Chronic hepatitis C virus (HCV) infection remains a public health problem worldwide. Traditional therapy leads to viral elimination in less than 50% of treated patients. New treatment using direct-acting antiviral agents (DAAs) has significantly increased the cure rate. These new DAA drugs directly interfere with different steps in the HCV life cycle. Thus, existing models that do not consider intracellular processes may not be optimal in analyzing data from patients treated with these drugs. In this talk, I will discuss recent advances in developing multiscale mathematical models that can study HCV dynamics under therapy with new DAAs. The models include both intracellular viral replication and extracellular cell infection. I will address model analysis, approximation, comparison with experimental data, as well as the implications for developing new treatment strategies for hepatitis C. (Received January 27, 2014)