

HIV infection stems from few viruses

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A new study reveals the genetic identity of human immunodeficiency virus (HIV), the version responsible for sexual transmission, in unprecedented detail.

The finding provides important clues in the ongoing search for an effective HIV/AIDS vaccine, said researchers at the University of Alabama at Birmingham (UAB). The UAB team found that among billions of HIV variants only a few lead to sexual transmission.

Earlier studies have shown that a ‘bottleneck’ effect occurs where few versions of the virus lead to infection while many variants are present in the blood. The UAB study is the first to use genetic analysis and mathematical modeling to identify precisely those viruses responsible for HIV transmission.

George M. Shaw, M.D., Ph.D., professor in the UAB departments of Medicine and Microbiology and senior author on the report, said the research sheds new light on potential vulnerabilities in the virus at a time when science, medicine and society are still reeling from the failure of a major HIV vaccine clinical trial.

“We can now identify unambiguously those viruses that are responsible for sexual transmission of HIV-1. For the first time we can see clearly the face of the enemy,” said Shaw, a project leader with the Center for HIV/AIDS Vaccine Immunology. The center is a National Institutes of Health-sponsored consortium of researchers at UAB, Harvard Medical School in Boston, Oxford University in England, the University of North

Carolina in Chapel Hill and Duke University in Durham, N.C.

The new HIV-1 findings are published online in the *Proceedings of the National Academy of Sciences*.

The new study was performed by sequencing many copies of the HIV envelope gene present in the viruses taken from 102 recently infected patients. The envelope gene encodes for a protein called Env that forms part of the outer covering of the virus, and is responsible for its infectiousness.

The researchers then used sophisticated mathematical models of HIV replication and genetic change to identify the virus or viruses responsible for transmission. In 80 percent of the newly infected patients, a single virus caused transmission, though each virus was different in each patient. In the other 20 percent of patients, two to five unique viruses caused transmission.

“Previously, researchers employed inexact methodologies that prevented precise identification of the virus that initiated infection,” said Brandon Keele, Ph.D., an instructor in UAB’s Department of Medicine and lead study investigator. “Our findings allow us to identify not only the transmitted virus, but also viruses that evolve from it.”

The UAB team said their work would lead to new research on how different HIV genes and proteins work together to make a virus biologically fit for transmission and for growth in the face of mounting immunity.

Statistics show that while the worldwide percentage of people infected with HIV has leveled off, the total number HIV cases is rising. In 2007, 33.2 million people were estimated to be living with HIV, 2.5 million people became newly infected and 2.1 million people died from AIDS,

according to the Joint United Nations Programme on HIV/AIDS (UNAIDS) and the World Health Organization.

Source: University of Alabama at Birmingham

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