Association of Baseline Characteristics and Plasma ALG-001075 to HBsAg Responses in HBeAg+ CHB subjects following ALG-000184±ETV treatment

WED-378 Contact information Kha Le kle@aligos.com

¹Aligos Therapeutics, Inc. ²Department of Medicine, School of Clinical Medicine, The University of Auckland, ⁴King's College Hospital, Institute of Liver Studies, ⁵Nanfang Hospital, Southern Medical University, ⁶The First Hospital of Jilin University, ⁶The First Hospital of Jilin University, ⁷ARENSIA Exploratory Medicine, Republican Clinical Hospital and Nicolae Testemitanu State University of Medicine and Pharmacy, Moldova

Introduction

- ALG-000184 is a prodrug of ALG-001075, a potent chronic hepatitis (CHB) capsid assembly modulator-empty that inhibits viral replication cccDNA establishment in vitro.
- The potent antiviral effects and favorable safety profile in HBeAg+ (subjects receiving 300 mg ALG-000184 ± Entecavir (ETV) ≤72 wee in HBeAg- CHB subjects receiving 300 mg ALG-000184 monother weeks from an ongoing study ALG-000184-201 are reported in pos WED-365 and WED-361, EASL 2024.¹
- Functional cure, defined as sustained hepatitis B surface antigen (I loss with virologic suppression after a finite treatment course, is or desired outcomes for new treatment approaches for the managem chronic hepatitis B (CHB).²
- Substantial reductions in HBsAg has been shown for ALG-000184 in HBeAg+ CHB subjects.³
- Identifying factors associated with HBsAg reductions would be critical patient identification and understanding of mechanism of action of ALG-000184 in CHB subjects.

Aim

To evaluate whether there is an association between baseline characteristics including demographics, baseline viral antigens, and ALG-001075 exposures to HBsAg responses in HBsAg+ CHB subje following ALG-000184 ± ETV treatment

Method

ALG-000184-201 is a multi-part, multi-center, double-blind, randomiz placebo-controlled study (NCT04536337). In Part 4, eligible treatme or currently-not-treated HBeAg+ CHB subjects that enrolled in Coho and 2 were randomly assigned (3:1) to receive oral daily doses of 1 300 mg ALG-000184, respectively or placebo in combination with en (ETV) x 12 weeks followed by open-label treatment with

100 mg ALG-000184 + ETV x \leq 12 weeks and 300 mg ALG-000184 $x \leq 96$ weeks, respectively. Those enrolled in Cohort B received operations of the second s daily doses of 300 mg ALG-000184 alone $x \le 96$ weeks.

A total of 22 subjects (n= 4, 9, and 9 in Cohorts 1, 2 and B, respective with \geq 24 weeks of ALG-000184 dosing were included in the analysi Baseline participant characteristics, including age, sex, ethnicity, boo weight, BMI, HBV genotype, HBsAg, HBeAg, HBcrAg and steady st plasma ALG-001075 exposures were included in the analysis. For b HBsAg, both continuous and categorical (stratified by $< \text{ or } \ge 4 \log_{10} I$ was examined.

Linear univariate and multiple regression models were used to deter associations between selected baseline variables, plasma ALG-0010 exposures and HBsAg reduction. The level of significance was set to sided P < 0.05. Association was also shown in graphical form.

References

¹MF Yuen et al. and Kosh A. et al., EASL 2024; ²Lok et al., Hepatology 2017; et. al, Poster 2023 EASL Conference

Tse-I Lin¹, Matthew McClure¹ and Sushmita Chanda¹

	Results
itis B ation and + CHB eeks and eapy ≤60 oster (HBsAg) one of the nent of 4 ± ETV itical to	 Baseline patient characteristics were similar for those strate In the univariate regression model, baseline HBsAg contines have a statistically significant association with the change In the multiple regression model, baseline HBsAg (< or ≥ 4 were shown to have a statistically significant association with the change shown to have a statistically significant association with the statistical signation of the statistical signation of the statistical statistical signation of the statistical signature shown to have a statistically significant association with the statistical signation of the statistical signature shown to have a statistically significant association with the statistical signature of the stati
	Figure 1: Maximum HBsAg Change Figure 2: Linear Regres
	from Baseline vs. HBsAg Baseline 2a: Overall Pat
d plasma jects	Change from Baseline (log ₁₀ (U/m ¹) 0.00 -0.50
nized, ent naïve orts 1 100 and entecavir	$\begin{array}{c} \begin{array}{c} \begin{array}{c} 0 \\ 0 \\ 0 \\ 0 \\ \end{array} \end{array} \\ \begin{array}{c} 100 \\ mg \\ ALG-000184 + ETV \\ \hline 0 \\ 300 \\ mg \\ ALG-000184 \\ monotherapy \end{array}$
4 + ETV	AUC ₀₋₂
en-label	Figure 3: Linear Regression Model HBV Antigen
tively) sis. ody state baseline JU/mL) ermine 1075 to a 2-	<section-header></section-header>
7; ³ Hou,	Multi-log reduction in HBV antigens appears to be mediated Higher baseline HBsAg (≥4 log ₁₀ IU/mL) and plasma ALG-0 treatment. Plasma ALG-001075 was associated with HBeAg

Kha Le¹, Man-Fung Yuen², Edward Gane³, Kosh Agarwal⁴, Jinlin Hou⁵, Junqi Niu⁶, Xieer Liang⁵, Alina Jucov⁷, Min Wu¹, Maida Maderazo¹, Lawrence M. Blatt¹,

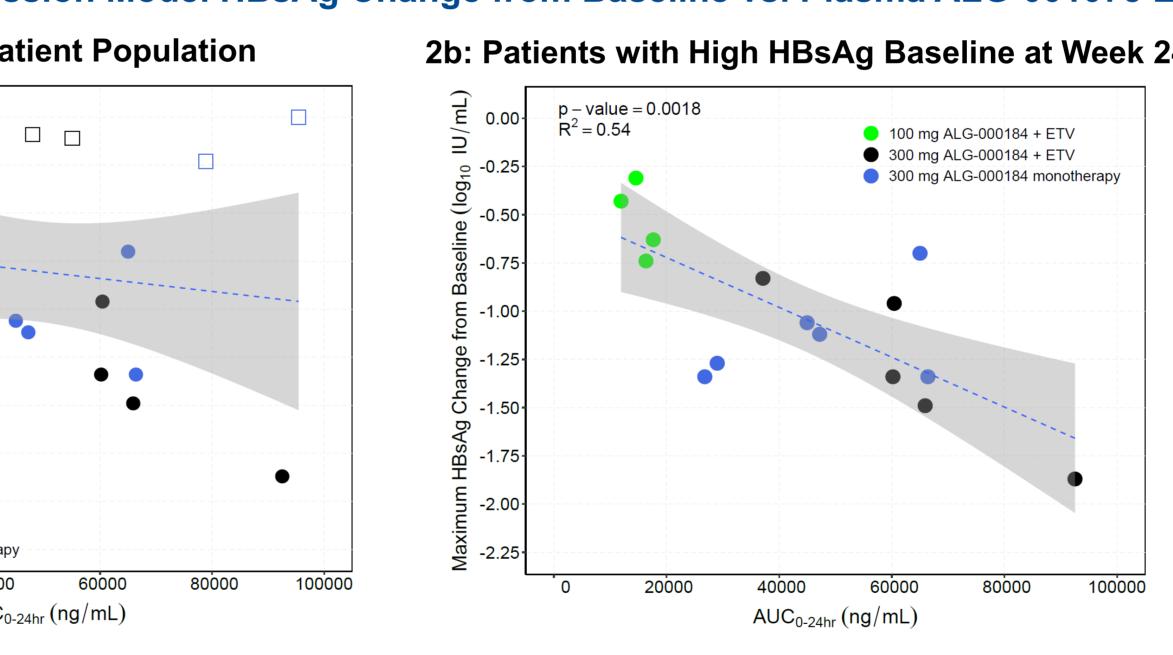
atified by HBsAg < or \geq 4 log₁₀ IU/mL and overall population (Table 1). nuous and categorical (< or \geq 4 log₁₀ IU/mL) variables were shown to from baseline in HBsAg at Week 24 (Table 2a, Figure 1).

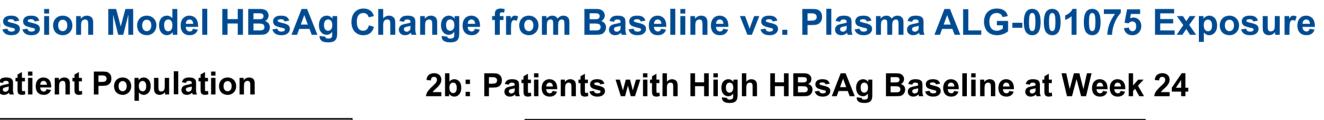
4 log₁₀ IU/mL) and steady state plasma ALG-001075 exposure (AUC) with the change from baseline in HBsAg at Week 24 (Table 2b).

ignificance in the univariate model but after adjustment for baseline atistical significance to the prediction (p=0.00416) (Table 2, Figures 2a

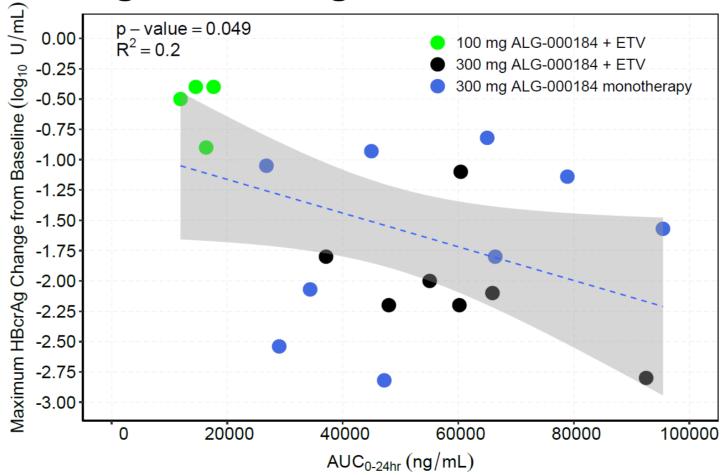
show significant reduction in HBsAg regardless of plasma ALG-001075

- en age, sex, ethnicity, HBV genotype, baseline HBeAg, HBcrAg or ALT r multiple regression models (Tables 2a and 2b).
- sociation with maximum change from baseline in HBsAg at Week 24 but tment for baseline HBsAg (Table 2b).
- eks 36 and 48 (data not shown).
- n HBeAg and HBcrAg irrespective of their baseline (Figures 3).





Change from Baseline and Plasma ALG-001075 Exposure Change in HBcrAg from Baseline vs AUC



ed by ALG-000184 secondary mode of action to lower cccDNA. 001075 levels were predictors of HBsAg response to ALG-000184 Ag and HBcrAg reduction.



	Baseline	Overall	
	<4 log ₁₀ lU/mL (n=5)	≥4 log ₁₀ lU/mL (n=17)	(n=22)
Age, years, mean(SEM)	40.0 (5.2)	32.4 (2.0)	34.1 (2.0)
Male, n (%)	4 (80%)	9(53%)	12 55%)
Asian, n (%)	5 (100%)	16 (95%)	21(95%)
Body Weight, kg, mean (SEM)	68.1(5.5)	59.3 (2.7)	61.2 (2.5)
BMI, kg/m², mean (SEM)	21.6(0.6)	22.0 (0.5)	22.0 (0.5)
HBV Genotype	B (1, 20%) C (4, 80%)	B (8/17, 47%) C (8/17, 47%) D (1/17, 5.9%)	B (9/22, 41%) C (12/22, 55%) D (1/22, 4.5%)
HBV DNA, log ₁₀ IU/mL, mean(SEM)	7.0 (0.3)	8.4 (0.1)	8.0 (0.16)
HBV RNA, log ₁₀ copies/mL, mean (SEM)	4.8 (0.56)	6.6 (0.27)	6.2 (0.29)
HBsAg, log ₁₀ IU/mL, mean (SEM)	3.5 (0.25)	4.7 (0.05)	4.4 (0.13)
HBeAg, log ₁₀ COI, mean (SEM)	2.1(0.34)	2.7(0.13)	2.6 (0.13)
HBcrAg, log ₁₀ U/mL, mean (SEM)	6.0±0.82 log ₁₀ U/mL	7.5±0.36 log ₁₀ U/mL	7.1±0.36 log ₁₀ U/m
ALT, U/L, mean (SEM)	47(7.0)	43 (7.4)	62 (17)

Table 2: Association of Patient Characteristics and Plasma ALG-**001075 Exposure to HBsAg Change from Baseline**

2a: Univariate Model

Maximum Change from Baseline in HBsAg at Week 2				
Age	0.02373 (0.01297)	0.08234		
Sex	Male 0.2668 (0.2508)	0.3		
Ethnicity	White -0.2824 (0.6129)	0.65		
Body Weight	0.01576 (0.01069)	0.1561		
BMI	0.06121 (0.05035)	0.2382		
HBV Genotype	C 0.478611 (0.247667) D -0.008889 (0.592038)	0.1645		
Baseline HBV DNA	-0.5095 (0.1291)	0.000797		
Baseline HBV RNA	-0.22511 (0.08135)	0.0119		
Baseline HBsAg	-0.5761 (0.1732)	0.003364		
Baseline HBsAg (≥ 4 log ₁₀ lU/mL)	-0.9479 (0.2211)	0.000359		
Baseline HBeAg	-0.08256 (0.20702)	0.6943		
Baseline HBcrAg	-0.07826 (0.07692)	0.3211		
Baseline ALT	0.001126 (0.004007)	0.7815		
AUC ₀₋₂₄	-3.361e-06 (5.081e-06)	0.5167		
C _{trough} (24hr)	1.816e-05 (1.692e-04)	0.9157		
Åge	0.02373 (0.01297)	0.08234		
Sex	Male 0.2668 (0.2508)	0.3		

2b: Multiple Regression Model

Maximum Change from Baseline in HBsAg at Week 24					
	Coefficient (Standard Error)	P-value			
Baseline HBsAg (≥ 4 log ₁₀ lU/mL)	-0.9479 (0.2211)	0.000359			
After Adjustment for Baseline HBsAg					
Age	0.009852 (0.010836)	0.37465			
Sex	Male 0.04946 (0.19836)	0.805756			
Ethnicity	White -0.0575 (0.4594)	0.901701			
Body Weight	0.004962 (0.008744)	0.57700			
BMI	0.01429 (0.04036)	0.727194			
HBV Genotype	C 0.28792 (0.19766) D 0.08646 (0.45718)	0.16244 0.85212			
Baseline HBV DNA	-0.2348(0.1969)	0.2477			
Baseline HBV RNA	-0.08017(0.08454)	0.35488			
Baseline HBeAg	0.2431(0.1616)	0.14891			
Baseline HBcrAg	0.01825(0.06314)	0.775699			
Baseline ALT	-0.002193 (0.003034)	0.478710			
AUC ₀₋₂₄	-9.735e-06 (2.943e-06)	0.00416			
C _{trough} (24hr)	-0.0002120 (0.0001157)	0.0844			

Acknowledgements

The authors wish to thank the subjects for participating in this clinical study. The Sponsor is grateful to the staff of the clinical sites, Novotech and TigerMed for assisting in the conduct of the study.