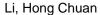
The presence of ancient human T-cell lymphotropic virus type I provirus DNA in an Andean mummy



Fujiyoshi, Toshinobu

Lou, Hong

Yashiki, Shinji

Sonoda, Shunro

Cartier, Luis

Nunez, Lautaro

Munoz, Ivan

Horai, Satoshi

Tajima, Kazuo

The worldwide geographic and ethnic clustering of patients with diseases related to human T-cell lymphotropic virus type I (HTLV-1) may be explained by the natural history of HTLV-I infection. The genetic characteristics of indigenous people in the Andes are similar to those of the Japanese, and HTLV-I is generally detected in both groups. To clarify the common origin of HTLV-I in Asia and the Andes, we analyzed HTLV-I provirus DNA from Andean mummies about 1,500 years old. Two of 104 mummy bone marrow specimens yielded a band of human ?-globin gene DNA 110 base pairs in length, and one of these two produced bands of HTLV-I-pX (open reading frame encoding p40(x), p27(x)) and HTLV-I-LTR (long terminal repeat) gene DNA 159 base pairs and 157 base pairs in length, respectively. The nucleotide sequences of ancient HTLV-I-pX and HTLV-I-LTR clones isolated from mummy bone marrow were similar to those in contemporary Andeans and Japanese, although there was microheterogeneity in the sequences