

Modeling of viral kinetics in patients chronically infected with hepatitis B and D

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Introduction - Virus kinetic models

 The dynamics of a virus population in vivo could be described by a simple ODE (Bonhoeffer et al., 1997; Nowak and May, 2000)

$$\frac{dT}{dt} = \lambda - mT - \beta TV$$
$$\frac{dI}{dt} = \beta TV - \delta I$$
$$\frac{dV}{dt} = pI - cV$$

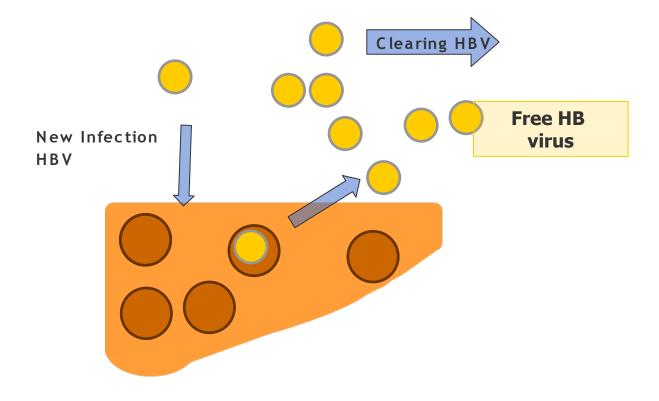


Introduction - Virus kinetic models

- Models for HIV, HBV, HCV monoinfection are an important tool for
 - Understanding dynamics of several viruses diseases
 - Quantifying effectiveness of anti-viral therapy
 - Comparing and optimizing anti-viral therapy
- Now: Introducing HBV-HDV-Viral kinetic model

Medical background - HBV

 Hepatitis B is a disease caused by HBV (hepatitis B virus) which infects the liver and causes an inflammation called hepatitis



Medical background - HBV

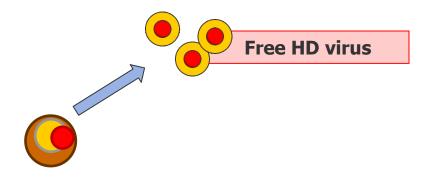
HBsAg: Hepatitis B surface Antigen 🔘



- Vast amount of HBsAg particles in blood serum
- Produced in liver cells
- HDV life-cycle relies on HbsAg
- HDV uses HBsAg as surface protein
- Anti-HBs: Hepatitis B surface antibody
 - Anti-HBs neutralizes HBsAg particels
 - Anti-HBs makes HBV noninfectious but cannot cure infected liver cells
- HBIG: Hepatitis B immune globulin
 - Blood plasma product administered after liver transplantation (LTX)
 - HBIG contains Anti-HBs and can prevent hepatitis B reinfection

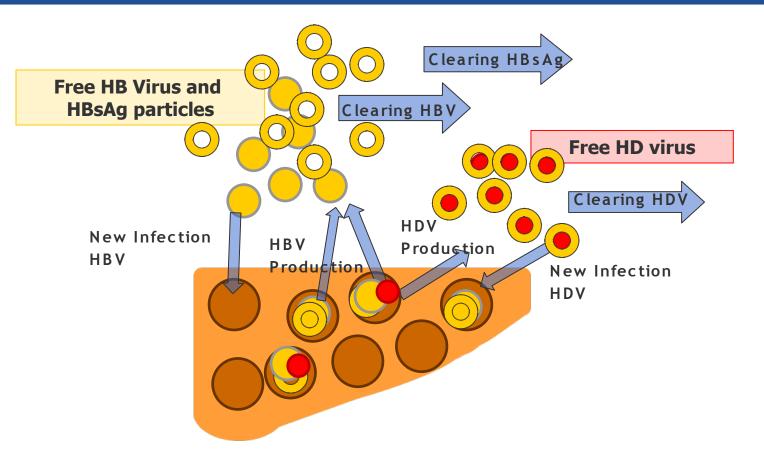
Medical background - HDV

- Delta hepatitis is the most severe form of chronic viral hepatitis
 - Frequently leading to end-stage liver disease and hepatocellular carcinoma
- Hepatitis D virus
 is a defective virus that is dependent for its life cycle on HBV-particles (HBsAg)
 - Therefore HDV-infection can only occur as coinfection or as superinfection with HBV-infection
 - Produced in liver cells which contain HBV and released to blood



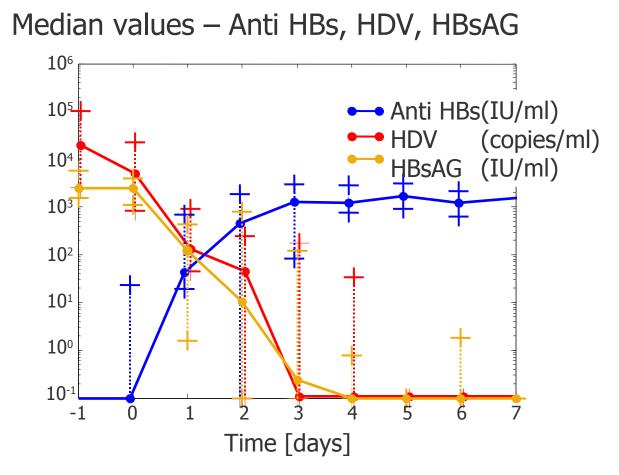


HBV-HDV-host-interaction

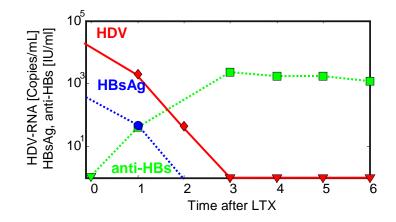


Material and Methods

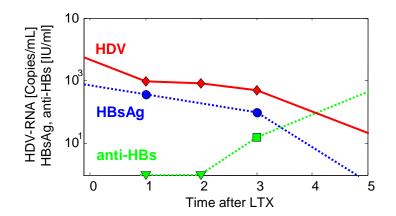
- The data: 25 coinfected patients who underwent liver transplantation
- Measured was:
 - HB Virus load (qualitative)
 - HD Virus load
 - HbsAg-level
 - Anti-HBs-level after transplantation
 - HBIG dose after transplantation
- Measured once before LTX and every 1,2,3 days after LTX
 - Until HBsAg became negative (Range: 1-13 days, except one patient who didn't achieved negativity at all)

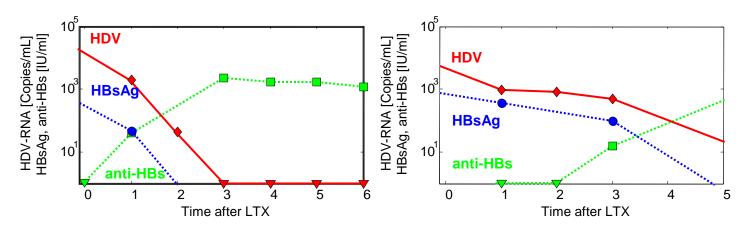


Kinetics of HDV-RNA, HBsAg and anti-HBs in representative patients



Kinetics of HDV-RNA, HBsAg and anti-HBs in representative patients





Kinetics of HDV-RNA, HBsAg and anti-HBs in two representative patients



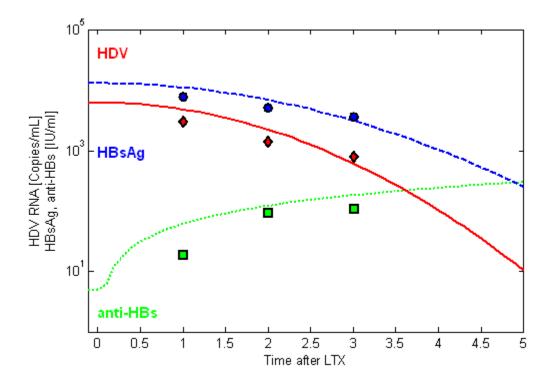
Model after liver transplantation

- Assume clearing of HBsAg and HDV due to anti-HBs
- No reinfection of the liver

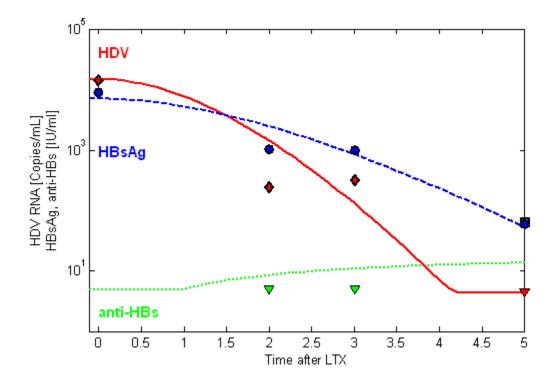
$$A = k_0 + (k_{\text{max}} - k_0) \cdot (1 - \exp(-kt))$$
$$\frac{dV_D}{dt} = -A c_D V_D$$
$$\frac{dH}{dt} = -A c_H H$$

Compartments	Kinetic parameters
A : Anti - HBs	c_D : Clearance of free HDV
V _D : Hepatitis D viremia	$c_{\rm H}$: Clearance of free HBsAg
H : HBsAg	k_0 : Initial anti - HBs level
	k: Rate of saturation
	\mathbf{k}_{\max} : Maximal saturation

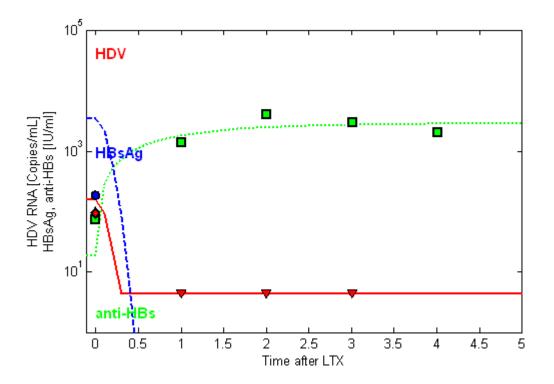




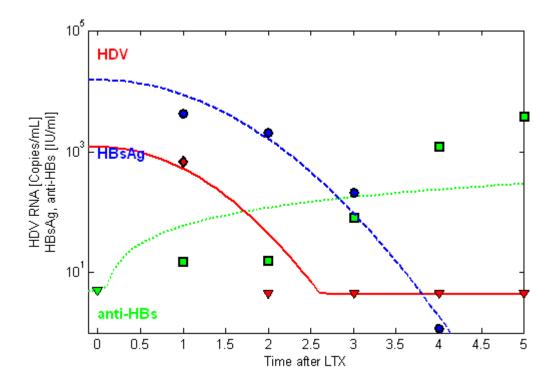




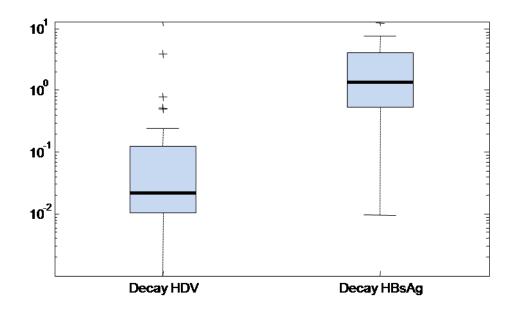














Results and Outline

- Overall similar kinetic pattern in HDV and HBsAG decline
 - Early HDV-RNA decline and HBsAg decline paralleled almost exactly in all 25 patients
- Nevertheless, two kinetic profiles were observed:
 - Most patients showed a relatively linear decrease (in logarithmic scale)
 - Some show a plateau phase in both, HBsAg and HDV DNA:
- Model modification to account for these profiles:
 - Directly model the single doses of HBIG in a PK-PD approach
 - Inclusion of possible time lags
 - Analyze if these plateaus can be explained by reinfection



Outline - the full model

Modelling virus-virus-host-interaction

$$\frac{dV_{B}}{dt} = p_{B} I_{B} - A c_{B} V_{B} + p_{DB} I_{DB}$$

$$\frac{dV_{D}}{dt} = p_{D} I_{D} - A c_{D} V_{D}$$

$$\frac{dI_{B}}{dt} = \beta_{B} T V_{B} - \delta_{B} I_{B} - \beta_{D} I_{B} V_{D}$$

$$\frac{dI_{DB}}{dt} = \beta_{D} I_{B} V_{D} - \delta_{DB} I_{DB}$$

$$\frac{dH}{dt} = p_{H} I_{B} - A c_{H} H + p_{HD} I_{DB}$$

$$A = k_{0} + (k_{max} - k_{0}) \cdot (1 - exp(-kt))$$

$$T = T_{max} - I_{B}$$

 $\frac{Compartments}{V_{B}} : Hepatitis B viremia$ $V_{D} : Hepatitis D viremia$ $I_{B} : Monoinfected cells$ $I_{DB} : Coinfected cells$ T : Target cells $T_{max} : Maximal contingent$ of target cells H : HBsAg A : Anti - HBs

Kinetic parameters

 $p_{B} : Viral production rate (free HBV)$ $p_{DB} : Viral production rate (free HBV)$ $p_{D} : Viral production rate (free HDV)$ $p_{H} : HBsAg production rate (free HBsAg)$ $p_{HD} : HBsAg production rate (free HBsAg)$ $c_{B} : Clearance of free HBV$ $c_{D} : Clearance of free HDV$ $c_{H} : Clearance of free HBsAg$ $\beta_{B} : De novo monoinfection rate$ $\beta_{D} : De novo coinfection rate$ $\delta_{B} : Monoinfected cell loss rate$ k : Treatment effect due to HBIG administration



Conclusions and Outline

- It seems as if HDV fully parallels HbsAg kinetics without differences in degradation rates
- The dynamics does not yet indicate reinfection but this has to be analyzed with more detailed data
- Modeling the observed plateau phase by introducing time lags
 - Considering time lags using the full model
 - Introduce pharmacokinetics (HBIG) as well
- Modeling appraoch may help to individualize HBIG dosing schemes in patients undergoing HBV/HDV-indicated or HBVindicated liver transplantation
 - Up to now HBIG is given at a fixed dose until HBsAG level is negative



References

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- Powers et al.: Kinetics of Hepatitis C virus Reinfection After Liver Transplantation. Liver Transplantation 2006, 12:207-216.



Thank you for your attention.