Parvovirus 4 Infection and Clinical Outcome in High-Risk Populations

Citation for published version:

Digital Object Identifier (DOI):
10.1093/infdis/jis291

Link:
Link to publication record in Edinburgh Research Explorer

Document Version:
Publisher's PDF, also known as Version of record

Published In:
The Journal of Infectious Diseases

Publisher Rights Statement:
© The Author 2012. Published by Oxford University Press on behalf of the Infectious Diseases Society of America. All rights reserved.

This is an Open Access article distributed under the terms of the Creative Commons Attribution Non-Commercial License (http://creativecommons.org/licenses/by-nc/3.0), which permits unrestricted noncommercial use, distribution, and reproduction in any medium, provided the original work is properly cited

General rights
Copyright for the publications made accessible via the Edinburgh Research Explorer is retained by the author(s) and / or other copyright owners and it is a condition of accessing these publications that users recognise and abide by the legal requirements associated with these rights.

Take down policy
The University of Edinburgh has made every reasonable effort to ensure that Edinburgh Research Explorer content complies with UK legislation. If you believe that the public display of this file breaches copyright please contact openaccess@ed.ac.uk providing details, and we will remove access to the work immediately and investigate your claim.
Parvovirus 4 Infection and Clinical Outcome in High-Risk Populations

Ruth Simmons,1 Colin Sharp,2,3 C. Patrick McClure,4 Janine Rohrbach,5 Helen Kovari,6 Eleni Frangou,7 Peter Simmonds,2 Will Irving,7 Andrí Rauch,7 Paul Bowness,5,6 Paul Klenerman,1,9 Ruth Simmons,1 Colin Sharp,2,3 C. Patrick McClure,4 Janine Rohrbach,5 and the Swiss HIV Cohort Study

1Nuffield Department of Medicine, Peter Medawar Building for Pathogen Research, 2Centre for Immunology, Infection and Evolution, and 3The Roslin Institute and Royal (Dick) School of Veterinary Studies, University of Edinburgh, 4School of Molecular Medical Sciences, National Institute for Health Research Biomedical Research Unit, University of Nottingham, and 5University Clinic of Infectious Diseases, University Hospital Bern and University of Bern, and 6Division of Infectious Diseases and Hospital Epidemiology, University Hospital Zurich, University of Zurich, Switzerland; and 7Department of Statistics, University of Oxford, and 8Weatherall Institute of Molecular Medicine, and 9National Institute for Health Research Biomedical Research Centre, John Radcliffe Hospital, Oxford, United Kingdom

Parvovirus 4 (PARV4) is a DNA virus frequently associated with human immunodeficiency virus (HIV) and hepatitis C virus (HCV) infections, but its clinical significance is unknown. We studied the prevalence of PARV4 antibodies in 2 cohorts of HIV- and HCV-infected individuals (n = 469) and the correlations with disease status. We found that PARV4 infection frequently occurred in individuals exposed to bloodborne viruses (95% in HCV-HIV coinfected intravenous drug users [IDUs]). There were no correlations between PARV4 serostatus and HCV outcomes. There was, however, a significant association with early HIV-related symptoms, although because this was tightly linked to both HCV status and clinical group (IDU), the specific role of PARV4 is not yet clear.

Parvovirus 4 (PARV4) is a recently discovered DNA virus of the Parvoviridae family that infects human populations worldwide [1–5]. It has been frequently found in intravenous drug users (IDUs) [4, 6] but is uncommon in healthy individuals in Western countries, suggesting parenteral transmission [4, 6]. Parvovirus 4 is associated with human immunodeficiency virus (HIV) and hepatitis C virus (HCV) infections [3]; hence we were interested in the effect PARV4 might have on disease progression. Parvovirus 4 has been found in many tissues, including the bone marrow of HIV-positive individuals [3] and the liver of HCV-positive individuals [1, 7], but is also found in plasma, cerebrospinal fluid, skin, and myocardium [1, 2, 4, 6, 8]. Despite the detection of viral DNA in so many organs, PARV4 has rarely been linked to specific symptoms, except for a recent study linking PARV4 to encephalitis [8] and in the individual in whom PARV4 was discovered, who presented symptoms including pharyngitis, vomiting, and arthralgias [2]. Determining a pathological association is problematic because PARV4 is so frequently found in individuals burdened with HCV- or HIV-related disease. However, as a common coinfection with these pathogens, it may have an important impact on clinical disease. This is of increased importance in light of the recent examination of immune responses to this virus [9]. This revealed sustained high-frequency T-cell responses associated with an effector memory phenotype consistent with persistent exposure to immunogenic viral antigen. Because the antigen can be expressed in both lymphoid and hepatic tissues [3, 7], an impact on both HCV and HIV pathogenesis is plausible.

We therefore studied the impact of PARV4 serostatus on HCV- and HIV-related disease progression. To do this, we tested for PARV4-specific antibodies in 2 prospective cohorts of HCV- and HIV-infected individuals (mono- and coinfected). Hepatitis C viral clearance, genotype, patient gender, age, alanine amino-transferase (ALT) levels, tissue histology (fibrosis), CD4 slopes, and Centers for Disease Control and Prevention (CDC) events were analyzed in relation to PARV4 serostatus.

METHODS

Study Subjects and Sample Collection

Local ethical approval (MREC/98/3/55 and http://www.shcs.ch/30-study-design) and informed patient consent were obtained for 2 cohorts, totaling 469 individuals (Table 1). The first, which consisted of 193 individuals from the Swiss HIV cohort [10], was made up of 99 HIV-positive, HCV-negative men who have sex with men (MSM) and 94 HIV-HCV coinfected IDUs. The first sample taken at least 1 year after the first positive HIV serology was used in experiments. The
second group, which consisted of 276 individuals from the Trent HCV cohort, was divided into 44 individuals who cleared HCV vs 232 who became chronically infected and, among chronically infected individuals, 143 who had persistently mild liver fibrosis (Ishak fibrosis score always 0 or 1, 1–5 biopsies were taken per individual, across 1–25 years) vs 98 who progressed to severe fibrosis (Ishak fibrosis score 5 or 6). The most recent plasma sample available was tested in this latter cohort. Plasma samples were taken by each center and frozen until required.

Serological Screening
Plasma samples from these individuals were tested in duplicate for anti-PARV4 immunoglobulin G (IgG), as described elsewhere [6].

CD4 Slopes and CDC Events
CD4 counts were available for 114 of 193 individuals of the Swiss HIV cohort prior to antiretroviral therapy. CD4 slopes were calculated using GraphPad Prism when at least 3 time points were available, spanning 6 months minimum. CD4 counts were plotted relative to time (day 0 was the first available sample date) to determine CD4 slopes, which were then compared to PARV4 serostatus using Mann–Whitney tests. Kaplan–Meier survival curves were drawn to compare time to reach CDC-B and CDC-C events and death, defined by the CDC as hallmarks of HIV-related disease [11].

Statistical Analyses
Statistical analyses were carried out using the Mann–Whitney test, Fisher’s exact test, and log rank (Mantel–Cox test) using GraphPad Prism software. For more detailed statistic analyses on the Trent HCV cohort, the open-source R software (http://www.r-project.org) was used to perform a logistic regression to analyze the simultaneous relationship of age, gender, main risk factor (IDU or MSM), and ALT with PARV4 serostatus. The HCV genotype was excluded because this information was not available for all individuals. The log odds of being PARV4 seropositive were modeled as a linear function of all variables potentially affecting this. The formula was:

\[
\text{Log odds (PARV4 serostatus)} \sim \text{age} + \text{gender} + \text{main risk factor} + \text{ALT}
\]

where “∼” implies relationship. The coefficients of the model have approximately normal distributions; therefore \( P \) values were obtained to compare individual coefficients. This analysis was carried out on 263 individuals of the Trent HCV cohort with complete data sets.

RESULTS
PARV4 Strongly Correlates With Intravenous Drug Use and Is Linked to CDC-B Event Occurrence
To address whether PARV4 has an impact on HIV disease progression, PARV4 serostatus was determined in 193 individuals from the Swiss HIV cohort (Table 1). First, we noted a striking association between PARV4 status and clinical group. In the HIV-positive, HCV-positive (IDU) group, a 95% prevalence of PARV4 was observed, compared with only 11% in the HIV-positive MSM group (\( P < .0001 \)). We next analyzed CD4 slopes in relation to PARV4 status using serial CD4 counts available for 114 patients: 49 PARV4 IgG− individuals with CD4 slopes ranging from −41.3 to 5 cells/µL/month (median, −6.2), and 65 PARV4 IgG+ individuals with CD4 slopes ranging from −32.6 to 7.6 CD4 cells/µl/month (median, −6.3; data not shown). Using this approach we could not detect a difference in CD4 T cell decline between serologic groups (\( P = .89 \)).

As another robust indicator of HIV disease progression, we assessed the occurrence of CDC-B and CDC-C events and death in PARV4-seropositive and -seronegative groups (Figure 1). The CDC-B symptoms were observed earlier in PARV4-seropositive individuals (\( P = 0.02 \)). The association was not significant for CDC-C or death or between clinical groups (MSM vs IDU; data not shown). Thus, we did observe a correlation between PARV4 serostatus and early HIV disease progression, but the very close association between PARV4 serostatus, risk factor for HIV

---

Table 1. Demographic Data and Parvovirus 4 (PARV4) Seroprevalence

<table>
<thead>
<tr>
<th>Cohort</th>
<th>Main Risk Factor</th>
<th>No.</th>
<th>HCV</th>
<th>HIV</th>
<th>Gender, % Male</th>
<th>HCV Genotype at Diagnosis</th>
<th>PARV4 Serostatus</th>
</tr>
</thead>
<tbody>
<tr>
<td>Swiss HIV</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>MSM</td>
<td>99</td>
<td>−</td>
<td>+</td>
<td>100%</td>
<td>N/A</td>
<td>11%</td>
<td></td>
</tr>
<tr>
<td>IDUs</td>
<td>94</td>
<td>+</td>
<td>+</td>
<td>74%</td>
<td>60% genotype 1, 40% genotype 3</td>
<td>95%</td>
<td></td>
</tr>
<tr>
<td>Nottingham Trent</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>66% IDUs</td>
<td>276</td>
<td>+</td>
<td>−</td>
<td>67%</td>
<td>40% genotype 1, 48% genotype 3</td>
<td>31%</td>
<td></td>
</tr>
</tbody>
</table>

Only 58 of 94 hepatitis C virus (HCV) genotypes for the Swiss HIV cohort were available. The percentages shown represent proportions of known genotypes. Abbreviations: HIV, human immunodeficiency virus; IDUs, intravenous drug users; MSM, men who have sex with men; N/A, not applicable.
transmission, and HCV serostatus makes the individual components of risk difficult to dissect.

**PARV4 Infection Is Also Common in HCV Mono-Infected Individuals**

The prevalence of PARV4 was also studied in 276 HCV-positive, HIV-negative individuals from the Trent HCV cohort. Thirty-one percent of individuals were PARV4 seropositive, and 36% in the IDU subset were PARV4 seropositive.

To determine if PARV4 serostatus affects clinical outcome in HCV-positive individuals, age, gender, HCV genotype, ALT levels, and main risk factor (IDU or non-IDU) were compared. No significant difference was seen between PARV4-seropositive and -seronegative individuals in gender, HCV genotype, age, or ALT levels ($P = .89$, .64, .26, and .34 respectively). We did, however, find a strong association between PARV4 serostatus and intravenous drug use as a risk factor ($P = .01$).

Next, the parameters of age, gender, ALT, and risk factor were analyzed together with PARV4 serology using a logistic regression framework. The results of this analysis show that only the IDU risk group significantly correlated with detection of PARV4 IgG ($P = .01$).

**PARV4 Does Not Affect the Progression of HCV-Related Disease**

To assess the impact of PARV4 infection on HCV disease progression, 276 individuals from the Trent HCV cohort were grouped by clinical outcome. Study subjects were divided by PCR status: either persistently positive ($n = 232$) or always negative ($n = 44$), an indication of spontaneous HCV clearance. Thirty-six percent of individuals who had cleared HCV were PARV4 seropositive vs 29% of individuals who remained viremic ($P = .37$; data not shown).

Longitudinal biopsy data was available for 241 of these individuals. They were divided into those who maintained a mild fibrosis score (Ishak score 0 or 1 over time; $n = 143$) and those who progressed to severe liver fibrosis (Ishak score 5 or 6; $n = 98$). Twenty-nine percent of the individuals with mild fibrosis were PARV4 seropositive vs 31% of those with progressive disease ($P = .78$; data not shown). Finally, the treatment outcome of 131 individuals from the Trent HCV cohort was compared with their PARV4 serostatus. No significant difference was seen between patients who did not respond to treatment or relapsed and those who had a sustained virological response ($P = .45$; data not shown).

**DISCUSSION**

This study confirms that PARV4 infection is common in HCV-positive individuals, and even more so in HCV-positive IDUs coinfected with HIV. Although PARV4 did not influence HCV persistence, disease progression, or treatment response, PARV4-seropositive HIV-infected subjects progressed faster to HIV CDC-B symptoms than PARV4-seronegative individuals. However, because this was tightly linked to both HCV status and clinical group (IDU), the specific role of PARV4 is not yet clear.

Thirty-one percent of the HCV-positive, HIV-negative individuals of the Trent HCV cohort were PARV4 seropositive. This is in accordance with our previous study that found 26% seropositivity in 84 HCV-infected individuals [9] and other studies that tested for PARV4 IgG [6] or viral DNA directly [12]. Parvovirus 4 infections are acute and resolve rapidly, followed by complete or almost complete clearance of viremia and only very low viral loads on reactivation [12]. Parvovirus 4 may therefore be relatively inefficiently transmitted compared with HCV and HIV-1.

In the Swiss HIV cohort, a striking 95% of the HIV-positive, HCV-positive IDUs were PARV4 seropositive. This is the
highest published figure for this clinical group, with other studies reporting 55%–85% [6]. Together with only 11% PARV4 seropositivity of the HIV-positive, HCV-negative MSM and 31% in the Trent HCV cohort, these data strongly indicate parenteral transmission of PARV4. Parvovirus 4 seroprevalence in HCV-positive, HIV-negative IDUs was still only 36%. This suggests that HIV infection in the Swiss cohort may be a marker for a more highly exposed IDU subset, although other factors such as differences in risk behavior, local epidemiology, and also an impact of HIV infection itself may potentially play a role. Parvovirus 4–specific antibodies were also present in non-IDU MSM, albeit in fewer individuals, which suggests unreported intravenous drug use or another transmission route because all these individuals were also HCV negative. The possibility of alternative routes of transmission is strengthened by studies in HIV-positive MSM [6], along with reports of the presence of PARV4 in the general population in Central Africa and in children in India [5, 8].

The study cohorts were not further analyzed for the rate of PARV4 seroconversion. These are prospectively clinically monitored groups, and the exposure rates do not necessarily reflect an active IDU status. Further studies to define the incidence of new PARV4 infections in active IDU cohorts are underway, and these will help define the duration of viremia and the timing of acquisition of antibody and T-cell responses.

These 2 cohorts have allowed us to study the relationship between PARV4 serostatus and age, gender, ALT levels, HCV genotype, HCV treatment outcome, and HCV or HIV disease progression. Although we found no correlation between PARV4 seropositivity and HCV disease, significant correlations were found between PARV4 and early HIV disease–related symptoms. However, this clear association is tightly linked to both HCV status and clinical group (IDU). Although there is clear evidence that PARV4 DNA persists in tissues, we did not test for viral DNA because PARV4 viremia is rarely detected [3].

Immunosuppression from HIV infection is known to accelerate HCV disease progression, linked to increased HCV loads and local immune activation in the liver [13, 14]. In the case of increased mortality in HCV-positive, HIV-positive cohorts, it is clearly hard to distinguish the impact of HCV infection per se and the impact of the associated risk factor of intravenous drug use or even another coinfection such as PARV4. The IDU profile may also affect subject compliance to treatment, which may allow the disease to progress faster.

The factors that determine HCV disease progression in those chronically infected are more complex, although they do include environmental factors such as alcohol use in addition to gender and age. Although PARV4 infection did not have a significant impact in our relatively small, although well-defined cohort, larger prospective studies could address this further.

PARV4 remains an intriguing virus that is not associated with clear symptoms. Further research on the pathogenesis of PARV4 infection, especially acute infection, is warranted given the extremely high prevalence of infection in HIV-positive, HCV-positive IDUs and the profound and long-lived T-cell responses elicited. Future studies to define its cellular and tissue targets may well shed further light on its pathogenesis, both as a single agent and in the context of coinfection.

Notes

Acknowledgments. We thank all the patients participating in the Swiss HIV cohort study (SHCS) and all the individuals and clinical staff at the different sites that have contributed to this study, the Swiss HIV Cohort Study, and the Trent HCV study.


Financial support. This work was supported by the Wellcome Trust (including WT091663MA), the National Institute of Health (NIH) (National Institute of Allergy and Infectious Diseases U19 AI082630/01), SHCS (grant 633), Swiss National Science Foundation (grants 34277 3345-062041 and 324730-116862), the Medical Research Council UK, and the Biomedical Research Centre. The development and use of the serological assay for anti-PARV4 antibodies was supported by an unrestricted investigator-initiated grant from Baxter Healthcare and by the NIH, National Institute of Child Health and Human Development (R01 HD41224). Funding to pay the Open Access publication charges for this article was provided by the Wellcome Trust.

Potential conflicts of interest. All authors: No reported conflicts.

The author has submitted the ICMJE Form for Disclosure of Potential Conflicts of Interest. Conflicts that the editors consider relevant to the content of the manuscript have been disclosed.

References


