



HAL
open science

Capture in the metabolic arena: co-selection of gamma and deltaretrovirus envelope glycoproteins and their receptors

Marc Sitbon, Hiroyuki Abe, Valérie Courgnaud, Donatella Giovannini, Felix Kim, Madakasira Lavanya, Nicolas Manel, Jawida Touhami, Wiliam Switzer, Pierre Castelnau, et al.

► To cite this version:

Marc Sitbon, Hiroyuki Abe, Valérie Courgnaud, Donatella Giovannini, Felix Kim, et al.. Capture in the metabolic arena: co-selection of gamma and deltaretrovirus envelope glycoproteins and their receptors. *Frontiers of Retrovirology: Complex retroviruses, retroelements and their hosts*, Sep 2009, Montpellier, France. pp.I20, 10.1186/1742-4690-6-S2-I20 . inserm-00668488

HAL Id: inserm-00668488

<https://inserm.hal.science/inserm-00668488>

Submitted on 9 Feb 2012

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.

Invited speaker presentation

Open Access

Capture in the metabolic arena: co-selection of gamma and deltaretrovirus envelope glycoproteins and their receptors

Marc Sitbon^{*1}, Hiroyuki Abe¹, Valérie Courgnaud¹, Donatella Giovannini¹, Felix Kim¹, Madakasira Lavanya¹, Nicolas Manel¹, Jawida Touhami¹, Wiliam M Switzer², Pierre Castelnau³, Emmanuelle Lagrue³, Lydie Nadal-Desbarats⁴, Karine de Guillen⁵, Christian Roumestand⁵ and Jean-Luc Battini¹

Address: ¹Institut de Génétique Moléculaire de Montpellier (IGMM), CNRS-UMR 5535, Université Montpellier 1 et 2, IFR 122, 34293 Montpellier Cedex 5, France, ²Centers for Disease Control and Prevention, Atlanta, Georgia, USA, ³Service de Neurologie et Neurochirurgie Pédiatrique, Centre de Pédiatrie Gatién-de-Clocheville, CHRU de Tours, 37044 Tours cedex 01 INSERM U930, France, ⁴INSERM U930, Université François Rabelais de Tours, 37032 Tours, France and ⁵Centre de Biochimie Structurale (CBS), UMR UM1/5048 CNRS/554 INSERM, 29 rue de Navacelles, 34090, Montpellier Cedex, 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):I20 doi:10.1186/1742-4690-6-S2-I20

This abstract is available from: <http://www.retrovirology.com/content/6/S2/I20>

© 2009 Sitbon et al; licensee BioMed Central Ltd.

Although all infectious and replication-competent retroviruses harbor an *env* gene, the origin of *env* remains unknown except for that of a few invertebrate retroviruses. It is generally admitted that infectious retroviruses have evolved from endogenous viral retrotransposons by insertion of an "external" gene that encodes for a fusion glycoprotein (*env* capture). In 2000, Malik *et al.* provided the first formal evidence for the origin of *env* in several invertebrate retroviruses. For instance, they showed that *env* of *Gypsy*, an infectious *Drosophila* retrotransposon, has been "captured" from a fusion protein-encoding gene of a baculovirus, a totally unrelated large DNA enveloped virus.

Vertebrate retroviruses cover 7 genera distinguished by their *gag* (capsid encoding) and *pol* (enzyme encoding) genes. The gammaretroviruses (murine leukemia viruses, MLV as a prototype) and deltaretroviruses (the human T cell leukemia virus, HTLV as a prototype) are the most distant genera according to their *pol* genes. However, we reported that HTLV *env* is most closely related to MLV *env*, sharing similar modular organization and motifs even within the receptor-binding domain (RBD), the Env most variable sequence. Accordingly, swapping the RBD-encoding regions between the two types of Env yielded func-

tional chimeras. We argued that this common ancestry between the *env* of remotely related retroviruses is also in favor of an *env* capture scenario by vertebrate retroviruses. Nonetheless, the origin of these *env*, and more specifically their RBD, remains unknown.

Based on the gammaretrovirus Env modular organization, we derived soluble RBD domains of different gamma and deltaretroviruses. This has been instrumental to the identification of Glut1, the major glucose transporter, as the cognate receptor of HTLV-1 and 2 Env. We further showed that Glut1 binds all known HTLV or S(imian)TLV types and that intracellular interaction of HTLV or STLV RBD with Glut1 modulates glucose transport and glycolysis. Of most interest is that, like Glut1, all of the receptors identified so far for gammaretrovirus Env belong to the family of multimembrane-spanning molecules and that those for which a function has been determined are all metabolite transporters (amino acids, inorganic phosphate, vitamins, etc.).

The selection as Env receptors of metabolite transporters that shuttles from cytoplasmic pools to the cell surface and the cytoplasmic interaction between RBD and their

cognate receptors have us to postulate that gamma and deltaretrovirus Env, and more particularly their RBD modules, are related to transporter chaperone molecules that modulate their cell surface translocation.

Publish with **BioMed Central** and every scientist can read your work free of charge

"BioMed Central will be the most significant development for disseminating the results of biomedical research in our lifetime."

Sir Paul Nurse, Cancer Research UK

Your research papers will be:

- available free of charge to the entire biomedical community
- peer reviewed and published immediately upon acceptance
- cited in PubMed and archived on PubMed Central
- yours — you keep the copyright

Submit your manuscript here:
http://www.biomedcentral.com/info/publishing_adv.asp

