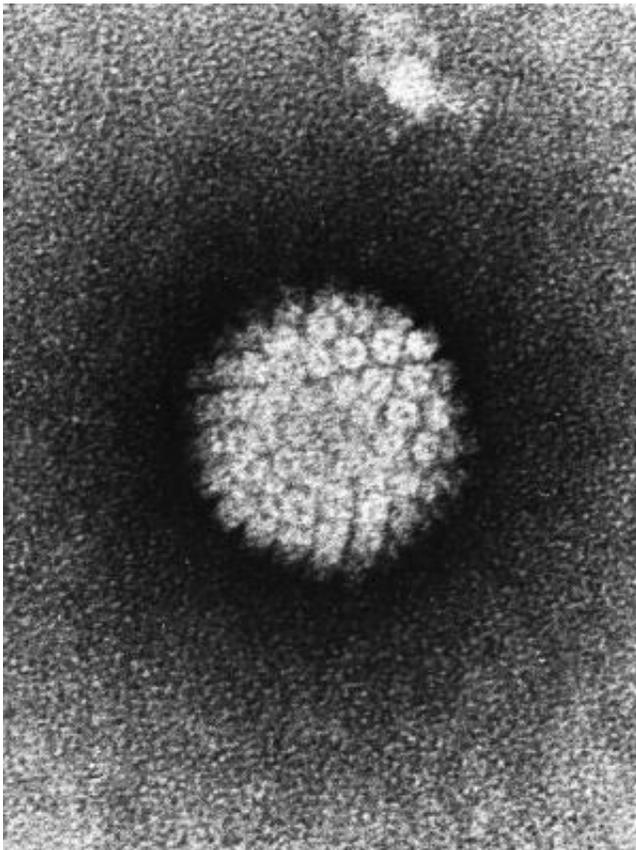


## Ancient hominid 'hanky panky' also influenced spread of STIs

October 17 2016

---



TEM of papillomavirus. Credit: Public Domain

With recent studies proving that almost everyone has a little bit of Neanderthal DNA in them——up to 5 percent of the human genome——it's become clear our ancestors not only had some serious hominid 'hanky panky' going on, but with it, a potential downside: the spread of

sexually transmitted infections, or STIs.

For wherever life goes, germs are soon to follow.

In the case of the most common STI, [human papillomaviruses](#) (HPVs), almost everyone hosts a number of infections, with strain HPV16 responsible for most cervical and oral cancers.

By reconstructing the ancestry and timing of the family tree of HPV16 in greater detail than ever before, and by comparing the evolutionary histories of viruses and humans, a new pattern has emerged. Now, researchers have generated compelling evidence that HPV16 co-diverged with archaic and modern humans—only to be repopulated at a much later date through their contact by Neanderthals, challenging the assumption that HPV16 co-evolved with modern humans. The study, by Ville Pimenoff at the Catalan Institute of Oncology and Ignacio Bravo at the French National Center for Scientific Research was published in the advanced online edition of *Molecular Biology and Evolution*.

During the evolution of HPV16, variants A and B/C/D co-diverged with archaic and modern humans, respectively. When populations of modern humans left Africa and had sexual intercourse with Neanderthals and Denisovans, they were infected by the viral variant that had evolved with [archaic humans](#), and this virus thrived and expanded among modern humans

This scenario finally explains unsolved questions: why human diversity is largest in Africa, while HPV16 diversity is largest in East-Asia, and why the HPV16A variant is virtually absent in Sub-Saharan Africa while it is by far the most common one in the rest world.

"Oncogenic viruses are very ancient," said Ignacio Bravo. "The history of humans is also the history of the viruses we carry and we inherit. Our

work suggests that some aggressive oncogenic viruses were transmitted by sexual contact from archaic to [modern humans](#)."

They propose that interactions between the host and viral genomes may explain why most humans are exposed to HPVs and cure the infection, while in a few unfortunate cases the infection persists and can lead to cancer. The different degree of archaic ancestry in our genomes could be partly responsible for differential susceptibility to cancer. Since HPVs do not infect bones, current Neanderthal and Denisovan genomes do not contain HPVs. As a next step, the authors hope to trace HPV sequences in ancient human skin remains as a more direct test of their hypothesis.

**More information:** Ville N. Pimenoff et al, Transmission Between Archaic and Modern Human Ancestors During the Evolution of the Oncogenic Human Papillomavirus 16, *Molecular Biology and Evolution* (2016). [DOI: 10.1093/molbev/msw214](https://doi.org/10.1093/molbev/msw214)

Provided by Oxford University Press

Citation: Ancient hominid 'hanky panky' also influenced spread of STIs (2016, October 17) retrieved 24 April 2024 from

<https://phys.org/news/2016-10-ancient-hominid-hanky-panky-stis.html>

This document is subject to copyright. Apart from any fair dealing for the purpose of private study or research, no part may be reproduced without the written permission. The content is provided for information purposes only.