Prevalence of Human Parvovirus B19, Bocavirus, and PARV4 in Blood Samples from the General Population of China and Lack of a Correlation between Parvovirus and Hepatitis B Co-Infection

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Abstract

Few comprehensive studies have investigated viraemia caused by human parvoviruses (HPAVs) in China. A total of 1626 of blood samples were collected from non-HBV and HBV infected Chinese subjects (adults, N = 1279; children, N = 347) from south-western and south-eastern China. DNA from three HPAVs was detected in blood samples using PCR-based assays. The epidemiological profiles and association with HBV co-infection were also analysed. Of the 1626 blood samples tested, 138 (8.49%) were found to exhibit HPAV viraemia, including 3.51% with B19, 3.75% with HBoV and 2.52% with PARV4. The presence of B19 DNA in both child and adult, as well as that of PARV4 DNA in adult, from the south-western region was significantly higher than that from the south-eastern region (P = 0.006 for B19 in children; P = 0.026 for B19 in adults; and P = 0.014 for PARV4 in adult). However, the frequency of HBoV DNA in adults from the south-western region was significantly lower than that observed in adults from the south-eastern region (P = 0.001). Furthermore, HBoV was more prevalence in male (4.9%) than in female (1.4%) individuals. In addition, no significant correlation between HBV and HPAV co-infection was found using serum samples from Chinese adults. In conclusions, the molecular prevalence of three HPAVs in blood samples exhibited variation among different populations depending on area, age and gender; No association between HPAV and HBV infection in adults was found. Our data provide a basis for improving blood safety and preventing HPAV infection in China.

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Introduction

Human parvoviruses (HPAVs) are small, non-enveloped, single-stranded DNA viruses. In recent years, the number of identified HPAVs has increased rapidly [1]. In addition to B19, which was the first HPAV known to cause erythematous infectiosum and a variety of other disease manifestations [2], the HPAV family now also includes human bocavirus (HBoV) and parvovirus 4 (PARV4), both of which were first reported in clinical samples in 2005 [3,4]. Several studies have shown that HBoV was detected in human respiratory secretions and feces and might associate with acute respiratory tract symptoms and gastrointestinal disease [5–7]. However, HBoV has also been frequently detected in asymptomatic patients and in patients co-infected with other pathogens [7]. PARV4 has been detected in blood, pooled plasma, and diverse tissue samples of HIV/AIDS patients who are also known injectable drug users [8,9]. However, the clinical significance of co-occurrence of PARV4 DNA in hepatitis B virus (HBV)-infected patients remains controversial [8–12].

Previous studies have suggested that B19, HBoV and PARV4 are the pathogenic members for human among parvovirus and likely to circulate globally [7,11,13–19]. Both HBoV and PARV4 was recently identified novel HPAVs. Little is known about the mode and frequency of transmission and their full pathogenicity of HBoV and PARV4 infection. Up-to-date, none reported the epidemiological profile of HBoV and PARV4 infection among general populations in China. In addition, few studies of HBoV DNA in blood samples are available [7,16,19,20].

In addition, the clinical significance of HPAV occurrence in patients co-infected with hepatitis remains controversial [14–16]. Co-infection of parvovirus B19 and PARV4 with HBV or hepatitis C (HCV) has been observed in patients with acute and chronic hepatitis [17,18]. In the southern region of China, HBV infection is endemic, with an HBsAg seroprevalence of approximately 7–9%
Detection of B19, HBoV and PARV4/5

Methods

Ethical Statement
All human sera were de-identified before use in the study, and all laboratories testing of samples were approved by the Ethical Review Committee of the National Institute for Viral Disease Control and Prevention (CNVCDC) and the Wenzhou Medical College (WMC). All work involving human blood samples was approved by the Ethical Review Committee of the CNVCDC and the WMC. The blood samples were collected as part of routine surveillance activities undertaken by CNVCDC and WMC, and so consent was waived by the Ethical Review Committee.

Study Groups
This study involved a total of 1626 blood samples from the southern region of China (Table 1). Samples were divided into groups as the southwest area (including several provinces such as Chongqing, Guizhou, Yunnan, Sichuan and Xizang) representing multi-ethnic and less-developed zone, and the southeast (Zhejiang and Jiangsu province) areas representing the costal and developed zone in China (Figure 1). The sample size and demographic characteristics of all participants were matched between southwest and southeast area. All samples were collected from health examination population and retrieved randomly from the Sample Bank of the CNVCDC and the WMC from 2005 to 2012. Serum specimens were tested for the presence of HBV, HCV and HIV-1 viral genomes using commercial real-time PCR kits. None were positive for HIV-1 or HCV RNA. HBsAg and HBeAg were assayed using commercial ELISA kits (Kehua Corporation, Shanghai). In this study, we used 347 serum samples from children and 1279 from adults. The cohort included the following: samples defined as healthy controls were serum-negative for HBV DNA, HCV and HIV-1 RNA; samples that were serum-positive for HBV DNA and HBV surface antigen (HBsAg) but negative for HBV e antigen (HBeAg) were termed HBV carriers; samples that were serum-positive for both HBsAg and HBeAg were termed chronic HBV infected patients. All serum samples from the Xizang area were Tibetan in origin; samples from the Sichuan areas were Han in origin.

Detection of B19, HBoV and PARV4/5

Nucleic acid was extracted from 200 µl samples of blood using QIAamp MinElute Virus Spin Kit (Qiagen, Mississauga, Ontario, Canada) according to the manufacturer’s instructions. Aliquots (10 µl) of the nucleic acids were subjected to a nested PCR assay for three HPAVs (B19, HBoV and PARV4), as described previously [11,13]. The primers used in this study are listed (Table S1). PCR amplicons for DNA sequencing were gel purified using the PCR Clean-Up System (Promega, Madison, Wisconsin) according to the manufacturer’s instructions. DNA sequencing was performed with specific primers using the ABI PRISM BigDye Terminator Cycle Sequencing Reaction kit (version 3.1) on an ABI PRISM 3130 DNA sequencer (Applied Biosystems, Foster City, California) following the manufacturer’s instructions.

Statistical Analysis
Eligibility and classification of samples were determined from the original medical record in the database. Univariate associations between age and the frequency distribution of viral pathogens were analysed by logistic regression. Univariate associations between the distributions of virus and co-detections and the clinical picture of illness were assessed by multinomial logistic regression analysis. Statistical significance was assessed by one-way ANOVA followed by Tukey’s test. The statistical analyses were performed using SAS (version 9.2; SAS Institute, Cary, NC, USA). P values <0.05 were considered to indicate statistical significance.

Results

Characteristics of Study Participants
The general demographic information of the subjects is listed in Table 1. Groups were formed based on gender, age, area, population, and HBV infection status among adults. Overall, a total of 1626 blood samples were screened for B19, HBoV and PARV4 in this study. A total of 966 (59.4%) samples were from male subjects and 347 (21.3%) were from children (all child samples tested negative for HBV). A total of 741 samples were collected from the population in the south-western region of China, including samples from 175 children and 566 adults; 885 samples were collected from the population in the south-eastern region of China, including samples from 172 children and 713 adults. A total of 125 samples were collected from the Tibetan population in Xizang and 528 samples were from the Han population in the Sichuan province. Cohorts were formed among healthy adult subjects (HBV negative, N = 563) and HBV-infected subjects (HBV positive, N = 716); the group was further subdivided into HBV carriers (N = 400, HBsAg HBsAg and chronic HBV patients (N = 316, HBsAg HBsAg ).

Distribution of HPAV Infection by Age, Gender, Area, and Population

All blood samples were screened using nested PCR for the DNA of three HPAVs: B19, HBoV and PARV4. Of 1626 blood samples tested, 138 (8.49%) exhibited HPAV infection, including 57 (3.51%) with B19, 61 (3.75%) with HBoV, and 41 (2.52%) with PARV4 (Table 1). We further analysed the distribution of HPAV infection by age, gender, area, and population. As shown in Table 2, we detected 20 (5.76%) with B19, 16 (4.61%) with HBoV, and nine (2.6%) with PARV4 in the child group (N = 347). There was no significant difference in the prevalence of the three HPAVs between male and female subjects. In addition, no significant difference in the prevalence of HBoV and PARV4 infection between subjects from the south-western and south-eastern regions was observed. However, the B19 positivity rate (9.1%) among children from the south-western region was significantly higher than that (2.3%) in children from the south-eastern region (P = 0.006). The prevalences of the three HPAVs in three age groups (<4 years, 4–5 years, and >5 years) were also determined (Figure 2). B19 and PARV4 infections increased among the 4–5-year-old group compared to those under the age of 4 years. However, HBoV positivity peaked among young children and then decreased with advancing age (6.73% for the <4 years group, 4.12% for the 4–5 years group, and 2.78% for the >5 years group).

In the adult sample group (N = 1279), we detected 37 (2.89%) with B19 infection, 45 (3.52%) with HBoV infection, and 32 (2.50%) with PARV4 infection. No significant difference was observed in B19 and PARV4 infection between male (N = 773)
Table 1. Demographic characteristics of all participants (N = 1626).

| Group Characteristics | Number | Percentage (%) |
|-----------------------|--------|----------------|
| Gender                |        |                |
| Male                  | 966    | 59.4           |
| Female                | 660    | 40.6           |
| Age (year)            |        |                |
| Children (1–14)       | 347    | 21.3           |
| Adults (18–81)        | 1279   | 78.7           |
| Area                  |        |                |
| Southwest             | 741    | 45.6           |
| Children              | 347    | 21.3           |
| Adults                | 404    | 25.4           |
| Southeast             | 885    | 54.4           |
| Children              | 404    | 25.4           |
| Adults                | 481    | 29.6           |
| Cohort in Adults      |        |                |
| HBV DNA(−)            | 563    |                |
| HBV DNA(+)            | 716    |                |
| HBsAg+ HBeAg−         | 400    |                |
| HBsAg+ HBeAg+         | 316    |                |
| HPAV DNA(+)           |        |                |
| Any                   | 138    | 8.49           |
| B19                   | 57     | 3.51           |
| HBoV                  | 61     | 3.75           |
| PARV4                 | 41     | 2.52           |

Table 2. Prevalences of B19, HBoV and PARV4 in different age, gender, and regional groups.

| Group               | B19   | HBoV  | PARV4  |
|---------------------|-------|-------|--------|
| Children (N = 347)  | 20 (5.76%) | 16 (4.61%) | 9 (2.6%) |
| Gender              |       |       |        |
| Male (N = 193)      | 14 (7.3%) | 10 (5.2%)  | 7 (3.6%) |
| Female (N = 154)    | 6 (3.9%)  | 6 (3.9%)  | 2 (1.3%) |
| P value             | 0.182 | 0.571 | 0.31   |
| Region              |       |       |        |
| Southwest (N = 175) | 16 (9.1%) | 8 (4.6%)  | 7 (4.0%) |
| Southeast (N = 172) | 4 (2.3%)  | 8 (4.7%)  | 2 (1.2%) |
| P value             | 0.006 | 0.972 | 0.185  |
| Adults (N = 1279)   | 37 (2.89%) | 45 (3.52%) | 36 (2.50%) |
| Gender              |       |       |        |
| Male (N = 773)      | 23 (3.0%) | 38 (4.9%)  | 16 (2.1%) |
| Female (N = 506)    | 14 (2.8%)  | 7 (1.4%)  | 16 (3.2%) |
| P Value             | 0.828 | 0.001 | 0.221  |
| Region              |       |       |        |
| Southwest (N = 566) | 23 (4.1%) | 9 (1.6%)  | 21 (3.7%) |
| Southeast (N = 713) | 14 (2.0%)  | 36 (5.0%) | 11 (1.5%) |
| P value             | 0.026 | 0.001 | 0.014  |

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and female (N = 556) subjects. However, the HBoV positivity rate (4.9%) in males was significantly higher than that (1.4%) in females. In addition, the prevalence of the three HPAVs exhibited significant differences between subjects from the south-western and south-eastern regions of China. Both B19 and PARV4 were more prevalent in south-western region samples (B19, 4.1% vs. 2.0%, \(P = 0.026\); PARV4, 3.7% vs. 1.5%, \(P = 0.014\)). In contrast, HBoV was more prevalent in south-western region subjects (5.0% vs. 1.6%, \(P = 0.001\)). The prevalence of three HPAVs among three adult age groups (18–30 years, 31–50 years, and >50 years) was also analysed (Figure 2). Both HBoV and PARV4 exhibited significantly lower infection rates (<1.43%) than B19 (3.82%) among the 18–30-year-old group.

Two populations (Han and Tibetan) from adjacent provinces (Sichuan and Xizang) in the south-western region were evaluated to assess the HPAV infection rates among ethnicities (Table 3). Among 528 subjects from the Sichuan Han population, we detected 17 (3.2%) with B19, nine (1.7%) with HBoV, and seven (1.3%) with PARV4. Among 125 subjects from the Xizang Tibetan population, we detected six (4.8%) with B19, none with HBoV, and 12 (9.6%) with PARV4. The prevalence of PARV4 in the Xizang Tibetan population was significantly higher than that in the Sichuan Han population.

A total of 16 cases with HPAV co-infection were identified (Table S2). Half of these were children, five of which exhibited co-infection with all three HPAVs (B19, HBoV and PARV4).

Comparison between Healthy and HBV Infection Adults

To explore the correlation between HPAV and HBV co-infection, we formed cohorts of healthy (HBV-negative) and HBV-infected adults; the HBV-infected group was further divided into HBV carriers (HBsAg\(^+\) HBeAg\(^-\)) and chronic HBV patients (HBsAg\(^+\) HBeAg\(^+\)) (Table 4). The B19 and PARV4 detection frequencies were similar in both healthy and HBV-infected adults. However, the HBoV positivity rate (6.6%) in healthy adults was higher than that (1.1%) in HBV-infected adults (Table 4). In addition, no significant difference in the prevalence of HPAVs between HBV carriers and chronic HBV patients was observed.

**Discussion**

The present study is the first comprehensive investigation of the epidemiological profiles of HPAVs among the general population in China using blood samples and PCR-based assays. The overall prevalence of HPAV viraemia in the general Chinese population was 3.51% B19, 3.75% HBoV and 2.52% PARV4. Groups were evaluated based on gender, age, and regional differences. We also compared the frequency of three HPAVs between HBV-infected subjects and healthy controls. We found several aspects of HPAV infection that had not been reported previously, and we increased the knowledge of the epidemiological profiles of HPAV infection in China.

As reported previously, transmission of parvovirus B19 occurs most commonly by personal contact or via blood, sexual intercourse, or a maternal-neonatal relationship, and it is usually associated with an expanding range of clinical disorders [14,16]. However, it has also been shown that B19 DNA can persist in healthy or immunocompetent individuals for long periods.

**Table 3.** Prevalences of B19, HBoV and PARV4 in Han and Tibetan populations in the south-western region.

|        | B19 | HBoV | PARV4 |
|--------|-----|------|-------|
| Han (Sichuan = 528) | 17 (3.2%) | 9 (1.7%) | 7 (1.3%) |
| Tibetan (Xizang = 125) | 6 (4.8%) | 0 | 12 (9.6%) |

\[P \text{ value } 0.554 0.297 0.001\]

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**Table 4.** Prevalences of B19, HBoV and PARV4 among healthy adults (HBV DNA negative), HBV carriers (HBsAg\(^+\) HBeAg\(^-\)) and chronic HBV patients (HBsAg\(^+\) HBeAg\(^+\)).

| Group | B19 | HBoV | PARV4 |
|-------|-----|------|-------|
| HBV DNA(−) (N = 563) | 18 (3.2%) | 37 (6.6%) | 16 (2.8%) |
| P value | 0.565 0.001 0.490 |
| HBV DNA(+) (N = 716) | 19 (2.7%) | 8 (1.1%) | 16 (2.2%) |
| P value | 0.774 0.488 0.633 |

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Author Contributions
Conceived and designed the experiments: RT LS YL WT. Performed the experiments: RT LS YL WZ JL MZ. Analyzed the data: RT SB YL WT. Contributed reagents/materials/analysis tools: LS WY MZ SB. Wrote the paper: RT WT.

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