Evolution of important livestock species

Modul no. 2: Conservation and Sustainable Use of Animal Genetic Resources
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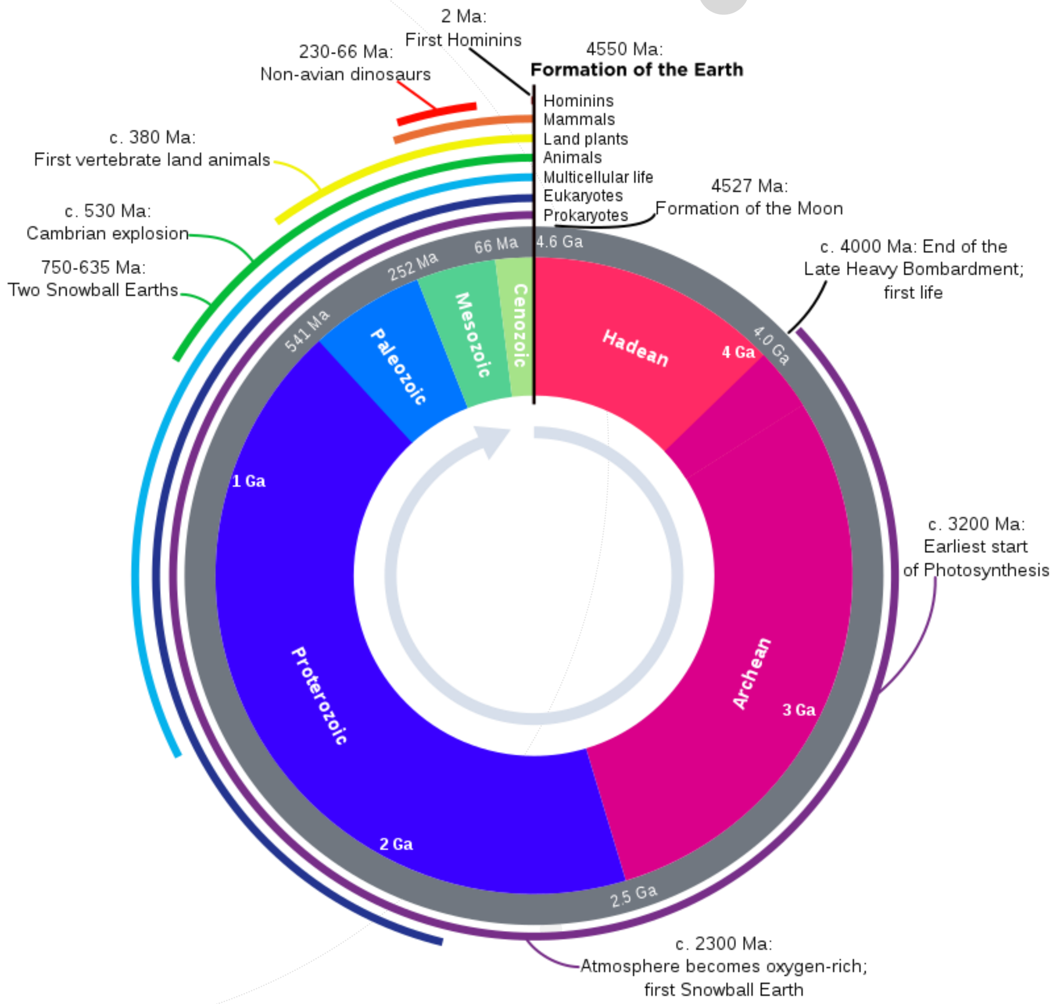
History of Earth and life



https://en.wikipedia.org/wiki/History_of_Earth

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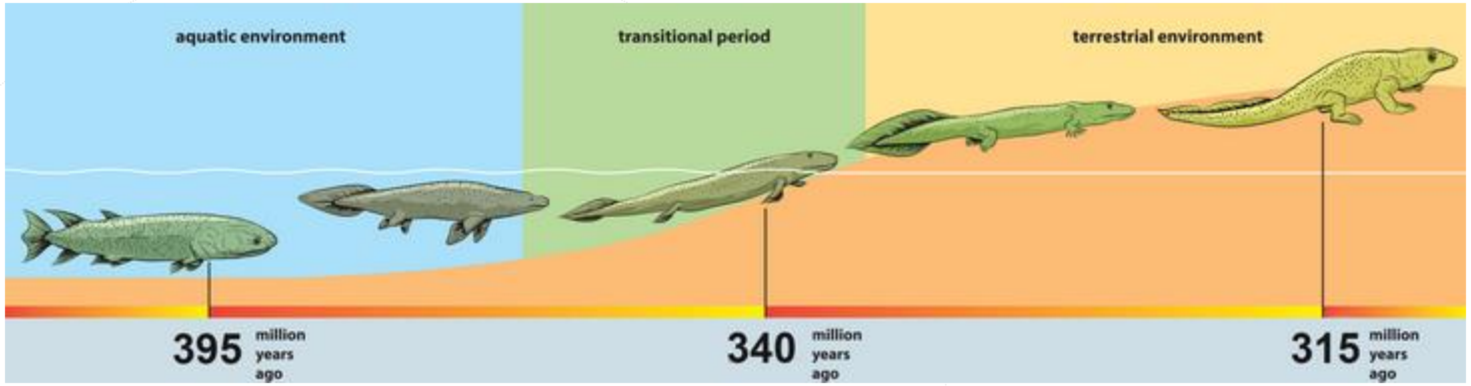
Evolution of animals



The ribbed medusa-like animal (*Dickinsonia*) is one of the oldest known animals living on Earth (about 558 million years old)

https://www.science.org/content/article/fossil-one-world-s-earliest-animals-according-fat-molecules-preserved-half-billion

The oldest fish, the 518-million-year-old *Metaspriggina walcotti*, was about 6 cm long, had a pair of large protruding eyes and a small pair of nasal capsules.

https://theconversation.com/the-oldest-fish-in-the-world-lived-500-million-years-ago-27710

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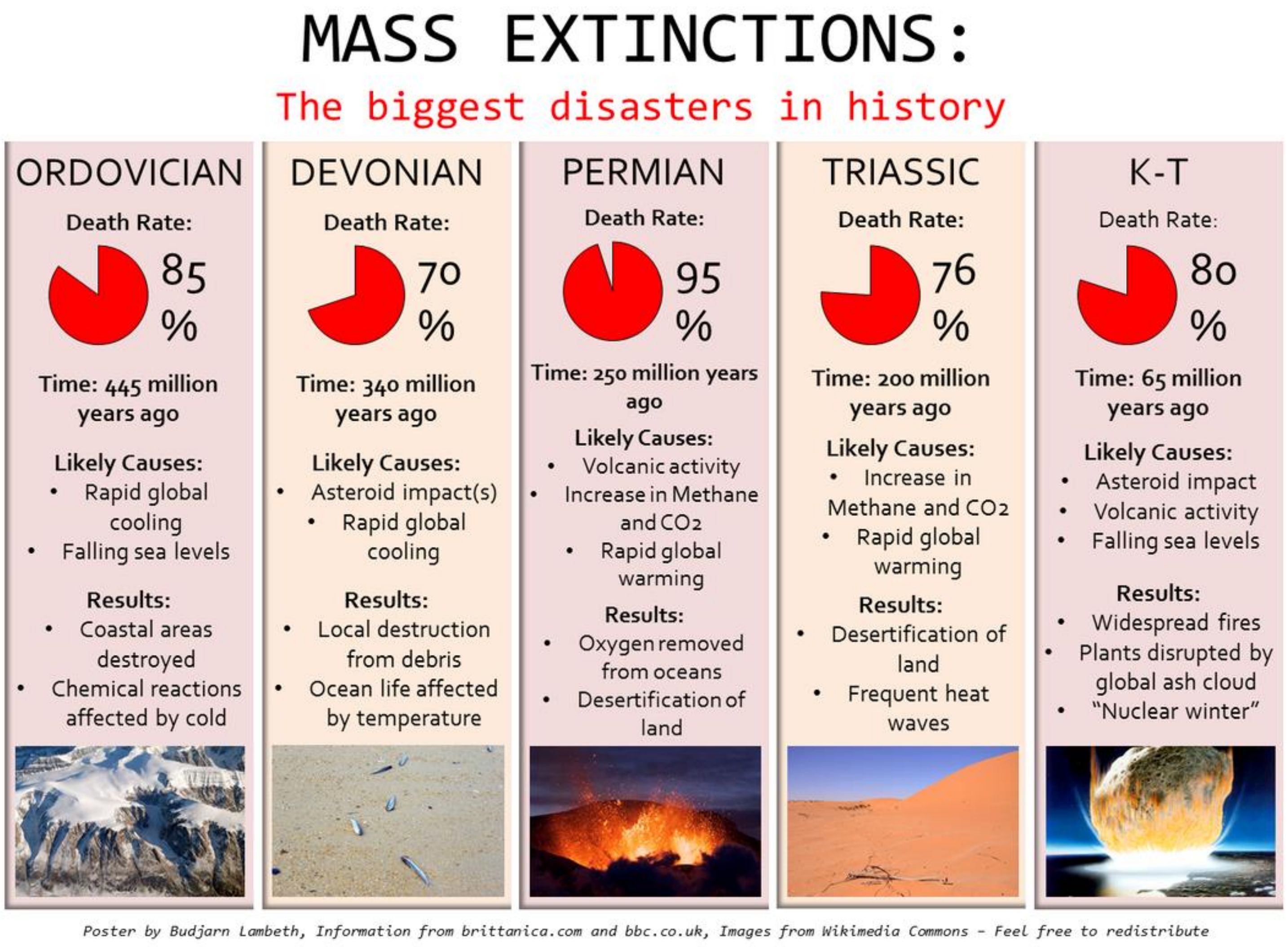

MASS EXTINCTIONS:

The biggest disasters in history

ORDOVICIAN	DEVONIAN	PERMIAN	TRIASSIC	K-T
Death Rate: 85 %	Death Rate: 70 %	Death Rate: 95 %	Death Rate: 76 %	Death Rate: 80 %
Time: 445 million years ago	Time: 340 million years ago	Time: 250 million years ago	Time: 200 million years ago	Time: 65 million years ago
Likely Causes: • Rapid global cooling • Falling sea levels	**Likely Causes:** • Asteroid impact(s) • Rapid global cooling	**Likely Causes:** • Volcanic activity • Increase in Methane and CO2 • Rapid global warming	**Likely Causes:** • Increase in Methane and CO2 • Rapid global warming	**Likely Causes:** • Asteroid impact • Volcanic activity • Falling sea levels
Results: • Coastal areas destroyed • Chemical reactions affected by cold	**Results:** • Local destruction from debris • Ocean life affected by temperature	**Results:** • Oxygen removed from oceans • Desertification of land	**Results:** • Desertification of land • Frequent heat waves	**Results:** • Widespread fires • Plants disrupted by global ash cloud • "Nuclear winter"

Poster by Budjarn Lambeth, Information from brittanica.com and bbc.co.uk, Images from Wikimedia Commons - Feel free to redistribute

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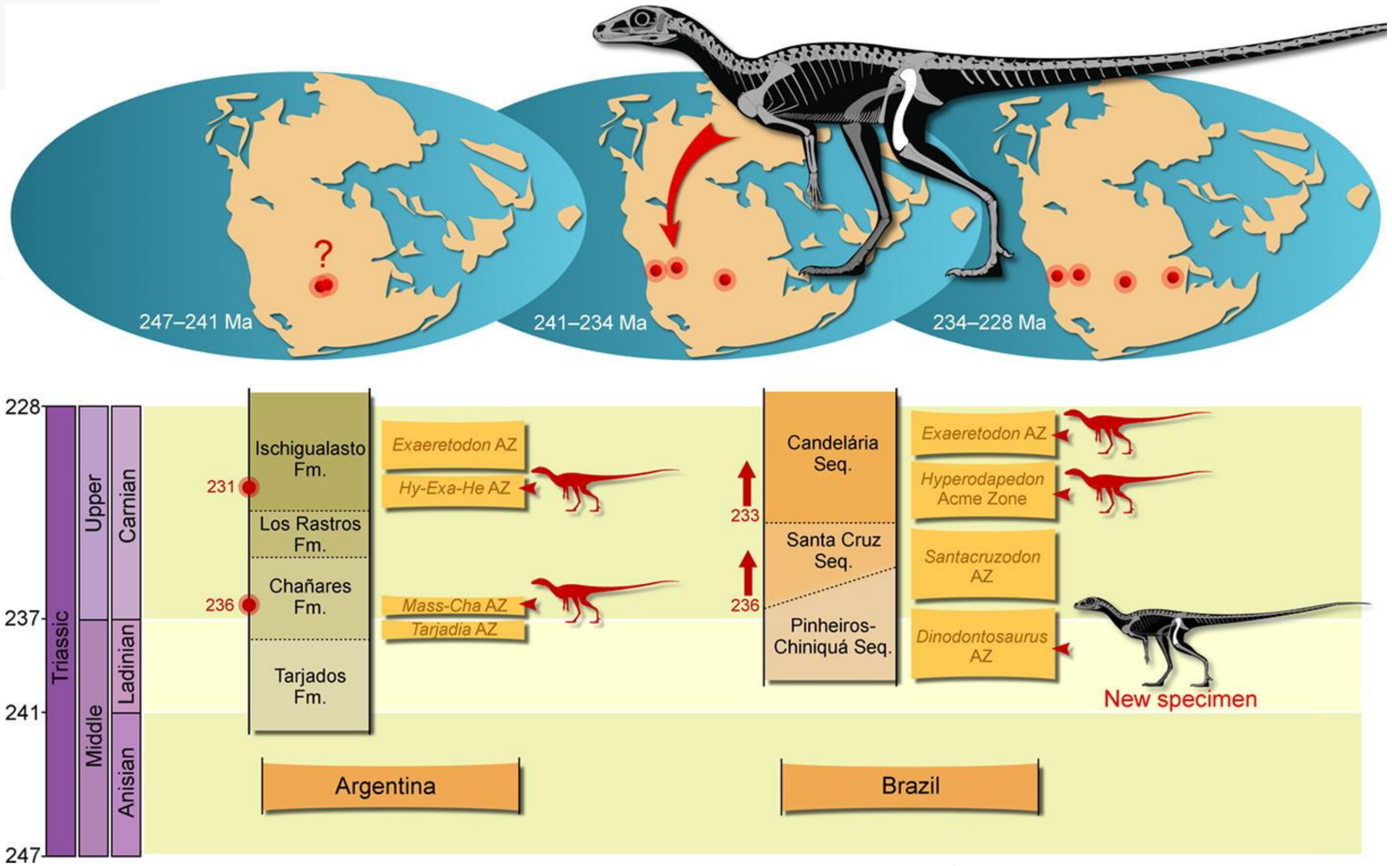

The first dinosauromorph from Middle Triassic sediments (240-230 million years ago) in Brazil.

The new sample is therefore potentially the oldest dinosaur from South America, thus narrowing the biogeographic gap between Africa and Argentina during the early dinosaur radiation. In addition, the new specimen provides evidence that dinosaurids lived in South America earlier than previously thought (Ladinian-Middle Triassic).
https://doi.org/10.1016/j.gr.2022.02.010

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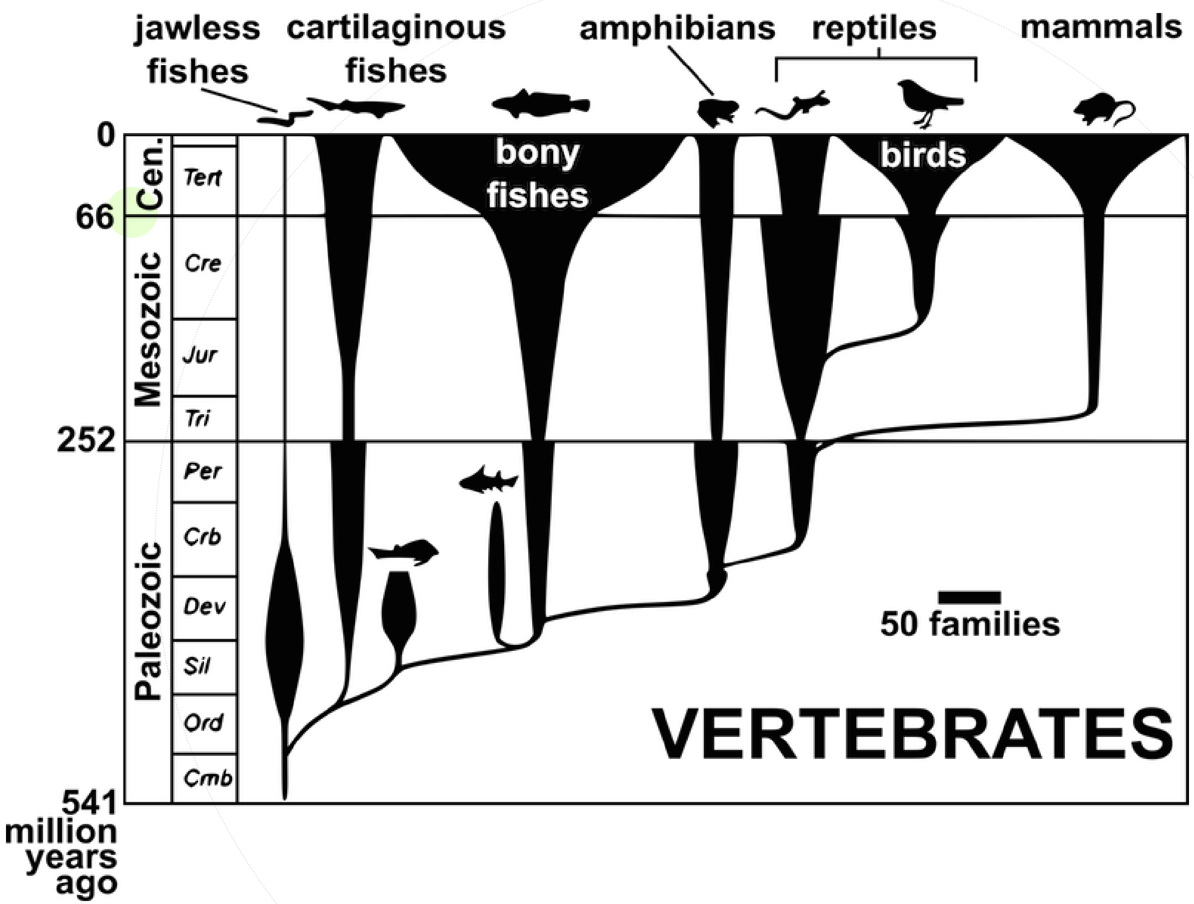

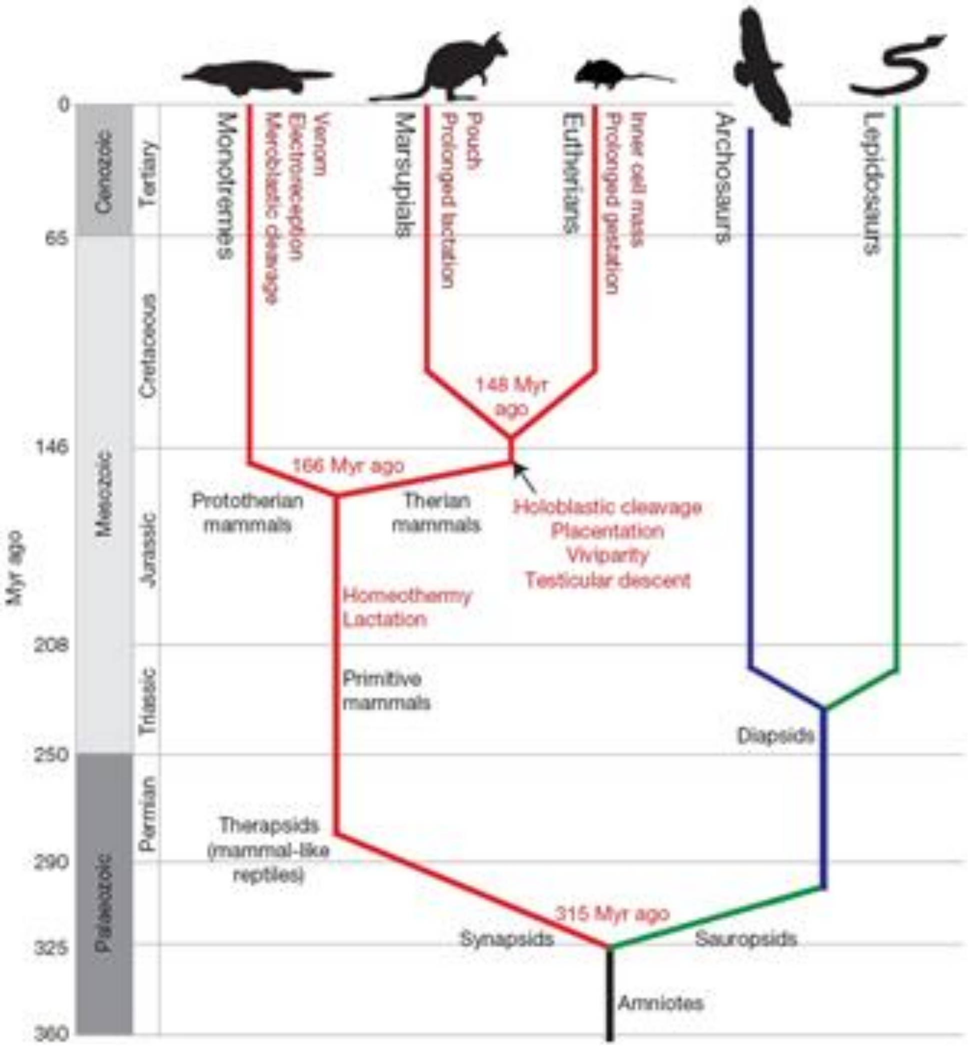

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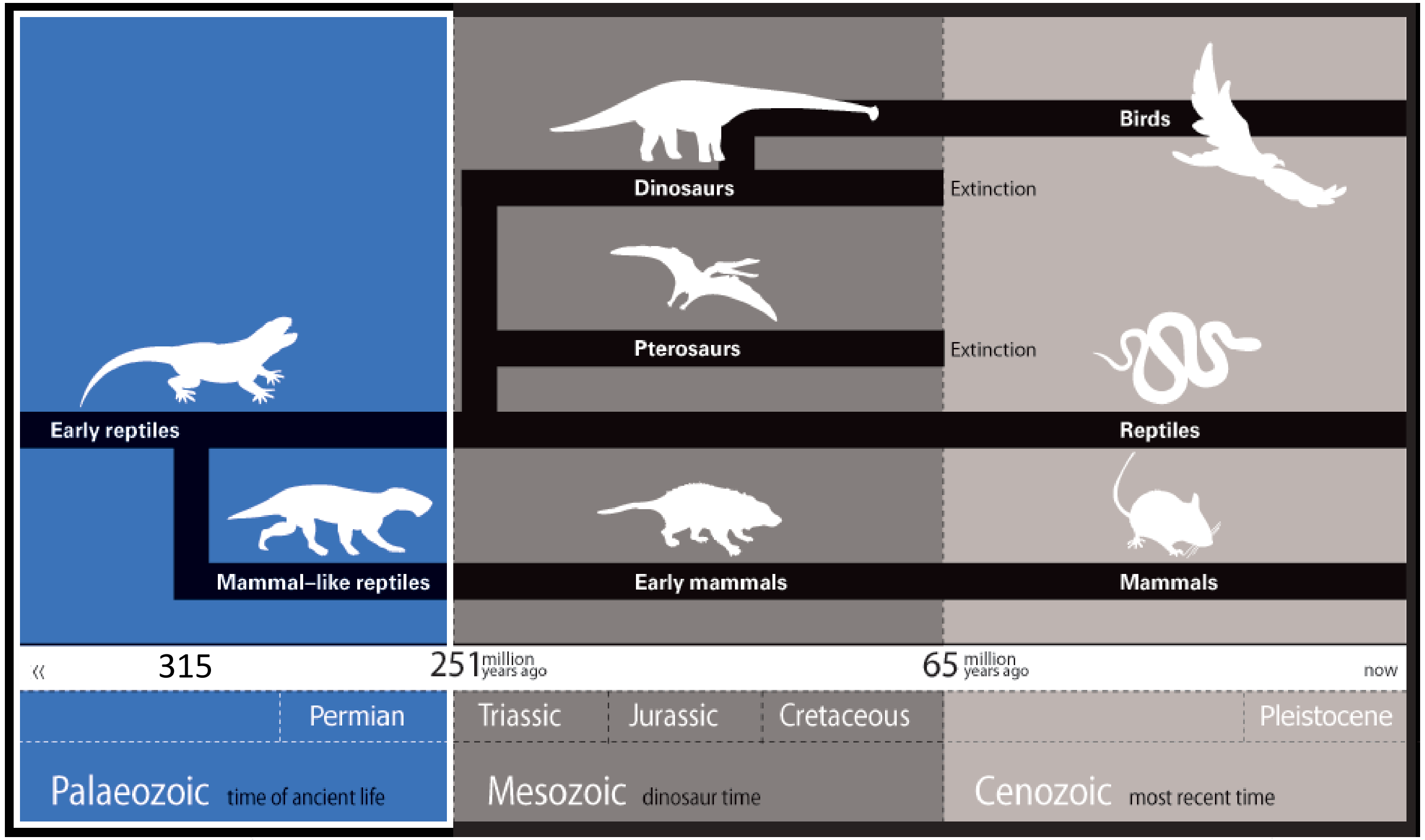

https://museumsvictoria.com.au/melbournemuseum/resources/dinosaur-walk/

- The ancestors of mammals are the **cynodont therapsids** (Cynodontia, Therapsida, Synapsida), reptiles that were one of the dominant groups of terrestrial vertebrates in the Triassic.
- Cynodonts produced a variety of forms during the Triassic that exhibit a mosaic of "old reptilian" and "new mammalian" characters to varying degrees.
- It is important to note, however, that the emergence of these characters was gradual. Determining the reptile/mammal boundary is essentially artificial and its exact location is very difficult and subjective. In other words, **mammals are advanced cynodonts**.

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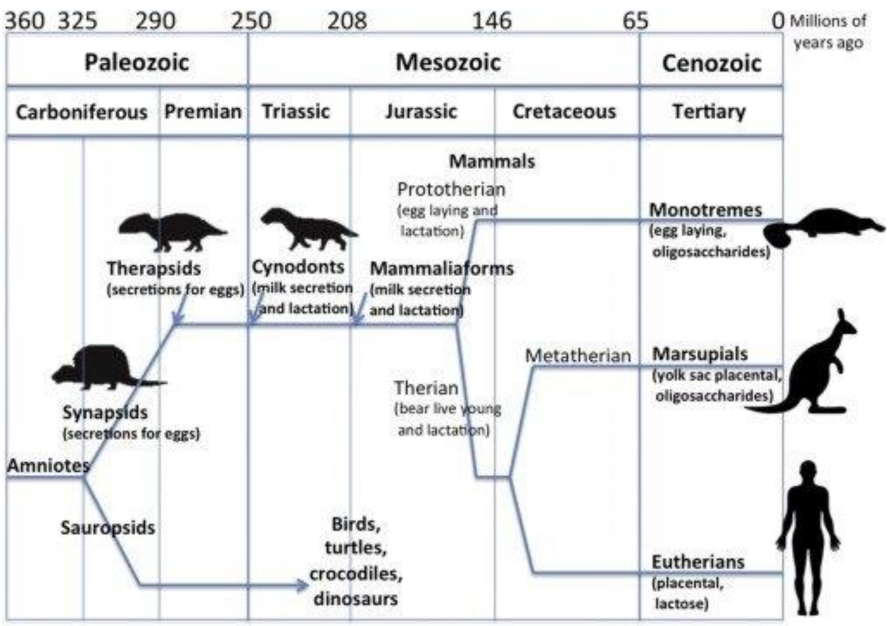
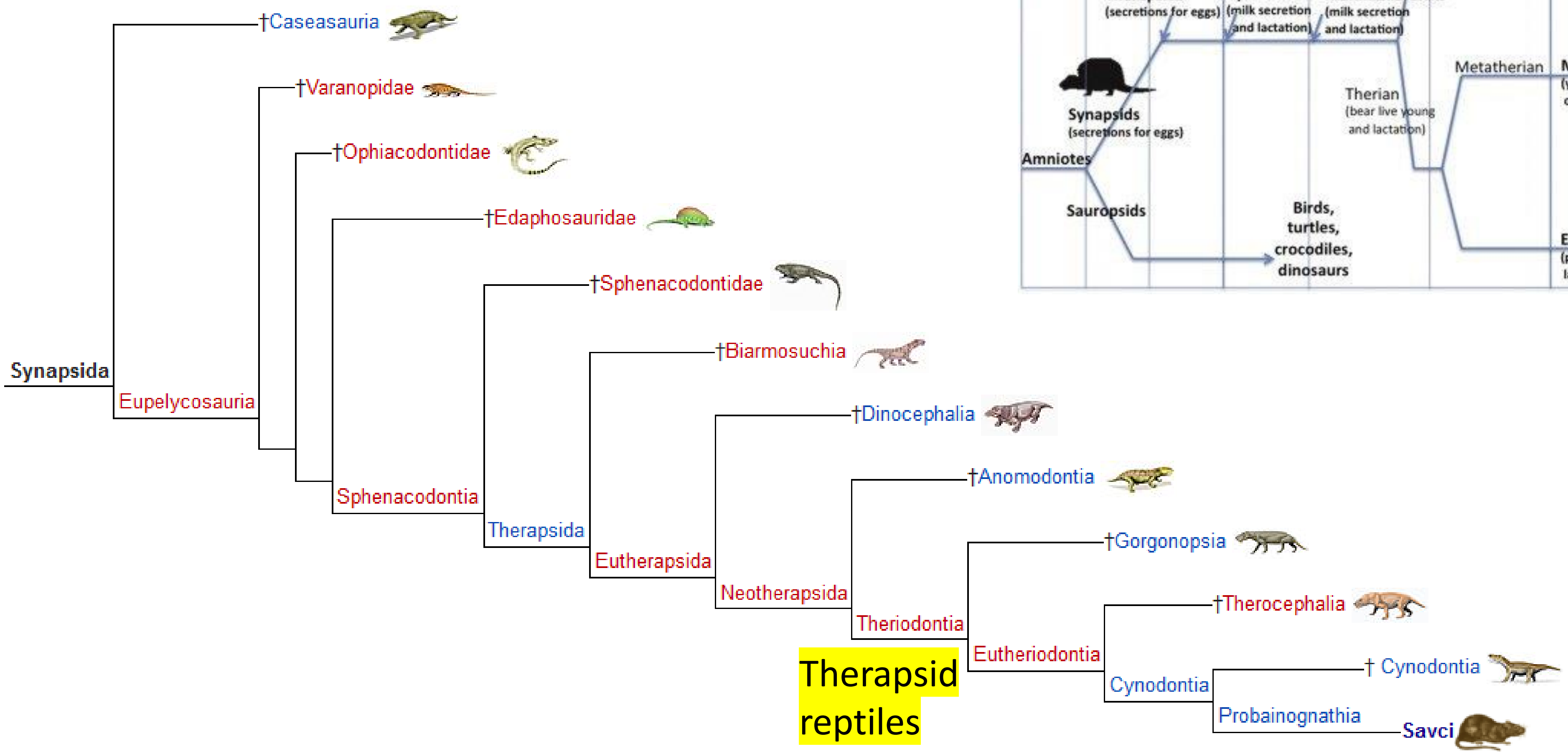
Reptile - *synapsida*

- from the Late Carboniferous to the Lower Cretaceous, since then they have lived only as mammals.





Therapsid reptiles

Perm - Triassic

Upper Triassic (200 Ma)

Sister Branch - *Sauropsida* -> reptiles and birds today

Reconstructing the genome of the common ancestor of all mammals

- Every modern mammal, from the platypus to the blue whale, descends from a common ancestor that lived about 180 million years ago.
- The scientists drew on high-quality genome sequences from 32 living species representing 23 of the 26 known mammalian orders. These included humans and chimpanzees, wombats and rabbits, manatees, domestic cattle, rhinoceroses, bats and marsupials. The genomes of chickens and Chinese alligators were also included in the analysis as comparison groups.
- The mammalian ancestor had 19 autosomal chromosomes (2n = 38) + 2 sex chromosomes.
- Scientists found nine whole chromosomes or fragments of chromosomes in the mammalian ancestor, whose gene order is the same as that of modern bird chromosomes (320 million years - conservation synteny).

Damas J. et al., Evolution of the ancestral mammalian karyotype and syntenic regions, *Proceedings of the National Academy of Sciences* (2022). DOI: 10.1073/pnas.2209139119

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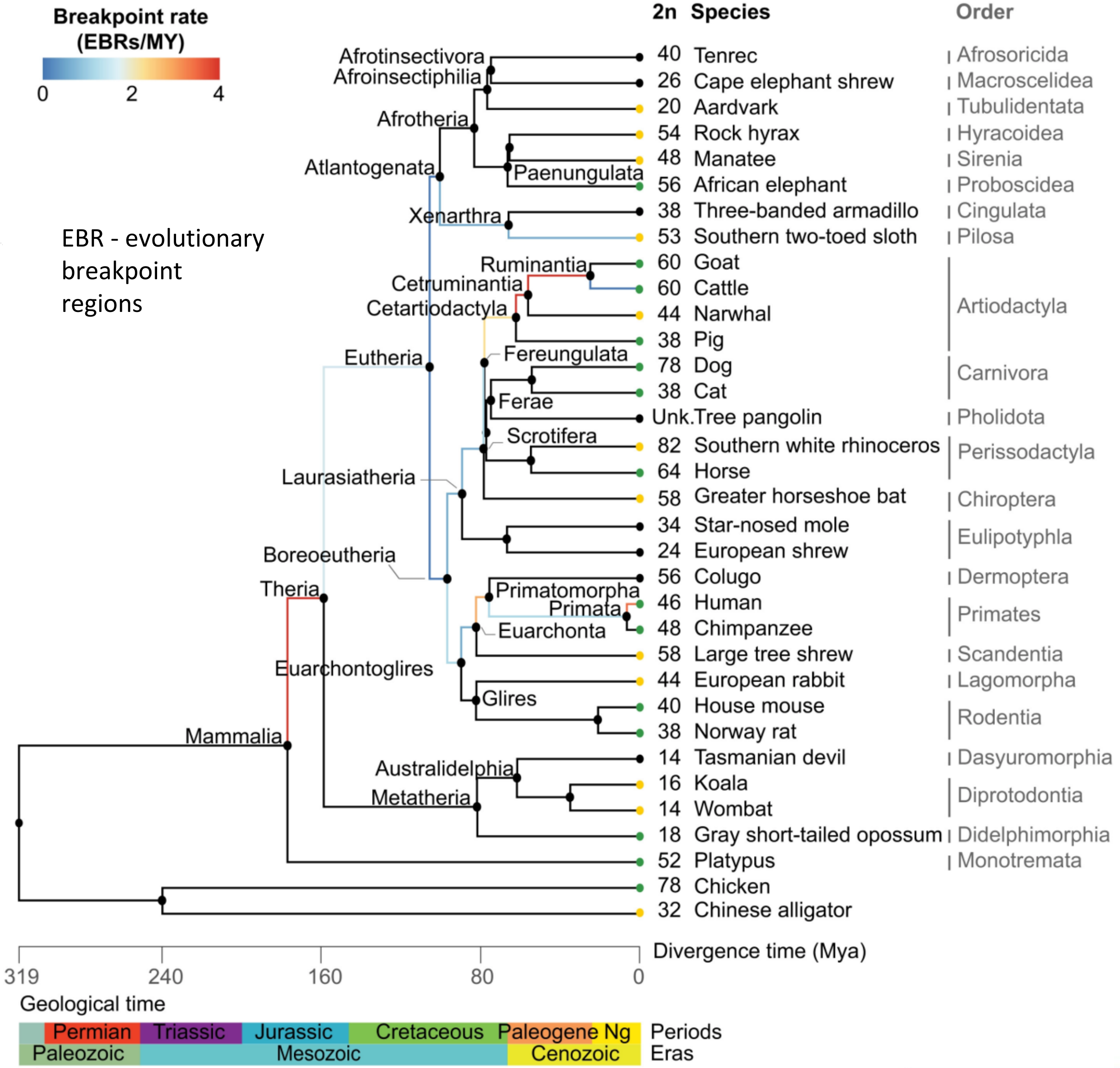
Mammalian radiation

- It is only in the Cenozoic (65 million years ago, the beginning of the Tertiary) that mammalian differentiation grows, increasing in size, flying mammals, marine mammals...
  - Archaic primates, proto-predators, anthropoids
- Extinct 37-22.5 million years ago and replaced by apes, artiodactyls, elephants, carnivores, rodents, bats, primates
- Late Tertiary - the modernisation of mammals (until today)
  - Specialised mammals
  - Horses with 3 fingers -> with 1 finger; Primitive dogs -> modern wolves and foxes
  - High diversity - a small remnant of mammal species diversity has survived to the present day
    - 2000 known families died out, today only 1000 families



EBR - evolutionary breakpoint regions

Phylogenetic tree of descendants and reconstructed ancestors. The colour of the branches represents the rate of breakpoints in the RACF (breakpoints per million years). Black branches represent undetermined breakpoint rates. The colors of the spikes represent the assembly sequence: black, scaffold-level genome assembly; green, chromosome-level genome assembly; yellow, chromosome-scale scaffold-level genome assembly. The numbers next to the species names indicate the diploid chromosome number (if known).

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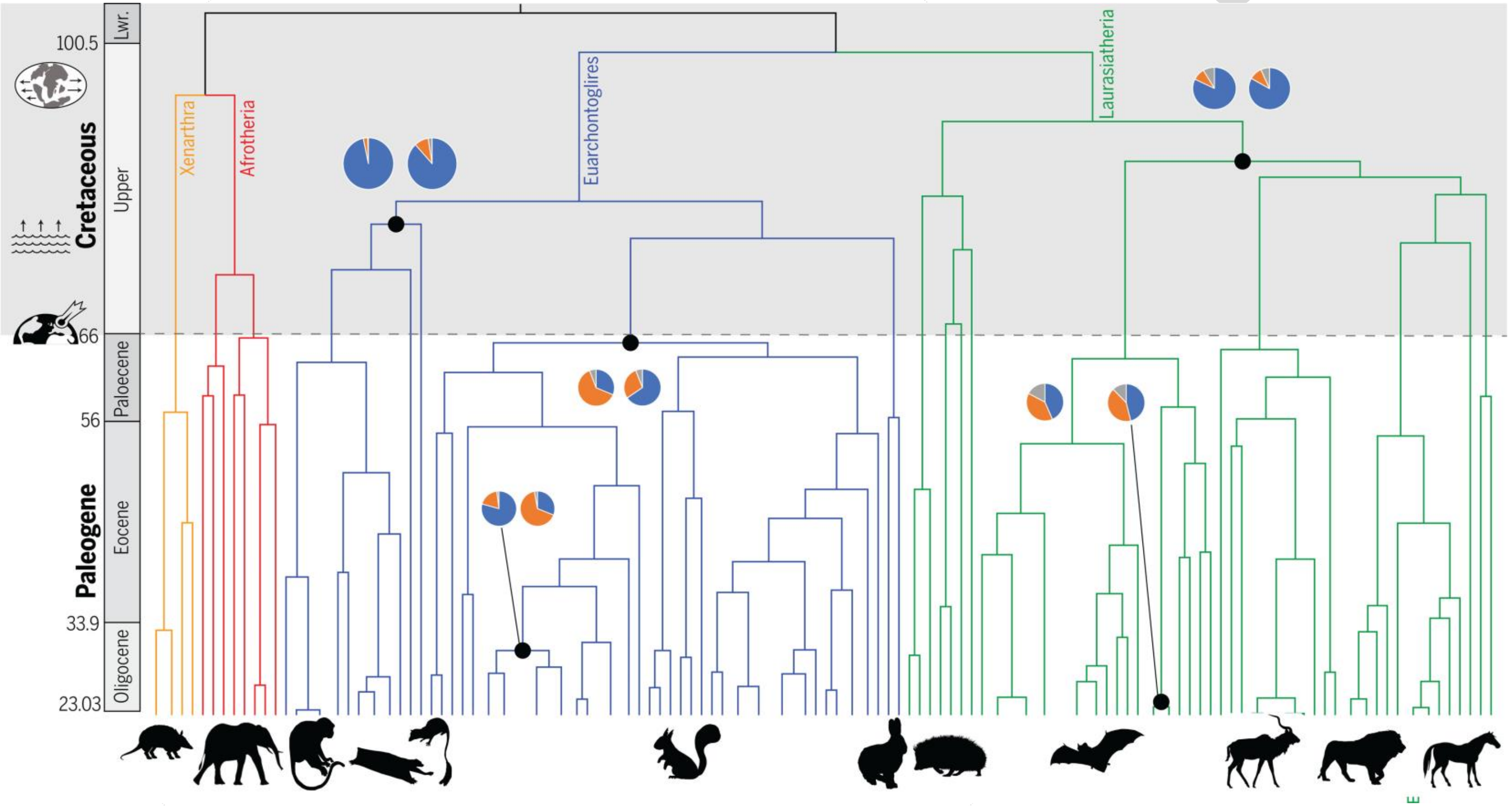
The timing of placental mammal evolution



The combination of Cretaceous continental fragmentation and lineage isolation, followed by the direct and indirect effects of the K-Pg extinction during rapid land emergence, synergistically contributed to the accelerated rate of placental mammal diversification during the early Cenozoic.

Genomic time trees reveal an accumulation of cladogenic events before and immediately after the Cretaceous-Paleogene (K-Pg) boundary, suggesting an important role for Cretaceous continental vicariance and K-Pg extinction in placental radiation.

https://www.science.org/doi/10.1126/science.abl8189

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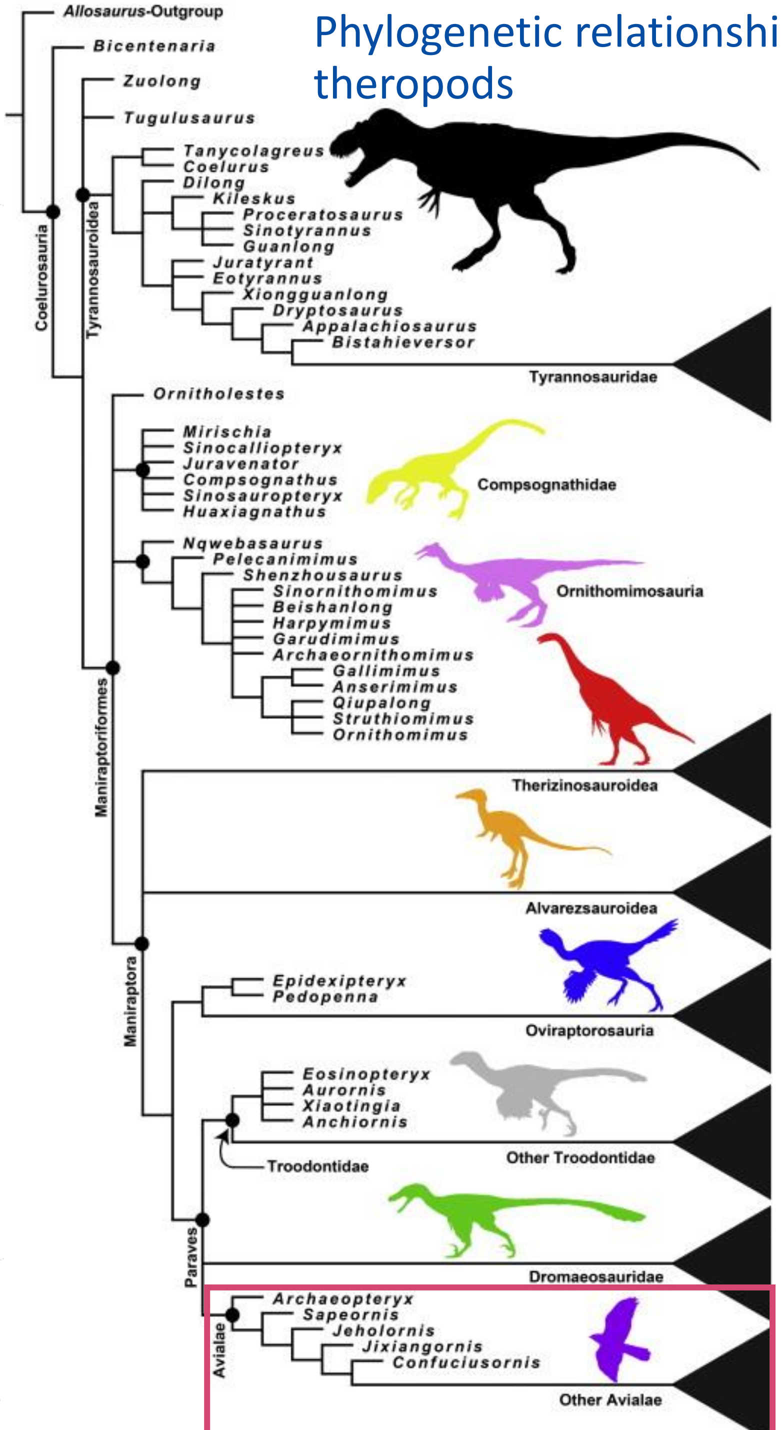
Bird radiation

- **Modern birds** have achieved their enormous diversity over a more than **150-million-year** evolutionary journey that began with their divergence from theropod dinosaurs, continued with the gradual and piecemeal adoption of a lethal body plan, and included two bursts of diversification: the first in the Mesozoic, when the small feathered winged dinosaur became fully formed, and the second, when the surviving species were given free rein to thrive after the end-Cretaceous extinction.

Phylogenetic relationships of coelurosaurian theropods



https://doi.org/10.1016/j.cub.2014.08.034

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„Ungulates“

- Evolutionarily very different groups of herbivorous mammals
- Cretaceous (141-65 million years ago) - no ungulates
  - Proto-ungulates - small body, primitive teeth, claws (close to carnivorans).
- True ungulates
  - They appear at the beginning of the Paleocene (65 million years) and diversify rapidly, in the Eocene their extinction, only some survived to the Oligocene (37-22.5 million years)
  - Families: *Hyopsodontidae*, *Phenacodontidae*
- **Artiodactyls**
  - Reduction of fingers to 2; reduction of teeth (upper incisors, canines), digestive system - rumination (in suborders of camelids and ruminants) - in the Upper Eocene (40 million years)

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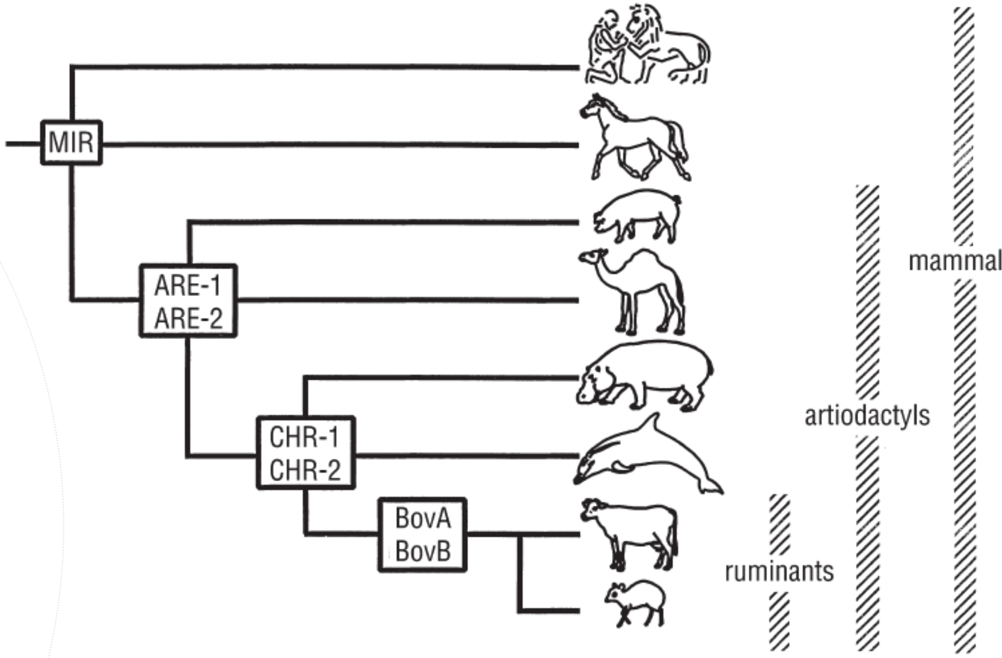
Cetartiodactyla - artiodactyls

- about 220 species - representatives live all over the world outside Australia and Antarctica
- Herbivores, occasionally omnivores
- They separated from other placental mammals 87.2 million years ago.
- Subordinate taxa:
  - suborder ***Suiformes*** Jaeckel, 1911 – **pigs, peccaries**
  - suborder *Tylopoda* Illiger, 1811 – **camels, llamas**
  - suborder *Ruminantia* Scopoli, 1777 - **Ruminants**
  - suborder *Cetancodonta* Arnason, Gullberg, Gretasdottir, Ursing & Janke, 2000 (**cetaceans, hippos**)



- Short interspersed repepeated elements (**SINE**)
- **M**ammalian-wide **i**nterspersed **r**epeats
  - Artiodactyl repeats (ARE)
  - Cetacean-hippopotamus-ruminant repeats CHR)
  - Ruminant repeats (Bov)

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- Superfamily Bovoidea – ox (cattle), buffalo, antelope, chamois, musk ox, goats and sheep
  - 187 fossil species known
  - Main distribution in the Pliocene (2 million years)
  - Northern Europe and Asia, from the end of the Pliocene southward and into Africa; migration also into North America
- Family *Bovidae*
  - Development began in the Middle Oligocene (25 million years ago); Centre of origin - tropics and subtropics of Central Asia
  - Direct ancestors - oldest genus Parabos (old Pliocene, 5-2 mya) in Eurasia, only in Pleistocene (Quaternary) -> North America (to South America by humans)
  - Finds of bison, ox and buffalo only in the Pleistocene (in sediments of older interglacial periods, suitable climate)

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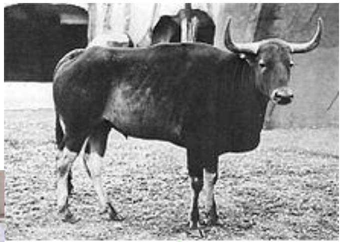
- Genus: ***Bos***
- Species: † **auroch** (*Bos primigenius*)
  Domesticated form: **cattle** (*Bos primigenius taurus*) and **zebu** (*Bos primigenius indicus)*
- Species: **gaur** (*Bos gaurus*)
  - Subspecies: Indian gaur (*Bos g. gaurus*)
  - Subspecies: Siamese gaur (*Bos g. readei*)
  - Subspecies: Malayan gaur (*Bos g. hubbbacki*)
  - Domesticated form: **gayal** (*Bos gaurus* f. *frontalis*)
- Species: **banteng** (*Bos javanicus*)
  - Subspecies: Javan banteng (*Bos j. javanicus*)
  - Subspecies: Bornean banteng (*Bos j. lowi*)
  - Subspecies: Burma banteng (*Bos j. birmanicus*)
  - Domesticated form: **Bali cattle** (*Bos banteng*)
- Species: **kouprey** (*Bos sauveli*) – mainly Cambodia
- Species: **wild yak** (*Bos mutus*)
  Domesticated form: **domestic yak** (*Bos mutus* f. *grunniensis*)



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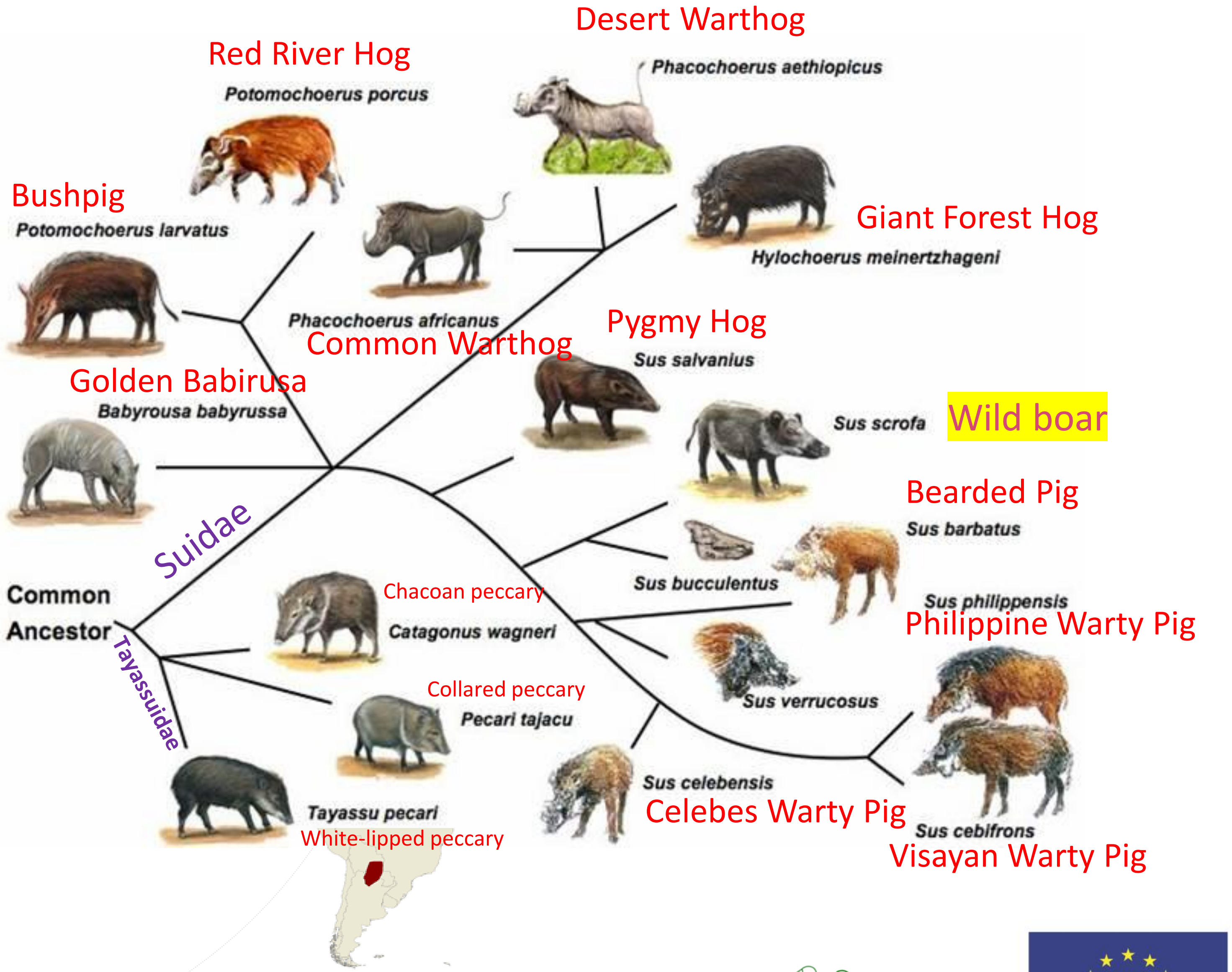
- Suborder: *Suina*
- Genera: *Suoidea*
  - Family: *Tayassuidae*
    - Genus: Catagonus , Pecar, Tayassu (all labeled as **pekari**)
    - Separated from pigs in SE Asia in the late Eocene, migrated to Eurasia, Africa and North America -> South America - only modern forms of peccaries live here
  - Family: ***Suidae***
    - Upper Eocene (Thailand, 35-40 million years ago)
    - Subfamily: ***Suinae***
      - Tribus:
        - ***Suini***
          - ***Genus: Sus***
        - *Babyrousini*
        - *Phacochoerini*
        - *Potamochoerini*



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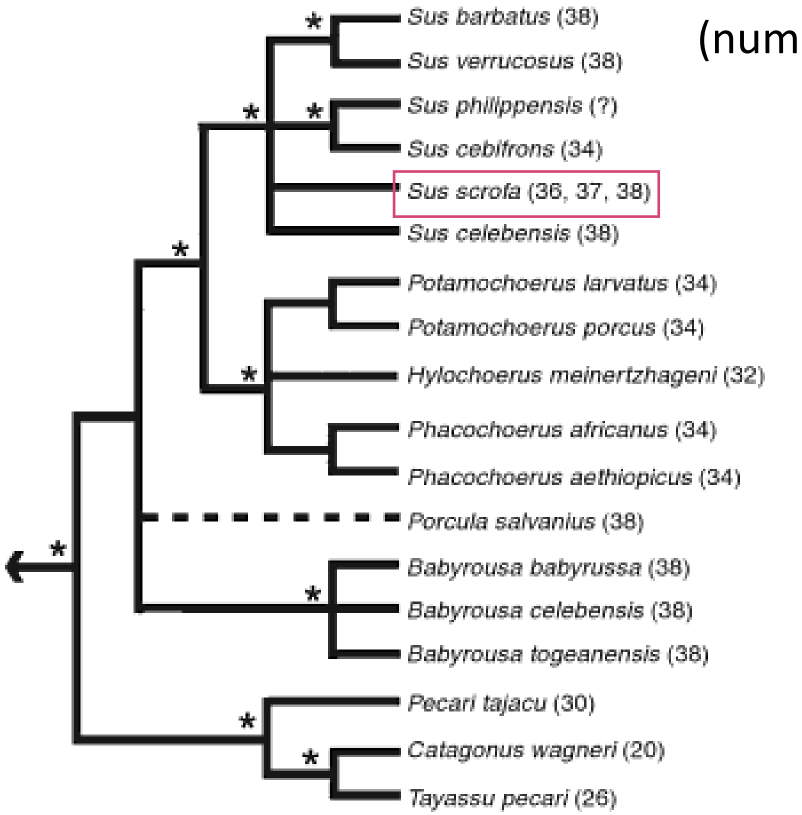
Cladogram by mtDNA and nuclear DNA sequences



(number of chromosomes)

Fig. 1.1. A cladogram depicting the relationships in the suborder Suiformes. This tree amalgamates information from several recent publications that have generated mitochondrial and nuclear DNA sequences. Polytomies indicate a lack of resolution with respect to branching order, and the dashed line leading to the pygmy hog represents the current uncertainty with regard to its position within the tree. Well-supported nodes are marked by asterisks, and diploid chromosome numbers are placed within parentheses following the species name. This tree will be revised as newly elevated species are included and new genetic and morphological data resolve the branching order.

The areas of these subspecies are close and the level of discriminating differences may be quite small, involving size, colour, proportions, skull characters and, in several cases, chromosome numbers. The variation in chromosome number is a result of two distinct Robertsonian translocations, which were found in the different geographical areas of the species (Tikhonov and Troshina, 1974; Bosma, 1976). The usual number of chromosomes in *S. scrofa* is 38 (Bosma *et al.*, 1995). However, translocation I involving chromosomes 16 and 17 and translocation II involving chromosomes 15 and 17 were found in Kyrgyzstani and European boars (Tikhonov and Troshina, 1978), and reduce the number of chromosomes to 37 in crosses (heterozygotes) and to 36 in homozygotes.

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Genus *Sus*

- Origin : islands of SE Asia -> SE Asia - - -> Middle East, North Africa, Europe
- 6-5.3 million years.
- According to morphological and molecular genetic data -> 3 evolutionary groups (differentiated during the Pliocene):
    - *S. cebifrons, S. celebensis,*
    - *S. barbatus*
    - *S. verrucosus, S. scrofa, S. ahoenobarbus*

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- *Sus scrofa* originated in SE Asia some 3-4 million years ago and spread to almost all of Eurasia within 1 million years.
- Wild boars were also found in the northern part of Sumatra, this population separated from the Eurasian pig about 1.5 - 2 million years ago.
- European and Asian wild boars diverged about 1 million years ago > very different low-frequency alleles at millions of loci in the genome and more than a million loci that are fixed for alternative alleles.

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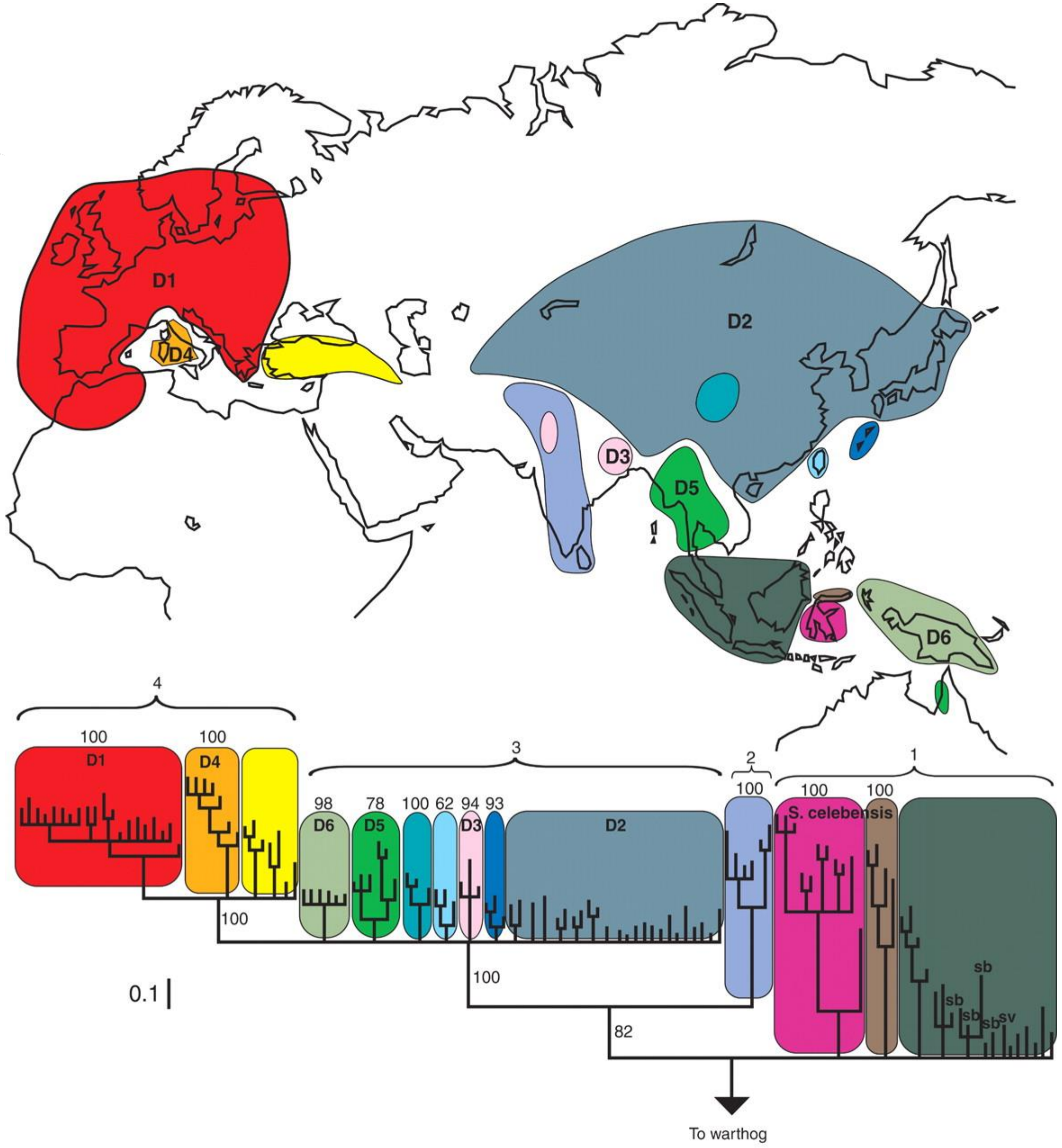
Independent pig domestication sites

Greger Larson, et al. 2005. Worldwide Phylogeography of Wild Boar Reveals Multiple Centers of Pig Domestication. Science 11 March 2005. Vol. 307. no. 5715, pp. 1618 - 1621. DOI: 10.1126/science.1106927.



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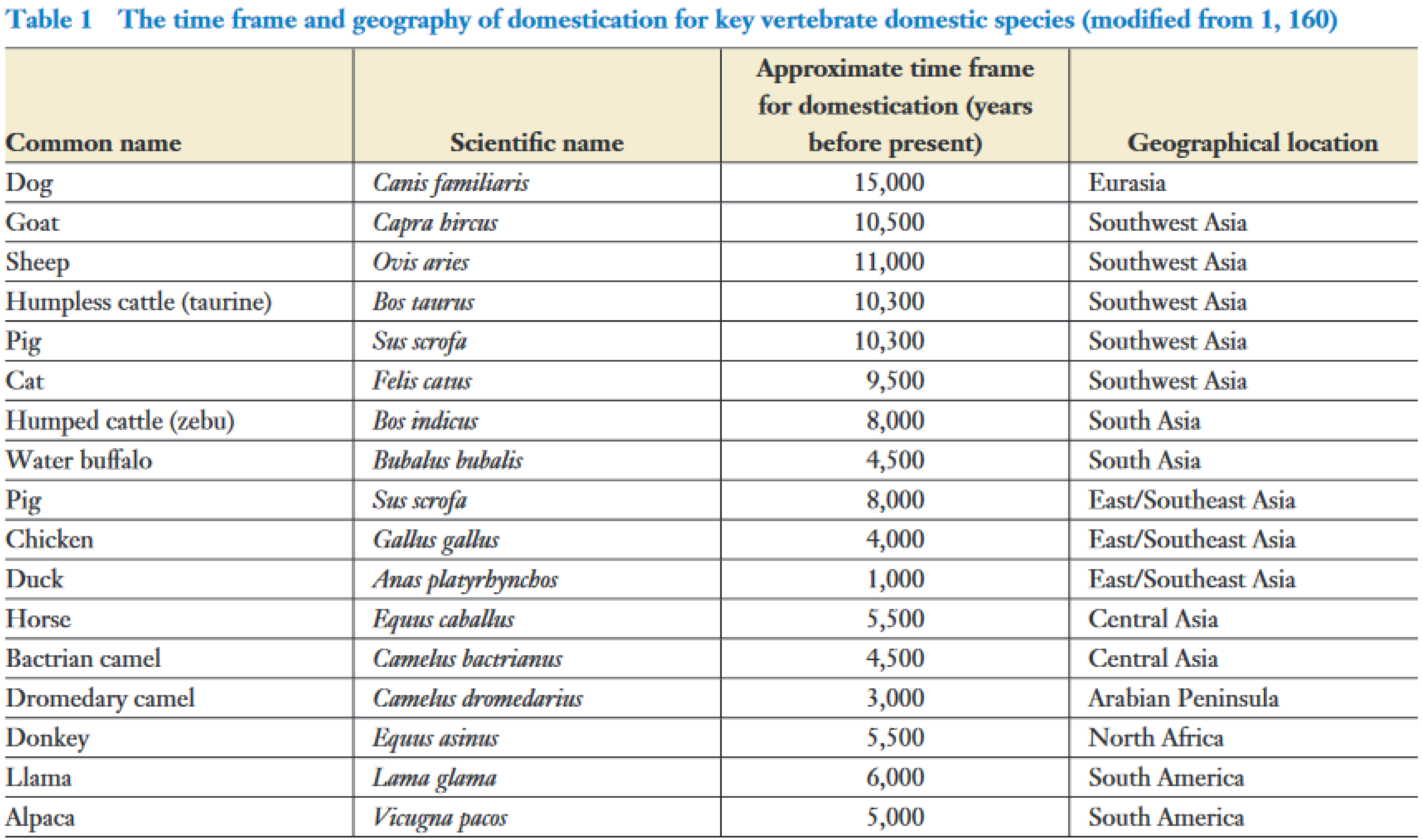

Table 1 The time frame and geography of domestication for key vertebrate domestic species (modified from 1, 160)

Common name	Scientific name	Approximate time frame for domestication (years before present)	Geographical location
Dog	*Canis familiaris*	15,000	Eurasia
Goat	*Capra hircus*	10,500	Southwest Asia
Sheep	*Ovis aries*	11,000	Southwest Asia
Humpless cattle (taurine)	*Bos taurus*	10,300	Southwest Asia
Pig	*Sus scrofa*	10,300	Southwest Asia
Cat	*Felis catus*	9,500	Southwest Asia
Humped cattle (zebu)	*Bos indicus*	8,000	South Asia
Water buffalo	*Bubalus bubalis*	4,500	South Asia
Pig	*Sus scrofa*	8,000	East/Southeast Asia
Chicken	*Gallus gallus*	4,000	East/Southeast Asia
Duck	*Anas platyrhynchos*	1,000	East/Southeast Asia
Horse	*Equus caballus*	5,500	Central Asia
Bactrian camel	*Camelus bactrianus*	4,500	Central Asia
Dromedary camel	*Camelus dromedarius*	3,000	Arabian Peninsula
Donkey	*Equus asinus*	5,500	North Africa
Llama	*Lama glama*	6,000	South America
Alpaca	*Vicugna pacos*	5,000	South America

DOI: 10.1146/annurev-animal-022516-022747

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