Retrovirology

Poster presentation

P16-13. A greater breadth of HIV-1-specific T cell responses detected using mosaic peptides compare to consensus peptides

H Yang*[1], H Yan[2], W Li[2], X Zhang[2], W Fischer[3], H Zhang[2], H Wu[2], BT Korber[3], AJ McMichael[1], X Xu[1] and N Goonetilleke[1]

Address: [1]MRC Human Immunology Unit, Weatherall Institute of Molecular Medicine, Oxford, UK, [2]YouAn Hospital, Capital Medical University, Beijing, PR China and [3]Los Alamos National Laboratory, Los Alamos, NM, USA

* Corresponding author

from AIDS Vaccine 2009
Paris, France. 19–22 October 2009

Published: 22 October 2009

Retrovirology 2009, **6**(Suppl 3):P242 doi:10.1186/1742-4690-6-S3-P242

This abstract is available from: http://www.retrovirology.com/content/6/S3/P242

Background

The accurate identification of HIV-1-specific T cell responses is important for determining the relationship between immune responses and viral control. Overlapping peptides were synthesized to span gag and nef core 'mosaic' proteins. Mosaic proteins were assembled from fragments of natural sequence using an optimized computational biology method (W. Fischer et al., Nature Medicine, 2007). These proteins resemble natural proteins and were designed to maximize the coverage of potential T cell epitopes. Whilst recent studies have shown that mosaic proteins are highly immunogenic in mice models (W.P. Kong et al., J Virol, 2009), it remains unknown whether mosaics when compared with consensus peptide sets will detect a greater breadth of T cell responses in natural HIV-1 infection.

Methods

Twenty-six HIV-1 clade B infected antiretroviral therapy naive individuals were included in the study. T cell responses were assessed by an IFN-γ-ELISPOT assay using overlapping consensus peptides that span the whole gag and the conserved nef region base on clade B virus and corresponding mosaic peptide sets.

Results

Initial studies in 26 patients demonstrated that mosaics detected a greater breadth of responses than consensus peptides in 16 subjects. In 7 subjects the same breadth of responses was detected and in 3 subjects consensus peptides detected more epitopes. Overall, T cells recognized an average of 5 mosaic peptides (range, 1–12) and 3 consensus peptides (range, 1–11) that was statistically significant ($p < 0.0001$, Wilcoxon signed-rank test using GraphPad Prism software).

Conclusion

Studies suggest an increased coverage of T-cell epitopes derived from natural infection by mosaic peptides. The inclusion of mosaic peptides is recommended to improve detection of HIV-1 specific T cells in natural infection.