Retrovirology

Oral presentation

Insights into the activation of transcription elongation by lentiviruses: structure of the Cyclin T1-Tat-TAR RNA complex

Kanchan Anand[1,2], Nadine Czudnochowski[1], Friederike Vollmuth[1], Antje Schulte[1] and Matthias Geyer*[1]

Address: [1]Max Planck Institute for Molecular Physiology, Dept. Physical Biochemistry, 44227 Dortmund, Germany and [2]EMBL Heidelberg, Structural and Computational Biology Programme, 69117 Heidelberg, Germany

* 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):O18 doi:10.1186/1742-4690-6-S2-O18

This abstract is available from: http://www.retrovirology.com/content/6/S2/O18

The replication of many retroviruses is mediated by a transcriptional activator protein, Tat, which activates RNA polymerase II at the level of transcription elongation. Tat interacts with Cyclin T1 of the positive transcription elongation factor P-TEFb to recruit the transactivation-response TAR RNA that acts as a promoter element in the transcribed 5' end of the viral long terminal repeat. Here, the structure of the cyclin box domain of CycT1 in complex with the Tat protein from equine infections anemia virus and its corresponding TAR RNA is presented. The basic RNA recognition motif of Tat adopts a helical structure whose flanking regions interact with a cyclin T-specific loop in the first cyclin box repeat. Together both proteins coordinate the stem-loop structure of TAR. Our findings show that Tat binds to a similar surface on CycT1 as the recognition motifs from substrate and inhibitor peptides were found to interact within Cdk/Cyclin pairs. With the first insights into the structural basis of CycT1-Tat-TAR recognition solved the rational identification of specific target sites to interfere with the tripartite complex assembly is becoming possible and the specificity for lentiviral vector systems apparent.