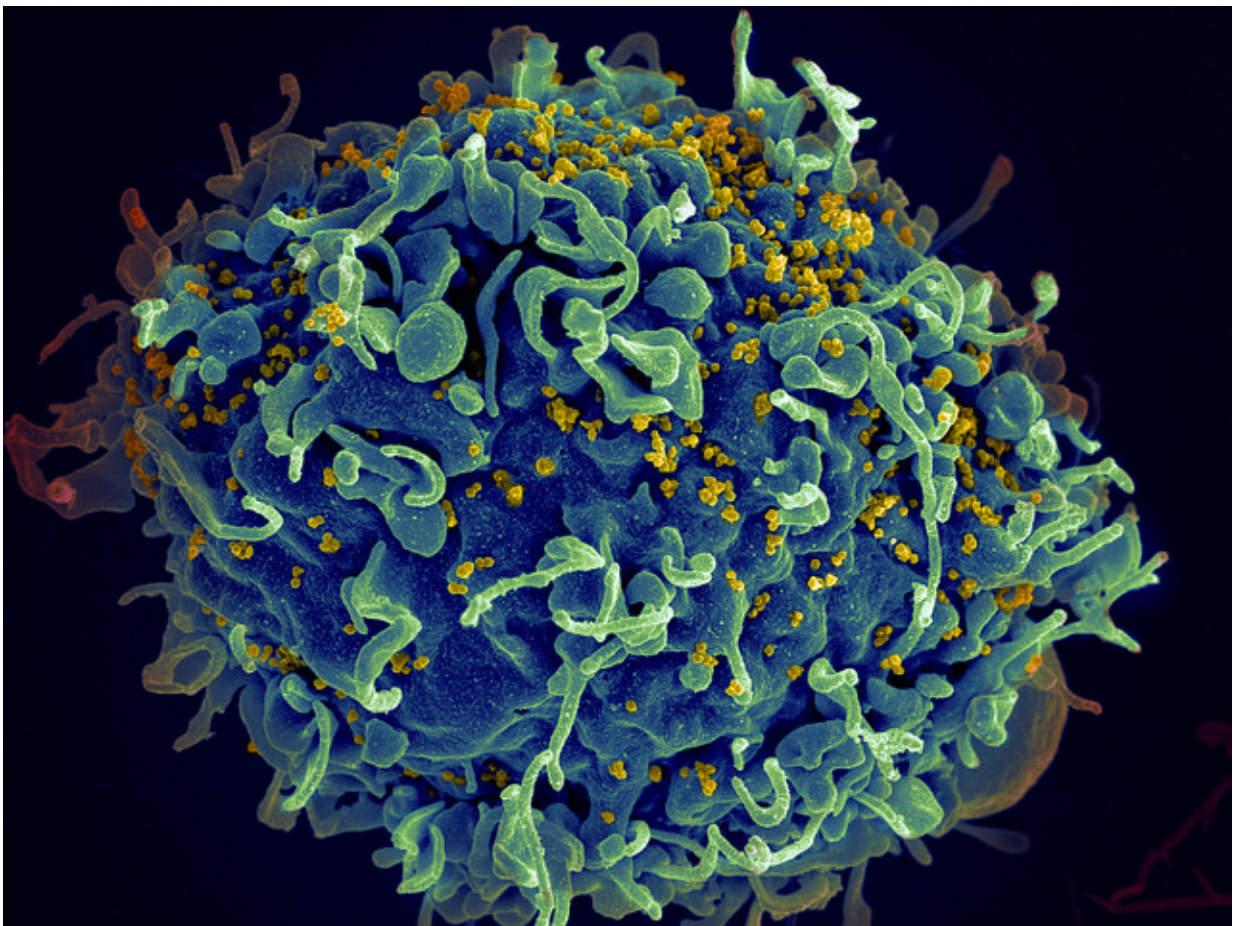


Genetics of both virus and patient work together to influence the course of HIV infection

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HIV, the AIDS virus (yellow), are infecting a human cell. Credit: ZEISS Microscopy / Flickr

Viral and human genetics together account for about one third of the differences in disease progression rates seen among people infected with the human immunodeficiency virus (HIV), according to new research published in *PLOS Computational Biology*. The findings suggest that patient genetics influences disease progression by triggering mutations in the HIV viral genome.

People with HIV experience different rates of [disease progression](#). HIV progresses faster in people with a higher [viral load](#)—the amount of genetic material from the HIV virus found in an infected person's blood.

Previous research has shown that an infected person's genetics and the genetics of their particular HIV strain both influence viral load. István Bartha of École Polytechnique Fédérale de Lausanne, Switzerland, and colleagues are now the first scientists to investigate the relative impacts of human and viral genetics on viral load within the same group of patients.

The researchers collected patient and viral genetic data from 541 people with HIV. They used a computational modeling method known as linear mixed modeling to determine how human and viral genetics might explain differences in viral load between the patients.

They found that genetic differences between HIV strains explain 29 percent of differences in viral load between patients, while human genetic variation explains 8.4 percent. Together, they explain just 30 percent of viral load variation, indicating that patient genetics exert most of its influence by inducing genetic mutations in the HIV virus as it multiplies inside the patient.

"Our paper demonstrates that the genetic make-up of both the patient and the infecting virus contribute to the clinical course of HIV infection," says study director Jacques Fellay.

Further research with a larger group of patients is needed to confirm and refine the findings. Nonetheless, "combining host and pathogen data gave us new insight into the genetic determinants of HIV control," Fellay says. "A similar strategy could be used to better understand other chronic infectious diseases."

More information: Bartha I, McLaren PJ, Brumme C, Harrigan R, Telenti A, Fellay J (2017) Estimating the Respective Contributions of Human and Viral Genetic Variation to HIV Control. *PLoS Comput Biol* 13(2): e1005339. DOI: [10.1371/journal.pcbi.1005339](https://doi.org/10.1371/journal.pcbi.1005339)

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