

The Oz Mammal Genomes initiative: Mammal genomics, evolution and conservation at a continental scale

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The Australo-Papuan region has a unique mammal fauna, which faces unique threats and poses important evolutionary and ecological questions. Genomic approaches have great potential to advance our understanding of the region's terrestrial mammals and their conservation. The Oz Mammal Genomes Consortium brings together museums, researchers, data specialists and wildlife management agencies to comprehensively tackle mammal genomics at a continental scale and at three different levels of resolution. There are few published genomes for Australian marsupials. We will develop well-assembled genomes from a broadly representative range of marsupial taxa, to facilitate new insights into evolution and to provide reference data for conservation studies. Genome projects are now underway for three priority species (fat-tailed dunnart, brush-tailed rock-wallaby and eastern bettong), with several additional species to follow. Our current understanding of evolutionary relationships among many mammal taxa remains incomplete. To improve resolution of genus and species boundaries we are generating comprehensive phylogenies of all extant and recently-extinct terrestrial mammals native to the Australo-Papuan region. We are using genome scanning methods to sequence over 1000 genes from around 500 taxa, including marsupials, rodents and bats. Finally, the availability of reference genomes and phylogenies will provide a solid base for population-level studies. We will develop conservation genomic datasets for a selection of threatened mammal species. Using a genome scanning approach we will measure genetic diversity and inbreeding, determine population structures, and identify adaptive variation. Species will be prioritised so that genomic data will contribute directly to urgent conservation management decisions.



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ABSTRACT BOOK