389

Prevalence and Characteristics of Hepatitis B Virus Mutations in Chronic Hepatitis B Patients on Oral Antiviral Therapy: The CHARM Study

60th Annual Meeting of the American Association for the Study of Liver Diseases October 30 - November 3, 2009 Boston, Massachusetts, USA SK Roberts¹, MC Ngu², SI Strasser³, J George⁴, GJ Dore⁵, SA Locarnini⁶, JJ Sasadeusz⁷, W Sievert⁸, K Mitchell⁹ and AM Elsome⁹ for the CHARM Study Group

¹The Alfred Hospital, Prahran, VIC; ²Concord Repatriation General Hospital, Concord, NSW; ³Royal Prince Alfred Hospital, Camperdown, NSW; ⁴University of Sydney at Westmead Hospital, Westmead, NSW; ⁵National Centre in HIV Epidemiology & Clinical Research, UNSW, Darlinghurst, NSW; ⁵Victorian Infectious Diseases Reference Laboratory, North Melbourne, VIC; ¹Royal Melbourne Hospital, Parkville, VIC; ³Monash Medical Centre, Clayton, VIC; ³Gilead Sciences Pty Ltd, East Melbourne, VIC.

GILEAD
Gilead Sciences Pty Ltd
128 Jolimont Road
East Melbourne
VIC 3002
AUSTRALIA
Tel: +61 (0)3 9272 4400
Fax: +61 (0)3 9272 4435

Introduction

- The advent of newer, more potent oral antiviral therapies (AVT) has been a significant advance in the treatment of chronic hepatitis B (CHB)
- However, long-term management of CHB may be compromised by the emergence of drugresistant mutations (genotypic resistance) that may lead to virologic breakthrough and progressive liver disease
- · Detection of genotypic resistance
- Facilitates treatment modification before viral or clinical rebound
 prevents the initiation of inappropriate, cross-resistant AVT
- However, resistance testing is not routine

Objective

The aim of the study was to describe the prevalence and nature of hepatitis B virus (HBV)
mutations that confer drug resistance in patients receiving AVT in a tertiary clinic outpatient
setting in Australia

Methods

- Multi-centre, cross-sectional, epidemiology study
- 18 Australian sites
- Entry criteria
- Adults with CHB attending tertiary outpatient clinics
- Receiving one or more AVT ≥6 months
- HIV, HCV, HDV co-infection, and/or concurrent immunomodulatory therapy excluded
- · Demographic and clinical data collected
- serology, AVT (current and treatment history), histology, patient-assessed compliance, and prior HBV mutations.
- HBV DNA quantification
- performed on all patients (Versant HBV DNA v3.0 assay; LLOQ = 351 IU/mL)
 Direct sequence analysis (catalytic region of HBV DNA polymerase, encoding amino acids 1-257) attempted on all patients with detectable HBV DNA

Figure 1. Patient Disposition

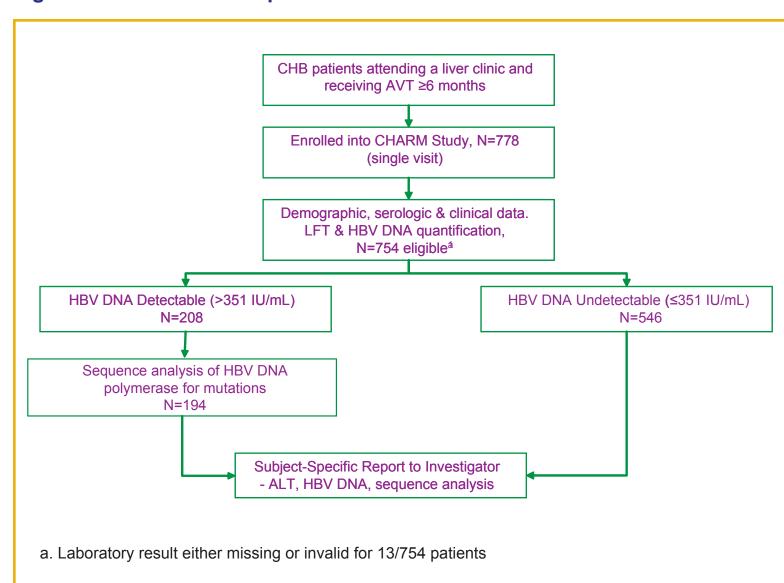


Table 1. Demographics

Parameter		N=754
Male		75%
Median age (range)		50 years (20-83)
	Asian	77%
	Caucasian	17%
Ethnicity	Aboriginal/Torres Strait or Pacific islander	3%
	African	2%
	Other	1%
Overseas born (non-Australian born)		93%
Known family history of liver disease		47%
Estimated mode of transmission	Birth/Early childhood	66%
	Horizontal	7%
	Other	27%
	1st regimen	39%
AVT	2 nd regimen	27%
	3 rd regimen	16%
	≥4 th regimen	18%

Table 2. Current AVT Regimen

Current AVT Regimen ^a	% (N=754)	Mean duration of current regimen ± SD (months)
Entecavir 0.5mg	25%	14 ± 5.7
Lamivudine	23%	48 ± 27.2
Adefovir + lamivudine	23%	19 ± 15.7
Entecavir 1.0 mg	10%	23 ± 15.2
Adefovir	8%	38 ± 21.9
Adefovir + entecavir ^b	4%	11 ± 7.6
Tenofovir DF + lamivudine	3%	13 ± 12.9
Tenofovir DF	2%	20 ± 9.3
Telbivudine	1%	29 ± 14.4
Adefovir + telbivudine	<1%	12
Tenofovir DF + entecavir 0.5 mg	<1%	9
Entecavir 1.0 mg + lamivudine	<1%	15 ± 0.4

a. Combinations reported if > 3 months duration

b. 28/30 received entecavir 1.0 mg; 1/30 received 0.5 mg entecavir; 1/30 dose of entecavir not reported

Table 3. Clinical CHB Status of Patients Receiving AVT

Parameter		HBV DNA Detectable (>351 IU/mL)	HBV DNA Undetectable (≤351 IU/mL)
		208/741 (28%)	533/741 (72%)
% with ≥1 drug resistance mu	utation detected	64%	N/A
Advanced fibrosis/cirrhosis ^a		25%	42%
Mean ALT (IU/L)		42	31
	≤40 IU/L	67%	81%
ALT	≤30 IU/L men/ ≤19IU/L women ^b	38%	51%

- a. Biopsy data only available for 506 patients; 132/208 (63%) HBV DNA detectable & 364/533 (68%) HBV DNA undetectable. Most recent biopsy information collected.
- b. Using The Royal College of Pathologists, Australia normal range ≤ 40 U/L. Central Lab normal range <50 U/L
- c. Prati D et al. Updated Definitions of Healthy Ranges for Alanine Aminotransferase Levels.
 Ann Intern Med 2002; 137: 1-9

Table 4. Clinical and Virological Characteristics of Patients with and without Drug-resistance Mutation

Results

	HBV DNA detectable			
Clinical and Virologic Characteristics	All (N = 208)	Drug-resistance mutation(s) (N=134)	No drug- resistance mutation(s) (N=74)	HBV DNA Undetectable (N=533)
HBeAg positive	63%	60%	69%	20%
Mean HBV DNA (IU/mL) ± SD	5.8 x 10 ⁵ ± 3.5 x 10 ⁶	5.4 x 10 ⁵ ± 2.4 x 10 ⁶	6.6 x 10 ⁵ ± 4.9 x 10 ⁶	N/A
Mean ALT (IU/L) ± SD	42 ± 45	44 ± 54	37 ± 22	31 ± 16
1 st oral AVT regimen	39%	19%	42%	43%
2 prior AVT regimen	27%	27%	28%	27%
3 prior AVT regimen	16%	21%	20%	15%
≥ 4 prior AVT regimen	18%	34%	9%	14%
Prior oral AVT	61%	81%	58%	57%
Mean duration of current oral AVT (months)	21 ± 22	23 ± 25	16 ± 15	27 ± 22
Mean duration of cumulative oral AVT (months)	54 ± 31	64 ± 26	35 ± 30	50 ± 31
Patient assessed non-compliance (≥1 dose missed in last 28 days)	14%	15%	12%	10%

Table 5. Most Common Drug-Resistance Mutations

Mutations ^a	Prevalence in viraemic patients (N=208)	Proportion of patients receiving active AVT regimen ^b
L180M + M204V/I	32 (15%)	18 (56%)
M204V/I	27 (13%)	12 (44%)
A181V/T	14 (7%)	4 (29%)
E164D + V173L + L180M + M204V/I	10 (5%)	8 (80%)
L80V/I + L180M + M204V/I	9 (4%)	6 (67%)
N236T	8 (4%)	2 (25%)
L180M +T184A/I/L/S + M204V/I	7 (3%)	5 (71%)
L80V/I + M204V/I	5 (2%)	4 (80%)
A181V/T + N236T	5 (2%)	2 (40%)
L180M + S202G + M204V/I	4 (2%)	0 (0%)
P120T + L180M + M204V/I	2 (1%)	1 (50%)
L180M + T184I + S202G + M204V/I	2 (1%)	1 (50%)

49% (60/123) patients with drug resistance mutations receiving inactive/sub-optimal AVT M204V/I reported in 80% of patients with drug resistance mutations

- a. Mutations reported in only 1 patient not presented
- b An active regimen is one to which the reported mutations are fully susceptible, i.e. it contains one or more AVT to which the mutations do not confer either resistance or reduced susceptible (ref: VIDRL classifications for HBV mutations).

Table 6. Patients with Genotypic Resistance to Current Regimen

Current AVT	% patients receiving an inactive/ sub- optimal AVT regimen ^a
Entecavir 1.0mg + lamivudine	1/2 (50%)
Entecavir 1.0mg	18/74 (24%)
Adefovir	8/60 (13%)
Telbivudine	1/8 (13%)
Lamivudine	19/170 (11%)
Adefovir + lamivudine	5/165 (3%)
Entecavir 0.5mg	5/190 (3%)
Adefovir + entecavir (0.5 or 1.0mg ²)	0/30 (0%)
Tenofovir + lamivudine	0/26 (0%)
Tenofovir	0/17 (0%)
Adefovir + telbivudine	0/1 (0%)
Tenofovir + entecavir 0.5mg	0/1 (0%)

8% (57/741) of patients are receiving an inactive/sub-optimal AVT

- a. Presence of a mutation or combination of mutations that confers reduced susceptibility/resistance to AVT
- b. 28/30 received 1.0 mg entecavir; 1/30 received 0.5 mg entecavir; 1/30 dose of entecavir not reported

Conclusions

- CHB patients receiving AVT in Australia are predominantly
- Overseas born (93%)
- Asian ethnicity (77%)
- HBeAg negative (68%)
- Male (75%)
- 39% of patients were receiving their first AVT regimen
- 18% had received ≥4 different regimens
- 28% of patients had a detectable viral load (>351 IU/mL)
- The majority (64%) of these patients had at least one drug resistance mutation
- Of those with drug resistance mutations
- Approximately 49% are not receiving active therapy
- The majority are
- HBeAg positive (60%)
- Treatment experienced, with approximately 1/3 receiving at least 4 regimens
- Cumulative treatment of approximately 5 years.
- 8% of all patients receiving oral antiviral therapy are receiving sub-optimal or inactive therapy
- 29% of patients with detectable HBV DNA
- These data support:
- The recommendation that genotypic resistance testing be considered in all patients who are HBV DNA positive
- That resistance testing should form part of the regimen selection process;
- That there is an urgent need for better education or referral advice in the treatment of CHB

Acknowledgements

Late Phase Group, Kendle PTY Ltd

The authors would like to thank the following on behalf on the CHARM Study group:

VIC

P. Angus
P. Angus
P. Desmond
P. Leggett
M-L Wong
MSW
MA

A. Zekrey
M. Levy
ACT
M. Levy
ACT
ACT
ACT

SA
H. Harley
CLD
B. Leggett
G. Macdonald
WA
WA

WA

WA

O. A. Zekrey
C. G. Jeffrey
Anna Ayres, VIDRL
Dr Scott Bowden, VIDRL