Pathogenicity and Immunogenicity of Attenuated, nef-deleted HIV-1 Strains In Vivo

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Abstract

In efforts to develop an effective vaccine, sterilizing immunity to primate lentiviruses has only been achieved by the use of live attenuated viruses carrying major deletions in nef and other accessory genes. Although live attenuated HIV vaccines are unlikely to be developed due to a myriad of safety concerns, opportunities exist to better understand the correlates of immune protection against HIV infection by studying rare cohorts of long-term survivors infected with attenuated, nef-deleted HIV strains such as the Sydney blood bank cohort (SBBC). Here, we review studies of viral evolution, pathogenicity, and immune responses to HIV infection in SBBC members. The studies show that potent, broadly neutralizing anti-HIV antibodies and robust CD8+ T-cell responses to HIV infection were not necessary for long-term control of HIV infection in a subset of SBBC members, and were not sufficient to prevent HIV sequence evolution, augmentation of pathogenicity and eventual progression of HIV infection in another subset. However, a persistent T-helper proliferative response to HIV p24 antigen was associated with long-term control of infection. Together, these results underscore the importance of the host in the eventual outcome of infection. Thus, whilst generating an effective antibody and CD8+ T-cell response are an essential component of vaccines aimed at preventing primary HIV infection, T-helper responses may be important in the generation of an effective therapeutic vaccine aimed at blunting chronic HIV infection.
Introduction
Despite considerable effort, all attempts to develop an effective human immunodeficiency virus (HIV) vaccine based on subunit or prime-boost strategies have failed to elicit sterilizing immunity and protect against infection with wild type virus (reviewed in [1-3]). Current World Health Organization estimates indicate 42 million people are infected with HIV and approximately 20 million have died from AIDS. Approximately 5 million new infections occur annually. The overwhelming majority of these individuals live in developing countries with little or no access to potentially lifesaving antiretroviral therapies. Moreover, HIV is predicted to become the leading burden of disease in middle and low income countries by 2015 [4]. Thus, the need for an effective preventative and/or therapeutic HIV vaccine has never been more urgent.

Since the discovery of HIV nearly 25 years ago, there have been significant advances in our knowledge of HIV immunology (reviewed in [5-7]). As early as 1990 subunit vaccines based on the HIV envelope protein were developed, based on the observation that vaccinated chimpanzees were protected against homologous HIV challenge [8]. However, it is unlikely that such vaccines will ever be able to illicit immune responses sufficient for protection against heterologous HIV strains and, in fact, these approaches have failed repeatedly in animal models. In addition, HIV envelope protein-based vaccines were not efficacious in 2 phase III vaccine trials in humans [9-12]. More sophisticated vaccine approaches have targeted cellular immunity by the development of DNA prime-boost strategies, and have achieved strong stimulation of antibody and cytotoxic T-lymphocyte (CTL) responses in monkeys. However, despite robust immunological responses, these strategies have ultimately failed to protect against challenge infection. A better understanding of the correlates of immune protection against HIV infection would greatly assist efforts to develop an effective HIV vaccine [13,14].

In addition to envelope and DNA prime-boost vaccines, various other strategies have been adopted in HIV vaccine development including the use of recombinant viral and bacterial vectors, synthetic peptides, live attenuated virus, and whole inactivated HIV particles. These strategies have been reviewed in detail recently [1-3,15], and are summarized in Figure 1. Other innovative vaccine strategies that have been recently explored include the use of peptide-loaded dendritic cells [16], and non-infectious viral particles surface-engineered to produce antigen presenting particles that mimic antigen presenting cells [17] to induce cellular immune responses. To date, sterilizing immunity to primate lentiviruses has only been achieved by the use of live attenuated simian immunodeficiency virus (SIV) and chimeric simian-HIV (SHIV) vaccines carrying major deletions in the nef gene and other accessory genes [18-21]. Passive infusion of broadly-neutralizing monoclonal antibodies in HIV animal models have also been shown to confer complete protection against challenge infection [22-25]. This provides proof of principle that protection against infection is possible with use of the appropriate antigen. However, nef-deleted virus is unlikely to be considered safe enough for use as a HIV vaccine, either because immunization may pose an immediate risk to individuals with weak immune systems, or because the attenuated vaccine strain could eventually evolve to a more pathogenic form [14]. Both of these outcomes have been demonstrated in macaque studies, whereby some animals vaccinated with nef-deleted SIV progressed to AIDS in the absence of wild type virus challenge [26,27]. Moreover, some individuals infected with nef-deleted HIV strains eventually experience CD4+ T-cell loss after many years of asymptomatic infection [28-31]. Nonetheless, studies of long-term survivors (LTS) naturally "vaccinated" with nef-deleted HIV, such as the Sydney blood bank cohort (SBBC) [32] and other rare cohorts [33-37], may provide unique insights into protective antibody and CTL responses, which may assist HIV vaccine development [14].

Epidemiology and Clinical History of the Sydney blood bank cohort
The SBBC consists of 8 individuals (subjects C98, C54, C49, C64, C18, C135, C83 and C124) who became
infected with an attenuated strain of HIV via contaminated blood products from a common blood donor (subject D36) between 1981 and 1984 [30,32,38]. The SBBC blood transfusion recipients have been referred to as recipients 7, 13, 12, 9, 10, 4, 8, and 5, respectively, in one previous study [30] and subjects A (C18), B (C64), C (C98), D (C54), E (C49) and F (C83) in an earlier publication [38]. Viral attenuation has been attributed to gross deletions in the nef/long terminal repeat (LTR) region of the HIV genome [32]. The clinical history and laboratory studies of the subjects from the first identification as SBBC members through 1998 has been described previously [30], and a detailed update of the clinical and laboratory data through 2006 has been described recently [39]. Briefly, despite being infected from a single source, SBBC members now comprise slow progressors (SP) who have eventually experienced decline in CD4 T-cells after many years of asymptomatic infection (subjects D36, C98, C54), and "elite" long-term nonprogressors (LTNP) who have had stable CD4 T-cell counts and low or below detectable plasma HIV RNA levels for more than 20 years without antiretroviral therapy (ART) and remain asymptomatic (subjects C49, C64, C135) [28,30,31]. Five SBBC members have died of causes either unrelated to- or not directly related to HIV infection (C98, C54, C18, C83, C124) (Table 1). The SBBC therefore provides a unique opportunity to study the pathogenesis of, and immune responses to nef-deleted HIV infection in a naturally occurring human setting.

### HIV isolates and viral phenotypes

To determine whether changes in viral phenotype were occurring in SBBC members, HIV isolation was attempted from peripheral blood mononuclear cells (PBMC) collected longitudinally from all subjects except C124 and C83 [28,40], by selected PBMC coculture techniques [40,41] (Table 2). For subjects with detectable but low HIV RNA levels (D36, C54, C98, C18), more than 10 HIV isolates were obtained from each of D36, C54 and C98 over a 5 to 6 year period between November 1994 and November 2000 [40]. Three HIV isolates were obtained from C18 over an 8 month period between July 1993 and March 1994. For subjects with consistently undetectable HIV RNA levels (C49, C64, C124, and C135), a single isolate was obtained from C64 from PBMC collected in February 1996. This was despite isolation attempts from 16 additional PBMC collections between November 1995 and March 2001 [40]. All isolates carried similar but distinct deletion mutations in the nef gene and LTR region [28,29,32,42], and were unable to synthesize Nef proteins detectable by Western blotting or immunofluorescence staining of infected cells (D. McPhee and A. Greenway, unpublished data). No isolates were obtained from longitudinal samples of PBMC collected from C49 or C135 over a 4 to 7 year period between February 1994 and October 2000, or from a single sample of PBMC obtained from C124 in March 1993 [40]. Thus, success of isolating nef-deleted HIV from SBBC members was strongly dependent on the presence of detectable plasma HIV RNA levels, with few exceptions.

### Table 1: Clinical history of SBBC members

<table>
<thead>
<tr>
<th>Subject</th>
<th>Sex</th>
<th>Date of Birth</th>
<th>Date Transfused</th>
<th>Antiretroviral Drugs</th>
<th>Clinical History and other information</th>
</tr>
</thead>
<tbody>
<tr>
<td>D36</td>
<td>M</td>
<td>6/4/1958</td>
<td>N/A</td>
<td>ABC, AZT, NVP</td>
<td>Diagnosed with moderate HIVD, 12/1998; SP.</td>
</tr>
<tr>
<td>C98</td>
<td>M</td>
<td>7/11/1937</td>
<td>1/2/1982</td>
<td>D4T, NVP, IND</td>
<td>Prednisone since 1995 for asthma; died 3/30/2001 from bronchial amyloidosis; death not related to HIV; SP.</td>
</tr>
<tr>
<td>C54</td>
<td>M</td>
<td>2/17/1928</td>
<td>7/24/1984</td>
<td>None</td>
<td></td>
</tr>
<tr>
<td>C49</td>
<td>F</td>
<td>6/9/1954</td>
<td>6/11/1984</td>
<td>None</td>
<td>Diagnosed with age-onset diabetes in 2004, managed by diet; chronic alcoholism; LTNP.</td>
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<tr>
<td>C64</td>
<td>F</td>
<td>3/20/1926</td>
<td>5/4/1983</td>
<td>None</td>
<td>Hypertension; hypercholesterolemia; LTNP.</td>
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<tr>
<td>C135</td>
<td>M</td>
<td>2/23/1946</td>
<td>2/11/1981</td>
<td>None</td>
<td>CCR5-A32 heterozygote; HLA-B57 positive; LTNP.</td>
</tr>
<tr>
<td>C18</td>
<td>M</td>
<td>10/12/1912</td>
<td>8/31/1983</td>
<td>None</td>
<td>Severe coronary atherosclerosis; died 11/1995 from bacterial pneumonia; death not related to HIV; LTNP.</td>
</tr>
<tr>
<td>C83</td>
<td>F</td>
<td>12/21/1964</td>
<td>12/30/1982</td>
<td>None</td>
<td>Prednisone since 1982 for SLE; intermittent cyclophosphamide, azathioprine, hydrocortisone; died from combined PCP and pneumococcal pneumonia 4/1987; uncertain if death was HIV related; HIV Progression status uncertain.</td>
</tr>
</tbody>
</table>

Dates shown are day/month/year. M, male; F, female; ABC, abacavir; AZT, zidovudine; NVP, nevirapine; 3TC, lamivudine; N/A, not applicable; HIVD, HIV associated dementia; SP, slow progressor; LTNP, long-term nonprogressor; IDDM, insulin-dependent diabetes melitis; SLE, systemic lupus erythematosus. *These data have been reported previously [30, 39].
<table>
<thead>
<tr>
<th>Subject</th>
<th>Virus isolate</th>
<th>Date</th>
<th>Years post-infection</th>
<th>CD4 cells (cells/µl)</th>
<th>HIV RNA (copies/ml)</th>
<th>Replication in PBMC</th>
<th>Coreceptor usage</th>
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<td>D36II</td>
<td>6/5/95</td>
<td>14.4</td>
<td>N/A</td>
<td>1400</td>
<td>++</td>
<td>CCR5, CXCR4, (CCR2b)</td>
</tr>
<tr>
<td></td>
<td>D36III</td>
<td>8/2/96</td>
<td>15.2</td>
<td>609</td>
<td>1100</td>
<td>++</td>
<td>NT</td>
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<td>D36IV</td>
<td>10/4/96</td>
<td>15.3</td>
<td>504</td>
<td>7700</td>
<td>++</td>
<td>NT</td>
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<td>D36V</td>
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<td>15.6</td>
<td>414</td>
<td>2600</td>
<td>++</td>
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<tr>
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<td>D36VII</td>
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<td>3200</td>
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<td>540</td>
<td>4000</td>
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<tr>
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<td>23/12/97</td>
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<td>22/1/99</td>
<td>18.1</td>
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<td>N/A</td>
<td>++</td>
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<td>++</td>
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<td>26/7/93</td>
<td>9.8</td>
<td>N/A</td>
<td>N/A</td>
<td>+++</td>
<td>CCR5, (CCR3, Gpr15)</td>
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<tr>
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<td>C18(3)</td>
<td>14/10/93</td>
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<td>N/A</td>
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<td>C18(4)</td>
<td>7/3/94</td>
<td>10.5</td>
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<td>2804</td>
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<td>7/11/94</td>
<td>10.3</td>
<td>2006</td>
<td>8200</td>
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<td>C54IV</td>
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<td>1504</td>
<td>3000</td>
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<td>C54 V</td>
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<td>11.4</td>
<td>1054</td>
<td>400</td>
<td>+/-</td>
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<td>1188</td>
<td>1500</td>
<td>+/-</td>
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<td>30/9/98</td>
<td>16.7</td>
<td>N/D</td>
<td>N/A</td>
<td>++</td>
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<td>++</td>
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<td>28/2/96</td>
<td>12.8</td>
<td>850</td>
<td>BD</td>
<td>+/-</td>
<td>CCR5</td>
</tr>
</tbody>
</table>

Dates shown are day/month/year. CD4 cells were measured by flow cytometry. Plasma HIV-1 RNA was measured by COBAS Amplicor HIV-1 Monitor Version 1.0 (Roche Molecular Diagnostic Systems, Branchburg, N.J.) prior to July 1999 and Version 1.5 after July 1999. HIV-1 RNA levels < 400 copies/ml (Version 1) or < 50 copies/ml (Version 1.5) were considered below detection. BD, below detection; N/A, not available; NT, not tested. ++++, replication kinetics similar to wild type primary HIV strains; ++, reduced levels of replication and/or delayed replication kinetics compared to wild type primary HIV strains; +/-, levels of HIV replication barely detectable or not detectable by RT assays, but detectable by measurement of extracellular p24 antigen [40].
When compared with wild type HIV isolates and isogenic controls with mutations in nef, replication capacity of SBBC isolates in PHA-activated PBMC was found to be consistent over time by viruses isolated from a particular subject, but heterogeneous between subjects and fell into 3 distinct phenotypes [28,40] (Table 2). Viruses isolated from C18 replicated rapidly to high levels similar to wild type HIV; viruses isolated from D36 and C98 replicated to lower levels; and viruses isolated from C54 and C64 were barely able to replicate to detectable levels. In contrast, all isolates replicated to equivalent levels in the C2-luc reporter cell line [41,43,44] expressing CD4, CCR5 and CXCR4. Thus, SBBC isolates except those from C18 appear to have attenuated replication capacity in PHA-activated PBMC. Inhibiting the in vivo replication of HIV in D36 by HAART demonstrated a prolonged in vivo virion half life, with a first-phase slope of decline of HIV RNA 0.18/day [45] which is slower than that in all previously studied individuals infected with wild-type HIV after commencement of ART [46-49]. Thus, the replication kinetics of D36 virus appears to be attenuated both in vitro and in vivo.

Analysis of coreceptor usage in transfected C2-Luc cells [41] showed that all isolates used CCR5 (R5) as the primary coreceptor for HIV entry, except viruses isolated from D36 prior to commencement of HAART which were dual tropic and used CCR5 and CXCR4 (R5X4) [28,40] (Table 2). These results showed that nef-deleted HIV was capable of undergoing a coreceptor switch from R5 to R5X4 in vivo. An isolate obtained from D36 after commencement of HAART was CCR5-restricted and had features of an early archived HIV variant, but was genetically similar to HIV present in a CSF sample obtained from D36 during HIV-associated dementia (HIVD) [28]. Thus, for D36, HIV present in CSF during HIVD was likely to be an early variant that underwent compartmentalized evolution in the CNS. Moreover, we showed for the first time that nef-deleted HIV is inherently capable of undergoing compartmentalized evolution in the CNS and causing neurologic disease in humans [28]. Stepwise quasispecies diversity was observed in SBBC SP, whereas C49 displayed stable quasispecies diversity most similar to early variants in the SBBC (B. Herring et al., manuscript submitted). Extended analysis of alternative coreceptor usage showed that D36 and C54 isolates could use CCR2b, C18 and C54 isolates could use CCR3, and C18 isolates could use Gpr15 for HIV entry, albeit at low levels [40] (Table 2). Whether expanded usage of alternative HIV coreceptors by SBBC isolates contributes to HIV pathogenesis in these individuals is uncertain, but the unique signature of coreceptor usage for viruses isolated from different SBBC members suggests independent evolution for each virus after infection of each cohort member. This interpretation is consistent with results of Env heteroduplex tracking assays, Env heteroduplex mobility assays and Env V1V2 length polymorphism assays which also demonstrated independent evolution of HIV Env in each subject ([50], and B. Herring et al., manuscript submitted).

**Changes in HIV pathogenicity**

To better understand changes in pathogenicity which may have contributed to HIV progression in D36, Jekle et al [51] used an ex vivo human lymphoid cell culture system to analyze the ability of 2 HIV viruses isolated from D36 to deplete CD4+ T-cells; one isolated in 1995 prior to the onset of AIDS (D36I) and another isolated in 1999 after the onset of disease progression (D36II) (Table 2). Although both D36 isolates were less potent in depleting CD4+ T-cells than reference X4 and R5X4 isolates with intact nef genes, the 1999 isolate induced greater levels of CD4+ T-cell cytopathicity than the 1995 isolate. Differences in CD4+ T-cell cytopathicity between the 2 isolates were evident in CD4+/CCR5- cells, but not evident in CD4+/CCR5+ cells suggesting an increased ability to use CXCR4 by the 1999 isolate. Further studies with the CXCR4 inhibitor AMD3100 showed that, although both isolates were functionally R5X4 [28,40] (Table 2), the 1999 isolate had preferential use of CXCR4 whereas the 1995 isolate had preferential use of CCR5 for HIV entry. These studies showed evolution of R5X4 strains in D36 to a variant with higher cytopathic potential that was associated with increased use of CXCR4 in vitro and HIV progression in vivo.

Consistent with results of the study by Jekle et al [51], we showed alterations in HIV cytopathicity by sequential D36 isolates in cultures of monocyte-derived macrophages (MDM). Compared with the highly macrophage tropic R5 ADA and R5X4 89.6 isolates, all D36 viruses replicated in MDM to low levels and had delayed replication kinetics [52]. There was no evidence of increased HIV replication in MDM by virus isolated from D36 after HIV progression. However, in support of the results obtained by Jekle et al [51], the 1999 isolate induced greater levels of HIV cytopathicity in MDM similar to that present in cultures infected with ADA or 89.6, characterized by the presence of many syncytia [52]. In contrast, earlier D36 isolates caused only few or occasional syncytia in MDM despite all D36 viruses replicating in MDM to similar levels. Thus, increased cytopathicity in MDM by the 1999 D36 isolate is most likely due to intrinsic pathogenic features of the Env that increase fusogenicity, similar to that which has been observed by particular neurotropic R5 and R5X4 viruses [53-55]. The increased Env fusogenicity may have contributed to greater cytopathicity by the 1999 D36 isolate and HIV progression in D36. Further studies to elucidate the molecular determinants of D36 Env that are associated with increased fusogenicity are in progress.
**T-cell pathogenesis**

The effect of long-term infection with nef-deleted virus on CD4+ T cells was studied in detail for six SBBC members [56]. Careful comparison with age- and transfusion-matched controls revealed the surprising result that SBBC members had an increased number of circulating CD45RO+ memory CD4+ T cells. This was unexpected, since these CD4+ T cells are widely believed to represent the main target of cytopathic HIV infection [57-60] (reviewed in [61]), and loss of these cells ultimately leads to acquired immunodeficiency. Therefore, this result is consistent with the hypothesis that nef-deleted HIV has reduced pathogenicity in vivo.

Nevertheless, in the SBBC subjects studied with detectable plasma viral load, C54 and C98, there was concomitant elevation of CD8+ T cell activation, whereas the SBBC subjects with undetectable plasma viral load, C49, C64 and C135 had normal levels of CD8+ T cell activation [56]. Therefore, within the SBBC, the situation was similar to the strong correlation seen between plasma viral load and CD8+ T-cell activation in subjects infected with wild type HIV [62]. Furthermore, as described above, subjects D36, C98 and C54 exhibited a clear CD4+ T cell decline, albeit at a relatively slow rate [28-30]. This interesting finding argues that pathogenicity within the SBBC was more closely correlated with levels of viral replication (as assessed by plasma viral load) and CD8+ T-cell activation than with viral pathogenicity dictated by the presence or absence of nef. This finding likely represents the ability of host factors to modulate the pathogenicity of nef-deleted HIV-1 [63,64]. CD8+ T cell activation may reflect lymphocyte turnover during HIV infection, which has been proposed to lead to disruption of normal homeostasis and eventual consumption of both memory and naive CD4+ T cells [65,66]. However, we did not find evidence of dramatically increased CD4+ T cell turnover in these subjects, as determined by expression of Ki-67 as a marker of cell proliferation [56].

**Evolution of nef/LTR sequence**

To determine whether an evolving nef/LTR sequence contributed to HIV progression in D36 and C98, we undertook a detailed longitudinal analysis of nef and LTR sequence changes occurring in D36, C98, C49, C54 and C64 over a 4 to 10 year period [29]. Sequential analysis of nef/LTR demonstrated a gradual loss of nef sequence that differed in magnitude between subjects. A large deletion of 128 bp emerged in D36 effectively removing the entire nef gene with the exception of the region surrounding the nef start codon, the polypurine tract which contains terminal signals for HIV integration, and a 90 bp region of the nef/LTR overlap region surrounding the negative regulatory element. The pattern of nef/LTR sequence loss in C54 was also similar, but less extensive than that observed in D36 and C98. However, the additional loss of nef/LTR sequence in C64 was comparatively minimal. These data are illustrated in Figure 2, where the nef/LTR sequences cloned from the earliest available and most recent blood samples of these subjects are compared. A more detailed longitudinal analysis of nef/LTR sequences in these subjects has been reported in Churchill et al [29]. Thus, viruses harboured by D36, C54, C98 and C64 appeared to be evolving in a convergent fashion toward a highly deleted, minimal nef/LTR structure containing only sequence elements that are absolutely essential for HIV replication [29]. The convergent
nature of the nef/LTR sequence changes implies the presence of strong selection pressures that maintain the ability of defective HIV genomes to persist in vivo. The highly evolved nef/LTR sequences harboured by D36, C54 and C98 were strikingly similar to those that remained dominant in C49 for at least 10 years (Fig. 2) [29]. Thus, the highly evolved nef/LTR structure appears to be stable, and in the case of C49 does not increase pathogenicity. However, taken together the results suggest the in vivo pathogenicity of nef-deleted HIV harboured by SBBC members is dictated by factors other than those that impose a unidirectional selection pressure on the nef/LTR region of the HIV genome. Due to the changes in the nef/LTR region, these other presumably host factors become more important in terms of disease outcome. This is exemplified by the marked variation from no disease progression with no detectable virus replication (C49 and C64), to no progression with a low viral load (C54), through to slow progression (D36 and C98).

Reversion to pathogenicity by nef-deleted SIV has been associated with restoration of a truncated Nef protein [26], acquisition of further deletions in the nef/LTR overlap region [67], and/or duplications of NF-xB binding sites in the LTR [67]. In contrast to the SIV studies, the in vivo evolution of nef-deleted HIV in SBBC members was unidirectional toward a smaller nef/LTR sequence and the majority of the additional sequence loss was within the nef-alone region [29]. Furthermore, none of the clones were capable of encoding Nef. Together, these results suggest improved viral replication by further deleting remnants of the nef gene. In addition, the presence of duplicated NF-xB binding sites in the LTR was not associated with clinical status of the SBBC subjects. Therefore, it is likely that viral factors that modulate the in vivo pathogenicity of nef-deleted HIV will be distinct from those in nef-alone SIV. Interestingly, the unidirectional evolution toward the minimal nef/LTR sequence observed in SBBC members was strikingly similar to the pattern of evolution in a slow progressor infected with a nef/LTR-deleted variant of HIV circulating recombinant form 01_AE [34]. The convergent pattern of nef/LTR evolution among viruses harboured by SBBC members is therefore unlikely to be due to a unique property of the infecting strain, but rather a positive selection that is common across clades.

Changes in transcriptional activity

Viruses harboured by SBBC members contain unique alterations of NF-xB and Sp-1 binding sites in the LTR that may affect transcriptional activity and thus, replication capacity [28,29,32]. Therefore, we examined the nucleotide sequence and transcriptional activity of nef/LTR clones obtained sequentially from D36 blood samples and from D36 CSF obtained during HIVD, to determine whether changes in LTR activity may contribute to neuropathogenesis of nef-deleted HIV-1 infection [68]. We found that the transcriptional activity of CSF-derived nef/LTR clones was up to 4.5-fold higher than blood-derived clones isolated before and during HIVD when tested under basal, PMA- and Tat-activated conditions. The presence of duplicated NF-xB and Sp-1 binding sites or a truncated nef sequence in blood-derived nef/LTRs was not sufficient to mediate large increases in transcriptional activity. However, CSF-derived nef/LTRs had duplicated NF-xB and Sp-1 binding sites coupled with a truncated nef sequence, which formed a regulatory unit that significantly enhanced LTR transcription [68].

Previous studies showed that LTR variants with augmented transcriptional activity enhance replication of HIV [69]. Therefore, to determine whether D36 nef/LTRs affect replication capacity of HIV in vitro, we produced and characterized full-length chimeric molecular clones of HIV NL4-3 carrying the nef/LTR nucleotide sequence of blood-derived D36 nef/LTRs or the CSF-derived D36 nef/LTR [68]. We examined the capacity of chimeric NL4-3 viruses carrying D36 nef/LTRs to replicate in PBMC compared with wild type NL4-3 and the NL4-3ΔNef deletion mutant [70]. Compared to wild type NL4-3, chimeric HIV containing the nef/LTR sequence of blood derived D36 viruses had attenuated replication kinetics, similar to NL4-3ΔNef. In contrast, chimeric HIV containing the nef/LTR of D36 CSF had enhanced replication capacity compared to wild type NL4-3. Thus, the nef/LTR derived from CSF of D36, which had augmented basal, PMA- and Tat-activated transcriptional activity compared to wild type and blood-derived D36 nef/LTRs, augmented replication of HIV in PBMC. Together, our results suggest unique features of the CSF-derived nef/LTR restore efficient replication capacity of nef-deleted HIV in PBMC by enhancing transcription. The results further suggest that nef and LTR mutations that augment transcription may contribute to neuropathogenesis of nef-deleted HIV.

Attenuation in other HIV genes

In addition to nef and LTR, mutations or polymorphisms in other HIV genes including gag, rev, tat, vif, vpr, vpu and env have been detected in SP or LTNP [71-78]. A previous study of HIV rev alleles isolated from a subject with long-term nonprogressive HIV infection showed a persistent Leu to Ile change at position 78 in the Rev activation domain which attenuated Rev function and HIV replication capacity [73], providing evidence that defective rev alleles may contribute to long-term survival of HIV infection in some patients. A subsequent study of naturally occurring rev alleles with rare sequence variations in the activation domain showed variable reductions in Rev activity [79], although it was unclear from this study whether the observed reductions in Rev activity would be sufficient to attenuate HIV replication capacity. Of note,
gene sequences [40]. We found a good correlation between total 
IgG responses in SBBC members and a detectable plasma 
VL, with plasma from C18, C54, D36 and C98 all being 
strongly reactive. Subjects C49 and C64, who consistently 
maintained undetectable HIV RNA copy numbers 
[29,30], had significantly reduced total IgG responses. 
Furthermore, subject C135, who has also had consistently 
undetectable HIV RNA levels has not fully seroconverted 
after more than 20 years of infection [40,42]. These stud-
ies highlight the importance of adequate antigenic stimu-
lization by nef-deleted HIV to drive antibody production. 
In contrast, we found that total IgG responses in the control 
group were uniformly potent, reflecting the fact that all 
these individuals had detectable VLs. Among SBBC mem-
bers, the strongest antibody responses were observed in 
individuals with low but detectable VL set points, less 
than approximately 10,000 RNA copies/ml. This is con-
sistent with a recent observation of an undetectable VL 
and weak, delayed antibody responses in an unrelated 
individual with nef-deleted HIV [34].

Recent studies have highlighted the change in HIV anti-
body responses with respect to antibody isotype switching 
after initial infection, in particular IgG3 reactivity to p24 
[82,83] Preliminary WB testing of p24 IgG3 responses in 
The SBBC LTNP indicated there was reactivity for those 
individuals with the most potent total IgG responses (C18 
and C54) (E. Verity, D. McPhee, K. Wilson, and D. Zotos, 
unpublished data). This hints at delayed isotype switching 
and hence delayed maturation of immune responses for 
at least some members of the SBBC.

Neutralization studies of nef-deleted HIV
In additional studies, we determined whether plasma 
from SBBC members had differences in ability to neutral-
ize nef-deleted HIV strains. We did this by comparing the 
ability of longitudinally collected plasma from SBBC 
members or from control LTNP cohort members to neu-
tralize the infectivity of HIV isolated from D36 and C18 
[40]. We found that, for SBBC plasmas, neutralization of 
D36 or C18 viruses strongly correlated with VL, replica-
cation capacity of the isolated virus, and the strength of anti-
HIV IgG responses. Plasma from SBBC members with 
undetectable VL was unable to neutralize the infectivity of 
these viruses. In contrast, plasmas from the control LTNP 
cohort were able to neutralize the infectivity of SBBC 
viruses with titres generally higher than that seen for SBBC 
members, but there was no correlation between neutrali-
zation and HIV RNA copy number or IgG responses in the 
control LTNP group.

Broad neutralizing antibody responses
A number of studies have suggested an increased fre-
cuency of LTNP and long term survivors (LTS) possess 
strong, cross-reactive neutralising antibody responses [84-
have demonstrated that the presence of a sustained Gag-specific CD8+ T-cell response is associated with protection against disease progression in cohorts of LTNP infected with nef-intact HIV [95-97]. In support, our studies have also shown that the distinguishing feature of LTNP harbouring nef-intact HIV is the predominance of Gag-specific CD8+ T-cell responses, which decline when these individuals start to progress (W.B. Dyer et al., manuscript in preparation). However, novel qualitative and quantitative differences in immune correlates of viral control may exist in LTNP infected with nef-deleted HIV. Longitudinal studies of T-cell responses in SBBC members have demonstrated a dominance of Pol-specific CD8+ T-cell responses rather than those against Gag [98] and W.B. Dyer et al., manuscript in preparation). This suggests that infection with nef-deleted HIV may give rise to a qualitatively different response, although a subset of SBBC members also had strong CD8+ T-cell responses to Gag [98]. Nonetheless, CD8+ T-cell responses to Gag or Pol did not discriminate SBBC LTNP from SP.

In contrast, longitudinal analysis of HIV-specific CD4+ T-cells showed that all SBBC nonprogressors able to completely control plasma HIV RNA levels to below detectable levels (C49, C64 and C135) had persistent and strong T-helper proliferative responses to HIV p24 antigen, whereas these responses were absent in all progressors with persistent viremia (C54, C98 and D36) (Fig. 3). The notable exception was C18 who had detectable but low plasma HIV RNA levels without evidence of CD4+ T-cell loss, and had detectable p24 T-helper responses over a short period of approximately 12 months leading up to his non-HIV related death at 83 years of age. In this subject, the p24 T-helper responses coincided with an exponential increase in CTL responses against Pol antigens, measured by memory CTL precursor frequency assay [98], and IFN-gamma ELISPOT responses (W. Dyer, unpublished data). However, it is difficult to interpret the significance of the T-cell responses in C18 given the short window of analysis. Together, although derived from a small cohort of individuals, these results suggest that immune suppression of nef-deleted HIV-1 by SBBC LTNP may be dependent upon persistent T-helper responses irrespective of the CD8+ T-cell and neutralizing antibody response to viral antigens.

**Conclusion**

The development of an effective HIV vaccine has been hampered by the lack of defined correlates of immune protection against HIV infection. Although nef-deleted strains of HIV are not suitable as live attenuated HIV vaccines due to safety concerns, the only lentiviral vaccines to date that have generated sterilizing immunity in animals are those based on live, attenuated viruses. To this end, studies of SBBC members naturally "vaccinated" with nef-

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**T-cell responses**

Analysis of cellular immune mechanisms suppressing nef-deleted virus in SBBC nonprogressors may provide insights relevant for HIV vaccine design. Several studies
studies of this unique cohort of individuals will provide HIV vaccine researchers with novel insights into immune mechanisms that may serve to prevent or control HIV infection.

Competing interests
The author(s) declare that they have no competing interests.

Authors’ contributions
The SBBC project is a multicenter consortium. PRG, DAM, JL, JSS, SMC, JM, BJB, ALC and MIC are principal SBBC investigators who, along with SRL contributed to the study design, analysis and interpretation of the data. EV performed the neutralization studies and helped determine the viral phenotypes. WBD and JJZ performed the T-cell experiments. MJG performed the nef cloning and sequencing. MR provided technical expertise and contributed intellectually. DG performed the viral phenotyping in conjunction with PRG. PRG wrote the manuscript. All authors helped edit the manuscript. All authors have seen and approved the final manuscript.

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