

Poster presentation

Open Access

Pentapeptide overlapping between human immunodeficiency viruses and *Homo sapiens* proteomes is higher than 90%

Darja Kanduc

Address: University of Bari, Bari, Italy
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):P44 doi:10.1186/1742-4690-6-S2-P44

This abstract is available from: <http://www.retrovirology.com/content/6/S2/P44>

© 2009 Kanduc; licensee BioMed Central Ltd.

We used sequence-to-sequence peptide matching to analyze the similarity level of the HIV-1, HIV-2 and HTLV polyprotein sequences to the human proteome. The following results were obtained: 1) pentapeptides from the viral polyproteins are widely, repeatedly and intensively represented in a large number of human proteins; 2) high level of similarity of viral versus human proteomes is still present even using esa- or eptapeptide motifs as probes for sequence identity scanning; 3) a relatively limited number of viral pentameric fragments (about 10% or less) are unique to the viruses with no similarity to the human host; 4) the distribution of the zero similarity pentapeptides is not random in the three main immunodeficiency virus strains, with a maximum clustering in the HIV-2 p160 aa 1007-1019 sequence. The data are important in relation to the role of molecular mimicry in the genesis and diagnosis of immunodeficiency diseases, and the use of low similarity amino acid sequences as a peptidome platform for anti-HIV vaccine constructs exempt from harmful collateral cross-reactions.