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.

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

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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.

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

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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