

Oral presentation

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Proteomic characterization of HIV-1 Tat interactome

VW Gautier*¹, N O'Donohu², S Pennington² and WW Hall¹

Address: ¹Centre for Research in Infectious Diseases, Conway Institute, University College Dublin, Dublin, Ireland and ²Protective Research Centre, Conway Institute, University College Dublin, Dublin, Ireland

* Corresponding author

from 2006 International Meeting of The Institute of Human Virology
Baltimore, USA. 17–21 November, 2006

Published: 21 December 2006

Retrovirology 2006, **3**(Suppl 1):S107 doi:10.1186/1742-4690-3-S1-S107

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The HIV-1 regulatory protein, Tat (86aa), displays pleiotropic activities, ultimately, contributing to HIV-1 pathogenesis. Sequence analysis reveals a unique arrangement of five distinct functional domains. Additionally, Tat has been described as a natively unfolded protein with fast dynamics. Collectively these findings suggest that Tat is a protein suited for multiple protein interactions and highlight how Tat can elicit multifaceted activities. To achieve the unprecedented comprehensive interaction map of Tat, we have designed and performed high-throughput affinity chromatography coupled with MS/MS.

We successfully identified a total of 270 proteins with size ranging from 15 kD to 400 kD, the majority of which have not been previously identified as Tat partners. The entire dataset was organised according to distinct cellular processes, which remarkably resulted in the wide functional distribution of the proteins over 15 categories. We then assigned each individual protein to their respective complexes and obtained functional interaction maps.

Our study clearly reveals that Tat is involved in supercomplexes encompassing a multitude of biochemical entities and particularly emphasises the scope of combinatorial control involved in the coordination of mRNA biogenesis and maturation, and DNA replication and repair by HIV-1 Tat.