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Genes, regulons, feathers and flight. The origin of the avian genome

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Gould Seminar Room (Room 235) Gould building, 116 Daley Road, ANU



For the past 10 years our lab has employed diverse approaches to understand the origins of the avian genome, which is distinguished from the genomes of mammals and non-avian reptiles in being small and less populated by transposable elements. In particular we have been intrigued by possible links between powered flight and smaller genome size, a hypothesis that receives some support from our work.

A major effort has been the development of BAC libraries from several reptiles and the emu as resources for interrogating genome evolution along the reptile-bird transition. Through these resources we have found that avian genomes exhibit a distinctive and simple landscape of simple sequence repeats and transposable elements as compared to reptiles.

More recently we have employed bioinformatic approaches to investigate distributions of intron sizes among extant amniotes and find that lineages characterized by powered flight (birds, bats) have detectably smaller introns than their non-volant sister groups.

Finally, we have recently investigated the phylogenetic distribution and abundance of conserved non-exonic elements (CNEEs) in amniotes, and find that long (> 500 bp) CNEEs underwent a differential retention in mammals and reptiles, despite originating from a common pool of about 8000 CNEEs in the common ancestor of amniotes.

Using a candidate gene approach, we have investigated the evolutionary dynamics of CNEEs associated with genes involved in feather development. We find that, while most coding regions associated with feathers arose long before the origin of birds, there was a spike in origination rates of feather CNEEs in the avian ancestor. Large scale sequencing of avian and reptile genomes will be crucial for refining these dynamics and providing a more detailed picture of the deeper origins of the avian genome.

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