

## Whole genome sequence analysis of human T-cell leukemia virus type 1 in Peru

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### Background:

Although human T-cell leukemia virus type 1 (HTLV-1) is known to have a low genetic diversity as compared to most other retroviruses, little is known about the relevance of genetic variations with pathogenicity of HTLV-1. Peru is a multiracial nation composed of Mestizo, Indihena, European Peruvians, African Peruvians, and Asian Peruvians including Chinese and Japanese. Peru has also a high prevalence of *Strongyloides stercoralis* (Ss) infection, and coinfection by Ss is a major risk factor for the development of adult T-cell leukemia/lymphoma (ATLL). To explore the relationship between susceptibility to coinfection with Ss and specific strain type of HTLV-1, we collected blood samples from HTLV-1-positive subjects who visited the Instituto de Medicina Tropical Alexander von Humboldt in Lima, and phylogenetic characteristics related to coinfection of Ss were assessed by the entire sequence of HTLV-1 genome.

### Methods:

Sequencing of the entire HTLV-1 genome was carried out using a target

enrichment-next generation sequencing. Of 67 samples tested, 25 were positive for Ss infection in the past or at the time of blood collection. The phylogenetic analysis was conducted with Maximum likelihood (ML) using RAxML on the entire HTLV-1 genome. The resulting trees were visualized in FigTree v1.4.

**Results:**

The majority of samples fell into HTLV-1 aA (cosmopolitan-transcontinental) subtype and clustered within the Latin American cluster. There was no clear evidence of the phylogenetic groups being associated with susceptibility to Ss infection. Phylogenetic analyses also showed that the Peruvian isolates showed more similarity to Iran and Germany aA strains than Japan aA, supporting the previous notion that HTLV-1aA was possibly introduced by its transcontinental dispersal out of Africa to South America during human migrations.

**Conclusion:**

Analysis of the obtained complete genome sequences of HTLV-1 would allow us to study the genetic variants important for its pathogenesis.

**Disclosure of Interest Statement:**

None.

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