

# Preface

Cladocera and Copepoda are the major groups of freshwater zooplankton. Among them are species with planktonic, benthic or epiphytic style of life. The latter two may have a short moment in their life when they can be seen among the euplanktonic species as meroplankton, and therefore we may simplify things by referring to almost all of them as zooplankton Wetzel (2001).

Progress on research in community and ecosystem ecology, as well as simple environmental monitoring or biodiversity assessment relies on an accurate enumeration of coexisting species, and this in turn requires that the specimens collected in the field must be properly identified to the species level (Gotelli 2004; Farnsworth et al. 2013). It has been recommended that the finest taxonomic level (species) should be used in water quality assessments (Feio et al. 2006). Therefore, progress on frontier research and applied environmental protection heavily depends on correct species identification. An unclear taxonomic status of many Cladocera and Copepoda species, the absence of reliable characters to discriminate specimens of the similar taxa, the lack of inclusion of many newest and valid species in the published and commonly available identification keys, as well as the use of very old keys listing species that are no longer valid result in biased data interpretation in ecological publications. One of the most recent Copepoda examples of wrong identification based on the old key is the new species description provided by Robertson (2014). Among the Cladocera, the species identification confusion exists because of poor original description (only 45–50% of cladoceran species are well described (Hamrova et al. 2012), subtle differences in the morphology of many similar species (Van Damme et al. 2011), unknown extent of phenotypic variation within the species, and an overlap of this variation with closely related species (Schwenk et al. 1998)). For example, *Acroperus harpae* has often been mentioned in the majority of ecological publications, whereas its sibling species *A. angustatus* is very rarely mentioned. In addition, many European regional published keys have treated *A. angustatus* as a subspecies or variety of *A. harpae*, which adds to the confusion (Sinev 2009). As another example, it is probably that just a few European Cladocera experts are able to distinguish *Chydorus ovalis* and *C. latus* from *C. sphaericus* (species described much over a century ago but their morphology is quite different) (Van Damme et al. 2011).

Another problem, not limited to the Cladocera and Copepoda, is the generic resolution provided by researchers inexperienced in the identification process. Such results are unreliable when assessing biodiversity (Nielsen et al. 1998). This is a well-known worldwide problem expressed years ago by Dumont (1997), who stated that “cripple descriptions of our forefathers are currently replaced by cripple descriptions by poorly trained workers from underequipped and underfunded laboratories ....” One of the solutions would be to design training courses, but such an approach has its obvious limitation. The more efficient solution would be a key, easy to use without prior long training and experience. A user-friendly, species-level taxonomic key, based on morphology, current nomenclature, and modern taxonomy using molecular tools, would fulfill the most pressing needs of both researchers and environmental managers. Such a key could reach many people at once, providing them with sufficient tools necessary to improve their species identification abilities. The radical technologies based entirely on DNA analyses (barcoding) are not feasible for the species identification needed by ecologists and managers (Gotelli 2004; Van Damme et al. 2011), but they are well suitable for phylogenetic research and discovering cryptic species (Bucklin et al. 2003; Bucklin and Frost 2009; Belyaeva and Taylor 2009). In the near future, genetic identification may be replaced by the newest method of mass spectrometry (Riccardi et al. 2012). Both methods, DNA barcoding and mass spectrometry, suffer the same major problems as the remaining methods, namely, determining at what point two groups of organisms are distant enough from each other to be separate species (Kunz 2012). The combined approach of genetic identification and morphological studies seems to be the best way, as it allows access to the level of phenotypic variation within and among populations necessary to identify taxonomically relevant traits (Billiones et al. 2004). These methods may then be combined with the newest mass spectrometry method. This approach is in an agreement with Kunz’s statement that “It is not sufficient to identify two organisms belonging to two different species by their diagnostic traits. It is more scientific to be able to explain the reasons that the organisms belong to two different species” (Kunz 2012). We should keep this statement in mind before we decide to describe a new species that slightly differs from the already known pool. Before describing a new species, the researcher who found a specimen that differs from the known species should refer to Winston (1999) for technical advice and especially to Kunz (2012) for recent theoretical background related to the principles of taxonomic classification. This is due to the fact that the newly discovered individuals with new traits are not necessarily a new species. The concept of traits assumes a central role in taxonomy, but traits have different meanings in the process of species identification (diagnostic meaning—used in the keys) and species description (definition meaning—used in taxonomy and while describing new species) (Kunz 2012).

Another obstacle, especially related to copepodologists during the identification process, is the mix of female and male characters used in genera-level keys to the calanoid copepods. Examples of this may be seen in keys provided by Dussart and Defaye (2001) and Boxshall and Halsey (2004). Even Borutzky et al. (1991), who provided separate keys for both calanoid copepod sexes, have used the mixed sexes

approach several times. Often, during the identification process, both calanoid copepod sexes are not available, and the user of such a key is stuck with an uncertain identification. Here, we provide separate male and female keys to the calanoid copepods, for both the genera and species levels.

Nonprofessional taxonomists have been responsible for describing more than half of the animal species discovered in Europe from 1998 to 2007 (Fontaine et al. 2010). The lack of trained professional taxonomists is one of the obstacles of the research progress or environmental monitoring implementation when collaboration with an experienced taxonomist is not always possible. The above is also true in all kinds of research involving freshwater Cladocera and Copepoda. Both groups of freshwater Crustacea have been described in several dozen monographs, not easily accessible, published in various languages equipped with scientific jargon understandable only to experts or more experienced researchers. Many professionals and especially undergraduate and graduate students are required to identify freshwater planktonic crustaceans during their research or lab projects. Many of them do not have the sufficient training in species identification and do not have access to published monographs needed to achieve the proper species identification. Therefore, here we propose a clear, easy-to-use, one-volume taxonomic dichotomous-pictorial key for genera and species identification of all (or almost all) planktonic Cladocera and Copepoda (Calanoida, Cyclopoida) currently (up to the end of November of 2015) reported from Europe. This is the first such key on the continental scale, covering the whole of Europe. According to current trends, researchers need to address ecological and environmental issues on a large scale, that is, across regions, continents, or globally (Preston and Rusak 2010; Schimel 2011). This is the only way in which we may study the geographic ranges and their limits to species distribution (Geber 2011). The extraordinary current rate of description of new species makes Europe an unexpected frontier for biodiversity exploration (Fontaine et al. 2010). The regional approach can eliminate another problem related to restricted geographical basis of many studies (single lake or lake district) which cannot take into account the phenotypic variation of the species (Schwenk et al. 1998). Also, various “local” taxonomic keys are often of limited use on a broader geographic scale and may be contradictory to each other due to the variation in analyzed traits (Schwenk et al. 1998). This key should help researchers as they may now use just one-reference key during the identification process, without searching through several dozen keys published years ago in various languages. Using the old keys could be a source of confusion or errors, as the old “local” keys do not provide the current more advanced taxonomical knowledge on the continental scale and often rely on several no longer valid species. This is why *Moina ephemeralis* and *M. weismanni* have been missing from zooplankton surveys in Central Europe—both of these species are missing in the identification keys (Petrušek 2002). The use of misleading, old identification keys is the source of erroneous identification. Cladocera and Copepoda literature is scattered among several dozen journals, which may be hard to track and obtain, especially in the recent quarter century publication boom. The proposed key is also a synthesis of recent changes and revisions, which include new species discovered and described during the last quarter of the century, published in several hundred

papers in various journals. The key should be relatively easy to use by almost any person, such as students and researchers with minimal or no prior expertise in the identification of these groups. We attempted to use autapomorphic characters and, whenever possible, almost a single character to distinguish between similar species, in an easy pictorial way, avoiding long verbal descriptions equipped with scientific jargon. Later, if a detailed morphology description or more information related to the identified species is needed, the reader may refer to more advanced monographs or papers cited in subsequent chapters. The idea of preparing this kind of key came from our years of experience in teaching undergraduate- and graduate-level courses spanning around half a century. Our area of study focused on limnology and the ecology of zooplankton (Cladocera, Copepoda), devoted mostly to the study of fresh and preserved field collection, and requiring students to identify zooplankton to the genus or species level. Students enrolled in such courses usually did not have the sufficient introduction to the morphology of crustaceans, which made identification very difficult, erroneous, or impossible. The use of advanced monographs was mostly impractical from the same reasons. Therefore, this manual should provide a useful and user-friendly key, allowing students, researchers, and also high school teachers or inexperienced amateurs, for rapid access to Cladocera and Copepoda species identification. Given that this manual is concerned only with the family, genera, and species identification of freshwater Cladocera and Copepoda, it is not necessary to discuss upper taxonomy divisions above the order, as their arrangement is in a constant state of flux, mostly caused by the recent progress of DNA phylogeny (Lecointre and Le Guyader 2006). However, the progress in taxonomy is not limited to DNA research, but also due to the progress caused by other broadly available modern technologies advancing taxonomical knowledge. Among the most important are high-resolution digital photography of specimens using both visible and ultraviolet images, improved by computer-assembled photomontages, genomic maps, advanced statistical analysis, and Internet publications (Wilson 2004; Dodson and Lee 2006; McKay 2013). All techniques mentioned above are the main driving force behind the progress of the knowledge of Cladocera and Copepoda we have been observing in the recent decades. This key provides a species-level overview of species of Cladocera and Copepoda (Calanoida and Cyclopoida) known from Europe. It is however not intended to be a monograph with a detailed species morphology description, as this approach would highly increase the volume to an impractical size. Such information has been provided in the cited references to published monographs and other papers. In this key, we provide only all relevant information needed for the proper species identification. Because of that, the species descriptions are limited to a single or few key characters. Keys to families, genera, and species are arranged into plates with an easy-to-use pictorial guide. In the subsequent chapter, all species are listed in alphabetical order, along with subspecies names and a list of known synonyms. Described also are recent changes in taxonomy status of the family, genera, or species. The key provides all relevant characters important for family, genera, and species identification as well as distinction from other similar groups or species. We provide written description and drawings for

most of the key characters in our keys. However, in a few exceptions (in Copepoda), when only written characters are available and when there is lack of published drawings or specimens for a verification, we sporadically provide diagrams for the symbolic visualization of a key character that is marked accordingly in the related plates. The identification process always should start at the beginning of the key. Otherwise, a single character missed during the identification may lead to the wrong result. Classification of Cladocera and Copepoda is in a permanent state of flux. The phylogenetic relationships within these groups are mainly focused on current DNA research, but are still far from the final arrangement. We present here the current state-of-the-art taxonomy for these groups. The morphology description of each group is given to the minimum level necessary for a reliable identification. The most important detailed descriptions of biology, morphology, biogeography, and ecology of these groups are given in monographs or papers cited in the introductory part of Cladocera and Copepoda and in subsequent chapters, in ecology notes, and synonym lists. The most recent important papers and monographs related to the given species are listed after the last valid species name, given at the end of the synonym lists. The provided maps of European distribution of each species are also based on these citations as well as on an unpublished worldwide biodiversity database of freshwater Cladocera and Copepoda maintained by L. A. Błędzki, as well as Illies (1978), the Freshwater Animal Diversity Assessment (FADA) project: Forró et al. (2008), Kotov et al. (2013), Boxshall and Defaye (2008), Boxshall and Defaye (2009), and Fauna Europaea (2012) the online service. Several authors made a good effort to elaborate patterns and mechanisms of the introduction (invasion) of species into certain European regions (Grigorovich et al. 2002). However, the biogeography of Cladocera and Copepoda in Europe is still not well known in some areas.

The next step after the proper species identification is (zooplankton) data analysis within a framework provided by modern community ecology, hardly relying on analytical methods (Hilborn and Mangel 1997; Scheiner and Gurevitch 2001; McCune and Grace 2002). Among them, the most important are experimental design, sampling, and data analysis, which in turn rely on statistical tests, where pseudoreplication (Hurlbert 1984) and null models for species diversity comparison in samples that have been standardized for abundance (Gotelli and Graves 1996) belong to the most ignored in published zooplankton analysis. This inspired us to prepare a short introduction to these problems as well as to useful statistical tests, which include the R statistics. It is now widely acknowledged that R proficiency is becoming increasingly more desirable as a scientific skill set and useful throughout the scientific community (Logan 2010). For that reason, we also provided some examples to illustrate how R can be used to perform biostatistical analyses. Our descriptions of these topics are brief, but we hope that they will help advance the understanding of the current trends in community ecology, of which Cladocera and Copepoda are a part and this will further equip researchers with better tools to make progress in the field. The advanced study of the properly identified species lays a solid base for modern three-dimensional biology (study of species across all levels of biological organization, diversity, evolution) (Wilson 2005).

We would like to encourage users of this key to share with us their constructive ideas, published papers, and information that may lead to improvements of the key or better knowledge of species morphology, ecology, and distribution. All such info can be sent to Leszek Błędzki at [lbledzki@mtholyoke.edu](mailto:lbledzki@mtholyoke.edu).

Freshwater Crustacean Zooplankton of Europe  
Cladocera & Copepoda (Calanoida, Cyclopoida) Key to  
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distribution, methods and introduction to data analysis  
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