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IN BRIEF

VIRAL EVOLUTION

Hypermutation of HIV-1 *in vivo*

Spontaneous mutation in RNA viruses is a major determinant of genetic diversity; however, knowledge of HIV-1 mutation rates has largely been limited to cell culture and *in vitro* studies. Cuevas *et al.* quantified the HIV-1 spontaneous mutation rate *in vivo*, based on the frequency of premature stop codons in HIV-1-derived cDNA in peripheral blood mononuclear cells (PBMCs) from infected human patients. The mutation rate in PBMCs was 2 orders of magnitude greater than that predicted by *in vitro* studies and 44 times higher than in plasma samples, suggesting that most viruses are lethally mutated within PBMCs and fail to reach the plasma. Further analysis revealed that 98% of mutations could be attributed to host editing by A3 cytidine deaminases. The HIV-1 mutation rate was lower in patients with rapidly progressing disease than in those with normal disease, highlighting the antiviral effect of hypermutation by A3. However, variation in the degree of A3-mediated editing suggested that, at low levels, A3 activity may enhance the genetic diversity and pathogenicity of HIV-1.

ORIGINAL RESEARCH PAPER Cuevas, J. M. *et al.* Extremely high mutation rate of HIV-1 *in vivo*. *PLoS Biol.* http://dx.doi.org/10.1371/journal.pbio.1002251 (2015)

GENOMICS

Identification of sORFs

Short open reading frames (sORFs) are abundant within eukaryotic transcripts and transcript regions that were previously thought to be non-coding, and evidence for their functionality has been increasing; however, the large-scale identification of functional sORFs has so far proved challenging. Using a new computational approach based on the presence of specific amino-acid-based evolutionary conservation features, Mackowiak *et al.* have identified over 2,000 novel sORFs in 5 animal species. The sORFs were located in transcripts that had been annotated as non-coding or in the presumed untranslated regions of canonical mRNAs, and some were conserved over long evolutionary distances. Mining of experimental data sets revealed that the newly identified sORFs are expressed and are often translated. The highly annotated results of this study represent a useful resource for further experimental functional analysis of sORFs.

ORIGINAL RESEARCH PAPER Mackowiak, S. D. *et al.* Extensive identification and analysis of conserved small ORFs in animals. *Genome Biol.* http://dx.doi.org/10.1186/s13059-015-0742-x (2015)

MICROBIAL GENETICS

Single-locus changes perturb community structure

The importance of bacterial social traits in determining the structure of microbial communities was unclear. In a new study, McClean *et al.* assembled freshwater microcosm communities comprising four bacterial species and one protozoan apex predator. By introducing single-locus deletions, the researchers created strains of one community member (*Bacillus subtilis*) that were constitutively on or off for biofilm formation, and measured the effects on overall community composition. Remarkably, these single mutations modified community structure more than the loss of *B. subtilis* itself and to the same extent as loss of the apex predator, demonstrating that social traits are a key determinant of community structure. The authors suggest that microevolution resulting from environmental changes may be as important as species extinctions in shaping microbial communities.

ORIGINAL RESEARCH PAPER McClean, D. *et al.* Single gene locus changes perturb complex microbial communities as much as apex predator loss. *Nat. Commun.* http:/dx.doi.org/10.1038/ncomms9235 (2015)