

Chapter 17

Perspectives: An Integrated Approach on Future Studies of the Lymnaeidae



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Abstract In this last chapter, we have briefly summarized several topics treated within the main chapters of this book on the Lymnaeidae. A call of attention is placed upon the integrativeness of research towards this group of snails, from classical to the state-of-the-art approaches. While certain areas of the Lymnaeidae study have been thoroughly covered, some have only been moderately or slightly explored and would need comprehensive research. Hence, we expose some challenges lying ahead for scientists and students that may find themselves passionate with the study of such an interesting family of freshwater snails.

17.1 On the Acknowledgment of Lymnaeid Species: From Identification to Phylogeny

“Integrativeness” is a keyword of current research in many fields of life sciences, from taxonomy to ecology and genetics. Sometimes, it is referred to as the “Age of Integration”, when the multidisciplinary and multi-faceted approaches to research are most welcome (Clamp and Lynn 2017). For research, to be “integrative” means to use data of various origins, taken from different sources and obtained following various methods and techniques. The trend towards integrativeness is markedly expressed in biological systematics, which is thought to rescue this discipline from long-lasting disregard and neglect as well as to overcome the so-called taxonomic impediment (Gomes et al. 2015; Cao et al. 2016; Vinarski 2020).

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This concluding chapter aims to review the existing challenges in the lymnaeid research and outline the benefits that different aspects of research can gain from the integrative approach.

The explicit application of the integrative taxonomic approach for classification of the pond snails has started relatively recently (Vinarski et al. 2016; Aksenova et al. 2018), however, the most prominent workers in the field always tried to utilize as many independent sources of data as possible, not using, of course, the very term “integrative taxonomy” (Hubendick 1951; Kruglov 2005). In other words, “taxonomy has been integrative for most of its history” (Valdecasas et al. 2008, p. 211).

Until now, only a very limited number of lymnaeid genera and species complexes has been studied on the “integrative” basis. We still lack molecular information on some small genera of the Lymnaeidae, whereas the phylogenetic relationships and taxonomic position of some other genera cannot be satisfactorily resolved because the available information is too scarce. The new classification scheme for the living Lymnaeidae published in this book (Aksenova et al. 2023, this volume) remains not finalized as the position of some taxa is not clear, and a large deal of further work is required to fulfil the task of classification.

Another challenge for the current lymnaeid systematics is the overload of synonyms and nominal species names in this family, which is among the highest among freshwater Mollusca (Lopes-Lima et al. 2021). Hubendick (1951) compiled a list of about 1150 nominal taxa (including *nomina nuda*) of the species and below-species rank which were established in this family between 1758 and 1950. Today, such a list is remarkably lengthier and approaches 1500 items (Vinarski, unpublished data). Apparently, only a minority of these names correspond to valid species, however, most of the nomenclaturally available names have not been reassessed since their description, and at least part of these can be suitable for the naming of cryptic species and other entities, which molecular taxonomy can reveal. One of the most urgent tasks of the integrative lymnaeid taxonomy is to link the genetically defined clades of the species rank to already existing species names. The use of old available names is much more preferable than introducing new ones, but such an approach requires a qualification of a “classical” taxonomist, who can work with museum collections and has experience with resolving issues related to zoological nomenclature. Unfortunately, it is not an uncommon situation today, when a team of “integrative” researchers does not include a professional taxonomist, which results in the inability to determine the proper taxonomic position of the revealed species-level clades or describe new species when it is needed. Hence, many current studies (not only in the taxonomy of freshwater Mollusca) suffer from evident incompleteness: their authors are unable to place their findings in a proper taxonomic context, i.e. name and describe biological species revealed by sophisticated analysis. The opposite examples are, of course, available (Aksenova et al. 2018; Mahulu et al. 2019; Vinarski et al. 2020, 2022).

The authors of such publications prefer to deal with “putative” species or “candidate species” rather than to undertake their formal description in accordance with the rules of zoological nomenclature (to give them binomial Latin names). Sometimes it is due to lack of information needed for the proper description, but not

rarely does it indicate the absence of an experienced taxonomist in the authors' team. This practice, however, should not be welcomed because the absence of taxonomic formalization of species hampers future progress in both the studies of biological diversity and conservation efforts (Pante et al. 2015; Vinarski 2020).

Thus, the most desirable kind of taxonomic work with lymnaeids is what combines molecular and morphological study with a thorough exploration of existing literature and available museum collections. Needless to say the truly integrative system of the family Lymnaeidae, both at the genus and below-genus levels, when it is reached will constitute a firm basis for biogeographic and ecological studies of the pond snails as well as for conservation purposes. The use of fossil-calibrated molecular trees with estimates of the absolute ages of certain evolutionary events will allow researchers to put the evolution of the family in a broad paleogeographic context (see, for example, Aksenova et al. 2018). The integrative approach is crucial for the studies of host–parasite systems which are formed by the pond snails and various trematode taxa, for example, for a deepened understanding of coevolution of these groups and the patterns of host specificity of helminths parasitizing the Lymnaeidae (Vázquez et al. 2022).

Up to now, virtually all integrative and molecular research on the pond snail systematics was based on either single-gene (like DNA barcoding) or multi-locus approaches, which has some apparent limitations. The mighty possibilities of the use of complete genomes for phylogeny and taxonomy of the family are still weakly used, and the complete mitochondrial genomes are available for only a few pond snail species (Feldmeyer et al. 2010, 2015; Liu et al. 2012; Qin et al. 2019). The time is ripe for extensive usage of the “omics-approach” for the purpose of lymnaeid classification.

The future of the Lymnaeidae taxonomy will probably benefit from the further advancements of the most innovative approaches, such as the use of machine learning and artificial intelligence (see Quenu et al. 2020; Klinkenbuß et al. 2020 for examples of the application of these techniques to systematic malacology). Today, such traditional tasks of classification as species delimitation are increasingly relegated to computers, which even creates a perspective of the predictable “dehumanization” of biological systematics, the extinction of the scientific community of taxonomists (Vinarski 2022). Are they doomed to repeat the fate of mammoths and the recent victims of the Sixth Extinction? Perhaps, the solution is that, after its “integrative” renewal, systematics will become a constituent part of a synthetic science of biodiversity (or *metataxonomy*), where taxonomic revisions and descriptions of new taxa, based on an integrated approach, are inseparable from reconstructions of phylogenies, historical biogeographical models, and other products of “non-descriptive” science (Vinarski 2020, 2022).

17.2 Lymnaeid Snails in Applied Medical Malacology

From an applied perspective, in this book we have reviewed several aspects of the lymnaeid studies including experimental models, biological invasions, or disease transmission by the lymnaeid snails. The processes leading to the introduction of lymnaeid snails, whether of natural or anthropic nature, are of particular importance and need further research (Lounnas et al. 2017; Schniebs et al. 2017). However, introduction not necessarily means invasion, and some alien lymnaeid species are unable to expand in the new site (López-Soriano and Quiñonero-Salgado 2020). Invasions are critical events bringing perils to local ecosystem health, threatening not only biodiversity but public health as well when the species is of medical importance. Examples exist within the Lymnaeidae in which introduced species end by resulting in main or relevant hosts of several parasites by either boosting an ongoing transmission (parasite spill-back) (Molloy and Anderson 2006; Carolus et al. 2019) or by bringing new pathogens into the introduction site (parasite spill-over) (Schols et al. 2021).

It is a fact that several lymnaeid species are important hosts of relevant parasites of wildlife, some of great zoonotic relevance (see Hurtrez-Boussès et al. 2023; Vázquez et al. 2023). However, we are still far from the complete understanding of the plethora of species interacting with lymnaeids, particularly in the microbial world (e.g. bacteria and protozoa). We have, to some extent, advanced in elucidating several host–parasite interactions of medical and/or veterinary interest, but mainly in helminth parasites. Within the latter, in the case of lymnaeid snails, the liver flukes (*Fasciola* spp.) have been thoroughly studied because of their relevance to both medical/veterinary health and meat/milk production (Dreyfuss et al. 2006; Rondelaud et al. 2014; Vázquez et al. 2018). However, we still lack several details on transmission dynamics (mainly related to environmental/climatic interaction), species–species (and genotypic–genotypic) compatibility, ecological risks, etc., that would ultimately determine the presence, susceptibility, and transmissibility by a given lymnaeid population. Following this line, if we dig deeper into the biology of lymnaeid–parasite interactions, research should be aimed at disentangling the effects of the environmental gradients over the population and transmission dynamics. How do differential levels of pollution (chemical, organic, etc.), human perturbations of heterogeneous sorts (habitat transformation, water diversion, etc.), climatic settings (tropical, temperate, alpine, etc.) affect lymnaeids? At the individual level, attention should be steered to the host’s microbiota interactions with pathogens, as we know it might play a major role in driving host–parasite interactions (Le Clec’h et al. 2022). Funding is, however, a big issue for this kind of investigation, but by succeeding in this, we will not only add to the general knowledge on lymnaeid biology, but also better tackle disease transmission.

In an attempt to support such research activities in the laboratory, we have devoted two chapters to explicitly applied works related to lymnaeid snails. Laboratory culture of snails is a fundamental activity to undertake much of the research we have discussed in several chapters. However, such a task has proved to be

challenging to researchers around the globe. Conditions needed to rear lymnaeids in the laboratory are quite heterogeneous, as we understand that across the phylogeny of Lymnaeidae we stumble upon species with contrasted patterns of ecological requirements. Thus, the study of lymnaeid ecology is fundamental and more studies should be heading this way. We can share some experiences in some model species (e.g. *Galba truncatula*, *Lymnaea stagnalis*, *Pseudosuccinea columella*, etc.) that range from aquatic to amphibious behaviour, but only solid ecological knowledge would enhance our understanding of more precise conditions that would ultimately translate in better results of our experiments. In this sense, performing experimental infections are critical steps for the general understanding of lymnaeid–parasite interactions, and many studies are routinely carried out in this regard (see Dreyfuss et al. 2023). Detailed conditions for lymnaeid infection, particularly with *F. hepatica*, in order to measure several parasitological variables are presented in this work.

All in all, we are confident this book will serve as a reference for scientists and students related to the study of the Lymnaeidae, but a broader range of readers such as teachers, parasitologists, malacologists, epidemiologists, paleobiologists, and surveillance and vector control authorities would benefit from the works detailed in their chapters.

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