

Results: In 2000 it was discovered 6216 HIV-positive, of which - 648 AIDS patients (diagnosis is put the first time), accounting for 10.42% of all detected HIV-infected. The number of newly diagnosed HIV-positive increased with each passing year, and the part of patients on III-IV stage of AIDS. In 2005, the percentage of patients already was 30.61% (from 13786 new cases of HIV infection - 4220 were already sick with AIDS), which exceeded the corresponding index in 2000 almost tripled ($r \leq 0,05$).

During the following years (2006-2008) despite the increasing of virus-carriage cases in the population, the proportion of AIDS patients with newly diagnosed was declined and in 2009 was 22.38% (from 19859 newly diagnosed HIV-infected the patients were 4446). However, the positive trend is not entrenched and the following year was marked by a significant increase in both the number of new HIV infections and the proportion of patients among them. As of July 1, 2014 the number of newly diagnosed HIV-positive was 10777, including 5459 (50.65%) - the new AIDS-patients.

Conclusions: Since 2000, the annual growth of HIV-carriers (except 2012) is observed. The proportion of AIDS-patients among the newly diagnosed HIV-positive during this period increased on 40.23 %. Thus, despite improving diagnosis of HIV/AIDS, the disease manifests itself mainly in stage III-IV, which leads to the searching of new, affordable and effective screening methods of population.

No conflict of interest

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Monitoring and Diagnostic Tools

Features of mineral metabolism disorders in patients Co-infected with HIV/HCV

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Background: Hepatitis C virus (HCV) and human immunodeficiency virus (HIV) are characterized by their wide distribution and ability to cause health disorders of the working population, thus causing significant morbidity and mortality worldwide. Chronic hepatitis C is observed in 60-70% of HIV-infected individuals, due to the common modes of transmission of viruses. Co-infection with HIV/HCV is an important public health problem, since viruses, acting synergistically accelerate the progression of liver disease. HIV accelerates the progression of chronic hepatitis C to cirrhosis and hepatocellular carcinoma, thus increases 'liver' mortality.

Trace elements have a significant impact on the metabolic processes in the body and have a close relationship with the enzymes, hormones, vitamins and other biologically active compounds. The content of trace elements in the blood is a valuable diagnostic feature in many pathological conditions. Insufficient knowledge of their content in patients co-infected with HIV/HCV proves the feasibility of studying their role in the pathogenesis of this disease.

Materials & Methods: Study on the work carried out at the Department of Infectious Diseases of Kharkiv National Medical University, located at the Regional Clinical Hospital of Infectious Diseases of Kharkiv and Kharkiv regional center for prevention and control of AIDS.

The content of trace elements (copper (Cu), iron (Fe) and zinc (Zn)) in serum were determined by atomic absorption spectrophotometry. Features of mineral metabolism were studied in 99 patients: 32 patients with chronic hepatitis C, 34 HIV-infected patients and HIV and 33 patients co-infected with HIV/HCV. The age of patients ranged from 20 to 52 years old. The comparison group consisted of 32 healthy subjects. Blood samples were taken for the study after signing the informed consent of the patients.

Results: Patients with chronic hepatitis C when compared to the control group, showed a reduction in the content of Zn, haptoglobin, increase Cu, Fe and ceruloplasmin. In patients with HIV infection and co-infection with HIV/HCV a reduction of these trace elements (Zn, Cu, Fe) and acute phase proteins (ceruloplasmin, haptoglobin) was established. In patients co-infected with HIV/HCV when compared with HIV infection only revealed a lower level of Zn ($p < 0.001$), and lower content

of ceruloplasmin and haptoglobin. Patients co-infected with HIV/HCV, compared with a group of chronic hepatitis C have lower values for all parameters ($p < 0.001$). From this it follows that HCV-infection potentiates microelement disorder manifestations in patients with HIV infection.

Conclusions: Comprehensive assessment of the degree of deviation from the control indices of the content of trace elements and activity of metal dependent acute phase proteins showed that it was typical for patients co-infected with HIV/HCV, and also higher than that of HIV-infected patients with a factor of 1.2 and 2.2 times greater than levels in chronic hepatitis C patients.

No conflict of interest

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Monitoring and Diagnostic Tools

Molecular-genetic analysis of HCV and HIV in HIV/HCV co-infected patients living in Grodno region of Belarus

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Background: Prevalence of HCV-infection among HIV-infected European patients according to WHO is 40% on the average. In Eastern and Southern Europe it is higher (47,7 and 44,9%, respectively) than in Northern Europe (24,5%) as there are more IDU in the first two regions.

In the Republic of Belarus HIV/HCV co-infection is one of the most widespread HIV associated infections, making up 40-50% in different regions of Belarus.

The aim of the research is to detect prevalence and phylogenetic relationship of various HCV

genotypes and HIV subtypes in patients with HIC/HCV co-infection living in Grodno Region of Belarus.

Material & Methods: Samples of blood plasma were taken from 36 HIV/HCV co-infected patients for the analysis of phylogenetic relationship between HCV genotypes. HCV RNA was extracted from these samples using a kit «RNA-sorb» (CRI of epidemiology, Russia) in accordance with instructions. To compare genetic sequences software «Clustal W» was used. HIV subtypes with phylogenetic relations were detected in 35 patients using RT-PCR module of the commercial test-system «Corbet Research». Sequencing of the purified fragments were performed in the genetic analyzer «ABI Prism 3100 Avant» («Applied Biosystems», USA). Design and synthesis of primer pairs to HIV gag and env genes was performed using GenBank database and nucleic acid synthesizer Expedite 8900, USA. Phylogenetic analysis of nucleotide sequence was performed using software «Mega 4» (trees were constructed with neighbor-joining method).

Results: According to molecular-genetic HCV analysis in 36 HIV/HCV co-infected patients 19 (52,8%) samples belong to 3a genotype, 6 (16,6%) – to 1b, 11 (30,6%) corresponded to 1a genotype. Nucleotide p-distances inside each group made 0,06; 0,08; and 0,02 for 3a, 1b and 1a genotype, respectively. All the samples, corresponding to 1a, 1b and 3a genotypes were clustered around standard samples, obtained from GenBank, and formed several phylogenetic groups, indicating one source of their origin. According to molecular-genetic HIV analysis in 35 HIV/HCV co-infected patients all 35 samples were positive for env gene and 33 (94,3%) belonged to A subtype, prevalence of which at present is 80-85% throughout Belarus; 2 samples belonged to B subtype. Mean evolutionary p-distance inside nucleotide HIV sequences for all examined samples belonging to A subtype made 0,04 for gag gene and 0,13 – for env gene, which indicates a prolonged circulation of the same strains throughout the country.

In phylogenetic analysis of 22 gag gene positive samples it was detected that 21(95,5%) of them belong to A subtype, forming joint phylogenetic group together with reference samples from Russia and Ukraine; 1 (4,6%) sample corresponded to B subtype. Considering gag gene this sample belonged to A subtype. Ma-ul sample belonged to B subtype according gag and env gene.