

Multiscale Modeling of Hepatitis C Virus Infection

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Mathematical models of viral infection and treatment for illnesses caused by agents such as HIV, hepatitis C virus (HCV) and hepatitis B virus, have been successful in uncovering basic features underlying the pathogenesis of these diseases, such the rate of viral production in infected individuals and the lifespan of infected cells. In the case of HCV infection, new direct acting antiviral agents that interfere with various intracellular molecular processes are in clinical trials and the two HCV protease inhibitors have been approved by the FDA. In order to model the action of these agents, new multiscale models that simultaneously consider intracellular events as well events at the cellular and extracellular level are needed. I will discuss our recent progress in this area and show that certain features of HCV infection that we had previously deduced based on analyzing patient responses to interferon and ribavirin therapy need to be revised based on new data and analysis using multiscale models. This work suggests that multiscale models that take into the consideration the molecular biology of viral replication and virion secretion from infected cells may be essential in order to deduce features of the biology of HCV infection from the response of patients to drug therapy.