

# Phylogenetic subtypes of human T-lymphotropic virus type I and their relations to the anthropological background

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Isolates of human T-lymphotropic virus type I (HTLV-I) were phylogenetically analyzed from native inhabitants in India and South America (Colombia and Chile) and from Ainu (regarded as pure Japanese descendants from the preagricultural 'Jomon' period). Their genomes were partially sequenced together with isolates from Gabon in central Africa and from Ghana in West Africa. The phylogenetic tree was constructed from the sequence data obtained and those of previously reported HTLV-I isolates and simian T-lymphotropic virus type I (STLV-I) isolates. The heterogeneity of HTLV-I was recently recognized, and one major type, generally called the 'cosmopolitan' type, contained Japanese, Caribbean, and West African isolates. The phylogenetic tree constructed in the present study has shown that this cosmopolitan type can be further grouped

into three lineages (subtypes A, B, and C). Subtype A consists of some Caribbean, two South American, and some Japanese isolates, including that from the Ainu,