Retrovirology

Poster presentation

P16-44. Investigating T cell immune responses in Cameroon, a country with broad HIV-1 genetic diversity

M Tongo*[1], E Ebong[1], L Zembe[2], E Mpoudi Ngole[1] and W Burgers[2]

Address: [1]Ministry of Research and Innovation, Institute of Medical Research and Studies of Medicinal Plants, YAOUNDE, Cameroon and [2]Institute of Infectious Diseases and Molecular Medicine, Cape Town, South Africa

* Corresponding author

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Background

HIV-1 diversity presents a challenge for the development of an effective HIV vaccine. Cameroon in central Africa, exhibits very broad HIV-1 genetic diversity. That makes it one of the few places in the world where vaccine efficacy can be tested against a broad range of subtypes and recombinants. The aim of the study is to assess cross-clade T cell responses in HIV-infected Cameroonians.

Methods

PBMCs were obtained from 36 HIV-1 infected blood donors. T cell responses were determined using the IFNγ ELISPOT assay using cryopreserved PBMC. Cells were stimulated with overlapping peptide pools derived from HIV-1 group M consensus Gag and Nef proteins. The first line assay used a pool-matrix screening approach, and this was followed by a confirmatory assay to identify single reactive peptides.

Results

Thirty-six samples were tested in the IFNγ ELISPOT assay; 32 (89%) responded to at least 1 peptide pool. The median magnitude response was 1995 spot forming units (SFU)/106 PBMC among the responders (range 130 to 12853). At the protein level the median response to Gag was 1083 SFU/106 PBMC, while the median response to Nef was 1070 SFU/106 PBMC. The median number of peptides recognized per individual was 5 (range 1 to 16) with no difference in number of peptides recognized in Gag and Nef ($p = 0.1793$). Most of the reactive peptides targeted the conserved regions both in Gag and Nef. The magnitude of the total response correlated inversely with CD4 count ($r = -0.4026$ $p = 0.0165$), but no relationship with viral load was evident. At the protein level, there was no relationship between the Gag or Nef response and CD4 count or viral load.

Conclusion

These data show that high magnitude T cell responses are detectable in HIV-1 infected Cameroonians using Group M peptide reagents, which likely reflects the broad HIV-1 genetic diversity in the population.