

OMIG

Oz Mammal Genomics

SALLY POTTER & MARK ELDRIDGE

A large project to sequence the genomes of Australia's mammals will provide the first complete picture of their interrelationships and evolutionary history – and aid their conservation.

Australia and its surrounding islands contain a significant proportion of the world's mammalian diversity, including the only monotremes (egg-laying mammals) as well as a great diversity of marsupials (pouched mammals) and many eutherian mammals such as bats and rodents. More than 300 terrestrial mammalian species are native to Australia, and 87% of these are found nowhere else. This level of unique biodiversity brings value to Australia at economic, social and scientific levels.

Australia's unique biological diversity is a result of the continent's long-term isolation. Over the past 40 million years the Australian continent has been completely isolated from other landmasses and has been drifting slowly northwards as a giant antipodean ark. This period of isolation has allowed much of our fauna to evolve, diversify and adapt independently of other continents.

For example, bats have a long evolutionary history in Australia, with multiple lineages independently colonising the continent from Asia and potentially also from South America before radiating into many unique species. Rodents have also invaded from Asia in two waves over the past five million years, resulting in the rapid evolution of diverse native species. Thus, Australian mammals provide many different answers to the question of how to survive and even thrive over the long-term on this increasingly arid continent.

The conservation of Australia's fauna is not only important ecologically but also for the Australian tourism industry. Iconic native mammals like the koala and kangaroo are a major attraction for international travellers and so the conservation of our unique biodiversity is also economically important.



We currently have the genomes of only two Australian marsupials, including the tamar wallaby.

Credit: Australian Wildlife Conservancy

From a scientific perspective, the marsupials provide an important biological comparison to other mammalian groups, including how their physiology, ecology, reproduction, immune systems and genes function and have evolved.

Australia's isolation has also meant that recently introduced species – especially rabbits, cats and foxes – have had a major negative impact on our mammal fauna, unlike other continents. Australia has the highest rate of mammalian extinctions in the world, with ~30 species becoming extinct over the past 200 years. In addition, 21% of our current terrestrial mammals are threatened. Humans have caused this through the introduction of feral animals, clearing of habitat, farming, and changed fire regimes. Currently, 62 Australian terrestrial mammal species are on the International Union for Conservation of Nature's Red List as Threatened, and another 39 species are listed as Near Threatened.

The extinction of mammal species in Australia is continuing apace. This has had profound consequences on the environment, and necessitates ongoing conservation efforts at a species and landscape level.

Genetic information has been a vital tool in conservation programs for Australian mammals over the past few decades, providing insights and guidance into captive breeding efforts and wild population management. Recent advances in DNA technology, along with diminishing costs, have now dramatically expanded the genetic information we can obtain. We have entered the genomic era, where instead of looking at genetic information from a small number of genes we can now access information across thousands of genes and even the entire genome of each species.

This gives greatly increased understanding and clarity to questions such as the relationships between individuals, the discovery of species, refining boundaries among already named species, and the evolutionary history of populations and species over both recent and ancient timescales. It can also yield important insights for conservation management, such as genetic predictions of which Tasmanian devils (*Sarcophilus harrisii*) are more likely to survive the spread of contagious facial tumours.

To take advantage of these scientific advances, a consortium of museum, university and CSIRO scientists, as well as government agencies and non-government organisations have come together to form the Oz Mammal Genomics (OMG!) Consortium. With a \$1 million investment from BioPlatforms Australia and co-funding from many participating institutions, the

Consortium aims to use genomic technology to improve our understanding and use of Australian mammals in science, as well as to enhance their conservation. This funding will enable researchers to collaborate and share valuable resources to address several major goals.

The major advantage of next-generation sequencing technology is the ability to economically and efficiently sequence whole genomes. While the human genome project took decades and hundreds of millions of dollars to complete utilising many laboratories across the world, genomes can now be sequenced in a few months in a single facility and cost only thousands of dollars.



Bandicoots such as *Perameles* (pictured here) are a highly distinct evolutionary lineage within Australian marsupials.

While several high quality genomes are available for bats and rodents, among Australian marsupials we currently only have genomes for the tammar wallaby (*Notamacropus eugenii*) and Tasmanian devil. These genomes have already provided valuable insights into gene evolution, organisation and function, as well as disease susceptibility and population history. Genomes from several other Australian marsupial species are currently being sequenced, including the koala (*Phascolarctos cinereus*).

A priority for the OMG Consortium is to produce a high-quality marsupial reference genome to anchor future genomic studies and to improve the availability of genomic resources across the diversity of Australian marsupials. In particular, the Consortium will be sequencing the genome of the fat-tailed dunnart (*Sminthopsis crassicaudata*) as it's a model marsupial species frequently used in laboratory studies and has the ancestral marsupial arrangement of $2n=14$ chromosomes. Other priority species include a representative bandicoot (*Isoodon* or *Perameles*), which is a highly distinct evolutionary lineage within Australian marsupials, and a representative of the chromoso-

mally diverse genus *Petrogale* (rock-wallabies), which is the focus of ongoing work on chromosomal speciation and includes numerous species of conservation concern.

Another major goal of OMG is to use a genomic approach to definitively and comprehensively establish the evolutionary relationships among Australia's terrestrial mammals. Our current knowledge of how native marsupial, rodent and bat species are related is limited and patchy. Recently extinct species are usually not included, and relations among extant species are often unresolved as they are typically based on data from only a few genes.



The fat-tailed dunnart (*Sminthopsis crassicaudata*) is a model marsupial species that's frequently used in laboratory studies, and has the ancestral marsupial arrangement of chromosomes.

However, recent technological advances in genomics will enable OMG to generate DNA sequences from thousands of genes from each of the ~300 Australian terrestrial mammal species as well as some closely related species from New Guinea and nearby islands. This will provide a significantly more robust and definitive understanding of their relationships and evolutionary history, and a framework for comparative analyses of their extinction risk.

One of the major advantages of a genomic approach is the ability to use fragmented DNA, which will enable us to access the huge number of mammalian skin and skull specimens housed in Australia's natural history museum collections. This will enable, for the first time, recently extinct species such as the thylacine, pig-footed bandicoot, white-footed rabbit-rat and other rare species that are only known from a handful of museum specimens to be incorporated into the analysis. This will provide the first complete picture of the interrelationships and evolutionary history of Australia's mammals, as well as provide a backbone for future studies.

We anticipate that this comprehensive coverage and unprecedented genetic power will lead to the clarification of species boundaries within many previously problematic species complexes, and so lead to the identification of new species that in many cases have remained undetected in museum collections. For example, in 2014 a new mammal species was discovered in northern Australia, Wilkins' rock-wallaby (*Petrogale wilkinsi*), which was first recognised from genetic studies of material from Australian museum collections. This discovery and others like it suggest that many new species await discovery, even in relatively well-known groups such as mammals. The identification of these hidden or cryptic species is an essential first step to their effective conservation.

A major aim of the OMG project is to provide detailed and state-of-the-art genetic information to assist in the on-ground management of threatened Australian mammal species. The Consortium includes state and territory wildlife management agencies, as well as non-government land managers (e.g. Arid Recovery, Australian Wildlife Conservancy, Bush Heritage Foundation) and zoos that are actively managing threatened mammal species through captive breeding, translocations and reintroductions.

Using genomic data, OMG will be able to assess the genetic impacts of habitat loss and fragmentation, population isolation and inbreeding on mammal species, as well as guide the selection of animals for reintroductions and captive breeding, and assess the effectiveness of these programs in maintaining genetic diversity. Some of the priority species that will benefit include the greater bilby (*Macrotis lagotis*), greater stick-nest rat (*Leporillus conditor*), burrowing bettong (*Bettongia lesueur*) and western barred bandicoot (*Perameles bougainville*).

The OMG Consortium comes at an opportune time to provide increased scientific power to the conservation of our threatened mammals, as well as to increase public awareness of Australia's unique mammal fauna and genomic capabilities. The data generated by OMG will provide an extensive and valuable research resource that will be used for decades to address fundamental questions of species biology, understand how the extraordinary mammals of Australia evolved, and hopefully turn the tide of mammalian extinctions in Australia.

Sally Potter is a Postdoctoral Researcher in the Research School of Biology at the Australian National University. Mark Eldridge is Principal Research Scientist in Terrestrial Vertebrates at the Australian Museum.