

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.

7.9

doi: 10.15789/2220-7619-2018-4-7.9

### 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

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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 Khanh Hoa province do not differ from the available estimated metaanalysis 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.

7.10

doi: 10.15789/2220-7619-2018-4-7.10

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

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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.

7.11

doi: 10.15789/2220-7619-2018-4-7.11

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

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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,