

HIV's path out of Africa: Haiti, the US then the world

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The AIDS virus entered the United States via Haiti, probably arriving in just one person in about 1969, earlier than previously believed, according to new research. After the virus, HIV-1, entered the U.S., it flourished and spread worldwide.

"Our results show that the strain of virus that spawned the U.S. AIDS epidemic probably arrived in or around 1969. That is earlier than a lot of people had imagined," said senior author Michael Worobey.

The research is the first to definitively pinpoint when and from where HIV-1 entered the United States and shows that most HIV/AIDS viruses in the U.S. descended from a single common ancestor. The actual ancestral HIV entered the U.S. long before the storied "Patient Zero," Worobey said.

"Haiti was the stepping stone the virus took when it left central Africa and started its sweep around the world," said Worobey, an assistant professor of ecology and evolutionary biology at The University of Arizona in Tucson. "Once the virus got to the U.S., then it just moved explosively around the world."

The strain that migrated to the U.S. in 1969, HIV-1 group M subtype B, is the first human immunodeficiency virus discovered. It is the dominant strain of the AIDS virus in most countries outside sub-Saharan Africa. Almost all the viruses in those countries descended from the one that emerged from Haiti, he said.

Worobey and his colleagues figured out when HIV reached the U.S. by conducting genetic analyses of archived blood samples from early AIDS patients.

Learning more about the genetic make-up of the various strains of HIV could help vaccine development, Worobey said.

The scientists' research paper, "The emergence of HIV/AIDS in the Americas and beyond," is scheduled for publication in the online Early Online edition of the *Proceedings of the National Academy of Sciences* the week of October 29.

Worobey's co-authors are M. Thomas P. Gilbert of the University of Copenhagen in Denmark; Andrew Rambaut of the University of Edinburgh in Scotland; Gabriela Wlasiuk of the UA; Thomas J. Spira of the Centers for Disease Control and Prevention in Atlanta, Ga.; and Arthur E. Pitchenik of the University of Miami in Fla. The National Institutes of Health, the David and Lucile Packard Foundation and a University Research Fellowship from The Royal Society funded the research.

Figuring out which path HIV/AIDS took as it began its world travels and when it moved from one country to another has long been a topic of scientific investigation and debate.

Worobey and his colleagues tackled the problem by using archived blood samples from AIDS patients to construct genetic family trees for HIV.

The team analyzed blood from five of the first AIDS patients identified in the U.S., all of whom were recent immigrants from Haiti. The team also analyzed genetic sequences from another 117 AIDS patients from around the world who were infected with subtype B, the virus strain that has spread most widely.

Once all the sequences were assembled, the researchers loaded the data into a computer and used Bayesian statistics to investigate all the family trees that were consistent with the genetic data. The researchers then evaluated all possible HIV family trees to determine how probable a particular family tree is.

For the hypothesis that, from Africa, HIV went to the U.S. first, the probability is 0.003 percent -- virtually nil.

For the hypothesis that HIV went from Africa first to Haiti and then on to the U.S., the probability is 99.8 percent, almost 100 percent.

The analysis also shows that the ancestry of most viruses in the U.S. can be traced back to one common ancestor -- the virus that came from Haiti in about 1969.

"Before this study, that had not been nailed down," Worobey said.

The research also reveals that Haiti has a much larger genetic diversity of subtype B than does the U.S.

"The U.S., Australia, Europe plus many countries have just a subset of the subtype B diversity you see in Haiti," Worobey said.

The virus moved from Africa to Haiti in about 1966, he said. Haiti has more diversity of HIV than does the U.S. and other countries because the virus has been there longer and had more time to mutate.

The finding helps explain the early observations of a high prevalence of AIDS in Haiti, Worobey said. "The virus had simply been there longer."

"The main challenge of developing a vaccine against HIV is its tremendous genetic diversity," he said.

Knowing the gamut of diversity within subtype B could be important for effectively developing and testing vaccines that will work in Haiti, Worobey said.

Worobey's next step is following the trail of HIV even further back in time using older archival samples.

Source: University of Arizona

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