

Untangling the molecular phylogeny of tapeworms.

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The diversity of tapeworms reaches far beyond of what is typically known about this group from the few representatives of biomedical and veterinary importance (e.g. *Taenia* spp., *Diphyllobothrium* spp.). The large diversity of life cycles (typically involving crustacean intermediate hosts and vertebrate definitive hosts) means they have successfully established themselves throughout aquatic (both marine and freshwater) and terrestrial habitats, where the majority of the ~6000 known species are found parasitizing elasmobranch and tetrapod hosts.

Over the past two decades, molecular data have produced an ever more stable and well-resolved backbone phylogeny, whilst increasing the number of orders from 12 to 19. In this talk, the recent contributions to the construction of the tapeworm backbone phylogeny will be recapped. Additionally, new molecular phylogenetic results will be presented that have been accumulated over the last 5 years from the NSF-funded Planetary Biodiversity Inventory project 'A survey of the tapeworms from vertebrate bowels of the earth'. This international collaborative project targeted previously unexplored hosts and/or geographic regions to increase the sampled diversity of tapeworms. The resultant phylogeny, based on two nuclear (18S and 28S rDNA) and two mitochondrial genes (16S rDNA and *cox1*), is composed of ~850 taxa, which represents the most significant contribution to tapeworm phylogeny, to date, allowing us to investigate the effects of host-use and phylogeography on the diversification patterns in this group.