MESAS REDONDAS

MOLECULAR EPIDEMIOLOGY OF HTLV-1

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The endemicity of the HTLV-1 in some populations living in remote areas of the globe, suggests the possibility of this virus to have infected human populations since thousand of years. The presence of HTLV-1 infected Efe Mbuti Pygmies and the separation of the African and non-Africans human populations being estimated to have occurred 75,000-287,000 years ago had shown that this genic flow occurred normally from pygmies to the neighboring populations. With all these evidences, it can be inferred that the HTLV-1 infection among the pygmies is oldest or resulted in more recent STLV interspecies transmissions. With the HTLV-1 endemicity among the ameridians, we could conclude that this vírus was also present in the American continent a long time ago, and it was brougth, probably, to the American continent around 15,000-35,000 years, during one or more Asian infected people migrations by the Bering Streit. Finaly, the absence of the no-humans primates in the Melanesia and Australia suggests that the HTLV-1 have existed among the Austronesian people that firstly settled the Melanésia and Austrália, around 60,000 years ago. The first HTLV-1 isolates from Japan and Caribbean showed a variability into the *env* sequence <3%, and the subsequent isolating in Congo of a divergent strain of HTLV-1 (<4%) has suggested that more distint strains could exist in particular geographic regions. It was confirmed when HTLV-1 strains were descovered in the Melanesia (8.5%). In the last years, the use of the phylogenetic analysis of the HTLV-1 LTR region has shown seven genetic subtypes: a or Cosmopolitan,; b or Central African; c or Melanesian,; d, from Central African Republic pygmies and from two patients in Cameroon and Gabon; e, from an Efe pygmy; and f, from Gabon. The HTLV-1 subtype g was recently described from Southern Cameroon. The Cosmopolitan subtype is divided into five subgroups: Transcontinental (A), Japanese (B), West African (C), North African (D), and Black Peruvian (E). Only the HTLV-1 strains of the Cosmopolitan subtype have been isolated from different endemic and no-endemics areas throughout the American continent. These strains must have been carried out of Africa by their human host either during the pre-Columbian ancient human migrations out of Africa, or possibly during the pos-Columbian slave trade between the XVI and XIX centuries. The subgroup E was characterized in Peru, in only two individuals, and the isolate Bl1Peru had a mtDNA type identical to that of some West African source populations. The strains of the Subgroup C were identified in the American places like the Caribbean area and French Guiana, excluding Brazil, where most people were brought from the West African continent, during the slave trade. As previously suggested, the relationship between Japanese and American Paleo-Indian people, and the recent Japanese immigrations to the New World could explain the presence of the subgroup B in the American continent. This HTLV-1a subgroup B has been characterized in British Columbia, Peru and Colombia, Northern, Southeast and Northeast of Brazil. Previous report suggests a post-Columbian spread of both the Japanese and Transcontinental subgroups, possibly through separate introductions from Africa, and from West and South Africa to the American continent. This subgroup A has been characterized in British Columbia, USA, Caribbean and in the Latin American countries: French Guiana, Chile, Colombia, Peru, Argentina and Brazil. The heterogeneity of HTLV subtypes and subgroups distribution shows little evidence of adaptation or natural selection, due either to immune selection pressures of the host, or to environmental factors. For this reason, HTLV provides an excellent evolutionary model, which may lead to new insights for controlling the spread and genetic evolution of these important human pathogens.