background sheet

Phylogenetics

Taxonomy: the classification of life

To make sense of biodiversity scientists have attempted to organise, or group, life forms. In the eighteenth century, Carl Linnaeus developed a system of classification that organised the living world into ranks, and introduced binomial nomenclature, or scientific names. Linnaean classification is hierarchical and groups organisms according to similarities and differences.

Traditional, or Linnaean taxonomy, transformed the way in which organisms were named, described and ranked. But these ideas were developed long before there was any scientific understanding of the evolution of life. In 1859, publication of Charles Darwin's work provided a new theoretical framework that saw a shift in focus of taxonomy.

The new taxonomy

As our understanding of relationships between organisms has changed, so has the focus of taxonomy. Modern taxonomy strives to reflect evolutionary history of organisms, by classifying them according to evolutionary relationships. This approach to taxonomy, known as phylogenetic systematics, uses a basic unit of classification called 'clade'.

Clade — a group consisting of an ancestral form and all living and extinct descendants of that ancestor. Members of a clade share a common ancestor to the exclusion of all other organisms.

The Linnaean classification system is still used in modern taxonomy, and in many instances phylogenetic analyses reflect Linnaean groupings. In some cases Linnaean groupings have been modified to reflect new understanding of evolutionary relationships by the addition of extra ranks, such as superorder.

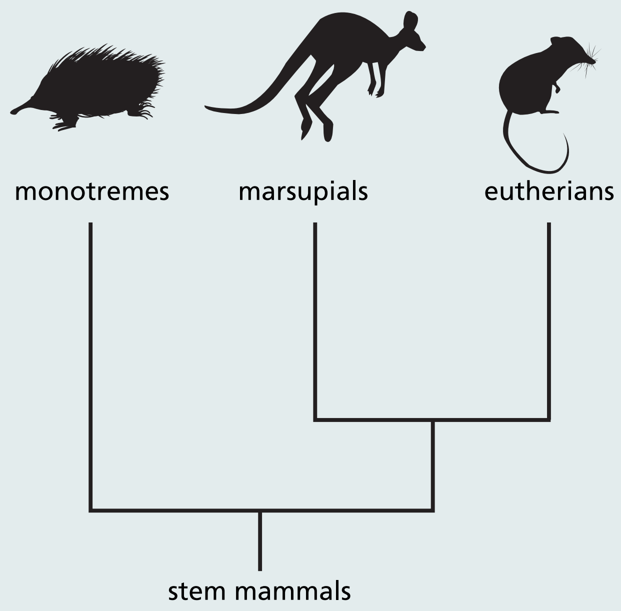

Figure 1: a cladogram

Evolutionary trees are used to represent evolutionary relationships (or common descent) amongst organisms. Each branch on a tree represents a clade. Clades can be nested within each other. This cladogram shows three clades (monotremes, marsupials and eutherians) nested within the mammal clade.

Molecular evidence for evolution

Prior to the 1970s, evidence for evolutionary relationships between organisms was based on similarities and differences of physical characteristics: fossil, anatomical and embryological features. Advances in DNA sequencing have enabled scientists to make use of large molecular datasets to establish evolutionary lineages of organisms. Similarities and differences in nucleotides of organisms provide strong evidence for shared common ancestry.

Revolutionising mammalian relationships

Modern molecular techniques have challenged many long-held beliefs about evolutionary relationships between organisms. The power of these techniques has resulted in new higher order groupings amongst eutherians (placental mammals) being proposed.

Investigations of proteins, individual genes and segments from multiple genes have resulted in the division of eutherians into four major clades: Afrotheria, Euarchontoglires, Laurasiatheria and Xenarthra.

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Evidence for four eutherian clades

These four eutherian clades weren't recognised before molecular evidence was available. However, based on morphological and fossil evidence, some groups within these clades had been established. These include: the evolutionary relationship between elephants, sea cows and hyraxes (order Paenungulata); relatedness of hares, rabbits and pikas (order Glires); and links between primates, tree shrews and colugos (order Euarchonta or Archonta). Clade Xenarthra has been recognised since 1975 on the basis of morphological evidence. Molecular data confirms this grouping.

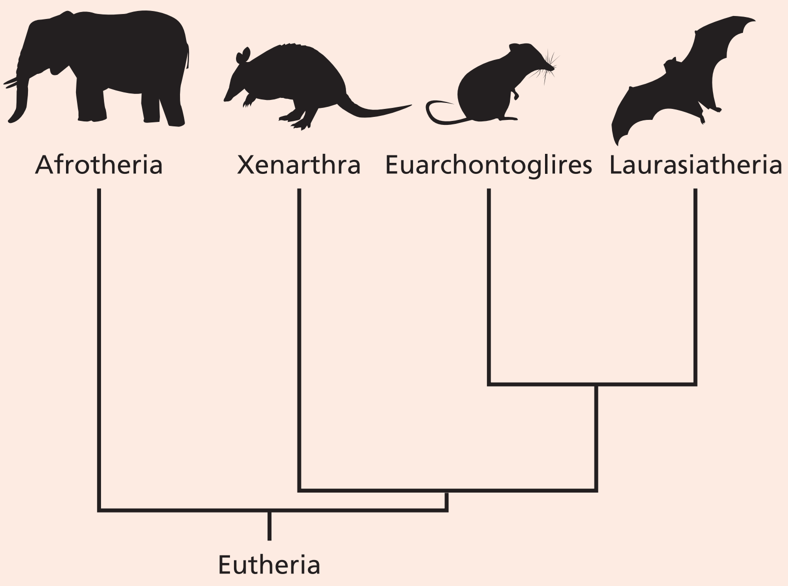

Figure 2: cladogram of the four eutherian clades

The major mammalian revisions

The most surprising revision of eutherian groupings is clade Afrotheria. This group of diverse mammals includes elephants, aardvarks and golden moles. Molecular evidence has also resulted in disbanding order Insectivora, once a vast group linking small, unspecialised, insectivorous mammals. Many mammals, once considered part of Insectivora, are now divided between the four major clades with similarities in form and function believed to be a result of convergent evolution. Another revision of eutherian organisation grouped cetaceans and even-toed ungulates to form the order Cetartiodactyla.

CLADE	MOLECULAR EVIDENCE
Afrotheria	• nine base pair deletion in BRCA1 • unique nuclear elements called AfroSINES • one 237-246 deletion in the apolipoprotein B alignment
Euarchontoglires	• eighteen amino acid deletion in exon 8 of the SCA1 gene • six base pair deletion in the PRNP gene
Laurasiatheria	• deletion in PLCB4 gene
Xenarthra	• three amino acid deletion in the eye lens protein aA crystalline

Figure 3: examples of molecular evidence supporting the four eutherian clades

Links with biogeography

Divergence of separate eutherian clades closely matches what is known about movement of continental landmasses. At the base of the eutherian tree there's a distinct division reflecting origin of one group of mammals in the northern hemisphere (Laurasiatheria and Euarchontoglires); and another in the southern hemisphere (Xenarthra and Afrotheria). The split of supercontinent Pangaea, into northern and southern landmasses, supports this evolutionary history. Further splits of the southern supercontinent, Gondwana, support the diversification of animals in clades Afrotheria and Xenarthra.

Conclusion

Within the field of evolutionary biology there is increasing integration of molecular, fossil and morphological evidence. In future, as more data from all sources become available, relationships within the eutherian orders are likely to be refined.