HTLV and miRNA

Introduction

T-cell lymphotropic virus type 1 (HTLV-1) is a retrovirus that was first discovered in the early 1980s (1). It is a complex virus that primarily affects the immune system, specifically the T-cells. HTLV-1 is known to be associated with various diseases, including adult T-cell leukemia/lymphoma (ATLL) and HTLV-1-associated myelopathy/tropical spastic paraparesis (HAM/TSP) (2). Over the years, researchers have dedicated significant efforts to understanding the biology, transmission, and clinical implications of HTLV-1(3). Previous research has shed light on the prevalence of HTLV-1 infection in different regions of the world, its modes of transmission, and the associated risk factors. Additionally, studies have explored the pathogenesis of HTLV-1-related diseases and have sought to develop effective treatment strategies. In terms of epidemiology, HTLV-1 is most prevalent in certain geographical areas, including parts of Japan, the Caribbean, Central and South America, and sub-Saharan Africa (4, 5). It is estimated that approximately 10 to 20 million individuals worldwide are infected with HTLV-1 (6). The prevalence varies significantly across different populations, with certain groups, such as indigenous communities in Australia and Japan, exhibiting a higher prevalence rate (7). The modes of transmission of HTLV-1 are mainly through sexual contact, blood transfusion, and mother-to-child transmission(8) . Sexual transmission is considered the most common route of infection, particularly in endemic areas(9). Additionally, HTLV-1 can be transmitted through infected blood and blood products, highlighting the importance of rigorous screening and testing procedures in blood banks(10). Vertical transmission from an infected mother to her child can occur during breastfeeding, which poses a significant risk for transmission in endemic areas where prolonged breastfeeding is common(9). Previous research has identified several risk factors associated with HTLV-1 infection. These include engaging in unprotected sexual intercourse with an infected individual, sharing needles or syringes, receiving contaminated blood transfusions, and being born to an infected mother (11). Additionally, individuals who have multiple sexual partners, engage in high-risk sexual behaviors, or have a history of sexually transmitted infections are also at an increased risk of HTLV-1 infection (12). Studies have also focused on understanding the pathogenesis of HTLV-1-related diseases. ATLL is a highly aggressive form of T-cell leukemia that develops in a subset of individuals infected with HTLV-1(8). It is characterized by the uncontrolled proliferation of T-cells and can result in organ infiltration, lymphadenopathy, and hematological abnormalities (13). HAM/TSP, on the other hand, is a chronic neurological disorder characterized by progressive spastic paraparesis and sensory disturbances (14). Both ATLL and HAM/TSP have a significant impact on the quality of life and overall prognosis of affected individuals (14). Efforts have been made to develop effective treatment strategies for HTLV-1-related diseases. However, due to the complex nature of the virus and its associated diseases, treatment options remain limited (15). Current therapeutic approaches mainly focus on managing the symptoms and complications associated with ATLL and HAM/TSP. These include supportive care, antiretroviral therapy, immunomodulatory drugs, and symptom-specific interventions (14). Additionally, efforts are being made to develop targeted therapies that directly inhibit HTLV-1 replication and prevent the progression of associated diseases (16).

MicroRNAs (miRNAs) are a class of small non-coding RNA molecules that have garnered significant attention in recent years due to their critical role in gene regulation (17). These tiny molecules, typically consisting of 21-25 nucleotides, play a crucial part in post-transcriptional gene silencing, thereby influencing various biological processes and viral infections In the context of Human T-cell lymphotropic virus type 1 (HTLV-1), miRNAs have emerged as key players in the modulation of viral replication, immune response, and disease progression (1, 13). Over the years, researchers have conducted extensive investigations to understand the role of miRNAs in HTLV-1 infection and its associated pathologies (18). Previous studies have identified specific miRNAs that are dysregulated in HTLV-1-infected cells and have explored their impact on viral replication, immune escape, and the development of HTLV-1-associated diseases (13). These findings have provided valuable insights into the molecular mechanisms underlying HTLV-1 infection and have opened up avenues for the development of novel therapeutic strategies (19). One of the key areas of research in miRNAs and HTLV-1 revolves around the dysregulation of specific miRNAs in HTLV-1-infected cells. It has been observed that HTLV-1 infection leads to alterations in the expression levels of several miRNAs, both in infected T-cells and in patient samples (20). These dysregulated miRNAs have been found to target critical cellular pathways involved in immune response, cell cycle regulation, and apoptosis. By modulating the expression of target genes, these miRNAs contribute to the establishment of a favorable environment for HTLV-1 replication and persistence (1, 21).

This review aims to provide a comprehensive overview of the current knowledge and future perspectives on the role of miRNAs in HTLV-1 infection and its protein intraction with miRNAs, fostering further research in this field and opening new avenues for the management of HTLV-1-related pathologies

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