Abstract

In recent decades, the European Arctic has experienced warming at a rate much faster than the rest of the globe, a phenomenon known as polar (or Arctic) amplification, driven largely by the loss of sea ice and the resulting reduction in surface albedo. According to IPCC reports from 2021 and 2022, this progressive degradation of the cryosphere drives profound structural and functional changes in ecosystems. Both rising air temperatures and the intensified influx of relatively warm, saline Atlantic waters (a process known as "Atlantification") shape Arctic marine ecosystems by modifying water mass transport, mixing processes, and the formation of frontal zones. This, in turn, leads to local, regional, and large-scale changes across open ocean waters, shelf areas, and fjords. Furthermore, the significant loss of sea ice and the shortening of its seasonal duration directly affect primary production and water-column stratification. These changes disrupt the synchronization between biotic and abiotic ecosystem components, affecting primary production and pelagic-benthic coupling, and, later, the structure of entire trophic food webs.

This study focuses on meroplankton, which consists mainly of the larvae of benthic marine invertebrates. Meroplankton represents a temporary component of the zooplankton community, inhabiting the water column exclusively during their early life cycle. The duration of a this pelagic phase ranges from a few hours to several months. During this time, larvae encounter a range of adverse environmental conditions, such as physico-chemical fluctuations, variable water currents, predatory pressure, and changes in food availability, which strongly determine their survival, proper development, settlement success on the seabed, and ability to colonize new areas.

Meroplankton plays a key role in the marine environment by pelagic and benthic ecosystems (a process known as pelagic-benthic coupling). It serves as a crucial component of the food web, acting as as prey for predatory zooplankton and juvenile fish – and actively contributes to carbon and organic matter cycling through phytoplankton consuming and participating in the microbial loop. Due to their short life cycles and high sensitivity to environmental shifts (including variations in temperature, salinity, or primary production dynamics), larval survival and supply directly shape the recruitment success and future structure of adult benthic populations. Consequently, meroplankton functions as a sensitive indicator for detecting both sudden disturbances and long-term ecosystem shifts, providing valuable insights into Arctic marine trajectories amid ongoing global warming.

However, to fully assess the potential of using meroplankton as an indicator of changes in Arctic ecosystems, it is necessary to revisit the fundamentals of their identification and of their diversity assessment. So far, identification methods based on traditional microscopic analysis have largely been limited to categorization at higher taxonomic levels (classes, orders, and, less frequently, families). Many zooplankton studies treat meroplankton as a single aggregate or focus only on the most abundant groups (e.g., Bivalvia veligers, or Echinodermata and Cirripedia larvae), while grouping other less abundant taxa with rare holoplankton in an "other" category. Such an approach results in the loss of key information regarding taxonomic composition and, consequently, the potential environmental impact on meroplankton or its role in carbon cycling. These limitations can be overcome by developing molecular methods such as DNA barcoding (analysis of individual specimens) and DNA metabarcoding (analysis of entire communities), which enable the determination of the true taxonomic composition of meroplankton. Nevertheless, each of these methods has its limitations: the traditional morphological approach delivers precise data on environmental abundance, population structure, and developmental stages (e.g., nauplius, cypris, veliger, zoea, megalopa) but lacks taxonomic resolution. On the other hand, molecular methods provide detailed taxonomic information, often to the species level, but do not allow for identification of developmental stages or estimation of exact individual abundance.

Therefore, the aim of this doctoral dissertation was to assess the variability, spatial distribution, and community structure of meroplankton in the European Arctic. The study targeted a key marine gradient, spanning the West Spitsbergen Current (WSC) and Kongsfjorden (Svalbard). Through a dual approach combining classical morphological identification and DNA metabarcoding, the work evaluates how integrating methodological frameworks improves analytical resolution and inference The study comprises four main research chapters in which the complementary use of different methodological tools was demonstrated, enabling more precise hypothesis verification and inference, as well as the full utilization of meroplankton as an indicator of environmental changes.

In **Chapter II**, an original atlas of pelagic larvae, complete with photographic documentation, was developed to serve as a reference for the consistent identification of material in **Chapters IV** and **V**. Serving as the primary methodological basis of the entire thesis, this atlas guarantees taxonomic continuity across all analytical steps in which morphological examination provides the common baseline.

To gain insight into the general structure of meroplankton and its spatial and temporal changes in the European Arctic, in **Chapter III** a large-scale, multi-year analysis of

meroplankton communities in the area influenced by the West Spitsbergen Current was conducted. This current transports relatively warm, saline Atlantic waters, driving the process of "Atlantification", which can carry boreal larvae to high latitudes. Using a 16-year time series (2001-2016), the spatial and temporal variability of meroplankton assemblages within the pelagic layer (mostly 200-0 m) was investigated. By categorizing sampling stations into shelf, main Atlantic water stream (core), and open water (offshore) zones, it was demonstrated that the structure of meroplankton communities in the West Spitsbergen Current region was shaped primarily by the properties of the inflowing Atlantic waters and the spatial zonation extending from the shelf toward the open ocean, rather than by a latitudinal gradient from south to north. The transition zone between the shelf and open waters constituted a more significant ecological barrier than geographic distance alone, whereas the main flow of the West Spitsbergen Current acted as a transit zone facilitating larval dispersal. It is worth noting that, in general, thermal phases (warm vs cold years) did not influence meroplankton variability. However, the meroplankton showed a strong response to specific hydrographic extremes. Cooler years (e.g., 2010) favoured higher taxonomic diversity and abundance peaks for certain groups (e.g., Cirripedia cyprids), whereas warm years (e.g., 2006) showed a significant decline in taxonomic richness over the 16-year study period. These patterns indicated that progressive warming led to a reduction in the number of taxa within the larval pool, as higher temperatures and the influx of Atlantic waters favoured only a few dominant groups, with Bivalvia veligers, for instance, accounting for up to 70% of the community in open waters and the main current during warm years, therefore displacing more diverse meroplankton assemblages. The results suggested that meroplankton can serve as a sensitive early-warning indicator of ecosystem changes, responding with a decline in diversity much more rapidly than long-lived adult benthic populations. Consequently, further warming may weaken pelagic-benthic coupling by shifting larval assemblages toward thermally tolerant, less diverse communities, thereby altering energy transfer between the pelagial and the benthos.

In the subsequent part of the study (**Chapter IV**), the influence of a selected environmental variable on the formation of meroplankton communities within the water column was investigated, assessing the role of a halocline as a physical environmental barrier to larval migration. A significant outcome of this work was the examination of halocline's impact on the vertical distribution of meroplankton in relation to environmental variables in the European Arctic (using the Kongsfjorden Transect as a study area). The hypothesis that a strong vertical salinity gradient (halocline) acts as a physical barrier shaping benthic larval communities was confirmed, as evidenced by significant differences in taxonomic composition and assemblage

structure above and below this layer. Specific taxa and larval morphotypes exhibited preferences for particular water layers, likely driven by differences in their salinity tolerances and responses to mixing dynamics. In the fjord environment, the presence of a halocline restricted vertical migration, promoting the retention of some larvae within the fjord. Conversely, on the shelf, where stratification was weaker and conditions were more dynamic, larval dispersal and exchange with adjacent waters were more evident. Furthermore, differences in the dominance of major groups were observed along the transect: the warmer, less dynamic conditions of the fjord favoured greater diversity among Polychaeta larvae (which preferred stable, deeper waters below the halocline), whereas the more dynamic conditions on the West Spitsbergen shelf promoted the dominance of Echinodermata larvae (concentrated above the halocline). The observed differences in the vertical distribution of major taxonomic groups above and below the halocline indicated that salinity-driven stratification (explaining around 30% of total meroplankton variation) was an important factor shaping meroplankton communities. Certain taxa occurred within specific layers, indicating differing tolerances or adaptive strategies to salinity and turbulence. In addition to Echinodermata larvae, Cirripedia cyprids were physically retained above the halocline. In contrast, Bivalvia veligers occurred throughout the entire water column, though they were also retained in high concentrations at the glacier-influenced inner-fjord station. Additionally, spatial sorting was noticed across the gradient, as Bryozoa occurred exclusively near the glacier, Gastropoda and Decapoda were found strictly inside the fjord, and Ascidiacea were present on the open shelf, indicating clear differences in ecological tolerances and retention strategies regarding salinity gradients and turbulence. Summing up, in fjordic systems, the presence of a halocline can lead to the retention of certain larvae within the fjord, whereas the more dynamic shelf environment, characterized by weaker stratification, enhances their dispersal and exchange with adjacent water masses.

In **Chapter V**, a multidisciplinary approach was used to characterize the structure of meroplankton in the Northeast Atlantic shelf region. The complementarity of the traditional morphological approach and modern molecular methods (DNA metabarcoding using two markers: V1-V2 region of 18S rRNA gene (18S) and cytochrome c oxidase subunit I gene fragment (*cox1*)) was used in assessing meroplankton structure and diversity on the Northeast Atlantic shelf. It was shown that traditional microscopic analysis is crucial for identifying larval developmental stages (e.g., zoea, megalopa, cypris, veliger) and analyzing population age structure, whereas DNA metabarcoding reveals hidden taxonomic diversity (enabling identification down to the genus and/or species levels), a capability particularly crucial for Bivalvia and Gastropoda larvae that are difficult to identify morphologically. Furthermore, the

application of two different genetic markers highlighted their distinct yet complementary analytical properties: the nuclear V1-V2 18S rRNA region effectively reflected large-scale shifts in the meroplankton community structure associated with different water masses, while the mitochondrial *cox1* marker provided higher taxonomic resolution and was more sensitive to micro-scale, station-specific shifts in larval composition. Combining these methods enabled detailed mapping of meroplankton diversity. It revealed that the Norwegian Coast (NC) and Barents Sea (BS) regions are the primary "hotspots" of taxonomic richness on the Northeast Atlantic shelf, although diversity drops markedly in the Atlantic Water (AW) zone and on the West Spitsbergen shelf (WS). Water salinity and temperature were the key environmental factors shaping these spatial patterns.

In summary, the comprehensive analysis of the spatial and temporal variability of the Arctic meroplankton diversity conducted in this study confirms that benthic invertebrate larvae are highly sensitive indicators of changes occurring in the marine environment. The demonstrated complementarity of classical morphological methods and modern molecular tools constitutes a highly recommended methodological approach. In addition, an atlas of larvae, accompanied by comprehensive photographic documentation, was developed as a reference for consistent identification throughout this thesis and as a lasting taxonomic resource for future studies. The use of DNA metabarcoding reveals previously hidden taxonomic diversity within the meroplankton, which, when combined with traditional developmental-stage analysis, elevates taxonomic resolution achieved. This approach not only facilitates a better understanding of pelagic-benthic coupling but, above all, establishes a solid foundation for formulating more precise research hypotheses and ensuring more accurate interpretation and inference in future meroplankton studies. Furthermore, it may enable the creation of a complementary standard for meroplankton analysis to support the long-term monitoring of changes in Arctic and sub-Arctic ecosystems driven by the observed global warming.