

Секция «Фундаментальная медицина»

Genotype distribution of hepatitis C virus infection in the general population
in Republic of Srpska
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Introduction: Hepatitis C virus (HCV) is a major cause of chronic liver disease and hepatocellular carcinoma worldwide. The most recent WHO estimate of the prevalence of HCV infection is 2%, ranging from 0.6% to 2.3% in North America, Northern and Western Europe and Australia. HCV has a high molecular diversity worldwide. A recent international standardization of the nomenclature proposed a classification into 6 genotypes (1 to 6) and more than 70 subtypes. Knowledge on the HCV genotype is now used for tailoring therapeutic modalities. The aim was to determine the distribution of HCV genotypes in Republic of Srpska.

Materials and methods: Our retrospective study included 139 patients. We observed newly registered patients since 2011 until 2014. Age of patients was between 5 and 77 years (45 years average). HCV viral load in every patient was determined with the quantitative COBAS AMPLICOR® HCV test v2.0 and with Real - time COBAS® TaqMan® HCV Test. We used The LINEAR ARRAY HCV Genotyping Test for the determination of HCV genotypes 1– 6. Descriptive statistics and chi-square test were used as statistical analysis methods.

Results: Genotype 1 was predominant, with 85 patients (61.2%) ($p < 0,0001$), followed by genotype 3 (28,1%), 4 (10,1%) and 2 (0,7%). Among genders also genotype 1 was predominant (men 60,2%, ladies 63%). There was no statistically significant difference in frequency of genotypes among genders. Genotype 4 was associated significantly with patients aged more than 40 years (16,6% vs 1.6% for patients aged less than 40 years, $p < 0.0001$). We were not able to find any association of genotypes and demographic data for the patients.

Conclusion: The genotype distribution is similar to other European countries, genotype 1 is predominant. Unfortunately genotype 1 is known as the most difficult to treat. We can assume that the main methods of transmission are blood transfusions and unsafe medical procedures. For the presence of genotype 4 viruses identified in our study, we can assume that their presence could be related to trip in Africa during working career.

Key words: HCV, genotypes, Republic of Srpska.

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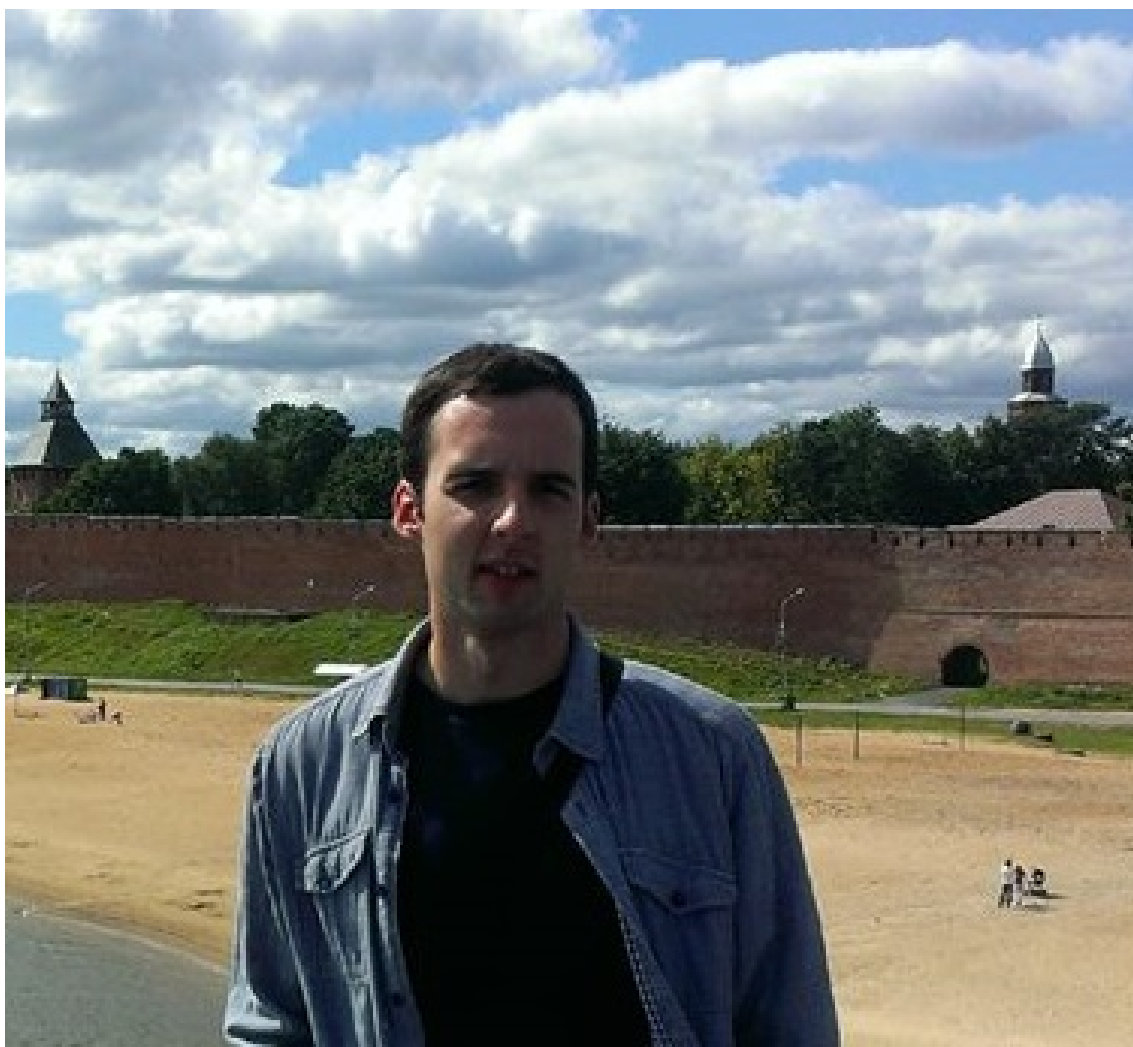


Рис. 1: Райко Чулибрк