Background: Acute intestinal infections (AII) represent one of the most significant health problems across the world. Among them, rotaviruses of group A (RV) and noroviruses (NV) play a leading role in the structure of viral diarrhea in infants and children up to 5 years. The aim of this work was to study the genetic diversity of noroviruses and rotaviruses circulating in different regions of Ukraine.

Methods & Materials: It was examined 537 fecal samples from children under the age of 5 years with AII in different geographical regions of Ukraine, representing north, south, east, west and center of the country and collected during the autumn and winter epidemic seasons of 2007–2012 yrs. (Fig. 1). Clinical specimens were tested for the presence of RV and NV with RT-PCR methods, ELISA and rapid tests based on immunochromatographic analysis. Genotyping of positive samples was performed via RT-PCR with set of primers, specific for different RV and NV genotypes.

Results: Results of the study showed that in Ukraine during epidemic periods in average 32.7% of the etiological agents of AII were RV and 53.3% were NV. RV were etiological agents in 34% of AII cases. Result of genotyping discovered diversity of four major genotypes of rotaviruses group A: G1P[8], G4P[8], G3P[8], G2P[4], with the dominance of genotype G1P[8] (32.8%) in the study period (Fig. 3).

Conclusion: We characterize the genetic spectrum of NV and RV circulating in Ukraine and their propagation characteristics in different regions of the country. It was shown that RT-PCR is the “gold standard” in the etiological diagnosis of AII, and simultaneous genotyping - the modern “tool” in the study of intestinal viruses, which is especially important in the context of the implementation of the programs of epidemic disease surveillance and prevention.

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Hepatitis C virus genotypes in population of prisoners and intravenous drug addicts in Croatia

Background: Hepatitis C virus (HCV) infection is an important sociomedical problem worldwide, and in Croatia as well. The aim of this study was to determine the differences in genotypes distribution of HCV in two risk groups, among prisoners and among intravenous drug addicts in north-western Croatia. Because of the dominant prevalence of genotype 3 in Croatian intravenous drug users, it is expected that HCV genotype 3 will be more prevalent in the intravenous drug addicts group than in the prisoners group in studied geographic area. The data about HCV genotype distribution in population of prisoners in Croatia are missing and generally the most prevalent genotype is subtype 1b.

Methods & Materials: The study included 67 seropositive patients with chronic HCV infection classified in two groups, the first group consisted of prisoners (n = 32) and the second one of intravenous drug addicts (n = 35). The patients from both groups underwent diagnostic procedures during 2010, when they were all anti-HCV positive and they not received any antiviral therapy. HCV RNA was detected from sera by using qualitative (COBAS AMPLICOR Hepatitis C Virus Test v. 2.0) and quantitative polymerase chain reaction (COBAS AMPLICOR HCV MONITOR Test v. 2.0) and genotyped (LINEAR ARRAY HCV Genotyping Test).

Results: HCV RNA was present in 52 of 67 samples (77.6%). The 88.6% prevalence of HCV RNA among anti-HCV-positive intravenous drug addicts was significantly higher than the 65.6% prevalence of HCV RNA among seropositive prisoners (p < 0.05). HCV genotype 3 was significantly more frequent among intravenous drug addicts than among prisoners (p < 0.01) and it was the predominant type in the intravenous addicts group (80.7%), while genotype 1 and 3 were equally distributed in the prisoners group.