RESEARCH NOTE

Bimodal distribution and set point HBV DNA viral loads in chronic infection: retrospective analysis of cohorts from the UK and South Africa [version 1; peer review: awaiting peer review]

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Abstract

Hepatitis B virus (HBV) viral load (VL) is used as a biomarker to assess risk of disease progression, and to determine eligibility for treatment. While there is a well recognised association between VL and the expression of the viral e-antigen (HBeAg) protein, the precise determinants and distribution of VL at a population level are not well described. We here report the distribution of HBV VL in two large cross-sectional population cohorts in the UK and in South Africa, demonstrating a consistent bimodal distribution. The right skewed distribution and low median viral loads are significantly different from the left-skew and higher viraemia in seen in comparable HIV and hepatitis C virus (HCV) cohorts. Using longitudinal data, we present evidence for a stable ‘set-point’ VL in peripheral blood during chronic HBV infection. These results are important to underpin improved understanding of HBV biology and to plan public health interventions.

Keywords

HBV, HIV, viral load, set point, distribution
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Introduction

Hepatitis B virus (HBV) DNA viral loads (VL) show wide variation between individuals with chronic hepatitis B (CHB) infection, and are used to determine treatment eligibility\(^1\). The relationship between HBV e-antigen (HBeAg)-positive status and high VL in CHB is well recognised, but there are few refined descriptions of VL distribution, and limited understanding of the biology that underpins these patterns. Set point viral load (SPVL), defined as a stable level of viraemia in peripheral blood during the initial years of chronic infection, is a concept well established in HIV\(^2\). However, despite many biological similarities between HIV and HBV viral replication cycles, SPVL has not been explored for CHB to date.

Developing improved insights into the distribution of VL at a population level is important for planning wider treatment deployment to support progress towards international sustainable development goals for HBV elimination, which set ambitious targets for reducing morbidity and incidence of new CHB cases\(^1\). Characterisation of HBV VL dynamics is also important for mathematical modelling, and for generating new insights into persistence, transmission and pathogenesis.

We have therefore set out to generate a preliminary description of the HBV VL distribution in independent cohorts from the UK and South Africa, to identify associated host characteristics, to compare with VL distributions in two other chronic blood-borne viral infections, HIV-1 and hepatitis C virus (HCV), and to seek evidence for SPVL in HBV infection.

Methods

We retrospectively collected VL measurements ± supporting metadata for adults with chronic HBV, HCV and HIV infection from four cohorts:

(i) HBV: UK dataset

We collected data for adults (>18 years) with CHB infection (defined as positive HBsAg on ≥2 occasions ≥ 6 months apart) from electronic records at Oxford University Hospitals NHS Foundation Trust, as part of the National Institute of Health Research Health Informatics Collaborative (NIHR-HIC), as previously described\(^3\). We assimilated VL results (Abbott M2000 platform) for 371 individuals off nucleoside analogue therapy over six years commencing 1st January 2011, for whom baseline HBeAg status was available in 351 (95%) cases. Age, sex and self-reported ethnicity (using standard ethnicity codes) were available for 352, 355 and 322 individuals, respectively. For longitudinal VL analysis, we only used data prior to commencing antiviral treatment, including patients with ≥2 measurements 26 months apart (n=299 individuals, 1483 timepoints). The upper limit of quantification is HBV DNA 10\(^7\) IU/ml.

(ii) HBV: South Africa dataset

We collected all HBV VL data from the South African National Health Laboratory Service (NHLS) recorded over a four year period commencing 1\(^{st}\) January 2015 (n=6506 individuals). These were generated using various commercial platforms in different NHLS labs across the country. Other metadata (HBeAg status, HIV status, treatment data) were not available. For the purposes of analysis, we excluded VL measurements below the limit of detection based on the assumption that the majority of these samples were taken on antiviral treatment (indicated for HBV infection ± HIV co-infection). All those above the laboratory limit of quantification were designated 1.7×10\(^8\) IU/ml. For analysis of longitudinal data, we included patients with ≥2 detectable VL measurements (n=874 individuals; 9578 timepoints).

(iii) HCV

Baseline HCV viral loads were collected for adults prior to commencing antiviral treatment between 2006–2018, representing 925 individuals, from the same source as the UK HBV data using the Abbott M2000 platform, and collected through the NIHR-HIC pipeline. The setting and characteristics of this study population has been previously described\(^4\).

(iv) HIV

HIV data were obtained from a UK database of HIV seroconverters between 1985-2014 through the BEEHIVE collaboration (n=1581)\(^5\). HIV VL was measured using COBAS AmpliPrep/COBAS TaqMan HIV-1 Test, v2.0 on samples collected starting at 6–24 months after infection. SPVL was defined as the average VL for each patient over time, as previously described\(^6\).

Statistical analysis

We used Graphpad Prism v.8.2.1 for analysis of VL distributions, skewness, and univariate analysis of patient parameters associated with HBV VL (Mann Whitney U test and Kruskall Wallis test). HBV and HCV VL are conventionally reported in IU/ml, but to make direct comparisons between VL in different infections, we also converted data into copies/ml (1 IU = 5.4 copies/ml for HBV\(^7\) and 2.7 copies/ml for HCV\(^8\)).

We used R package (version 3.6.1) to assess within and between patient VL variability, using longitudinal data from UK HBeAg-negative adults, and from South African individuals with detectable VL. A large contribution of between-host variation would provide support for SPVL. We defined total variation, between-individual and within-individual variation according to analysis of variance (ANOVA). Specifically, the calculations are as follows:

\[
Variation_{total} = \sum_{i=1}^{n} \sum_{t=1}^{n_i} (x_{it} - \bar{x})^2
\]

\[
Variation_{between-individual} = \frac{1}{n} \sum_{i=1}^{n} n_i (\bar{x}_i - \bar{x})^2
\]

\[
Variation_{within-individual} = \sum_{i=1}^{n} \sum_{t=1}^{n_i} (x_{it} - \bar{x}_i)^2
\]

\(n\) denotes the number of individuals; \(n_i\) represents the number of data points for individual \(i\); \(x_{it}\) denotes the viral load of
patient \( i \) at time point \( t \); \( \bar{x} \) is the mean of viral loads of all data points; \( \bar{\mu}_i \) is the mean of viral loads of patient \( i \).

### Ethics

Data collection for the UK cohort was approved as part of the NHS Health Informatics Collaborative (NHIC Hepatitis Theme C Database) by the NRES Committee South Central-Oxford C (ref: 15/SC/0523), allowing routine clinical data to be collated and analysed in anonymised form as described previously\(^8\). South African data collection was approved by the Health Sciences Research Ethics Committee at the University of the Free State (ref: UFS-HSD2019/0044/2603). In both cases, approval was given without the need for individual patient consent, as data were collected in anonymised form without identifying details.

### Results

Our UK HBV cohort was 56% male, median age 42 years, with diverse ethnic backgrounds (among 322 individuals with self-reported ethnicity data, 38% were Asian, 34% White, 24% Black, 4% Arabic, <1% other). Overall, median HBV VL was 3.4 \( \log_{10} \) IU/mL; 95% CI 3.2 – 3.5 \( \log_{10} \) IU/mL (equivalent to median 4.2 \( \log_{10} \) copies/ml). There was a bimodal VL distribution with two peaks:

(i) **HBeAg-negative infection** (accounting for 304/351 (87%) of measurements): median VL 3.2 \( \log_{10} \) IU/mL (95% CI 3.0 – 3.4); right-skewed distribution (Figure 1A);

(ii) **HBeAg-positive infection** (accounting for 47/351 (13%) of measurements): median VL 7.6 \( \log_{10} \) IU/mL (95% CI 5.6 – 8.2); left-skewed distribution (Figure 1B).

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**Figure 1.** Distribution of viral loads (VL) for adults with chronic infection with Hepatitis B virus (HBV), HIV and Hepatitis C virus (HCV). Panels A-C show VL distribution in HBV infection; D shows VL distribution in HIV infection; E shows VL distribution in HCV infection. Number of individuals represented, median viral load, and skewness of distribution are reported on individual panels A-E. IU/ml is standard approach to quantification for HBV and HCV (panels A, B, C, E), versus copies/ml routinely reported for HIV (panel D). In order to make a direct comparison between the three viruses, all values were converted into copies/ml for panel F.
In the South African dataset (HBeAg status not determined), median HBV VL was 4.6 log_{10} IU/mL (95% CI 3.9 – 4.0), with a bimodal distribution and right-skew (Figure 1C,2). Median HIV VL was 4.5 log_{10} copies/mL and median HCV VL was 6.0 log_{10} IU/ml (6.4 log_{10} copies/ml), with a left skew and no bimodal distribution (Figure 1D,E,2). Median viraemia was significantly different between HBV, HIV and HCV (p<0.0001; Figure 1F).

For the UK data we investigated whether sex, age or ethnicity had any influence on VL; the only significant association was lower VL with increasing age in the HBeAg-positive group (p=0.01 by Kruskal Wallis, Supplementary Figure 1; extended data3).

Inter-patient variation accounted for 82.7% and 88.0% of the variability in UK and South African longitudinal datasets respectively, whilst within-patient variation accounted for 17.3% and 12.0%. This provides support for a stable SPVL within individuals with CHB.

Discussion
In this short report, we describe a consistent bimodal distribution of VL in CHB in a diverse UK population and a large South African dataset, in keeping with previously published studies (e.g. 10), and reflecting the role of HBeAg in immunomodulation1. However, descriptions of this pattern have not previously been carefully refined.

HBV viral loads in HBeAg-negative infection are significantly lower than HCV and HIV, which may relate to differences in viral population structure, viral fitness, host immune responses, and the availability of target cells. These factors might also explain why HIV, HCV and HBeAg-positive infection have left skew VL distributions, whereas HBeAg-negative infection has a right skew. This is the first study to demonstrate the concept of SPVL in HBV infection, with between-host factors explaining >80% of the variation in VL during HBeAg-negative CHB. Missing metadata is a limitation for further analysis of our South African dataset, and longer term aspirations will be to investigate larger VL datasets together with more robust longitudinal clinical and laboratory data.

Whole genome sequencing has the potential to increase our understanding of HBV, but approximately 50% of cases fall below the current sequencing threshold12. This means that at present there is a significant ‘blind spot’ in sequence data, preventing analysis of sequence variants in individuals with VL below the population median. Enhanced descriptions of HBV VL may shed light on the biology of chronic HBV infection, inform mathematical models of viral population dynamics within and between hosts, improve understanding of risk factors for transmission and disease progression, underpin optimisation of viral sequencing methods, and help to stratify patients for clinical trials and treatment.

Data availability
Underlying data
Figshare: Supporting data for an analysis of HBV viral load distribution and set point in chronic infection: retrospective analysis of cohorts from the UK and South Africa. https://doi.org/10.6084/m9.figshare.11365082.v2

This project contains the following underlying data:
- 191217 HBV VL data South Africa.xlsx (Including baseline VL data for each patient in the South African patient cohort and longitudinal values where measured)
- 200115 HBV VL metadata file.xlsx (Including baseline VL data for each patient in the UK patient cohort and longitudinal values where measured)

Extended data
Figshare: Supporting data for an analysis of HBV viral load distribution and set point in chronic infection: retrospective analysis of cohorts from the UK and South Africa. https://doi.org/10.6084/m9.figshare.11365082.v2

This project contains the following extended data:
- 200115 Suppl Fig 1.pdf

Supplementary Figure 1: Relationship between hepatitis B viral load, HBeAg status and (A) sex, (B) age, and (C) ethnicity, in a cohort of adults with chronic hepatitis B virus infection recruited in Oxford, UK.

Data are available under the terms of the Creative Commons Attribution 4.0 International license (CC-BY 4.0).

References


8. NHIC Hepatitis Theme Database V1 - Health Research Authority [Internet]. [cited 2020 May 21]. Reference Source


