

The extraordinary evolution of REVs

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A new study by Anna Maria Niewiadomska and Robert Gifford, of The Aaron Diamond AIDS Research Center, New York, reveals that reticuloendotheliosis viruses (REVs), which originated in mammals, spread to birds as a result of medical intervention. Their findings will be published August 27 in the open access journal *PLOS Biology*.

"We became intrigued by these viruses", says Gifford, "...because their distribution in nature suggests something very unusual has occurred during their evolution."

The reticuloendotheliosis viruses (REVs) are retroviruses that were first identified in the 1950s as agents of virulent disease in poultry. DNA sequences derived from REVs are also present in the genomes of other, unrelated viruses that infect birds, including the gallid herpesvirus-2 (GHV-2) and fowlpox virus (FWPV), an avian cousin of the [smallpox virus](#).

Gifford's research focuses on 'endogenous viral elements' (EVEs) – snippets of viral DNA that can be found in the genomes of more complex cellular organisms – they are akin to 'fossil' evidence that a [viral genome](#) integrated into a [host genome](#) at some point in the host's evolutionary history. This study was prompted when Niewiadomska discovered ancestors of REV among these 'fossilized' [viral sequences](#). These sequences, which were identified in the echidna and ring-tailed mongoose genomes, allowed the scientists to link the REVs that circulate in birds today to a viral infection that occurred in mammals over 8 million years ago.

Next, by combining genetic information with spatiotemporal and historical data, the authors have come up with an attractive proposal for how REVS spread into birds. Their findings suggest that REVs spread into birds very recently, during experimental studies of *Plasmodium lophurae* - a [malaria parasite](#) that was isolated in the late 1930s from a pheasant housed in Bronx Zoo. By contaminating stocks of this parasite, the rogue retrovirus may have spread into poultry and subsequently into avian cell culture systems, inserting its genetic material into the GHV-2 and FWPV genomes along the way. The authors surmise that these larger viruses, and possibly the vaccines created against them, subsequently provided vehicles for the further dissemination of REV into the environment. Data presented in the study indicate this process is ongoing, and impacts wild birds as well as domestic poultry.

Besides shedding light on the origin and evolution of REV, the study draws attention to the unintentional role that medical interventions can play in enabling the emergence of viruses, and a need to monitor viral genetic diversity. "Unfortunately, the law of unintended consequences applies in the realm of infectious disease research," says Gifford. "While we can't escape that fact, we can use modern sequencing technologies to survey viral genetic diversity, so that changes in the ecology and evolution of important viral pathogens can be monitored and responded to more effectively. Our analysis of REV illustrates how such an approach might work."

More information: Niewiadomska AM, Gifford RJ (2013) The Extraordinary Evolutionary History of the Reticuloendotheliosis Viruses. *PLoS Biol* 11(8): e1001642. [DOI: 10.1371/journal.pbio.1001642](https://doi.org/10.1371/journal.pbio.1001642)

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