Arctic Ocean Biodiversity and DNA Barcoding – A Climate Change Perspective

Katarzyna S. Walczyńska, Maciej K. Mańko, and Agata Weydmann

Abstract

Global changes are initiating a cascade of complex processes, which result, among other things, in global climate warming. Effects of global climate change are most pronounced in the Arctic, where the associate processes are progressing at a more rapid pace than in the rest of the world. Intensified transport of warmer water masses into the Arctic is causing shifts in species distributions and efforts to understand and track these change are currently intensified. However, Arctic marine fauna is the result of different recurring colonization events by Atlantic and Pacific Ocean populations, producing a very confounding evolutionary signal and making species identification by traditional morphological taxonomic analysis extremely challenging. In addition, many marine species are too small or too similar to identify reliably, even with profound taxonomic expertise. Nevertheless, the majority of current research focusing on arctic marine communities still relies on the analysis of samples with traditional taxonomic methods, which tends to lack the necessary taxonomic, spatial and temporal resolution needed to understand the drastic ecosystem shifts underway. However, molecular methods are providing new opportunities to the field and their continuous development can accelerate and facilitate ecological research in the Arctic. Here, we discuss molecular methods currently available to study marine Arctic biodiversity, encouraging the DNA barcoding for improved descriptions, inventory and providing examples of DNA barcoding utilization in Arctic diversity research and investigations into ecosystem drivers.

Biodiversity of the Arctic Ocean

Today’s Arctic marine biodiversity is highly impacted by newly formed current systems that bring warmer waters and their boreal inhabitants from the Atlantic and Pacific Oceans through the Fram and Bering Straits, respectively (Piepenburg et al. 2011). In the past, the resident diversity was primarily shaped by recurrent invasions, habitat fragmentation, and processes associated with glacial and interglacial periods, like bathymetric changes (e.g., Hewitt 2000, 2004; Ronowicz et al. 2015; Weydmann et al. 2017).

The Quaternary glaciation and deglaciation events were associated with global sea level fluctuations often exceeding 100 m, which lead to recurrent eradication of shelf biota and favored the survival of bathyal species and those thriving in isolated refugia, with subsequent recolonizations from the Atlantic and Pacific Oceans (Golikov and Scarlato 1989). In addition, the presence of ice sheets covering the open ocean further limited the dispersal of planktonic organisms (including larval stages of the benthic fauna) in the transarctic perspective (Hardy et al. 2011). The relatively recent, dynamic glacial history of the area have created complex evolutionary patterns, often blurring species delineations and hampering traditional morphological taxonomic methods, whereby, e.g., cryptic taxa can be easily overlooked (Hardy et al. 2011). Evidence for the underlying processes can also be gleaned from paleoceanographic data (Gladenkov and Gladenkov 2004). The geology of the Bering Strait, for example, revealed that, since its first opening at the Miocene–Pliocene boundary, this gateway between the Pacific and Arctic Oceans has been opened and closed repeatedly, providing opportunities for multiple invasions (Gladenkov and Gladenkov 2004; Hardy et al. 2011) from both sides (during the first 0.9–1.0 Ma after opening the prevailing currents flowed southward; Haug and Tiedemann 1998).

The five oceanic basins of the Arctic Ocean (Canada, Makaroff, Amundsen, Nansen and Eurasian Basin) are separated by mid-oceanic ridges that limit dispersal of the
deep-sea species within the Arctic (Bluhm et al. 2011a), but also their inflow of waters from the adjoining oceanic regions (Carmack and Wassmann 2006). These dispersal barriers, together with the glacial history of the area, have resulted in isolated assemblages of distinctive marine biota, while maintaining the close relatedness to species found in neighboring oceanic regions (Bucklin et al. 2010).

Once thought to be relatively poor, the biodiversity of the Arctic Ocean is now considered to be at an intermediate level (Hardy et al. 2011), with the number of extant species estimated to about 8000 (Bluhm et al. 2011b). However, this number is dynamically increasing, with new taxa described ever more frequently (see e.g. Matsuyama et al. 2017) and estimates of several thousand yet undescribed species (Bluhm et al. 2011b; Appeltans et al. 2012). The ecologically harsh, but diverse setting of the Arctic Ocean underlies the local biodiversity (see Table 1). Sea ice, for example, aside from aforementioned dispersal limitation, constitutes a unique ecosystem where sympagic (ice-associated) organisms thrive (Bluhm et al. 2009a). This group includes many endemic taxa and those of panarctic distribution (Bluhm et al. 2009a), but remains largely unstudied with many taxa still awaiting descriptions (see Piraino et al. 2008).

The diversity level of each Arctic marine ecological group is also tightly coupled with the highly specific ecosystem functioning of the Arctic. Seasonality, with light and dark periods lasting for large parts of the year (polar day and night, respectively), and the variable sea ice extent, govern the phenology of the whole ecosystem. Algal blooms, as main energy source for secondary producers and thus higher trophic levels, follow a two-part succession. The first ice algae bloom appears towards the end of winter, which is succeeded by a second bloom of planktonic algae, once the sea-ice melts (Leu et al. 2015). Both phases are significantly restricted in duration, due to light availability and water stratification (Sakshaug 2004). When the sea ice melts, surface waters warm up and, together with the presence of the fresh melt water, limit water mixing and consequently the amount of nutrients available to autotrophs, thus terminating the bloom (Sakshaug 2004). In spite of limited primary production, the trophic web of the marine Arctic is relatively rich and diverse. It can probably be explained by lower metabolic rates of organisms from higher trophic levels, resulting from permanently low temperatures in the Arctic Ocean (Bluhm et al. 2011b).

Most of the primary production is spatially restricted to shelves, and thus the most diverse community of consumers can be found there (Piepenburg et al. 2011; Wei et al. 2010). Availability of concentrated organic matter attracts primary consumers (zooplankton), which later become easy prey for secondary consumers (e.g. macrozooplankton, fish, seabirds) at shallow depths. Ungrazed organic matter, metabolic products and remains of the organisms sink to the bottom, where they fuel the complex benthic community. This concentration of biomass in the shelf regions draws the attention of top predators, like sea birds and marine mammals, for whom the Arctic shelves constitute the main forage areas (Wei et al. 2010).

The tight coupling between the functioning of the diverse marine Arctic ecosystems and environmental drivers renders them particularly susceptible to changes. The most detrimental anthropogenic impacts affecting the state of the Arctic Ocean usually include enterprises like shipping (including tourism), oil and gas exploration and fisheries related damages (ACIA 2004). However, the factor with the most obvious impact on the future of the marine Arctic is clearly climate change (IPCC 2014). An increase in sea surface temperatures reduces the geographic extent and thickness of the sea-ice cover directly, inducing a habitat loss for sympagic organisms, but also initiating regional shifts in species distributions or declines in primary production on a larger scale (Bluhm et al. 2011a; IPPC 2014).

In spite of insufficient amounts of decadal biodiversity studies encompassing the broad range of Arctic ecosystems, rapid (year-to-year) changes in different aspects of species biology have already been detected. On the autecological scale, these changes included e.g., biomass, diet or fitness (see review by Wassmann et al. 2011). On a broader view, the climate change driven modifications in Arctic communities are leading to a northward extension of the distribution ranges of boreal species (see examples in Hegseth and Sundfjord (2008) for phytoplankton; Weydmann et al. (2014) for zooplankton; Bluhm et al. (2009b) for zoobenthos; Mueter and Litzow (2008) for fish; Piatt and Kitaysky (2002) and CAFF (2010) for sea birds; Moore (2008) for marine mammals), replacing the long-lived and slow growing Arctic organisms with their smaller and short-lived boreal counterparts (e.g., Berge et al. 2005; Węsławski et al. 2010), while population of more susceptible, and usually less plastic species decline (e.g., Gilchrist and Mallory 2005).

| Table 1 | Species diversity of marine Arctic biota of different ecological groups |
|---------|---------------------------------------------------------------|
| Ecological group | Number of species |
| Unicellular eukaryotes | 2106 (1027 sympagic; 1875 planktonic) |
| Sea ice fauna | At least 50 |
| Zooplankton | 354 |
| Seaweeds | c. 160 |
| Zoobenthos | c. 4600 |
| Fish | 243 |
| Seabirds | 64 |
| Marine mammals | 16 |

Modified after Bluhm et al. (2011b)
DNA Barcoding

Biodiversity studies represent the first step to provide a baseline for detecting the effect of climate change on marine biota. A precise identification of all ecosystem components will allow to analyze interspecific interactions and will enable to determine factors, which influence its functioning. Until recently, most of the biodiversity research has been based on morphological analyses, which have many limitations, what might result in underestimation of diversity. In the marine environment, cryptic speciation is common, resulting in genetically differentiated lineages that are indistinguishable morphologically (Bickford et al. 2006). Nonetheless, their recognition is important, as they can have different functions in ecosystems (Fišer et al. 2015). Similarly, the identification of very small organisms or early life stages may be problematic, resulting in identification restricted to the phylum or family level.

A promising auxiliary approach is the use of molecular methods for identification and discrimination of species, known as DNA barcoding, which enables not only the assignment of unknown species, but it also enhances the discovery of new species (Bucklin et al. 2011), by matching their genetic fingerprint to a known barcode reference. Its development in recent years enabled more accurate species identification (Hebert et al. 2003), and the effectiveness of this approach has been established for several large groups of organisms (Bucklin et al. 2011), due to contribution of big, international projects, like Barcode of Life (www.barcode-of-life.org). Here, species identification is achieved by the analysis of a short DNA sequence from a specific gene region, called “the barcode”, by comparing it with the library of reference barcode sequences derived from species of known identity (Hajibabaei et al. 2007). The method is based on the assumption that genetic differences between sequences within a species (intraspecific variability) are smaller than genetic differences among species (interspecific variability), reflected in the so-called “barcoding gap” (a min. % difference between intra- and interspecific variability), can be used to match the specimen’s barcode in the database, if an appropriate reference sequence is available. The presence, extent, and “position” of the barcoding gap differs between species, and hence there is a need to use different markers for different groups of organisms. One of the most commonly used markers in animals is a 648-base fragment at the 5′ end of mitochondrial gene cytochrome c oxidase I (COI), as it has no introns (in some groups of animals), limited recombination and many copies per cell (Hajibabaei et al. 2007). Other popular markers include the genomic ITS (internal transcribed spacer I and II), 18S and the mitochondrial 16S rDNA. The number of sequences in databases like GenBank or BOLD are constantly increasing at a very fast rate. Hajibabaei et al. (2007) summarized the number of available sequences in public databases, and in only few years these numbers have increased several times. Information on popular markers used for DNA barcoding and the corresponding number of available sequences per organism group are presented in Table 2.

Like all identification methods, DNA barcoding has its flaws, as it requires a reference sequence in the database based on accurately identified organisms. Even though the development of Gen Bank is very dynamic – new sequences are submitted every day – sequences from many organisms are lacking whilst other sequences may be present under a wrongly identified species name. Nevertheless, molecular methods may have advantages over morphological methods in species identification as there is a lack of unique diagnostic morphological or morphometric characteristics separating species, but it can also be performed by a person without specialized taxonomic knowledge. An integrative approach using both molecular and morphological analyses, has been shown to strengthen species identification in previous polar taxonomic studies and provided the most reliable taxonomic resolution (Heimeier et al. 2010) as compared to using either method alone.

Indeed, identification of organisms based on nucleotide sequences it is not always 100% accurate, which has led to the use of the term Operational Taxonomic Unit (OTU) or – in case of barcoding – Molecular Operational Taxonomic Unit (MOTU), instead of “species”. Studies have been carried out where the function of particular organisms in the ecosystem have been attributed to MOTUs (Ryberg 2015).

In the following sections we will provide examples to illustrate the use of DNA barcoding in Arctic diversity research and how can it be useful for detecting and monitoring of different processes in several important groups of marine organisms.

Plankton

Plankton is a very diverse group, containing very small organisms like viruses, heterotrophic single-cell organisms (bacterioplankton), autotrophic organisms (phytoplankton) and bigger animals (zooplankton). The diverse planktonic communities encompass both the tiniest autotrophs, like unicellular algae Synechococcus and Prochlorococcus, which are responsible for the production of approximately 60% of the atmospheric oxygen, as well as the siphonophores, which can grow to about 40 m in length (Robison 1995). Yet another important component of the plankton are pelagic copepod crustaceans, which in many regions of the World’s Ocean are the key species of the pelagic food webs, constituting up to 70% of the whole plankton biomass (Soreide et al. 2008). Their relatively short life cycles, high reproductive outputs, lack of direct anthropogenic pressure and distributions depen-
dent on the local hydrography make the plankton ideal for monitoring climate related changes in biodiversity (Hays et al. 2005). However, uncertainty in the taxonomic identification impedes further reasoning on climate-driven alterations of pelagic ecosystems.

Arctic zooplankton is characterized by a high seasonality and a strong spatial diversification resulting from distinct biogeographic origins of species (Blachowiak-Samolyk et al. 2008; Weydmann et al. 2014). A good example of such structuring of the plankton, comes from the analysis of the Calanus species complex. Three species of Calanus copepods coexist in the European Arctic: C. finmarchicus, C. glacialis and C. hyperboreus. In spite of similarities in their morphology and life cycles, there are some striking differences such as the type of lipids that characterize these congeners, what should be taken into account, as they play a role in the lipid-based energy flux in the Arctic (Falk-Petersen et al. 2008). So far, C. finmarchicus was considered a boreal species, C. glacialis a typical Arctic shelf species, and C. hyperboreus the Arctic open-water species (Falk-Petersen et al. 2008). Their distribution ranges were clearly established, and in areas where they coexisted, species identification just followed the size criterion (Unstad and Tande 1991). However, the accuracy of this method, has been questioned, because of the potential interspecific hybridization and growth plasticity (Gabrielsen et al. 2012; Nielsen et al. 2014), which already has been documented by Parent et al. (2012) in the Arctic and Northwest Atlantic.

Hence, the distribution records of these three key planktonic species may have to be revised whilst knowledge on exact distribution ranges is crucial for the understanding of ecosystem functioning. In the Arctic, little auks (Alle alle), an ecologically important sea bird species, mainly feed on Calanus glacialis. With the observable increase of Atlantic water inflow to the Arctic (Polyakov et al. 2011), the distribution of this Arctic copepod is predicted to decline, while a northward range expansion is expected for its boreal sister-species C. finmarchicus. This comparatively much smaller Atlantic counterpart, C. finmarchicus, is an undesirable food source for little auks since it is not as energy rich as C. glacialis, and thus capture of a sufficient amount of C. finmarchicus comes with more energy expenses (Wojczulanis-Jakubas et al. 2013). In order to validate the hypothesis of distribution shifts between those two species, Lindeque et al. (2004) employed both morphological (based on the prosome length) and molecular (barcoding of the 16S rDNA gene) methods for species identification. Results obtained by molecular techniques proved that Calanus species co-occur and have wider distribution than it was established based on morphological analysis.

Another example illustrating the efficiency of molecular methods for plankton species identification is a study on pandidal hydromedusae. Four morphologically similar genera are currently co-existing in the Arctic: Catablema, Halitholus, Leuckartiara and Neoturris. The taxonomic features used for species delineation are often inconspicuous and in some cases assumed to be growth-dependent, and thus variable within the species (see comments in Schuchert 2007). Besides the need to thoroughly re-examine the life cycle of some of these species, molecular methods can be a solution for the identification problems. In the case of Hydrozoa, the use of 16S rDNA as barcode marker has certain advantages over COI (Lindsay et al. 2015), and therefore initiatives aiming at supplementing sequence data, using this particular gene should be encouraged (see project HYPNO, Dr. Aino Hosia, https://artsdatabanken.no/Pages/168312).

**Microorganisms**

Microorganisms, are particularly important as primary producers for the functioning of marine ecosystems, but they also play an important role in all biogeochemical processes (Sogin et al. 2006). Nonetheless, knowledge is limited due to the difficulties associated with the investigation of small organisms like pico- (0.2–2 μm), and nanoplankton (2–20 μm). Previous research in the Arctic has shown strong seasonal variations in microorganism communities, related to changes in irradiation. However the development of molecular techniques in recent years enabled further investigation of their diversity (Marquardt et al. 2016). Genetic analyses proved that microorganisms in Arctic waters are of greater importance than previously believed. Furthermore, they are also widely spread during polar night: in fjords and

### Table 2: Common molecular markers. Numbers of available sequences in GenBank on 01.02.2017

| Marker | Region     | Animals       | Plants       | Protists     | Fungi     |
|--------|------------|---------------|--------------|--------------|-----------|
| COI    | Mitochondrial | 2,219,762    | 30,511       | 1162         | 2043      |
| 18S    | Genomic    | 161,263      | 25,130       | 9264         | 583,384   |
| 16S    | Mitochondrial | 345,915      | 4072         | 5221         | 382,418   |
| ITS1   | Genomic    | 47,842       | 82,880       | 33,235       | 481,840   |
| ITS2   | Genomic    | 61,956       | 88,157       | 14,535       | 236,705   |
| CYTB   | Mitochondrial | 413,039      | 619          | –            | 15,090    |
| rbcL   | Plastid    | –            | 45,737       | 31,463       | –         |

**Animals Plants Protists Fungi**

K. S. Walczyńska et al.
open ocean, deep and shallow water (Vader et al. 2015), which is particularly interesting as our knowledge regarding processes during the dark season was limited for a long time due to logistic difficulties with conducting research in winter. It should be taken into account that temperature increase and decrease in sea ice cover may influence the community structure of microorganisms and this effect has the potential to be translated to all upper trophic levels (Berge et al. 2015).

One of the most common methods used in the analysis of microorganisms, is barcoding based on the comparison of DNA and RNA derived OTU. While DNA is a very stable molecule and able to persist outside of the source organism for a long time, RNA is less stable and degrades rapidly. RNA analysis is therefore useful in informing about the current situation in the water column. In Svalbard waters, 4000 OTUs were differentiated based on DNA and only 2000 OTUs based on RNA (Marquardt et al. 2016). Differences can be explained by the fact that DNA is stable and may be present in the water column even after the death of an organism, but may also be caused by the high number copies of rRNA genes (Gong et al. 2013). The result of this research based on molecular data, has shown a high activity of heterotrophic groups during the polar night. It also revealed that species considered as autotrophic can become mixotrophic during winter. Based on a seasonal analysis of DNA and RNA, a succession of different microbial groups was demonstrated and their presence explained by particular environmental preferences, which may suggest that increasing temperatures will significantly influence community composition (Marquardt et al. 2016). Another study, in which microorganism communities were compared before and after the Record Sea Ice Minimum in the Arctic in 2007 (next were observed in 2012 and 2016), the genetic diversity of microorganisms appeared to be much lower (Comeau et al. 2011). This may be the result of particular adaptations to the sea-ice environment, as some are known to belong to the sympagic community. Differences in the community composition of Bacteria and Archaea, responsible for carbon and nutrient cycles, may influence productivity, but also the release of CO₂ from the Arctic Ocean (Legendre and Le Fèvre 1995). These findings underline the importance of future research focusing on the ecology and functions of microorganisms to predict consequences of forthcoming changes.

**Benthos**

Some areas of the Arctic Ocean, especially the continental shelves, are well-recognized for their tight benthic-pelagic coupling, inferred from the high amount of carbon fixed near the oceans’ surface that sinks ungrazed to the seafloor, where it fuels benthic communities (Ambrose Jr. and Renaud 1995; Renaud et al. 2008). In the Arctic, biogenic sedimentation is far greater than at lower latitudes, thus explaining the high biomass of benthos thriving there (Petersen and Curtis 1980; Ambrose Jr. and Renaud 1995). Even with winter-limited primary production these benthic communities are relatively stable (Dunton et al. 2005).

The Arctic benthos is composed of a relatively young community that acquired lot of its current form during Quaternary glaciations (Zenkevitch 1963). The ice-mediated inflow and -outflow of mature organisms and their offspring, the isolation in refugia, and species extinctions led to the present day state of the Arctic benthic biodiversity (Hardy et al. 2011; Ronowicz et al. 2015). Although much is known about the current state of the Arctic benthos, a higher spatial and taxonomic resolution for biodiversity data is needed for an improved inferring of its future.

High phenotypic plasticity (e.g., in body pigmentation) further impedes species identification and hence the understanding of environmentally-dependent spatial diversification of benthic communities (Hardy et al. 2011). Bottom-dwelling polychaetes of the Arctic properly portray this trend. Until recently, this speciose group was perceived as lacking geographic structure on the global scale (Fauvel 1984). However, the use of molecular methods revealed numerous phenotypically indistinctive sibling species whilst it confirmed the presumed cosmopolitism of others (Carr et al. 2011). Hence, morphology-based taxonomy coupled with COI barcoding better resolved the diversity of Arctic polychaetes, showing that almost 25% of the over 300 “species” examined, were in fact complexes of two or more divergent lineages (Carr et al. 2011). Using COI sequences, Carr et al. (2011), were also able to retrace possible historical changes in distribution ranges of polychaetes found on Canadian coast of the Arctic, suggesting the Pleistocene glaciation as the main factor responsible of the increased diversification observed in this taxon.

Similar studies were conducted on echinoderms of the Canadian Arctic (Layton et al. 2016). Out of 141 taxa examined, 118 constituted morphologically distinctive species, while the remaining 23 were taxa assigned to different genera but not representing recognized species (Layton et al. 2016). It may suggest that in this area 23 morphologically indistinctive species new to science, or new for this region, may exist. Interestingly, with the sole usage of COI sequences, these authors also discussed various aspects of the phyleogeography of echinoderms. For example, they pointed out that all species, where no pronounced spatial genetic structure could be observed between specimens collected in two or three oceanic regions of Canada, possessed a planktonic larval stage, which may justify the high levels of gene flow (Layton et al. 2016).

The above examples illustrate the utility of barcoding in delineation of the species composing the benthic communities of shallow shelf areas of the Arctic. Unfortunately, similar studies, focusing on the deep ocean assemblage remain uncommon, mostly because of the obvious difficulties of sampling below certain depths (Layton et al. 2016). One of
the few examples of such studies, is Song et al. (2016), who used combined morphological and molecular approach to investigate the collections of Chinese National Arctic Research Expeditions in the Bering Sea. By means of 16S rDNA sequences, a new species, Sertaria xuelongi, was described and the potential biogeographic origin of this species discussed. By comparing 16 sequences of S. xuelongi and of other congeneric species from the northwest of France, Iceland, and the Chukchi Sea, they suggested that these species are of Pacific origin, but may in fact constitute a significant part of the deep-sea benthic fauna of the Arctic (Song et al. 2016).

As mentioned earlier, important factors in shaping nowadays Arctic diversity were glaciation processes, during which species were forced into refugia in order to survive, what caused long-term isolation and thus differentiation of the species. After glaciation ceased, some of the expanding species went in secondary contact, however, undergoing processes were much more complicated (Maggs et al. 2008). One of the interesting examples is blue mussel, Mytilus edulis, which was gone for a long time from Svalbard waters, however warming of the Arctic enabled its re-appearance (Berge et al. 2005). It has been proven that blue mussels can create hybrids with other species, like Mytilus trossulus and Mytilus galloprovincialis in different Arctic regions, what leads to local adaptations (Mathiesen et al. 2017). This topic has not been investigated well yet, nonetheless it requires more insight as Mytilus spp. are ecosystem engineers and global warming opens new paths for invasions of boreal species in the Arctic.

Nekton

The benthic and planktonic organisms discussed above constitute food sources for higher trophic levels, which in the Arctic are primarily nektonic vertebrates. Aside from marine mammals and sea birds, this group is represented by a speciose community of fish. In the Arctic, there are 243 species of fish (Bluhm et al. 2011a), comprising several key species like polar cod and capelin (Hop and Gjøsæter 2013) as well as species with unique traits including the longest living vertebrate, the Greenland shark (Nielsen et al. 2016).

The biogeography of this ecologically and economically important group remained, unfortunately, largely unknown. Only recently, Mecklenburg et al. (2011) have improved the taxonomic identification of all Arctic species, thereby improving the resolution available for the spatial structure of their diversity. COI barcoding, combined with morphological analyses, allowed them to revise the biogeographic origin of species, showing that some of the past fish records from Arctic waters were misidentified. They found that a majority Arctic fish species (59%) are cosmopolitan species with boreal distribution, while the remaining 41% are Arctic, mainly-Arctic, and boreo-Arctic species (Mecklenburg et al. 2011). Such detailed knowledge on the biodiversity is required to trace the climate-change derived alteration of, for example, species distribution. The study also shows the hidden potential of the simultaneous morphological-molecular approach to taxonomy. In this particular case, it could be used to resolve the cod mother identity, or to acquire data of unprecedented species-resolution (Carr and Marshall 2008).

For some fish species like Arctogadus glacialis, Boreogadus saida complete genomes are available (Breines et al. 2008). There is a high interest in postglacial colonization of fishes like Salvelinus fontinalis (Pilgrim et al. 2012), Coregonus nasus (Harris and Taylor 2010) or Coregonu lavaretus (Östbye et al. 2006). We can also find lots of studies about genetic diversity of different species (Kai et al. 2011; Kovpak et al. 2011), as in the future it might be crucial for adaptations to a changing environment.

The overall low number of species and distinctive morphology allow a relatively easy acquisition of high-resolution data on marine mammal diversity by means of classic taxonomic methods. Furthermore, such approaches have already revealed pronounced modifications in species ecology and biology, by detecting shifts in distribution ranges, decrease in body size and size of the separate populations, as well as alterations of food migrations (Kovacs et al. 2010). All of these changes might affect marine mammal species populations. Even though molecular research does not focus on biodiversity, it may cover a wide range of other aspects, like evolution, population genetics or phyleogeography.

Future Perspectives

The Arctic Ocean is warming three times faster than the global average (IPCC 2014), thus further changes in species composition and entire ecosystem functioning are inevitable. Temperature has an impact on many aspects of physiological processes and it can affect reproduction, growth, and survival. Changes in single species distributions can effect entire ecosystems through all trophic levels, as was shown for the case of a potential mismatch between phytoplankton blooms and reproduction of Calanus glacialis in Arctic waters (Søreide et al. 2010). Hence, using only traditional methods might not be enough to timely observe what is going on in this fragile ecosystem. Kędra et al. (2015) emphasized the lack of biodiversity research in some Arctic areas, especially in the deep-sea region, but also the lack of research predicting direction of changes in species distribution resulting from global change.

DNA barcoding has been proven a useful tool in biodiversity assessment, however, the evolution of molecular methods is very fast, including the development of new approaches such as metabarcoding. This method involves the extraction...
of DNA from an entire sample, without the need of picking out single individuals, like larvae or other targeted groups of mesozooplankton. It is based on the New Generation Sequencing (NGS) technology, where millions of short sequences (reads) are produced allowing to screen entire genomes or transcriptomes in order to obtain a higher resolution of spatio-temporal patterns of species distribution (Bucklin et al. 2016). This technique is becoming increasingly available as sequencing is getting cheaper. Commonly used genetic markers for metabarcoding are 16S, 18S and 28S, while COI is not often used as it requires specific primers (Deagle et al. 2014). So far, metabarcoding has mainly been used for microorganism research, however, it might also be used for monitoring of zooplankton for which the dynamic changes may not be detected with other tools. It is now also possible to obtain DNA from environmental samples (environmental DNA, eDNA), like water or soil, without prior isolation of target organisms, as they continuously expel DNA into their surroundings from where it can be collected (Thomsen and Willerslev 2015). This approach can provide information about the presence and type of organisms which were in a particular location in the recent past, like fishes or whales (Sigsgaard et al. 2016). Metagenomics represent an even more advanced method, for which entire genomes present in environmental samples are analyzed. Yet it is mostly applied on microorganisms, since not enough reference genomes exist for metazoans (Wooley et al. 2010). Nevertheless, as mentioned at the beginning of this chapter, databases are growing at an enormous speed and new genomes are published every day, what means that analyses of metagenomes of different ecological groups will become possible in the nearest future. Metagenomics significantly exceeds beyond species identification, in biodiversity research it allows for investigation of uncultured microbial populations. It is a very powerful tool, which enables exploration of metabolic diversity, isolation and identification of enzymes and it may be an effective way to produce novel bioresources (Kodzius and Gojobori 2015).

Currently, the analysis of high-throughput sequence (NGS) data requires an in-depth knowledge in bioinformatics. Moreover, the obtained results are rather qualitative than quantitative, e.g. based on presence/absence of DNA in a sample, however, this is currently being improved. Nonetheless, until these methods are not optimized for converting number of sequences into abundances of organisms in the field, the best method remains the integrative taxonomic approach, which combines molecular with morphological data.

In conclusion, molecular data are a promising tool for detecting the influence and consequences of global warming on different communities. Standard molecular methods have been successfully applied in Arctic research and their fast development will render analysis even more feasible and cost-effective. The use of DNA barcoding should be emphasized for long-time monitoring studies. Considering the opportunity of acquiring fast results, however, caution should be taken with regard to the choice of an adequate molecular marker, a careful analysis of the data and if possible, the application of an integrative approach by supporting these results with morphological analyses.

Knowledge on the existing biodiversity is the baseline for many studies, e.g. on ecological and physiological aspects. In order to investigate the future of the Arctic ecosystems, further research should focus on combining data obtained from biodiversity assessments with modelling and experiments, in which molecular tools can be used as well.

Appendix

This article is related to the YOUMARES 8 conference session no. 8: “Polar Ecosystems in the Age of Climate Change”. The original Call for Abstracts and the abstracts of the presentations within this session can be found in the appendix “Conference Sessions and Abstracts”, chapter “9 Polar Ecosystems in the Age of Climate Change”, of this book.

References

ACIA (Arctic Climate Impact Assessment) (2004) Impacts of warming Arctic. Cambridge University Press, Cambridge

Ambrose WG Jr, Renaud PE (1995) Benthic response to water column productivity patterns: evidence for benthic-pelagic coupling in the Northeast Water Polynya. J Geophys Res 100:4411–4421

Appeltans W, Ahyong ST, Anderson G et al (2012) The magnitude of global marine species diversity. Curr Biol 22:2189–2202

Berge J, Johnsen G, Nilsen F et al (2005) Ocean temperature oscillations enable reappearance of blue mussel _Mytilus edulis_ in Svalbard after 1000 years of absence. Mar Ecol Prog Ser 303:167–175

Berge J, Renaud PE, Darnis G et al (2015) In the dark: a review of ecosystem processes during the Arctic polar night. Prog Oceanogr 139:258–271

Bickford D, Lohman DJ, Hodsi NS et al (2006) Cryptic species as a window on diversity and conservation. Trends Ecol Evol 22(3):148–155

Blachowiak-Samolyk K, Sareide J, Kwasniewski S et al (2008) Hydrodynamic control of mesozooplankton abundance and biomass in northern Svalbard waters (79–81°N). Deep Sea Res Part 2 55:2210–2224

Bluhm BA, Gradinger RR, Schnack-Schiel SB (2009a) Sea ice meio- and macrofauna. In: Thomas DN, Dieckmann GS (eds) Sea ice, 2nd edn. Wiley-Blackwell, Oxford, pp 357–393

Bluhm BA, Iken SL, Minckes BI et al (2009b) Community structure of epibenthic megafauna in the Chukchi Sea. Aquatic Biol 7:269–293

Bluhm BA, Geburk A, Gradinger R et al (2011a) Arctic marine biodiversity: an update of species richness and examples of biodiversity change. Oceanography 24(3):232–248

Bluhm BA, Gradinger R, Hopcroft RR (2011b) Arctic Ocean diversity: synthesis. Mar Biodivers 41:1–4

Brenes R, Ursvik A, Nymark M et al (2008) Complete mitochondrial genome sequences of the Arctic Ocean codfishes _Arctogadus glacialis_ and _Boreogadus saida_ reveal oriL and tRNA gene duplications. Polar Biol 31:1245–1252
Bucklin A, Hopcroft RR, Kosobokova KN et al (2010) DNA barcoding of Arctic Ocean holozoo plankton for species identification and recognition. Deep Sea Res Part 2 57:40–48

Bucklin A, Steinke D, Blanco-Bercial L (2011) DNA barcoding of marine Metazoa. Annu Rev Mar Sci 3:471–508

Bucklin A, Lindeque PK, Rodriguez-Ezpeleta N et al (2016) Metabarcoding of marine zooplankton: prospects, progress and pitfalls. J Plankton Res 38:393–400

CAFF (2010) Arctic biodiversity trends 2010: selected indicators of change. CAFF International Secretariat, Akureyri

Carmack E, Wassmann P (2006) Food webs and physical–biological coupling on pan-Arctic shelves: unifying concepts and comprehensive perspectives. Prog Oceanogr 71:446–477

Carr SM, Marshall HD (2008) Intraspecific phylogeographic genomics from multiple complete mtDNA genomes in Atlantic Cod (Gadus morhua): origins of the “Codmother” transatlantic vicariance and midglacial population expansion. Genetics 180:381–389

Carr CM, Hardy SM, Brown TM et al (2011) A tri-ocenric perspective: DNA barcoding reveals geographic structure and cryptic diversity in Canadian polychaetes. PLoS One 6(7):e22232. https://doi.org/10.1371/journal.pone.0022232

Comeau AM, Li WKW, Tremblay J-E et al (2011) Arctic Ocean microbial community structure before and after the 2007 record sea ice minimum. PLoS One 6(11):e27492. https://doi.org/10.1371/journal.pone.0027492

Deagle BE, Jarmen SN, Coissac E et al (2014) DNA metabarcoding and role of cross-shelf advective processes. Deep Sea Res Part 2 52:3462–3477

Falk-Petersen S, Mayzaud P, Kattner G et al (2008) Lipids and life strategies of the cytochrome c oxidase subunit I marker: not a perfect match. Biol Lett 10:140562. https://doi.org/10.1098/rsbl.2014.0562

Dunton KH, Goodall JL, Schenborn SV et al (2005) Multi-decadal synthesis of benthic-pelagic coupling in the western Arctic: role of cross-shelf advective processes. Deep Sea Res Part 2 52:3462–3477

Falk-Petersen S, Mayzaud P, Kattner G et al (2008) Lipids and life strategy of Arctic Calanus. Mar Biol Res 5:18–39

Fausch K (1984) Polychaete distribution patterns, or: can animals with Palaeozoic cousins show large-scale geographical patterns? In: Hutchings PA (ed) Proceedings of the first international polychaete conference, Sydney, The Linnean Society of New South Wales, pp 1–6

Fišer Z, Altermatt F, Zaksek V et al (2015) Morphologically cryptic amphipod species are “ecological clones” at regional but not at local scale: a case study of four Niphargus species. PLoS One 10(7):e0134384. https://doi.org/10.1371/journal.pone.0134384

Gabrielsen TM, Merkel B, Soreide J et al (2012) Potential misidentifications of two climate indicator species of the marine arctic ecosystem: Calanus glacialis and C. finmarchicus. Polar Biol 35:1621–1628

Gilchrist HG, Mallory ML (2005) Declines in abundance and distribution of the ivory gull (Pagophila eburnea) in Arctic Canada. Biol Conserv 121:303–309

Gladenkov AY, Gladenkov YB (2004) Onset of connections between the Pacific and Arctic Oceans through the Bering Strait in the Neogene. In: Herman Y (ed) The Arctic Seas during the Neogene period. In: Herman Y (ed) The Arctic Seas during the Neogene period. Springer, Netherlands, pp 175–187

Golikov AN, Scarlato OA (1989) Evolution of Arctic ecosystems. Evolution of Arctic ecosystems. Springer, Netherlands

Gladenkov AY, Gladenkov YB (2004) Onset of connections between the Pacific and Arctic Oceans through the Bering Strait in the Neogene. In: Herman Y (ed) The Arctic Seas during the Neogene period. Springer, Netherlands, pp 175–187

Gong J, Dong J, Liu X et al (2013) Extremely high copy numbers and polymorphisms of the rDNA operon estimated from single cell analysis of Oligotrich and Peritrich ciliates. Protist 164:369–379

Hajibabaei M, Singer GAC, Hebert PDN et al (2007) DNA barcoding: how it complements taxonomy, molecular phylogenetics and population genetics. Trends Genet 23:167–172

Hardy SM, Carr CM, Hardman M et al (2011) Biodiversity and phylogeography of Arctic marine fauna: insights from molecular tools. Mar Biodivers 41:195–210

Harris LN, Taylor EB (2010) Pleistocene glaciations and contemporary genetic diversity in a Beringian fish, the broad whitefish, Coregonus nasus (Pallas): inferences from microsatellite DNA variation. J Evol Biol 23:72–86

Haug GH, Tiedemann R (1998) Effect of the formation of the Isthmus of Panama on Atlantic Ocean thermocline circulation. Nature 393:673–676

Hays GC, Richardson AJ, Robinson C (2005) Climate change and marine plankton. Trends Ecol Evol 20:337–344

Hebert PDN, Cywinska A, Ball SL et al (2003) Biological identifications through DNA barcodes. Proc R Soc Lond B 270:313–321

Hegseth EN, Sundfjord A (2008) Intrusion and blooming of Atlantic phytoplankton species in the high Arctic. J Mar Syst 74:108–119

Heimeler D, Lavery S, Sewell MA (2010) Using DNA barcoding and phylogenetics to identify Antarctic invertebrate larvae: lesson from a large scale study. Mar Gen 3:165–177

Hewitt GM (2000) The genetic legacy of the quaternary ice ages. Nature 45:907–913. https://doi.org/10.1038/35016000

Hewitt GM (2004) Genetic consequences of climatic oscillations in the quaternary. Philos Trans R Soc Lond Ser B Biol Sci 359:183–195

Hop H, Gjøsæter H (2013) Polar cod (Boreogadus saida) and capelin (Mallotus villosus) as key species in marine food webs of the Arctic and Barents Sea. Mar Biol Res 9:878–894

IPCC (Intergovernmental Panel on Climate Change) (2014) Climate change 2014: synthesis report. Contribution of working groups I, II and III to the fifth assessment report of the IPCC. IPCC, Switzerland

Kai Y, Orr JW, Sakai K et al (2011) Genetic and morphological evidence for cryptic diversity in the Careproctus rastrinus species complex (Liparidae) of the North Pacific. Ichthyol Res 58:143–154

Ködra M, Moritz C, Choy ES et al (2015) Status and trends in the structure of Arctic benthic food webs. Pol Res 34:23775. https://doi.org/10.3402/polar.v34.23775

Kodzius R, Gojobori T (2015) Marine metagenomics as a source for bioprospecting. Mar Gen 24:21–30

Kovacs KM, Moore S, Lydersen C et al (2010) Impacts of changing sea ice conditions on Arctic marine mammals. Mar Biodivers 41:181–194

Kovpak NE, Skurikhina LA, Kukhlevsky AD et al (2011) Genetic divergence and relationships among smelts of the genus Osmerus from the Russian waters. Russ J Genet 47:958–972

Layton KKS, Corstorphine EA, Hebert PDN (2016) Exploring Canadian echinoderm diversity through DNA barcodes. PLoS One 11(11):e0166118. https://doi.org/10.1371/journal.pone.0166118

Legendre L, Le Fèvre J (1995) Microbial food webs and the export of biogenic carbon in oceans. Aquat Microb Ecol 9:69–77

Leu E, Mundy CJ, Assmy P et al (2015) Arctic spring awakening – steering principles behind the phenology of vernal ice algal blooms. Prog Oceanogr 139:151–170

Lindeque PK, Harris R, Jones MB et al (2004) Distribution of Calanus spp. as determined using a genetic identification system. Sci Mar 68:121–128

Lindsay DJ, Grossmann MM, Nishikawa J et al (2015) DNA barcoding of pelagic cnidarians: current status and future prospects. Bull Plankton Soc Jpn 62:39–43

Maggs CA, Castilho R, Foltz D et al (2008) Evaluating signatures of glacial refugia for North Atlantic benthic marine taxa. Ecology 89:108–122

Marguardt M, Vade A, Stühner El et al (2016) Strong seasonality of marine microbial eukaryotes in a High-Arctic fjord (Isfjorden, in West Spitsbergen, Norway). Appl Environ Microbiol 82:1868–1880

Mathiesen SS, Thyrring J, Hemmer-Hansen J et al (2007) Genetic diversity and connectivity within Mytilus spp. in the subarctic and Arctic. Evol Appl 10:39–55

Matsuyama K, Martha SO, Scholz J et al (2017) Ristella vestitilina n. gen. et sp., a new bryozoan genus and species (Gymnolaemata:
Cheilostomata) from an Arctic seamount in the Central Greenland Sea. Mar Biodivers. https://doi.org/10.1007/s12526-017-0645-z

Mecklenburg CW, Møller PR, Steinke D (2011) Biodiversity of arctic marine fishes: taxonomy and zoogeography. Mar Biodivers 41:109–140

Moore SE (2008) Marine mammals as ecosystem sentinels. J Mammal 89:534–540

Mueter FJ, Litzow MA (2008) Sea ice retreat alters the biogeography of the Bering Sea continental shelf. Ecol Appl 18:309–320

Nielsen TG, Kjellerup S, Smolina I et al (2014) Live discrimination of Calanus glacialis and C. finmarchicus females: can we trust phylogenetic differences? Mar Biol 161:1299–1306

Nielsen J, Hedeholm RB, Heinemeier J (2016) Eye lens radiocarbon reveals centuries of longevity in the Greenland shark (Somniosus microcephalus). Science 353:702–704

Østbye K, Amundsen P, Bernatchez L et al (2006) Parallel evolution of ecomorphological traits in the European whitefish Coregonus lavaretus (L.) species complex during postglacial times. Mol Ecol 15:3983–4001

Parent GJ, Plourde S, Turgeon J (2012) Natural hybridization between Calanus finmarchicus and C. glacialis (Copepoda) in the Arctic and Northwest Atlantic. Limnol Oceanogr 57:1057–1066

Petersen GH, Curtis MA (1980) Differences in energy flow through major components of subarctic, temperate and tropical marine shelf ecosystems. Dana 1:53–64

Pilgrim BL, Perry RC, Barron JL et al (2012) Nucleotide variation in the mitochondrial genome provides evidence for dual routes of postglacial recolonization and genetic recombination in the northeastern brook trout (Salvelinus fontinalis). Gen Mol Res 11:3466–3481

Piepenburg D, Archambault P, Ambrose WG Jr (2011) Towards a pan-Arctic inventory of the species diversity of the macro- and megabenthic fauna of the Arctic shelf seas. Mar Biodivers 41:51–70

Polyakov IV, Alexeev VA, Ashik IM et al (2011) Fate of early 2000s Arctic warm water pulse. Bull Am Meteorol Soc 92:561–566

Renaud PE, Morata N, Carroll ML et al (2008) Pelagic-benthic coupling in the western Barents Sea: processes and time scales. Deep Sea Res 2(55):2372–2380

Robison BH (1995) Light in the ocean’s midwaters. Sci Am 273:60–64

Ronowicz M, Kukli & Unwin Ltd, London

Sakshaug E (2004) Primary and secondary production in the Arctic Seas. In: Stein R, MacDonald R (eds) The organic carbon cycle in the Arctic Ocean. Springer, Berlin, pp 57–82

Schuchert P (2007) The European athecate hydroids and their medusae (Hydrozoa, Cnidaria): Filifera Part 2. Rev Suisse Zool 114:195–396

Sigsgaard EE, Nielsen IB, Bach SS et al (2016) Population characteristics of a large whale shark aggregation inferred from seawater environmental DNA. Nat Ecol Evol 1:0004. https://doi.org/10.1038/s41559-016-0004

Song X, Gravili C, Wang J et al (2016) A new deep-sea hydroid (Cnidaria: Hydrozoa) from the Bering Sea Basin reveals high genetic relevance to Arctic and adjacent shallow-water species. Pol Biol 39:461–471

Søreide J, Falk-Petersen S, Hegseth EN et al (2008) Seasonal feeding strategies of Calanus in the high-Arctic Svalbard region. Deep Sea Res Part 2 55:2225–2244

Søreide J, Leu E, BERGE J et al (2010) Timing of blooms, algal food quality and Calanus glacialis reproduction and growth in a changing Arctic. Glob Chang Biol 16:3154–3163

Thomson PF, Willerslev E (2015) Environmental DNA – an emerging tool in conservation for monitoring past and present biodiversity. Biol Conserv 183:4–18

Unstad KM, Tande KS (1991) Depth distribution of Calanus finmarchicus and C. glacialis in relation to environmental conditions in the Barents Sea. Polar Res 10:409–420

Vander A, Marquardt M, Meshram AR et al (2015) Key Arctic phototrophs are widespread in the polar night. Polar Biol 38:13–21

Wassmann P, Duarte CM, Agusti S et al (2011) Footprints of climate change in the Arctic marine ecosystem. Glob Chang Biol 17:1235–1249

Wei CK, Rowe GT, Escobar-Briones E et al (2010) Global patterns and predictions of seafloor biomass using random forests. PLoS One 5(12):e1000667. https://doi.org/10.1371/journal.pone.0010006

Whitfield JB, Seibel BA, Hare MB et al (2010) The biological oceanography of boreal and arctic coastal waters of the eastern Bering Sea. In: Stein R, MacDonald R (eds) The organic carbon cycle in the Arctic Ocean. Springer, Berlin, pp 393–408

Weydmann A, Przyłęcka A, Łużyński M et al (2017) Postglacial expansion of the Arctic keystone copepod Calanus glacialis. Mar Biodivers. https://doi.org/10.1007/s12526-017-0774-4

Weydmann A, Carstensen J, Goss Szczeklo I et al (2014) Shift towards the dominance of boreal species in the Arctic: inter-annual and spatial zooplankton variability in the West Spitsbergen current. Mar Ecol Prog Ser 501:41–52

Whitfield JB, Seibel BA, Hare MB et al (2010) The biological oceanography of boreal and arctic coastal waters of the eastern Bering Sea. In: Stein R, MacDonald R (eds) The organic carbon cycle in the Arctic Ocean. Springer, Berlin, pp 393–408

Weydmann A, Przyłęcka A, Łużyński M et al (2017) Postglacial expansion of the Arctic keystone copepod Calanus glacialis. Mar Biodivers. https://doi.org/10.1007/s12526-017-0774-4

Wojcizalus-Jakubas K, Jakubas D, Stempieniewicz L (2013) Alcyon – sztandarowy gatunek Arktiki. Kosmos 62:401–407

Wooley JC, Godzik A, Friedberg I (2010) A primer on metagenomics. PLoS One 6(2):e1000667

Zenkevitch L (1963) Biology of the seas of the U.S.S.R. George Allen & Unwin Ltd, London

Open Access This chapter is licensed under the terms of the Creative Commons Attribution 4.0 International License (http://creativecommons.org/licenses/by/4.0/), which permits use, sharing, adaptation, distribution and reproduction in any medium or format, as long as you give appropriate credit to the original author(s) and the source, provide a link to the Creative Commons license and indicate if changes were made.

The images or other third party material in this chapter are included in the chapter’s Creative Commons license, unless indicated otherwise in a credit line to the material. If material is not included in the chapter’s Creative Commons license and your intended use is not permitted by statutory regulation or exceeds the permitted use, you will need to obtain permission directly from the copyright holder.