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HOT NEWS

Dolutegravir shows efficacy in HTLV-1 infection

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HTLV-1 is a retrovirus that infects humans and is biologically close to HIV, the AIDS virus. Both are transmitted sexually, vertically, and parenterally. HTLV-1 may produce clinical manifestations in 10% of carriers, which characteristically include adult T-cell leukemia/lymphoma (ATLL) and a subacute neurological disease known as tropical spastic paraparesis or HTLV-1 associated myelopathy (HAM). The prognosis for ATLL is very poor and allogeneic stem cell transplantation is currently the best approach *(López-Pereira et al., Bone Marrow Transplant 2026)*. With respect to HAM, unfortunately many patients end up in a wheelchair and with urinary and fecal incontinence.

Antiretrovirals designed to treat HIV infection have been investigated to see if they could be equally effective in patients infected with HTLV-1. The results obtained so far have been not very encouraging, using, among others, zidovudine *(Machuca et al., Virus Res 2001)* or raltegravir *(Treviño et al., J Antimicrob Chemother 2012)*.

More recently, research has been carried out to determine whether newer, more potent antiretrovirals, such as dolutegravir, a second-generation integrase inhibitor, could be effective against HTLV-1. Last year, it was demonstrated in a mouse model that the combination of dolutegravir and tenofovir was able to reduce the transmission of HTLV-1 *(Cooney et al., 1999. Cell 2025)*.

Researchers in Brazil, where HTLV-1 is endemic, have recently published the results of a phase II clinical trial conducted in two hospitals in Salvador de Bahia. They examined 83 individuals infected with HTLV-1, 53 of them with symptoms. They compared dolutegravir with oral vitamin C. Over the course of 1 year, a reduction in proviral load and clinical improvement were observed in many of the patients who received dolutegravir, but not in the rest *(Brites et al., Clin Infect Dis 2026)*.

The results of the Brazilian study are the first to robustly demonstrate the efficacy of dolutegravir in HTLV-1 infection. There is no doubt this trial will trigger the design of multiple clinical studies aimed at reducing transmission (vertical and sexual), the risk of HTLV-1 disease, and the management of already sick patients *(Meyerowitz, Clin Infect Dis 2026)*.

Although HTLV-1 infection is considered a neglected disease, it is estimated that there are about 10 million people infected in the world. The regions with the highest endemicity are sub-Saharan Africa, South America, and the Caribbean. In Spain, there is a multicenter group and a national registry of cases *(de Mendoza et al., J Clin Virol 2023)*. To date, 555 infected people have been reported, 68% Latin Americans and 11% Africans.

HTLV-1 in sub-Saharan Africa

Several species of African monkeys depict high rates of infection with simian T-lymphotropic virus type 1 (STLV-1), the retrovirus that infects apes and that, as in other zoonoses, has passed to the human species in which we call HTLV-1. In monkeys, STLV-1 can also cause lymphoma and leukemia. The jump from the animal reservoir to humans most likely occurred over thousands of years during the hunting and consumption of monkeys infected by native Africans *(Mossoun et al., J Virol 2017)*.

The genomic sequence of new HTLV-1 isolates from 52 infected African patients has recognized a large genetic variability *(Cassar et al., Emerg Microbes Infect 2026)*. These findings confirm that the global dispersal of HTLV-1 had its ancient epicenter in Africa. On the

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other hand, a recent Spanish collaborative study conducted in Ivory Coast has suggested that the prevalence of HTLV-1 infection could be decreasing in some endemic areas of sub-Saharan Africa *(Konan et al., J Med Virol 2026)*.

HTLV-1 in Latin America

HTLV-1 infection is endemic and shows relatively high prevalence rates in many countries in South America, Central America, and the Caribbean. Phylogenetic studies show that there have been two major waves of HTLV-1 arriving in the Americas. The first is pre-Columbian, with the migrations of more than 1,500 years ago through the Behring Strait, which reached populations in the Andean mountain range, from the Incas in Peru to the Mapuche in Chile *(Zanella et al., Virus Res 2022)*.

The second introduction of HTLV-1 in America is more recent. It reached above all Brazil and the Caribbean, with African slaves arriving from the sixteenth century *(Amoussa et al., Infect Genet Evol 2017)*. It is interesting to note that the colonialism exercised by the English and Portuguese in America, with a significant traffic in African slaves, explains the large presence of African variants of HTLV-1 in Brazil and the British Caribbean islands, such as Jamaica, Trinidad and Tobago, etc. On the contrary, in the central and southern America conquered by the Spanish, the predominant variants of HTLV-1 are almost all pre-Columbian *(Enríquez-Vera et al. Virol J 2026)*.

The radical difference in variants of HTLV-1 in the Americas has at least three historical reasons, as the Spanish historian Elvira Roca Barea masterfully discusses in her book "*Imperiophobia and Black Legend*" (2016). First, the Spanish administrative organization in America was in viceroyalties, with recognition of the local indigenous population instead of the colonial submission arranged by the English. Second, the Spanish Crown's tolerance of the indigenous people, who were considered citizens, and "*mestizos*" allowed for a high survival of natives. In contrast, conditions imposed by colonialist for locals in North America were harder, and few Indians left. Finally, the legislation of the Spanish Crown, with Francisco de Vitoria at the head, did not accept slavery overseas, so African immigration was scarce.