

## 7. HIV, HEPATITIS AND OTHER SOCIALLY SIGNIFICANT INFECTIONS

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### THE ANALYSIS OF TRANSMITTED HIV-1 VARIANTS AMONG ACUTELY INFECTED PEOPLE WHO INJECT DRUGS USING NGS APPROACH

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The phenomenon of a genetic bottleneck, i.e. transmission of one or a few variants of the virus, has been widely studied for sexual transmission, but for people who inject drugs (PWID) the available data are not conclusive.

The objectives of the study were real-time detection and follow-up of individual cases of acute HIV-1 infection (AHI) and analysis of the genetic variability with SGA and NGA approaches.

We analyzed full-length *env* genes of transmitted strains using single genome amplification (SGA) and Bayesian Evolutionary Analysis Sampling Trees (BEAST) approach. We also implemented the PrimerID Illumina MiSeq approach for ultra-deep sampling of a fragment of the *env* gene to look for the presence of minor transmitted variants.

Among PWID screened for the study 25% were seropositive. The calculated AHI incidence was 9.3 per 100 person-years. We report 7 cases of acute HIV-1 infection among active PWIDs and 8 potential sexual partners of PWID. Among all the cases studied by SGA and PrimerID approaches we detected a homogeneous viral population likely produced from a single viral variant.

We also detected one case of a secondary infection from a different donor. Adding to previously published data we have analyzed 19 cases of AHI subtype A in St. Petersburg, and at least 74% had a homogeneous viral population confirming a strong genetic bottleneck during parenteral transmission.

The data confirm our original discovery of the genetic bottleneck in HIV transmission among PWID.

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### VIRAL HEPATITIS B AND C IN THE ARKHANGELSK REGION: LONG-TERM DYNAMICS OF INCIDENCE AND CROSS-SECTIONAL STUDY OF MARKERS AMONG ADULT POPULATION

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Viral hepatitis B and C (VHB and VHC) represent a serious problem for national health care, affecting the young working population of the country.

The purpose and objectives were to analyze the long-term incidence of VHB and VHC in the Arkhangelsk region and to study the prevalence of VHB and VHC markers among adult population in Arkhangelsk city.

The statistical data forms reported to the federal level were used and a population-based study was carried out as a part of the Norwegian-Russian project. A quota sampling method was used to recruit 1243 adults aged 18–39 years. All participants were tested on VHB Antigen (HBsAg), VHB core antibodies (anti-HBc), VHB surface antibodies (anti-HBs) and VHC (sum antibodies) using an enzyme-linked immunosorbent assay.

Over the past 30 years, the incidence of acute VHB (AVHB) in the Arkhangelsk region decreased in 40 times, the incidence of chronic VHB (CVHB) — in 2.8 times. Nowadays, the incidence of CVHB is in 15 times higher compared with the incidence of AVHB; the incidence of CVHC is in 87 times higher compared with the incidence of AVHC. The prevalence of VHB markers (HBsAg and/or anti-HBc) was 11.8% in men and 10.2% in women in a population-based study. Among men, 1.1 and 1.3% of women were positive on HBsAg; 41.8% of men and 50.9% of women were positive only on anti-HBs. All three tests were negative in 46.4% of men and 38.9% of women. Among men, the percentage of positive for VHC markers was 6.4%, among women — 4.3%. Co-infection of VHB and HCV was found in 1.5% of men and 0.3% women.

Despite the progress made in the control of VHB and VHC, a pool of sources of infections remains in the population. Therefore, preventive work should be continued.

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### IMMUNOPATHOGENESIS HIV AND MATHEMATICAL MODELING

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The study of HIV immunopathogenesis is the most important prerequisite for the search of new and improving the existing antiviral and immunomodulating medicines and vaccines used for the treatment and prevention of HIV infection.

The accumulated data of the HIV infection and the functional human physiological system reactions on it indicate that multifactorial mechanisms, which determine the development, course and outcomes of HIV infection, are mediated by a great number of physiological and pathological processes with various positive and negative feedbacks.

Due to the complexity of HIV interactions with the human body, the completely new interdisciplinary and interdisciplinary approaches are in urgent need. These approaches should include various bioinformatics and system analysis methods for the identification of immunobiological protection factors in HIV infection and comprehensive understanding of its pathogenesis. Thus, the advances in genome screening for the cellular proteins with anti-HIV activity identification may serve as the base for the promising approach for the HIV treatment and prevention. In turn, the methods of multiscale mathematical modeling