

# Ancient HTLV type 1 provirus DNA of andean mummy

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The worldwide geographic and ethnic clustering of patients with diseases related to human T cell lymphotropic virus type 1 (HTLV-1) may be explained by the natural history of HTLV-1 infection. The genetic characteristics of indigenous people in the Andes are similar to those of the Japanese, and HTLV-1 is generally detected in both groups. To clarify the common origin of HTLV-1 in Asia and the Andes, we analyzed HTLV-1 provirus DNA from Andean mummies about 1500 years old. Two of 104 mummy bone marrow specimens yielded a band of human  $\beta$ -globin gene DNA 110 base pairs in length, and one of these two produced bands of HTLV-1-pX (open reading frame encoding p(40x), p(27x)) and HTLV-1-LTR (long terminal repeat) gene DNA 159 base pairs and 157 base pairs in length, respectively. The nucleotide sequences of ancient HTLV-1-pX and HTLV-1-LTR clones isolated from mummy bone marrow were similar to those in contemporary Andeans and Japanese, although there was microheterogeneity in the sequences