

# HTLV-1 Infection and Pathogenesis

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Since the discovery of the human T-cell leukemia virus-1 (HTLV-1), cellular and animal models have provided invaluable contributions in the knowledge of viral infection, transmission and progression of HTLV-associated diseases. HTLV-1 is the causative agent of the aggressive adult T-cell leukemia/lymphoma and inflammatory diseases such as the HTLV-1 associated myelopathy/tropical spastic paraparesis (HAM/TSP).

In this entry, authors recapitulate the most effective animal models applied to investigate the pathogenesis of HTLV-1-associated diseases such as transgenic and humanized mice, rabbit and monkey models.

Keywords: HTLV ; humanized mice ; ATL

## 1. Introduction

Human T-cell leukemia virus type 1 (HTLV-1), isolated in the early 1980s from T cell lines derived from patients with cutaneous T-cell lymphoma and human adult T-cell leukemia, was the first human retrovirus to be discovered [1][2]. Since then, four HTLV types have been isolated in humans and have been phylogenetically associated with the simian STLV viruses [3][4]. In contrast to the HIV retrovirus, no efficient therapy is yet available to avoid the onset of the most alarming diseases caused by HTLV-1. In vivo, HTLV-1 infects mainly CD4+ T cells, the key cells in the triggering and establishment of the adaptive immune response. Besides being the etiological agent of adult T-cell leukemia/lymphoma (ATL), in 3–5% of infected subjects, HTLV-1 causes immune hypersensitivity conditions like arthritis, uveitis, and most importantly, the HTLV-1-associated myelopathy/tropical spastic paraparesis (HAM/TSP), a fatal chronic inflammatory neurological disorder [5][6][7][8]. Most infected people, however, remain asymptomatic, highlighting the role of the immune system in the control of infection [9][10][11]. Worldwide, more than 20 million subjects are infected by HTLV and, despite advances in treatment, patients with aggressive ATL generally have a poor prognosis [12][13].

HTLV-1 persistent infection is likely associated with the ability of the virus to evade the host's immune response. Immune evasion might correlate with high proviral load and thus to disease outcome. HTLV-1 infection occurs exclusively through cell-to-cell contact, and the number of infected cells in vivo significantly impacts on viral spreading [14]. After primary infection, the clonal expansion of infected cells, rather than the novo infection of cells, represents the main route for HTLV-1 to establish persistent and chronic infection [15] (Figure 1).

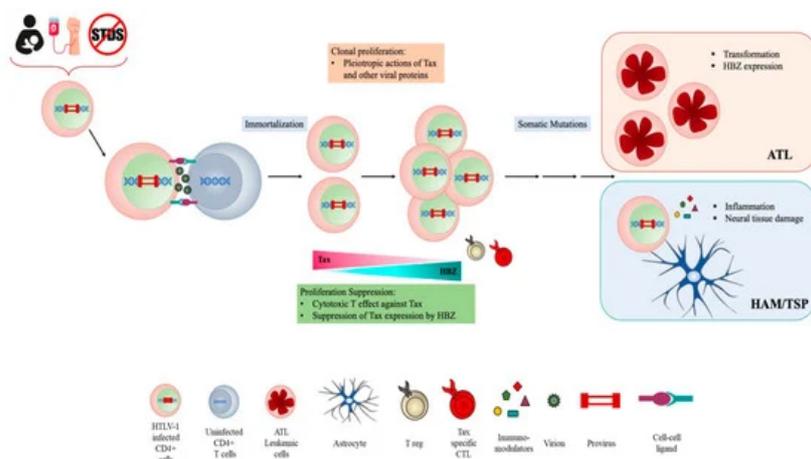


Figure 1. HTLV cell infection and transmission.

The proviral genome is integrated into the host genome and contains, in addition to structural proteins Gag, Pol and Env, a unique pX region coding for several regulatory and nonstructural proteins Tax, Rex, p12, p13, p30 and HTLV-1 basic zipper protein (HBZ), which is encoded by the antisense viral transcript. Among them, Tax and HBZ are thought to play

key roles in HTLV-1 infection and oncogenesis. Transgenic mice expressing Tax or HBZ develop neoplastic diseases, indicating that they function as oncogenes [16][17][18][19]. Tax is a potent activator of viral transcription and exerts pleiotropic effects on cell signaling deregulating different cellular pathways thus mainly contributing to HTLV-1 induced neoplastic transformation. However, the frequent loss of Tax expression from ATL cells suggests that the viral protein is mainly involved in the onset of leukemic transformation. By contrast, HBZ is ubiquitously expressed, playing a crucial role in the maintenance of oncogenic process and disease progression. Furthermore, recent reports from our laboratory have demonstrated that HBZ subcellular localization could be a prognostic marker of HTLV-1-disease progression, as HBZ is expressed solely in the cytoplasm of asymptomatic carriers (AC) and HAM/TSP subjects, while in tumor cells isolated from leukemic patients, it is also present in the nucleus [20][21][22]. HBZ antagonizes many of the activities of Tax and suppresses Tax-induced viral transcription, thus the interaction between Tax and HBZ may significantly affect the outcome of HTLV-1 infection [23][24][25].

Although intensive studies in recent years have contributed to shedding light on the mechanisms of viral replication and host response, several aspects of HTLV-1 pathogenesis remain poorly understood, including the intimate molecular mechanism(s) of tumorigenesis, the progression of HTLV-1 leukemia toward the aggressive form, and the possibility of enhancing the host response to avoid or at least delay disease onset.

## **2. Animal Models**

Animal models, including mice, rats, rabbits, squirrel monkeys, baboons, macaques, and even fruit flies, although not the natural hosts of HTLV infection, may help in elucidating some aspects of HTLV infection, persistence, host immune response, and diseases-associated developments [26][27][28][29][30]. In the following sections, we will discuss the most recent advances in the knowledge of HTLV infection and pathogenesis derived by studies in animal models.

### **2.1. Mouse Models**

Although immunocompetent murine cells are not productively infected with HTLV-1, xenograft and transgenic mice are widely used for the study of HTLV-1 infection and related diseases. Starting from the late 1990s, when the C3H/HeJ and BALB/c strains were used to establish persistent infection injecting HTLV-1-producing MT-2 cell intraperitoneally in neonatal mice, several HTLV immunocompromised mouse models have been further developed [31][32][33][34]. The development of SCID mice, unable to perform VDJ recombination of B- and T-cell receptors because of a nonsense mutation in the PRKDC (Protein Kinase, DNA-Activated, Catalytic Subunit protein kinase) gene, has generated animals with severe combined immunodeficiency (SCID). These mice allow the engraftment of human cells. By introducing additional genetic mutations, several other types of SCID immunocompromised mouse strains become available, i.e., NOD-SCID mice, in which SCID mutation is present in a non-obese diabetic (NOD) genetic background mouse that shows NK cell dysfunction, low cytokine production, and T- and B-cell deregulation; NSG and NOG mice, in which different mutations in the interleukin-2 receptor common subunit  $\gamma$  (IL2R- $\gamma$ C) leading to a complete loss of T, B, and NK cells, are introduced into the NOD/SCID background; and BALB/c mice deficient in IL2R- $\gamma$ C and the recombina-activating gene 2 (Rag2) (BRG), which are impaired in T- and B-cell differentiation and have high levels of NK-cell activity [35].

SCID xenograft mouse models can reproduce some features of HTLV-1 disease, such as multiple organ engraftments with ATL cells, expression of parathyroid hormone-related protein (PTHrP), a mediator of hypercalcemia in ATL patients, and increased levels of IL2 R $\alpha$  and  $\beta$ -2 microglobulin [36][37][38]. These xenograft mouse models have contributed to the recapitulation of splenomegaly and lymphoma similar to ATL pathologic features [39]. Several studies have reported the successful engraftments in NOG mice of HTLV-1-transformed cell lines, ATL cells, and PBMCs from asymptomatic HTLV-1 carriers [40][41][42]. Engrafted SCID mice have also been used to assess the tumorigenic potential of ATL cell lines [43]. In NOG mice, a highly tumorigenic ATL cell was selected by serial xenotransplantation of patient leukemic cells and used to study features of ATL such as the involvement of carbonic anhydrase IX (CA9), a membrane-associated enzyme that regulates cellular pH. It was found that CA9 is upregulated and promotes tumorigenicity of ATL-derived cells [44]. A highly penetrant in vivo model of HTLV-1-induced T-cell lymphoma was established by intraperitoneally engrafting immune-compromised NOD/SCID mice with tumorigenic HTLV-1-transformed SLB1 and MET-1 lymphoma T cell lines. In this model, a cooperative role was found between the viral p30II latency regulatory factor and the cellular TP53-induced glycolysis and apoptosis regulator (TIGAR) in cancer progression, highlighting TIGAR involvement in tumor lymphocyte infiltration [45]. NOD/SCID mice injected with leukemic cells (MET-1) from a patient with ATL were proposed as preclinical in vivo murine models of ATL [46]. In this model, the ATL therapeutic efficacy of selected compounds has been reported. Among other treatments, the efficacy of daclizumab, a monoclonal antibody against the IL-2R- $\alpha$  (CD25), combined with depsipeptide, a member of the cyclic peptide class of HDAC inhibitors, was tested by analyzing the survival of the



In addition to the numerous studies aimed at dissecting the molecular function of the Tax and HBZ viral protein in in vitro cellular model interesting contributions towards interpreting their role in vivo in the lymphoproliferative process have been derived using humanized mouse models. Recently, the contribution of the Tax PDZ binding motif (PBM) to T-cell proliferation was analyzed in humanized mice carrying a human hemato-lymphoid system. It was shown that Tax-PBM enhanced HTLV-1-mediated T-cell proliferation compared to a PBM-deleted mutant, and that this domain is required for T-cell proliferation. Furthermore, comparative transcriptome analyses of T cells derived by humanized mice infected with wt and mutant Tax showed that the absence of PBM is associated with the deregulation of genes involved in T-cell signaling and proliferation, apoptosis induction, and cytoskeletal organization [62]. Taking advantage of humanized mice, the role of HBZ in altering the expression of the receptor activator of NF- $\kappa$ B ligand (RANKL), a regulator of osteoclast differentiation, was evaluated in vivo. In this HTLV-1-infected humanized mouse model, treatment with denosumab, a monoclonal antibody against human RANKL, resulted in reduced bone loss [63].

### 2.1.2. Transgenic Mouse Models

Transgenic mice have been generated mostly to analyze the oncogenic potential of Tax and HBZ viral protein. Indeed, Tax expression in transgenic mice is sufficient to induce tumors, confirming the in vivo oncogenic potential of Tax [27][64]. An interesting transgenic mouse model was developed by introducing the firefly luciferase gene driven by the HTLV-1 LTR (LTR-LUC) in transgenic Tax mice. The double transgenic Tax-Luc mice develop lymphoma, splenomegaly, hypercalcemia, osteolytic bone lesions, and persistent activation of neutrophils [65]. The same team demonstrated that IL-15-deficient Tax-LUC mice developed an aggressive lymphoma and an increased expression of IL- $\alpha$ , thus suggesting IL-15 and anti IL-1 $\alpha$  as potential targets for ATL therapies [66].

To restrict Tax expression to the thymus, Tax transgenic mice have been generated using lymphocyte-specific protein-tyrosine kinase (lck) promoters. These Lck-Tax mouse models develop lymphoma and leukemia after a long latency period of almost 18 months and present most of the characteristics of acute ATL patients [67][68]. Tax transgenic models have also been used to test in vivo the efficacy of ATL therapy [69]. SCID mice injected with spleen cells from Tax transgenic mice developed ATL-like tumors. Treatment of these mice with arsenic/IFN- $\alpha$  or synthetic retinoid ST11926 compound resulted in a significant increase in animal survival [70][71]. In addition, normal syngenic mice injected with ATL cells from Tax-transgenic mice showed inefficient Tax-specific T-cell induction and ATL cells elimination [72].

As for Tax, the in vivo role of HBZ has been studied in HBZ transgenic (HBZ-Tg) mice. HBZ is the only regulatory/accessory gene encoded by HTLV-1 to be expressed in all ATL patients and necessary for the proliferation of ATL cells [23]. Mice expressing HBZ under the Granzyme B promoter (Gzmb-HBZ) developed lymphoproliferative disease and hypercalcemia [73]. HBZ transgenic models in which HBZ expression is restricted to CD4<sup>+</sup> are preferentially used to study the inflammatory process correlated with HTLV-1-mediated pathogenesis. These HBZ-Tg mice develop systemic inflammation and T-cell lymphoma [74], and show higher levels of the immunosuppressive cytokine IL-10 and dysfunctional Treg cells [23][75]. In an interesting HBZ-Tg-based model, it was recently demonstrated that HBZ plays a pivotal role in dysregulating the cytokine signaling modulating the IL-10/JAK/STAT signaling pathway. As expected, in HBZ-Tg the loss of IL-6 and expression of IL-10 accelerates inflammation and lymphomagenesis [25]. HBZ-Tg-derived T-cell lymphoma has also been used to establish an HBZ-induced T cell line, named Ht48, which has been used to test an HBZ-targeted HTLV-1 vaccine. This model identified a candidate peptide (HBZ157-176) for vaccine development by using rVV-vaccinated mice [76].

PBMC-humanized NSG mice and HBZ-transgenic (Tg) mice, which develop systemic inflammation, were recently used to validate the efficacy of administration of pentosan polysulfate (PPS), a semisynthetic glycosaminoglycan, to counteract HTLV-1 infection and pathological sequelae. PPS blocked HTLV-1 infection in huPBMC NSG and suppressed the development of dermatitis and lung damage in HBZ-Tg mice, supporting the therapeutic use of PPS in the treatment of HTLV-1-induced inflammatory diseases [77].

Tax-transgenic (Tax-Tg) and HBZ Tg mouse models have contributed to identifying functional ATL stem cells (ATLSC) and determining that c-kit, a common surface marker of ATLSCs, is a key regulator of ATL disease initiation and progression [78]. Unexpected results were obtained using a double transgenic mouse model expressing both Tax and HBZ in CD4<sup>+</sup> cells. These mice developed T-cell lymphoma but not ATL-like leukemia, suggesting that the balancing effect of Tax/HBZ expression is critical for oncogenic outcome [79]. Mouse models of acute-type ATL can be rapidly generated by transplanting in vitro-induced T cells that have been retrovirally transduced with HBZ. In this model, it is possible to study the cooperative action of HBZ and host factors in contributing to ATL development [80].

## 2.2. Rat Models

Rat models have been useful in the study of HAM/TPS pathology. HTLV-1-infected Wistar-King-Apekman (WKA) rat strain develops spastic paraparesis and clinical symptoms similar to the humans with HAM/TPS [81]. Rats have also been used to study mother-to-child transmission (MTCT) of HTLV-1. Recently an MTCT model was developed using orally HTLV-1-infected rats that did not have antibody responses against viral antigens. In this model, rats inoculated with ILT-M1, an IL-2-dependent HTLV-1-infected T cell line derived from an HAM/TPS patient, transmitted HTLV-1 to their offspring at a high rate (50–100%), and the rate of transmission correlated with the PVL of the infected mother rats [82]. This model has been also proposed for studying the neutralizing potential of antibodies against HTLV-1 envelope gp-46 (LAT27) through antibody-dependent cellular cytotoxicity in MTCT [83][84].

The role of host factors in supporting viral infection has also been investigated in rat models. Human CRM1 (hCRM1) protein, a member of the importin  $\beta$  family, acts as a cofactor of Rex-dependent viral mRNA transport. Transgenic CRM1 rats intraperitoneally inoculated with HTLV-1-infected cells exhibited a much higher HTLV-1 viral production than wild type rats, and presented more extensive invasion of the thymus by HTLV-1, supporting the in vitro evidence of the key role of CRM1 in HTLV-1 infection [85]. Rat models were also used to test the effect of vaccines based on HTLV-1 Tax-specific cytotoxic T lymphocyte immunity response, the oncolytic potential of vaccinia viruses (VVs) and the ability of siRNA Tax downregulated HTLV-1-infected cells to develop tumors in T-cell-deficient nude rats [86][87][88]. These studies confirm the significant roles of Tax in activating cytotoxic host immune response to the virus and in the survival of infected cells in vivo.

## 2.3. Rabbit Models

Rabbits are well established and reproducible models to study HTLV-1 transmission, immune responses, and viral determinants required for HTLV infection. Rabbits can be infected with HTLV, but do not develop HTLV-associated diseases; nevertheless, they produce a persistent infection and represent a useful animal model for studying the early steps of infection [29][89][90]. New Zealand White (NZW) rabbits injected with an HTLV-1 carrying a PBM-deleted form of Tax-1 showed that this domain was important for the establishment and maintenance of persistent infection [91]. A similar model was used to demonstrate in vivo that HBZ enhances infectivity and persistence and that the HBZ leucine zipper domain is critical for HBZ functional activity, whereas HBZ is dispensable for immortalization/transformation of primary T lymphocytes in cell culture [92]. In rabbits, APH-2 studies have demonstrated that compared to HBZ, APH is not required for viral persistence [93]. In addition, rabbit models have been successfully applied to demonstrate that the HTLV-1 accessory proteins p12, p13 and p30 are necessary to establish the infection and maintain viral loads in vivo [60][94][95].

Recently the NZW rabbit model was also used to study epigenetic regulation of HTLV-1 gene expression in vivo, demonstrating that the CCCTC binding site present in the overlapping p12 and HBZ sequences of the HTLV-1 genome is dispensable for persistent infection [96]. Particularly worthy of note are studies in rabbit models that have contributed to better defining the differences in the HTLV-1 and HTLV-2 tropisms. It has been possible to determine that at early steps of infection, at the entry step, the tropism is almost the same, represented by CD4+ and CD8+ T cells, although, consistent with reports in humans, HTLV-1 establishes a more robust infection in both CD4+ and CD8+ T cells, compared to HTLV-2 [97].

## 2.4. Non-Human Primate Models

Non-human primates are susceptible to HTLV-1 infection and develop HTLV-1-associated diseases, including leukemia. Squirrel monkeys, cynomolgus monkeys, rhesus macaques, and pig-tailed macaques have been used to study HTLV immune response, viral persistence, and ATL-like disease. In squirrel monkey *Saimiri sciureus* injected with HTLV-1-immortalized PBMCs, the spleen and lymph nodes were shown to serve as major reservoirs for HTLV-1 [98]. p12, p30, and HBZ have been found to be essential for establishing and maintaining HTLV-1 infection in macaques, but not in rabbits [98]. Furthermore, by inoculating macaques intravenously with lethally  $\gamma$ -irradiated B-cell lines producing mutated viral clones, it was shown that p12 and p8 are necessary for efficient viral persistence and spread [59]. The non-human primate models have contributed to recapitulating the initial steps of viral infections, including viral genome reverse transcription and persistent clonal expansion of infected cells [99]. Squirrel monkeys, as well as macaque rhesus, have also been used to evaluate the immunogenicity of experimental vaccines against HTLV-1 [76][100]. However, due to the high cost and restrictive regulations related to their application in experimental research, non-human primate models remain of very limited use in the study of HTLV-1.

## 2.5. Transgenic Fly Model

A Tax and HBZ transgenic *Drosophila melanogaster* fly model was recently proposed as a suitable model for studying HTLV-I transformation, persistence, and epigenetic modification. The *in vivo* fly model demonstrated that Tax activates the chromatin polycomb repressive complex 2 (PRC2), which acts on the regulation of the expression of genes involved in cell survival, proliferation, or apoptosis. In this model, HBZ does not induce transformation or NF- $\kappa$ B activation, but its expression abolishes Tax-mediated PRC2 activation in flies expressing both Tax and HBZ [30][101].

## 3. HTLV-1-Related Virus and Animal Models of Leukemogenesis

### 3.1. HTLV-1/BLV Models

Bovine leukemia virus (BLV) is a retrovirus closely related to HTLV-1 that causes B-cell lymphoma in ~5% of infected animals and has been proposed as a model for investigating the transmission, latency and pathogenesis of both BLV and HTLV [89][102]. In addition to cattle, BLV may infect sheep, and both species can develop leukemia and lymphoma. Sheep experimentally infected with BLV represent an interesting model for studying leukemia/lymphoma, as they systematically develop leukemia/lymphoma in a shorter period of ~20 months. In this model, it is possible to monitor all stages of the viral-induced disease, from infection, through asymptomatic stages, to terminal leukemia, recapitulating the development of HTLV-1-associated human malignancy. BLV sheep models have contributed to defining the viral and host determinants for viral persistence and latency and to exploring the efficacy of potential cancer treatment and viral vaccine [103][104][105]. Recently, comparative analyses of HTLV-1/BLV proviral integration sites in the host genomes were performed from the primary tumors and asymptomatic stages of the infection using high-throughput sequencing mapping and RNAseq [106]. This study demonstrated that HTLV/BLV proviruses are integrated close to cancer driver genes, the expression of which may be cis-perturbed, contributing to malignant progression in the polyclonal expansion of the infected cells. Proteome analysis of sheep lymphocytes in the course of BLV-induced leukemia identified novel potential protein markers of disease progression such as spleen trypsin inhibitor, CXCL4/PF-4, thrombospondin, vasodilator-stimulated phosphoprotein, and the fibrinogen alpha chain that are worthy of further investigation in HTLV-induced leukemia [107]. Defining the genetic and epigenetics factors that characterize the sheep BLV leukemia also offers the opportunity to test antiviral gene target therapies.

### 3.2. STLV Models

STLV-1 naturally infects non-human primates such as the Japanese rhesus macaque, *Mandrillus sphinx*, and *Papio anubis* and, like HTLV-1, causes ATL adult T-cell leukemia and lymphoma. [108]. Compared to HTLV-1 infection, Japanese monkeys infected by STLV-1 present similar host immune responses to viral protein and similar clonality of virus-infected T cells, representing a valid model for studying persistent infection and for developing immune-based therapy and prophylaxis [108]. Administration of anti-CCR4 antibodies to STLV-1-infected Japanese macaques resulted in a reduced proviral load *in vivo*, which is consistent with its efficacy in patient ATL treatment [109]. Furthermore, a long-lasting decrease in the number of STLV-1-infected cells *in vivo* was observed when Japanese macaques were treated with the humanized anti-CCR4 monoclonal antibody mogamulizumab, which enhances T-cell responses to viral antigens and suppresses CCR4+ Treg cells [110]. Recently, the effect of monoclonal antibodies on CD8 and CD16 was also explored in Japanese macaques infected with STLV-1; although not conclusive, the results suggested that depletion of CD8+ cells was able to modify the clonal proliferation of the infected cells [111].

In *Papio papio* baboons naturally infected with STLV-1, it was observed that the combined treatment with valproate, an inhibitor of histone deacetylases, and azidothymidine, an inhibitor of reverse transcriptase, caused a strong decrease in the proviral load and an increase in the STLV-1 specific cytotoxic T-cell population [112]. Due to the similarity with the human immune system, STLV-1-infected baboons have been proposed as a model for testing HTLV-1 vaccines based on immunogenic Tax epitopes. In this model, distinct Tax epitope-rich regions have been shown to be targeted by STLV-1-specific CD8+ T cells [113].

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