Global mapping of HIV-1 and host-macrophages molecular interactions.

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HIV-1 *in vitro* models using human primary macrophages are strongly limited by the low rate of productive infection and latency and the difficulty of studying separately the molecular modulations occurring in productively infected, latent and bystander cells (uninfected and abortively infected cells not expressing HIV-1 proteins).

We developed a collection of replicative reporter viruses allowing the sorting of these different populations (productive, bystander and latent cells) through an immunomagnetic capture of small surface epitopes (HA, HSA) or flow-cytometry sorting of fluorescent proteins (ZsGreen, E2-Crimson) co-expressed with the viral genome in productive and latent cells.

We used these vectors to isolate infected Macrophages and analyzed their transcriptomic and proteomic profiles using high throughput RNA sequencing combined with Protein Mass Spectrometry analysis. Integrated bioinformatics analysis of -omics data allowed us to detect with a high resolution the modulated transcripts and proteins controlling the successful replication of HIV-1 in macrophages.

We identified several new genes, miRNA, lncRNA and proteins, as well as not-previously described cellular pathways that could be keys for a specific eradication of infected and latent cells. The acquired data shed new light on HIV-1 replication mechanisms and will allow the emergence of new specific inhibitory strategies against the constitution of persisting virus reservoirs.