

Cologne Evolution Colloquium

Molecular Basis of
Evolutionary Innovations
SFB 680

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Within-host evolution of HIV

RNA viruses rapidly evade host immune responses by changing targeted proteins. We used deep sequencing of HIV populations from many consecutive samples to track virus evolution and quantify competing tendencies of immune escape and rapid replication. Accurate measurements of minor variant frequencies allowed us to estimate the landscape of fitness cost at almost all positions of the HIV genome. In addition to HIV RNA from plasma samples during untreated HIV infection, we sequenced latently integrated HIV genomes after many years of therapy. By comparing these sequences to pre-treatment samples, we quantify establishment, turn-over, and maintenance of the latent HIV-1 reservoir.

Wednesday, May 3, 2017, 17:00

University of Cologne, Institute for Theoretical Physics
Conference Room 2, Ground Floor

Hosted by Michael Lässig