

Biodiversity of Cyclophyllidea species in rodents of western China and the “out of the Qinghai-Tibet Plateau, QTP” hypothesis of this order based on its differentiation and biogeography

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Abstract

The Cyclophyllidea comprise the most species-rich order of tapeworms (Platyhelminthes, Cestoda) with, for helminths, perhaps the most severe health impact on wildlife, livestock, and humans. Rodent biodiversity of the Qinghai-Tibet Plateau (QTP) and its surrounding ranges provide a significant reservoir for numerous species of Cyclophyllidea. We collected cyclophyllidean species from QTP and Xinjiang province in China, resolving four unsequenced and likely new species. Phylogenetic construction of partial 18S rDNA, 28S rDNA and mitochondrial (*mt*) genes provided high nodal support for the categorisation of the three of the putative new species, assigning each respectively to the genera *Hydatigera* (ex *Eospalax fontainieri*), *Mesocestoides* (ex *Neodon irene*) and *Paranoplocephala* (ex *Neodon irene*). Poor nodal support for the unidentified (‘new’) species collected from pika (*Ochotona curzoniae*) in Yushu county, Qinghai province. Combined with the current investigation, the other three cyclophyllidean species found in this study (*Taenia caixuepengi*, *Taenia crassiceps* and *Versteria mustelae*) may be widely distributed in western China. The phylogenetic reconstructions based on 28S rDNA and *cox1-nad1* indicate that some families and genera may require taxonomic revision. Estimates of divergence time based on *mt* genes showed that the differentiation rate of tapeworms was strongly associated with the rate of change in the biogeographic scenarios caused by the uplift of the QTP, i.e. species differentiation of Cyclophyllidea was driven by host-parasite co-evolution caused by the uplift of QTP. We propose an “out of QTP” hypothesis for the radiation of cyclophyllideans.

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