Insect Friends and Relations

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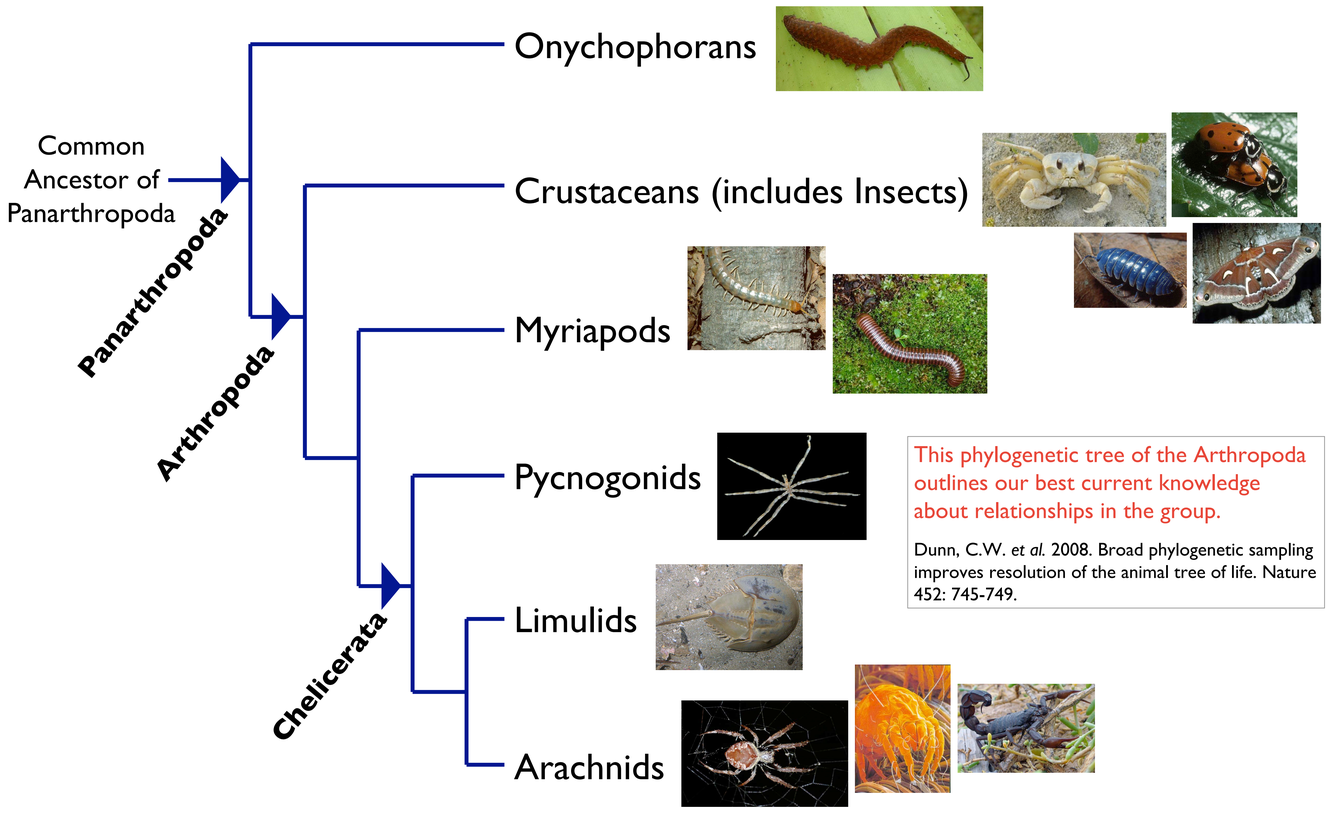
What do we know about arthropod relationships?



This phylogenetic tree of the Arthropoda outlines our best current knowledge about relationships in the group.

Dunn, C.W. *et al.* 2008. Broad phylogenetic sampling improves resolution of the animal tree of life. Nature 452: 745-749.

Unraveling arthropod phylogeny

There are about 1,100,000 described arthropods – 85% of multicellular animals! Segmentation, jointed appendages, and the development of pattern-forming genes profoundly affected arthropod evolution and created the most morphologically diverse taxon on Earth. With our ability to sequence DNA, describe whole genomes, compare gene rearrangements, and study protein structure and function, our ability to unravel their relationships is improving.

Five groups of arthropods are commonly recognized:

- **trilobites** (all extinct; ~4,000 species);
- **crustaceans** (crabs, shrimp, isopods, and their kin; ~67,000 species);
- **hexapods** (insects and their kin; ~1,000,000 species);
- **myriapods** (centipedes, millipedes, and their kin; ~13,000 species); and
- **chelicerates** (horseshoe crabs, spiders, mites, ticks, sea spiders, and the extinct eurypterids; ~70,000 species).

Most scientists currently agree that:

1. Insects are crustaceans: Hexapoda had an ancestor within the Crustacea.
2. Centipedes, millipedes, and the lesser-known symphylans and pauropodans had a common ancestor: Myriapoda are monophyletic.
3. Land spiders, mites, ticks, and scorpions (arachnids) are the sister taxon of horseshoe crabs (limulids), and sea spiders (pycnogonids) are the sister taxon to all of those.
4. Velvet worms (onychophorans) are ancestral to the phylum Arthropoda.

What is less clear, and under intense current study, is whether: (1) crustaceans or chelicerates are the basal arthropod lineage, and (2) where trilobites appear in the arthropod phylogenetic tree.

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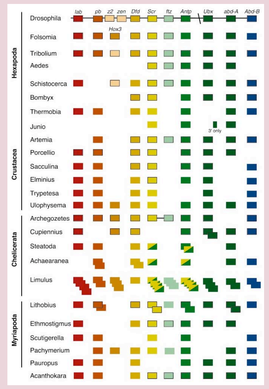
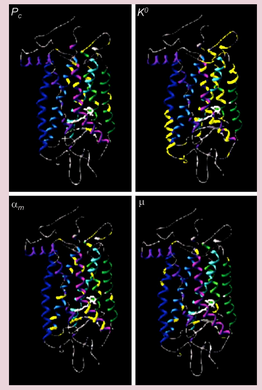
How do we know that? Examples of lines of evidence:

Genetics and Genomics



Genomic approaches can look at patterns of occurrence of whole genes across taxa to identify patterns of common ancestry.

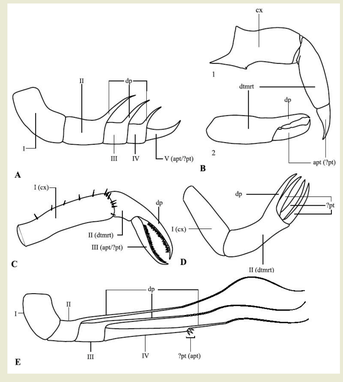
Cook, C. E., Smith, M. L., Telford, M. J., Bastianello, A., Akam, M. 2001. *Hox* genes and the phylogeny of the arthropods. Current Biology 11: 759-763.



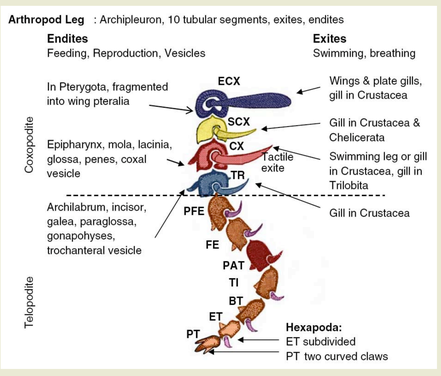
The figures at left show the protein structure of opsins (visual pigments). Yellow identifies areas of the protein that have important evolutionary and functional differences. This provides information about how the opsin gene family has evolved across different taxa.

Porter, M. L., Cronin, T. W., McClellan, D. A., Crandall, K. A. 2007. Molecular characterization of crustacean visual pigments and the evolution of pancrustacean opsins. Molecular Biology and Evolution 24(1): 253-268.

Morphology

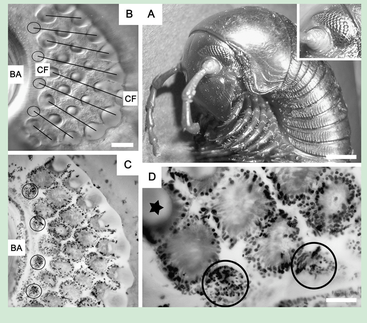


Comparing similarities and differences among arthropod appendages is a fertile source of information about patterns of ancestry. Morphological evidence can be especially valuable because it is available for both living and fossil taxa.



[Left:] Cotton, T. J., Braddy, S. J. 2004. The phylogeny of arachnomorph arthropods and the origin of the Chelicerata. Transactions of the Royal Society of Edinburgh: Earth Sciences 94: 169-193.
[Right:] Kukalová-Peck, J. 2008. Phylogeny of higher taxa in Insecta: finding synapomorphies in the extant fauna and separating them from homoplasies. Evolutionary Biology 35: 4-51.

Development



Eye structure in growing Diplopoda (left) and Crustacea (right) can be used to compare cell-by-cell development through time. That tells us about common evolutionary history.

Harzsch, S., Hafner, G. 2006. Evolution of eye development in arthropods: phylogenetic aspects. Arthropod Structure and Development 35: 319-340.