# Trends in Genetics | Genome of the Month

# Neoceratodus forsteri (Australian lungfish)

## Manfred Schartl<sup>1,2,\*</sup> and Axel Meyer<sup>3</sup>

<sup>1</sup>Developmental Biochemistry, Biocenter, Am Hubland, University of Würzburg, 97074 Würzburg, Germany

<sup>&</sup>lt;sup>3</sup>Department of Biology, University of Konstanz, Universitätsstraße 10, 78457, Konstanz, Germany



Trends in Genetics

Figure 1. Australian Lungfish. Photo taken by Tom Schedl, Research Institute of Molecular Pathology (IMP), Vienna.

## Lessons Learned from the Genome

In the Devonian era, lobe-fined fishes conquered land, giving rise to all land vertebrates. With ~43 Gb, the Australian lungfish, *Neoceratodus forsteri*, has the largest sequenced chromosome-quality animal genome. Its size is continuing to grow due to huge intergenic regions and introns with ~90% still active repeat content whose components resemble tetrapods more than ray-finned fish. Synteny to other vertebrate macrochromosomes is maintained just as its conserved ancient homology of all microchromosomes to the ancestral vertebrate karyotype. Lungfish are the closest living relatives to tetrapods, underscoring their importance for understanding innovations associated with terrestrialization. Preadaptations to land life include gaining limb-like expression of developmental genes in lobed fins, increased rates of evolution and duplication of genes associated with obligate air breathing such as lung surfactants, and the expansion of odorant receptor gene families that detect airborne odors.

#### Fun fact about the Genome

The lungfish genome is the largest animal genome that has ever been sequenced. It is 14 times larger than that of humans. This exceeds the genome size of the axolotl, the previous record holder in the animal kingdom, by  $\sim$ 30%. Several lungfish chromosomes each contain more DNA than the entire human genome combined.

#### **Resources**

<sup>i</sup>www.ncbi.nlm.nih.gov/bioproject/PRJNA644903

### Literature

- 1. Kemp, A. (1986) The biology of the Australian lungfish, Neoceratodus forsteri (Krefft 1870). J. Morphol. 190, 181–198
- Amemiya, C.T. et al. (2013) The African coelacanth genome provides insights into tetrapod evolution. Nature 496, 311–316
- 3. Meyer, A. et al. (2021) Giant lungfish genome elucidates the conquest of land by vertebrates. Nature 590, 284–289
- 4. Irisarri, I. et al. (2017) Phylotranscriptomic consolidation of the jawed vertebrate timetree. Nat. Ecol. Evol. 1, 1370–1378
- 5. Woltering, J.M. et al. (2020) Sarcopterygian fin ontogeny elucidates the origin of hands with digits. Sci. Adv. 6, eabc3510

#### **GENOME FACTS:**

The Australian lungfish genome spans 43 Gb and is organized into 17 macrochromosomes and 10 microchromosomes

The 37 Gb assembly has full chromosome size and an N50 of 1.67 Gb.

The sequence assembly contains 31 120 annotated protein-coding genes.

Greater than 90% of the genome consists of transposons and repetitive DNA with long interspersed nuclear elements (LINEs) as the most prominent component.

Many transposable elements are still active, thus the lungfish genome continues to expand.

The genome assembly is freely available.

#### SPECIES FACTS:

The Australian lungfish is the only surviving species of the Neoceradontidae, endemic to Australia and one of only six extant lungfish species. Its populations are small and it is a critically endangered species.

Lungfish are the closest relatives of the land-living vertebrates, the tetrapods, with which they share the last common ancestor about 420 million years ago.

The Australian lungfish has changed little compared with 100 million-year-old fossils (genus *Ceratodus*) and is therefore considered by some to be a living fossil.

Some of its biological features are preadaptations that permitted relatives of these lobe-fined fish to conquer land.

The fleshy fins of the Australian lungfish have an anatomical bone structure that is recognizable to be similar to that of tetrapod limbs, including human extremities. With them, the Australian

\*Correspondence: phch1@biozentrum.uni-wuerzburg.de (M. Schartl).



<sup>&</sup>lt;sup>2</sup>The Xiphophorus Genetic Stock Center, Texas State University, 601 University Drive Centennial Hall 419, San Marcos, TX-78666, USA

# **Trends in Genetics | Genome of the Month**

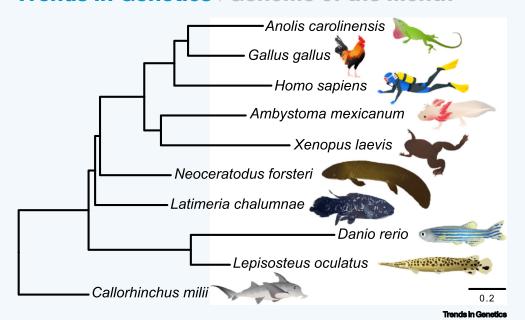


Figure 2. Phylogenetic Tree. (Reproduced, with permission, from [3]).

lungfish moves around in the water reminiscent of the locomotion of salamanders, with whom they also share the ability to regenerate severed limbs. They also have lungs, requiring them to breathe air in order not to drown.

TAXONOMY AND CLASSIFICATION:

KINGDOM: Animalia PHYLUM: Chordata SUBPHYLUM: Vertebrata CLASS: Sarcopterygii SUBCLASS: Dipnoi

ORDER: Ceratodontiformes FAMILY: Neoceratodontidae GENUS: Neoceratodus SPECIES: forsteri

- Meyer, A. and Wilson, A.C. (1990) Origin of tetrapods inferred from their mitochondrial DNA affiliation to lungfish. J. Mol. Evol. 31, 359–364
- 7. Meyer, A. and Dolven, S.I. (1992) Molecules, fossils and the origin of tetrapods. J. Mol. Evol. 35, 102-113
- 8. Meyer, A. and Wilson, A.C. (1991) Coelacanth's relationships. Nature 353, 219
- Brinkmann, H. et al. (2004) Complete mitochondrial genome sequences of the South American and the Australian lungfish: testing of the phylogenetic performance of mitochondrial data sets for phylogenetic problems in tetrapod relationships. J. Mol. Evol. 59, 834–848
- Brinkmann, H. et al. (2004) Nuclear protein-coding genes support lungfish and not the coelacanth as the closest living relatives of land vertebrates. Proc. Natl. Acad. Sci. U. S. A. 101, 4900–4905
- 11. Irisarri, I. and Meyer, A. (2016) The identification of the closest living relative(s) of tetrapods: phylogenomic lessons for resolving short ancient internodes. *Syst. Biol.* 65, 1057–1075

