

Challenges of HIV-1 subtype diversity

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A review article in the *New England Journal of Medicine* explores the genetic variation of HIV-1 and its implications for preventing and treating the disease. Francine McCutchan, Ph.D., a researcher with the U.S. Military HIV Research Program, co-authored the article, which appeared in the April 10, 2008 edition.

HIV-1 is classified into several subtypes, or clades, which are denoted by letters. Subtype B is most prevalent in the Americas, whereas clades A, C and D are most prevalent in Sub-Saharan Africa, the region that remains most severely affected by the pandemic.

Advances in full-genome sequencing, along with expanded disease surveillance, have enabled researchers to identify circulating and recombinant forms of the disease as well.

“Given the diversity of HIV-1, gathering and classifying its strains has been very challenging. Nevertheless, this data provides the foundation for understanding the virus, its spread and how to combat it,” said Dr. McCutchan.

The authors address the implications viral diversity has on HIV prevention, vaccine development and antiretroviral therapy. For example, subtypes and their interaction with the human host may influence disease progression and transmission. They cite a cohort study in the Rakai district in Uganda, which suggested that HIV-1 disease progression is more rapid, and the risk of death is greater, among persons infected with subtype D (with recombinant forms or multiple

subtypes) than those infected with subtype A.

Source: Henry M. Jackson Foundation for the Advancement of Military Medicine

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