ability than the strains found in American Indians (ref. 3 and Fig. 1*a*). All HTLV-I strains found in American Indians from Latin America, including the strains ARGSOT and SIB170, discussed by Li *et al.*[1], belong to just one variant of this Transcontinental subgroup, tightly clustering with virus also found in Latin-American Black populations, but not with Japanese HTLV-I strains. The other Latin-American strains outside this tight cluster belong to other ethnic populations. The obvious conclusion is that the virus was transmitted from Black populations to American Indians. Our recent 'molecular clock' calculations also clearly show that the time frame in which the genetic variability in American Indians from Latin America could have been established is more concordant with a post-Columbian transmission from Black slaves rather than from Mongoloid populations following Bering strait migrations[9].

To verify whether the separation between the HTLV-I sequences found by Li *et al.*[1] in the Andean mummy and the ones found in the contemporary Japanese Ainu and Chilean populations could have dated more than 1,500 years ago, we did 'molecular clock' calculations. The fragments sequenced for the mummy sample were very conserved, allowing no phylogenetic resolution within the Cosmopolitan HTLV-I subtype. The evolutionary distances (Fig. 1*b*), however, show that the distance from HTLV-Ib (chosen as outgroup) is not substantially less than for the other strains sequenced by Li *et al.*, as would be expected in a comparison of a 1,500-year-old strain with contemporary strains. On the contrary, most of the contemporary strains even had smaller distances (although not significantly so) to the outgroup (Fig. 1*b*, underlined). Thus, the mummy strain has in fact all the characteristics of a contemporary strain.

Therefore, we find it premature to conclude that the HTLV-I sequence reported by Li *et al.* actually originates from a 1,500-year-old American Indian mummy.

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Tajima and Sonoda reply—In Latin America, the prevalence of HTLV-I is decreasing and at present is not as high (up to 10%; ref. 10) as reported previously. The same phenomenon can be seen in an endemic island in Japan that had a high prevalence of HTLV-I in 1985 (23% in 2,582 adults from 2–50% among 123 villages; ref. 11) and now has a very low prevalence rate in young adults (down to 3%). The rates of transmission of HTLV-I may have easily changed over time depending on transmission routes and infectious conditions. Therefore, it seems reasonable that one of two Andean mummies about 1,500-year-old is positive for HTLV-I.

In investigating the origin of HTLV-I, it is very important to select the appropriate source of materials from natives of South America. Some African HTLV-I strains have spread around the world, and many native people have recently been infected with HTLV-I from other ethnic groups, especially through prostitutes and drug users in large cities. To obviate these confounding factors, we have collected blood samples in very isolated villages in the Andes[10]. It is important to note that Andean samples from Quechua in Cusco[3] would not be suitable to investigate ethnic relationship between Andean HTLV-I and its African lineage, because that city represents an admixture of many ethnic groups whose HTLV-1 may have come from several lineages.

The evolutionary speed of HTLV-I is as slow as 0.4×10^{-7}–6.8×10^{-7} base substitutions/year (ref. 12), which is 100 times less than the estimate for HTLV-II (0.3×10^{-4}–1×10^{-4}; ref. 13). Based on the HTLV-II 'time clock', all of the Transcontinental subgroup of HTLV-I might have been spread throughout the 'New Continent' during the last 100–400 years. Based on the HTLV-I evolutionary speed, however, aboriginal strains of HTLV-1 among Mongolian populations in South America and Asia, including Japanese and Ainu, produce distinct ethnic clusters separating in the period 10,000–40,000 years BP (before present).

We propose that Asian Mongolians with HTLV-I moved into Andes during the prehistorical period long before the colonial era. Our results with HTLV-I DNA extracted from a 1,500 year-old Andean mummy substantiate this.

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