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Building a basis for the molecular phylogeny of the order Gyrocotylidea

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The order Gyrocotylidea Poche, 1926 represents the most basal extant group of tapeworms that are specific parasites of cartilaginous fishes (Holocephali, Chimaeriformes). The systematics of the group was mainly revised in 80s, when the validity of many species specific morphological traits was questioned. After PBI project, the order harbors 10 valid species of single the genus *Gyrocotyle*. In 2020, Bray *et al*. described two new species from the North Atlantic, *G. haffi* and *G. discoveryi*, based on molecular data and generated sequences for other species. In our work, we collected alive gyrocotylideans from two fish hosts from the East China Sea off Taiwan, and type species *G. rugosa* Diesing, 1850 from Atlantic coast off Argentina. The tapeworms were examined as hologenophores to find morphological features, which correspond with different genotypes. Our genetic analyses were inferred from three genes (COI, 28S rRNA, 18S rRNA), and revealed unexpected interrelationships among isolates of the genus *Gyrocotyle*, as each of the four genotypes from Taiwan clustered with isolates of distinct gyrocotylideans from the North Atlantic. Three genotypes of *Gyrocotyle* from Taiwan were morphologically almost indistinguishable from each other but represented distinct genetic lineages; *Gyrocotyle* sp. genotype 4 exhibited a clear genetic and morphological distinctness, though its formal description as a new species would be premature, as only one specimen was found. Additionally, specimens of *G. rugosa* provided the first genetic data on the type species of the genus. The finding of some specimens of *Gyrocotyle* sp. genotype 3 in *Chimaera phantasma*, and another one in *C.* cf. *argiloba*, together with the putative conspecificity of an unidentified gyrocotylidean from *Callorhinchus milii* off Australia and *G. rugosa* from *C. callorynchus* off Argentina, are evidence that one gyrocotylidean species may parasitize several holocephalan species. We believe, that the taxonomic problems and conflicts between morphological and molecular data within this group can only be resolved if hologenophores from type hosts and localities of nominal taxa are properly characterized genetically and morphologically.