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HCV genotypes distribution in the Nizhny Novgorod area HIV-positive population

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Background

The number of people infected due to intravenous drug use remains at a level of 50% so far, despite the HIV sexual transmission rate increasing. Chronic hepatitis C (HCV) infection is currently one of the most clinically relevant co-morbidities (>80%) in the population of HIV-positive drug-users. Due to the wide use of HAART and prevention of opportunistic diseases, life expectancy of HIV-infected individuals has increased and chronic viral hepatitis has become one of the principal causes of death side-by-side with tuberculosis. We started HCV treatment in 2007. Prior to treatment, all HCV co-infected patients required an HCV genotype testing.

Methods

The HCV genotypes distribution in the HIV-infected residents of the Nizhny Novgorod area was studied. We investigated the 366 blood samples taken from 366 patients by polymerase chain reaction method (PCR) using the "AmpliSens-50-R" test-system and the Bio-Rad MyCycler Sample Loading Tray.

Summary of results

HCV genotype 3a predominated in our cohort samples (43.9%) and the remainders were type 1b (33.6%) and type 1a and 2 with low distribution (5.5% and 3.3%, respectively). In 20 samples we have found mixed 1b+3a genotypes; in 30 cases genotypes were not detected.

Conclusion

In the Nizhny Novgorod area, a distribution of HCV genotypes among HIV-infected individuals was observed

with a higher prevalence of genotype 3a (43.9%) by comparison with the population of Russia (10.5%). As has been shown in previous research, HCV genotype 3a is a favorable prognostic factor for achieving in most cases a sustained virologic response. Our findings have potential implications for appropriate patient selection for HCV treatment, as individuals carrying this genotype are more likely to respond to therapy.