

EDITORIAL

Marsupial Research Springs to the Forefront

Skippy, Blinky Bill, Fatso the Wombat, Caramello Koala, the Qantas flying kangaroo: are they just Aussie icons, or can they be useful tools for basic and medical research?

Australia has by far the largest number of marsupial families, yet the first marsupial genome to be sequenced is that of the South American grey short-tailed opossum (*Monodelphis domestica*), and the sequencing of the genome of the first Australian marsupial (the tammar wallaby *Macropus eugenii*) would not be underway without dollar for dollar funding from the USA. Recently, an article appeared in the news about a compound identified from the wallaby genome that is more potent than penicillin. Australians and the Australian government should be more proactive in exploiting the use of marsupial models for research!

What are marsupials? Why are there so many in Australia? How can they be useful models for research?

Mammals can be divided into three groups:

- (i) eutherians: often erroneously referred to as 'placental mammals' e.g. humans, bats and whales
- (ii) marsupials: e.g. kangaroos, wombats and antechinus in Australia and opossums in the Americas
- (iii) monotremes: egg laying mammals e.g. platypus and echidna in Australia and zaglossus in Papua New Guinea

To understand why there are so many marsupials in Australia, we must consider the movement of tectonic plates across the earth's surface. About 180 million years ago, the original land mass on earth (Pangea) divided into two: Laurasia (in the north) and Gondwanaland (in the south), but connections between the two existed, in particular around what is now North and South America. The fossil record indicates that marsupials originated in what is now North America, and migrated to what has become South America, while those in the north mostly died out. From South America marsupials migrated across Gondwanaland. When

Gondwanaland separated into South America, Antarctica and Australia, marsupials in the Antarctic died out due to the cold, and the vast majority of marsupials in the Americas became extinct due to predation by large eutherian carnivores. Australia lacked large carnivores, moved north to warmer climes and marsupials flourished.

Novel aspects of marsupial adaptation that can be exploited in basic and medical research include:

- Marsupials are born at an extremely undeveloped stage compared with eutherian mammals
- Two joeys (pouch young) at different stages of development in the same pouch receive milk from teats of the same mammary gland, but with totally different milk compositions
- Marsupials diverged from eutherian lineages about 150 million years ago, therefore marsupial genome sequencing can reveal more useful information for human genomics than that of chicken (diverged too long ago) or another eutherian (diverged too recently)

This Showcase on Research presents articles from four laboratories on different aspects of biology being investigated using marsupial models, on how these models offer advantages over available eutherian models, and on commercial applications. Jenny Graves and Elizabeth Kuczek discuss discoveries arising from sequencing the kangaroo genome; Lynne Selwood describes the insights into early embryogenesis from marsupials, including whole conceptus culture; Kevin Nicholas and colleagues write about endocrine regulation of lactation and milk composition; and Norman Saunders and colleagues give an update on the marsupial model for spinal cord regeneration.

These articles comprise four examples where marsupial models reveal superior insights into both basic research and the consequences for medicine and industry.

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Cover Illustration

Members of the kangaroo family have wonderful large chromosomes. Chromosome painting shows that the chromosomes of different species are all very similar. Here tammar wallaby chromosomes have been physically separated by flow sorting. DNA from tammar chromosomes two (green), seven (pink) and X (white) have been tagged with different fluorochromes and hybridised back to the chromosomes of another species (the swamp wallaby *Wallabia bicolor*), whose enormous chromosomes are shown to be fusions of tammar chromosomes.

Image supplied by Roland Toder and Rachael O'Neill, Department of Genetics, La Trobe University, VIC.

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