**NEWS**

**Better Understanding of the HIV Epidemic through an Evolutionary Perspective**

With the abundance of sequencing data, scientists can use ever more powerful evolutionary biology tools to pinpoint the transmission and death rates for epidemics such as HIV, which has remained elusive to a cure. Reconstructed evolutionary trees, called phylogenies, can trace a family of viral mutations over time. When combined with epidemiology, tree construction can allow for a greater insight into the dynamics of disease transmission and how a pathogen eludes its host to spread infection.

Leventhal et al. (2014) from the ETH Zurich in Switzerland report on a new method that successfully combines evolutionary tree studies and epidemiology, using viral sequence data from ten transmission clusters of the Swiss HIV Cohort Study. For some clusters, the HIV epidemic appears saturated, with very few new cases appearing, while in others, new infections were still common. Overall, HIV transmission was characterized by initial rapid spread within subpopulations that slows down to only a small number of infections.

“Using a novel methodology, we were able to estimate the number of individuals that are at risk of becoming infected within transmission clusters of the Swiss HIV epidemic and found that many of these clusters are characterized by initial rapid infection of most at risk individuals within a cluster, followed by a slowdown of new infections within each cluster,” said Leventhal.

This allowed the team, for the first time, to estimate not only HIV transmission and death rates but also the total susceptible population size within certain transmission groups from viral sequence data. Their model can successfully predict how the number of infected and susceptible individuals will vary over time, giving new insight and predictions into how an ongoing epidemic will continue to develop and help guide future public health intervention strategies.

**Reference**


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**Out of Eurasia, a Great Primate Evolutionary Bottleneck?**

On the road to our modern human lineage, scientists speculate there were many twist and turns, evolutionary dead ends, and population bottlenecks along the way. But how large were population sizes of common ancestors of the great apes and humans, and does genetic analysis support the prevailing views of a great bottleneck in primate evolution?

Using inferred evolutionary rates of more than 1,400 genes and ancestral generation times, researchers trace population histories backwards across evolutionary time to estimate population sizes for common ancestors. Their results show that the population sizes of lineages leading to human and chimpanzees dramatically shrunk over evolutionary time, from approximately 1,200,000 in number to 30,000 (Schrago 2014).

This population reduction coincides with bio-geographical data that suggests a great ape ancestral migration event from Eurasia to Africa during the late Miocene period, from approximately 12 to 5.5 Ma, with a 5-fold reduction in effective population size between the ancestor of the Eurasian and African great apes and the ancestor of African great apes alone, suggesting that the Homininae diversified after a dispersal event from an Eurasian ancestor.

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