Host genomics of the HIV-1 reservoir size and its decay rate during suppressive antiretroviral treatment


BACKGROUND
The primary hurdle for the eradication of HIV-1 is the establishment of a latent viral reservoir early after primary infection. Here we investigated the potential influence of human genetic variation on the HIV-1 reservoir size and its decay rate during suppressive antiretroviral treatment (ART).

SETTING
Genome-wide association study and exome sequencing study to look for host genetic determinants of HIV-1 reservoir measurements in patients enrolled in the Swiss HIV Cohort Study (SHCS), a nation-wide prospective observational study.

METHODS
We measured total HIV-1 DNA in peripheral blood mononuclear cells from study participants, as a proxy for the reservoir size, at three time points over a median of 5.4 years, and searched for associations between human genetic variation and two phenotypic readouts: the reservoir size at the first time point and its decay rate over the study period. We assessed the contribution of common genetic variants using genome-wide genotyping data from 797 patients with European ancestry enrolled in the Swiss HIV Cohort Study and searched for a potential impact of rare variants and exonic copy number variants using exome sequencing data generated in a subset of 194 study participants.

RESULTS
Genome- and exome-wide analyses did not reveal any significant association with the size of the HIV-1 reservoir or its decay rate on suppressive ART.

CONCLUSIONS
Our results point to a limited influence of human genetics on the size of the HIV-1 reservoir and its long-term dynamics in successfully treated individuals.

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