

# Clinical and Public Health Implications of Human T-Lymphotropic Virus Type 1 Infection

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**SUMMARY** Human T-lymphotropic virus type 1 (HTLV-1) is estimated to affect 5 to 10 million people globally and can cause severe and potentially fatal disease, including adult T-cell leukemia/lymphoma (ATL) and HTLV-1-associated myelopathy/tropical spastic paraparesis (HAM/TSP). The burden of HTLV-1 infection appears to be geographically concentrated, with high prevalence in discrete regions and populations. While most high-income countries have introduced HTLV-1 screening of blood donations, few other public health measures have been implemented to prevent infection or its consequences. Recent advocacy from concerned researchers, clinicians, and community members has emphasized the potential for improved prevention and management of HTLV-1 infection. Despite all that has been learned in the 4 decades following the discovery of HTLV-1, gaps in knowledge across clinical and public health aspects persist, impeding optimal control and prevention, as well as the development of policies and guidelines. Awareness of HTLV-1 among health care providers, communities, and affected individuals remains limited, even in countries of endemicity. This review provides a comprehensive overview on HTLV-1 epidemiology and on clinical and public health and highlights key areas for further research and collaboration to advance the health of people with and at risk of HTLV-1 infection.

**KEYWORDS** clinical methods, clinical therapeutics, diagnostics, epidemiology, human T-cell leukemia virus, oncogenic virus, pathogenesis, public health, sexually transmitted diseases, virology

## INTRODUCTION

Human T-lymphotropic virus type 1 (HTLV-1) is estimated to affect 5 to 10 million people globally (1) and can cause severe and potentially fatal disease, including adult T-cell leukemia/lymphoma (ATL) (2–5) and HTLV-1-associated myelopathy/tropical spastic paraparesis (HAM/TSP) (6). The burden of HTLV-1 infection is geographically concentrated, with high prevalence in discrete regions and populations. While most high-income countries have introduced HTLV-1 screening of blood donations, few other public health measures have been implemented to prevent infection or its consequences.

Gaps in knowledge and limited information about HTLV-1 have made it difficult for health care workers, researchers, policy makers, and people living with HTLV-1 infection to advance the clinical and public health response to HTLV-1. In recognition of this, the World Health Organization (WHO) held the first Global Consultation on HTLV-1 with member states and partners in November 2019, followed by the publication and launch of a series of documents, including a technical report (7), fact sheet, and meeting report (8) in March 2021. The recommendations outlined in these reports focused on the need to address HTLV-1 through a global public health approach. This review provides a comprehensive overview on HTLV-1 epidemiology and clinical and public health and highlights key areas for further research and collaboration to advance the health of people with and at risk for HTLV-1 infection.

## GLOBAL OCCURRENCE OF HTLV-1

In 1977, researchers in Japan described a novel, rapidly progressing lymphoid malignancy, which became known as ATL (9). In addition to unique clinical and hematological features, the geographic distribution of patients by place of birth was notable, with almost all having been born on the southwestern island of Kyushu, a region now recognized as endemic for HTLV-1. The clustering of ATL cases led to the hypothesis that an oncogenic viral infection should be considered in disease causation (9). Shortly after, HTLV-1 was isolated from a patient with cutaneous T-cell lymphoma (10) and, following further serological and virological evidence, was determined to be the causative agent of ATL.

Once the association between ATL and HTLV-1 was established, epidemiological surveys of HTLV-1 prevalence were carried out across many countries and population groups, as well as investigations of transmission, disease progression, and associations

with diseases other than ATL. The data on prevalence demonstrated a highly heterogeneous global distribution, with focal occurrence in various parts of the world. Even in areas where infection with HTLV-1 has been found, it occurs as endemic clusters, often within, or close to, populations with much lower prevalence. Given the substantial heterogeneity both within and between geographic areas, characterizing specific countries or even localities within countries as high versus low prevalence is not straightforward. The European Centre for Disease Prevention and Control proposed defining high prevalence as more than one in 10,000 positives among first-time blood donors, or 1% in the general population (11). Categorical thresholds such as these may not reliably define country or region level prevalence, but they are useful measures to inform policy decisions around cell and tissue donation screening practices. How HTLV-1 infection persists within discrete communities and geographies over time may be the result of a founder effect (the result of prolonged viral transmission within isolated groups), but this remains to be fully elucidated (1). A consistent finding is that HTLV-1 prevalence increases with age and, in most populations, is higher in adult females than adult males.

Genetically, HTLV-1 has been classified into seven subtypes, each with a characteristic geographic distribution explained by population migration. The cosmopolitan subtype A is the most widespread globally and classed further into subgroups (transcontinental, Japanese, West African, North African, Senegalese, and Afro-Peruvian) (1). Subtypes B, D, E, F, and G are found in specific parts of Africa, while subtype C is found in Australia and Oceania.

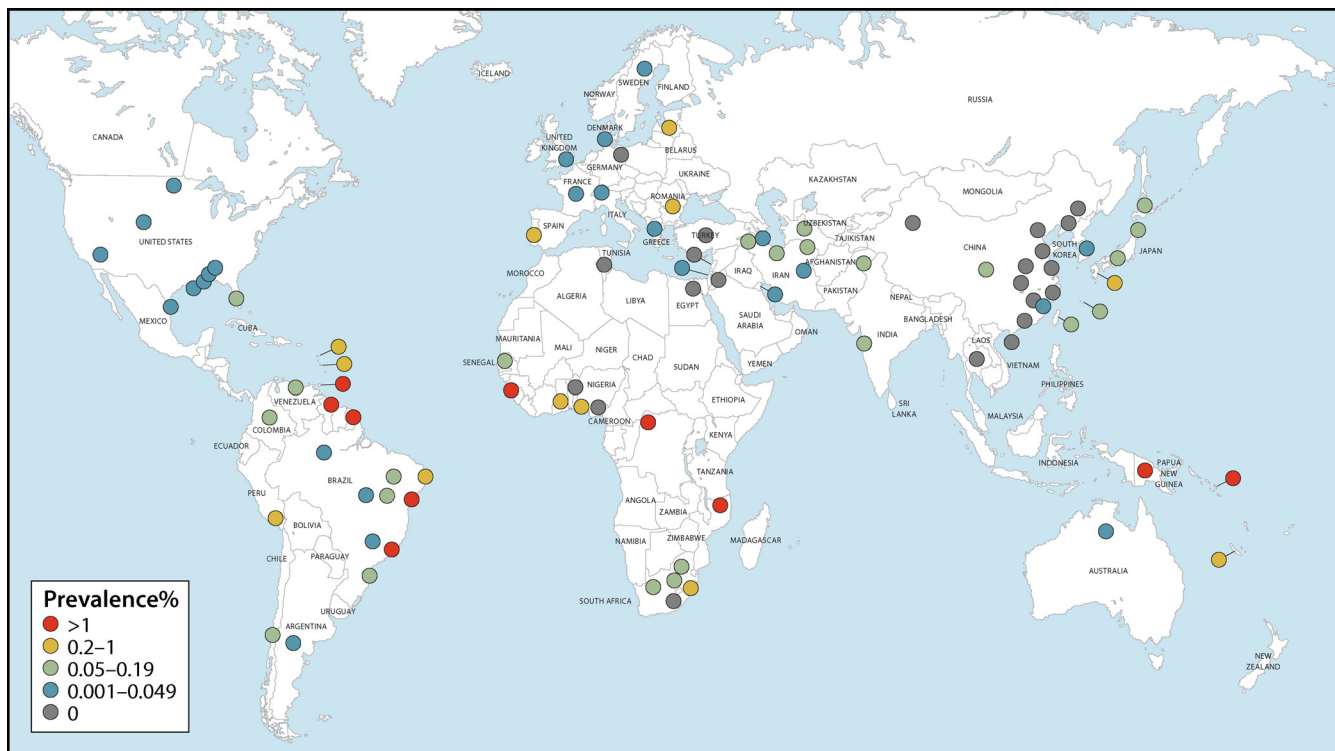
HTLV-1 likely originated from the genetically similar simian T-lymphotropic virus type 1 (STLV-1), a retrovirus endemic among many nonhuman primates in intertropical Africa. The greater genetic diversity of HTLV-1 subtypes in Africa may be the result of repeated zoonotic transmission events from human encounters with STLV-1 endemic nonhuman primates. Accordingly, higher prevalence of HTLV-1 is reported in people bitten by nonhuman primates with strikingly similar sequence homology to the STLV-1 sequences present in native primate species (12).

The number of people living with HTLV-1 worldwide was estimated in 2012 to be in the range of 5 to 10 million (1). Countries and regions broadly regarded as having focal areas where HTLV-1 is endemic include Japan (13–15), Iran (16–18), the Americas (19–27), the Caribbean (28–31), Melanesia (32–35), Central and West Africa (36–40), and Australia (41–43) (Fig. 1; see also Fig. 2 and 3). The paucity of reliable prevalence data from several highly populated countries, such as India and Nigeria, complicates calculations of global prevalence. Since estimations are based on and limited to known areas of endemicity, the available data are likely an underestimate of true global prevalence. The following overview on global occurrence of HTLV-1 reports prevalence data from studies ( $n = 186$ ) whose methodological quality was critically appraised and where infection was validated by confirmatory testing. Data were excluded ( $n = 400$ ) if no original prevalence data were reported, confirmatory testing was not carried out, or the sampling methodology was not representative of the general population.

### African Region

The WHO African region likely has the largest number of people living with HTLV-1 worldwide. High prevalence has been consistently detected in many populations and communities, with little change since the first studies conducted in the 1980s. Countries with well-defined areas of endemicity include Cameroon, Democratic Republic of the Congo, Gabon, Guinea, and Guinea-Bissau. In general, countries of central and west Africa are best characterized, with most prevalence data drawn from surveys in blood donors and pregnant women. A limited number of large community surveys in the general population have been carried out in countries of endemicity, notably Gabon and have been repeated to demonstrate the persistence of geographically localized infection over time. There remain large areas in north and east Africa with little reliable prevalence data.

For West Africa, prevalence data are available for Benin, Côte d'Ivoire, The Gambia, Ghana, Guinea, Guinea-Bissau, Nigeria, Senegal, and Togo, with prevalence ranges



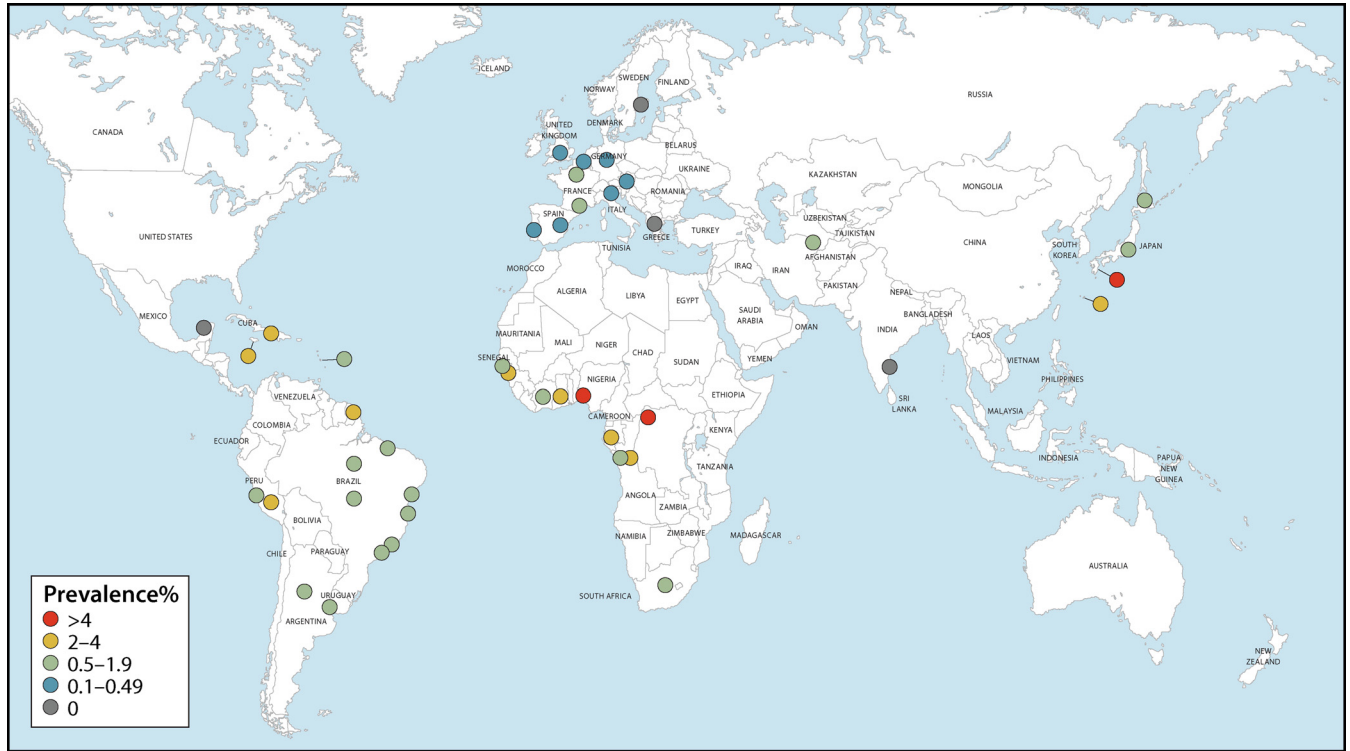
**FIG 1** Global distribution of HTLV-1 seroprevalence among blood donors. These data were extracted from 65 critically appraised peer-reviewed publications reporting original prevalence data subject to confirmatory testing.

from 0 to 1.2% among blood donors, 1.2 to 2.2% among pregnant women, and 1 to 3.6% among the general population.

The highest prevalences are in Guinea-Bissau, demonstrated by three large general population studies reported prevalences ranging from 2.3 to 3.6%, with considerable variation by sex and age (37, 44, 45). In the capital city Bissau, seroprevalence increased with age from 0.5 and 1.1% in men and women aged 15 to 24 years, to 5.6 and 8.8% in those 55 years and above, respectively (37). Prevalence appears to have remained stable over time at 3.6% in 2000, 2.3% in 2009 (44), and 3% in 2018 (37, 44). A nationwide serosurvey among pregnant women found an overall prevalence of 2.2% (46). In contrast to many other countries where HTLV-1 is endemic, the distribution of infection in Guinea-Bissau appears to be relatively homogeneous (46).

The situation is similar in Guinea, with an overall prevalence of 1% in the general population (39) and a higher prevalence in the southern region of Samoé (2%). Seropositivity increased from 0.5% in children aged 10 years or younger to 5.7% in people aged 40 years or older. One blood donor study carried out in 1993 reported a prevalence of 1.2% (47). Although few studies report prevalence data from Cote d'Ivoire, one survey from the late 1980s found high levels in several population groups, including 1.9% among pregnant women, 2.2% among the general adult population, and 7.4% among female sex workers (48). Likewise, while there is some evidence of elevated prevalence in Nigeria, available studies are limited. Prevalence in blood donors ranged from 0% in the south-eastern city of Enugu to 0.73% in the capital of Lagos (49–51), while among pregnant women in the southwestern city of Ibadan a high prevalence of 5.5% was reported (52). In Benin, a national general population survey reported an overall prevalence of 1.5%, with substantial variation by geography, age, and sex (53).

In Accra, the capital of Ghana, antenatal screening detected a prevalence of 2.1% (54). Little reliable evidence is available for Senegal, with one study in 2006 reporting a seroprevalence of 0.14% among 4,900 blood donors (55), with five of the seven positive cases from the south Casamance region, indicating a potential region of endemicity. Among



**FIG 2** Global distribution of HTLV-1 seroprevalence among pregnant women. These data were extracted from 37 critically appraised peer-reviewed publications reporting original prevalence data subject to confirmatory testing.

pregnant women from several regions across the Gambia, the prevalence was 1.2% (56). In Togo, HTLV-1 among outpatients the prevalence was 1.2% (57).

The prevalence in Central Africa countries is similarly high, ranging from 0.3 to 8.7% in the general population (36, 38, 58–63) and from 2 to 4.6% in pregnant women (64–67) in reports from Equatorial Guinea, Cameroon, Gabon, and the Democratic Republic of the Congo. The best-investigated country in Central Africa is Gabon, with four large population-based surveys carried out since the late 1980s (38, 58–60). Prevalences in the general population varied regionally, ranging from 2.2 to 12.5% (59). Higher positivity was associated with older age, exceeding 13% in people over 60 years (59). The prevalence in Gabon is generally high across all regions but is particularly high in the eastern provinces. A national survey of pregnant women across five provinces reported an overall prevalence of 2.1% (65) and, consistent with the general population studies, found clusters of higher prevalence in the eastern provinces (65).

The prevalence in the Democratic Republic of the Congo was similarly high. Among pregnant women, the HTLV-1 prevalence was 3.7 to 4.6% (64, 66) and 3.2 to 7.3% among female sex workers in Kinshasa (64, 68). The seroprevalence in blood donors from three regions (Basankusu, Gemena, and Dungu) was 4% (66).

For Cameroon, two studies reported on populations inhabiting rural areas in south and southeastern rainforest regions and found overall HTLV-1 seroprevalences of 2.6 and 2.9% in Pygmy populations, with particularly high rates in people over 60 years (11.3%) (61, 62). The HTLV-1 prevalence in Bantu populations was lower (1.3%) (61). The epidemiology of HTLV-1 in Equatorial Guinea has not been well described and is limited to one early study that reported a prevalence of 0.26% in the general population (69).

East African countries appear to have lower HTLV-1 prevalences than elsewhere in Africa. Data on HTLV-1 in Ethiopia comes from one study in 2012 that found no cases among 556 outpatients attending a rural hospital in a central part of the country (70). In Rwanda, one general population study reported prevalences of 0.2% in a rural setting and 0.3% in an urban sample (71).





In Brazil, there is high prevalence across several regions, particularly in the north and northeast of the country. The prevalences in first-time blood donors were reported to be 0.01% in Ribeiro Preto in the southeast and 0.6% in the northeastern state of Piau (90, 91). The city of Salvador has the highest overall prevalence of HTLV-1 in Brazil (21). Here, the prevalences in pregnant women, in general populations, and in blood donors were 0.85, 1.50, and 1.40%, respectively (92, 93). The prevalence among pregnant women ranged from 0.11% in Sau Paulo to 0.58% in Rio de Janeiro (94–98). Although men who have sex with men are infrequently studied with respect to HTLV-1, one survey reported a 0.70% prevalence (99).

Tumaco in Colombia's southwest was found to have high rates of suspected HTLV-1-related neurological disease. Subsequent serological surveys reported prevalence of 2.8% in the general community, exceeding 14% in people older than 50 years. Outside of Tumaco, a prevalence of 0.05% in blood donors was found in the city of Medellin in Colombia's central northwest (100).

In Peru studies have focused largely on indigenous communities among whom HTLV-1 is considered endemic, in particular the Shipibo-Conibo and Quechua people (19, 87, 88). Depending on geographic location, prevalence in Quechua communities varied considerably from 0 to 10% (88, 101, 102). Shipibo-Conibo communities within the Amazon region have similarly high levels of HTLV-1, with population-based studies reporting prevalences of 4.1 and 5.9% in Shipibo-Conibo women (19, 87). Consistent with other findings, high levels of HTLV-1 were found in female sex workers in Lima, with an overall prevalence of 9.6% increasing to 17.5% in women between 35 and 60 years old (103). The prevalence among pregnant women in French Guiana ranged from 3.8 to 5.7% (26, 84, 86). Importantly, women from the Noir-Marron population accounted for approximately 90% of all positive cases (85).

Population-based studies in Honduras showed clustering of HTLV-1 in cities along the Atlantic coast (89). Higher prevalence was reported in people of Afro-Caribbean descent (8%) than in people of American-European ancestry (0.5%) (89). In Georgetown Guyana, the prevalence in blood donors was 1.3%, with positivity associated with Guyanese-African and Guyanese-Indian ethnicity, older age, and female sex (27). In Panama, the overall seroprevalence in the general population was 0.6% (104).

In Argentina the prevalence ranged from 0.03% in blood donors to 0.1% in pregnant women (20, 105, 106). Data from Chile and Venezuela are derived from blood donor studies, with both reporting an overall prevalence of 0.1% (24, 107). For Chile, the prevalence in first-time blood donors was 0.1%, with a higher prevalence in Valparaiso in the north (0.17%) than in Concepcion (0.05%) in the south (24). For Venezuela, one study in Caracas found a 0.1% prevalence among blood donors (107).

The Caribbean has several high-prevalence regions. Prevalences ranged from 0.3 to 0.6% in blood donor studies (30, 108–110), 5.2 to 6% in general population studies (29, 111), and 1.2 to 3.8% in pregnant women studies (28, 112–116). In Guadeloupe, one blood donor survey reported an overall HTLV-1 prevalence of 0.33%, with geographic variation ranging from 0.21% in the southern regions of Basse Terre to 1.15% on the island of Marie Galante (31, 110). Among pregnant women in northern rural Haiti, 2.2% were found to be HTLV-1 positive (28). In addition, antenatal surveys carried out in French Guiana reported a prevalence of 4.2% in pregnant women of Haitian background (86). In Jamaica, a large population-based survey found a prevalence of 6% (29), while the prevalence in pregnant women ranged from 2 to 3.8% (113, 114, 116). HTLV-1 prevalence in the French overseas territory of Martinique was 2.4% among pregnant women (115), and 0.35% among first-time blood donors (108, 109). One blood donor study in Trinidad and Tobago reported an HTLV-1 prevalence of 1.5% (30).

### South-East Asia Region

Although HTLV-1 in the WHO South-East Asia Region appears rare, most countries have substantial gaps in reliable prevalence data. Indonesia, Thailand, and India were the only countries with prevalence data where positive screening results were subject to confirmatory testing. No positive cases are reported in blood donors or population-

based studies from Thailand and Indonesia (117–119). In India, one small blood donor study found prevalence of 0.14% (120). Nevertheless, case reports of ATL and HAM/TSP from India reflect the need for larger-scale studies to fully determine the extent and distribution of HTLV-1. Given the limited data and large population size, it is not possible to characterize the epidemiology of HTLV-1 in India.

### Eastern Mediterranean Region

The overall prevalence of HTLV-1 in the WHO Eastern Mediterranean Region is generally low, with the Islamic Republic of Iran as the exception. In blood donor studies, zero prevalences are reported for Egypt, Saudi Arabia, Oman, Tunisia, Lebanon, and Jordan (121–128). Screening of blood donors in Kuwait found a prevalence of 0.07%, with the majority of positive cases of non-Kuwaiti origin (129). In Pakistan, one blood donor study in the northern city of Rawalpindi found an HTLV-1 prevalence of 0.2% (130). A prevalence of 0.06% was reported in a cohort of outpatients in northern Egypt (131).

Seroprevalence data in Iranian blood donors ranged from 0.05 to 0.7% and were associated with region and age (16, 17, 132–135). In Iran, HTLV-1 is described as a significant health issue particularly in the northeastern province of Razavi Khorasan. In Mashhad, the capital of Razavi Khorasan, a population-based survey reported an overall prevalence of 2% exceeding 12% in people older than 65 years (18). Two blood donor studies in Mashhad found prevalences of 0.7 and 0.18% (17, 132) and 1.5% among pregnant women (136).

### Europe Region

The prevalence of HTLV-1 in the WHO Europe region is generally low. Blood donor studies range between 0 and 0.006% prevalence in Denmark, France, Germany, Greece, Sweden, Switzerland, the United Kingdom, Israel, and Turkey (137–146). Countries with higher prevalence include Portugal, Turkmenistan, Latvia, and Romania, with prevalences among blood donors ranging from 0.2 to 0.64% (147–150). In pregnant women, prevalence ranges from 0 to 0.02% in Belgium, Germany, Greece, Italy, Portugal, Slovenia, Spain, and Sweden, with higher prevalences reported in the United Kingdom (0.03%) and Paris, France (0.1%) (142, 151–154). One study examining prevalence among people who inject drugs found no cases of HTLV-1 (155).

Detection of positive cases in the United Kingdom (138, 156), France (140, 151, 157, 158), Portugal (148), Italy (151, 159), Spain (154, 160), The Netherlands (161), Greece (146), and Sweden (142) was generally associated with people from, or with sexual partners from, high-prevalence regions. Despite the role population migration plays in the detection of cases within these countries, there is little evidence of expansion beyond known regions of endemicity.

The notable exception in the Europe Region is Romania, which, for reasons unknown, is the only true country of endemicity in the Europe region. In Romania, the detection of ATL prompted a seroepidemiological survey that found a high prevalence of 0.64% among blood donors (149). The origin of HTLV-1 in Romania is unknown, and no reliable epidemiological surveys have been carried out since the mid-1990s. Nevertheless, evidence of higher prevalence in people of Romanian origin has been substantiated in part by the detection of higher rates of HTLV-1 in Romanian immigrants (145).

### Western Pacific Region

HTLV-1 is found in several countries in the WHO Western Pacific Region, with multiple focal areas of high prevalence in Australia, Papua New Guinea, Solomon Islands, and southwest Japan. Prevalence ranged between 0.007 and 2% in blood donors (13, 15, 32, 33, 162–170) and between 0.5 and 39% in general population studies (34, 35, 41, 171–175). High levels of HTLV-1 infection have been found in communities in Papua New Guinea and Central Australian Aboriginal communities.

In Australia, HTLV-1 occurs at extremely high prevalences among Aboriginal people living in central Australia. Here, the first case of HTLV-1 was reported in 1988. Available



evidence indicates that Aboriginal people in Central Australia have a prevalence of HTLV-1 infection 1,000 to 10,000 times higher than the Australian population as a whole, in which prevalence can only be inferred from routine testing in blood donors (41, 176). In 2016, a community-based survey in central Australia found an HTLV-1 prevalence of 33.3% (41). Between 2014 and 2018, a larger community-based survey in the same region found a similar HTLV-1 prevalence in adults of 39% and a lower prevalence of 6% in children aged 3 to 17 years (175). As with overseas studies, prevalence increased with age but, in contrast to most other populations affected by HTLV-1, was higher in older men than women (34).

For Papua New Guinea, studies reporting prevalence data are more than 20 years old. The available data indicate a high prevalence of 14.6% in the Madang province (173). Similarly, prevalence among Hagahai communities in Madang province was 14.2%, increasing to 35% in people older than 40 years (34). The overall prevalence among outpatients in the Solomon Islands was 3.5%, increasing to 7.4% in people aged 40 to 49 years (33). For blood donors in Honiara, the prevalence ranged from 0.7 to 2% (33, 170).

In China there was substantial regional variability, with clustering of elevated prevalence in the southeast (166, 172). Higher-prevalence regions include the province of Fujian and Kinmen County (164–166, 172). Prevalence was greater in Fujian born blood donors (0.02%) compared to non-Fujian born blood donors (0.003%) (166). In central China and Beijing, HTLV-1 is uncommon (164, 177).

For Taiwan, screening for HTLV-1 among blood donors between 1996 and 1999 reported an overall prevalence of 0.058%, with an annual decline in seropositivity from 0.13% in 1996 to 0.032% in 1999 (163). One community-based study reported an overall prevalence of 0.48% among people aged 18 years and older (174).

In Japan there was an estimated 10% decline between 1988 and 2012 in the number of people in Japan living with HTLV-1, from 1.2 million to 1.08 million (15, 178). The overall seroprevalence among first-time blood donors was 0.3%, with substantial regional variability by region from 0.06% in eastern Japan to 1.95% in the southwesternmost island of Kyushu (15). The prevalence among pregnant women from national antenatal screening data was 0.14% and, as in the case of blood donors, was highest in Kyushu (0.6%) (14).

Data on prevalence in South Korea are derived from blood donor studies (167–169), the most recent of which reported a low overall prevalence of 0.007% (168). For New Caledonia, the prevalence in adults aged 60 to 96 years was 0.06%, with all positive cases obtained from female donors (1.3%) (32). One large population-based study in Vanuatu reported an overall HTLV-1 prevalence of 0.62%, with regional variability ranging from 0% in the northernmost province of Torba to 1.93% in the northwesternmost province of Sanma (35).

### Issues Related to Evaluation of HTLV-1 Prevalence and Burden of Infection

While a number of reports have evaluated HTLV-1 prevalence in various populations across the world, there remain many highly populated countries with ill-defined or undetermined HTLV-1 prevalence. Prevalence data have been collected across a broad time period from various populations and cohorts. During this time, screening and diagnostic methods have evolved considerably, constraining the validity of geographic and times-series analyses. With few prevalence surveys representative of general populations with reasonable sample sizes, the majority of prevalence data are derived from studies centered on routine screening practices such as those in blood donors and in pregnant women. Although blood donor screening is advantageous on the scale on which it can be carried out, this method favors selection of people at low risk of blood-borne viral infections, reducing the generalizability to the broader population. Similarly, screening of pregnant women provides a more accurate estimation of HTLV-1 in the general population but tells us little about the older cohort who likely have higher rates of infection.

In addition to the gaps in HTLV-1 prevalence data, systematically collected information on HTLV-1 related diseases is limited. In addition, there are knowledge gaps

concerning the variation in HTLV-1 infection within countries of endemicity and within subpopulations that may be at higher risk, e.g., people who inject drugs and men who have sex with men. A standardized approach to monitoring both HTLV-1 and its associated diseases is needed in order to improve and inform public health decision-making and responses both nationally and globally.

### HTLV-1 VIROLOGY AND PATHOGENESIS

HTLV-1 is a human type C retrovirus (family *Retroviridae*, genus *Deltaretrovirus*) which predominantly infects CD4<sup>+</sup> T lymphocytes (179, 180). The sequence variability within the seven reported HTLV-1 subtypes (A to F) is low. These subtypes have been determined phylogenetically via analyses of the long terminal repeat (LTR) and *env* regions (181, 182), with the genetic divergence within subtype reported to reach 2.7% in the *gp21-env* gene (183). The HTLV-1 genome is encoded on two copies of positive single-stranded RNA. Single-stranded RNA is converted to double-stranded DNA and inserted into the human host cell DNA. When integrated into the host genome as provirus, persistent infection is established. In early infection, cell-to-cell transmission of HTLV-1 (through formation of a virological synapse and/or viral biofilm) is likely to predominate, resulting in polyclonal infection of CD4<sup>+</sup> and CD8<sup>+</sup> T lymphocytes. In established infections, HTLV-1 infection is maintained by clonal expansion of infected cells as described below, a process dependent on host cell DNA polymerase.

The HTLV-1 genome encodes structural proteins typical of a retrovirus (*gag*, *pol*, and *env*), along with proteins specific to HTLV-1, encoded by a unique region in its genome, named *pX*. Encoded in the *pX* region are nonstructural regulatory proteins, including *p13*, *p12*, *p30*, and *p40* (*Tax*), and on the minus (complementary) strand of *pX* is HTLV-1 basic leucine zipper factor (*HBZ*). *Tax* and *HBZ* proteins are important for understanding HTLV-1 biology and pathogenesis.

As a retrovirus, HTLV-1 shares similarities with HIV-1 but differs very substantially in disease association and causation. Unlike HIV-1, HTLV-1 infection does not result in death of T lymphocytes; rather, it is thought to initially cause cell cycle arrest before undergoing further modification during the chronic phase of infection, leading to cell proliferation which can, in turn, lead to malignant transformation of these cells (184). HTLV-1 and its proteins (notably *Tax* and *HBZ*) interact with host cell proteins (often transcription factors) and alter their function. The net effect (of *Tax* and *HBZ*) in HTLV-1-infected cells is cellular proliferation, induction of genetic instability, and inhibition of apoptosis, leading to the persistent clonal expansion of infected cells and the promotion of oncogenesis (185).

Initially, the clonality of HTLV-1-infected T cells is heterogeneous and unstable, but it becomes stabilized over a long clinical latency, during which *HBZ* drives mitotic expansion of latently infected cells that are largely quiescent (186, 187). Recent data have indicated that *Tax* expression occurred intermittently in an ATL cell line, MT1, where it induced the expression of antiapoptotic factors via *NF-κB* to facilitate altruistic cell survival (188). In agreement with these results, *Tax* and HTLV-1 plus-strand mRNA transcripts have also been shown to be expressed in intense bursts in lymphocytes of infected individuals cultured *ex vivo* (189). These results—in combination with the known clastogenic and proinflammatory activities of *Tax* (190), likely delivered in small doses repeatedly over decades—may begin to explain the oncogenic and inflammatory effects associated with HTLV-1.

Both cellular and humoral responses are mounted by the host immune system against HTLV-1. Class 1-restricted CD8<sup>+</sup> T lymphocytes (cytotoxic T cells) identify and destroy HTLV-1-infected-T cells. A balance between CD8<sup>+</sup> T cell killing and HTLV-1 proviral replication through clonal expansion of host cells leads to a steady-state HTLV-1 proviral load. HTLV-1 also induces a proinflammatory, type 1 helper T cell (Th1) response in CCR4<sup>+</sup> CD4<sup>+</sup> T cells (191, 192), characterized by the production of interferon gamma, the induction of B cells, and the development of cell-mediated immunity. Antibodies to *Gag* proteins are produced within the first 2 months of infection,

**TABLE 1** Commercially available HTLV diagnostic immunoassays

Assay type	Assay (manufacturer) <sup>a</sup>	Principle of assay
Enzyme immunoassay	Elecsys HTLV-I/II (Roche Diagnostics)	One-step double-antigen sandwich chemiluminescent immunoassay (ECLIA); detects antibodies to viral recombinant antigens gp21 and p24.
Enzyme immunoassay	Abbott Architect rHTLV-I/II (Abbott Laboratories)	Two-step chemiluminescent immunoassay (CLIA); detects antibodies to viral synthetic peptide gp46 and recombinant antigen gp21.
Enzyme immunoassay	Ortho Avioq HTLV-I/II Microelisa (Avioq, Inc.) <sup>*</sup>	Detects antibodies to purified viral lysate and recombinant HTLV-1 p21E antigen.
Enzyme immunoassay	Abbott Prism HTLV-I/HTLV-II (Abbott Laboratories) <sup>*</sup>	Three-step sandwich chemiluminescent immunoassay (CLIA); detects antibodies to HTLV-1 and HTLV-2 antigens.
Enzyme immunoassay	Murex HTLV I+II (Diasorin)	Detects antibodies to HTLV-1 and HTLV-2 antigens.
Enzyme immunoassay	Gold ELISA HTLV-1/2 (Rem Indústria e Comércio LTDA)	Uses recombinant antigens (gp46 and gp21) fixed on microplate; detects anti-HTLV-1 and HTLV-2 IgM, IgG and IgA antibodies in human serum or plasma by EIA.
Line immunoassay	Inno-LIA HTLV-I/II (Fujirebio, Inc.)	Purified recombinant proteins (rp19, rp24: I/II and rgp21: I/II) and synthetic peptides (gp46: I/II and p19: I) fixed on nylon membrane.
Particle agglutination	Serodia-HTLV-I PA (Fujirebio, Inc.)	Gelatin particle-coated cell culture derived HTLV-1 antigens are agglutinated in presence of antibodies to HTLV-1 in human serum/plasma.
Western blot	HTLV Blot 2.4 (MP Diagnostics) <sup>*</sup>	Seropositivity criteria for HTLV-1 includes reactivity to p19 Gag, with or without p24 Gag, and to GD21 with the presence of rgp46-I peptide, MTA-1.

<sup>a</sup>\*, FDA licensed.

followed by antibodies specific for envelope proteins. Anti-Tax antibodies may develop later in the course of infection. While host immune responses appear to be relatively effective in controlling (but not eradicating) HTLV-1, the CD8<sup>+</sup> and Th1 T cell responses generate inflammatory cytokines, which play a role in the pathogenesis of HAM/TSP and other inflammatory conditions (193). Tax also upregulates expression of other host genes which may be involved in HTLV-1 disease pathogenesis, including interleukin-2 (IL-2), granulocyte-macrophage colony-stimulating factor, and tumor necrosis factor alpha (194).

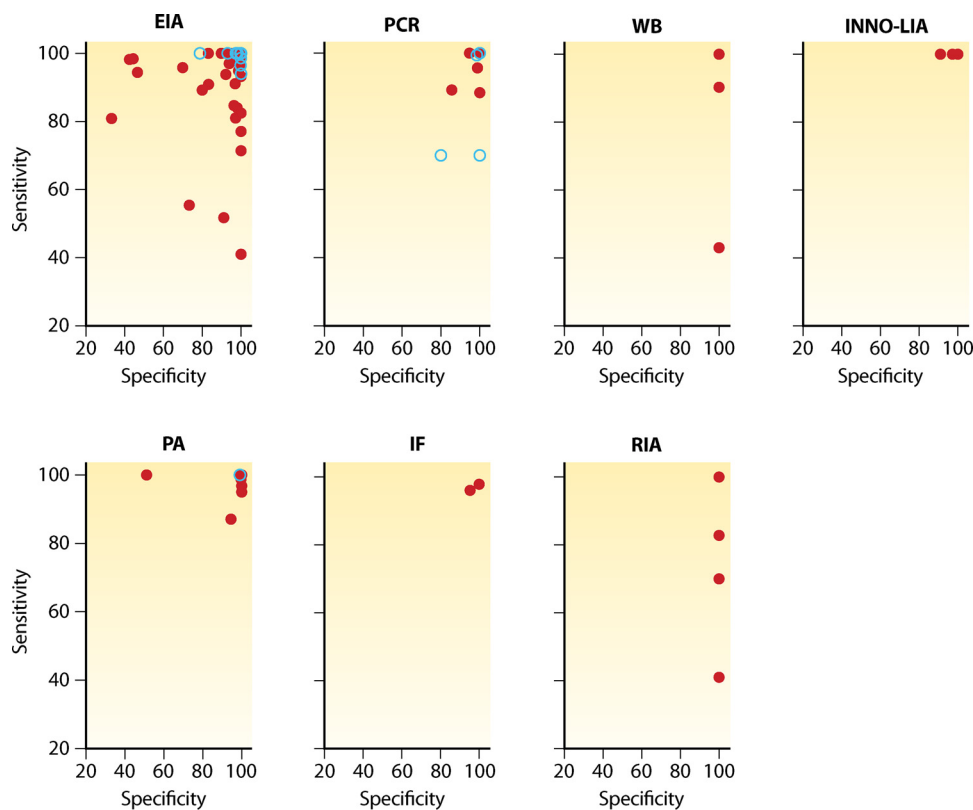
## HTLV-1 TESTING AND DIAGNOSIS

### HTLV-1 Serology

The formation of HTLV-1-specific antibodies is considered to only take place in people who have acquired chronic infection. After acquisition of infection, seroconversion may take 40 to 65 days. In early reports, there were even longer times to seroconversion, with periods of several years reported in infants (195, 196) and in people who were immunocompromised (197, 198), probably due to the past use of lower-sensitivity assays.

HTLV-1 structural proteins are the common targets for the serological tests. These include Gag proteins (capsid [p24], nucleocapsid [p15], and matrix [p19]) and Envelope glycoproteins (gp46 [or its precursor gp61/68], and gp21). One of the regulatory proteins, Tax, is a less frequently used target. While it has been suggested that variability is greatest in the antigenic profile of the Envelope gp46 protein across HTLV-1 subtypes (a to g) (199), there does not appear to be an association between HTLV-1 subtype and the sensitivity of current commercial serological tests (200). More recently, serological assays have used both gp46-I and gp46-II proteins to differentiate between HTLV-1 and HTLV-2 infection (201).

The most widely available serological tests are enzyme immunoassays (EIAs) (Table 1). Epidemiological surveys, and blood and transplant donor screening programs typically use EIAs because of their high sensitivity, simplicity, and throughput capacity. While first-generation EIAs had relatively low specificity, they have been improved with the addition of recombinant proteins, though specificity is still lower than the other serological assays, including Western blot and line immunoassays (INNO-LIA) (7, 202)



**FIG 4** Sensitivity and specificity of 165 HTLV-1 diagnostic assays. Data were extracted from 65 peer-reviewed publications. Gray dots indicate data extracted pre-2009 and black circles post-2009, highlighting improved sensitivity and specificity of more recent assays. EIA, enzyme immunoassay; IF, immunofluorescence assay; INNO-LIA, line immunoassay; PA, particle agglutination; RIA, radioimmunoassay; WB, Western blot.

(Fig. 4). False-positive results can occur as a result of cross-reactivity with antigens produced by other pathogens or autoantigens (203–205). Definitive diagnosis of HTLV-1 infection therefore requires confirmatory testing with either another serological assay or a molecular test.

The two main confirmatory serological tests are Western blotting, considered to be the “gold standard,” and INNO-LIA (201). The role of the Western blot as the gold standard, however, has been questioned with the arrival of molecular testing. Furthermore, its use has been hampered by the lack of a standard set of criteria for positivity and the consequent difficulties in interpreting results deemed “indeterminate” (61, 206). In the late 1980s, the U.S. Centers for Disease Control and Prevention (CDC) and the World Health Organization had similar definitions of Western blot positivity, requiring detection of anti-Gag (CDC, p24 only; WHO, p19 or p24) and anti-Envelope (CDC, gp46 or precursor gp61/68; WHO, gp46 and/or gp68) antibodies (207). In 1992, the CDC modified criteria to include reactivity to the anti-Gag (p24) and anti-Envelope (gp46) or the recombinant GD21 protein (a truncated recombinant portion of gp21) (208). In 1996, the HTLV European Research Network defined its own criteria which required the detection of at least one anti-Gag (p19 or p24) and two anti-Envelope (gp21 and gp46) antibodies, whether native or recombinant (209, 210). Based on these definitions, some samples considered positive according to WHO criteria would be classified as “indeterminate” based on CDC and European criteria. In addition to this complexity, commercial Western blot kits are also available with their own manufacturer-defined criteria for positivity.

Indeterminate Western blot results can pose a significant issue, particularly if other confirmatory assays are not available. The proportion of indeterminate Western blot results reported has ranged from 0 to 68%, with the highest proportion in studies from

Central Africa and Zaire (61, 206). A number of factors have been identified as associated with “false” positivity, including (i) cross-reactivity with structural proteins from other HTLV types (211, 212); (ii) cross-reactivity with *Plasmodium falciparum* proteins in particular gp21 (203–205), a particular issue in areas where HTLV-1 and malaria are co-endemic (61, 206); and (iii) nonspecific cross-reactivity with host or other pathogen proteins (213). Given the limitations of Western blotting, it has been proposed that line immunoassay or molecular tests be considered for routine use as confirmatory assays (214). For the line immunoassay, INNO-LIA (Fujirebo), positivity is defined by reactivity to p19, p24, gp46, and gp21.

### HTLV-1 Molecular Testing

Highly specific molecular diagnostic methods can detect HTLV-1 nucleic acid sequences by PCR in peripheral blood and tissue. Targeting the DNA provirus integrated into host cell genomes, this group of tests includes qualitative, quantitative real-time (Q) and droplet digital (dd) methods (215). Qualitative tests are often performed on whole blood or other tissues to confirm diagnosis.

Potential PCR targets include the *pol*, *env*, and *tax* regions. However, it is important to note that deletions in the HTLV-1 provirus can impact test sensitivity. While *pol* and *env* are prone to deletion (200, 216), pX (which includes *tax*) and 5'-LTR are highly conserved (215), suggesting that *tax* should be a focus for molecular diagnostic assays. Another factor which can affect the sensitivity of PCR testing is the proportion of potential target cells in a specimen with integrated HTLV-1 genomes. Another potential limitation for implementation of PCR testing, particularly in resource-limited settings, is the need to acquire and store cellular samples.

HTLV-1 proviral load can be quantified and is expressed as the number of HTLV-1 DNA copies detected per fixed number of peripheral blood mononuclear cells (PBMCs). It appears to remain relatively stable over time in an individual with HTLV-1 infection (usually <100 copies per 10,000 PBMCs [ $<1\%$ ] in asymptomatic infection) (217), as discussed in the transmission and health consequence sections of this review, is a strong predictor of both the risk of onward transmission and disease development (218–221). No HTLV-1 proviral load assay is produced commercially but would clearly be valuable in public health and clinical applications.

### HTLV-1 Testing and Diagnosis Algorithms

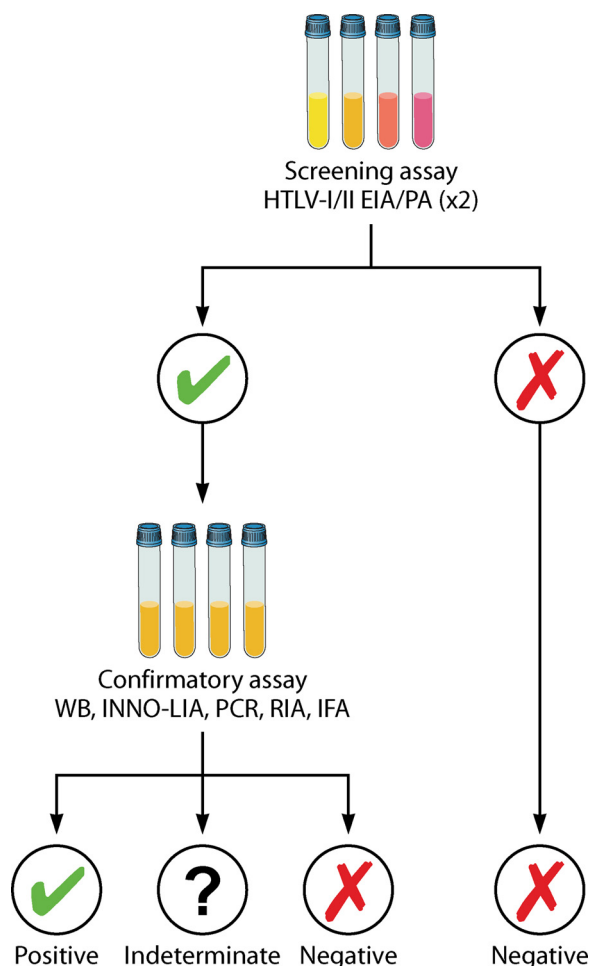
Current testing algorithms use a stepwise process to confirm HTLV infection, based on positive results on at least two different assays. A typical algorithm involves use of a sensitive serological test (usually an EIA) that, if positive will often be repeated, followed by a more specific confirmatory test (Western blot, INNO-LIA, or PCR) (Fig. 5). Most EIAs do not distinguish between HTLV types so the confirmatory tests are also important for this. In general, serum or plasma is used for immunoassays and PBMCs are used for PCR.

At the WHO global consultation on HTLV-1 held in 2019, an expert group recommended that appropriate testing strategies should be selected on the basis of context and setting. For instance, it may be acceptable in low-prevalence settings to use a testing strategy that can produce a quick result, even if it does not have optimal sensitivity in situations such as organ donation, where timeliness is critical. However, more labor-intensive confirmatory testing is essential for individuals with suspected HTLV-1-associated disease.

### Cost of Testing

Cost is a critical consideration when selecting the appropriate testing algorithm for large-scale, routine use (222, 223). In the context of serological screening of blood donors, Stigum et al. (224) calculated that at a prevalence of 1 in 100,000, the cost was \$9.2 million per life saved through screening or \$420,000 per quality adjusted life year (QALY). At a prevalence of 1 in 10,000, the cost was \$0.9 million per life saved and \$41,000 per QALY. In low-prevalence, high-income settings, measures have been taken





**FIG 5** HTLV-1 testing algorithm. Testing algorithms for HTLV-1 have generally required two or three assays. An EIA-based method is used for screening plasma or sera given high sensitivity, simplicity, and potential for high throughput. Positive samples are then retested, either with the same EIA or an alternative. Finally, repeatedly reactive plasma or serum samples are confirmed by another assay type, either Western blot, INNO-LIA, or PCR. EIA, enzyme immunoassay; IFA, immunofluorescence assay; IMMO-LIA, line immunoassay; PA, particle agglutination; RIA, radioimmunoassay; WB, Western blot.

to improve the cost-effectiveness, such as screening blood donors only at their first donation (e.g., Sweden) or using pooling of specimens (e.g., Wales and Scotland) (223).

**HTLV-1 Testing: Whom To Test and When?**

There are few published guidelines and strategies on who should be offered testing for HTLV-1 and when. Clinical recommendations are diverse and include testing pregnant women (i.e., Japan [225]), infants born to mother with HTLV-1 infection (i.e., Brazil [226, 227], Chile [228], and Japan [225]), sexual partners of people with HTLV-1 infection (i.e., Brazil [226, 227] and Chile [228]), people who inject drugs (i.e., Brazil [226, 227] and Chile [228]), people who engage in sex work (i.e., Brazil [226, 227] and Chile [228]), and people with occupational exposure to HTLV-1 infection (Australia [229]). There is little information on the implementation and uptake of these recommendations.

**HTLV-1 TRANSMISSION: ROUTES AND RISK FACTORS**

Transmission of HTLV-1 is generally understood to require direct contact between infected and uninfected cells in bodily fluid such as breastmilk, blood, and semen (230). From a public health perspective, the most important ways that transmission occurs are from mother to infant, via sexual contact, and through transfusion of cellular blood products (Table 2).

**TABLE 2** Routes and rates of HTLV-1 transmission

Transmission route (references)	Detail (references)	Reported rates (%)
Maternal exposure (56, 116, 136, 196, 232, 234, 235, 239, 241, 246, 247, 249, 250, 456–460)	Through breastfeeding; limited evidence of intrauterine or peri-partum transmission	3.2–46
Sexual intercourse (87, 102, 254–256, 258–262, 461)	More frequent from male-to-female than female-to-male (252–255)	2–65
Therapeutic use of blood products and organ transplant (266, 268, 269, 462)	Primarily via products containing cellular components (i.e., whole blood, red blood cells, platelets)	28–86
Other blood contact <sup>a</sup>	Blood contact through nonsterile skin penetrating procedures; reported examples include injection of illicit drugs (79, 463–465) and traditional religious self-flagellation practices (466, 467)	NA <sup>b</sup>

<sup>a</sup>Injecting using nonsterile equipment is considered very high risk, and other forms of blood contact are not well documented.

<sup>b</sup>NA, not applicable.

### Mother-to-Child Transmission

Evidence of vertical transmission emerged soon after the discovery of HTLV-1, with the detection of infected lymphocytes in the breast milk of mothers with HTLV-1, and high rates of infection in children born to mothers with HTLV-1 (231, 232). Transmission estimates have ranged from 3.2 to 46%, with an average around 20%.

HTLV-1 has been detected in several specimen types, including breast milk (231), peripheral blood, and cord blood samples (233), while proviral DNA has been detected in placental tissue and breast milk (234) but not in cord blood (196, 232, 235). These findings, as well as the very low prevalence of infection in formula fed children born to HTLV-1-positive mothers, indicate that transmission *in utero* or during delivery is rare (236, 237) and that the major risk to infants is from breastfeeding (237, 238).

Furthermore, multiple epidemiological studies have shown that duration of breastfeeding is a strong predictor of mother-to-child transmission of HTLV-1. Breastfeeding for more than 6 months leads to transmission rates exceeding 30% (239, 240), while shorter duration conveys a much lower rate (116, 239–244). There is also a strong association between maternal proviral load in peripheral blood and breast milk and the risk of mother-to-child transmission (234, 245–250).

### Sexual Transmission

HTLV-1 has been detected in both cervical secretions (237, 251) and seminal fluid (230), indicating the biological plausibility of sexual transmission. A wide range of transmission rates have been reported in epidemiological studies of heterosexual couples (Table 2). In general, male-to-female sexual transmission is more likely than from female to male, based on studies in which one member of a couple is positive and the other negative for HTLV-1 infection (252–255).

Several factors have been associated with an increased risk of heterosexual transmission of HTLV-1 (Table 3), including longer duration of a sexual relationship (253, 254) and older age of the male partner (253). A higher proviral load is a risk factor in both cross-sectional and longitudinal studies (253, 254, 256, 257). Cross-sectional surveys in populations considered to be at higher risk of acquiring sexually transmitted infections (102, 256, 258, 259), including sex workers, people attending STI clinics, and men who have sex with men), and investigations of sexual partners of people with HTLV-1 (253, 254, 257, 260) have identified a range of risk factors for sexual transmission. These include the number of sexual partners (261), a history of condomless sex (254), sex during menses, vaginal douching before and after sexual intercourse (102), earlier sexual debut (262), and other sexually transmitted infections, particularly ulcerative conditions such as syphilis or herpes simplex virus infection (102, 254, 258, 259, 261).

Such cross-sectional studies can generally not distinguish whether other sexually transmitted infections function as a cofactor facilitating the transmission of HTLV-1 or whether HTLV-1 and other sexually transmitted infections are driven by common causal factors related to sexual behaviors. It is also not clear whether the populations assessed as being at higher risk of sexually transmitted infection in fact had increased

**TABLE 3** Risk factors for HTLV-1 transmission

Transmission route	Risk factor (references)
Maternal exposure	Breastfeeding duration, particularly longer than 6 mo (116, 239–244) Higher maternal HTLV-1 proviral load (234, 245–247, 249, 250)
Sexual intercourse	Condomless sex (254) Earlier age at first sex (262) No. of partners (261) Current or past sexually transmissible infections (102, 254, 258, 259, 261, 468) <sup>a</sup> Sex during menses and vaginal douching pre- and postintercourse (102) Higher HTLV-1 proviral load (253, 254, 256, 257) Duration of sexual relationship (253, 254)
Therapeutic use of blood products	Shorter storage duration (266, 268, 269)

<sup>a</sup>It is difficult to distinguish sexually transmitted infections as a cofactor for HTLV-1 transmission from the alternative explanation that both HTLV-1 and other sexually transmitted infections are driven by sexual behavior as the common causal factor.

prevalence of HTLV-1 infection compared to the general populations in the settings from which they were drawn.

### HTLV-1 Transmission through Blood and Blood Products

Evidence of transmission via blood transfusion emerged in the 1980s, when it was found that HTLV-1 prevalence in people who had received transfusions of cellular blood products was substantially higher than those with no history of blood transfusion or transfusion with acellular blood products (Table 2). Specific populations at higher risk were people with conditions—including thalassemia, (HTLV-1 prevalence, 6%), sickle cell anemia (4%), renal dialysis (20%), and neonatal complications (2%)—requiring therapeutic blood product transfusion (263–265). Transfusion of whole blood from a donor with HTLV-1 infection carries a risk of transmission exceeding 80% (266). A similar high risk applies in cases of a solid organ transplant from a donor with HTLV-1 infection (267).

A shorter duration (<14 days) of storage of blood has been associated with increased risk of transmission, likely because of the reduced lymphocyte viability in older blood units (266, 268, 269) and use of immunosuppressive therapy by recipients of positive blood products (Table 3) (268).

### Other Routes of HTLV-1 Transmission

Investigations of household members have found higher than expected prevalence of HTLV-1 infection following a diagnosis in a household member but no evidence for routes of transmission other than those described above (270).

## HEALTH CONSEQUENCES OF HTLV-1 INFECTION

Most people with HTLV-1 infection do not appear to develop health conditions that can be directly linked to the infection. However, there is a subgroup of people who experience severe complications (Table 4). The most well recognized are adult T-cell leukemia-lymphoma (ATL) and HTLV-1-associated myelopathy/tropical spastic paraparesis (HAM/TSP), both of which can only be diagnosed in a person with HTLV-1 infection. Subsequently, HTLV-1-associated uveitis (HAU) and infective dermatitis were defined as disease entities that could only occur in a person with HTLV-1 infection.

Several other health conditions involving a range of organ systems, including lung disease and other infectious diseases, have also been assessed. A recent systematic review and meta-analysis of epidemiologic studies examined published associations between HTLV-1 infection and all-cause mortality, and a range of inflammatory, infective, and malignant conditions (271) (Table 4).

**TABLE 4** Diseases associated with HTLV-1 infection

Category	Disease	Lifetime risk <sup>a</sup>
Diseases for which HTLV-1 infection is required for diagnosis		
Cancer	Adult T-cell leukemia-lymphoma	5%
Inflammatory conditions	HTLV-1-associated myelopathy/tropical spastic paraparesis	2%
	HTLV-1-associated uveitis	<1%
	Infective dermatitis	Unknown
Diseases with epidemiological evidence of an association with HTLV-1 <sup>b</sup>		
Cancer	Lymphoma other than ATL	
Inflammatory conditions	HTLV-1-associated pulmonary disease (bronchiectasis, bronchitis, bronchiolitis)	
	Rheumatoid arthritis, Sjogren's syndrome	
	Seborrheic dermatitis (adults and children), eczema (children)	
Other infectious diseases	Tuberculosis	
	Disseminated strongyloidiasis and <i>Strongyloides</i> hyperinfection syndrome	
	Urinary tract infection	
	Dermatophyte infection	
	Community-acquired pneumonia	

<sup>a</sup>Lifetime risk among people with HTLV-1.

<sup>b</sup>Epidemiological evidence quality very limited to moderate. (Data from reference 271.)

### Adult T-Cell Leukemia-Lymphoma

In 1979, a novel virus (subsequently named HTLV-1) was isolated from a patient with a cutaneous T-cell malignancy in the United States (10), following initial reports of a similar clinical syndrome in Japan, which had been named ATL (9). The causal role of HTLV-1 in the pathogenesis of ATL was determined (2–5, 272–276), and HTLV-1 was declared carcinogenic to humans in 1996 by the International Agency for Research on Cancer (IARC) (277).

There are four recognized clinical subtypes of ATL: acute, lymphomatous, chronic, and smoldering (278–280) (Table 5). People with ATL may present with skin lesions (nodules, ulcers, and generalized papular rash), lytic bone lesions, lymphadenopathy, hepatosplenomegaly, hypercalcemia, and symptoms related to lung and other organ involvement. Lymphocytes with a characteristic appearance, referred to as “flower cells,” may be seen on blood film. Opportunistic infections may occur due to immunosuppression related to dysfunctional HTLV-1-infected T cells. Mortality is high for people diagnosed with aggressive forms of ATL (acute and lymphomatous), with a median survival less than 12 months (279, 280).

Knowledge of ATL occurrence, progression, and treatment largely come from Japan (280). In 2018, it was estimated by IARC that there were 3,600 cases of ATL worldwide, approximately one-third in Japan, which also had the highest reported incidence (281) (Fig. 6). Given underdiagnosis and underreporting of HTLV-1 and ATL in many parts of the world, the estimated global burden of ATL was likely to be very conservative. Of countries with cancer registries, few have coding systems that allow the routine analysis of ATL as a distinct entity.

While ATL incidence generally increases with age (Fig. 7), age at diagnosis is markedly higher in Japan (median, 68 years; range, 34 to 100 years) (280) in comparison with Brazil (mean age, 44 years; range, 13 to 78 years) (282), and Jamaica (mean age, 43 years; range, 17 to 85 years) (283). Similarly, in a U.S. series, the median age at ATL diagnosis was 50 years (range, 22 to 82 years), with most cases (93%; 83/89) among immigrants to the United States from the Caribbean, Latin America, or Africa (284). In the 2018 IARC analysis, little difference was seen when stratified by gender, in contrast to previous cohort and population-based surveillance studies in which incidence was higher among men than women (Fig. 7) (285–288).

The estimated lifetime risk of ATL among people with HTLV-1 infection is approximately 5% (276, 285–289). The incidence of ATL among people with HTLV-1 has

**TABLE 5** Diagnostic criteria and classification of clinical subtypes of ATL

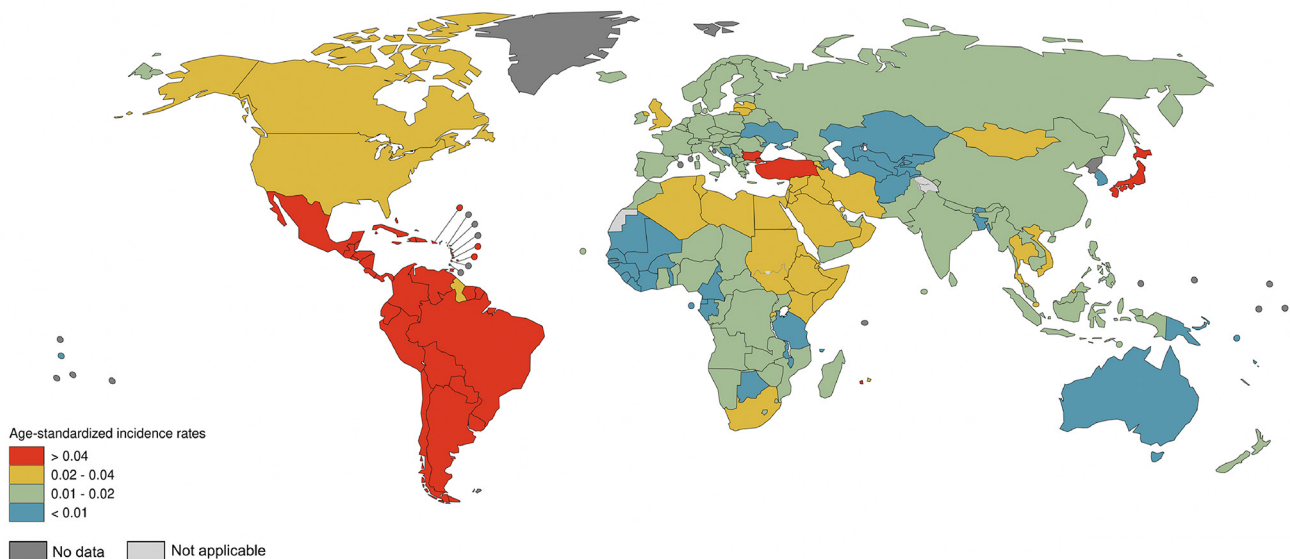
Criterion or classification	Diagnosis <sup>a</sup>			
	Acute	Lymphomatous	Chronic	Smoldering
Diagnostic criteria				
Anti-HTLV-1 antibody	Yes	Yes	Yes	Yes
Lymphocyte count ( $\times 10^9/L$ )	Any (often $\uparrow\uparrow\uparrow$ )	$<4$	$\geq 4$	$<4$
Abnormal T lymphocytes	Yes*	$\leq 1\%$	Yes*	$\geq 5\%$
Flower cells	Yes	No	Occasional	Occasional
Lactate dehydrogenase	Any (often $\uparrow$ )	Any	$1.5\times-2\times$ ULN	$<1.5$ ULN
Hypercalcaemia	Possible	Possible	No	No
Lymphadenopathy	Possible	Yes	Possible	No
Involvement of:				
Skin	Possible	Possible	Possible	Possible
Lung	Possible	Possible	Possible	Possible
Lymph node	Possible	Yes	Possible	No
Liver	Possible	Possible	Possible	No
Spleen	Possible	Possible	Possible	No
Central nervous system	Possible	Possible	No	No
Bone	Possible	Possible	No	No
Gastrointestinal tract	Possible	Possible	No	No
Clinical presentation:				
Ascites	Possible	Possible	No	No
Pleural effusion	Possible	Possible	No	No
Disease burden <sup>b</sup>				
Proportion (%) of ATL cases	50	26	13	11
Median survival (mo)	8.3	10.6	31.5	55.0

<sup>a</sup>\*, For diagnosis of acute or chronic ATL: abnormal T lymphocytes  $\geq 5\%$  in peripheral blood or histology-proven tumor + abnormal T lymphocytes  $< 5\%$  in peripheral blood.

<sup>b</sup>Based on data from people with ATL in Japan from 2000 to 2011. (Data from references 278, 279, and 280.)

ranged from 0.5 to 7.1 per 1,000 person-years in Japan (272–276, 290), and although data are limited, ATL incidence in regions outside Japan appears to be within a similar broad range (291–293).

Factors associated with diagnosis of ATL include older age, younger age at HTLV-1 infection, duration of HTLV-1 infection ( $>20$  years), family history of ATL, and higher HTLV-1 proviral load (276, 281, 285, 287–291, 294–299). Among cohort studies of



**FIG 6** Age-standardized incidence rates of ATL worldwide per 100,000 population. Age-standardized incidence rates are reported for the general population and are not specific for people with HTLV-1 infection. (Adapted from references 7 and 281.)



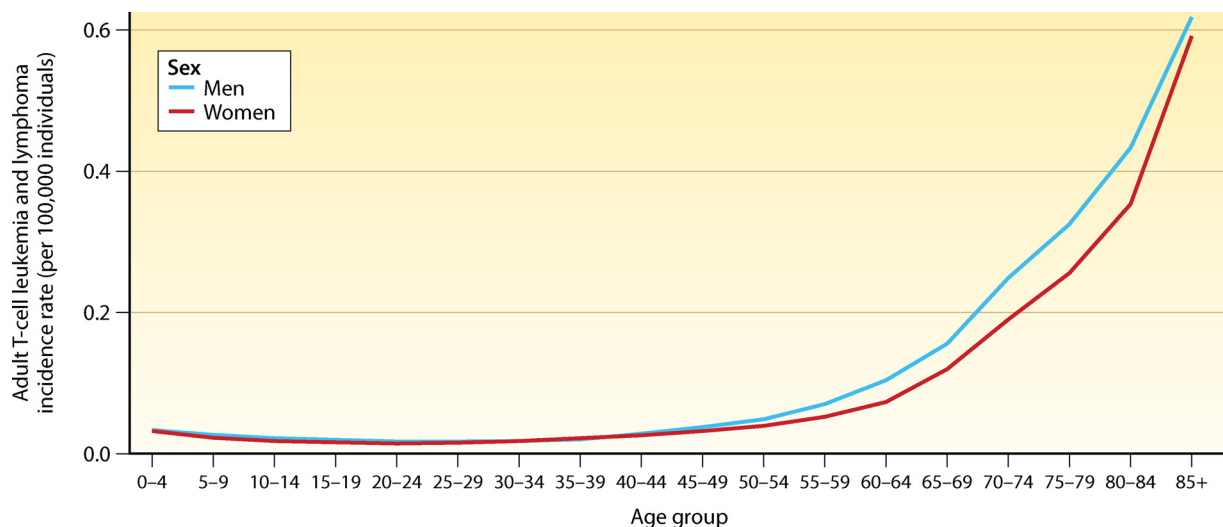


FIG 7 ATL incidence by age and sex in 2018. (Adapted from references 7 and 281.)

people with HTLV-1 infection, no cases of ATL have been diagnosed in those with a baseline proviral load of fewer than 400 copies per 10,000 PBMCs (276, 291). In addition, cross-sectional and case-control studies have suggested that HLA type, HTLV-1 antibody titer, soluble interleukin-2 receptor (sIL2R) level, and *Strongyloides stercoralis* coinfection may be associated with ATL (276, 291, 295–299). sIL2R and HTLV-1 antibody titer are correlated with HTLV-1 proviral load, while *Strongyloides stercoralis* coinfection has been associated with higher HTLV-1 proviral load and oligoclonal expansion of infected T cells (298), which may shorten the time between HTLV-1 infection and ATL development.

### HTLV-1-Associated Myelopathy/Tropical Spastic Paraparesis

HAM/TSP is a chronic inflammatory disease of the central nervous system, characterized by progressive spastic weakness of the lower limbs, lower back pain, and bowel and bladder dysfunction (300, 301). An association between HTLV-1 and a chronic progressive myelopathy of previously unknown etiology, “tropical spastic paraparesis” (TSP) (6, 302, 303), was noted in 1985, followed by the description of a comparable syndrome, “HTLV-1-associated myelopathy” (HAM), in Japan in 1986 (304). Recognizing that these were the same clinical entity, the WHO proposed standardized diagnostic criteria for HAM/TSP in 1988 (301). Detection of HTLV-1 in blood or cerebrospinal fluid (CSF) by serological or molecular methods is required to make the diagnosis. The defining pathological features of HAM/TSP are an inflammatory phase involving perivascular lymphocytic infiltration of the spinal cord (with relative sparing of the posterior columns), followed by scarring, atrophy, and neurodegeneration (193).

HAM/TSP should be considered in people with HTLV-1 who present with gait abnormalities, lumbar pain, and bladder, bowel, or sexual dysfunction. Specific neurological manifestations of HAM/TSP include a spastic gait, lower limb weakness, hyperreflexia, and clonus, as well as an extensor plantar response. Weakness of the lower limbs tends to be more marked proximally. Bowel and bladder symptoms (urinary incontinence or retention [early feature], constipation [usually a late feature]), and sexual dysfunction (impotence or decreased libido) are common. Sensory symptoms (including paraesthesia) may be present, and vibration sense impaired, but there should not be a discrete sensory level. Onset of HAM/TSP symptomatology is usually insidious but may be sudden. While symptoms are typically slowly progressive, a spectrum exists, from static to rapidly progressive. Findings on examination of CSF in support of a diagnosis of HAM/TSP may include a mild pleocytosis, a mild to moderate increase in protein concentration, and positive antibody and/or molecular tests for HTLV-1. Notably, a definite diagnosis of HAM/TSP may be difficult, particularly in settings with limited health care.

The cumulative lifetime risk of HAM/TSP among people with HTLV-1 infection has been estimated to be approximately 2%, with higher risk in women than men (305–307). However, there are contrasting geographic findings, with different methods of cohort recruitment and case finding, probable underdiagnosis, and wide confidence intervals (CIs) signaling uncertainty in the reported estimates. In a Caribbean study based on registry data, the estimated lifetime risk was 1.7% (1.3% in men and 1.8% in women) (306), whereas in a Japanese study based on passive case reporting, the estimated lifetime risk was 0.23% in those who had acquired infection in infancy (0.18% in men and 0.26% in woman), with even lower estimates among those infected at an older age (305). In two cohorts among people with HTLV-1, HAM/TSP incidence was 5.3 per 1,000 person-years (95% CI = 0.3 to 10.9) in Brazil (308) and 1.8 per 1,000 person-years (95% CI = 0.2 to 6.7) in the United States (307).

A higher HTLV-1 proviral load has been associated with the development (305–307, 309–314) and progression (315) of HAM/TSP. In a cohort study conducted in Martinique, higher HTLV-1 proviral load (>1,000 per 10,000 PBMCs) was associated with shorter time from HAM/TSP onset to being wheelchair dependent (315). Other factors that influence HTLV-1 proviral load, including HTLV-1-specific cytotoxic T-cell responses (316) and HLA type (314, 317), also appear to moderate the risk of HAM/TSP.

Older age (315) and markers of CSF inflammation (318, 319) have also been associated with progression. Markers of CSF inflammation, namely, CXCL10 and neopterin, may be useful for documenting disease activity, the risk of neurological disease progression, and potentially the response to treatment (318, 319).

HAM/TSP can result in substantial disability and reduced quality of life. The mental health and social impact of HAM/TSP appear to be considerable (320) but have not been systematically evaluated. Unlike ATL, HAM/TSP is not life-threatening, but like many severe progressive neurological conditions it may indirectly contribute to reduced life expectancy, particularly in resource-limited settings (315).

Other forms of neurological disease, which do not fulfil diagnostic criteria for HAM, may be underrecognized among adults and children with HTLV-1 infection (321–323). A spectrum of predominantly urinary and motor abnormalities without overt myelopathy (including leg weakness, impaired gait, hyperreflexia, impaired vibration sense, and neurogenic bladder) have been reported and appear to occur more frequently among people with HTLV-1 compared to those who are uninfected (175, 321, 322), although there has been a marked variation in frequency across study cohorts (5 to 50%) (175, 321, 322). Case reports suggest that such presentations can be precursors of HAM/TSP, but they may also remain as isolated syndromes.

### **HTLV-1-Associated Uveitis**

In 1989, an association between HTLV-1 infection and eye disease was suggested, with initial case reports stemming from a region of HTLV-1 endemicity in southern Japan (324). HTLV-1-associated uveitis (HAU) was subsequently recognized as a specific syndrome following clinical, epidemiological, and laboratory investigation (325–330). Ocular pathogenesis appears to be related to lymphocyte-driven inflammation mediated by HTLV-1-infected CD4<sup>+</sup> T cells (328, 329).

HAU should be considered in people with HTLV-1 who present with uveitis, particularly “intermediate uveitis” (localized to the vitreous and peripheral retina), after other etiologies have been excluded. HAU may occur in adults and children, is more likely in women, and can involve one or both eyes. Blurred vision and “floaters” are common presenting symptoms. Many cases involve a single episode of mild to moderate uveitis with spontaneous or corticosteroid-induced (topical or systemic) resolution in weeks. Recurrence and even sight-threatening complications are uncommon but can include retinochoroidal degeneration, glaucoma, and corticosteroid-induced cataracts (331–333).

Based on limited data, HAU appears to occur in less than 1% of people with HTLV-1 infection (334, 335). It can occur as an isolated condition or in association with other HTLV-1-related diseases, including ATL and HAM/TSP, which may precede or follow it (331–333). In the Japanese HAM-net cohort, the incidence of uveitis among people

**BOX 1 Diagnostic criteria for infective dermatitis**

- **Erythematous, scaly, exudative, and crusted lesions on scalp, retroauricular areas, neck, axillae, groin, paranasal and perioral skin, ears, chest or abdomen, with at least 3 involved sites.**
- Crusting around the nostrils.
- **Chronic relapsing** clinical course with **prompt response to antibiotics but recurrence on discontinuation.**
- Diagnosis of **HTLV-1 infection** (by serology or molecular testing).

*Note: Items indicated in boldface are mandatory for diagnosis. Data from references 339 and 340.*

with HAM/TSP was 6.5 (95% CI = 3.3 to 12.7) per 1,000 person-years (335). As with ATL and HAM/TSP, HAU appears to be associated with higher HTLV-1 proviral load (336).

**Infective Dermatitis**

Infective dermatitis was the first, and so far only, pediatric syndrome to be linked to HTLV-1 infection (337). In 1966, a severe exudative eczema was described in Jamaican children and labeled “infective dermatitis” (338). An association with HTLV-1 was suggested decades later (337, 339) and led to the publication of diagnostic criteria for a specific HTLV-1 syndrome in 1998 (339), with revisions suggested in 2012 (340). Despite being initially described in children, cases have subsequently been diagnosed in adults. Similar to HAM/TSP and HAU, the pathophysiology of infective dermatitis appears to be characterized by an exacerbated Th1 immune response (341).

Essential clinical features include chronic relapsing dermatitis, generally involving the scalp and retroauricular skin, with prompt response to antibiotic treatment, and recurrence on discontinuation (see Box 1). In a case-control study comparing the clinical, pathological, and immunological features of infective dermatitis ( $n = 50$ ) and atopic dermatitis ( $n = 35$ ), all (100%) people with infective dermatitis had antibodies to HTLV-1 compared to 14% of those with atopic dermatitis (339). Other features were similar between groups, with frequent growth of *Staphylococcus aureus* and beta-hemolytic streptococci from involved skin and no distinguishing skin biopsy findings. As such, clinical assessment and diagnosis of HTLV-1 infection are required to differentiate infective dermatitis from other skin conditions, including atopic and seborrheic dermatitis (342).

Minimal data exist on the incidence and burden of infective dermatitis or on factors that predict occurrence among children with HTLV-1. In one study from Jamaica, the risk of infective dermatitis was 2% by age 4 (343). Infective dermatitis has been associated with higher HTLV-1 proviral load (341) and diagnosis of ATL and HAM/TSP later in life (340, 341, 344–350). In a case series from Brazil ( $n = 42$ ), 20 (48%) people with infective dermatitis were diagnosed with HAM/TSP as a child or adolescent and one with ATL as an adult (340, 351).

As with other diseases linked to HTLV-1, there is marked geographic variation in reporting. Whereas case series of infectious dermatitis have been published from Africa (342, 352), the Caribbean (338), and South America (340, 351), few cases have been reported in Japan. The reasons for this apparent regional difference are unclear, but lack of recognition and diagnosis may be an issue.

**HTLV-1-Associated Pulmonary Disease**

HTLV-1 infection has been associated with spectrum of chronic lung disease, including bronchiectasis, bronchitis, and bronchiolitis, across varied populations, geographic regions, and HTLV-1 subtypes (271). Lung disease among people with HTLV-1 infection was first reported in 1987, with lymphocytic alveolitis diagnosed in five people with

HAM/TSP in Japan (353). Subsequently, radiological assessment of people with HTLV-1a infection in Japan demonstrated a variety of abnormalities, with the most frequent being features consistent with bronchiolitis, bronchiectasis, and interstitial pneumonia (354, 355). Correlation of radiological and histological features on lung biopsy was also noted, with lymphocyte infiltration along bronchioles and into bronchovascular bundles and the interstitium (355).

Over the last decade, clinical research among Aboriginal people in central Australia has shown that HTLV-1 was associated with radiologically confirmed bronchiectasis, bronchitis, and bronchiolitis in community and hospital-based cohorts (175, 356, 357). Notably, higher HTLV-1 proviral load was associated with diagnosis of bronchiectasis (175) and death due to bronchiectasis (356) in this population. The prevalence of bronchiectasis has been found to be substantially higher among a clinic-based cohort of people with HTLV-1 infection (3.4%) in the United Kingdom compared to the general population (0.1%) (358). The proposed pathophysiology of lung disease in HTLV-1 infection has been likened to that of HAM/TSP, driven by a chronic inflammatory process involving the lungs (359).

Considering evolving evidence, diagnostic criteria for a new entity, HTLV-1-associated pulmonary disease, have been proposed (359), including HTLV-1 infection, along with radiological evidence of bronchiolitis, bronchiectasis, or interstitial pneumonia, and exclusion of other causes of lung disease. Other criteria could include an HTLV-1 proviral load greater than 1,000 copies per 10,000 mononuclear cells in induced sputum or bronchoalveolar lavage fluid and peribronchiolar or interstitial lymphocyte infiltrate on lung biopsy. While these require validation, the framework would support further work in the area, particularly if considering evaluating potential pharmacological and non-pharmacological interventions. For broad clinical use, “definite” and “probable” categories may be required in the proposed diagnostic criteria, with use of high-resolution CT imaging, bronchoscopy, and quantitative HTLV-1 PCR included as supplementary rather than obligatory, since they may not be feasible in many regions where HTLV-1 is endemic.

### **Tuberculosis**

Several studies have reported associations between HTLV-1 and tuberculosis (360–366). The one cohort study reported a relative risk of incident tuberculosis of 2.30 (95% CI = 1.60 to 4.10) among people with HTLV-1 (360), and a meta-analysis found a pooled odds ratio of 2.25 for the association (95% CI = 1.48 to 3.43) (271).

### ***Strongyloides stercoralis* Infection**

Regions of endemicity overlap for HTLV-1 and *Strongyloides stercoralis*, with the natural history of each apparently modified by coinfection with the other (367). *Strongyloides stercoralis* infection is associated with higher proviral load in people with HTLV-1 and is a predictor of subsequent ATL (298). Conversely, strongyloidiasis in people with HTLV-1 is associated with a higher parasite burden and greater risk of dissemination and hyperinfection syndrome than in people who do not have HTLV-1 (368). Given the importance of a robust Th2 response in dealing with parasitic infections, the hyperinfection syndrome among people with HTLV-1 appears to be mediated by an aberrant response with an increase in regulatory T cells, decreased production of IL-5, and a reduced eosinophil number, with resultant downregulation of the host defense against the parasite (369).

*Strongyloides* screening is routine in some centers caring for people with HTLV-1 infection. Limitations to accurate diagnosis of strongyloidiasis include low sensitivity of stool microscopy, variable specificity of serology, and limited access in endemic settings to molecular testing, now considered to be the most reliable method. Conflicting findings on the association between HTLV-1 and uncomplicated strongyloidiasis may be due to differing diagnostic methods (175, 370).

Effectiveness of standard treatment for *S. stercoralis* infection may also be reduced in the presence of HTLV-1 infection. A systematic review and meta-analysis favored

ivermectin over albendazole for efficacy and over thiabendazole for safety (371). The study populations included people with and without HTLV-1 but did not draw separate conclusions. Published evidence and clinical experience support the use of ivermectin at 200  $\mu\text{g}/\text{kg}$  with the duration depending on the severity of the strongyloidiasis presentation among people with HTLV-1.

### **HTLV-1 Infection and All-Cause Mortality**

HTLV-1 infection has been associated with a 60% increased risk of death from any cause, based on a meta-analysis of eight longitudinal studies (271). Consistency of the finding was high across geographic areas (273, 274, 372–378). Despite its lethality, ATL cannot account for this substantial increase in risk of death among people with HTLV-1 infection, nor can any other disease or combination of diseases. The spectrum of pathology associated with HTLV-1 may be broader than generally recognized. Relatively few studies have investigated the role of HTLV-1 proviral load as a predictor of disease progression and mortality. Proviral load and HTLV-1 antibody titer (which is correlated with proviral load [379]) predicted mortality in African (374) and Japanese (273) studies, respectively.

## **MANAGEMENT OF HTLV-1 INFECTION AND HTLV-1-ASSOCIATED DISEASE**

### **Asymptomatic HTLV-1 Infection**

There is no direct evidence that screening asymptomatic people for HTLV-1 infection can affect the outcome of their infection, and there is no intervention known to prevent the development of HTLV-1-associated disease. Nevertheless, there will be people who for various reasons, such as blood donation or contact tracing, are diagnosed with HTLV-1 infection in the absence of symptoms, so it is reasonable to consider what additional investigation and management might be of value.

Management may include periodic clinical and laboratory assessment to (i) monitor for development of ATL, HAM/TSP, and other diseases known to be associated with HTLV-1; (ii) screen for relevant comorbidities and coinfection such as *Strongyloides stercoralis* and tuberculosis; and (iii) assess the risk of other infections known to be transmitted by the same pathways as HTLV-1, including HIV, HBV, HCV, syphilis, *Chlamydia trachomatis*, and *Neisseria gonorrhoea*, depending on local epidemiology and transmission risk (see Box 2). Education and counselling may reduce the risk of onward transmission and could include information regarding modes and efficiency of transmission, prevention, disease associations, and the probability of developing diseases due to HTLV-1. People diagnosed with HTLV-1 infection should be made aware that infection is lifelong and that they should not donate blood or other tissue. HTLV-1 proviral load is the only known prognostic indicator and may help in assessing risk of HTLV-1-associated disease and transmission, but the test is largely unavailable for routine clinical use outside a few high-income settings.

### **Adult T-Cell Leukemia/Lymphoma**

There is substantial variation across ATL subtypes regarding short-term prognosis and management, with the aggressive subtypes (acute and lymphomatous) having the worst prognosis. Other negative prognostic factors include poor ECOG (Eastern Cooperative Oncology Group) performance status at diagnosis, age over 40 years, extensive disease, hypercalcemia, a high serum lactate dehydrogenase, and relapsed or refractory disease of any subtype (380). However, regardless of subtype and despite therapeutic advances, overall long-term survival for people diagnosed with ATL remains poor.

International recommendations for the management of ATL were first published in 2009 (380) and then updated in 2019 (381). Depending on subtype and treatment history, management options could include interferon-based antiviral therapy (382–386), chemotherapy (387–396), biologic agents (397–400), and hematopoietic stem cell transplantation (401–408). Management strategies are also dictated by local availability of specific agents and therapeutic modalities. As first-line therapy, guidelines state that



## BOX 2 Assessment of people diagnosed with HTLV-1 infection

### Initial assessment\*

History and examination

History: Address patient concerns about the infection; identify household and sexual contacts who might require further testing; assess risk factors for acquisition; assess host factors that may be associated with an increased risk of HTLV-1-associated disease.

Examination: Including assessment of gait and skin.

Full blood count (including differential) and blood film.

Electrolytes urea and creatinine.

HTLV-1 proviral load (if available).

*\*Consider screening for relevant coinfection, including Strongyloides stercoralis, tuberculosis, HIV, HBV, and HCV. Consider screening for other sexually transmitted infections, including syphilis, Chlamydia trachomatis, and Neisseria gonorrhoea.*

### Follow-up assessment†

History and examination

Full blood count (including differential) and blood film

Electrolytes urea and creatinine

*†Consider yearly follow-up for people with asymptomatic HTLV-1 infection. Timing of follow-up assessment is based on expert opinion. More frequent review may be clinically indicated.*

*Note: Clinical recommendations are based on the expert opinion and publications from the UK (NHS) and Australia (ASHM): <https://www.england.nhs.uk/wp-content/uploads/2013/06/b07-human-t-cell-lympho.pdf> and <https://hivmanagement.ashm.org.au/human-t-cell-leukemia-virus-coinfection/>.*

interferon alpha and zidovudine should be considered for people with symptomatic smoldering ATL, favorable or unfavorable chronic ATL, and acute ATL, while intensive multi-agent chemotherapy be considered for people with lymphoma-type ATL (381). More recent attention has focused on the use of biological agents, with or without chemotherapy (397–400). Mogamulizumab, a first-in-class humanized anti-CCR4 monoclonal antibody, has been evaluated in patients that are CCR4<sup>+</sup> chemotherapy naive (398) or who have relapsed or refractory ATL (397, 399), with subsequent regulatory approval in multiple jurisdictions. While allogeneic hematopoietic stem cell transplantation can improve survival in aggressive ATL (406), most patients are ineligible due to age, the availability of a stem cell source, and the lack of an adequate response to primary therapy.

### HTLV-1-Associated Myelopathy

No curative treatment for HAM/TSP is available. Options for management include medications aimed at altering the disease course (“disease-modifying therapy”) or relieving symptoms. The International Retrovirology Association published consensus guidelines for the management of HAM/TSP in 2020, with a focus on agents that may be disease modifying (409). Due to a dearth of published evidence, most recommendations in the guidelines are based on expert opinion (409).

Corticosteroids (including pulsed methylprednisolone for induction and oral prednisolone for maintenance) have been the mainstay of disease-modifying therapy. Pilot trials and cohort studies suggest that any benefit is transient and limited to improvements in pain and spasticity (410–414). Retrospective observational studies have been cited in support of oral prednisolone (410, 413–415). In one of these studies, which compared people with HAM/TSP who were ( $n = 57$ ) and who were not ( $n = 29$ ) treated with low-dose oral prednisolone (mean follow-up, 3.4 years), the overall annual mean change in Osame motor disability score

(OMDS [a higher score means greater disability]) was  $-0.13$  in the corticosteroid group and  $+0.12$  in the untreated group (415). The HAMLET-P randomized controlled trial comparing prednisolone with placebo among people with HAM/TSP is in progress (416).

As with ATL, biological agents have been used in HAM/TSP. In an uncontrolled phase I/IIa trial ( $n = 21$ ), the safety and efficacy of mogamulizumab was assessed among people with glucocorticoid-refractory HAM/TSP (417). In the phase I study, dose-dependent declines in CCR4<sup>+</sup> T cells, HTLV-1 proviral load, and CSF inflammatory markers (CXCL10, neopterin) were seen. In the phase IIa extension ( $n = 19$ ), both HTLV-1 proviral load and CSF neopterin concentration had fallen by nearly 50% at week 24, and clinical measures improved, particularly in those with shorter duration of disease (<10 years) and mild disability (OMDS <5).

Given the low incidence of HAM/TSP and much of its occurrence being in resource-limited settings, there are substantial challenges in developing a robust evidence base to standardize clinical trial assessment and reporting, and guide management. The International Retrovirology Association has recommended that management of people with HAM/TSP be guided by speed of disease progression (409), highlighting the varied natural history of HAM/TSP. Given the uncertainties about treatment options, all patients with HAM/TSP should be considered for enrollment in a clinical trial, if available, regardless of severity and duration of disease.

#### EPIDEMIOLOGICAL AND CLINICAL COMPARISON OF HTLV-1 AND HTLV-2

Both HTLV-1 and HTLV-2 are retroviruses that integrate into T lymphocytes and cause lifelong infection. They share the same routes of transmission and increasing prevalence with age and have geographic distributions that are at once dispersed and focal, with some overlap. However, they differ in some key epidemiologic and clinical respects. HTLV-2 is endemic among a large number of Indigenous populations in North America and South America, and unlike HTLV-1, is prevalent in urban areas among people who inject drugs, with high prevalence detected in this population in several European, South-East Asian, and North American cities (418–422). High prevalence in people who inject drugs is likely the result of direct blood-to-blood contact via reuse of syringes and needles. It remains unclear why HTLV-1 is not also found at high prevalence among these populations despite common modes of transmission (423).

Unlike HTLV-1, HTLV-2 has not been shown to cause malignancy, but myelopathy and other neurological manifestations can occur, albeit less frequently than with HTLV-1 (1% versus 4% in a prospective cohort) (307, 321). The natural history of myelopathy may also differ, with HTLV-2 cases presenting with more mild, slowly progressive signs and symptoms (307). As with HTLV-1, a range of neurological symptoms related predominantly to lower limb motor and bladder function are more common among people with HTLV-2 than in the general population (321). HTLV-2 infection has been associated with an increase in all-cause mortality (373) and additional under-recognized health consequences (424), though the evidence is more limited than for HTLV-1 and is largely drawn from a blood donor cohort in the United States. There is limited evidence to support an association between HTLV-2 infection and acute bronchitis (425), and there are insufficient data to comment on an association with chronic lung disease (426).

#### PREVENTION OF HTLV-1 TRANSMISSION

At the WHO Global Consultation in 2019, a key recommendation was that policies for prevention of sexually transmitted infection and blood borne viral infections be adapted to incorporate HTLV-1. This recommendation effectively echoed the first WHO statement on HTLV-1 prevention in 1992, (427), which proposed consideration of HTLV-1 preventive measures related to breastfeeding, injecting drug use, and sex.

Evidence for HTLV-1 prevention measures comes principally from observational studies originally conducted to investigate specific transmission pathways. There has been very little prospective evaluation of preventive interventions at the population level. Development of a vaccine would be ideal and is considered biologically feasible given

low antigenic variability. HTLV-1 proteins have been tested as vaccine immunogens, but preclinical evaluation is hampered by the selection of a representative animal model (428–432). No candidate vaccine has progressed to late-stage clinical trials (432).

Japan is the only country to have implemented a national policy on HTLV-1 prevention. Other countries have a policy on one or more of the interventions aimed at preventing maternal HTLV-1 transmission and transmission through donated blood or tissue. Many countries have policies related to preventing sexually transmitted and blood-borne infections that contain elements likely to reduce the risk of transmitting or acquiring HTLV-1 infection. Specifically, condom use is likely to reduce sexual transmission risk, and the use of sterile injecting equipment is likely to reduce the likelihood of transmission related to injected-drug use. There do not appear to be any policies or guidelines specifically aimed at the prevention of HTLV-1 infection through sexual exposure or injecting drug use.

### Preventing Mother-to-Child Transmission

**Duration of breast feeding.** Several investigations have demonstrated that shortening the duration of breastfeeding or eliminating it altogether substantially lowered the risk of mother-to-child transmission of HTLV-1 infection. These studies, predominantly from Japan, include a 20-year evaluation showing that the prevalence of HTLV-1 infection among formula-fed children was significantly lower than that in breastfed children (244) (Table 6). Among breastfed children, the prevalence was much lower among children who fed for less than 6 months than among those fed longer ( $\geq 6$  months). These results conclusively confirmed findings from earlier evaluations (235, 240, 241, 243, 433).

Any consideration of reduced duration of breastfeeding must take into account the numerous benefits of breastfeeding to both the infant and the mother (434). The balance must be weighed particularly carefully in contexts where safe alternatives to breastfeeding are not readily available, even in settings of high HTLV-1 prevalence.

**Freeze-thaw method.** Freezing and thawing breastmilk disrupts the morphology of and results in a loss of function of cells contained in breastmilk, and has been demonstrated to impair the viability and infectivity of HTLV-1 antigen positive cells (435). Once thawed, the risk of HTLV-1 transmission from the breastmilk of seropositive mothers is substantially reduced. In a 12-month follow-up of 13 infants given exclusively frozen-thawed breast milk, none acquired HTLV-1 infection (436). This method relies on individual access to a high level of technology so not be feasible in low-resource settings.

**Policies and guidelines: prevention of mother-to-child transmission.** Policies aimed at the prevention of mother-to-child HTLV-1 transmission involve screening women for HTLV-1 during pregnancy and then recommending a shortened duration of breastfeeding—or its avoidance altogether—in those found to have HTLV-1 infection. Japan is the only country that has implemented a nationwide program based on these principles (244, 437). All women are offered HTLV-1 testing in pregnancy, and those found to have infection are encouraged and supported to either formula feed their newborn, breastfeed for a shorter term (up to 3 months), or feed with thawed frozen milk.

National or local policies relevant to prevention of mother-to-child transmission have also been developed or are in development in other countries, including Australia, Brazil, Chile, France, and the United Kingdom (228, 438–440). Policies and recommendations differ, tailored to local epidemiology and infrastructure. Antenatal HTLV-1 screening is recommended in some regions of Brazil (438, 441). In France, screening is recommended for pregnant women and milk donors born in endemic regions (the Caribbean, Africa, Japan, South-East Asia), while the United Kingdom recommends screening of all breast milk donations. Universal antenatal screening has not been recommended outside Japan, and all available policies state that decisions regarding breastfeeding are in the hands of individual women, who should be provided with information tailored to local circumstances, including socioeconomic factors and health infrastructure at a community level and, at the individual level, HTLV-1-associated conditions, and HTLV-1 proviral load if available).

**TABLE 6** Prevalence of HTLV-1 among children born to women with HTLV-1 infection, by feeding method

Study	Country of research	Study design	Child age at survey (yrs)	No./total no. (%)		
				Breast fed	Formula fed	OR (95% CI)
Ando et al., 1989 (433)	Japan	Prospective cohort	2	24/31 (77.4)	1/30 (3.3)	4.3 (1.6–11.2)
Tsuji et al., 1990 (235)	Japan	Retrospective cohort	1–13	17/44 (39)	0/10 (0)	Unable to calculate
Takahashi et al., 1991 (241)	Japan	Retrospective and prospective cohort	1–25	24/229 (10.0)	9/158 (5.7)	2.0 (0.9–5.1)
Hirata et al., 1992 (240)	Japan	Retrospective and prospective cohort	0–19 (mean, 5.5)	18/97 (18.6)	10/78 (12.8)	1.5 (0.6–4.0)
Takezaki et al., 1997 (243)	Japan	Prospective cohort	0–3	15/115 (13.0)	4/162 (2.5)	5.9 (1.8–25.1)
Hino et al., 2011 (244)	Japan	Retrospective and prospective cohort	NA <sup>a</sup>	89/567 (15.7)	29/1152 (2.5)	7.2 (4.6–11.5)

<sup>a</sup>NA; not applicable.

### Preventing Transmission through Screening of Blood and Tissue

Serological assays for HTLV-1 screening became available in the middle to late 1980s and, by the mid-1990s, HTLV-1 screening of blood donors was implemented in many high-income countries and countries where HTLV-1 is endemic (223). Blood donor screening policies include testing of donations for the presence of HTLV-1, discarding those found positive; deferral or exclusion of people whose history provides evidence they are at higher risk of HTLV-1 acquisition; or technologies, such as leucoreduction, that remove infectious organisms, including viral particles in the process of manufacturing plasma-derived blood products. Studies from Japan and the United States in the late 1980s and early 1990s showed that universal antibody screening of blood donors reduced the rate of HTLV-1 seroconversion among whole-blood recipients (442–444) (Table 7).

In low-prevalence settings, there is ongoing debate regarding the cost-effectiveness of universal screening (222). Prinsze and colleagues note that there are substantial gaps in knowledge regarding screening strategies, as well as contradictory findings from the limited available research (445). A study from the United Kingdom used a lookback method to review outcomes in people receiving blood components from HTLV-positive donors (446) and found that filter-leukoreduced or buffy coat-reduced blood products effectively reduced the risk of HTLV infection. Buffy coat-reduced products made up the minority (14%) of the total, and should not be equated with filter reduction, since this approach is known to be less effective. Because HTLV-1 is almost always cell associated, leukoreduction may be as effective as blood donation screening (445).

### POLICIES AND GUIDELINES: SCREENING OF BLOOD AND TISSUE DONATION

Mandatory antibody screening against HTLV-1 for all blood donations has been implemented in 23 countries (Table 8). The first were Japan and the United States, both in 1988 (447), followed by Canada, Caribbean nations (Dominican Republic, Haiti, and Jamaica), and French overseas departments (French Guiana, Guadeloupe, and Martinique) in 1989. For Argentina, China, Iran, and Venezuela, mandatory screening was implemented in areas designated endemic for HTLV-1. First-time donors are screened in Denmark, France,

**TABLE 7** Impact of screening on HTLV-1 transmission through blood products

Study	Country of research	Study design	HTLV-1 screening	Prior to implementation of donor screening (%)	Postimplementation of donor screening (%)
Kamihira et al., 1987 (442)	Japan	Before and after comparison	PA	53.6	0.9 ( $n = 1$ ) <sup>a</sup>
Nelson et al., 1992 (443)	United States	Before and after comparison	ELISA and confirmatory WB/RIPA	0.0039 ( $n = 2$ )	0.0
Inaba et al., 1999 (444)	Japan	Prospective cohort	Second-generation PA		0.021 ( $n = 1$ ) <sup>b</sup>

<sup>a</sup>One seroconversion occurred due to blood being used from a different donation center that did not screen.

<sup>b</sup>Follow-up of patient failed to confirm whether or not seroconversion was due to transfusion.

**TABLE 8** Countries and territories with policies or guidelines on screening of blood donations for HTLV-1<sup>a</sup>

WHO region <sup>b</sup>	All donations	First-time donors only	Specific areas	Leucoreduction <sup>c</sup>
Africa region	Gabon (only at the National Centre for Blood Transfusion [no national formal policy])			
Eastern Mediterranean region	Saudi Arabia (469)		Iran (Khorasan) (470)	
Europe region <sup>d</sup>	French Guiana, Greece, Ireland, Israel, Netherlands, Romania, United Kingdom (222, 448, 471)	Denmark, Finland, France, Guadelupe, Martinique, Portugal, Sweden (27, 108, 448, 472)		Austria, Belgium, Czech Republic, Finland, France, Germany, Greece, Ireland, Italy, Malta, Netherlands, Norway, Poland, Portugal, Romania, Slovakia, Slovenia, Spain (222, 448, 471–474)
Region of the Americas	Brazil, Canada, Chile, Colombia, Dominican Republic, Haiti, Jamaica, Peru, USA, Uruguay (208, 226, 228, 438, 475–482)		Argentina, Venezuela (438, 483)	
Western Pacific region	Australia, China (Taiwan), Japan, New Zealand (163, 222, 447, 455, 484)		China (222, 484)	

<sup>a</sup>Adapted from reference 7 (published under a CC BY-NC-SA 3.0 IGO license).

<sup>b</sup>No information was available for the South-East Asia region.

<sup>c</sup>All blood or cellular components, or on medical request.

<sup>d</sup>Includes overseas departments of France: French Guiana, Guadelupe, Martinique.

Guadelupe, Martinique, Portugal, and Sweden, and while Norway adopted a similar policy in 2000, first-time donor screening was ceased due to the absence of positive cases in 2007 (448). In the African Region, Gabon appears to be the only country conducting routine HTLV-1 screening of all blood donations at the National Center for Blood Transfusion; however, there is no formal national screening policy or guideline.

For organ transplant and donation, few policies and guidelines for HTLV-1 screening exist, with no global consensus. In the United States, mandatory screening of deceased organ donors was eliminated in 2009 due to the presumed very high false-positive rate in this low-prevalence setting, leading to organ donor wastage (449, 450). Current guidance nevertheless recognizes that potential health issues are associated with HTLV-1 in organ donation (450). In 2012, a directive adopted by the European Commission required HTLV-1 testing of all donors of cells and tissues from high-prevalence areas for HTLV-1 infection or those whose sexual partners or parents come from such areas (451). The United Kingdom requires that all donors of tissues and cells be tested for HTLV-1 at the time of donation (452). In Spain, screening for HTLV-1 in organ and tissue donors from endemic countries is recommended, as well as for individuals with sex partners or parents from high-prevalence regions.

## DISCUSSION AND FUTURE DIRECTIONS FOR RESEARCH AND PRACTICE

Recent advocacy from concerned researchers, clinicians and community members emphasized the potential for improved prevention and management of HTLV-1 infection (453). It is also clear that, despite all that has been learnt in the 4 decades following the discovery of HTLV-1, major gaps in knowledge across clinical and public health aspects of HTLV-1 need to be filled to ensure optimal control and prevention and inform policy and guideline development. The WHO consultation in late 2019 was the first global forum to consider recommendations on public health aspects of HTLV-1 and has already led to policy shifts in addressing this ancient human infectious disease (7, 8)

Robust surveillance data are needed to direct policy, service implementation, and health system investment. On the best available evidence, the geographic distribution of HTLV-1 infection remains highly focal, but prevalence in some highly populous countries has not been well characterized by surveys, making it difficult to estimate

the global burden of infection beyond recognized areas of endemicity. Reports of ATL and HAM/TSP in heavily populated countries or regions with little to no HTLV-1 prevalence data highlights a requirement for wider tracking. In addition, knowledge gaps persist on prevalence variations within endemic regions and on prevalence among subpopulations that may be at higher risk, including men who have sex with men and people who inject drugs. Countries can build on existing surveillance networks (which may include making HTLV-1 nationally notifiable) or build new ones to gather reliable epidemiological data, allowing more accurate assessment of the burden of infection and related morbidity and mortality.

Cost-effective HTLV-1 testing approaches and strategies tailored to local infection patterns and settings, as well as the purpose of testing, are needed, particularly in low- and middle-income countries. Current commercially available serological assays have high sensitivity and specificity and are optimally used when combined for diagnosis. Molecular tests, with even better performance, are also available, but broad uptake is constrained by lack of commercial production and limited access outside high-income settings. Transitioning from the "gold standard" Western blot to the use of INNO-LIA or PCR for confirmatory testing is conceptually appealing but comes with cost and health system implications (214). Complementary to improving access to HTLV-1 testing is the need for clearer guidance on testing and for whom it should be offered. Populations who have been considered include (i) people attending sexual health clinics, (ii) donors and recipients of blood or tissue, (iii) both pregnant women and children born to women with HTLV-1, and (iv) people who inject drugs (453). Clinical consensus and guideline development focused on HTLV-1 testing, including who should be offered testing and how to communicate test results, will be of benefit to clinicians, policy makers and, most important, people and communities at risk of HTLV-1.

There is no biomedical prevention intervention currently available for HTLV-1 infection. A vaccine would be ideal but has never progressed beyond early preclinical development. Modes of HTLV-1 transmission are well established, but additional information is required to optimize prevention strategies. While breastfeeding duration has been associated with the risk of mother-to-child transmission, decisions regarding cessation or shorter duration of breastfeeding must be weighed against the numerous demonstrated benefits of breastfeeding to both the infant and mother, particularly in settings where safe alternatives are not readily available. The role of sexual contact in sustaining transmission in endemic settings is suggested by the clearly increasing HTLV-1 prevalence with age (87, 102, 252, 253, 258, 261, 262). More-detailed analyses of age-specific patterns of prevalence, starting in childhood and covering all adult age groups, will help to clarify the role of sexual transmission in different settings. At a biological level, higher proviral load is a well-established risk factor for transmission, but it is at present not known whether a person with a low or undetectable proviral load represents a transmission risk to sexual partners. HTLV-1-specific prevention strategies are at present limited to screening of blood donations, generally only in high-income countries and, in regions of endemicity in a small number of countries, offering testing to pregnant women followed by counselling to limit breastfeeding for those found to have HTLV-1 infection. Existing public health interventions related to the prevention of blood-borne viruses and sexually transmitted infections, including safe sex promotion and harm reduction strategies for drug injecting, are likely to be effective in reducing the risk of HTLV-1 transmission.

The burden of diseases attributed to HTLV-1 appears to be highly variable across affected populations. The reasons for apparent regional differences are unclear but lack of recognition, and diagnosis may be an issue, highlighting the need for education and testing in the appropriate clinical context. Beyond ATL and HAM/TSP, HTLV-1 infection may have other substantial negative health impacts that are either unknown or under acknowledged, as suggested by the substantial increase in all-cause mortality observed among people with HTLV-1 across three continents. There is a lack of systematically collected information on HTLV-1 infection and related diseases, with few examples of directed initiatives (454, 455). Although many countries have cancer registries,



most coding systems do not distinguish ATL as a distinct entity. Japan has specific coding for ATL and HAM/TSP and reports the diseases in separate national registries. International collaboration will provide the basis for better understanding the apparent geographic differences in disease development and foster clinical research networks that can be used to investigate new therapeutic options.

Awareness of HTLV-1 among health care providers, communities, and affected individuals remains limited, even in countries of endemicity. Placing HTLV-1 firmly on the global health agenda and linking where appropriate to control strategies and research for other infectious diseases will advance the health and wellbeing of people living with and at risk for HTLV-1 infection.

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