SONATA BIS project "Implementing molecular models for the HIV and HCV transmission networks surveillance to inform clinical interventions".

Lay summary

Currently both Human Immunodeficiency Virus (HIV-1) and hepatitis C virus (HCV) are controllable diseases - in case of HIV treatment with antiretrovirals leads to the reduction of the viral loads to undetectable levels, reduction of the risk of disease progression and infectivity. On the other hand, HCV treatment with new directly acting antiviral drugs has led to possibility of viral eradication in >90% of cases. These successes may be hindered by the development of viral drug resistance and rapid transmission within the closely related networks which may further fuel the spread of the epidemics. The objective of this study is to aid the understanding how the viruses spread and how the resistance is developing (namely: to understand the infection and transmission dynamics) to guide and improve HIV and HCV prevention and elimination strategies. For this purpose new research team will be created brining together experienced medical specialists, bioinformaticians biologists and modeling experts.

Research carried out will involve creation of the large scale database for the integration of data, introduction of the novel techniques allowing for the deep, specific and sensitive investigations of the virus evolution and dynamics of spread between people. Computer-based modelling of the infections (phylogeny) will be used to ultimately create the guidelines stating possible improvement in the prevention of HIV and HCV. All this will benefit human populations allowing for the reduced infection risk in the future.

The reasons for the selection of the project topics are possibility to use scientific novel tools - both biotechnologic (obtaining virus genetic sequences) and bioinformatic (creation of the model for which reflect how the viruses spread) for combating these deadly infectious diseases; the ultimate aim is to eliminate both HIV and HCV from human population.