
Understanding and tackling jellification: from polyp to bloom

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This thesis is about the phenomenon of jellyfish blooms, which are sudden and massive increases in jellyfish abundance that can have negative impacts on various aspects of human society and the marine ecosystem. Jellyfish can potentially have a significant impact on economy, tourism and environment, especially when they form blooms. They can reduce the fishery production and the fish stocks by competing with or preying on fish, affecting the livelihoods of fishermen and the food security of many people. They can also sting humans and other animals, causing pain, irritation, allergic reactions or even death in some cases, which can deter people from swimming or visiting beaches where jellyfish are present. Moreover, they can clog the cooling systems of power plants, desalination plants, and other industrial facilities that use seawater, causing damage, disruption, or shutdown of the operations, resulting in economic losses and environmental risks. Furthermore, they can alter the biogeochemical cycles of the ocean, such as the carbon, nitrogen, and phosphorus cycles, affecting the primary production, the oxygen levels, and the nutrient availability of the water, influencing the marine biodiversity and ecosystem functioning. Finally, they can transport non-indigenous species (NIS) or pathogens across different regions, as they can act as hosts, vectors, or carriers, introducing new diseases, parasites, or invasive species to the native communities, threatening their health and diversity.

The thesis focuses on the occurrence and causes of jellyfish blooms in the Belgian Part of the North Sea (BPNS), which is a region that has been reported to experience frequent jellyfish blooms in the last decades. The aim was to answer two main research questions: (1) Can jellyfish blooms in the BPNS be predicted on the basis of environmental DNA (eDNA) metabarcoding? and (2) What are the possible factors that contribute to jellyfish blooms in the BPNS?

To answer the first question, the thesis uses both traditional morphology and eDNA metabarcoding to identify and quantify the gelatinous zooplankton in the BPNS over the course of six months. Traditional morphology involves counting and measuring the jellyfish specimens collected by nets, while eDNA metabarcoding involves extracting and sequencing the DNA fragments from the seawater samples and comparing them with a reference database. In this research project, we applied nanopore sequencing, which is a novel and portable technique that can generate long DNA reads in real time. We targeted a 500 – 1000 bp fragment of the 18S rDNA gene, which is a universal marker for eukaryotes. We focused on two phyla of gelatinous zooplankton: Cnidaria and Ctenophora, which include the most common and problematic jellyfish and ctenophore species.

The thesis compared the spatial and temporal patterns of jellyfish abundance obtained by both methods and evaluated the advantages and limitations of each method. We also identified the species and life stages of the gelatinous zooplankton detected by eDNA metabarcoding and discussed the implications for jellyfish monitoring and management. eDNA metabarcoding detected seven different species of Cnidaria and Ctenophora in the BPNS, but it could not predict jellyfish blooms, as there was no significant correlation between the eDNA reads and the morphological counts. We also found that eDNA metabarcoding can detect the presence of jellyfish larvae and polyps, which are the asexual and sessile stages of the jellyfish life cycle, but it could not distinguish them from the medusae, which are the sexual and free-swimming stages. We concluded that eDNA metabarcoding is a useful tool for jellyfish detection, but it needs to be complemented by other methods for jellyfish quantification and identification.

To answer the second question, the thesis reviewed the literature and discussed the possible factors that contribute to jellyfish blooms in the BPNS and other regions of the world. We considered both abiotic and biotic factors, such as water temperature, salinity, pH, turbidity, nutrient availability, predation, competition, symbiosis, and parasitism. The role of human activities, such as overfishing, eutrophication, aquaculture, global warming, and the introduction of non-indigenous species (NIS) was also considered, as these factors can alter the benthopelagic food web and create favorable conditions for jellyfish blooms. Our findings suggest that jellyfish blooms are the result of complex and multifactorial interactions between environmental and anthropogenic drivers, and that they may vary depending on the region, the season, and the species. It is concluded that jellyfish blooms are likely to become more frequent and severe in the future due to the ongoing changes in the marine ecosystem and the human society.

The thesis ends with a discussion of the implications and recommendations for the management and mitigation of jellyfish blooms. We argue that jellyfish blooms are not only a nuisance, but also a symptom of a larger problem: the degradation and imbalance of the marine ecosystem. To reduce the frequency and intensity of jellyfish blooms, changes have to be made that act directly on the causes of these blooms, such as reducing nutrient pollution, overfishing, transport of NIS, the amount of artificial substrate and global warming. It is acknowledged that these changes are not easy to implement, as they require a significant economic cost in the short-medium term and a global cooperation in the long term. The thesis also suggests that besides preventing jellyfish blooms, it is also important to adapt to them and to find ways to use them as a resource, such as for food, fertilizer, medicine, or biofuel. It is concluded that jellyfish blooms are a challenge and an opportunity for the human society and the marine ecosystem, and that they require a holistic and interdisciplinary approach to understand and manage them.