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Monkey gene that blocks AIDS viruses evolved more than once

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Researchers at Harvard Medical School have identified a gene in Asian monkeys that may have evolved as a defense against lentiviruses, the group of viruses that includes HIV. The study, published February 29 in the open-access journal *PLoS Pathogens*, suggests that AIDS is not a new epidemic.

The gene, called TRIM5-CypA, well characterized elsewhere (*AIDS*, 2007; *PNAS*, 2008), is a hybrid of two existing cellular genes, TRIM5 and CypA. The combination produces a single protein capable of blocking infection by viruses closely related to HIV. Surprisingly, this is actually the second time researchers have identified a TRIM5-CypA gene in monkeys. The other hybrid gene, called TRIMCyp, was discovered in 2004 in South American owl monkeys.

Normally, evolutionary biologists assume that similar DNA sequences, present in the same location in the genomes of two or more species, evolved only once. In this scenario, the gene arises first in a common ancestor and is subsequently inherited by all the species that descend from that ancestor. In the case of TRIM5-CypA and TRIMCyp, this does not appear to be the case.

TRIM5-CypA was not found in monkeys closely related to the Asian macaques, and in fact, was not found in every macaque individual tested. Likewise, owl monkey TRIMCyp was not found in any other species of South American primate. Researchers interpret this to mean that the two genes arose independently, once in owl monkeys and once in macaques.

More tellingly, even though the protein sequences specified by the two TRIM5-CypA genes are similar, at the DNA level it is obvious that the molecular events leading to formation of the two genes were different.

Evolutionary biologists refer to the acquisition of a similar adaptation in different species as “convergent evolution,” an example being the independent appearance of flight in both birds and bats. The Harvard team’s genetic evidence indicates that the two TRIM5-CypA genes constitute an unambiguous and particularly striking example of convergent evolution. Moreover, the kinds of molecular events required to construct the two TRIM5-CypA genes are thought to be rare.

That the process occurred at least twice during primate evolution suggests that the combination of the TRIM5 and CypA genes provided a strong evolutionary advantage to the individuals in which they originally appeared. An intriguing possibility is that the newly formed genes prevented infection by prehistoric viruses related to modern AIDS viruses. If so, this could mean that AIDS-like epidemics are not unique to our time, but in fact may have plagued our primate ancestors long before the modern AIDS epidemic.

Citation: Newman RM, Hall L, Kirmaier A, Pozzi L-A, Pery E, et al. (2008) Evolution of a TRIM5-CypA Splice Isoform in Old World Monkeys. PLoS Pathog 4(2): e1000003. doi:10.1371/journal.ppat.1000003 (www.plospathogens.org/doi/ppat.1000003)

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