

Emergence of recombinant forms of HIV: dynamics and scaling

The emergence of drug resistant forms of HIV often underlies the failure of current antiretroviral therapies for HIV infection. Specific mutations in the HIV genome confer resistance to individual drugs.

Recombination, a process similar to sexual reproduction in higher organisms, can accelerate the accumulation of resistance mutations by mixing the contents of distinct viral genomes and expedite the failure of therapy. The dynamics of the emergence of recombinant forms of HIV in infected individuals remains poorly understood.

In a study publishing in *PLoS Computational Biology* on October 26, 2007, researchers Suryavanshi and Dixit from the Indian Institute of Science, Bangalore, India present a new model of HIV dynamics that provides a detailed account of the emergence and growth of recombinant forms of HIV following infection with diverse viral genomes.

Analysis of experimental data using the model establishes the high rate of HIV recombination and elucidates the origins of scaling relationships that link the relative prevalence of recombinant forms of HIV to the overall extent of infection. The model provides a framework for predicting the development of multi-drug resistance in HIV patients.

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