

Viral 'fossils' study on birds finds fewer infections than in mammals

December 12 2014

In a contribution to an extraordinary international scientific collaboration the University of Sydney found that genomic 'fossils' of past viral infections are up to thirteen times less common in birds than mammals.

"We found that only found only five viral families have left a footprint in the bird genome (genetic material) during evolution. Our study therefore suggests that birds are either less susceptible to viral invasions or purge them more effectively than mammals," said Professor Edward Holmes, from the University of Sydney's Charles Perkins Centre, School of Biological Sciences and Sydney Medical School.

"The results shed light on virus-host interactions across 100 million years of bird evolution."

Professor Holmes is one of 200 scientists worldwide who have taken part in the ambitious scientific effort to sequence, assemble and compare the full genomes of 48 bird species.

After four years of collaboration the findings are published in *Science* and simultaneously in associated publications on 12 December. Their insights include how birds arrived at the spectacular biodiversity of more than 10,000 species.

Professor Eddie Holmes is an author on the first flagship paper published in *Science*.

"This exciting flagship paper presents a comprehensive history of how bird genomes have evolved along with a new family tree for birds. It also briefly covers our research on viral fossils in birds, covered in more detail in *Genome Biology*," said Professor Holmes.

"One of the most striking findings is the small size of bird genomes, and the small number of fossil viruses seems to match this," said Holmes.

Together with his postdoctoral student Jie Cui, now at Duke-NUS in Singapore, Professor Holmes screened 48 avian genomes for 'viral fossils'; that is, copies of viruses that have been incorporated into the avian [genome](#) and then passed on through generations.

"Using comparative genomics we have shown that birds carry far fewer of these viral or genomic fossils than mammals. Only five viral families have visited during bird evolution, with retroviruses and hepadnaviruses (like hepatitis B virus) the most common," said Professor Holmes.

"Clearly, our next question is whether the small genomes carried by [birds](#) somehow favour a reduction in the number of these viral fossils?"

Nine academics including Professor Simon Ho from the University's Faculty of Science and Associate Professor Jaime Gongora from the Faculty of Veterinary Science have also contributed their expertise to the international project and are authors on articles published in *Science* and simultaneous publications in *Genome Biology*, *GigaScience* and other associated journals.

Provided by University of Sydney

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