HTLV-1 infections

Charles R M Bangham

Abstract
Human T lymphotropic virus type 1 (HTLV-1) causes disabling and fatal diseases, yet there is no vaccine, no satisfactory treatment, and no means of assessing the risk of disease or prognosis in infected people. Recent research on the molecular virology and immunology of HTLV-1 shows the importance of the host’s immune response in reducing the risk of these diseases, and is beginning to explain why some HTLV-1 infected people develop serious illnesses whereas most remain healthy life long carriers of the virus. These findings might be applicable to other persistent virus infections such as human immunodeficiency virus, hepatitis B, and hepatitis C.

Keywords: human T lymphotropic virus type 1; adult T cell leukaemia/lymphoma; tropical spastic paraparesis; myelopathy

Epidemiology
HTLV-1 is widespread in the tropics and subtropics. There are large endemic foci in the Caribbean, southern Africa, and South America. In Africa, HTLV-1 is also present in southern Africa, India, the Middle East, and many islands in the tropics. In Europe and North America, the virus is found chiefly in certain immigrant groups and in intravenous drug users. Within the endemic areas, the distribution of HTLV-1 is typically uneven: the seroprevalence varies widely, between 0.1% and 30% of adults, often with great differences between neighbouring towns. There is an unexplained predilection for coastal areas.

The dominant modes of transmission of HTLV-1 in endemic areas are from mother to child in breast milk, and sexual transmission in adults; male to female transmission is about four times as frequent as female to male transmission. However, transmission by infected blood products has been a major problem in endemic regions, especially in Japan. Blood for transfusion is now screened routinely for HTLV-1 in several countries, including Japan, the USA, and Brazil. In Japan, screening of blood products and counselling on breast feeding has been followed by the beginning of a downward trend in the age dependent seroprevalence of HTLV-1.

The virus
HTLV-1 was first isolated and identified from a patient with a cutaneous T cell malignancy. Similarities in the clinical picture and the abnormal T cell morphology led to the suggestion that HTLV-1 was also involved in ATL, which had been described in Japan a few years earlier. Subsequent seroepidemiological and molecular work confirmed this connection.

HTLV-1 is a complex type C retrovirus, in the subfamily Oncovirinae. Like other retroviruses, it has an envelope derived from the host cell membrane, and two copies of the positive sense RNA genome. The genome of 9032 nucleotides contains the gag, pol, and env genes found in replication competent exogenous retroviruses. In addition, HTLV-1 encodes two non-structural, regulatory proteins: Tax, the transcriptional transactivator of the virus, and Rex, the regulator of viral mRNA splicing. The Tax protein is required for rep-
The clinical features of ATL are those of a high serum concentrations of lactate dehydrogenase. Laboratory findings often include hyperglobulinemia, and are usually CD25 positive (IL-2 receptor). The leukaemic cells are almost invariably CD4 positive. Southern blot analysis indicates the presence of HTLV-1 in the CD4 positive T cell. The cellular receptor for the virus has been mapped to chromosome 17q25 but has not yet been identified. Intercellular adhesion molecule 1 (ICAM-1), ICAM-3, and vascular cell adhesion molecule also facilitate entry of HTLV-1 into the cell, but are not the main receptors for the virus.

Diseases associated with HTLV-1 (table 1)

<table>
<thead>
<tr>
<th>Disease</th>
<th>Refs</th>
</tr>
</thead>
<tbody>
<tr>
<td>Adult T cell leukaemia/lymphoma</td>
<td>10, 11</td>
</tr>
<tr>
<td>HTLV-1 associated myelopathy/tropical spastic paraparesis</td>
<td>24, 25, 26</td>
</tr>
<tr>
<td>Polyneuropathy</td>
<td>27</td>
</tr>
<tr>
<td>Arthropathy</td>
<td>28</td>
</tr>
<tr>
<td>Infective dermatitis</td>
<td>29</td>
</tr>
<tr>
<td>Uveitis</td>
<td>30</td>
</tr>
</tbody>
</table>

HTLV-1 ASSOCIATED MYELOPATHY/TROPICAL SPASTIC PARAPARESIS

In the mid 1980s a French group in Martinique discovered an association between HTLV-1 seropositivity and chronic progressive myelopathy of previously unknown aetiology, known as Jamaican neuropathy or tropical spastic paraparesis. An association with a similar disease was described in Japan by Osame and his colleagues, who called the disease HTLV-1 associated myelopathy; subsequently it was established that these are the same condition.

<table>
<thead>
<tr>
<th>Subtype</th>
<th>% Total</th>
<th>Median survival (months)</th>
<th>Five year survival</th>
</tr>
</thead>
<tbody>
<tr>
<td>Acute</td>
<td>55</td>
<td>6.2</td>
<td>5.0%</td>
</tr>
<tr>
<td>Lymphomatous</td>
<td>20</td>
<td>10.2</td>
<td>5.7%</td>
</tr>
<tr>
<td>Chronic</td>
<td>20</td>
<td>24.3</td>
<td>26.9%</td>
</tr>
<tr>
<td>Smouldering</td>
<td>5</td>
<td>–</td>
<td>62.8%</td>
</tr>
</tbody>
</table>

The mean age at diagnosis: 60 years in Japan, but 40 years in the Caribbean and Brazil; the reason for this disparity is unknown. Men are more commonly affected than women (approximately 1.5 : 1 male to female ratio).

The disease often responds initially to standard chemotherapeutic regimens, but early relapse is common, and the disease typically becomes refractory to further chemotherapy after two to six months. Recently, considerable progress has been made with the discovery that a combination of interferon α and AZT (zidovudine) can prolong life expectancy by between six months and two years. However, fundamental improvements in the management of this aggressive condition are needed.

HTLV-1 associated myelopathy/malignant lymphoma, and their prognoses

The lifetime risk of ATL is about 5% in people infected before the age of 20 years; the incidence is approximately 0.1% infected individuals/year. There is a wide disparity in the mean age at diagnosis: 60 years in Japan, but 40 years in the Caribbean and Brazil; the reason for this disparity is unknown. Men are more commonly affected than women (approximately 1.5 : 1 male to female ratio).

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The proviral load of HTLV-1

The proviral load of HTLV-1 is unusually high compared with other retrovirus infections: a typical healthy carrier of HTLV-1 carries the provirus in about 0.1–1% of peripheral blood mononuclear cells (PBMCs). However, the provirus load is, on average, even higher in the chronic inflammatory diseases such as HAM/TSP, ranging up to 30% of PBMCs. The proviral load appears to be stable over many years in most individuals. In a recent case control study in Japan, we found that the prevalence of HAM/TSP rises very sharply once the proviral load exceeds 1% of PBMCs (fig 1).

This association between HAM/TSP and a high proviral load of HTLV-1 has been recognised for several years, and it is widely believed that healthy carriers of HTLV-1 with a high proviral load cause HAM/TSP and the other features of HAM/TSP. Therefore, to answer these questions we must first understand something of the immune response to HTLV-1.

Immune response to HTLV-1

Antibodies against the Gag protein of HTLV-1 (mainly p24) are the first to appear after infection. Other responses to HTLV-1 infections have included corticosteroids, anabolic steroids, zidovudine (AZT), and vitamin C, but none gave lasting benefit. Recently, Taylor and colleagues have obtained evidence that lamivudine (3TC) 150 mg twice daily can reduce the provirus load of HTLV-1. Again, the effects—symptomatic improvement and reduction in provirus load—were temporary, but it is possible that drug regimens that produce a more sustained reduction in proviral load will provide some benefit, particularly if started early in the course of clinical disease. These exciting preliminary findings are shortly to be tested in a randomised, placebo controlled trial.

OTHER DISEASES ASSOCIATED WITH HTLV-1

In addition to ATL and HAM/TSP, HTLV-1 has been associated with a range of chronic or subacute inflammatory conditions in different tissues (table 1). These associations are weaker than those with ATL and HAM/TSP, and it is not yet agreed that HTLV-1 is the likely cause in each condition.

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Antibodies against the Gag protein of HTLV-1 (mainly p24) are the first to appear after infec-
tion, and predominate in the first two months, followed by anti-Env antibodies. About 50% of individuals subsequently produce antibodies to the Tax protein.

The cellular immune response has not been studied systematically in the early stages of infection with HTLV-1. However, in the chronic phase, most infected individuals make a very strong cell mediated immune response to the virus. The cytotoxic T lymphocyte (CTL) response to HTLV-1 has been studied in particular detail, because animal experiments in many virus infections indicate the special importance of these cells in limiting viral replication. In addition, the mononuclear cell infiltrate found in the spinal cord in the areas of demyelination consists predominantly of T cells, which are mainly CD8 positive (the usual phenotype of antiviral CTLs), at least in the chronic phase.

Anti-HTLV-1 CTLs are unusual in their extreme abundance: up to 10% of circulating CD8 positive T cells can recognise just one epitope of the virus. The anti-HTLV-1 CTLs are unusual in two further respects: they are chronically activated, and most recognise a single viral protein, the Tax protein. How does the virus persist in the face of such a strong immune response? Speculatively, do mutations in the Tax protein lead to escape from recognition by CTLs? Putative CTL escape mutations in Tax were indeed identified by Niewiesk et al. However, the selection pressure on the tax gene, presumably exerted by the Tax specific CTLs, was only evident in the healthy carriers of the virus, not in the patients with HAM/TSP. We concluded that the HTLV-1 specific CTLs might play an important part in limiting the replication of the virus, so determining the individual’s proviral load of HTLV-1 and their risk of inflammatory diseases such as HAM/TSP.

**HLA-A*02 protects against HTLV-1 associated myelopathy**

This conclusion suggested in turn that individual variation in the “efficiency” or “strength” of the anti-HTLV-1 CTL response might explain why some HTLV-1 infected people develop a high proviral load and diseases such as HAM/TSP, whereas others effectively suppress the replication of HTLV-1 and remain healthy. To test this hypothesis, we have compared the frequencies of polymorphic candidate genes between asymptomatic carriers and patients with HAM/TSP in Kagoshima (in southern Japan) in collaboration with Professor M Osame. This study has produced a clear result: patients who carry the human major histocompatibility complex (HLA) allele, HLA-A*02 (HLA-A2) have only half the risk of developing HAM/TSP as those who lack this allele. Because HLA class I genes are known to determine the specificity of CTLs, this observation suggests that HLA-A*02 restricted CTLs are particularly efficient at controlling HTLV-1 replication, and strongly supports the hypothesis that the CTL response to the virus is an important determinant of the risk of disease. In further support of this conclusion, healthy carriers of HTLV-1 who possessed the HLA-A*02 allele had a significantly lower proviral load of HTLV-1 than those who lacked this allele.

Because HLA-A*02 is common in Kagoshima, as in all major human populations, its protective effect is very important at the population level: the presence of HLA-A*02 at its observed frequency prevents approximately 28% of potential cases of HAM/TSP in Kagoshima.

The results of this study also confirmed previous indications that the class II HLA gene, HLA-DRB1*0101 (HLA-DR1) appears to increase the risk of HAM/TSP; the reason for this association is not yet explained. However, the predisposing effect of HLA-DRB1*0101 is seen only in people who lack HLA-A*02. That is, the HLA-A*02 associated protection appears to be dominant.

Many HLA disease associations have been described. However, in most cases the HLA allele is associated with predisposition to disease, not with protection, and the reason for the association is not clear. The association of HLA-A*02 with protection from HAM/TSP is, by contrast, the only clear example of an effective antiretroviral vaccine will elicit a strong and persistent CTL response to the virus.

**Pathogenesis of HAM/TSP**

The recent results, summarised above, cast light on the reasons for individual variation in disease risk in HTLV-1 infection. However, the mechanism of pathogenesis of HAM/TSP and the other inflammatory diseases remains a matter for speculation. By exclusion of other possibilities, we and others have suggested that the tissue damage in the central nervous system (CNS) is caused by lymphocytes, chronically activated by the HTLV-1 Tax protein acting as an antigen and/or a mitogen, which migrate into the CNS as a result of the Tax induced upregulation of adhesion molecules on their surface. HTLV-1 infected or activated lymphocytes have indeed been shown to secrete large amounts of certain cytokines and metalloproteinases, which might be toxic in high local concentrations in the CNS. However, it must be emphasised that this is a speculative scheme at present. It is to be hoped that the results of further genetic studies on the risk of HAM/TSP will suggest pathways of pathogenesis that can be subjected to experimental testing.

**HTLV-1 is a highly dynamic infection**

Because of the relative constancy of the HTLV-1 genome sequence, and the difficulty in detecting HTLV-1 proteins in freshly isolated blood cells, it has been generally believed that the virus is largely latent; that is,
The lessons learned will throw light on many other persistent virus infections, including HIV-1, hepatitis B, and hepatitis C.

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