

Contribution ID: 239

Type: Oral Presentation

Predicting mechanism of action and quantifying anti-viral effects of cytokines against hepatitis B virus

Tuesday, 10 July 2018 11:00 (30 minutes)

Hepatitis B Virus (HBV) is widespread infectious disease and more than 240 million people are chronic infected so far. Although some patients can suppress the viral load under detection limits by current drug treatments, these are not effective for over 60% of patients. The obstacles for developing effective drugs are the existence of a reservoir in infected cells, which is known as covalently closed circular DNA (cccDNA). Because cccDNA remains in infected cells for a long time, the replication of HBV is not completely inhibited. We need new effective drug that can decrease the concentration of cccDNA persistently. In this study, we carried out cell culture experiments that can be measured the time course of the concentration of cccDNA, intracellular HBV DNA and extracellular DNA. Then, we added several kinds of cytokines in this experiment, and measured the same time course data. Furthermore, to investigate mechanism of action and quantify the anti-viral effect of each cytokine, we established a mathematical model that can capture the dynamics of intracellular HBV replication and fitted this model to the our time course data. Finally, we investigated which cytokines can decrease the concentration of cccDNA. This framework that combining viral experiment and mathematical model would be helpful to find a chemical that have desired mechanism of action.

Primary authors: Mr KAKIZOE, Yusuke (Systems Life Sciences, Graduate school of Kyushu University); Dr IWAMOTO, Masashi (National Institute of Infectious Diseases); Dr WATASHI, Koichi (National Institute of Infectious Diseases); Dr IWAMI, Shingo (Department of Biology, Kyushu University)

Presenter: Mr KAKIZOE, Yusuke (Systems Life Sciences, Graduate school of Kyushu University)

Session Classification: Frontiers in viral dynamics

Track Classification: Minisymposium: Frontiers in Viral Dynamics