Retrovirology

Poster presentation

P17-05. Dealing with HIV-1 diversity

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Background

One of the big roadblocks in development of HIV-1/AIDS vaccines is the enormous diversity of HIV-1, which could limit the value of any HIV-1 vaccine candidate currently under test.

Methods

To address the HIV-1 variation, we designed a novel T cell immunogen, designated HIVconsv, by assembling the 14 most conserved regions of the HIV-1 proteome into one chimaeric protein. Each segment is a consensus sequence from one of the four major HIV-1 clades A, B, C and D, which alternate to ensure equal clade coverage. The gene coding for the HIVconsv protein was inserted into a number of vaccine vectors, which were used in a multiple heterologous prime-boost combination.

Results

Complex vaccination regimen induced strong, broad, polyfunctional HIV-1-specific CD8 and CD4 T cell responses non-human primates.

Conclusion

This vaccine approach provides an attractive and testable alternative for overcoming the HIV-1 variability, while focusing T cell responses on regions of the virus that are less likely to mutate and escape. Furthermore, this immunogen has merit in its simplicity. The potential of complex heterologous regimen will be discussed. Phase I clinical trials in healthy and HIV-1-infected individuals testing HIVconsv vaccines have been funded and are under preparation.