Australia has the highest rate of recent mammal extinction on the planet. It is an alarming fact. Australia is recognised globally as one of only 17 ‘megadiverse’ countries that have extraordinarily high levels of biodiversity, and collectively these countries account for around two-thirds of the world’s biodiversity. Bioplatforms Australia is investing in the Oz Mammals Genomics Initiative, which will support genomic data collection, data access and international collaboration in an endeavour to reduce extinction rates of Australia’s unique mammal fauna.

Reversing the cycle of mammal extinction

Australia is home to many different rock-wallabies, a marsupial group with unusually diverse chromosomes. Sequencing a rock-wallaby genome will help us to understand chromosomal evolution.

Clue to survival is in the DNA

Active collaboration domestically and internationally is key to effective outcomes. The Oz Mammals Genomics consortium brings together museums, universities and wildlife management agencies to comprehensively tackle mammal genomics at three different levels of resolution.

First, the initiative aims to sequence whole genomes from at least eight different mammal species. Second, it will generate a comprehensive phylogenomic (evolutionary) framework for Australian mammals, including species that have recently become extinct. Finally, conservation genomic resources will be developed for a range of threatened species.

Australian marsupials are genetically distinct and developmentally unique. This means that marsupial genomes are especially important comparative resources for understanding mammalian diversity world-wide.

The Oz Mammals Genomics initiative is an Australia-wide collaboration involving researchers from more than 30 institutions. Core members include: Australian Museum, Australian National Wildlife Collection, Centre for Biodiversity Analysis, Department of Parks and Wildlife Western Australia, Museum Victoria, South Australian Museum, Queensland Museum, University of Adelaide, University of Canberra and the Western Australian Museum. Ongoing international collaborations include the Natural History Museum, London (UK), University of Otago, Dunedin (NZ), and the Museum of Vertebrate Zoology, Berkeley (USA). The project is also involved with the Genome 10K project, EDGE and the IUCN Conservation Genetics Specialist Group.

We have an engaged domestic and international community now with the capacity to tackle collaboratively the urgent problem of mammal extinction.

The Western chestnut mouse is one of many native rodents unique to Australia. Phylogenomic studies will improve our understanding of how rodents arrived in Australia and how they diversified as they spread across the continent.

The Critically Endangered Christmas Island flying-fox could be the last native mammal left on Christmas Island. Genomic information will help us to understand how to conserve this species and other Australian bats.
Phylogenomic research will improve our understanding of relationships among different groups of mammals

Our understanding of the evolutionary relationships among different groups of mammals 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 species, including marsupials, rodents and bats.

Eight new marsupial genomes will be sequenced as part of the Oz Mammals Genomics Initiative

Conservation genomic datasets will help us to understand extinction risks for threatened mammals

The availability of whole genomes and phylogenies will provide a solid reference base for conservation genomics. We will prioritise research to focus on threatened mammal species where genomic resources can contribute directly to urgent management decisions. For example, knowledge of genetic diversity, inbreeding, and population genetic structure can help managers decide which animals to breed in captive populations, or which populations to use as sources for reintroductions. The Oz Mammals Genomics initiative is currently contributing to conservation genomics projects for the rufous hare-wallaby (pictured), burrowing bettong, New Holland mouse, Christmas Island flying-fox, and several bandicoot species.

For more information, please visit: https://data.bioplatforms.com/organization/about/bpa-omg

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