

# Phylogenetic dating analysis of HTLV-1 from Chile suggests transmissions events related to ancient migrations and contemporary expansion

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? Human T-cell lymphotropic virus type 1 (HTLV-1) is a globally-spread virus. It is estimated that there are about 5?10 million infected people in the world. HTLV is endemic in Chile, with higher seroprevalence among indigenous people. However, little is known about HTLV-1 genetic diversity, its introduction and dispersion in this country. To gain insights into these issues, a phylogenetic dating analysis was conducted based on Chilean and closed related long terminal repeat sequences. The time tree reconstruction showed that the introduction of HTLV-1aA occurred several times in Chile. It was hypothesized that these introductions took place at least in two different historical moments: (i) during the ancient human migrations and (ii) during/after the European colonization of South America. The present study contributes toward understanding the evolutionary history of HTLV-1 in Chile and South America. © 2020 The Authors