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Detection of Human T-cell Leukemia Virus Type 1 in adult T- cell Leukemia by RT-qPCR

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ABSTRACT

Human T-cell Leukemia Virus Type 1 (HTLV-1) is a retrovirus associated with serious hematological and neurological disorders. Understanding its epidemiological distribution is essential for effective prevention and control strategies. Human samples from Leukemia patients were collected from November 16, 2024, to January 1, 2025. The age range of the patients was 18 years to 80 years. The RT-qPCR method was used to detect Human T-cell Leukemia Virus Type 1 in all samples; the results showed Twenty-five positive cases for *Human T-cell Leukemia Virus Type 1* . The population groups studied were divided into five age groups: 18-27, 28-37, 38-47, 48-57, and 58-67 years. The first group (18-27) had the highest number of infected cases at 56%, compared to the age group (28-37 at 12%, 38-47 at 8%, 48-57 at 14%, and the age group 58-67 at 8%). The samples were collected from Hospital, Middle Euphrates Cancer Center in Najaf province. The findings revealed that individuals aged 18 to 27 years had the highest infection rate with Human T-cell Leukemia Virus Type 1 (HTLV-1). Additionally, the infection was more prevalent among males compared to females.

KEYWORDS

Leukemia, Human T-cell Leukemia Virus Type 1, RT-qPCR

Introduction

Human T-Leukemia Virus Type 1 (HTLV-1), A member of the Retrovirus Family, is linked to a 57% rise in overall mortality. the prevalence of *HTLV-1* and *HTLV-2* infections varies, with *HTLV-1* being particularly associated with this significant increase in death rates (Marinho *et al* .,2024).

The First Retrovirus identified to be associated with human cancer, discovered by gallo and colleagues, affects approximately ten million people worldwide. this enveloped virus has a virion diameter of 80–100 nm and contains two single-stranded rna strands, each about 9 kb in length, within its nucleocapsid core. the virus employs sophisticated molecular mechanisms to evade immune detection and remains latent in infected individuals for extended periods (Jetly *et al*.,2024).

The Seroprevalence of *Human T-Cell Leukemia Virus* in adults varies widely, ranging from 0.1% to as high as 40%, with rates increasing with age and being more common

in individuals assigned female at birth. *HTLV-1* primarily targets and infects CD4+ T Cells, often maintaining a state of low transcriptional activity during the early stages of infection, which typically remains asymptomatic. however, symptoms may emerge later in life (Wang *et al.,*2024).

Human T-Cell Leukemia Virus Type 1 (HTLV-1) is a Retrovirus that mainly targets and infects CD4+ T Cells, leading to a persistent, lifelong infection. globally, an estimated 10–20 million people are infected with *HTLV-1*, with higher prevalence rates observed in endemic regions like Japan. although the majority of those infected do not show symptoms, about 5% develop to all due to associated immunosuppression. even asymptomatic *HTLV-1* carriers exhibit immune system abnormalities, increasing their susceptibility to opportunistic infections (Nozuma *et al.,* 2025) .

The *Human T-Cell Leukemia Virus* is primarily transmitted through breastfeeding and, less commonly, through sexual contact. the lifetime risk of *HTLV-1* carriers developing Adult T-Cell Leukemia/Lymphoma (ATLL) is estimated to be 6–7% for males and 2–3% for females. htlv-1-encoded proteins like tax and hbz, play crucial roles in the process of cancer development. these somatic changes drive the clonal expansion of *HTLV-1*-infected cells, resulting in distinct genomic and transcriptomic patterns and alterations in the cellular microenvironment (Kogure &Kataoka, 2025) .

The Adult T-Cell Leukemia (ATLL) highly aggressive disease resulting from the dysfunction of CD4+ T lymphocytes, which are essential for the host's adaptive immune response. *HTLV-1* infection disrupts the function and differentiation of T cells, enabling them to evade immune detection. this immune imbalance in atll is further exacerbated by the accumulation of genetic and epigenetic alterations in key genes related to host immunity. additionally, angiogenesis, the process of forming new blood vessels, plays a critical role in the development and progression of cancer (Lubov *et al .,*2024).

The Adult T-Cell Leukemia (ATLL) remains a significant cause of mortality worldwide, driven by the emergence of transformed cells with an exceptional ability to proliferate rapidly. this process is marked by sustained dysregulation in protein synthesis, which disrupts the translational control of growth-promoting transcripts. among the various types of cancer, ATLL stands out as a highly aggressive and dangerous form of lymphoma. the primary cause of ATLL is infection with *HTLV-1*, with the acute subtype being the most common. unfortunately, the prognosis for patients with acute ATLL is poor, often with survival limited to only a few months (Pourrezaei, 2025).

The Wide range of clinical manifestations and varying prognoses in patients with ATLL have resulted in its classification into four subtypes: acute, lymphoma, chronic, and smoldering. for patients with acute and lymphoma types (aggressive ATLL), intensive chemotherapy is typically advised. however, those with aggressive ATLL often face a very poor prognosis due to inherent resistance to chemotherapy and frequent infectious complications caused by immunodeficiency. in contrast, patients with chronic and smoldering types (Indolent ATLL) generally have a more favorable prognosis, and a strategy of watchful waiting until disease progression is usually recommended (Sato, 2025).

Materials and methods

A Case-Cross study was designed on 100 total blood, including 47 females and 53 males, obtained from patients with leukemia. twenty of them *developed Human T- cell Leukemia Virus Type 1 (HTLV-1)*. These were compared with 75 samples from negative infection *HTLV-1*. The ages ranged from 8 month to 80 years during the interval from December 2024 Until January 2025. verbal consent was obtained from all participants before sample collection.

Real-time qPCR technique

This method was used to diagnose *Human T- Leukemia virus type 1 (HTLV-1).* The primers were designed based on the NCBI sequences of *Human T Leukemia virus type 1 (HTLV-1)* as shown in table (1). SolisGreen qPCR Mix (Solis BioDyne , Teaduspargi 9, 50411 (EU)) and Viral RNA were extracted using the viral RNA Extraction Kit (Magzol Reagent RNA Extraction Kit) (Magen, Lot No. R480101-MFG, Chin). This technique was performed at Faculty of Veterinary Medicine, at University of Kufa by using an Agilent Technologies Stratagene Mx3005p (Iraqi Biotechnology Company).

Table 1. Primers for *Human T-Leukemia virus type 1* used, design based on NCBI

Primer		Sequence	product size
HumanT-cell Leukemia virus Type-1 pol gene	Forward	AACCCACAACATCAGATGCC	20 bp
	Reverse	AATGGCCTGAAGCAAAGAGG	20 bp

Results and Discussion

In this study, a total of 100 whole blood samples were collected from leukemia patients presenting with diverse clinical conditions, with age years ranging from 18 years to 80 years. Molecular screening for *HTLV-1* infection was conducted using real-time quantitative PCR (RT-qPCR).

The total samples analyzed, 25 (25%) are confirmed positive for *HTLV-1*, while 75 (75%) tested negative. The viral load was inferred from the cycle threshold (Ct) values obtained during amplification, which reflect the relative concentration of *HTLV-1* proviral DNA in each sample. As shown in (Figure1) lower Ct values correspond to higher viral loads, indicating a stronger presence of *HTLV-1* in those patients.

This data provides a clear indication of *HTLV-1* prevalence among leukemia patients in the studied population and supports the utility of RT-qPCR as a sensitive and specific method for detecting *HTLV-1* in clinical specimens across a wide age range.

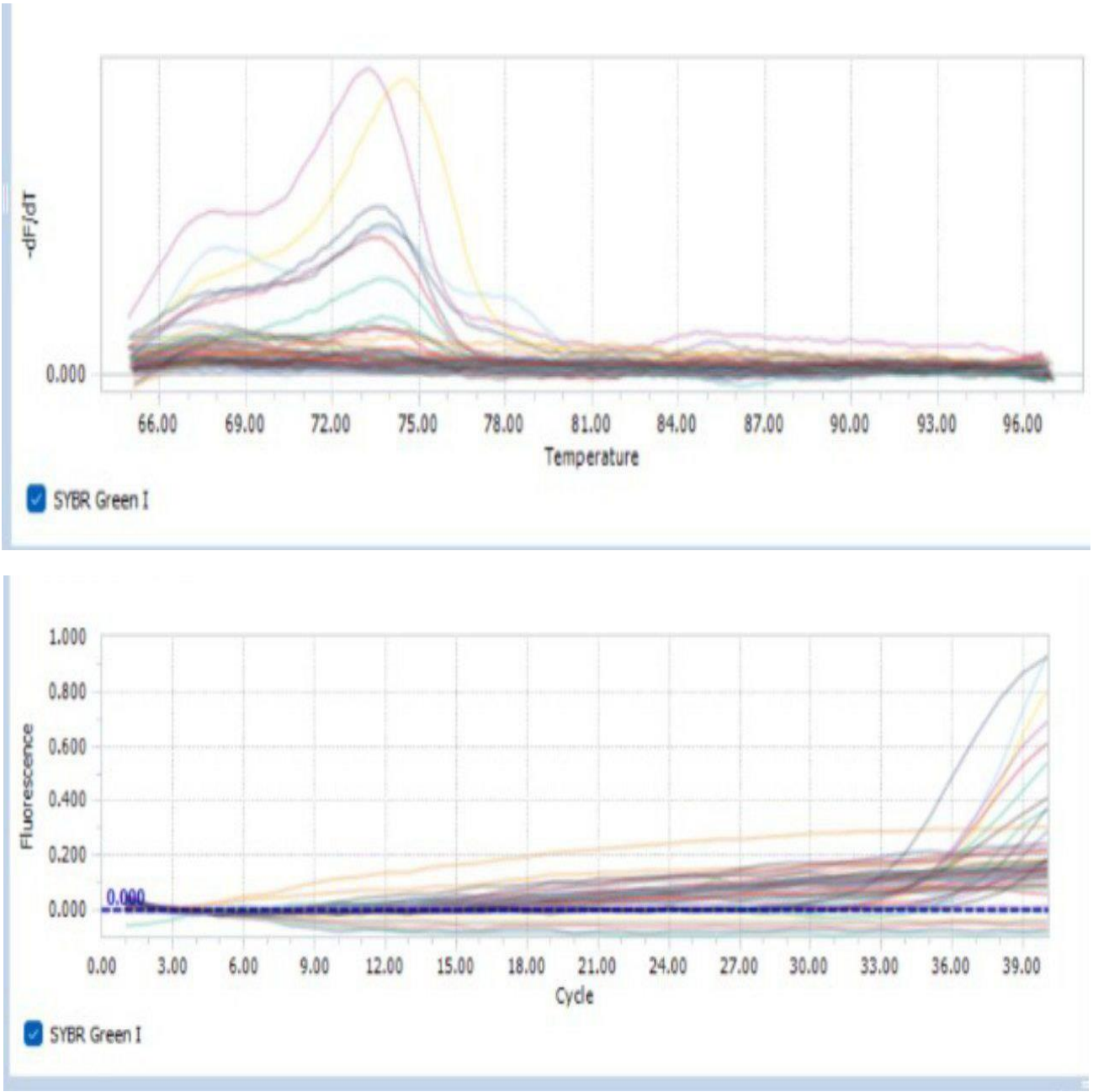

Figure 1. Detection of *Human T-cell Leukemia virues Type -1* by RT-qPCR in Leukemia patient

The current study, whole blood samples were collected from patients diagnosed with leukemia across several hospitals. This methodological approach is consistent with the findings of Alameedy (2022) who also employed total blood samples in leukemia patients for *HTLV-1* analysis.

Branda *et al*., (2025) conducted a study that utilized multiple real-time RT–PCR tests to investigate *HTLV-1* infection in leukemia patients. Their findings suggest that the proportion of positive samples was significantly influenced by geographical distribution and the nature of patient recruitment. regional differences and the specific causes of infection appear to impact the detection rate. Furthermore, their study observed that some patients transitioned from acute to chronic disease states, highlighting the importance of longitudinal follow-up in *HTLV-1* surveillance. It was noteworthy that sample collection from different regions might yield variable prevalence rates depending on local epidemiology and testing protocols.

In a related investigation by Oloumbou *et al*., (2025), *HTLV-1* diagnosis began with ELISA-based serological screening for *HTLV-1* antibodies. Among the cohort, 19 cases of non-Hodgkin's lymphoma were documented, with two cases testing positive for *HTLV-1*. These two patients underwent detailed clinical evaluation used the Levine point-score classification system and the Shimoyama criteria, which led to a probable diagnosis of

adult T-cell leukemia (ATL), with subsequent clinical subtype investigation.

In our current dataset, 25 out of 100 tested samples (25%) were confirmed *HTLV-1* positive. Among these, 16 were male and 9 were female (Figure 2).

The As a researcher, the number of males in collecting samples from the number of visitors is greater than the number of females. and the second possibility is that the large number of infections is due to biological and hormonal differences that affect the development of the immune system and T cells in the body.

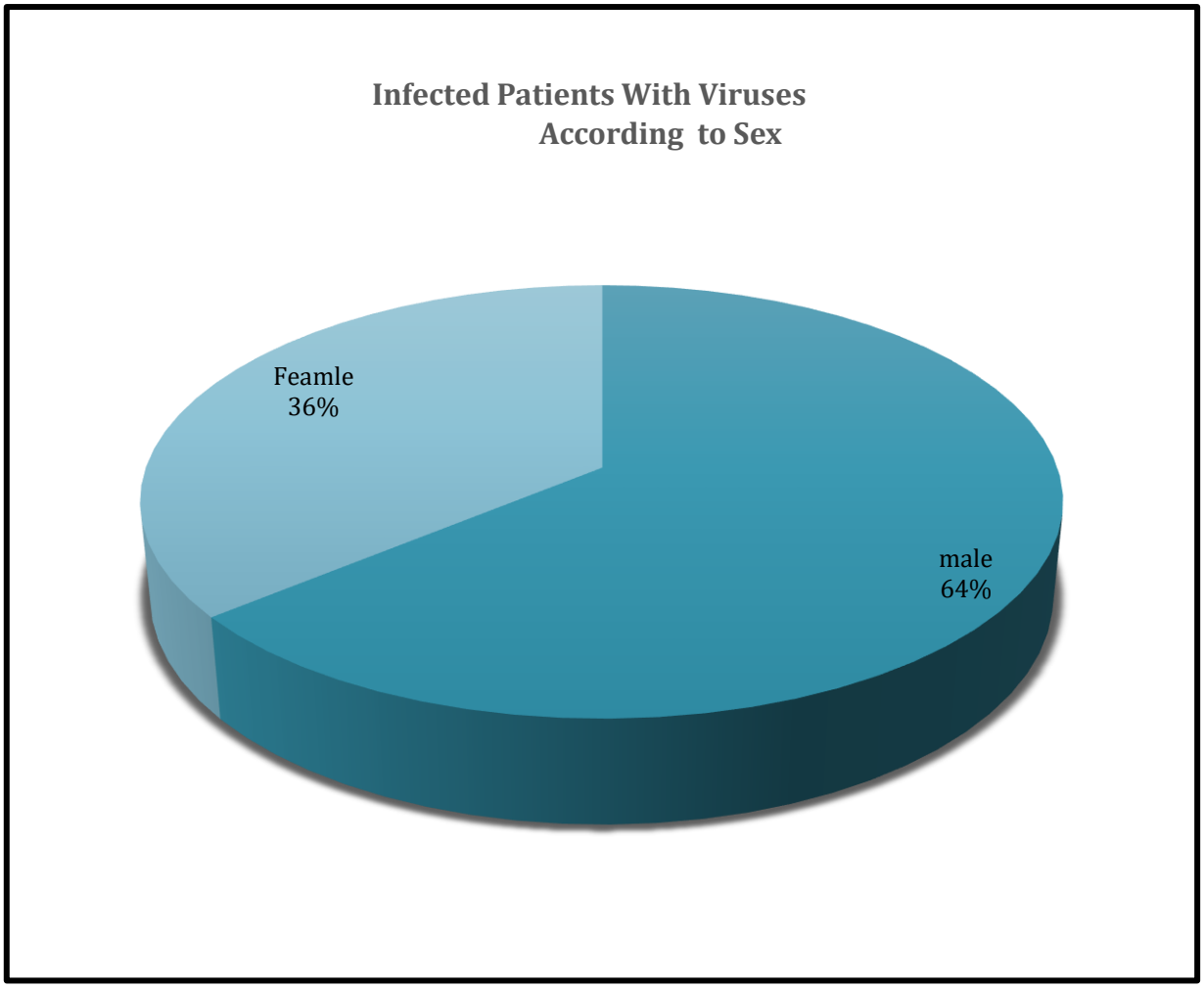

Figure 2. The percentage of patients infected leukemia within *HTLV-1* according sex

This distribution was consistent with the findings reported by Malpica *et al*., (2025), where *HTLV-1* was detected in 1,061 males (59%) and 733 females (41%) out of 1,794 patients. The Similarly, Soares *et al*., (2025) examined 228 individuals, of whom 39.47% were male and 60.53% were female. Six individuals (2.7%) tested seropositive for *HTLV-1*, confirmed by qPCR. Among these confirmed cases, four (66%) were male and two (33%) were female, with age ranges between 51 and 73 years.

Rosadas *et al*., (2024) conducted a study involved 296 participants, of which 24% were male and 76% were female. *HTLV-1* proviral load (PVL) was quantified used real-time PCR by measuring copies of the *HTLV-1* Tax gene. These findings further support the trend of higher *HTLV-1* prevalence in males, possibly attributed to biological and hormonal differences that influence T-cell immunity and viral susceptibility. It was also plausible that sampling bias or shorter collection windows may underestimate infection rates among females.

Table 2. The Distribution of Patients According to Age years Groups

Age group (years)	No. Positive(case)	Percentage %
18-27	14	56%
28-37	3	12%
38-47	2	8%
48-57	4	16%
58-67	2	8%

The distribution of *HTLV-1* infection across age groups in this study revealed that individuals aged 18–28 years represented the highest number of positive cases (14 patients), while those aged 58–67 years had the lowest prevalence (2 cases), as illustrated in (Table .2). According to Araujo (2023), the overall prevalence of *HTLV-1* infection was estimated at 3.6%, with 2.0% among males and 1.6% among females. Among pregnant women, the prevalence was reported at 0.49% (Leal *et al*., 2025).

The A population-based cohort reported by Chen *et al*., (2025) included 674 males (58.8%) and 473 females (41.2%), with ages ranged from 7 to 86 years and a median age of 50 years. In this group, 81 individuals (7.1%) tested positive for *HTLV-1* antibodies, comprising 39 males and 42 females.

The Further clinical data were obtained from 44 patients with confirmed *HTLV-1* infection via Western Blot (Torres *et al*., 2025). Among them, 23 (52%) were pediatric cases, 16 (37%) were adults, and 5 (11%) were pregnant women. The adult subgroup had a mean age of 48.5 ± 14.5 years, with 56.25% being female. All patients were residents of southwestern Colombia, particularly Buenaventura (37.5%) and Cali (31.3%).

The Several factors may explain the higher prevalence of *HTLV-1* infection observed among adults including the first long incubation period HTLV-*1* can remain latent for decades, with clinical symptoms manifesting only after prolonged periods. Second gradual pathogenesis the virus targets and stimulates T-cell proliferation slowly over time, which contributes to disease progression in later life. Third transmission pathways Infections in childhood commonly occur through breastfeeding, blood transfusions, or later-life sexual contact. Fouth host susceptibility: Individual differences in immune response, genetic predisposition, and lifestyle factors may influence viral replication and disease development.

Conclusion

The findings revealed that individuals aged 18 to 27 years had the highest infection rate with Human T-cell Leukemia Virus Type 1 (HTLV-1). Additionally, the infection was more prevalent among males compared to females.

References

1. Alameedy, F. (2022). Detection of G Protein-Coupled Receptors of Human T-cell Leukemia Virus Type 1 and Cytokines Study. Virology & Mycology, 11, 228.
2. Araujo, C., & Adele, B. (2023). Sex, age, and risk group variations among individuals infected with HIV, HTLV-1, and HTLV-2. Brazilian Journal of Sexes, 4(4), 638–655.
3. Branda, F., Romano, C., Pavia, G., et al. (2025). Human T-Lymphotropic Virus (HTLV): Epidemiology, genetics, pathogenesis, and future challenges. Viruses, 17(5), 664.
4. Jetly, S., Singh, S., Khatri, M., et al. (2024). Human T-cell leukemia virus type 1 (HTLV-1). In P. L. Bhukya & A. Subbaiyan (Eds.), Emerging Human Viral Diseases (Vol. II). Springer.
5. Ji, H., Chang, L., Yan, Y., et al. (2023). Development and validation of a duplex real-time PCR for the rapid detection and quantitation of HTLV-1. Virology, 20.
6. Joanne, C., Gbenjo, D., Georgia, M., et al. (2023). Do leukemia: What primary care physicians need to know. Journal of Primary Care, 107(4), 397–405.

7. Kogure, Y., & Kataoka, K. (2025). Clinical and therapeutic significance of genetic profiling in adult T-cell leukemia/lymphoma. Leukemia, 15, 107676.
8. Leal, G., Cunha, G., Anna, A., et al. (2025). Prevalence and first detection of HTLV-2 in a pregnant woman in rural Brazil. Acta Tropica, 265, 107632.
9. Radygina, L. V., & Mochalova, L. V. (2024). Diseases caused by human T-lymphotropic virus type 1 (HTLV-1). MIR Journal, 11(1), 57–69.
10. Malpica, L., Idrobo, H., Pavlovsky, A., et al. (2025). Epidemiology, clinical features, and outcomes of peripheral T-cell lymphoma in Latin America: An international, retrospective cohort study. Haematology, 12(4), 258–268.
11. Marinho, A., Okita, T., Guimarães, A., et al. (2024). The global prevalence of HTLV-1 and HTLV-2 infections among immigrants and refugees—A systematic review and meta-analysis. Viruses, 16(10), 1526.
12. Nozuma, S., Yoshimura, A., Pai, C., et al. (2024). Geographic characteristics of HTLV-1 molecular subgroups and genetic substitutions in East Asia: Insights from complete genome sequencing of HTLV-1 strains isolated in Taiwan and Japan. PLOS Neglected Tropical Diseases, 18(2), e0011928.
13. Oloumbou, F., Lentombo, L., Nkoghe, J., et al. (2025). Clinical and molecular evidence of HTLV-1 infection in inpatients diagnosed with diseases previously described as associated with this infection. PLOS Neglected Tropical Diseases, 19(5), e0013075.
14. Pourrezaei, S., Letafati, A., Molaverdi, G., et al. (2025). RAB3GAP2 dysregulation in adult T-cell leukemia/lymphoma (ATLL) compared to acute lymphoblastic leukemia (ALL): A molecular perspective. BMC Research Notes, 18, 28.
15. Rodrigues, S., Salustiano, S., Santos, V., et al. (2022). Monitoring of HTLV-1-associated diseases by proviral load quantification using multiplex real-time PCR. Journal of NeuroVirology, 28, 27–34.
16. Rosadas, C., & Taylor, P. (2022). HTLV-1 and co-infections. Frontiers in Medicine, 9, 812016.
17. Sato, F., Okada, Y., Asayama, M., et al. (2025). Centrilobular nodules are predictive chest computed tomography (CT) findings related to adult T-cell leukemia/lymphoma development in human T-lymphotropic virus type 1 carriers. Clinical Radiology, 81, 106765.
18. Soares, C., Lopes, T., Neto, G., et al. (2025). High prevalence and risk factors for infection with human T-lymphotropic viruses 1 and 2 in the municipality of Ananindeua, Pará, Northern Brazil. Viruses, 17(6), 765.
19. Torres-Hernández, D., Martínez, K., Marmolejo, C., et al. (2025). A cross-sectional view of HTLV-1: From childhood to adulthood in an endemic region of Colombia. Preprints, 1(10), 20944.
20. Wang, T., & Tiana, T., et al. (2024). Current state of therapeutics for HTLV-1. Viruses, 16(10).