russia). The confidence interval (95% CI) was calculated by the Wilson method.

Totally, anti-HCV was detected in 9 (3.63%; 95%, CI 1.92−6.75) of 248 adults from Kindia; in 3 (1.17%; 95%, CI 0.40−3.39) of 256 adults from Khanh Hoa. The uncertain results of the anti-HCV were obtained in 6 (2.42%; 95%, CI 1.11−5.18) of 248 residents of Kindia; one (0.39%; 95%, CI 0.07−2.18) of 256 residents of Khanh Hoa. RNA HCV was detected only in one (0.39%; 95%, CI 0.07−2.18) of 256 adults from Khanh Hoa, while RNA HCV was not detected in serum blood samples from Kindia.

The results of the occurrence of HCV markers in apparently healthy residents of both Kindia Prefecture and Kanh Hoa province do not differ from the available estimated metaanalisys data on the HCV prevalence in West Africa and South-East Asia. In order to assess the dynamics of the epidemic process, it is necessary to study HCV infection in different ethnic groups throughout the territory of both countries.

POLYMORPHISM THE *CCR2* GENE IN THE ST. PETERSBURG POPULATION

N.E. Lyubimova, A.V. Semenov
St. Petersburg Pasteur Institute, St. Petersburg, Russia

HIV infection is one of the main socially significant diseases of the world population. Resistance/susceptibility to HIV-1 infection is different. Chemokine receptors such as *CCR2* play an important role during infection with HIV-1. The gene for the chemokine receptor *CCR2* locates in the short arm of chromosome 3. The replacement of nucleotide *G* by nucleotide *A* at position 190 in the *CCR2* gene results in the replacement of the amino acid valine by isoleucine at position 64 (*CCR2-V64I*) in the primary sequence of the protein. This replacement slows the development of AIDS in HIV-infected. In Europeans the allele frequency of *CCR2-V64I* is 8−10%, blacks — 15−17%, Mongols — 20−25%. Knowing the frequency of polymorphic allele distributions can help predict the epidemic situation in the region. The aim of the work was to study the frequency of alleles of the *CCR2* gene in St. Petersburg.

The study examined a group of 411 conditionally healthy donors aged 0 to 95 years living in St. Petersburg. Genomic DNA was isolated from biological samples using commercial kits (Interlabservice, Russia). *CCR2* genotype polymorphism was detected by pyrosequencing on the PyroMark Q24 instrument (Qiagen) using primers of our own design.

Factors "sex" and "age" had no a significant influence on the frequency of distribution of the studied alleles. The distribution of genotype frequencies in the studied population does not differ from the Hardy−Weinberg Equilibrium. Wild-type genotype (*GG*) was detected in 320 people. 6 people were carriers of the genotype *AA*, and 85 people were heterozygotes (*GA*). Frequency genotype of the *CCR2* wild-type (*GG*) was 77.9%. Heterozygotes (*GA*) were 20.7%, homozygotes *AA* were 1.4%. The frequency of allele *G* was 0.88, allele *A* was 0.12. Thus, more than 20% people of the population in St. Petersburg have a protective allele of the *CCR2* gene.

The high incidence of allele *CCR2* makes it reasonable to screen HIV-infected people and groups at risk for HIV infection. The obtained data can be used to predict the development of the AIDS epidemic in St. Petersburg.

RECONSTRUCTION OF RECOMBINATION SITES IN GENOMES OF GENOTYPE 2 HEPATITIS C VIRUS STRAINS USING BIOINFORMATICS METHODS

A.I. Paramonov[1], Yu.P. Dzhioev[2], I.V. Kozlova[1], L.A. Stepanenko[2], I.V. Malov[2], S.I. Malov[2], V.I. Zlobin[2]
[1]*Scientific Center of Family Health and Human Reproduction Problems, Irkutsk, Russia; *[2]*Institute of Biomedical Technology, Irkutsk State Medical University, Irkutsk, Russia*

Hepatitis C virus (HCV) is an important human pathogen, causing an estimated 180 million chronic infections and annually 3−4 million new infections worldwide. Due to its genetic heterogeneity, HCV has been classified into seven major genotypes and about 80 subtypes. Although the different genotypes and subtypes share basic biological and pathogenic features they differ in clinical outcomes, response to treatment and epidemiology. HCV recombination raises many questions concerning its mechanisms and effects on the epidemiological and physiopathological features of the virus. The first natural recombinant strain of HCV was identified as recently as 2002. Since then,