



HAL
open science

What do we learn from a Genome Wide Association Study performed on HIV-1 infected Long Term Non Progressors individuals?

Julien Guergnon, Cyril Dalmasso, Ioannis Theodorou, Agostino Riva

► To cite this version:

Julien Guergnon, Cyril Dalmasso, Ioannis Theodorou, Agostino Riva. What do we learn from a Genome Wide Association Study performed on HIV-1 infected Long Term Non Progressors individuals?. *Retrovirology*, 2009, 6 (Suppl 2), pp.O27. 10.1186/1742-4690-6-S2-O27 . inserm-00622545

HAL Id: inserm-00622545

<https://inserm.hal.science/inserm-00622545>

Submitted on 12 Sep 2011

HAL is a multi-disciplinary open access archive for the deposit and dissemination of scientific research documents, whether they are published or not. The documents may come from teaching and research institutions in France or abroad, or from public or private research centers.

L'archive ouverte pluridisciplinaire **HAL**, est destinée au dépôt et à la diffusion de documents scientifiques de niveau recherche, publiés ou non, émanant des établissements d'enseignement et de recherche français ou étrangers, des laboratoires publics ou privés.

Oral presentation

Open Access

What do we learn from a Genome Wide Association Study performed on HIV-1 infected Long Term Non Progressors individuals?

Julien Guernon^{*1}, Cyril Dalmasso², Ioannis Theodorou¹, Agostino Riva³ for the GISHEAL and PRIMO studies groups^{4,5}

Address: ¹INSERM UMR-S 945, School of Medicine Pierre et Marie Curie, Paris, France, ²University Paris 11, Villejuif, France and Genome Institute of Singapore, Singapore, ³Department of Cytomorphology, School of Medicine, University of Cagliari, Cagliari, Italy, ⁴GISHEAL study group School of Medicine Pierre et Marie Curie, Paris, France; Dominique Costagliola, INSERM U720, University Pierre et Marie Curie, Paris, France and ⁵PRIMO study group INSERM U802, University Paris-Sud 11, Le Kremlin Bicêtre, France

* Corresponding author

from *Frontiers of Retrovirology: Complex retroviruses, retroelements and their hosts* Montpellier, France. 21-23 September 2009

Published: 24 September 2009

Retrovirology 2009, **6**(Suppl 2):O27 doi:10.1186/1742-4690-6-S2-O27

This abstract is available from: <http://www.retrovirology.com/content/6/S2/O27>

© 2009 Guernon et al; licensee BioMed Central Ltd.

Background

Previous Genome Wide Association Studies performed on Elite Controllers and control HIV-1 infected individuals have shown that the MHC locus is predominantly responsible for containing plasma viremia below a threshold of detection. Here we performed a GWAS on a cohort of 160 HIV-1 infected Caucasian Long Term Non Progressors (LTNP) from the EC-funded European-African "GISHEAL" Consortium in order to explore whether novel genetic factors could account for the LTNP phenotype (i.e. maintenance of CD4 T cell counts >500 cells/ μ l and good health conditions without therapy).

Results

Frequencies of the SNPs found in LTNP were challenged vs. those of seroconverters of the French "PRIMO" cohort. Most of the SNPs strongly associated to LTNP phenotype were found in the MHC region (figure 1), especially encompassing class I and class III genes. Since 6 of the 10 top SNPs are in the HLA-B region, we confirm previous studies showing that class I HLA-B27 and HLA-B57 alleles are strongly correlated to the LTNP condition. In addition, about 65% of our LTNP naturally resist to HIV disease progression independently of HLA-B27/B57; in this regard, quite strikingly, 11 over 32 SNPs with a Q-value <

0.05 are located in MHC class III region in GISHEAL LTNP cohort.

Conclusion

Thus, our findings support the concept that different MHC loci significantly contribute to long-term control of HIV disease progression in the absence of antiretroviral therapy and provide novel evidence of a seminal role of MHC class III gene polymorphisms in determining the LTNP phenotype.