Implications of HBsAg from Integrated DNA for Clinical Trial Design

Bruce D. Given, MD HBV Forum 3, October 24, 2017



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Hepatitis B Virus Life Cycle





All HBV RNA derived from cccDNA can be targeted with one siRNA

 All HBV transcripts, including pregenomic RNA, have common sequence and terminate with the same polyadenylation signal.

HBV Transcript Map



Single siRNA can reduce all HBV proteins



Co-injection of chol-siHBVs with NAG-MLP in HBV mouse model



6 mg/kg NAG-MLP + 6 mg/kg chol-siRNA Wooddell et al, Mol Ther 2013 May; 21(5) 973-85



Strong reduction of serum viral markers using either chol-siHBV-74 or -77 with NAG-MLP after a single dose

Decreased HBsAg

- 3-4 log reduction with both chol-siHBVs
- > 2 log reduction for 1 month

Decreased HBeAg to LOD Decreased HBV DNA

~ 3 log reduction of HBV DNA for ~ 1 month

HBsAg data in NUC- experienced HBeAg neg patients show less than expected activity



Batch analyzed Cohorts 1-4 with ARC-520/placebo

Chimp dosing and sampling timeline



- Monitor safety and efficacy
 - Blood collection performed regularly throughout study
 - Periodic liver needle biopsies



Differential HBsAg Reduction Observed in Chimpanzees with ARC-520



HBeAg positive responded better than HBeAg negative chimps



Response to ARC-520 in NUC-experienced, HBeAg positive patients



- High level KD of HBcrAg and HBeAg (cccDNA derived)
- Lower KD of HBsAg

4 mg/kg ARC-520



Representative HBV transcript profiles in HBeAg+ and HBeAg- chimps (Illumina RNA-seq analysis)



- Fewer transcripts with HBV poly(A) signal in HBeAg- vs HBeAg+ chimps
- In HBeAg- chimps, frequency of reads is reduced in region near DR1 : known for high frequency integration
- Are these transcripts coming from integrated HBV DNA?

Process of HBV dsL DNA integration and theoretical production of HBsAg





siRNA Designed to Target RNA Derived From HBV Integration Products in HBeAg- Chimps



- siHBV-i targets HBsAg RNA even if expressed from integrated HBV DNA
- siHBV-i gave deep reductions in HBsAg in HBeAg- chimps, similar to those observed using ARC-520 in HBeAg+ chimps



HBV Transcripts in HBeAg+ vs. HBeAg- Chimps PacBio Single Molecule Real-Time (SMRT) Sequencing



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ARC-520 Phase2a explored 4 HBV groups

Think of the groups as quadrants Defined by HBeAg status and NUC experience





ARC-520 Results Lead To New Understanding of Role of Integrated HBV DNA



HBcrAg reduction after 4 mg/kg ARC-520 dose



 HBeAg status and previous NUC affect HBsAg response HBcrAg data confirms potent antigen reduction in all patients



HBV DNA in hepatocytes of HBeAg pos and HBeAg neg





HBsAg reduction in HBeAg negative patients

HBeAg neg



HBeAg pos

 Even with undetectable circulating HBV DNA, HBV RNA, HBcrAg and HBeAg significant amounts of HBsAg persist



Where we believe this leaves us

- Integration has been shown to occur as early as acute infection
 - ~10% of circulating virions contain dsL DNA, instead of RC DNA
 - Largely studied as a means of assessing clonality and for possible oncogenic effects
 - Has been mostly viewed as a result of "failed" reverse transcription
 - Generally hasn't been considered as transcriptionally active
- These results should make us ask if this isn't instead an effective viral response to host immunological pressure
- If so, even with complete loss of cccDNA activity, HBsAg may persist if the host can't also control transcription from integrants or eliminate cells with active transcription from integrants
 - A question for the field: Is this what we historically have referred to as the "inactive carrier" state?



Acknowledgments

- The University of Hong Kong
 - MF Yuen
 - Frank YF Lam
 - Michael KL Ko
 - Loey LY Mak
 - Elvis WP To
 - Wai-Kay Seto
 - Danny Ka-Ho Wong
 - Ringo Chi-Hang Wu
 - John Chi-Hang Yuen
 - Charles Tze-Kin Cheng
- The Chinese University of Hong Kong
 - Henry Chan
 - Vincent WS Wong
 - Grace LH Wong

- Victorian Infectious Diseases Reference Laboratory
 - Stephan Locarnini
 - Kathy Jackson
 - Renae Walsh
- Arrowhead Pharmaceuticals
 - Chris Woodell
 - Diamond Martin
 - Christine Wooddell
 - Caroline LaPlaca Davis
- Clinical Advisory Board
 - Robert Gish
 - Stephan Locarnini
 - CL Lai
 - Carlo Ferrari
 - Johnson Lau

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