Blame It on the Chimps: Researchers Resolve Evolutionary Origins of Human Herpes Viruses

A leading sexually transmitted disease, the herpes virus, infects more than two-thirds of all people. An evolutionary question for scientists has been why humans are the only primate species that harbor two forms of the herpes simplex virus (HSV): HSV-1 (causing cold sores) and HSV-2 (genital herpes).

Wertheim et al. (2014) used a novel model of molecular evolution to demonstrate that HSV-1 likely infected the last common, ancient ancestor of chimpanzees and humans at estimates of 6 Ma. Although HSV-2, which leads to more severe complications for people, arose by an entirely different means, jumping from species to a species when, around 1.6 Ma, an ancestor of modern chimpanzees first passed on HSV-2 to an early hominid species.

“Before we were human, there was still cross-species transmission into our evolutionary lineage,” study author Joel O. Wertheim.

Since that time, when the ancient split first introduced HSV-2 into ancient hominids, the herpes virus has remained a scourge that has been passed down all the way to modern humans.

Reference

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Study Shows Use of High Doses of Antibiotics to Clear Infections May Have the Potential to Promote Increased Cross-Resistance in Clinics

Antibiotic resistance has become an increasing public health concern, with MRSA infections and last lines of antibiotic drug treatments having to be increasingly deployed in hospitals and clinics.

Oz et al. (2014) utilized an experimental evolution approach to evolve 88 different *Escherichia coli* populations against 22 antibiotics, under “strong” and “mild” selection conditions. After 21 days, they isolated bacterial clones, measured the resistance to each antibiotic, and performed whole-genome sequencing of resistance clones to tease out the genetic changes that could be responsible for antibiotic resistance.

Their results demonstrate that the evolution of cross-resistance depends on selection strength. Overall, they found evidence for higher cross-resistance in the strongly selected strains and higher numbers of pathway-specific mutations. The study yielded important new insights into the increased emergence of drug resistance with the use of high doses of antibiotics, as well as hypersensitivities to exploit for new antibiotic therapies.

Reference

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