



MEETING ABSTRACT

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# HLA-G 14 bp insertion/deletion polymorphism is not associated to proviral load levels and presence of HAM/TSP in Peruvian HTLV-1 infected individuals

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## Introduction

High HTLV-1 proviral load (PVL) has been associated with HAM/TSP disease in HTLV-1-infected individuals. Human leukocyte antigen (HLA) complex plays an important role in the immune response against virus-infected cells. One mechanism involves HLA-G binding to KIR2DL4 and modulates the activities of Natural Killer and CD8+ T cells. The 14-bp insertion/deletion in the 3'UTR exon 8 of HLA-G affects the HLA-G-mRNA-stability and therefore the HLA-G-protein levels. We analyzed the distribution of the 14-bp ins/del polymorphism among HTLV-1-infected individuals to evaluate its effect both on PVL and HAM/TSP.

## Subjects and methods

394 unrelated HTLV-1-infected Peruvian individuals were included in this analysis (254 asymptomatic carriers [AC] and, 140 HAM/TSP). HLA-G 14-bp ins/del and KIR2DL4 were genotyped with PCR specific primers. PVL was determined by real-time quantitative PCR using human the endogenous retrovirus 3 as reference gene. Associations of KIR-HLA-G ins/del with PVL or HAM/TSP were evaluated through multivariate logistic and linear regression analysis using R-software.

## Results and conclusions

KIR2DL4 was observed in all the individuals evaluated. The predominant genotype was +14-bp/-14-bp, both in AC (50.8%) and HAM/TSP (50.7%,  $P>0.05$ ). HLA-G 14-bp ins/del showed no effect on PVL ( $P>0.05$ ), nor with the presence of HAM/TSP in comparison to AC ( $P>0.05$ ). This finding does not agree with the trend of high PVL observed for the -14-bp/-14-bp genotype, compared to +14-bp/-14-bp, +14-bp/+14-bp genotypes, in a Brazilian population. Our results stress the importance of replication studies in independent populations to demonstrate the association of host genetic factors with PVL or disease outcome in HTLV-1-infected subjects.

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