UDC 578.891(571.56)

Genetic Characteristic of Virus C Hepatitis in the Republic of Sakha (Yakutia)

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Resume: Genetic characteristic of virus C hepatitis in the Republic of Sakha (Yakutia) is presented. Genotyping of virus of hepatitis C was carried out in the laboratory of the Central Research Institute of Epidemiology of the Federal Service of Supervision in the Sphere of Protection of the Rights and Well-being of Consumers (Rospotrebnadzor) of the Russian Federation, Moscow with application of PCR-test-system. This test-system allows identification of 4 genotypes of virus C hepatitis: 1a, 1b, 2a, 3a. During the years of 2007-2010 163 samples of viral RNA of the chronic hepatitis C patients from the Republic of Sakha (Yakutia) were genotyped.

Keywords: chronic virus C hepatitis (ChHC), hepatitis C virus (HCV), polymerase chain reaction (PCR).

Introduction: In spite of the fact that it quite recently became possible to study HCV, researchof it can be considered successful. There is no vaccine because of virus Chigh mutagenicity. Prevalence of virus C hepatitis beats all records in the world. According to various classifications 6, 11 and more genotypes and more than 90 subtypes of HCV are known [1, 2]. Millions of various quasitypes of HCV can exist in the organism of a person. Their existence can be explained by virus «escaping» of immune control of an organism that makes for occurrence of continually varying antigenic viral structures. There is constant «competition» between formation of new antigenic variants and development of antigen-neutralizing antibodies. And each time virus appears«a winner» but not human immune system.Some people became HCV carriers for a long (sometimes lifelong) period because of very high mutability of the virus. Genotyping of HCV in various regions of the world revealed that genotypes 1a, 1b, 2a and 3a are prevailed [7].Genotype 1b is dominating in Russia and it is registered in 50-56 % of cases in central part of Russia and in 80-83% - in the Far East [8, 9].

The purpose of research: studying of HCV genotype in patients suffering chronic virus C hepatitis in the Republic of Sakha (Yakutia).

Materials and methods: During the years of 2007-2010 163 samples of viral RNA of the chronic hepatitis C patients from the Republic of Sakha (Yakutia) were genotyped by means of PCR. 3 genotypes of HCV (1b, 2a, 3a) were registered, 2 genotypes (mixt) were isolated from a small amount of samples.

Genotyping of HCV was carried out using PCR-test-system in the laboratory of the Central Research Institute of Epidemiology of the Federal Service of Supervision in the Sphere of Protection of the Rights and Well-being of Consumers (Rospotrebnadzor) of the Russian Federation in Moscow (V.N. Chulanov - the head of the laboratory, Doctor of biological sciences).This test-system allows identification of 4 genotypes of virus C hepatitis: 1a, 1b, 2a, 3a.

Results and discussion:genotype 1b of HCV was registered more frequently – in 116 patients (71.2%). Genotype 3a was found in 26 patients (16%) and genotype 2a – in 14 patients (8.6 %). Two genotypes (mixt) were isolated in a small amount of samples: 1b+3a - in 3 samples (1.8%), 1b+2a - in 1 sample (0.6%), 1b+1a – in 2 samples (1.2%) and 1a+2a – in 1 sample (0.6%).

The same as in the Russian Federation genotypes 1b and 3a of HCV were revealed more frequently in chronic hepatitis C patients in the Republic of Sakha (Yakutia) - in 71.2% and 16% of studied cases accordingly. In Yakutia genotype 1b was found asethiologic factor of hepatitis C in 116 cases

(71.2%), less frequently 3a genotype – 16%. Unlike chronic hepatitis C patients from other regions of Russia presence of two genotypes in different combinations was revealed in the population of Yakutia. It should be noted that in the population of Yakutia genotypes 3a, 2a were met independently or in combination of other genotypes. They are known as seldom revealed genotypes in chronic virus C hepatitis patients (3a – 16%, 2a – 8.6%) [3].Interrelation of infection of virus C hepatitis and its genotype was confirmed by Russian and foreign researchers. Thus, 3a (in Yakutia – 16%) and 1a genotypes are more often revealed in patients addicting drug intravenously whereas 1b genotype is more often revealed in chronic virus C hepatitis patients infected as the result of medical parenteral manipulations [4, 5, 6].Combinations of genotype 1b with other genotypes (1b+3a, 1b+2a, 1b+1a, 1a+2a) in chronic hepatitis C patients in Yakutiaprove variety of ethiologic structures of the disease, severity of clinical course, resistance to antiviral therapy (Fig.1).

163 serum samples from chronic hepatitis C patients were studied, 75 of them with genotypes 1b, 2a, 3a of HCV were distributed according to age, sex and ethnic attribute of patients.

Prevalence of ChHC according to sex and depending on virus genotype was the following: 1b, 2aand 3a genotypes prevailed in women – 56%, 58% and 62%, in men it was – 44%, 42% and 38% accordingly.

Prevalence of ChHC according to age and depending on virus genotype is presented in Table 1. Average age distribution of patients depending on virus genotype did not reveal any significant difference in men and women. Average age in men with 1b genotype was 39.8±7.8, in women – 36.9±10.7. Difference in distribution of ChHC patients with 2a genotypeaccording to age was not revealed. Average age in men was 43.4±16.9, in women – 42.5±9.4. Average age of patients with 3a genotype was in men – 30.3±4.1 and in women – 32.8±8.7.

Distribution of ChHC patients according to their ethnic attribute and depending on virus genotype is presented in Figure2. Genotypes 1b and 2a prevailed in indigenous population – 80%, 58.3% whereas genotype 3a prevailed in Russian population and in other nationalities – 61.5%.

Conclusion: Thus, it was established that in the Republic of Sakha (Yakutia) as well as through Russia genotypes 1b (71.2%) and 3a (16%) prevailed. It can be explained by the fact that 1b genotype has greater viral load in comparison with other genotypes of HCV and it is almost unresponsive to antiviral therapy.Distribution of ChHC according to sex and depending on virus C genotype showed women prevalence.Distribution of ChHC patients according to their ethnic attribute and depending on virus genotype revealed that genotypes 1b and 2a prevailed in indigenous population. Virus genotyping is highly informative both for therapeutic prognosis and for epidemiological studies.

References:

Akimkin V.G. Hospital-acquired Infection of Virus B and C Hepatitis: Epidemiology and Preventive Measures // Epidemiology and Infectious Diseases. – 2006. - №6. – P. 13-17.

Aleinik M.D., Ryabikova T.F., Bakaeva I.A., Makarevich I.K. Epidemiologic Characteristic of Virus B Hepatitis Prevalence and Ways ofAntiepidemic Measures Perfection // In the book: «Viral Hepatitis». – Gorkij, 1988. – P. 5-9.

Bazarova M.V. Clinicoepidemiologic Estimation of Efficiency of Hepatitis B Vaccination in Newborns of Women Infected Virus B Hepatitis // Abstract of Cand.ofMed.Siences Dissertation. – Moscow, 2002. – 27 p.

Vasilieva E.A., Sologub T.V., Mukomolov S.L.Comparative Clinico-laboratory Characteristic of Virus B and C Hepatitis Acute Form Patients // In the book: «Actual Problems of Infectious Pathology». – St.Petersburg, 1993. – V.2. – P. 81.

Viral Hepatitis / A.G. Rakhmanova, V.K. Prigozhina, V.A. Neverov, et al // St.Petersburg. – 1995. – 35 p.

Viral Hepatitis in the Russian Federation: Analytical Review / Ed. A.B. Zhebrun. – St.Petersburg, 2000. – Vol. 3. – 256 p.

Maertens G., Stuyver L. Genotypes and Variation of Hepatitis C Virus // The Molecular Medicine of Viral Hepatitis / Ed. T.J. Harrison, A.J. Zuckerman. – 1977. – P. 183-233.

Sprengel R., Kaleta E.E., Will H. Isolation and Characterization of Hepatitis B Virus Endemic in Herons // J. Virl. – 1998. – Vol. 62, №10. – P. 3832-3839.

Krugman S., Giles J.P., Hammond J. Hepatitis Virus: Effect of Heat on the Infectivity and Antigenicity of the MS-1 and MS-2 Strains // J. Infect. Dis. – 1970. – Vol. 122, №5. – P. 432-436.