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HIV favors active genes

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Tudor P Toma Email: t.toma@ic.ac.uk

Replication of HIV requires integration of the proviral cDNA into human DNA within chromosomes, but the mechanism for selecting these sites has been poorly understood. In the August 23 Cell, Astrid Schröder and colleagues at The Salk Institute, La Jolla, California show that HIV-1 chooses active genes and local hotspots for integration in the human genome (*Cell* 2002, **110**:521-529).

Schröder *et al.* mapped 524 sites at which HIV cDNA had integrated into the human genome sequence and observed that these genes were strongly favored as integration acceptor sites. Active genes were the preferred integration targets, and in particular genes that became activated in cells after infection by HIV-1. In addition, they found regional hotspots for integration, including a 2.4 kb region containing 1% of sites.

"The findings may have implications for developing more effective gene therapies", says Frederic Bushman, senior author of the paper. "For example, data on preferred integration sites could guide the choice of gene-delivery vectors to minimize possible toxicity from integration and inform surveillance for possible malignancy due to integration at characteristic hotspots," he concludes.

References

1. Schröder ARW, Shinn P, Chen H, Berry C, Ecker JR, Bushman F: HIV-1 integration in the human genome favors active genes and local hotspots. *Cell* 2002, 110:521-529., [http://www.cell.com/]

2. The Salk Institute, [http://www.salk.edu/]