



New Therapies to More Effectively Eliminate Viral Replication and Increase Cure Rates in CHB Patients

Richard Colonno, Uri Lopatin, Sandy Liaw, Ran Yan, Dawei Cai and Qi Huang

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Strategic Approaches Being Pursued To Improve Cure Rates





Our Focus is on Finding More Effective Antivirals – WHY?



Prolonged Nuc Therapy Fails to Eliminate Viral Replication



PCR-detectable HBV DNA persists in 70-80% of patients despite TDF treatment for 5 years¹

Learnings from EASL 2019

- Detected DNA represents *infectious virus*²
 - Residual viremia refractory to Nuc therapy
 - Likely accounts for poor cure rates
- Over 80% of circulating HBsAg derived from integrated DNA³
 - HBsAg may not be an appropriate biomarker of cccDNA loss
 - HBsAg does NOT lead to reinfection and is NOT a marker of ongoing infection
- Appropriate biomarkers of cure is an open question in the field
 - If DNA and RNA are undetectable, there is likely no remaining infectious virus
 - cccDNA ONLY source of pgRNA and virus

¹Marcellin, et al., Poster 1861 AASLD 2014; ²Burdette et al., PS-150 EASL 2019; ³Podlaha et al., SAT-91 EASL 2019

New Therapies are Needed to Increase Cure Rates in CHB



Nucleos(t)ide Pol Inhibitors (Nuc)

- Current "Standard of Care" for HBV
- Safe, well tolerated, with minimal resistance
- Reduce HBV DNA

But Fail to

- Fully eliminate virus
- Prevent new cccDNA formation
- Provide finite treatment duration

Cure is not possible without elimination of residual virus

Remaining Virus Able to Re-infect Liver When Nuc Therapy Stops



Time (years)

To improve cure rates...must eliminate residual virus to prevent reinfection

LLQ = lower limit of quantification.

HBV Viral Load

Key Findings of cccDNA Biosynthesis Studies



- Genetic source of resistance shown to be cccDNA
- pgRNA closely reflects genetic composition of cccDNA pools
- Turnover of cccDNA from sensitive to resistant and from resistant to sensitive occurs in 12-16 weeks
- Suggests relatively rapid biologic turnover of both pgRNA and cccDNA pools and/or infected cells
- No evidence to support existence of inactive subpopulation of cccDNA, as genetic changes are observed in the entire population of cccDNA

Results indicate that existing cccDNA has a limited half-life, suggesting that therapies inhibiting establishment of new cccDNA may lead to higher cure rates for patients with HBV *Huang et al. Poster Thr-216 EASL Apr 2019*

Critical Inhibitory Elements of New Treatment Paradigms

Eliminate Residual Virus Replication



.....To Stop New Infection of Hepatocytes

Block Generation of New cccDNA



....To Allow Decay of Existing cccDNA



CIs Block Viral Replication and cccDNA Establishment



Core Protein Inhibitors (Cls)

- Inhibit multiple steps in viral replication cycle
- Achieve deeper levels of viral inhibition than Nucs alone

AND.....

Can block the formation of cccDNA

Goal is to use combination therapy to increase cure rates with finite treatment duration

Superior Antiviral Effectiveness vs. ETV in Culture Assays



Core Inhibitors Inhibit Establishment of cccDNA in Infected Cells

Infection of Primary Human Hepatocytes



Huang Q, et al. Poster 922 AASLD Nov 2017

Relative Potency in Blocking cccDNA Generation



Interim Review of ABI-H0731 Phase 2a Studies (EASL - Apr 2019)



| Study | 201 | | 202 |
|-------------------------------------|-------------------------|---------------------|--------------------|
| Demographics | HBeAg + (n = 47) | HBeAg – (n = 26) | HBeAg + (n =25) |
| Asian (%) | 87 | 81 | 96 |
| Genotype B,C (%) | 83 | 46 | 88 |
| Mean Baseline Values | | | |
| ALT (U/L) | 27 | 25 | 57 |
| HBV DNA (log ₁₀ lU/mL) | BLQ | BLQ | 7.8 |
| HBV RNA (log ₁₀ copy/mL) | 5.9 ^a | ≤ 2.3 ^b | 8.0 |
| HBsAg (IU/mL) | 5,569 | 2,970 | 57,179 |
| HBeAg (PEU/mL) | 29 | N/A | 791 |

a 37/47 patients with baseline RNA > 200; b 4/26 patients with RNA > 200 copies)

| Metrics at Time of Interim Analysis | | | |
|-------------------------------------|----|-------|-------|
| - | D1 | Wk 12 | Wk 24 |
| Study 201 | 73 | 65 | 11 |
| Study 202 | 25 | 24 | 12 |

Blinded, Pooled Safety – Well Tolerated with Favorable Safety Profile

Blinded Summary of TEAEs (Studies 201 and 202) at interim data cut

- No SAEs or treatment related discontinuations or interruptions
- Adverse events were mostly mild, infrequent, and considered unrelated to study drug
- No Flares on treatment
- No clinical AE > grade 2
- 3 patients with rash considered "possibly related" (2x grade 1, 1x grade 2); none associated with systemic findings
- 1 patient in each study with a grade 2 AE considered possibly related to study drug
 - Macular/maculopapular rash-resolved on antihistamine (Study 201)
 - ALT increase-resolved with continued treatment (Study 202)

Study 202: Superior DNA Reductions with 731 Combination



*Statistically significant at (P < .05 or better)

Lalezari et al. Oral LB-07 EASL Apr 2019

| Mean Log ₁₀ HBV DNA Decline | | | |
|--|------|-----------|---------|
| Week | ETV | ETV + 731 | P Value |
| 12 | 3.29 | 4.54 | <.011 |
| 24 | 3.99 | 5.94 | <.005 |

HBV DNA assessed by Roche Cobas qPCR; LOQ = 20 IU

- Significantly faster and deeper reductions in HBV DNA levels, as early as Week 2 (P=.03)
- Among subjects with abnormal ALT at entry, more rapid ALT normalization seen in combination arm
 - 5/7 vs. 0/5 by Week 4 (P <.05)
 - 7/7 vs. 2/5 by Week 12 (P <.05)

Study 202: Superior RNA Reductions with 731 Combination



| Mean Log ₁₀ HBV RNA Decline | | | |
|--|------|-----------|---------|
| Week | ETV | 731 + ETV | P Value |
| 12 | 0.44 | 2.27 | <.005 |
| 24 | 0.61 | 2.54 | <.005 |

HBV RNA assessed by RT qPCR; LOQ = 200 copies/mL

• All patients on combination achieved a rapid decline in RNA levels

Study 201: Elimination of Detectable Virus Only on Combination

At Week 24, longitudinal serum samples were assayed for detectable virus using sensitive PCR assay



Nuc Monotherapy

HBV DNA PCR Assay To Quantitate Low Level Viremia

- DNA purified from longitudinal serum samples (0 24 Wk)
- PCR amplification (40-45 cycles) using individually optimized primers

Residual viremia not eliminated by Nuc



731 Combo Therapy

Residual viremia decline below detection (2-5 IU/mL)

Study 201: RNA Reductions to BLQ Only on Combination



Results for HBeAg Positive Patients with RNA >LOQ at Baseline (N = 38)

Lalezari et al. Oral LB-07 EASL Apr 2019

Study 201: Summary of Results at Time of Interim Analysis

Patients Treated 24 Weeks*

| Treatment | Nuc | 731 + Nuc |
|----------------------------------|-----------------------|-----------|
| DNA (TND ¹) | 0/4 (0%) | 5/6 (83%) |
| RNA (<200 Copies/mL) | 0/3 (0%) ² | 3/6 (50%) |
| $HBeAg \ge 0.5 Log_{10} Decline$ | 0/3 (0%) | 1/6 (17%) |
| $HBsAg \ge 0.5 Log_{10} Decline$ | 0/4 (0%) | 0/6 (0%) |

 $^{\rm 1}$ Target not detected by ASMB semi-quantitative PCR $^{\rm 2}$ a 4th subject on Nuc was BLQ at baseline

*Subjects with available data

- Antigen declines anticipated to follow elimination of residual viremia and RNA
- High level expression of HBsAg from integrated sequences limits ability of Core Inhibitors to decrease HBsAg levels from this source
- Study subjects continue to be treated and monitored in open label Study 211

ASMB Core Inhibitor Program Summary

- Core inhibitors have the potential to be the backbone of future HBV regimens
 - Highly potent antivirals that disrupt viral replication at multiple steps
 - Potential to eliminate residual viremia (deficiency of Nuc therapy)
 - Inhibit the generation of new cccDNA

• Summary of Interim Data for Phase 2a Studies on ABI-H0731

- Favorable safety profile (AEs and lab abnormalities generally considered unrelated, grade 1 and transient)
- Combination of 731+Nuc demonstrated superior antiviral activity vs. Nuc alone
 - In Rx-naïve patients, faster and deeper declines in HBV DNA observed starting at Week 2
 - DNA reductions to below limits of high-sensitivity PCR assay observed in Nuc "suppressed" patients
 - Significant HBV RNA declines In both studies
- Elimination of residual viremia will likely be required to prevent new cccDNA formation and increase cure rates

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Thank You!

