Project summary

It is estimated that at least 20 million people worldwide are infected with the oncogenic retrovirus, human T-cell leukemia virus type 1 (HTLV-1). HTLV-1 infection is common in southwestern Japan, sub-Saharan Africa, the Caribbean islands, some regions of South America, the Middle East and Austro-Melanesia. Infected individuals are at risk of developing a rapidly progressive malignancy, adult T-cell leukemia (ATL), and a debilitating and sometimes fatal neurologic condition, HTLV-I associated myelopathy/tropical spastic paraparesis (HAM/TSP).

According to the current most accepted model, two viral proteins (TAX and HBZ) are hypothesized to have the highest impact on viral replication and cell transformation. The modes of action of TAX and HBZ are remarkably pleiotropic and involve a variety of cell signaling pathways. Besides a role of these proteins, more recent evidence from the laboratory has highlighted epigenetic modulation of gene expression by the HBZ ribonucleic acid. By disrupting the basal transcription machinery, HBZ RNA indeed inhibits sense transcription of the HTLV-1 provirus. Unpublished ChIP-sequencing using TBP antibody also indicates that the HBZ RNA targets specific chromatin domains of the host cell. Furthermore, HBZ RNA disrupts interactions between lncRNAs and mediators of the Polycomb repressive complex. The project aims at understanding these epigenetic regulations to further elucidate the mechanisms of HTLV-1 pathogenesis.

Candidates:
- should hold a PhD degree in molecular biology, biochemistry, medicine, veterinary medicine or equivalent
- demonstrate expertise in retrovirology, preferably HTLV.
- master bioinformatics

Location:
Laboratory of Cellular and Molecular Epigenetics of the University of Liège, Belgium *https://www.gigacme.uliege.be/cms/c_4222777/en/gigacme*

Contract:
Renewable one-year contract

Application:
CV, motivation letter and names of two referees should be sent to: luc.willems@uliege.be