

# Taxonomy, Biodiversity, and Ecology of Parasites of Aquatic Organisms: A Special Issue

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Parasitism is ubiquitous and one of the most successful lifestyles on Earth, with more than 200 independent transitions from non-parasitic ancestors considered only in the kingdom Animalia [1]. Besides representing a large portion of global biodiversity, parasites are also broadly known for their crucial role in ecosystems, influencing host population dynamics and structuring food webs, among other key biological services [2].

One of the primary challenges which parasitologists face is in confidently assessing the biodiversity of parasite species, understanding their distribution, identifying the factors that drive this biodiversity, and discerning the reciprocal selection pressures involved in the intricate host–parasite relationship. A key milestone in addressing this challenge is represented by the seminal contribution of Poulin and Morand [3], which offers a comprehensive overview of existing studies and perspectives, laying the groundwork for future research endeavors on this field.

The accurate estimation of parasite diversity is compromised by multiple issues, encompassing logistical constraints, permissions required for sampling a diverse range of hosts, the so-called taxonomic impediment (see Brooks and Hoberg [4]), contentious taxonomy pertaining to both parasites and hosts, the existence of cryptic species, etc. Furthermore, the lack of suitable methods for obtaining such estimates includes an additional layer of complexity to this problem [5]. The correct circumscription of species boundaries and hence, the diversity of a particular group of parasitic organisms, also affects the explanatory power of ecological studies. Obtaining a high taxonomic resolution is considered one of the best practices in studies of parasite community ecology [6].

In this way, integrative taxonomy, i.e., the combination of multiple pieces of evidence to strengthen taxonomic hypotheses, has proven to be a highly valuable approach for enhancing our understanding of parasitic groups. It contributes significantly to elucidating taxonomic problems, ensuring consistency and greater stability in taxon identification. This, in turn, facilitates an improved integration of ecological and historical (or phylogenetic) approaches in the study of parasite diversity, as recommended by Poulin and Morand [7].

Parasite species associated with hosts from various aquatic environments serve as excellent models for in-depth studies using integrated approaches. Regions like South America, characterized by a variety of ecosystems and a diverse range of hosts, have been shown to harbor a significant portion of global parasite diversity, yet still remains underexplored [8].

Given the high biodiversity of hosts and parasites in aquatic environments, along with the pressing need for robust taxonomic studies that accurately unveil the diversity of parasites worldwide, the proposal for this Special Issue (SI) on “Taxonomy, Biodiversity, and Ecology of Parasites of Aquatic Organisms” emerged. This SI comprises seven research articles that employ integrative approaches, primarily combining morphological, ecological, and molecular evidence, to address taxonomic and evolutionary questions related to a broad spectrum of parasitic organisms from different geographical regions (Figure 1).



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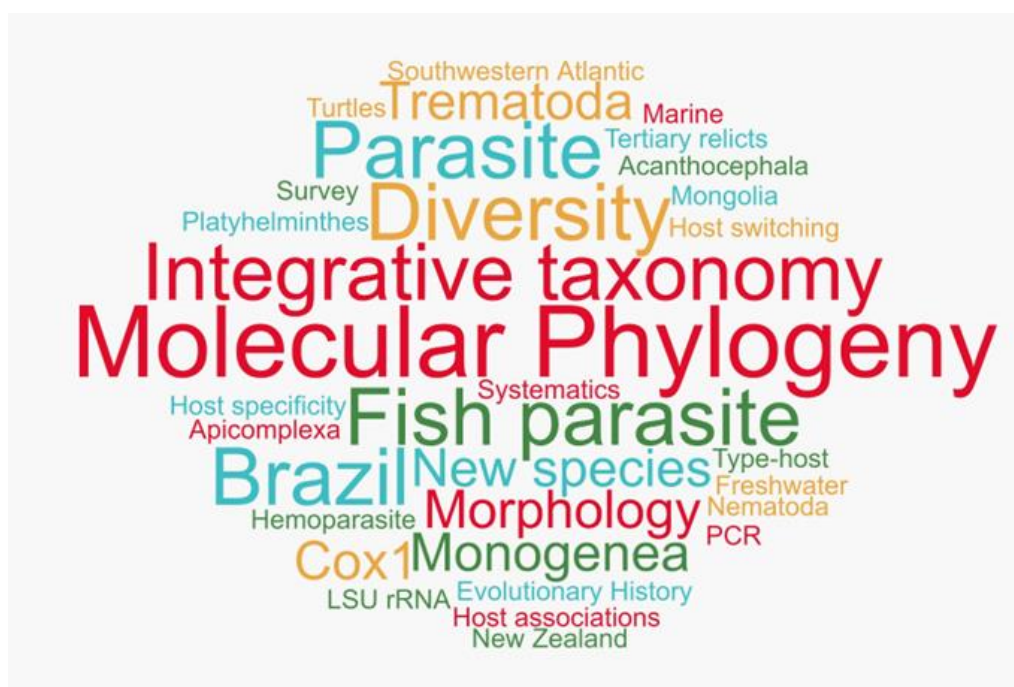
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**Figure 1.** Word cloud showcasing the most frequent words extracted from the Abstract and Keywords sections of the Special Issue manuscripts. Generated with <https://www.wordclouds.com> (accessed on 8 November 2023).

The first paper published in this SI, and the only one focused on unicellular eukaryotes, i.e., apicomplexan parasites (Apicomplexa), sheds light on the diversity of hemogregarines parasitizing freshwater turtles from Brazil. Úngari et al. [9] described as many as six new species of *Haemogregarina* based on morphological, histopathological, and molecular data. The authors have also highlighted that there are likely many other hemogregarines to be discovered in Brazilian chelonids, as only a small portion of the potential hosts has been scrutinized for hemoparasites.

Bennett et al. [10] conducted extensive morphological and molecular prospecting of acanthocephalans (Acanthocephala) in New Zealand waters. A wide range of coastal animals (32 out of 168 species investigated), representing intermediate, definitive, or accidental hosts, were reported harboring 13 acanthocephalan species. Among these host–parasite associations, one geographical and nine host records were new to science. Additionally, the authors found at least two species hitherto undescribed. This large-scale survey of acanthocephalans from aquatic organisms in New Zealand has paved the way for further biodiversity-monitoring endeavors that clearly should not ignore parasites, as claimed by the authors.

Monogenea is a group of parasitic flatworms (Platyhelminthes) typically known for its strict host specificity; however, certain species are reported to infest multiple unrelated hosts. Tabor da et al. [11] addressed this issue by subjecting alleged representatives of *Encotylabe spari* from marine fish off Brazil to morphological, morphometric, and molecular analyses. As a result, they described two new species of *Encotylabe* and called for a critical re-evaluation of specimens previously assigned to *E. spari*.

Ailán-Choke et al. [12] provided phylogenetic reconstructions for the Philometridae, a highly diverse group of dracunculoids (Nematoda) parasites of fish worldwide. They further mapped morphological and life history traits onto the phylogenies to assess the systematic value of these characteristics. Additionally, the authors investigated host–parasite cophylogenetic patterns. As a result, they listed several attributes that were found to be phylogenetically informative, e.g., the morphology of the male tail, habitat, and

geographical origin. They also demonstrated that host switching, host–parasite coevolution, and allopatry have played roles in the evolutionary history of the group.

Sokolov et al. [13] resolved a long-standing question regarding the taxonomy of *Diplostomum numericum* (Platyhelminthes, Trematoda). Based on morphological, molecular, and ecological data gathered from newly collected metacercariae from cyprinid fish in Russia, including the host type, they confirmed the validity of this species (now resurrected). Moreover, they demonstrated the conspecificity of *Diplostomum* sp. lineage 3 of Blasco-Costa et al. [14], and suggested that *D. numericum* may also be conspecific with *D. colymbi*.

The convoluted and contentious taxonomy of the species-rich *Gyrodactylus* (Platyhelminthes, Monogenea) was the focus of Lebedeva et al.'s [15] paper. They subjected *Gyrodactylus* specimens from Mongolian “relict” fishes to morphological and molecular analyses. Besides reporting 12 species of *Gyrodactylus*, including three previously undescribed, the authors discussed the processes underlying the successful radiation of this monogenean group in Central Asia.

Last but not least, Pinto et al. [16] redescribed a poorly known paramphistomoid trematode (Platyhelminthes, Trematoda), *Kalitrema kalitrema*, from loricariid catfishes *Hypostomus* spp. in Brazil, and assessed the phylogenetic interrelationships of this species. Furthermore, they reinforced that a new subfamilial classification scheme for Cladorchiidae is needed to reflect the evolutionary history of the group.

The research featured in this SI underpins that, beyond its fundamental role in describing and naming biological entities, integrative taxonomy also proves to be instrumental in acquiring meaningful insights into intermingled fields such as biogeography, evolution, and ecology. We hope this SI will be a valuable resource for readers, aiding them in advancing their own research.

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