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Host laboratory:

IBS <https://www.ibs.fr/>

Host group/team:

Epigen: Epigenetics & molecular pathways

Title of the M2 research internship:

Nuclear import of HIV-1 Rev : a comprehensive analysis of molecular interactions with host cell proteins

Project summary:

Background: The HIV-1 regulatory protein Rev is a nucleocytoplasmic shuttling protein essential for viral replication. Rev mediates the specific nuclear export of viral RNA transcripts needed to synthesize new viral particles. Rev is synthesized in the early phase of infection and is imported into the nucleus by direct interaction with host cell proteins Importin β (Imp β) and Nucleophosmin (NPM1) (1-3). The interaction between Rev and Imp β is essential for Rev nuclear import (4), while the Imp β -dependent interaction between Rev and NPM1 enhances the nuclear import of Rev (5). However, despite the crucial role of Imp β and NPM1 in the viral infection cycle (4,6), the molecular basis of these interactions remains poorly understood.

Preliminary results: We recently characterised the interaction between Imp β and Rev through extensive biochemical, biophysical and computational analyses, allowing us to report the first 3D structural model of the Imp β /Rev complex (7). Preliminary data by electron microscopy (negative stain and cryo-EM) indicate that this complex is suitable for single particle analysis. Additionally, we identified NPM1 domains that interact directly with Rev as well as with Imp β , suggesting the existence of a ternary complex that may play a regulatory role during the viral infection cycle.

Aims: The overall project aims to (i) determine the EM structures of Rev in complex with Imp β and NPM1, (ii) characterise the Rev/NPM1 interaction by a set of biochemical and biophysical techniques, (iii) study the dynamics of Imp β /Rev/NPM1 complex formation by cross-linking/mass spectrometry analyses and (iv) investigate the effect of Rev, Imp β and NPM1 point mutations on Rev nuclear import in human cells by fluorescence microscopy.

According to his/her interest and background, the student will participate in one or more of these objectives.

Techniques: Protein purification, fluorescence polarization, ITC, SEC-MALLS, mass photometry, crosslinking, native mass spectrometry, cell culture, fluorescence microscopy, negative-stain, cryo-EM, NMR.

Keywords:

HIV-1, protein complex, structural biology

Relevant publications of the team:

Spittler D, Indorato RL, Boeri Erba E, Delaforge E, Signor L, Harris SJ, Garcia-Saez I, Palencia A, Gabel F, Blackledge M, Noirclerc-Savoie M, Petosa C. 2022. Binding stoichiometry and structural model of the HIV-1 Rev/importin β complex. *Life Sci Alliance* 5. <https://doi.org/10.26508/lsa.202201431>

Ben Fadhel N, Signor L, Petosa C, Noirclerc-Savoie M. 2019. Phosphomimetic mutations modulate the ability of HIV-1 Rev to bind human Importin β in vitro. *Matters* (ISSN: 2297-8240). <https://hal.univ-grenoble-alpes.fr/view/index/docid/3605154>

Coscia F, Estrozi LF, Hans F, Malet H, Noirclerc-Savoie M, Schoehn G, Petosa C. 2016. Fusion to a homo-oligomeric scaffold allows cryo-EM analysis of a small protein. *Sci Rep* 6:30909. <https://doi.org/10.1038/srep30909>

Cingolani G, Petosa C, Weis K, Muller CW. 1999. Structure of importin-beta bound to the IBB domain of importin-alpha. *Nature* 399:221-9. <https://doi.org/10.1038/20367>

References

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2. Li et al. 2005 <https://doi.org/10.1038/sj.cr.7290370>
3. Nouri et al. 2015 <https://doi.org/10.1371/journal.pone.0143634>
4. Truant & Cullen 1999 <https://doi.org/10.1128/MCB.19.2.1210>
5. Szébeni et al. 1997 <https://doi.org/10.1021/bi962793i>
6. Passos-Castilho et al. 2018 <https://doi.org/10.1016/j.virol.2017.12.021>
7. Spittler et al. 2022 <https://doi.org/10.26508/lsa.202201431>