

Poster presentation

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Structural basis for HIV-1 DNA integration in the human genome

Fabrice Michel¹, Sylvia Eiler¹, Florence Granger¹, Jean-François Mouscadet², Marina Gottikh³, Alexis Nazabal⁴, Stéphane Emiliani⁵, Richard Benarous⁶, Dino Moras¹, Patrick Schultz¹ and Marc Ruff*¹

Address: ¹IGBMC, UDS, U596 Inserm, UMR7104 CNRS, 67404 Illkirch; France, ²Laboratoire de Biotechnologie et Pharmacologie Génétique Appliquée, CNRS, UMR8113, ENS-Cachan, 94235 Cachan, France, ³Belozersky Institute of Physico-Chemical Biology, Moscow State University, 119992 Moscow, Russia, ⁴CovalX, Technoparkstrasse, 1, CH-8005, Zürich, Switzerland, ⁵Institut Cochin, Université Paris Descartes, CNRS (UMR8104), Inserm, U567, Paris, France and ⁶CellVir SAS, Evry, France; Hybrigenics SA, Paris, France

* Corresponding author

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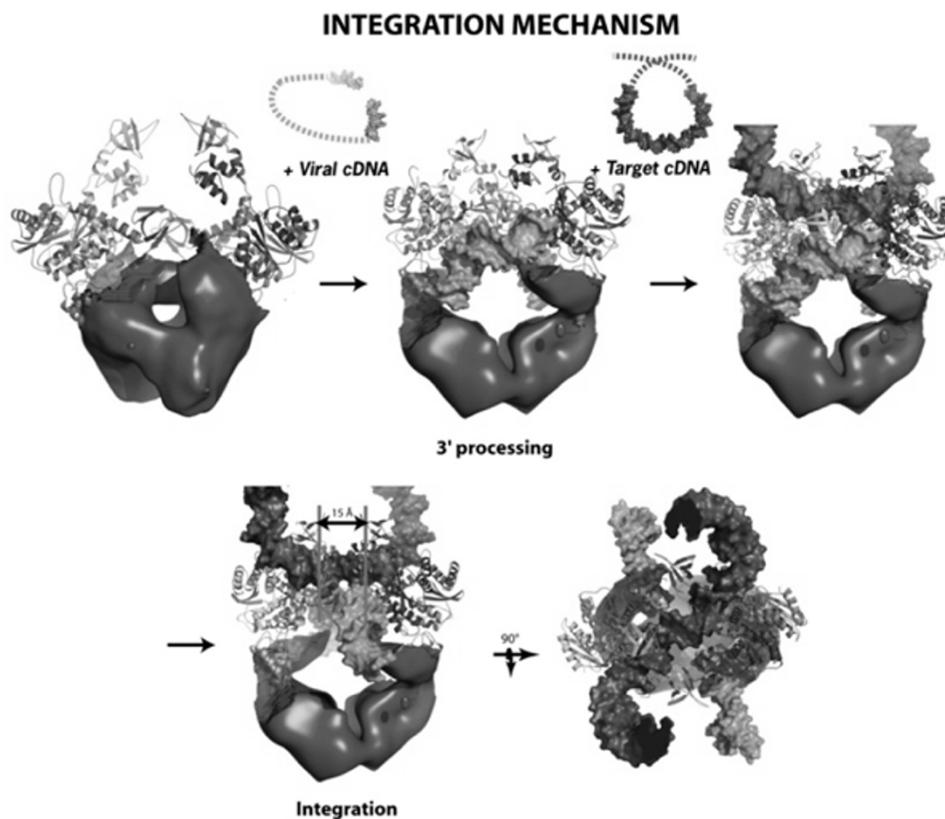
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Integration of the human immunodeficiency virus type 1 (HIV-1) cDNA into the human genome is catalyzed by the viral integrase protein that requires the lens epithelium-derived growth factor (LEDGF), a cellular transcriptional coactivator. In the presence of LEDGF, integrase forms a stable complex *in vitro* and importantly becomes soluble by contrast with integrase alone which aggregates and precipitates. Using cryo-electron microscopy (EM) and single-particle reconstruction, we obtained three-dimensional structures of the wild type full length integrase-LEDGF complex with and without DNA [1]. The stoichiometry of the complex was found to be (integrase)₄-(LEDGF)₂ by mass spectrometry analysis and existing atomic structures were unambiguously positioned in the EM map. *In vitro* functional assays reveal that LEDGF increases integrase activity likely in maintaining a stable and functional integrase structure. DNA-Protein cross-linking experiments show specific interaction between viral DNA and the C-terminal domain of integrase. Upon DNA binding, IN undergoes large conformational changes. Cryo-EM structure underlines the path of viral and target DNA and a model for DNA integration in human DNA is proposed (see fig. 1, overleaf).

**Figure 1**

Proposed mechanism for the integration of viral cDNA into the host genome: The LEDGF envelope is represented in blue; the integrase tetramer is shown as atomic structures. The viral DNA is in orange and the target DNA in red. On target DNA binding, there is a conformational change of the integrase proteins to position the viral DNA for the integration within 5 bases pairs in the target DNA.

References

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