

Study uses herpes virus to track human migration across the globe

By tracking the Herpes Simplex Virus Type-1 (which is generally associated with cold sores), scientists from the University of Wisconsin have further solidified the “out of Africa” theory of human migration. They used a genomic analysis of the different HVS-1 strains from around the world, which works “particularly well for this study because it is easily spread by physical contact as well as easy to collect.”

In general, the paper suggests that the data “supports the “out of Africa model” of human migration with HSV-1 traveling and diversifying with its human host”. There was one North American derived strain which they found was related to the East Asian family of the virus. They estimated the “divergence time” between this strain and its relatives as around 15,000 years which corresponds “with the estimated time period in which the North American continent was populated from Asia, approximately 15,000 years BP.”

Read the full, original story here: [“Follow the Herpes”](#)

Additional Resources:

- [“Hitchhiking virus confirms saga of ancient human migration,”](#) Phys.org
- [“Using HSV-1 Genome Phylogenetics to Track Past Human Migrations,”](#) PLOS One