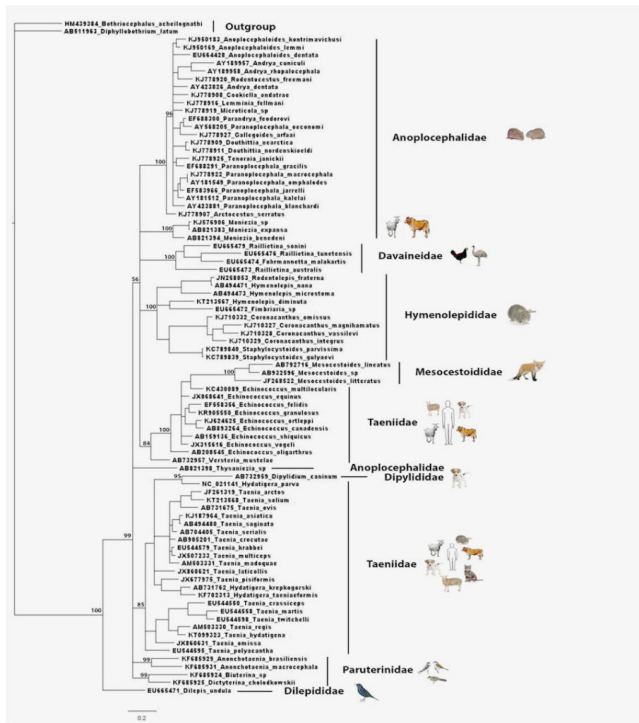


Cyclophyllidean tapeworms: phylogeny reconstructed

'Parasite' is a term used collectively to describe organisms that have the ability to survive at the expense of another organism (the host). They are notorious in being capable of parasitizing a vast range of organisms (insects, crabs, snails, fishes, amphibians, reptiles, birds, mammals including humans etc.) as their intermediate and/or final host. The host provides basic necessities for their survival, perpetuation and in addition, bears the cost of this association with its health. Many a times the body of the host gets severely damaged leading to its death. Many organisms of the worm group [that includes flatworms (Trematoda), tapeworms (Cestoda) and roundworms (Nematoda)] are obligate parasites and cause infections and inflict injury to their animal hosts. Within Cestoda one such parasitic group called 'Cyclophyllidea' comprises the tapeworms inhabiting the intestine of their (avian or mammalian) host. Some of the species included in this group of tapeworms are well known causative agents of serious medical conditions in humans as well as domestic and wild animals. The diseases caused by tapeworms, despite of having global occurrence and being more common in Asia, are yet classified as 'Neglected Tropical Diseases' by World Health Organization.



adult worms as well as their larval stages also adds to the complicatedness, and thus, attaining taxonomic stability in such groups becomes challenging. Today, with the advancement in the field of molecular biology we can make use of DNA of an organism to address a number of problems. DNA of an organism, which offers valuable information, can be used to study different aspects of its biology.

By comparing a small region of the genome of 83 tapeworms and depicting the results in the form of a phylogenetic tree (which is used to show evolutionary relationships among organisms), we tried to deduce the phylogenetic relationships among the different tapeworm families within the Cyclophyllidea group and look for possible loop holes in the current taxonomy of the group.

We found that the tapeworms of the family Dilepididae (that make use of fish-eating birds as their definitive host) showed early divergence from the ancestral lineage, indicating that these parasites represented the primitive forms in this group. Further, in the course of diversification, the parasites evolved to infect terrestrial animals starting from the avian all the way to the mammalian host. The human tapeworms, *Taenia* and *Echinococcus*, are currently placed under the same family, i.e., Taenidae; however, considering their position in the phylogenetic (evolutionary) tree, there is a need to revise the taxonomic status of these tapeworms. Infact, our analysis showed that *Taenia* tapeworms are quite primitive, whereas *Echinococcus* represents a much advanced group. Another family of tapeworms, Anoplocephalidae (known to parasitize both small rodents and higher mammals), showed a beautiful clustering pattern with parasites of rodents clubbed in a single clade, whereas those occurring in higher mammals erected separately. Such clustering pattern indicates that diversification in this family of tapeworm parasites is a result of selection of novel host lineages.

In addition, the families Anoplocephalidae, Davaineidae, Hymenolepididae and Mesocestoididae and the genera *Echinococcus* and *Versteria* (both members of Family Taeniidae) were included in the crown clade, suggesting that these tapeworms represent the most derived forms in Cyclophyllidea.

In conclusion, studying phylogeny using molecular data gives significant insights into evolutionary relationships that exist among various groups, which inturn helps in resolving taxonomic issues.

Sunil Sharma¹, Damanbha Lyngdoh¹, Bishnupada Roy¹, Veena Tandon^{1,2}

¹Department of Zoology, North-Eastern Hill University, Shillong 793022, Meghalaya, India

²Biotech Park, Lucknow 226021, Uttar Pradesh, India

Publication

[Molecular phylogeny of Cyclophyllidea \(Cestoda: Eucestoda\): an in-silico analysis based on mtCOI](#)

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