HBsAg, Subviral Particles and Their Clearance in Establishing Functional Cure of Chronic HBV Infection

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Getting rid of therapy in chronic HBV infection



Latent cccDNA – the barrier to true cure

Inside the nucleus, the HBV genome (cccDNA) is chromatinized – the HBV minichromosome





Heterochromatic form – condensed (inactive / latent)^{1,2}

Very slow turnover Insoluble - bound to nuclear scaffold^{14,15} Immunologically silent

Effective barrier to sterilizing cure

Persists in resolved¹⁰ and occult¹¹ HBV infection – reactivated by immunosuppression¹⁶⁻¹⁹ Persists despite biopsy negative for cccDNA during NUC therapy Rapid rebound with NUC withdrawal in the presence of HBsAg²⁰

1. Levrero et al., J Hepatol. 2009; 51: 581-592

- Hong et al., Hepatol. 2017; 66: 2066-2077 Huang et al., Hepatol. 2020; epub Mar 19 Yuen et al., Hepatol. 2018; 68: 46A

- Lucifora et al., Science 2014; 343: 1221-1228

Xia et al., Gastroenterol. 2016; 150: 194-205 Li et al., Ści Rep. 2017; 7: 12715

- Liu et al., PLoS Path. 2013; 9: e1003613
- Palumbo et al., PLoS One 2015; 10: e0142599 9.
- 10. Bloom et al., Genes 2018; 9: 207

11. Troperger et al., PNAS 2015; 112: E5715-E5724 12. Rivière et al., J Hepatol. 2015; 63: 1093-1102 13. Hensel et al., Epigenetics & Chromat. 2018; 11: 34 14. Cam et al., Cell 2009; 136: 610-614 15. Chen et al., Nuc Acids Res 2016; 44: 6482-6492

16. Loomba and Jiang, Gastroenterol. 2017; 152: 1297-1309 17. Wang et al., Hematologica 2019; 104: 435-443 18. Zhang et al., J Immunother Canc. 2019; 7: 322 19. Kuo et al., Sci Rep. 2020; 10: 2456 20. Lai et al., JHEP Rep. 2020; 2: 100112

Targeting cccDNA inactivation / clearance

Capsid assembly modulators:

Efficient HBV DNA and RNA declines are a result of their antiviral mechanism¹
negligible effects on cccDNA to date¹⁻⁵ (HBeAg, HBcrAg) in monotherapy
96% rebound rate following 12-18 months of vebicorvir (ABI-H0731) + NUC therapy⁶

Can we do better with novel CAMs? NUCs already have good activity against cccDNA!

6. <u>https://investor.assemblybio.com/node/10876/pdf</u>

NUCs target cccDNA inactivation / clearance



1. Carey et al., Hepatol. 2020 72: 42-57

- 2. Bommel et al., Hepatology 2015; 61: 66-76
- 3. Lai et al., J Hepatology 2017; 66: 275-281
- 4. Van Campenhout et al., Clin Microbiol Inf 2016; 22: 571.e6
- 5. Liu et al., Alimentary Pharmacol Therap 2020; 52: 692-700

6. Suslov et al. J Heptaol 2021; 74: 794-800

Silencing of cccDNA within the first 12 weeks of therapy^{2,5} Reduction of cccDNA burden within 1st year of therapy³ or with HBeAg seroconversion⁶ HBsAg persists during NUC therapy despite cccDNA inactivation/clearance

The challenge of controlling HBsAg production in the liver

Subviral particles (SVP) constitute 99.99% of circulating HBsAg



Present in HBeAg positive and negative infection³

Transaminase flares signal removal of integrated HBV DNA from the liver

1. Tu et al., Viruses 2017; 9: 75

2. Yang et al., J Cancer 2018; 9: 3225-3235

3. Budinska et al., Emerg Microb Inf. 2018; 7: 142

Production of excess SVP drives chronicity of HBV infection

Immunoinhibitory properties of SVP

| Immune function | Target of inhibition | Effect observed |
|--------------------|-----------------------------------|-------------------------------------|
| Innate | TLR function | In vitro, in vivo |
| | Cytokine signalling | <i>In vitro,</i> in humans |
| | Monocyte and macrophage function | In vitro |
| | Dendritic cell function | In vitro |
| | NK cell function | <i>In vitro, in vivo,</i> in humans |
| Adaptive | Sequester anti-HBs | In vitro |
| | HBV specific B-cell function | In humans |
| | HBV specific CD4+ T-cell function | In humans |
| | HBV specific T-cell tolerance | In vitro, in vivo |
| | HBV specific T-cell exhaustion | <i>In vivo,</i> in humans |

The path to functional cure



What is "potent" HBsAg (SVP) reduction?

0.5 - 1 log₁₀ IU/mL reduction from baseline **Should not be described as "potent"**!

- Rare with CAMs in the absence of NUCs
- Common with NUCs and pegIFN and RNAi
- Consistent with inactivation of cccDNA
- Abundant circulating HBsAg still present
- Predicts clinical futility for achieving functional cure¹⁻³

> 4 log₁₀ IU/mL reduction from baseline Potent HBsAg loss predicting functional cure⁴⁻⁷

- Associated with strong therapeutic transaminase flares and HBsAg loss⁸⁻¹⁵
- Allows withdrawal of NUC therapy with sustained virologic control or functional cure¹⁶⁻¹⁹

• NUCs: <1% per year of therapy²⁰ more likely in GT A²¹

- PegIFN: 6% with 48 weeks of therapy²²
- PegIFN + NUCs: 9% with 48 weeks of therapy²²
 - Mostly restricted to GT A, more likely with HBeAg positive infection^{22,23}
- Rarely observed with RNAi (dsRNA) or antisense

•pegIFN + NUCs + NAPs: 70% with 48 weeks of therapy²⁴

GT A, GT C and GT D, HBeAg positive or negative^{24,25}, HBV / HDV co-infected²⁶

- 1. Brunetto et al., Hepatol. 2009; 49: 1141-1150
- 2. Rijckborst et al., Hepatol. 2010; 52: 454-461
- 3. Sonneveld et al., Heaptol. 2013; 58: 872-880 Wiegand et al., Antiviral Ther. 2008; 13: 547-554
- Moucari et al., Hepatol. 2009; 49: 1151-1157 5.
- Marcellin et al., Alimen Pharmacol Ther. 2016; 44: 957-966
- 7. Ahn et al., Dig Dis Sci. 2018; 63: 3487-3497
- 8. Wong et al., Liv Int. 2018; 38: 1760-1769 9. Jeng et al., J Viral Hep. 2018; 25: 421-428 10. Nagaoka et al., Hepatol Res. 2016; 46: E89-E99 11. Yano et al., Biomed Rep. 2017; 7: 257-262 12. Hall et al., J Hepatology 2020;73: S69 13. Choi et al., J Hepatology 2020; 73: S866 14. Farag et al., J Hepatology 2020; 73: S877

15. Bazinet et al., J Viral Hepatitis 2021: epub Feb 8 16. Liang et al., Ailment Pharmacol Ther. 2011; 34: 344-352 17. Chan et al., Antiviral Ther. 2011; 16: 1249-1257 18. Lee et al., Clin Mol Hepatol. 2016; 22: 382-389 19. Chen et al., J Viral Hep. 2018; 25: 590-597 20. Chevaliez et al., J Hepatol. 2013; 58: 676-683 21. Marcellin et al., J Hepatol. 2014; 61: 1228-1237

- 22. Marcellin et al., Gastroenterol. 2016; 150: 134-144
- 23. Brunetto et al., J Hepatol. 2013; 59: 1153-1159
- 24. Bazinet et al., Gastroenterology 2020; 158: 2180-2194 25. Al-Mahtab et al., PLoS One 2016; 11: e0156667
- 26. Bazinet et al., Lancet Gastro Hepatol 2017; 2: 877-889

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Approaches to targeting SVP

All oligonucleotide-based **Specific activity requires delivery to hepatocytes**

GalNAc RNAi

Inhibition of HBsAg synthesis Designed to engage RISC-mediated cleavage of HBV RNA dsRNA stimulates innate immunity via TLR3 – <u>sequence independent!</u>²⁻⁴ Cannot be fully quenched without blocking RISC-loading!⁵

GalNAc antisense

Inhibition of HBsAg synthesis Designed to engage RNAse H mediated cleavage of HBV RNA ssDNA (CpG) stimulates innate immunity via TLR9² ssRNA (U-rich) stimulates innate immunity via TLR7²

Nucleic acid polymers

Single point mutation abolishes hydridizationdependent mRNA cleavage¹

Similar pharmacodynamic response with optimal dosing

Well described ability to stimulate innate immunity

1. Vickers et al., J. Biol. Chem. 2003; 278: 7108-7118

2. Kawai and Akira Int Immunol 2009; 21: 317-337.

TLR-independent RNAi pharmacodynamic signatures (true RNAi effect)



150 165 180

135

Days after First Dose

195 210

LNP-RNAi

(Alnylam – PCKS9) Effect saturated at 0.3 mg/kg

GalNAc-RNAi (Arrowhead - ANGPTL3)

Very low interpatient variability in response

Saturated effect (~1 log₁₀ decline) with multiple dosing 2 weeks after first dose

Effect saturated at 100mg

Residual intact target mRNA remains!

Seo et al., Cell Host & Microbe 2013; 14: 435-445

Cytoplasmic RISC competition with endogenous miRNA Deactivation of RISC by TLR3 activation

TLR-independent GalNAc-antisense pharmacodynamic signatures (true antisense effect)

Graham et al., NEJM 2017; 377: 222-232





Very low interpatient variability in response

Saturated effect (~1 log₁₀ decline) with multiple dosing 2 weeks after first dose

Intact residual target mRNA remains!

Antisense is consumed in RNAseH mediated target mRNA cleavage

Equivalent pharmacodynamic response as RNAi





Expected HBsAg response with efficient target engagement by antisense / RNAi



Oligonucleotide partitioning influences TLR activation



GSK 3228836 and 3389404

antisense targeting HBx → targets mRNA from cccDNA and integrated HBV DNA





GalNAc drives hepatocyte targeting Weak HBsAg response indicates HBV mRNA is not efficiently cleaved Development halted!

Kupffer cells targeted without GalNAc Strong HBsAg response limited to 3 patients with low HBsAg at baseline Consistent with TLR9 stimulation of innate immunity (cccDNA silencing)

Theodore et al., HEPDART 2019 O15

Roche RG6004 (RO7062931)

GalNAc LNA antisense gapmer targeting HBx→ targets mRNA from cccDNA and integrated HBV DNA



Highly variable and weak HBsAg response indicates minimal cleavage of HBV mRNA Escape mutants present at baseline or rapidly fixed via cccDNA turnover

Development of RG6004 / RO7062931 halted

Yuen et al., J Hepatology 2020 73: S51

ARB-1467 (TKM-HBV)

LNP: one RNAi targeting HBx and two RNAi targeting HBsAg (+ETV or TDF)

Optimum design for efficacy:

High efficiency targeting to hepatocytes (LNP) Targeting of HBsAg (two loci) and HBx: covers cccDNA and integrated HBV DNA best effort against mutational escape





Highly variable and weak HBsAg response indicates minimal cleavage of HBV mRNA

Escape mutants present at baseline or rapidly fixed via cccDNA turnover

Eley et al., Hepatology 2017; 66: 23A

ARB-1467 (TKM-HBV)

LNP: one RNAi targeting HBx and two RNAI targeting HBsAg (+ETV or TDF)

HBsAg

HBcrAg



Weak HBsAg response indicates HBV mRNA not efficiently cleaved



Agarwal et al., Hepatology 2017; 66: 22A

Development of ARB-1467 halted

ARC-520 (single dose) LNP: two RNAi targeting HBsAg (+ETV or TDF)

High efficiency targeting to hepatocytes



ARC-520 (multiple dose) LNP: two RNAi targeting HBsAg (+ETV or TDF)



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JNJ-3989 (ARO-HBV) Two GalNAc-RNAi targeting HBx and HBsAg (+ETV)



JNJ-3989 (ARO-HBV) Two GalNAc-RNAi targeting HBx and HBsAg (+ETV)



Gane et al., J Hepatology 2020;73: S20

JNJ-3989 (ARO-HBV) GalNAc-RNAi + ETV + CAM (JNJ-6379)

LP4 – AASLD 2019

400mg GalNAc RNAi dosing!

HBsAg response during first 2 weeks

- absent (7/12 participants)
- $<< 1 \log_{10}$ from baseline (12/12 participants)

Delayed HBsAg response > 4 weeks

12/12 participants

HBV mRNA cleavage negligible or absent

HBsAg response consistent with TLR3 stimulation / cccDNA silencing Figure 1: Individual Changes in HBsAg Levels over Time with JNJ-3989, JNJ-6379 and NA Treatment.



7. Kumar et al., Immunology 2005; 117: 11-21

Observation of upper respiratory tract infections consistent with TLR3-mediated lung inflammation¹⁻³ Also observed for ARC-520 (LNP), ARO-AAT (GalNAc) and ALN-AAT (GalNAc)

Increased cytokine responses in humans consistent with TLR3 activation observed with ARC-520⁴⁻⁷

- Sköld et al., Blood 2012; 120: 768-777
- Murray et al., Am J Resp Care Med. 2008; 178: 1227-1237
- Stowell et al., Respir Res. 2009; 10: 43 3.

- Schluep et al., Clin Pharmacol Drug Dev. 2017; 6: 350-360
- Yang et al., Am J Heart Circ Physiol 2006; 291: H2334-H2343 5.
- Dia et al., FASEB J 2015; 29: 4978-4988 6.

VIR-2218 (ALN-HBV02) GalNAc-RNAi targeting HBx (+ETV)



Hypervariable response in HBsAg



HBsAg response during first 4 weeks

- Absent (1/6 participants)
- $<< 1 \log_{10}$ from baseline (4/6 participants)

Delayed HBsAg response > 4 weeks

- 6/6 participants
- Hypervariable responses





HBV mRNA cleavage minimal or absent in most patients **Delayed HBsAg response consistent with TLR 3 simulation**

Grade 3 upper respiratory tract infection reported! (likely TLR3-mediated)

AB-729 GalNAc-RNAi targeting HBx

HBsAg reduction from baseline



HBsAg response during first 2 weeks

- Absent (3/6 @60mg, 2/5 @ 90mg)
- << 1 log₁₀ from baseline (all participants)

Delayed HBsAg response > 4 weeks

• All participants

HBV mRNA cleavage minimal or absent in most patients

Delayed HBsAg response > 1 log₁₀ from baseline consistent with TLR 3 simulation

> http://www.arbutusbio.com/portfolio/ab-729-galnac-rnai.php Gane et al., APASL 2021

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RG6346 (DCR-HBVS) GalNAc-RNAi targeting HBsAg (+ NUCs)



Large error bars indicate highly variable HBsAg response Overall weak HBsAg response indicates mRNA cleavage is minimal or absent

Reporting of individual patient responses is CRITICAL for proper interpretation of HBsAg response to RNAi / dsRNA

Yuen et al., AASLD 2020, LO-9

RNAi / antisense for HBV (???) The clinical story so far....

HBsAg response is much stronger with targeting of RNAi to Kupffer cells / periphery (GalNAc)

- Responses should be much stronger with targeting to hepatocytes with RNAi effect
- Indicates an immunostimulatory mechanism is involved in HBsAg response to RNAi

HBsAg response to antisense is much weaker than RNAi with optimal dosing

• Response should be equivalent! Weak HBsAg response to antisense confirms lack of RNAi effect

HBsAg response is weak or absent 2 weeks following start of antisense / RNAi in most patients

- No cleavage of HBV mRNA is occurring no targeting of integrated HBV DNA
- Escape mutants are present at baseline or rapidly evolve during treatment
- Consistent with prevalence of numerous HBV quasispecies and rapid turnover of cccDNA

HBsAg response > 1 log₁₀ from baseline (after 1 month) in all patients with GalNAc-RNAi

- Inconsistent with well characterized pharmacological limitation of RNAi in humans
- Absent with LNP-RNAi (more efficient hepatocyte targeting and minimal TLR exposure)
- Consistent with TLR3 mediated HBsAg response to dsRNA in vivo
- Consistent with TLR3-mediated side effects and cytokine signalling observed with RNAi in humans
- Indicates HBsAg responses to RNAi are driven by TLR3-mediated cccDNA silencing

Moving forward to correctly interpret RNAi / dsRNA clinical data in HBV

- RNAi = dsRNA = TLR3 stimulation (sequence independent, cannot be blocked without losing RNAi activity)
- Disclose individual patient responses to HBsAg, HBV RNA, HBcrAg, and HBeAg, separate according to HBeAg status
- Exclude patients with HBsAg < 1000 IU/mL (these will respond better to TLR3 stimulation)
- Disclose correlation between baseline HBsAg and HBsAg response on therapy

Nucleic acid polymers (NAPs)

Oligonucleotides with sequence independent activity Anneal to the exposed hydrophobic face of an uncomplexed amphipathic α -helix Amphipathic Nucleic acid alpha helix polymer Base Base S==P=0 s-P=0 induced uncharged state by local Base Base hydrophobic environment Charged state Uncharged state (induced)

Broad spectrum antiviral activity

HBV, HDV, HCV, HSV, CMV, RSV, PI-3, LCMV, HIV, Influenza, Ebola, Marburg, Lassa Fever, Coronaviruses, prion disease + others

Vaillant. ACS Inf Dis 2019; 10: 675-687

Broad-spectrum activity of NAPs in viruses with class 1 fusion proteins Conserved amphipathic α-helices provide a common antiviral target for NAPs



- 4. Hastie et al., Nat Struc Biol 2016; 23: 513-521
- 5. Lamb and Jardetzky Curr Op Struc Biol 2007; 17: 427-436
- 6. Eckert and Kim Annu Rev Biochem 2001; 70: 777-810
- 11. Tortorici et al., Nat Struct Mol Biol 2019; 26: 481-489
- 6 12. Chang et al., PLoS Pathogens 2012; 9: e1003563
- 13. Zuccola et al.. Structure 1988: 6: 821-830

In vivo activity – active against liver / lung / spleen viral infections (consistent with demonstrated accumulation of NAPs in liver, lungs and spleen)

Mechanism of action of NAPs in HBV



Amphipathic α-helical interactions in the J-domain of DNAJB12 consistent with conserved target interface

Boulon et al., AASLD 2020 LP-42

Antiviral effects of NAPs



Clinical optimization of NAPs

REP 2055 1st gen clinical candidate



Equivalent activity *in vitro*, *in vivo* and in humans

Activity is length and phosphorothioation dependent

40mer phosphorothioate¹ High affinity and selectivity for J-domain of DNAJB12

Activity is sequence independent Repetitive adenosine / cytidine sequence¹ (safety) Eliminates secondary structure, quenches immunoreactivity in ssDNA or ssRNA²

REP 2139 improvements

All naturally occurring with no impact on antiviral activity

2'O-methylation of all ribose sugars in backbone

- Improves solubility, reduces off target protein interactions
- Enhanced nuclease stability
- Quenches immunoreactivity

Optimizes chelate complex formation (required for well tolerated administration)

5-methylation of cytosine

Quenches immunoreactivity

Exclusion of locked nucleic acids early in development (e.g. ALG-10133)

- Not naturally occurring, hepatotoxic
- Induces strong 2° structure and substantially reduces oligonucleotide flexibility reduces binding to J-domains
- Unsuitable for clinical use with NAPs (additional undisclosed property)
 - 1. Vaillant. ACS Inf Dis 2019; 10: 675-687
 - 2. Real et al., Sci Reports 2017; 7: 43838

REP 2139 Lead clinical candidate



Integrating NAPs into existing therapies

REP 2055 monotherapy HBeAg positive chronic HBV infection



REP 2139-Ca monotherapy (calcium chelate complex) HBeAg positive chronic HBV infection



Due to chelate complex formulation HBsAg response alone is insufficient for high rates of control

Antiviral response with REP 2139 is improved with addition of immunotherapy



Improved HBsAg and anti-HBs response

All participants on combination therapy achieve < 0.05 IU/mL HBsAg on therapy

2 year follow-up post therapy:

3/9 with virologic control

1/9 with functional cure

Al-Mahtab et al., 2016 PLoS One 11: e0156667

REP 401: Putting the pieces of the puzzle together



REP 401: NAPs dramatically improve responses with TDF + pegIFN



REP 401: NAPs dramatically improve response over TDF + pegIFN



Dramatic increase in host mediated transaminase flares¹

- occur in 95% of participants²
- no alteration in liver function / asymptomatic²
- correlated with functional cure (when HBsAg is also < 1 IU/mL)²
- Signals the removal of cccDNA and integrated HBV DNA

Consistent with the safe and beneficial nature of host mediated transaminase flares during therapy with approved agents, even in cirhottics³

- Bazinet et al., Gastroenterol. 2020; 158: 2180-2194
 Bazinet et al., J Viral Hep 2021; 28: 817-825
 Vaillant, Viruses 2021; 131: 745
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REP 401: Transition to NAP addon from TDF + pegIFN elicits similar responses



Bazinet et al., Gastroenterol. 2020; 158: 2180-2194

REP 401: Outcomes

| Completed treatment and 24-48 weeks of follow-up | | 36 |
|--|---|-----|
| Clinical | Normal ALT | 89% |
| response | Normal liver median stiffness | 56% |
| | < 1000 IU/mL | 72% |
| HBsAg | < 1 IU/ml | 50% |
| response | ≤ LLOQ (0.05 IU/mL) | 42% |
| | Seroconversion | 53% |
| HBV DNA | ≤ 2000 IU/mL | 78% |
| response | Target not detected (TND) | 47% |
| | Virologic control (Inactive HBV) (HBV DNA ≤ 2000 IU/mL, normal ALT) | 39% |
| Virologic response | Functional cure (HBsAg < LLOQ, HBV DNA TND, normal ALT) | 39% |
| | Clinical benefit, no therapy required (low risk of progression, reduced risk of HCC) | 78% |

Bazinet et al., Gastroenterol. 2020; 158: 2180-2194 Bazinet et al., Hepatol Comm 2021, in press All with:

- HBsAg < 0.005 IU/mL (ARCHITECT[®] NEXT)
- No HBsAg immunocomplexes
- HBV RNA target not detected
- HBcrAg < LLOQ



Summary

| Subviral particles (SVP): The Key to Functional Cure | > 99.99% of circulating HBsAg Prevent immune control and function of immunotherapy Removal during therapy is essential for functional cure Cannot be targeted by direct acting antivirals (NUCs / CAMs) |
|---|--|
| Integrated HBV DNA: | Bulk of SVP production in HBeAg negative infection HBsAg specific T-cell response is required to target efficiently Therapeutic transaminase flares signal removal of integrated HBV DNA from the liver |

RNAi acts like dsRNA in human HBV infection:

Negligible targeting of HBV mRNA (and integrated HBV DNA) in most subjects HBsAg response likely reflects TLR3-mediated inactivation of cccDNA *Can TLR3 activation with dsRNA play a role in functional cure?*

NAPs: Target SVP assembly / secretion from cccDNA and integrated HBV DNA Allow efficient, host-mediated clearance of HBsAg

> Immunotherapy used in combination is associated with: high rates of asymptomatic host-mediated transaminase flares high rates of functional cure, silencing of cccDNA and removal of integrated HBV DNA

Transition to SC administration in cirrhotics in REP 501 study (HBV / HDV) will improve convenience for all patients.