Preserving the Baltic Sea

The Baltic Sea is environmentally and economically important, but it is under threat as a result of human activities. Dr Birgitta Bergman is leading a research project that aims to help restore these waters by discovering more about the microbial populations that live within them.

Could you begin by explaining your research objectives?

Triggered by the discovery in recent decades of the enormous importance of bacteria and viruses in oceans, we realised that our knowledge of the diversity and role of microbes in one of the largest seas in Europe, the Baltic Sea, is still rudimentary. We hypothesised that if we are to preserve and maintain the full function of these waters in the future, a holistic view covering all organismal segments is necessary.

The objective of our research, therefore, is to understand the role of microbes in this unique brackish water ecosystem that is threatened by anthropogenic activities causing eutrophication and pollution. The life of the Baltic Sea is dependent on its largely overlooked organismal segment. The fundamental knowledge generated in our programme is critical for all future risk assessments and management action plans, and will help predict future scenarios in a changing climate, hence promoting the welfare of the ecosystem. No microbes, no life.

Your research group received a three-year grant from the Baltic Sea 2020 Foundation for a research programme on metagenomic analyses of all microbes in the Baltic Sea. What is the aim of this programme?

In recent years we have widened our research focus beyond cyanobacteria as we realised that, to get a comprehensive view of how microbial life is orchestrated and regulated in the Baltic Sea, we needed to visualise and understand all microbes, such as heterotrophic bacteria and viruses – including what they are doing and how they interact with cyanobacteria. To achieve this goal we needed the most up-to-date, potent and efficient ‘-omics’ technologies. The objective of the funded Microbial Metagenomics in the Baltic Sea (MiMeBS) programme is therefore to understand the identity and role of microbes in this brackish water body.

This study employs metagenomic analyses. Why is this approach so valuable to the study of microbial populations, and are you using any other techniques?

The metagenomic approach advances our understanding of microbial biodiversity, distribution and potential functions in a way that was inconceivable just a decade ago. Besides metagenomic analyses we also examine the metatranscriptome of the same microbes, which gives the actual function of a given microbe at a particular place and time. Complementary techniques are also used to achieve complete genomes of key microbial players in the Baltic Sea, as is imaging to verify identities, interactions and activities.
and so on. Such multi-OMIC/genomic data will enable us to promote Baltic Sea ecosystem health evaluations and risk assessments.

A major challenge in microbiology is linking genetic diversity to function. How do you hope to overcome this using a holistic approach?

First and foremost, our research relies on exploring the enormous microbial metagenomic dataset generated in MiMeBS in order to identify the vast array of microbes present in time (over seasons) and space (along a transect), as well as their genetic make-up predicting functions. We now also examine microbial functions by sequencing and analysing their metatranscriptomes.

To what extent are your efforts collaborative in nature?

Our research efforts are highly collaborative. Besides my biology team at Stockholm University, Sweden, researchers at the Craig Venter Institute in La Jolla, USA, are critical to the success of the programme. This institute performs the crucial sequencing and the development of bioinformatics tools for our analyses. In addition, parts of the sequencing activities are performed at the Science for Life Laboratory in Stockholm, and researchers with complementary skills at other Swedish universities are also engaged.

Have you made any significant findings you wish to discuss?

Most importantly, our data clearly show that there is a rich microbial biodiversity in the Baltic Sea. These microbes range from eukaryotic phytoplankton to well-known bacteria such as SAR11, from an unexpected large variety of cyanobacteria to large numbers of viruses and cyanophages; and this microbiome encompasses a mix of benign and pathogenic microbes. Furthermore, it is apparent that salinity, followed by nutrient availability, are the environmental factors that primarily govern the distribution of these microorganisms.

Interestingly, we have also identified distinct changes in the core metabolic pathways of bacteria, depending on their localisation along the salinity gradient. These profound differences in their genetic backgrounds (related to processes such as respiration) may explain why freshwater and marine microbes rarely mix in nature – answering a long-standing open question. Through our approach we have managed to identify the existence of large populations of uniquely adapted unicellular pico-cyanobacteria with novel pigment gene organisations, which dominate under non-bloom conditions.

To better understand the crucial role of microbial populations in the Baltic Sea, the MiMeBS project team, based at Stockholm University, Sweden, is using environmental genome shotgun sequencing to an extent that has never before been attempted in this water body.

THE BALTIC SEA is one of the largest brackish water bodies on Earth and has provided a multitude of valuable services to humans for 8,000 years. Today, 90 million people in nine surrounding countries live close to its shores or depend on these services. This semi-enclosed water reservoir has a pronounced and unusual salinity gradient that has led to a unique composition and organisation of the organisms living within.

The Baltic Sea, however, is under threat from anthropogenic activities such as overfishing, population growth and pollution. Negative developments – the increasing occurrence of toxic cyanobacterial summer blooms and severe reductions in fish stocks – require urgent action. So far, there has been limited progress in restoring the waters of the Baltic Sea, and the prognosis could be dire if its health and vitality continue to degenerate.

In recent years, genomic techniques have clearly shown that microbial communities play a critical role in the dynamics and biogeochemical cycles of aquatic ecosystems. Therefore, in order to effectively manage this important water body for future generations, the countless bacteria and viruses that drive, form and dictate the life within must be identified, and their functions understood and preserved.

SEEING THE LITTLE

Now, the collaborative Microbial Metagenomics in the Baltic Sea (MiMeBS) programme – involving researchers at Stockholm University in Sweden and collaborators from the J Craig Venter Institute in the US – is aiming to uncover, for the first time, a holistic view of the ‘hidden’ diversity and metabolic capacities of microorganisms in the region. Led by Dr Birgitta Bergman, the principle of MiMeBS is that “to see the little is to understand the whole”.

All life in the Baltic Sea ultimately depends on microorganisms as primary producers and generators of nutrient resources. “If we ignore the potentially most vital life-supporting organisms in the ecosystem simply because we cannot see or cultivate them, we cannot understand how to save and support the wellbeing of organisms of commercial value such as shellfish and fish,” explains Bergman.

UNPRECEDEDNT APPROACH

In partnership with J Craig Venter Institute and the newly established, high-throughput facility at the Stockholm Science for Life Laboratory, Bergman’s team is using metagenomic and organism-oriented approaches to genetically identify microbes, ranging from microeukaryotes to bacteria, and from cyanobacteria to viruses. The project is also characterising microbial diversity and following, at the metagenomic and metatranscriptomic levels, the flow of energy and macronutrients like carbon, nitrogen, phosphorous and iron.

The MiMeBS approach allows the unprecedented detection of enormous numbers of microbes, revealing information about their identity, potential functions and thereby their role in the Baltic Sea. This is in sharp contrast to most previous studies which relied on analysis of just one or a few microbes at a time using light microscopy and cultivation-dependent techniques. “This approach also opens up the potential for the efficient identification of environmental factors that dictate the existence of microbial populations and their activities,”

LEFT: ON BOARD SORCERER II: DURING THE MiMeBS SAMPLING EXPEDITION IN THE BALTIC SEA
LEFT TOP: FILAMENTS OF THE CYANOBACTERIUM DOLICOSPERMUM SP.

PART OF A CYANOBACTERIAL ‘BLOOM’ IN THE BALTIC SEA COMPOSED OF DIFFERENT CYANOBACTERIA SUCH AS NODULANA (CURLED COLONIES) AND OF APHANIZEMONI (BUNDLES OF STRAIGHT FILAMENTS) INTERMIXED WITH SMALL BACTERIA.
INTELLIGENCE

MiMeBS
MICROBIAL METAGENOMICS IN THE BALTIC SEA

OBJECTIVES

To expose the role of the Baltic Sea microorganisms to obtain information on their influence on the food-webs depending on microbes – from zooplankton to finfish and shellfish – and thereby on the human population of surrounding countries. Additionally, to increase understanding of the yearly recurring massive surface blooms of nitrogen-fixing cyanobacteria.

TEAM

Dr John Larsson, Dr Karolina Ininbergs, Dr Martin Ekman and Dr Johan Eriksson

Narín Celepli and Lotta Berntzon (PhD students)

KEY PARTNERS

Researchers at J Craig Venter Institute, La Jolla, California, USA

FUNDING

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BIRGITTA BERGMAN is Full Professor in Plant Physiology at Stockholm University and is associated with the Science for Life Laboratory in Stockholm. She is a member of the Royal Swedish Academy of Sciences. Her research focus is on interactive and evolutionary aspects of symbiotic and free-living cyanobacteria. Currently her team is using ‘-omics’ approaches to explore the biodiversity and role of aquatic microbial populations (virus to plankton) in marine and brackish waters.

states Bergman. “Such data are also predictive in nature and therefore extremely valuable, considering the rapid changes that may be imposed on our aquatic environments on a short- and long-term basis,” she adds.

MULTITUDE OF ORGANISMS

The southern Baltic Sea is connected to the North Sea via the Danish sounds, which allows restricted salt-water inflow, creating a salinity of 15 practical salinity units (psu) in this area. Large river outflows mean that salinity in the north is close to zero. This 1800 km long, north to south salinity gradient is rarely found elsewhere in nature. So far, the MiMeBS team has identified a vast abundance and diversity of microbes, and demonstrated that this is dictated by the salinity gradient. “From these data it was possible, for the first time, to explain why the microbial community diversity varies to such an extent between fresh and marine waters,” Bergman explains.

The Swedish researchers have also observed that, unlike higher organisms such as macroalgae and fish, Baltic Sea microorganisms can adapt throughout this highly unusual gradient of salinity and macronutrients. For instance, they have discovered that populations of unicellular cyanobacteria are much more prominent and have a novel type of genetic pigment organisation, not seen in any other waters, that allows them to capture light.

Other aspects of the Baltic Sea microbiome being explored by the MiMeBS project include the identification of microbes which pose a threat to human health, such as bacterial and viral pathogens. The team is also searching for genes involved in microbial vitamin production, as vitamin deficiency in the Baltic Sea is thought to be the cause of diseases and reduced fish stocks.

CYANOBACTERIAL BLOOMS

In a second phase of MiMeBS, the project team will focus on the annual surface blooms of nitrogen-fixing cyanobacteria. These are widespread and common phenomena across the globe in both the ocean that are not influenced by human activities. These blooms can benefit aquatic ecosystems through the delivery of energy and nutrients, however, in the Baltic Sea ongoing anthropogenic eutrophication has increased the intensity of these often toxin-producing blooms.

In this context, the team showed that one recently discovered cyanobacterial toxin BMAA, accumulates in Baltic sea food webs and the researchers are currently elucidating if and to what extent this toxin may cause neurodegenerative diseases in humans.

Little is understood about what factors initiate the mass occurrence of cyanobacterial blooms at water surfaces; why they produce a number of highly toxic secondary metabolites; and what factors cause them to collapse. Bergman is following their cycle in the Baltic Sea over seasons; identifying and cataloguing all cyanobacteria and their associated microbial partners – as well as their gene expression – in order to identify the cellular processes in which they are involved. By using various ‘-omic’ based technologies and other analyses, the team hopes to uncover knowledge which may provide instruments or markers to better predict and master ‘unwanted’ blooms.

PRESERVING AND MANAGING

Findings from the MiMeBS project will answer many questions about key players in the Baltic Sea ecosystem, providing both a crucial knowledge base as well as the information required to manage this body of water in a scientifically sound manner in the future: “As long as this knowledge base is missing, we will run into problems trying to understand the causes and consequences of unwanted phenomena in Baltic Sea food-webs, such as fish death,” Bergman reflects. Her team’s results will directly contribute to better preserving and managing. Their data will be used to predict the effects of eutrophication, pollution and future climate change, and will be fed into environmental models that are used as tools for management programmes in this unique ecosystem.