



The first marsupial genome sequence

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URLs

Entrez gene

XIST

http://www.ncbi.nlm.nih.gov/entrez/query.fcgi?db=gene&cmd=Retrieve&dopt=full_report&list_uids=7503

The grey, short-tailed opossum (*Monodelphus domestica*) has become the first metatherian (marsupial) to have its genome sequenced. The draft sequence sheds light on genome evolution in eutherian (placental) mammals.

The authors used whole-genome shotgun assembly to sequence 3,475 Mb (covering 97%) of the opossum genome, which consists of eight large autosomes and one short sex chromosome, and encodes ~18,000–20,000 protein-coding genes. Eighty-two percent of the predicted genes have human orthologues, and most others also showed homology to human genes, but could not be classed as orthologues with certainty.

One surprising finding from comparing the opossum and human genomes is that most sequence innovation in the human genome following the eutherian split from the metatherian lineage has occurred in non-coding sequences (20% being lineage-specific in eutherians),

rather than in coding sequences (only 1% are absent in metatherians). Many of these non-coding sequences are in regions surrounding important developmental genes, indicating that they are functional regulatory elements. The authors found a high degree of overlap between eutherian-specific sequences and transposable elements (16%), which might have served as a driving force in the evolution of the eutherian genome.

The opossum sequence has also helped to answer a long-standing question about eutherian X-chromosome evolution: no homologue for the X-(inactive)-specific transcript (*XIST*) gene was identified in the opossum X chromosome, indicating that this gene is indeed a recent evolutionary innovation that coincided with the evolution of random X inactivation, which is specific to eutherians.

The opossum genome shows reduced rates of segmental duplication in comparison with other amniotes (1.7% and 2.5–5.3%,

respectively). Reflecting this, analysis of gene expansions revealed that the metatherians have one-third fewer lineage-specific duplications than humans. Eutherian-specific duplications have occurred in genes that are involved in sensory perception, immunity and detoxification.

As well as evolutionary insights, the genome sequence will facilitate research into features of the opossum that might have medical relevance; for example, opossums are currently being used as models in studies into development, genetic imprinting, immune function, malignant melanoma and regenerative medicine.

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ORIGINAL RESEARCH PAPER

Mikkelsen, T. S. *et al.* Genome of the marsupial *Monodelphus domestica* reveals innovation in non-coding sequences. *Nature* **447**, 167–177 (2007)

FURTHER READING Dermitzakis, E. T., Reymond, A. & Antonarakis, S. E. Conserved non-genic sequences — an unexpected feature of mammalian genomes. *Nature Rev. Genet.* **6**, 151–157 (2005)

WEB SITE

<http://www.broad.mit.edu/mammals/opossum>