RETROVIROLOGY

ORAL PRESENTATION Open Access

A NKG2D Thr72Ala polymorphism is not associated with HAM/TSP and proviral load values in Peruvian HTLV-1 infected patients with HAM/TSP and asymptomatic carriers

Cynthia Bernia*, Jason Rosado, Giovanni López, Eduardo Gotuzzo, Michael Talledo

From 17th International Conference on Human Retroviruses: HTLV and Related Viruses
Trois Ilets, Martinique. 18-21 June 2015

Background

NKG2D is an activating receptor mainly expressed on Natural Killer (NK) cells, its ligands has an abnormal expression in virus infected cells and tumoral cells. The SNP rs2255336 G/A generates a substitution of alanine to threonine (NKG2D Thr72Ala) associated with a low and high cytotoxic activity of NK cells respectively. This study investigated the association between the NKG2D Thr72Ala polymorphism with HAM/TSP and PVL values in Peruvian HTLV-1 infected patients with HAM/TSP and asymptomatic carriers.

Methods

215 Peruvian HTLV-1 infected patients (142 asymptomatic carriers (AC) and 73 HAM/TSP) were evaluated. NKG2D Thr72Ala polymorphism were genotyped by polymerase chain reaction using allele-specific primers, 37 ancestry informative markers (AIM) were genotyped to correct by population stratification using the first three principal components. Proviral load (PVL) was measured using the endogenous retrovirus 3 (ERV-3). Association of the NKG2D Thr72Ala polymorphism with HAM/TSP and PVL were performed by univariate analysis using Pearson's chi-square test and Mann-Whitney U-test and by multivariate analysis using logistic regression and linear regression analysis. STATA software was used for all analysis.

Results

The NKG2D Thr72Ala polymorphism with G/G genotype showed a higher prevalence in asymptomatic carrier (64.13%) respect to HAM/TSP patients (34.87%), however these differences were not statistically significant (P>0.05). No association was found between the different genotypes of NKG2D Thr72Ala with PVL (P > 0.05), or with the presence of HAM/TSP (P > 0.05). The assessment of the association between allele G (OR = 2.3760; CI = 0.7744 to 7.2901) or the allele A (OR = 0.4209; CI = 0.1372 to 1.2914) with the presence of HAM/TSP were not statistically significant (P > 0.05).

Conclusions

The results of this study indicate the need to evaluate the association of polymorphisms in NKG2D gene with HAM/TSP and PVL in other independent populations of HTLV-1 infected individuals in order to verify an association of disease state with host genetic.

Published: 28 August 2015

doi:10.1186/1742-4690-12-S1-O37
Cite this article as: Bernia *et al.*: A NKG2D Thr72Ala polymorphism is not associated with HAM/TSP and proviral load values in Peruvian HTLV-1 infected patients with HAM/TSP and asymptomatic carriers. *Retrovirology* 2015 **12**(Suppl 1):O37.

* Correspondence: cynthiabernia@yahoo.com.pe
Inst de Med Trop Alexander von Humboldt, Univ. Peruana Cayetano Heredia, Lima, Peru