

# The African Coleacanth Genome

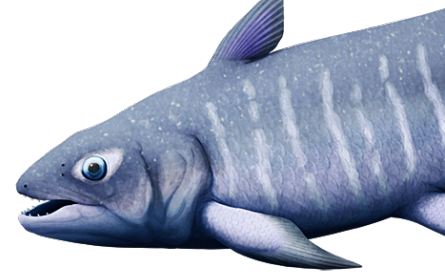
**Nashmeiah Alshammeri**

Intro. To Genomics 485

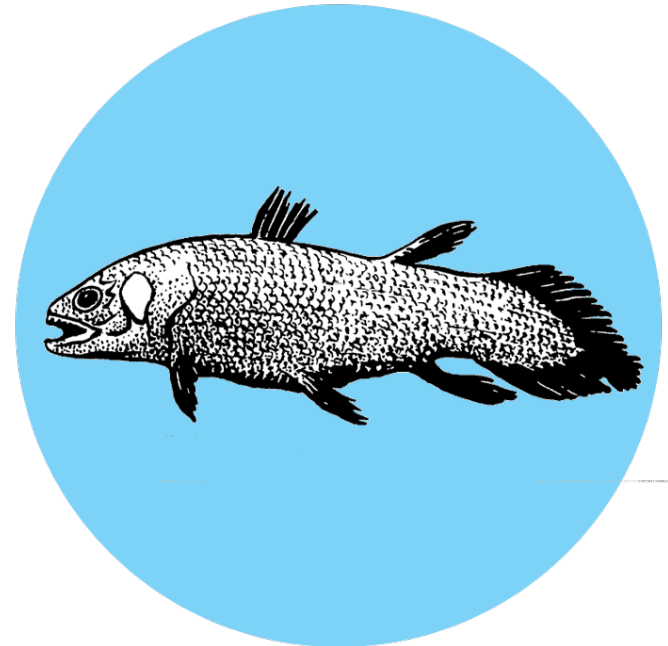
Fall 2020



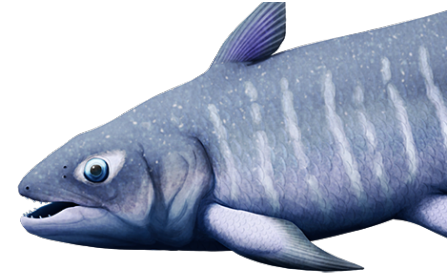
# Outline



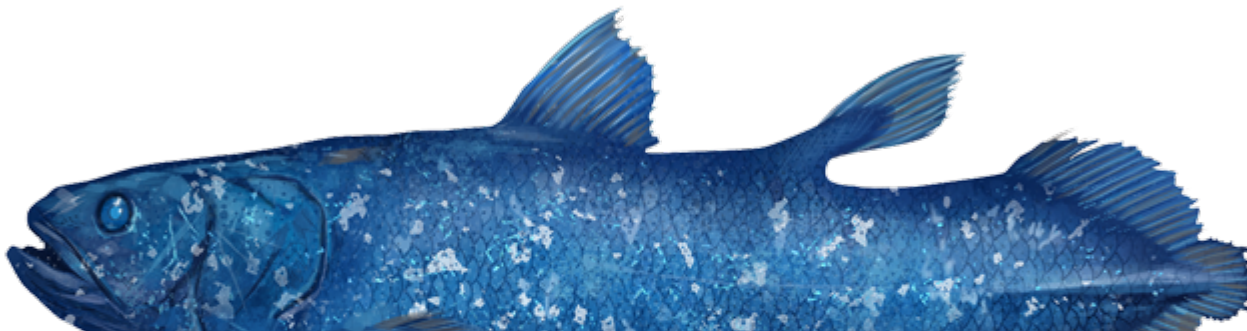
- General information
- Genome paper
- General genome information
- Sequencing strategy
- Sequencing Methods
- Genome assembly
- Genome outcome



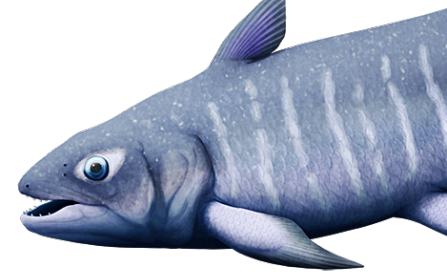
# General information



- Lineage of lobe-finned fish (extinct 70 million years ago).
- the only living member of its group.
- over 1m long, bluish in colour.
- had conspicuously fleshy fins that resembled the limbs of terrestrial vertebrates.



# General information

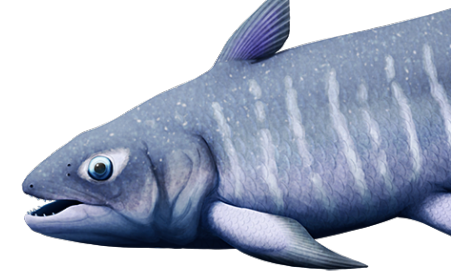


- Geographical distribution of coelacanth
- Unique locomotion
- Scientific name:  
*Latimeria chalumnae*





# Genome paper



nature

[Explore Content](#) ▾ [Journal Information](#) ▾ [Publish With Us](#) ▾

[nature](#) > [articles](#) > [article](#)

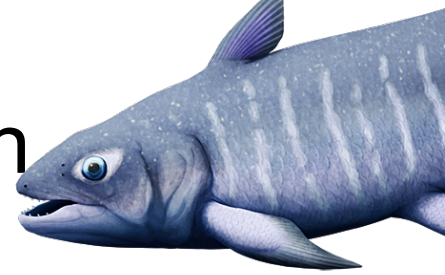
[Open Access](#) | Published: 17 April 2013

## The African coelacanth genome provides insights into tetrapod evolution

Chris T. Amemiya<sup>1,2\*</sup>, Jessica Alföldi<sup>3\*</sup>, Alison P. Lee<sup>4</sup>, Shaohua Fan<sup>5</sup>, Hervé Philippe<sup>6</sup>, Iain MacCallum<sup>3</sup>, Ingo Braasch<sup>7</sup>, Tereza Manousaki<sup>5,8</sup>, Igor Schneider<sup>9</sup>, Nicolas Rohner<sup>10</sup>, Chris Organ<sup>11</sup>, Domitille Chalopin<sup>12</sup>, Jeramiah J. Smith<sup>13</sup>, Mark Robinson<sup>1</sup>, Rosemary A. Dorrington<sup>14</sup>, Marco Gerdol<sup>15</sup>, Bronwen Aken<sup>16</sup>, Maria Assunta Biscotti<sup>17</sup>, Marco Barucca<sup>17</sup>, Denis Baurain<sup>18</sup>, Aaron M. Berlin<sup>3</sup>, Gregory L. Blatch<sup>14,19</sup>, Francesco Buonocore<sup>20</sup>, Thorsten Burmester<sup>21</sup>, Michael S. Campbell<sup>22</sup>, Adriana Canapa<sup>17</sup>, John P. Cannon<sup>23</sup>, Alan Christoffels<sup>24</sup>, Gianluca De Moro<sup>15</sup>, Adrienne L. Edkins<sup>14</sup>, Lin Fan<sup>3</sup>, Anna Maria Fausto<sup>20</sup>, Nathalie Feiner<sup>5,25</sup>, Mariko Forconi<sup>17</sup>, Junaid Gamielidien<sup>24</sup>, Sante Gnerre<sup>3</sup>, Andreas Gnirke<sup>3</sup>, Jared V. Goldstone<sup>26</sup>, Wilfried Haerty<sup>27</sup>, Mark E. Hahn<sup>26</sup>, Uljana Hesse<sup>24</sup>, Steve Hoffmann<sup>28</sup>, Jeremy Johnson<sup>3</sup>, Sibel I. Karchner<sup>26</sup>, Shigehiro Kuraku<sup>5,†</sup>, Marcia Lara<sup>3</sup>, Joshua Z. Levin<sup>3</sup>, Gary W. Litman<sup>23</sup>, Evan Mauceli<sup>3,†</sup>, Tsutomu Miyake<sup>29</sup>, M. Gail Mueller<sup>30</sup>, David R. Nelson<sup>31</sup>, Anne Nitsche<sup>32</sup>, Ettore Olmo<sup>17</sup>, Tatsuya Ota<sup>33</sup>, Alberto Pallavicini<sup>15</sup>, Sumir Panji<sup>24,†</sup>, Barbara Picone<sup>24</sup>, Chris P. Ponting<sup>27</sup>, Sonja J. Prohaska<sup>34</sup>, Dariusz Przybylski<sup>3</sup>, Nil Ratan Saha<sup>1</sup>, Vydianathan Ravi<sup>4</sup>, Filipe J. Ribeiro<sup>3,†</sup>, Tatjana Sauka-Spengler<sup>35</sup>, Giuseppe Scapigliati<sup>20</sup>, Stephen M. J. Searle<sup>16</sup>, Ted Sharpe<sup>3</sup>, Oleg Simakov<sup>5,36</sup>, Peter F. Stadler<sup>32</sup>, John J. Stegeman<sup>26</sup>, Kenta Sumiyama<sup>37</sup>, Diana Tabbaa<sup>3</sup>, Hakim Tafer<sup>32</sup>, Jason Turner-Maier<sup>3</sup>, Peter van Heusden<sup>24</sup>, Simon White<sup>16</sup>, Louise Williams<sup>3</sup>, Mark Yandell<sup>22</sup>, Henner Brinkmann<sup>6</sup>, Jean-Nicolas Volf<sup>12</sup>, Clifford J. Tabin<sup>10</sup>, Neil Shubin<sup>38</sup>, Manfred Scharl<sup>39</sup>, David B. Jaffe<sup>3</sup>, John H. Postlethwait<sup>7</sup>, Byrappa Venkatesh<sup>4</sup>, Federica Di Palma<sup>3</sup>, Eric S. Lander<sup>3</sup>, Axel Meyer<sup>5,8,25</sup> & Kerstin Lindblad-Toh<sup>3,40</sup>

The discovery of a living coelacanth specimen in 1938 was remarkable, as this lineage of lobe-finned fish was thought to have become extinct 70 million years ago. The modern coelacanth looks remarkably similar to many of its ancient relatives, and its evolutionary proximity to our own fish ancestors provides a glimpse of the fish that first walked on land. Here we report the genome sequence of the African coelacanth, *Latimeria chalumnae*. Through a phylogenomic analysis, we conclude that the lungfish, and not the coelacanth, is the closest living relative of tetrapods. Coelacanth protein-coding genes are significantly more slowly evolving than those of tetrapods, unlike other genomic features. Analyses of changes in genes and regulatory elements during the vertebrate adaptation to land highlight genes involved in immunity, nitrogen excretion and the development of fins, tail, ear, eye, brain and olfaction. Functional assays of enhancers involved in the fin-to-limb transition and in the emergence of extra-embryonic tissues show the importance of the coelacanth genome as a blueprint for understanding tetrapod evolution.

# General Genome information



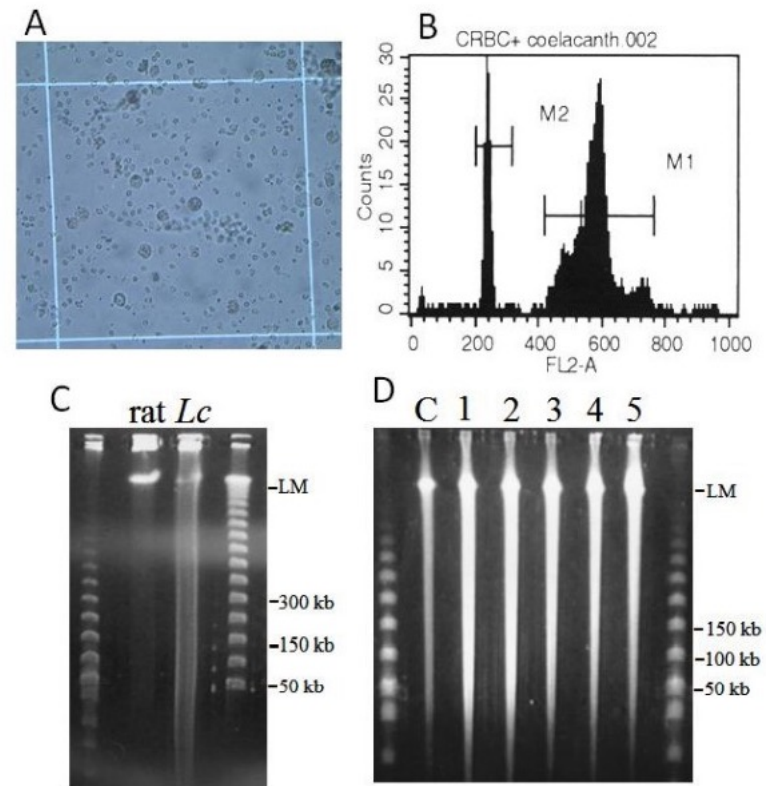
- 48 chromosomes
- The protein-coding genes are slowly evolving  
( contribute to ? )
- Is it important to examine the changes in genes  
and regulatory elements ?

# Sequencing Strategy

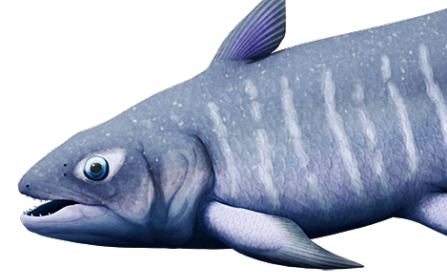


- DNA source: Blood sample

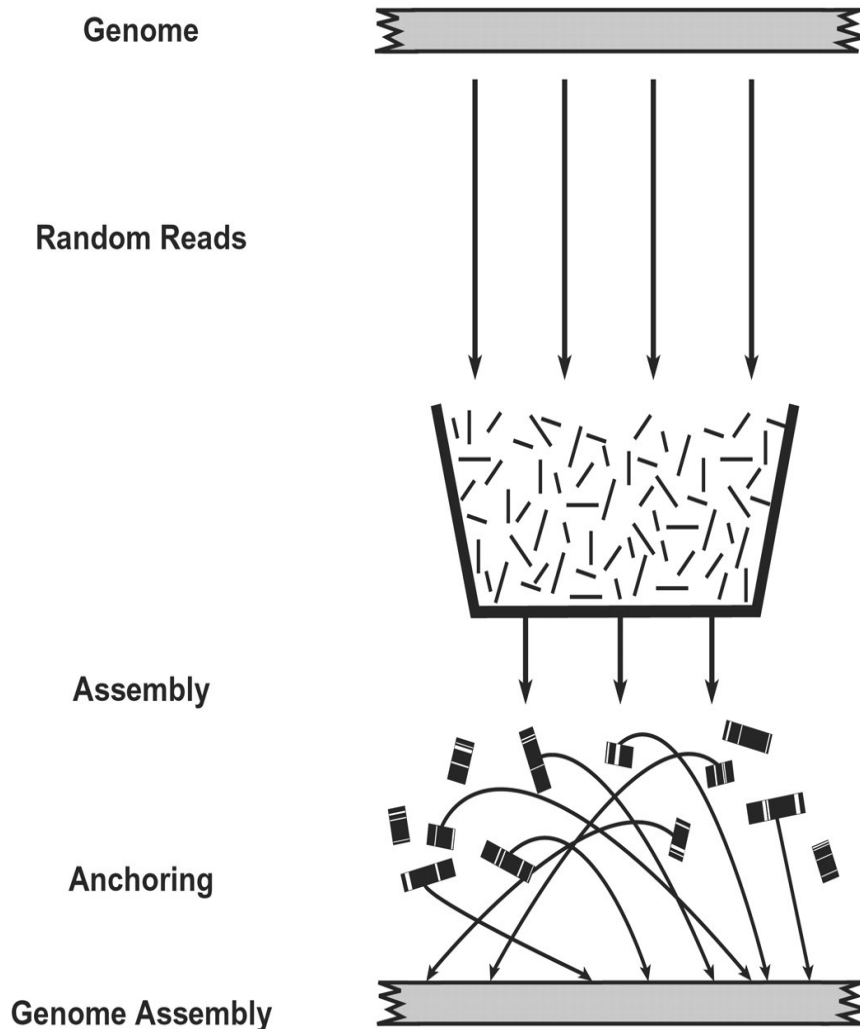
- A. Microscopic phase-contrast examination.
- B. Flow cytometric analysis of blood sample.
- C. Agarose-embedded *Latimeria* genomic DNA was run on a pulse field gel along with a similarly prepared sample from brown Norway rat.
- D. Agarose-embedded DNA was subjected to an *EcoRI*-*EcoRI* methylase competition reaction prior to electrophoresing.



# Sequencing Strategy



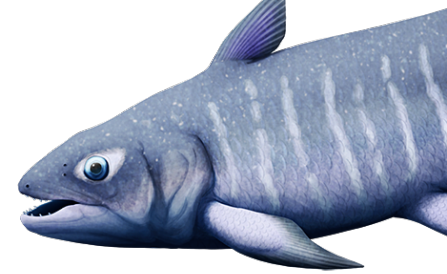
## WHOLE-GENOME SHOTGUN



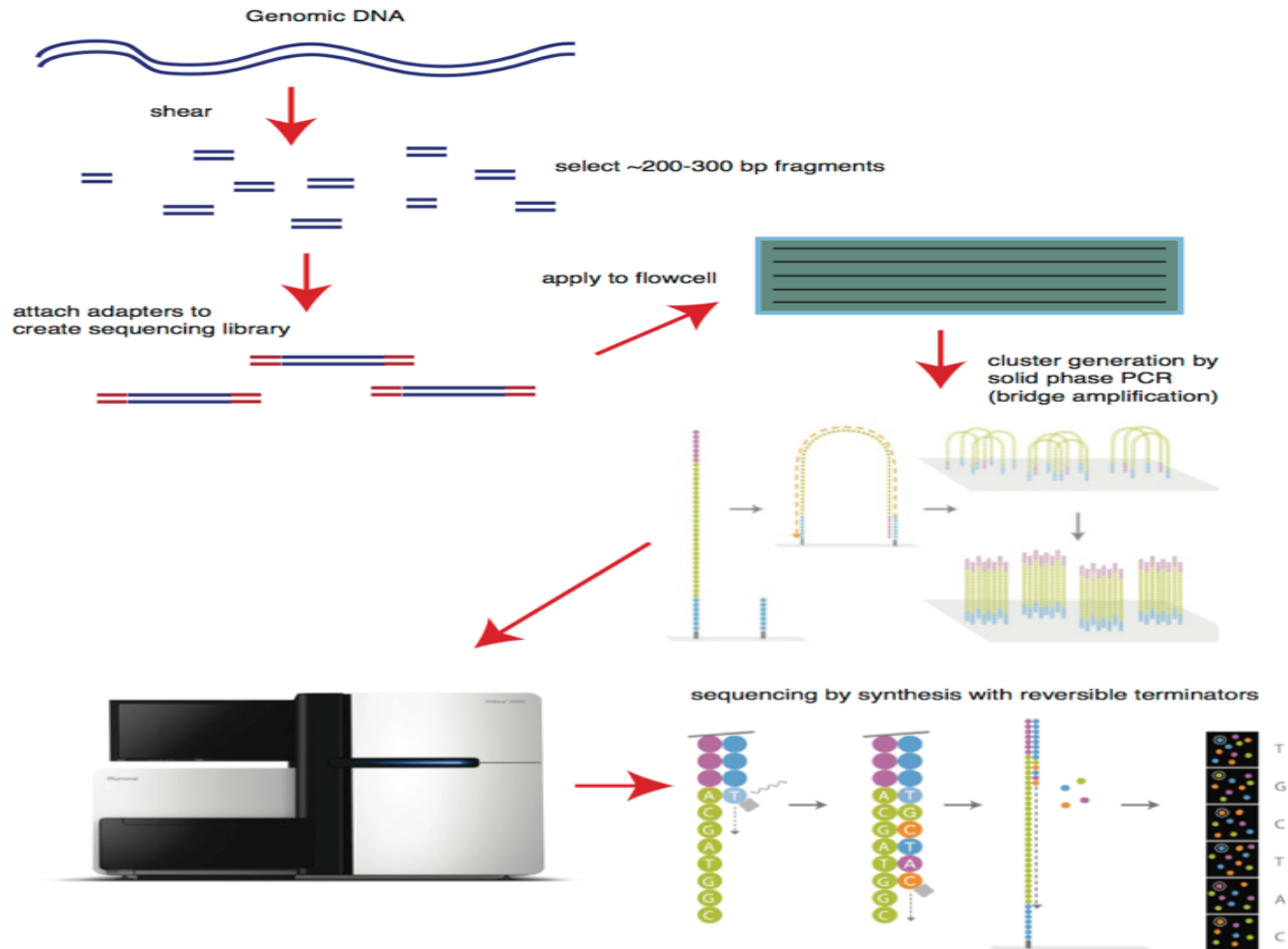
whole genome shotgun  
sequencing



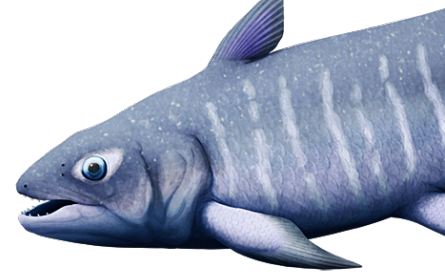
# Sequencing Method



- Illumina sequencing technology

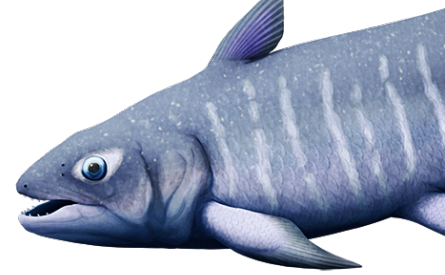


# Genome Assembly



- Assembled genome size = 2.86 Gb
- Assembly by ALLPATHSLG<sup>55</sup> (short read genome assembler)
- Contig N50 size of 12.7 Kb
- Scaffold N50 size of 924 Kb

# Genome Annotation



- The genome assembly was annotated separately by both:

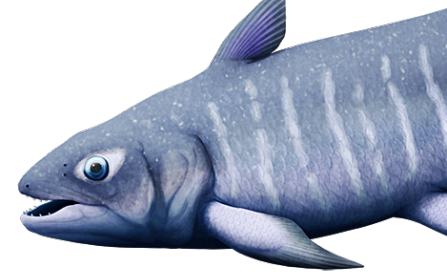
## 1. The Ensembl gene annotation pipeline

19,033 protein-coding genes containing 21,817 transcripts

## 2. MAKER13

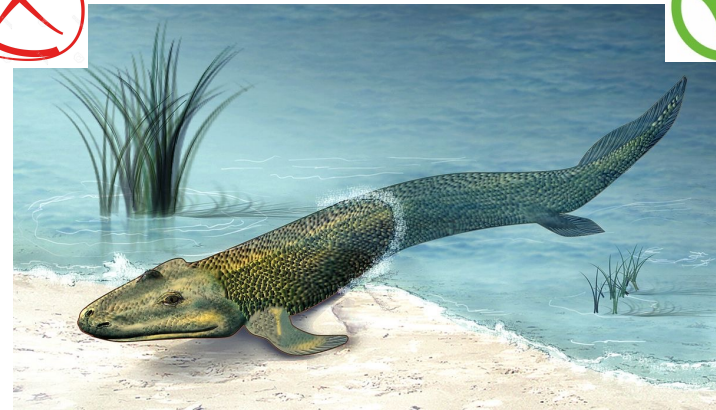
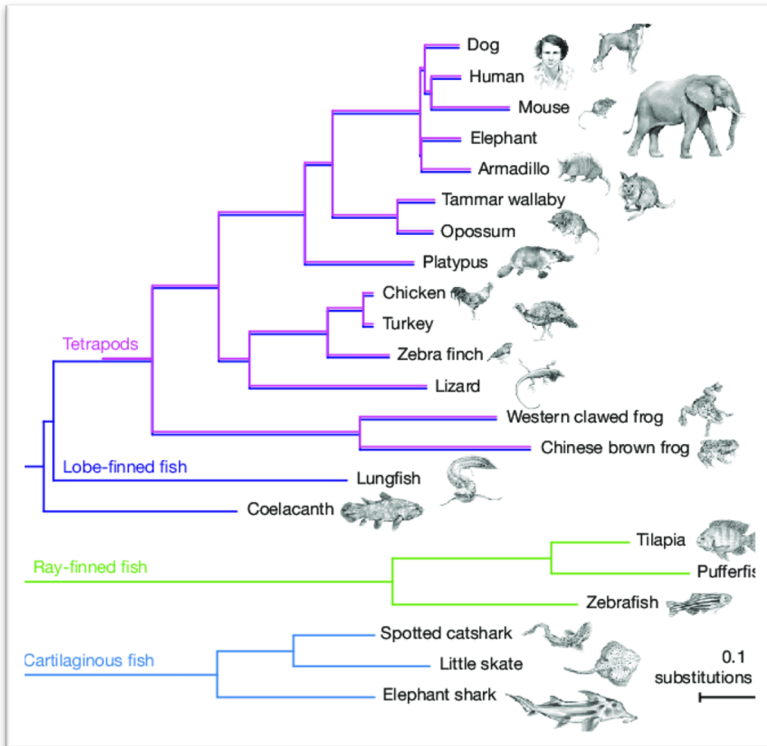
29,237 protein-coding gene annotations

# Genome Outcome

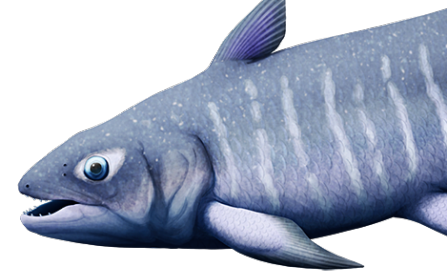


phylogenomic analysis:

Lung-fish NOT coelacanth closest living relative of tetrapods



# Genome Outcome

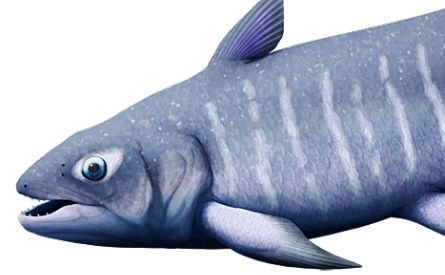


- the water-to-land transition

critical characters in the morphological transition from water to land are reflected in the loss of specific genes along the phylogenetic branch leading to tetrapods

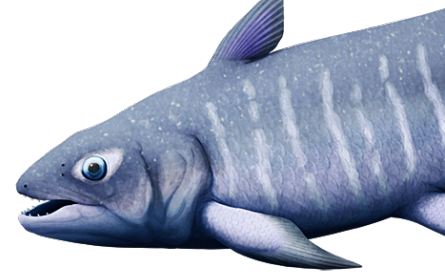


# Genome Outcome



- The coelacanth lacks immunoglobulin-M
  - all other major components of the immune system are present
  - two IgW genes

# Question



- Why it is important to sequence animals?
- Why it is important to use more than one assembly ?

# Thank You

