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POSTER PRESENTATION

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# Continuous evolution of HIV-1 more than ten years after infection in an elite neutralizer

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## Background

The viral evolution of HIV-1 and its escape to autologous neutralizing antibodies (Nabs) during the early years of infection have been analyzed in depth. In contrast, little is known about neither the long-term evolution of the virus in patients who developed broadly Nabs (bNabs) nor the mechanism of escape in presence of these bNabs.

## Methods

We have studied the viral population infecting an HIV-1 infected long term non progressor (LTNP) who had developed Nabs toward all tier 2/3 viruses (6 clades) tested, 9 years after infection, and was then followed up over 7 years. Sixty-nine env clones issued from sequential blood samples collected from 9 years to 16 years post-infection were obtained. Thirteen infectious clones representative of the genetic diversity of variants present at the different time-points were selected. Pseudotyped viruses harboring these different envelopes were generated and their sensitivity to neutralization was analyzed.

## Results

Evidence of ongoing viral evolution was found, supported by both the phylogenetic analyses that showed a continuous diversification and an increasing divergence over-time. The mean autologous neutralization titers of the sequential sera toward the 13 env variants significantly increased during the period of late follow-up. The env pseudoviruses displayed a broad range of sensitivity to the autologous sera, with the most resistant variant identified at the last visit suggesting that it represented a late emerging escape variant. We identified 5 amino acids substitutions that appeared associated with escape to

bNabs. They were V319I/S, R/K355T, R/W429G, Q460E and G/T463E, in V3, C3 and V5 regions.

## Conclusion

This study showed that HIV-1 may continue to evolve in presence of both broadly neutralizing antibodies and increasing autologous neutralizing activity more than 10 years post-infection. Such material may provide opportunities to reveal the molecular determinants of escape of HIV-1 to highly potent broadly neutralizing antibodies.

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