1124-92-316 **Stanca M Ciupe*** (stanca@vt.edu), Blacksburg, VA 24060, and **Andrea Carracedo Rodriguez** and **Matthias Chung**. *Complex Hepatitis B virus profiles during antiviral therapy - mathematical and numerical investigation.* Preliminary report.

In this study, we investigate the hepatitis B virus dynamics following initiation of drug therapy. Data from human clinical trials have shown that HBV DNA follow complex profiles such as biphasic, triphasic, stepwise decay and rebound. We utilized a deterministic model of hepatitis B virus dynamics following antiviral therapy to uncover the mechanistic interactions behind the hepatitis B virus dynamics. Analytical investigation of the model was used to separate the parameter space describing virus decay and rebound. Uniform Monte Carlo sampling of the parameter space was used to determine the virological, pharmacological and immunological factors that separate the types of virus decay. We found that the level of liver infection at the start of therapy best separates the decay patterns. Moreover, drug efficacy, ratio between division of uninfected and infected cells, and the strength of cytotoxic immune response are important in assessing the amount of liver damage experienced over time and the duration of therapy leading to virus resolution in each of the observed profiles. (Received September 12, 2016)