ORAL PRESENTATION



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Vaccine responses to conserved regions of the HIV-1 proteome are associated with an increased capacity to inhibit multiple virus isolates ex vivo

A Ashraf^{1*}, J Kopycinski¹, H Cheeseman¹, F Lala¹, J Czyzewska-Khan¹, A Spentzou¹, DK Gill¹, M Keefer², J Excler³, P Fast³, P Hayes¹, JH Cox³, J Gilmour¹

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Background

The majority of assays currently used to assess HIV-1 vaccine candidate immunogenicity in humans fail to predict protection against HIV-1 acquisition or control of viraemia. However, a correlation between in vivo and ex vivo control mediated by CD8+ T-cell populations has been described using an ex vivo virus inhibition assay (VIA) in chronically infected individuals and vaccinated non-human primates. Here we attempt to relate the specificity of vaccine-induced virus-specific CD8 responses to the inhibition of HIV-1 ex vivo.

Methods

Using peptide epitope mapping, we assessed the breadth and specificity of CD8 T-cell responses induced by vaccination using two adenovirus serotype 35 (Ad35) vectors containing gag, reverse transcriptase, integrase and nef (Ad35-GRIN) and env (Ad35-ENV), respectively, derived from HIV-1 subtype A isolates. The conserved regions targeted by these 25 subjects were related to the capacity of vaccine-induced CD8 T-cells to inhibit replication of a cross-clade panel of HIV-1 isolates using the VIA.

Results

A median of 4 peptides were recognised in vaccinated individuals (range 1-9). When related to the log reduction of p24 production as measured in the VIA, mapping data suggest that targeting immunodominant responses towards highly conserved regions of the HIV-1 proteome tended towards an increased ability to inhibit multiple clades of HIV-1 ex vivo.

¹International AIDS Vaccine Initiative (IAVI), Imperial College London, London, UK Full list of author information is available at the end of the article

Conclusion

These data support the plausibility of inducing conserved CD8+ T cell responses using a consensus HIV-1 subtype A sequence in an adenovirus-based vector.

Author details

¹ International AIDS Vaccine Initiative (IAVI), Imperial College London, London, UK. ² University of Rochester School of Medicine & Dentistry, Rochester, NY, USA. ³ International AIDS Vaccine Initiative (IAVI), New York, NY, USA.

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