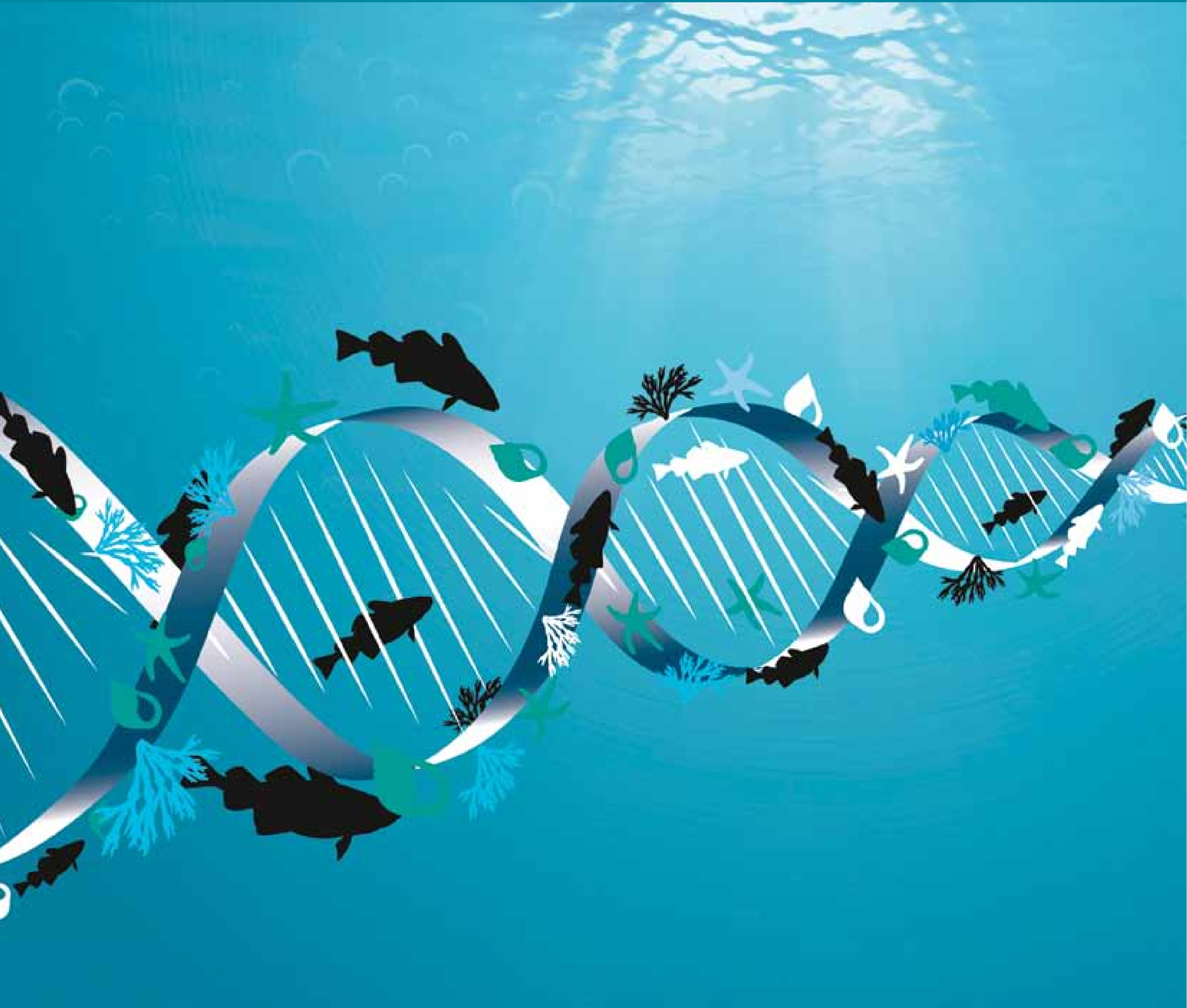
CeMEB in progress

Highlights in midterm from
the Linnaeus Centre for Marine Evolutionary Biology



CeMEB

The Linnaeus Centre for Marine Evolutionary Biology

Topics for research

What is the potential for evolutionary change in key marine species?

How far have organisms evolved following recent large-scale environmental changes?

Which mechanisms at molecular and organismal level drive rapid adaptation?

What is the role of plasticity in the evolution of new adaptations?

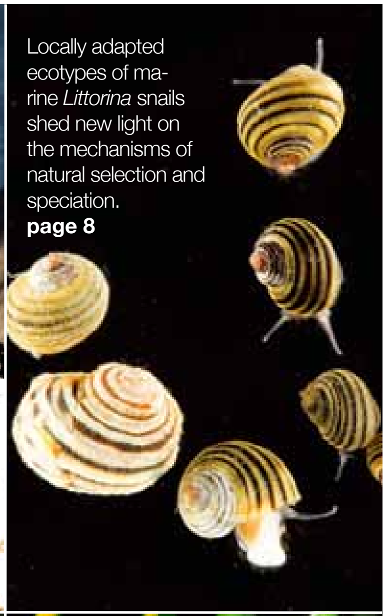
How and when do new species evolve?

Global scale processes are causing environmental change faster than ever before. To ensure biodiversity and natural resources for future generations, the scientific community is expected to increase our knowledge basis to help policy makers develop management strategies.

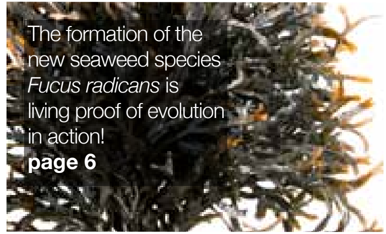
The Linnaeus Centre for Marine Evolutionary Biology, CeMEB, is well suited to rise to the challenge. We do this by the contribution to new knowledge of fundamental importance; by providing understanding about the mechanisms and rates of adaptation of organisms under changing conditions.

CeMEB started in July 2008 when the project was selected for a ten-year Linnaeus grant awarded by the Swedish Research Councils. 2013 marks the half-way point. This publication presents CeMEB activities, including some of the many interesting results.

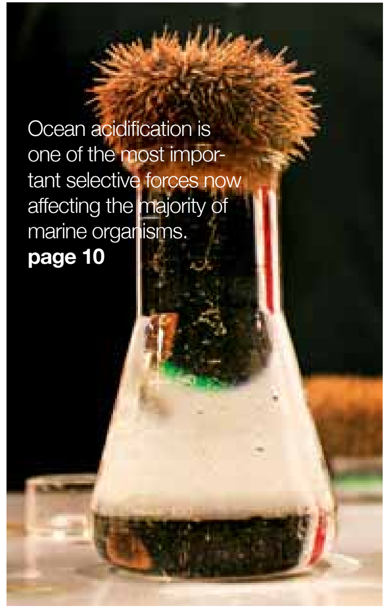
"In the light of the disappearing biodiversity it is important to understand what is going on at the other end – how populations adapt to new environments and how new species are formed."
page 4



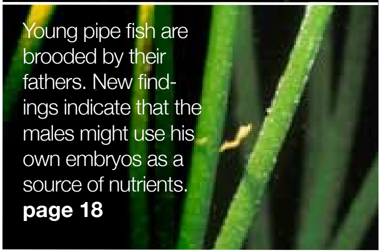
Locally adapted ecotypes of marine *Littorina* snails shed new light on the mechanisms of natural selection and speciation.
page 8



The formation of the new seaweed species *Fucus radicans* is living proof of evolution in action!
page 6



Ocean acidification is one of the most important selective forces now affecting the majority of marine organisms.
page 10



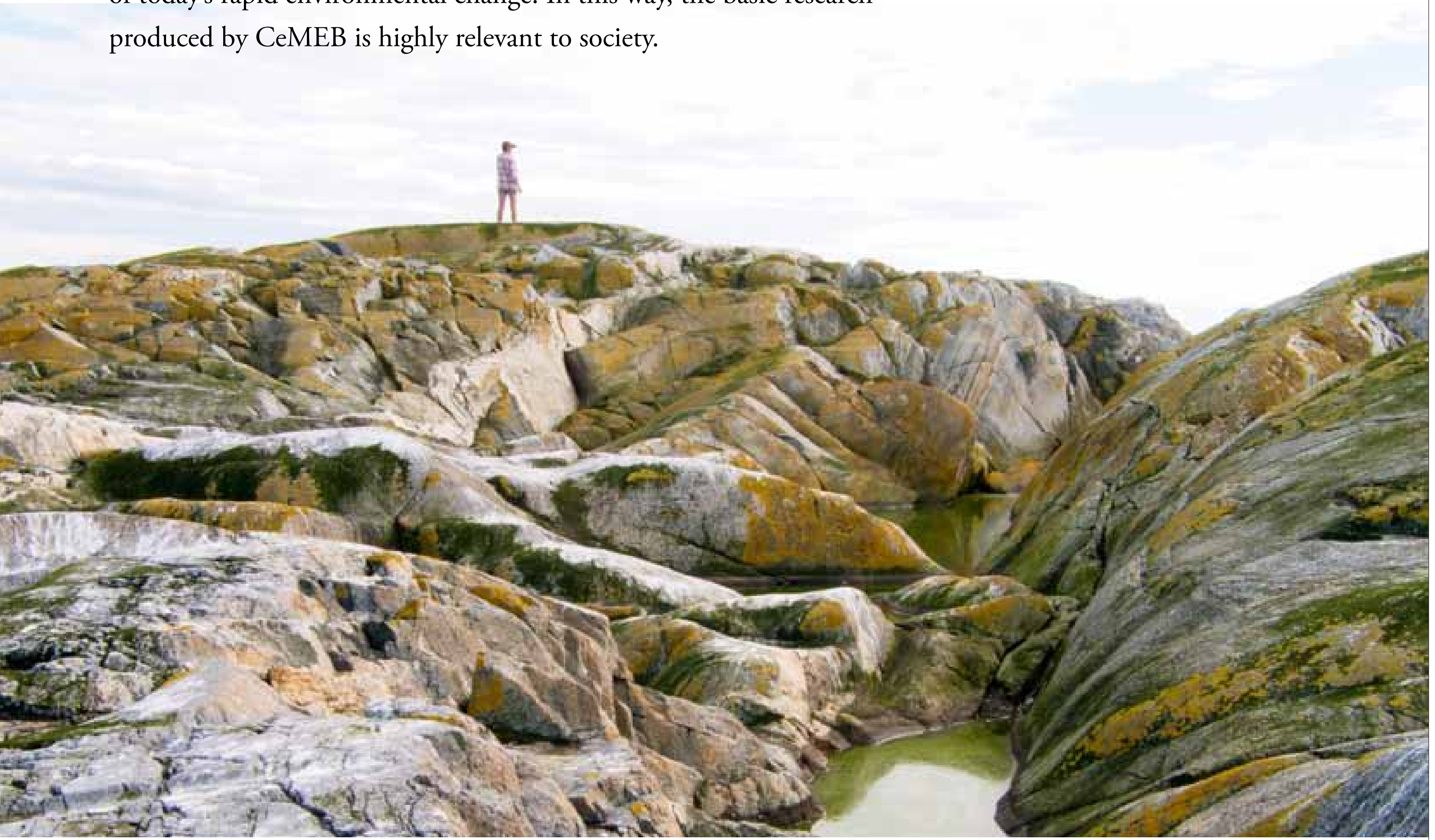
Young pipe fish are brooded by their fathers. New findings indicate that the males might use his own embryos as a source of nutrients.
page 18

In CeMEB, sharing a laugh is an important basis for first-class science.
page 24

Table of contents

Studying the past to picture the future

Evolution is the only known process to generate new biodiversity. Still, we know very little about its mechanisms. Understanding the ways of evolution will make us better prepared to face the consequences of today's rapid environmental change. In this way, the basic research produced by CeMEB is highly relevant to society.



Today we know that evolution is not only a historical process working on time-scales of several thousands of years. Evolution is going on right now – and much faster. We must realize that the formation of biodiversity is not only affected by natural changes, but also by human activites such as fishery and global warming.

This raises questions, CeMEB director Kerstin Johannesson explains: Are we managing fish and other natural resources in a sustainable way? And do we allow for biodiversity to adapt to future environmental conditions?

To understand the mechanisms of natural selection, local adaptation, plasticity and the formation of new species is of prime interest in CeMEB. The results are relevant not only to science but also to society as a whole, because it can help forecast the effects of human impact on biodiversity.

– New techniques for decoding DNA and finding the function of specific genes provide fantastic opportunities to study how organisms adapt to changing environments, says Kerstin Johannesson. In a few years from now we hope to be able to answer questions such as: What is crucial for the survival of key species when the enironment changes due to global change?

A great deal of diversity on the genetic level is essential for the adaptation of species to future environmental changes. But for most species, especially in the sea, we don´t know how much genetic diversity there is, and we don´t know how it is distributed.

> “Discussing evolutionary issues with colleagues with a completely different background broadens the perspective and gives new insights”

– Mapping genetic diversity and identifying population structure is a major task, Kerstin Johannesson explains. This is important information for management, so they can prioritize which populations to protect.

Another problem is that we don´t know which genes will be important in the future, and thus especially important to preserve. But sometimes we have a hint. For example, we most certainly know that the Baltic Sea will be less salty in the future. Therefore, genes for handling low salinities are probably crucial for the survival of marine species in that environment.

Half way through the project, CeMEB has produced many interesting results and many more are in the pipeline. You can read about some of them on the following pages.

One success-factor for the project is the interdisciplinary mix of scientists. At the CeMEB Assembly twice a year everybody gets together.

– Discussing evolutionary issues with colleagues with a completely different background broadens the perspective and gives new insights, Kerstin Johannesson explains. Mathematicians and physicists in the project add skills we evolutionary biologists are lacking, for example, to design models to which we can add field data and test our hypotheses.

A balanced mix of male and female participants might be another strength of the project:

– My experience is that a gender neutral environment performs better, with a more open atmosphere, says Kerstin Johannesson.

Looking forward Kerstin Johannesson is excited about what will come out of the genomes that CeMEB presently is disentangling. The DNA of eight marine species are sequenced to describe their complete genomes; the most important genes are identified and their functions traced.

– The genomes provide tools to understand the significance of genetic differences we find in nature, and to identify which genes are important for different adaptations, Kerstin Johannesson explains.

CeMEB is funded for ten years by a Linnaeus grant. Long-term funding makes it possible to perform long-term experiments, lasting over several generations, and this is a great advantage in evolutionary research. Kerstin Johannesson also points out the unique research environment the Linnaeus Centres provide:

– The Centres are forums where scientists can let loose to concentrate on exciting research issues. Adminstrative matters like finances are dealt with in other settings. This is truly a sanctuary for research and great ideas!

Name: Kerstin Johannesson

Position: Professor in marine ecology at Department of Biological and Environmental Sciences – Tjärnö, University of Gothenburg.

Age: 57

Residence: Tjärnö, Strömstad.

Family: Husband and two grown-up children, two cats.

Other scientific responsibilities: Coordinates Gothenburg Centre for Marine Research, member of The Royal Swedish Academy of Sciences and Miljöforskningsberedningen for the Swedish Government.

Most memorable research moment: When we discoverded the new alga species *Fucus radicans* which is endemic to the Baltic Sea.

Unknown talent: I am quite proud to say that I built the glass-enclosed veranda of my house.

The evolution of new biodiversity

Just recently, the sea was considered an open system with very limited possibilities for populations to develop genetic differences and eventually evolve into new biodiversity. Today, we know this is not true. CeMEB aims to understand the fundamental components of evolution in the sea. We explore the topic from several perspectives; tracking down the history of today's marine species from the DNA, and use models to predict the future.

In the northern Baltic Sea bladder wrack *Fucus vesiculosus* coexists with a smaller and morphologically distinct wrack, *F. radicans*. The two species might have separated only 400 years ago, according to Rick Pereyra.

The formation of a unique Baltic Sea species

A few years ago a new brown alga was discovered in the Baltic Sea. This alga, *Fucus radicans*, has not been found anywhere else in the world. Research in CeMEB has confirmed that the species was formed within the Baltic Sea, possibly only 400 years ago.

The common bladder wrack *Fucus vesiculosus*, is the most dominant and ecologically important perennial large brown alga in the Baltic Sea. Like many other marine species in the Baltic, it immigrated from the Atlantic about 4000 to 8000 years ago.

In the northern Baltic Sea, the bladder wrack coexists with the smaller wrack *Fucus radicans*. This is a new species for science, discovered only a few years ago. Now, the question is, did these wracks enter the Baltic as two separated species – or has *F. radicans* evolved more recently, inside the Baltic Sea?

To take a closer look into this Rick Pereyra and his colleagues sampled *F. radicans* and *F. vesiculosus* from localities inside and outside the Baltic (Norway, Lysekil, White Sea/Russia) and used DNA markers to compare the different populations.

– Our analyses clearly show that *F. radicans* is a separated species, Rick Pereyra says. Also, the results reveal a close relationship with the Baltic populations of *F. vesiculosus*, which support the hypothesis that *radicans* has evolved inside the Baltic.

Both species can reproduce asexually, which is an advantage since the low salinity of the Baltic Sea has a negative impact on the mobility of fucoid sperm. In *F. radicans* clonal reproduction is the main strategy, and probably this plays a significant role for the rapid speciation process, Rick Pereyra explains.

The two species probably split up as recently as 400 years ago, representing one of few examples in nature of extremely rapid species formation.

– This is really exciting, Rick Pereyra says. The rise of a new species is very rare to see in nature. When we have the genome sequenced in both species, we will sort out the mechanisms of this rapid speciation even more.

Isopods – marine colonisers of the Baltic

Among the marine species which managed to colonise the Baltic Sea despite the low salinity, are some isopods of the family *Idotea*. To find out more about their early history, PhD student Sonja Leidenberger analysed DNA-sequences from mitochondria (the cells' power system) in populations along a salinity gradient from Tvärminne in Finland to Bergen on the Norwegian west coast.

In accordance with previous studies of marine colonizers, she found that the genetic variation in the Baltic populations is lower compared to the Atlantic ones. This indicates that the Baltic populations have passed through a ”bottleneck”, where many individuals were wiped out and, with them, a lot of genetic variation was lost.

– If *Idotea* species in the Baltic Sea are already genetically constrained today with a low genetic diversity, says Sonja Leidenberger – how will they be able to manage the rapid climate changes we are facing within the next fifty years? And if they don´t, what does that mean for the already species-poor ecosystem Baltic Sea?

Originally marine wracks do better in low salinity

Bladder wrack *Fucus vesiculosus* successfully colonized the Baltic Sea less than six thousand years ago. According to a study performed by PhD student Daniel Johansson, after only 3 000 generations the immigrants have already evolved traits optimizing life in the new environment.

While bladder wrack from the west coast grew more slowly in the low Baltic salinity compared to full marine salinity in laboratory experiments, individuals from the Baltic Sea grew faster in low salinity.

– The fact that wracks from the Baltic Sea grow better in low salinity than in the marine salinity of its "original" environment, confirms that this is probably a result of local adaptation rather than a sign of individual tolerance, says Daniel Johansson. The Baltic Sea wrack has moved its "functional optimum" to the lower salinity.

Top: Sonja Leidenberger looking for isopods (below) among the seaweed.

Bottom: Daniel Johansson genotyping bladder wrack (above) in the DNA-lab.

Local adaptation and reproductive isolation in a marine snail

The rough periwinkle is a small marine snail, common on rocky shores in the North Atlantic. The snail exhibits an extreme variation in shell morphology as a consequence of local adaptation to varying habitats.

In Spain, Great Britain and in Sweden, the snail *Littorina saxatilis* is found in two morphologically divergent variants. One is big and has a thick shell, adapted to life on sheltered shores facing heavy predation from crabs. The other is smaller with a thin shell and a bigger foot, adapted to cling on to shores exposed to strong waves. These characteristics are to a large extent inherited and the variants represent two ecotypes, locally adapted to their environments through natural selection.

The ecotypes often live close to each other and thus regularly meet in contact zones. The strong local adaptation has also led to the evolution of a partial reproductive barrier. So perhaps they will eventually evolve into two separate species?

With help from Suzanne Sadedin from the University of Tennessee in the US, Marina Panova took a peek into the future using a mathematical model. The model is fed with data such as habitat characteristics, survival rates, number of offspring, etc., and comes up with different scenarios, very much like a computer game.

The model showed that evolution of ecotypes could be very fast, forming populations adapted to either crab predation or wave exposure in only 500 generations. But, and a bit surprisingly – this model didn´t strongly signal that the ecotypes will evolve into separate species.

– This is explained by the hybrids, snails living in the contact zones between the crab and wave environments, Marina Panova explains. They probably act as a bridge transporting genes from one ecotype to the other, keeping the two variants connected. Often, hybrids are not very successful and there is a selection for mechanisms preventing hybridization, but the *Littorina saxatilis* hybrids are well-adapted to the zone between the two habitats.

Nevertheless, the ecotypes have done it half-way through, and as such represent the initial steps of a speciation event. A follow-up study involving colleagues from Spain and the UK show that partial reproductive barriers between ecotypes can evolve despite ongoing exchange of genes. Furthermore, the study demonstrates that partial reproductive barriers have evolved repeatedly – and independently – in as widespread places as the coasts of Galicia and Bohuslän.

– This makes the ecotypes particularly tractable as a model system to explore further, not least when we soon will have the whole snail genome sequenced, says Marina Panova.

The rough periwinkle is common on rocky shores of the Atlantic. Marina Panova studies speciation processes using the periwinkle as a model organism.

Rapidly spreading genes in slowly moving snails

The marine snail *Littorina fabalis* varies in size, with a larger ecotype snail dominant on wave exposed shores and a smaller ecotype on more sheltered shores. Previous studies show that the two ecotypes produce different types of arginine kinase (AK), an enzyme involved in the energy production in muscle tissue and possibly under different selection pressure depending on the degree of wave exposure. PhD student Mårten Duvetorp identified the AK-gene in the snails´ chromosomes to look for genetic differences.

As expected, the DNA-sequence differed between the two ecotypes. Snails from sheltered shores carried nine mutations with effects on the protein level, which were not found in the "exposed" ecotype.

– This is an exceptionally large difference, Mårten Duvetorp says. Also, every single snail from sheltered shores carried these mutations, regardless of their geographical origin, such as Sweden and Wales. We expected to find at least some variation due to the distance between countries but found none.

A likely explanation is that individuals carrying the highly mutated variant of AK gene have been extremely successful and thus, through natural selection, have spread very recently across a large geographic area.

A new way to calculate asymmetrical gene flow

If you want to find out how populations are related it is essential to understand how individuals migrate between the different populations. But migration patterns are complex with individuals seldom travelling equally in all directions. The methods available to calculate such "asymmetric migration" are very complicated, PhD student Lisa Sundqvist explains. In collaboration with some colleagues she has developed an alternative approach:

– It´s very simple, and based on traditional methods for measuring genetic differentiation. But we have added a component, an imaginary population of migrants. We compare the genes of the populations of interest with these migrants, and from this we can calculate how the populations contribute to each other.

Top: Snails of *Littorina fabalis* live among brown algae on shores all over Europe.

Below: Modelled protein structure of AK-enzyme from snails on sheltered shores. Parts with blue colour are mutation sites.

Bottom: Using a new method for calculating asymmetric migration, the genetic differentiation found in marine diatoms on the Swedish westcoast was matched to local oceanography.

Human impact and evolution

Today, human activities impose new types of selection pressure on populations and species. The capacity of organisms to adapt rapidly is critical to our future reliance on essential marine ecosystem services. CeMEB looks into the evolutionary response of changing environments. How are marine populations, species, and ecosystems affected over time? Which are the mechanisms underlying adaptation? Can models be used to forecast the effects?

Sam Dupont (right) and colleagues investigate how seawater acidification affects sea urchin larvae. Under decreased pH conditions (pH 7.9 and 7.7 as compared to 8.1), the larvae grow slower and spend more time in the plankton, thus being exposed to predation for a longer period.

Effects of ocean acidification on larval development

An important selective force now affecting marine organisms is ocean acidification. Studies show that the response varies among species. While some species may disappear within decades others seem to be able to cope with the new environment. And some may even benefit.

In laboratory experiments, Sam Dupont and his colleagues investigated the impact from seawater acidification on sea urchin larvae. Special attention was placed on pH regulation mechanisms.

Using microelectrodes and a fluorescent pH sensitive dye they measured extracellular and intracellular pH inside larvae. The results demonstrate that the larvae are "leaky"; pH in the extracellular compartments surrounding the calcifying cells decreases when the larvae are exposed to more acidic waters. But still the larvae manage to maintain pH inside the calicifying cells, and can proceed with the calcification of the endoskeleton.

– Our work shows that ocean acidification is not a matter of calcification but rather an energetic problem, says Sam Dupont. Regulating pH speeds up the metabolism and demands a lot of energy. As a consequence, larval growth is slowed down and the pelagic life stage lasts longer with increased mortality from predation.

This ability to buffer ocean acidification through pH regulation differs between species. For example, larvae and juveniles of the big sea star *Crossaster papposus* actually grow faster and with no visible negative effects at low pH. This sea star is born with a "lunch packet" and doesn´t need to eat during its larval stage. Instead all energy reserves can be used to quickly grow out of the dangerous pelagic stage. *C. papposus* could thus be an example of a species that may be well adapted to deal with the threat of ocean acidification, with potentially important consequences for the ecosystem as this sea star is a powerful predatory species.

A natural archive

When analyzing sediment cores from the Mariager Fjord in Denmark, Anna Godhe and her colleagues discovered that resting cells of the planktonic diatom *Skeletonema marinoi* remain undisturbed in the anoxic sediment. Like a natural archive, cells from different time periods are preserved in distinct layers and can be revived for DNA and other analyses.

This allowed for genetic analyses of diatoms from different time periods. The results show that through the last one hundred years one single population has dominated the fjord. Diatoms from the 1980´s had a slightly but significantly different genetic composition, which might indicate a response to natural selection from the heavy eutrophication in the fjord at this time.

The concept with one historical population and environmentally selected generations is now carried on into a new project, combining the different competences available in CeMEB, Anna Godhe explains:

– In order to identify genetically encoded adaptations we plan to sequence and compare the genomes of several different generations of diatoms. Big discrepancies possibly mirror genes important for adaptation to environmental changes due to eutrophication.

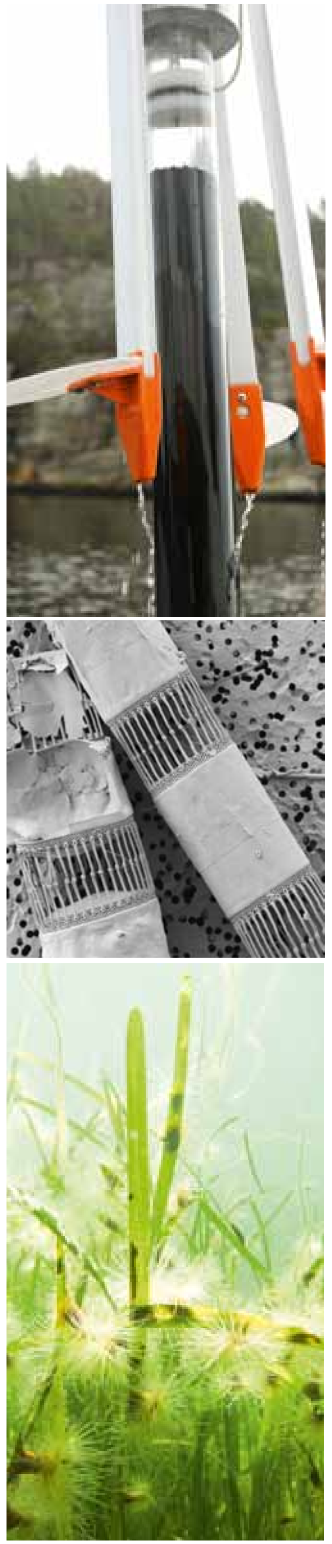
Biodiversity improves ecosystem resistance

Together with Lars Gamfeldt and other researchers at the University of Gothenburg, Jon Havenhand investigated the effects of simulated climate warming and ocean acidification in seagrass ecosystems with three species of herbivores and the fast growing alga *Cladophora*.

They found warming increased algal growth, but this was kept under control by the herbivores. However, when the scientists simulated and added another human impact, overfishing of large predatory fish, the grazers lost control and the algae took over.

Fewer big fish means that the numbers of small fish increase. These intensify predation on the herbivores - especially the shrimp which is also the most efficient grazer. Under today´s conditions with no climatic pressure, the two remaining herbivores still managed to keep the algae in control, even when the shrimp was absent.

– Our results clearly show the importance of biodiversity for the ecosystem´s potential to stay unaffected and maintain its services, says Jon Havenhand. Not only the *numbers* of species involved, but also *which* species.



Top and middle: Will revived diatoms *Skeletonema marinoi* from one-hundred-year-old-sediments be more sensitive to today's eutrophication?

Bottom: Shallow seagrass meadows provide valuable ecosystem services such as nursery areas for fish and clearing sediment and nutrients from coastal waters.

Chemical war in the sea

The invasive red algae *Bonnemaisonia hamifera* is not consumed by common native herbivores because it has a strong chemical defence. But it offers the grazers an effective refuge against fish predation. As a consequence the herbivores graze down neighbouring native algae, and promote the success of the invading species.

Bonnemaisonia hamifera is a red algae native to the West Pacific. It was introduced to the North Atlantic probably by ship traffic, and has become an invasive species dominating in many algal communities. On the Swedish west coast, *Bonnemaisonia* was first reported in 1902 and since then it has rapidly expanded to become one of the most common filamentous algae.

How is it that a newcomer can be so successful and outcompete native algae with a long history of local adaptation? This is a research issue for Swantje Enge. In feeding experiments she and her colleagues have shown that *Bonnemaisonia* is not as heavily grazed by isopods and other herbivores as native species are, such as e.g *Ceramium virgatum* and *Polysiphonia fucoides*. Also, they found that the alga produces a feeding deterrent, an organic brominated compound not known among native algae in the area. Still, in the field they observed that the herbivores aggregated in large numbers in *Bonnemaisonia*. Could it be that the algae provided some kind of protection?

Further experiments revealed that *Bonnemaisonia* offered the herbivores an effective refuge against fish predation, probably due to its morphology. At night-time the herbivores left the shelters of *Bonnemaisonia* and attacked neighbouring, more tasty algae.

– So, the herbivores not only avoid eating *Bonnemaisonia*, says Swantje Enge. They actually help the invader to outcompete native algae. Our experiment shows that without the herbivores, *Bonnemaisonia* is not a very efficient competitor.

– From a management perspective, understanding why some species become invasive and how they interact in their new ecosystem, can provide valuable knowledge and perhaps prevent future invasions, Swantje Enge concludes.

Swantje Enge assessed the palatability of the invasive red alga *Bonnemaisonia* and found that native herbivores strongly preferred native algae. This could be tracked down to an organic compound produced by the alien, not known in the native algae.

Why are you a member of CeMEB?

Magnus Alm Rosenblad
Researcher at Dept of Chemistry and Molecular Biology, University of Gothenburg

For the last ten years I have been working with identification of genes in genome sequences, which is really fun. And here within CeMEB I have the opportunity to do this with 8 or 10 different genomes – it´s Christmas every day!

Kristina Snuttan Sundell
Professor at Dept of Biological and Environmental Sciences, University of Gothenburg

There was a request for more physiological experience in the project, especially within the area of salinity acclimation/adaptation, where my expertise in osmoregulation fitted very well. For me, not being an evolutionary scientist, I learn a lot and experience many new things which is very stimulating.

Sam Dupont
Researcher at Dept of Biological and Environmental Sciences, Kristineberg, University of Gothenburg

I am studying the impact of global changes on marine life but I like to see myself not as the guy documenting the disaster. In CeMEB we also try to identify solutions. By exploring the genetic diversity in the sea we can find resilient organisms, some "climate proof" strains we can use in, for example, aquaculture.

Sonja Leidenberger
PhD at Dept of Biological and Environmental Sciences, Kristineberg, University of Gothenburg

Joining CeMEB was a big advance for me, because there are so many competences I could benefit from in the project – beside my supervisors. So I am really happy that I was a part of CeMEB during my PhD!

Jörgen Ripa
Associated member. Assistant professor at Dept of Biology, Lund University

This is a way for me to expand my network, to find interesting collaborators and approaches to get involved in. I think CeMEB is a very creative atmosphere and people are really engaged, more so than in other projects that I´ve been involved in.

Genetic modifications close to contaminated sites

Pulp mill effluents are known to affect fish in several ways, for example causing reduced fertility and influence sexual differentiation. Associated CeMEB member Mats Grahn and his PhD students at Södertörn University wanted to know whether the effluents could also act as a selective force and drive local adaptive changes.

They compared DNA in sticklebacks from polluted areas and from adjacent reference sites in the Baltic Sea, and found a clear change in the genotype composition in fish living near the pulp-mills. They also managed to identify and sequence pieces of DNA that were affected by the effluents, and could align them to the stickleback genome which is known from before.

– Our results clearly show that alterations in natural environments caused by humans can have evolutionary consequences for the animals living there, Mats Grahn says. And the response can be very fast.

Declining ice cover – predicted effects on seals

Even for moderate scenarios of future warming, sea ice in the Baltic Sea is expected to reduce by the end of the twenty-first century. This will have severe effects on the Baltic ringed seals who require stable ice with ridges and a decent snow cover for successful reproduction.

To analyse future effects of a warmer climate, Karin Hårding and colleagues linked models for seal population dynamics to existing climatic models, using historical data on seal population size, ice-coverage and time series of winter temperatures.

The analyses predict a strong negative impact on the Baltic ringed seal. The subpopulation in the Gulf of Riga is particularly affected, at risk of going extinct with a predicted number of only 75 seals at the end of the 21st century.

– Linking population dynamics to different climate models can help us identify vulnerable species, says Karin Hårding. Climate acts directly at the selection of individuals through the impact on survival and fertility, and obviously influences evolution of species such as the ringed seals in the long run.

A novel tool to study adaptive evolution

After genomics and proteomics time has come for *metabolomics*. This is a new technique for characterization of small molecule metabolites found in an organism. In CeMEB, metabolomic methods are developed to study how plant defenses evolve in response to changing environments, e.g. increased temperature, using bladder wrack *Fucus vesiculosus* and eelgrass *Zostera marina* as model species. Since the metabolites express the activity of genes, metabolomics offers an opportunity to study the relationship between genotype and phenotype; i.e. how the genotype response to environmental change.

Top: The three-spined stickleback is a well-studied model organism in evolutionary biology.

Bottom: Göran Nylund checks the liquid chromatography-mass spectrometer used for metabolomic analyses.

Managing genetic resources

Exploitation of marine resources causes genetic changes – often depletion – in populations and species. Still, to secure the long-lasting use of valuable species and ecosystems, a broad genetic variation is necessary. The research at CeMEB provides knowledge for informed management and conservation of marine biodiversity. This involves understanding the genetic structure of species, including how local populations are connected to each other.

Using genetic tools to trace which stock a caught fish derives from could prevent the depletion of local populations, says Carl André.

The necessity of a genetic perspective in fish stock management

There is growing scientific evidence that many fish species live in biologically separated populations that don´t mix. Using new genetic tools in fisheries management can reduce the risk for biodiversity loss and secure future catches.

When Carl Andre´participated in a study of population structure of Skagerrak cod together with collaeagues at Institute of Marine Research in Norway, they found a pattern of genetic differentiation on distances of a few kilometers only. This is remarkable, considering that cod has planktonic larvae drifting for several weeks or more.

Today, a management unit for fishing cod, for example, may very well contain several biologically separated populations, Carl André explains. As a consequence, local populations could be depleted, unnoticed. This has happened on several occasions, the cod crash in New Foundland 1992 perhaps being the most well known.

We are, however, slowly approaching a more genetically informed management. This requires cheap, simple and reliable tools to trace individual fish back to a specific population.

– The research in CeMEB contributes to this, Carl André says. In the cod genome, several thousands of new genetic markers were recently discovered. Together with Centre for Ecological and Evolutionary Syntheses (CEES) at the University of Oslo, we have identified a selection of these markers that can be used to link individual fish to populations in the Baltic Sea, Kattegatt and the North Sea.

Genetically informed management is already today put into practice in some places. For example, in the large Lofoten fishery where routines have been introduced to protect coastal cod populations. Genetic spot tests are carried out on the landings, and if the amount of coastal cod is too high the fishery is temporarily closed down.

BaltGene Wiki

For most marine species, knowledge of genetic diversity and how to manage it is very poor. The web site "BaltGene Wiki" contains information about genetic biodiversity of key species in the Baltic Sea. The site is based on results from the BONUS+ project BaltGene, which was coordinated by CeMEB director Kerstin Johannesson.

– This is a first attempt to generate management relevant scientific conclusions and transfer these to end-users, says Kerstin Johannesson. The research in CeMEB will produce new results which will be used to develop the site further.

For more information visit http://baltgene.tmbl.gu.se

Restoring local cod

The project CodS explores the possibility of restoring local cod stocks which previously existed in Bohuslän. An important part is to map the genetic structure of cod in Skagerrak and the North Sea.

– We use DNA from contemporary cod, but also from old tissue samples collected in the 1900th century, Carl André says. Studying the DNA helps us understand how populations are maintained through history and the potentials for future recovery.

CodS, in which CeMEB is the coordinating partner, is a collaborative multidisciplinary project with colleagues in Norway and Denmark, covering ecological, financial and legal aspects of future restoration.

Optimising MPA networks

Dispersal is a key factor explaining how species are geographically distributed and genetically structured. Thus, studying dispersal patterns is essential for understanding many ecological and evolutionary processes.

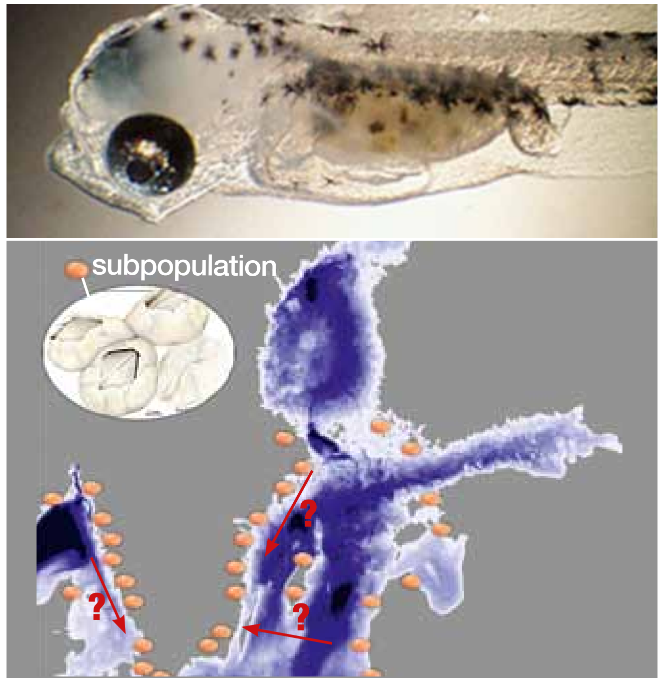
In CeMEB, Per Jonsson has joined forces with colleagues investigating patterns and mechanisms of gene flow, and has helped out to explain barriers to genetic exchange made up by ocean currents. As a spinoff effect, his research has become hot stuff in management.

Together with collegues, Per Jonsson has developed a scientific tool for designing optimal networks of marine protected areas, MPAs. This tool can be used to visualize how areas are biologically connected in terms of larval dispersal, and is based on biological data for the species of interest, maps of the sea bed, network theory and on detailed ocean current models.

– There is a very great interest from end-users, Per Jonsson says. Right now we are assisting the Swedish Agency for Marine and Water Management (HaV) with suggestions on how to select new Natura 2000-areas in Kattegat and Skagerrak.

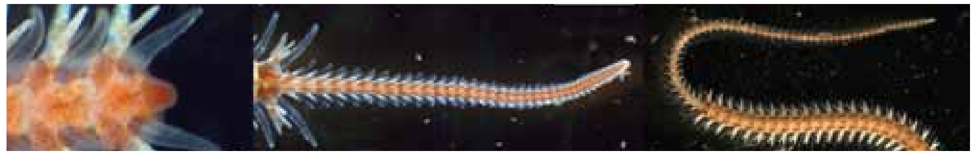
Bottom: Geographically separated subpopulations of many marine species are connected via planktonic larvae carried by waves and ocean currents.

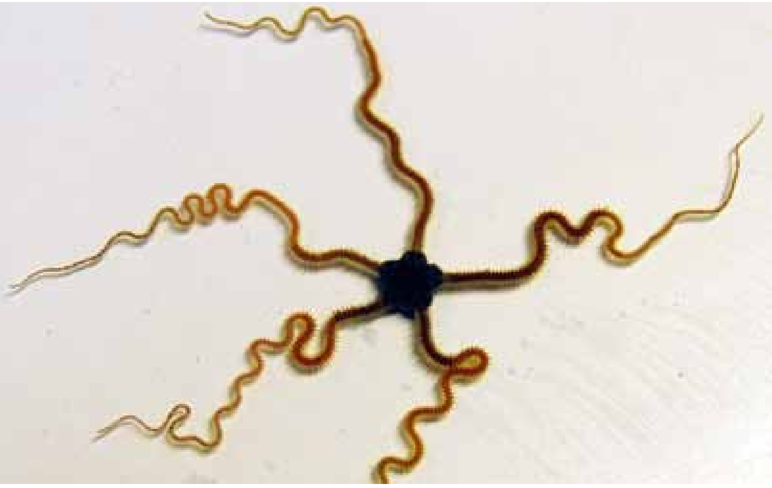
Below: A cod larva.



Understanding the ways of nature

Understanding the way nature ”works” is a challenge. At CeMEB, we explore the molecular and genetic mechanisms behind traits that are important for fitness and survival. Theoretical models are used to evaluate the benefit of behavioural strategies. Besides insight into evolution, knowing the ways of nature can also be the basis for future applications.





Brittlestars *Amphiura filiformis* regenerate lost arms very quickly. Above, three different stages of regeneration, from the left: after 1 week; after 3 weeks and after 5 weeks (95 percent differentiated). Olga Ortega-Martinez investigates which genes are involved in the process.

Molecular and genetic mechanisms of regeneration in brittle stars

Imagine being able to regrow a cut finger or leg. Or a damaged liver or an exhausted heart. Well, for some organisms this is easy! To study them might help us understand how it could be done. Olga Ortega-Martinez is one of the scientists putting pieces to the puzzle.

Brittle stars like *Amphiura filiformis* have a remarkable ability to regenerate lost or damaged tissues, particularly their arms. The majority of brittle stars in a population show evidence of arm damage due to predation from plaice and other demersal fish, so this ability certainly comes in handy.

Understanding the complex interactions within and between different cell types during regeneration is a hot issue for many scientists around the world. One of them is Olga Ortega-Martinez, using *A. filiformis* as a model organism. The brittle stars are easy to collect and keep in aquaria, and they regenerate lost arms very quickly – in only five weeks!

Olga Ortega-Martinez and her colleagues sampled arm tissue from brittle stars in different stages of regeneration. Using DNA microarray technology they analysed and compared the activity of thousands of genes during different stages of arm regeneration.

– Our results give insight into the molecular control required during the various stages of regeneration, Olga Ortega-Martinez explains. And with the genome information we expect to have in a year from now, we will be able to understand which genes are actually involved.

The very first stage of brittle star arm regeneration involves a massive production of new, undifferentiated cells, similar to a cancer process. In the brittle stars this phase is stopped and the cells start to specialize, while in human cancer it is not. This is an interesting fact, making this truly basic research relevant to medical science as well.

– People don´t always realise this, but behind applied research such as on cancer, there are always years and years of basic research, Olga Ortega-Martinez concludes.

Immune defence system in sea stars similar to in humans

In collaboration with French immunologist Michel Leclerc at Université d’Orléans, Olga Ortega-Martinez and her colleagues studied gene activity in the primitive immuno organ of the common sea star *Asterias rubens*.

They exposed sea stars to substances known to trigger the immune defence, and identified genes responsible for producing proteins in the defence process. When the DNA was sequenced and matched to genes with known function in other species, they found that the antibody-like substances produced by the sea stars are similar to the T-cells and macrophages involved in the human immune system.

– Of course, this is exciting, says Olga Ortega-Martinez. But it is too early to claim that we have found the missing link between vertebrate and invertebrate immune system – which is the ultimate goal for this type of research.

Computing the growth of barnacles

When PhD student Anna-Lisa Wrange studied salinity tolerance in the barnacle *Balanus improvisus*, her experiment included more than 3000 baby barnacles. To compare the growth of individuals in different treatments she planned to measure their diameter from photographs at four occasions during the experiment. This meant about 12 000 measurements in total – which would take forever if measured one by one.

Fortunately, she got lucky enough to find CeMEB associate member Torbjörn Lundh from Chalmers University of Technology. He developed a mathematical script that could scan the photos and measure the size of the barnacles in a computer. The process also included an analysis of the measurements, using a theoretical growth model to describe how growth patterns varied in different salinities.

– Understanding a new research area, in this case, biology, is stimulating and very challenging, says Torbjörn Lundh. Future collaboration could, for example, include developing more complex growth models adjusted to barnacle biology, which could be used to study evolutionary strategies for growth in different environments.

A robot helps out with massive testing

Working with fast growing organisms such as yeast with generation times of about two hours provides almost endless opportunities to study the evolutionary consequences of natural selection. The only limit is the scientist’s own handling time.

But PhD student Martin Zackrisson found a helping hand; a ”robot” which helps him explore the selective forces of different salinities. In experiments he exposes genetically modified strains of the bakery yeast *Saccharomyces cerevisiae* to varying salinities. Using the robot he can perform more than 100 000 different experiments in a week.

– The ultimate goal is to understand the evolution of salinity tolerance, says Martin Zackrisson. The yeast cells provide simple model systems to study basic principles applicable to any cells, including animals.

Top: Martin Zackrisson uses a robot to manipulate a high number of yeast cultures.

Below: A mathematical script and a theoretical growth model was used to compare the performance of barnacles in different salinities.

Brooding fathers suck the life out of their offspring

The broad-nosed pipefish has a pregnancy process resembling that of mammals – only it´s the father who is expecting. But is he really as caring as it seems?

The little pipefish *Syngnathus typhle* inhabits shallow waters along the coasts of Europe. In the summer, males can be seen in eelgrass meadows where they perform delicate dances to court females. If pleased, she will transfer her eggs into the male´s brood pouch, where he fertilises them. He will then keep the growing embryos in the pouch for 4-5 weeks before he gives birth to a brood of fully developed tiny pipefish individuals.

Previous studies have shown that the brood pouch has a placenta-like structure through which the male provides the developing embryos with nutrients and oxygen. When Lotta Kvarnemo and her colleagues studied brooding pipefish in aquaria they discovered that nutrients may travel both ways:

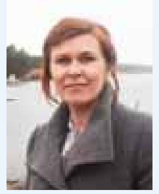
– It is well known that, on average, around 20 percent of the eggs in the brood pouch are lost and do not result in fully developed young, Lotta Kvarnemo says. We tagged eggs with 14C-labelled amino acids which allowed us to trace the fate of nutrients from reduced embryos – and found that these nutrients were transferred to the male´s brood pouch, liver and muscle tissue. The fathers actually absorb nutrients from these embryos through the skin of the broad pouch.

From the mothers' point of view, of course this is not very desireble, as Lotta Kvarnemo points out. But the males need energy while they brood the eggs and they don´t seem to eat very much after they get "pregnant". So perhaps absorbing an embryo or two increases his prospects of staying alive through the pregnancy. In that case, the female, too, probably benefits from this behaviour.

Female pipefish often mate and give eggs to several males. Results from a later study show that males brooding eggs from more than one mother lose fewer offspring compared to males brooding eggs from one single female. So "Never put all your eggs in one basket" seems a very appropriate advice in the pipefish world.

Pipefish males get pregnant and rear their young in a brood pouch on the belly. Lotta Kvarnemo studies the evolution of parental care and other reproductive behaviours using pipefish as a model.

How does CeMEB contribute to our society?



Marina Panova
Researcher at Dept of Biological and Environmental Sciences, Tjärnö, University of Gothenburg

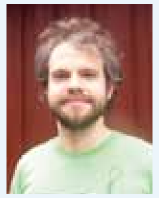
CeMEB brings our knowledge about evolution to time scales that are related to human activities. We still tend to think about evolution as something that happened a million years ago, and that it will take another million years to see the reactions to changes that we are causing now. But that is probably not the case.

Staffan Bensch
CeMEB Advisory Board. Professor at Dept of Biology, University of Lund

CeMEB puts a lot of effort into understanding how global change, including ocean acidification and changing salinities, will affect the ecosystems. The effects will, of course, have direct consequences for fisheries, the recreational use of the coastal environments and so on.

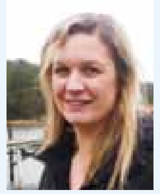
Anna Godhe
Professor at Dept of Biological and Environmental Sciences, University of Gothenburg

CeMEB will increase the understanding of how dynamic the environment is. For example, we are used to think of species as definite units but all species are changing continuosly. This is important for management to take into account, but also as public general knowledge.



Mårten Duvetorp
Ph D Student at Dept of Biological and Environmental Sciences, Tjärnö, University of Gothenburg

CeMEB improves our understanding on how environmental change affects the possibilities for species to adapt in the future. This information can guide society on where to put resources to get the most impact.



Hannah Wood
Researcher at Dept of Biological and Environmental Sciences, Kristineberg, University of Gothenburg

There is plenty of work in CeMEB about climate change and understanding how species will respond and their potential for adaptations. The more we can inform the policy makers of the implications of climate change through our work, the more that can contribute to decisions that protect the marine environments.

The battle of fertilization

In many animal species females mate with several males but not all of them become fathers. This indicates that mate choice can be going on inside the female – after copulation.

This was what PhD student Sara Hintz Saltin and her colleagues found in breeding experiments with *Littorina saxatilis*, a small marine snail known to be extremely promiscuous often mating with up to twenty different males. They kept females in small aquaria with a varying number of males, and after the experiment parents and offspring were genotyped using microsatellite markers to establish the fatherhood. The results clearly showed that the males didn´t contribute equally to the offspring production – sometimes, one single male had fathered more than half the brood.

– This pattern indicates sexual selection after copulation, Sara Hintz Saltin says. Either by sperm competition between different males, or by females discriminating between males' sperm. But the details of this battle of fertilization are still a snail secret!

Models show promiscuity is positive to colonization

Using mathematical models PhD student Marina Rafajlović explored possible genetic benefits from the vast promiscuity observed in *Littorina saxatilis*. And yes, she found that it has its advantages, especially during colonization.

L. saxatilis doesn´t have pelagic eggs or larvae, and thus the snails spread very slowly to new environments. But now and then a pregnant female might get a lift to a new place, perhaps on a drifting algae or on a seabird's foot. The offspring in a brood from a female who mated with many males often represents a broader genetic variety compared to the offspring from females mating only with one male. Thus, promiscuous – pregnant – females bring more genes into a new population; according to the models they might increase genetic diversity by up to 300 percent.

– This increases the chance for a colonizing population to sustain in the new environment, Marina Rafajlović explains. With a lot of genetic variation the population is better equipped to withstand diseases and other trials.

When no sex may be beneficial

Genetic data from brown algae *Fucus radicans* sampled all over the Baltic Sea reveals a remarkable distribution pattern with a few sexually reproducing populations and several dominated by asexual clones. On the Swedish coast, in particular, many of the populations are almost completely dominated by a single widespread female clone.

To investigate how such a pattern could develop, a theoretical model was formulated by physicist David Kleinhans. The model uses biological and oceanographic data, and the results suggest that the observed population structure is likely to have emerged – simply by chance!

– This is a good example of fruitful collaboration between biologists and theoreticians, Kerstin Johannesson explains. The model helped us formulate and test different hypotheses. It showed that there is a great advantage being asexual when a new area is being colonized. A single clone may "take over" large areas of distribution, which is exactly what we observed in this new alga species.

Female snails *Littorina saxatilis* often mate with several males. Genetic analyses of the offspring indicates that maybe the female can decide after copulation which males will fertilize the eggs and become fathers.

The Baltic Sea – a Darwinian lab

How can organisms colonize and survive in new habitats with novel conditions? Does it “require” evolutionary adaptation or can high tolerance at the individual level do the job? The answers can give us clues about how nature will respond to the environmental changes we are facing today. The Baltic Sea with its young history and natural salinity gradient provides CeMEB with an excellent model system to study rapid evolution.

The bay barnacle can endure desiccation and fluctuating salinities. Understanding how species handle varying environments can help us predict the impact and spread of invasive species, says Anna-Lisa Wrange, where tolerant species can spread and establish more rapidly, potentially posing serious threats to existing local biodiversity.

Plasticity – an alternative strategy to handle environmental change

Some species seem to be able to colonize any type of environment. The bay barnacle is found worldwide and can endure a broad range of environmental conditions, including extreme salinity variations.

The bay barnacle *Balanus improvisus* is believed to originate from the US, and was first recorded in the Baltic Sea in the mid 1800’s. Today it is found all over the Baltic Sea, even in the very north of the Bothnian Bay.

Living attached to hard substrates including boat hulls, in coastal areas and estuaries, the bay barnacle is known for its ability to tolerate a wide range of salinities – from fully marine environments to almost freshwater. But what about barnacles living in more stable environments? Can they adapt to local circumstances and perhaps optimise physiological processes such as growth and reproduction, and even possibly lose some of its tolerance range?

To explore this, PhD-student Anna-Lisa Wrange designed a laboratory experiment with barnacle larvae raised from adults collected at three geographical sites, representing different salinity regimes. The idea was to see if barnacles would perform better in their “own” salinity, indicating possible genetic differences between populations due to local adaptation.

The results show that salinity had the same effects on the barnacles irrespective of their origin. This indicates that barnacles from different sites are not genetically different from each other, but rather expressing high plasticity – an ability to adjust individually to different environments.

– Interestingly, low salinity had positive effects on growth, reproduction and survival but negative effects on shell strength and early growth, Anna-Lisa Wrange says. This suggests that there may be trade-offs between different fitness-related traits in different environments.

Handling low salinities

Although much is known about the bay barnacle´s ecology, it is not fully understood at a molecular level how they acclimatize to different salt concentrations and how they osmoregulate, the mechanisms to maintain their internal water balance.

The sodium-potassium pump Na+/K+-ATPase is a protein responsible for iontransport across cellmembranes in animals. It is likely that it plays an important role for osmoregulation in the bay barnacle too. To get detailed information on the molecular structure of the encoded protein, Ulrika Lind together with Anders Blomberg and colleagues isolated and sequenced DNA-segments from barnacles. They found that the gene was differently expressed under different salinities.

– This is a first step towards identifying genes that are crucial for low salinity tolerance in the bay barnacle, Ulrika Lind says. It can help us understand how this particular barnacle – and perhaps other marine species – could colonize the Baltic Sea.

Stronger defence strategies

In the Baltic Sea, bladder wrack *Fucus vesiculosus* encounters a different ecosystem compared to its original marine provenance in the Atlantic. Among other things, the Baltic Sea lacks a major enemy – grazing *Littorina* snails. According to influential hypotheses, escape from specialist natural enemies will lead to a reduction in defence levels. Thus, bladder wrack in the Baltic Sea should save resources and produce less bad tasting – and expensive – chemicals to defend themselves against grazers.

– But our laboratory experiments showed completely the opposite, Göran Nylund says. Individuals from the Baltic Sea contained more than 50 percent higher levels of defence chemicals phlorotannins than plants from Skagerrak.

Also, in feeding trials with isopod *Idotea balthica* which is the dominant grazer in the Baltic, wracks from the Baltic were the least preferred.

– Our study suggests that the high grazing pressure from *Idotea* has selected for increased resistance towards generalist grazing in bladder wrack inside the Baltic Sea, Göran Nylund concludes.

Marine isopods cope in the Baltic Sea

The isopod *Idotea balthica* is very common in the Baltic Sea, but is originally a true marine species. Hannah Wood and her colleagues are interested in how the species was able to colonize the Baltic Sea and the very low salinity there. They sampled isopods from three areas in the Baltic Sea with varying water salinity, and compared growth and other physiological responses in different salinities in aquaria. It turned out the isopods did very well in all salinities, no matter which area – and salinity – they originated from.

– This indicates that the isopods have a pre-existing ability to cope with lower salinities through physiological plasticity which is a more rapid process than evolutionary adaptation, Hannah Wood explains. Insights from studies like this can help us understand how organisms will respond to ocean acidification and other rapid environmental changes.

Top: Isopod experimental set up.

Middle: Ulrika Lind and Anders Blomberg.

Bottom: Bladder wrack produce defence chemicals against grazers.

IMAGO – Infrastructure for MArine Genetic model Organisms

In the sub-project IMAGO, CeMEB develops new marine model organisms for research. They will advance the issues addressed at CeMEB to the level of understanding the genetic background and mechanisms involved in the evolutionary processes.

IMAGO involves assembling the genome sequences of eight marine species from coastal ecosystems in the North Atlantic.

– Knowing the DNA-sequence of a species opens up the use of new modern technologies for studying ecology and evolution in the sea, CeMEB deputy director Anders Blomberg explains.

But there are many challenges to overcome, as he points out:

– The genetic diversity in many marine species is enormous! Also, in some species we find that parts of the DNA are repeated at several places in the genome, which confuses the assembling process.

Presently, the project has sequenced several millions of short pieces of DNA, approximately one hundred nucleotides each, which eventually will be put together to chromosomes. Assembling these pieces correctly has linked skilled bioinformaticians to CeMEB. Later steps will be to identify individual genes in the genomes and trace their functions, a work that will be completed in part by gathering all available competences in the international research society.

Knowing the whole DNA-sequence of a species provides opportunities to understand what traits are involved in genetic differences observed, to manipulate the genomes and to test experimentally the function of specific genes. For simple organisms like the marine yeast *Debaryomyces hansenii* this is already ongoing. For the more complex organisms, this is a long-term goal but cross-breeding experiments are in progress to unveil the genetic background of specific traits. For example, artificial selection of cultured lineages of the snail *Littorina saxatilis* with different growth rates provides possibilities to identify genes involved in shell size.

– In the same way as medical scientists are searching for the genetic background to cancer, we are tracing the genes behind traits involved in local adaptation and speciation, Anders Blomberg explains.

The IMAGO project will provide a service to scientists irrespective of membership of CeMEB, both through cultures of organisms available for research, and through the extensive genome information, which will be shared internationally through open access data bases.

– Data from IMAGO will have relevance not only for evolutionary research but also for other fields of science, such as toxicology, medical research and biotechnology, Anders Blomberg concludes.

The eight **IMAGO** species are relevant key species from the northern Atlantic with a well-known biology. They can complete their life cycle in the laboratory which is a prerequisite for the successful cultivation of breeding lineages.
Follow the genome sequencing at www.cemeb.science.gu.se/research

Disentangling the genomes – step by step

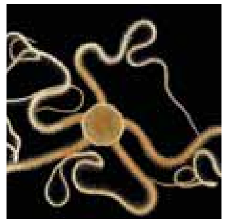
Basically you extract DNA from the organism of interest, and cut it into fragments which are sequenced to get "reads"; short pieces of the genome about 100 base pairs long. These reads are assembled into longer sections and eventually put together to genes in a kind of trial-and-error procedure.

Magnus Alm Rosenblad is one of the CeMEB bioinformaticians, helping out with the IMAGO genomes:

– The amount of data is huge, he explains. For example, right now we have about one billion reads from the *Littorina saxatilis* genome. After the reads have been assembled, you still have several hundred thousands of DNA-pieces that should be put in the right order. And often the genes you find lack the beginning or end, which is a big challenge.

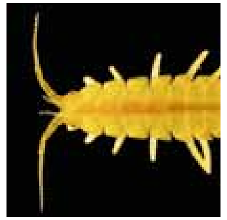
In the process the DNA-pieces are compared with already known gene sequences from other organisms found in databases. Powerful computers can make millions of comparisons which might take up to a week each.

– Getting the genomes together requires a lot of computers capable of storing and processing vast amounts of information, says Magnus Alm Rosenblad. We have to buy new hard drives all the time!

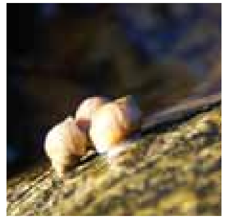


Brittlestar
Amphiura filiformis
Has the capacity to regenerate arms and is an emerging model for regeneration and stem cell biology in biomedical research.

Bladderwrack
Fucus vesiculosus
Extensive morphological and ecological variation among populations in which several cases show large genetic and chemical differences.



Baltic isopod
Idotea balthica
A key species in the Baltic Sea. Controls the growth of *Fucus vesiculosus* and is a major food source for many fish species, including commercially important species.



Rough periwinkle
Littorina saxatilis
This species is considered to be one of the rare examples of ongoing speciation in the presence of gene flow (sympatric speciation).

Diatom
Skeletonema marinoii
Generation time 24 hours which makes it ideal for studies of phenotypic response. Can be revived from sediment archives.

Sand goby
Pomatoschistus minutus
Is able to adapt to a wide range of salinities – but not to fresh water. All life stages are staple food for cod and other large commercial fishes.

Marine yeast fungus
Debaryomyces hansenii
Occurs globally and show extreme tolerance to salt/dehydration stress.

Bay barnacle
Balanus improvisus
An important fouling organism and a potential source for various areas of biotechnological research.

Glimpses of CeMEB activities

Based on the belief that the best research is produced in an open and encouraging atmosphere a range of activities are going on at CeMEB. Members gather to exchange ideas during meetings and workshops on several occasions every year. The young scientists are invited to inspiring classes and courses.

CeMEB Assemblies

The CeMEB Assemblies are an important part of the strategy for promoting discussions and development of the research within the centre. Taking place twice every year the programme always includes oral presentations of results, but also plenty of time for discussions and informal chatting. New research collaborations are often formed during these meetings. To stimulate the discussions recognised colleagues from national and international institutions are invited.

Workshops

CeMEB members are encouraged to suggest workshops for special purposes. Several such informal meetings have been arranged, for example "*Littorina* genomics", and "*Idotea-Gobiid* genomics". International scientists in the field are invited to these workshops.

Supporting the young

To support PhD students and young researchers CeMEB runs regular classes in, for example, writing scientific papers and how to write applications. A programme to encourage young members´ career development has been initiated where the coordinator, Eva Marie Rödström, offers individual coaching.

Advanced Courses

CeMEB involves leading researchers in marine evolutionary biology and a comprehensive network linking top international scientists in the field. To benefit from this competence and the marine infrastructure at the University of Gothenburg, CeMEB arranges advanced international courses for young scientists and students. The courses gather participants from all over the world and are run once a year.

Internal newsletter

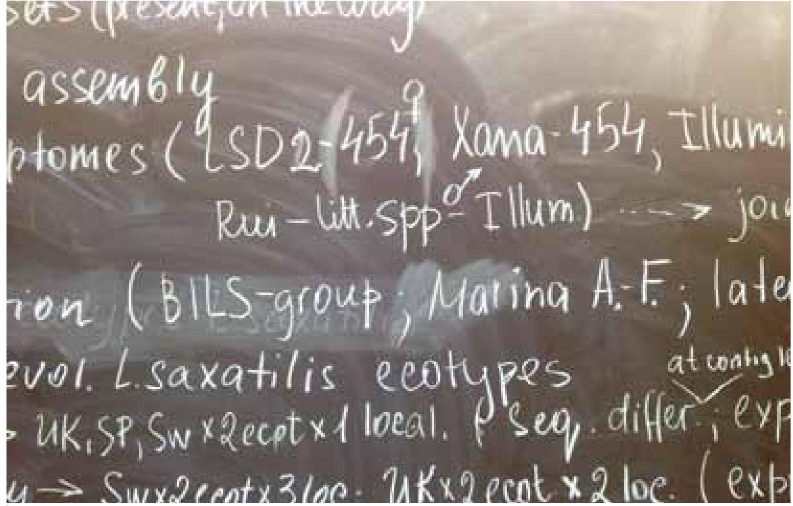
CeMEB Newsletter is compiled by coordinator Eva Marie Rödström and distributed at least once every month. The newsletter keeps the members updated on what´s going on; coming events, interesting conferences – and shares the good news of additional funding and accepted publications.

Reaching out

CeMEB web-site contains pages in Swedish particularly written for the non-scientific audience. Research breakthroughs are announced as press-releases. Members give newspaper interviews and publish popular science papers on research topics of CeMEB.

CeMEB scientists have participated in International Science Festivals in both Gothenburg and Stockholm, giving oral presentations on evolutionary topics and teaching school classes in experimental evolutionary research.

A CeMEB ambition is that results should be implemented and used in future management of marine resources. Several members have on-going collaborations with public authorities such as SEPA and the Swedish Agency for Marine and Water Management, and international assignments, such as the Ocean Acidification International Coordination Centre.



CeMEB facts

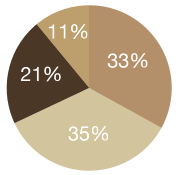
The strength of CeMEB is a fruitful integration of dedicated scientists from different disciplines, and the availability of unique marine infrastructure. CeMEB is funded by a ten-year Linnaeus grant and started in July 2008. The centre is hosted by the University of Gothenburg.

The people

CeMEB brings together research groups at the University of Gothenburg from the departments of Biological and Environmental Sciences, Chemistry and Molecular Biology, Physics, and Mathematical Sciences. In total, the centre has nearly 70 members. The scientists involved represent competence in evolutionary biology, molecular biology, genetics, physiology and theoretical biology, in addition to bioinformatics and modelling.

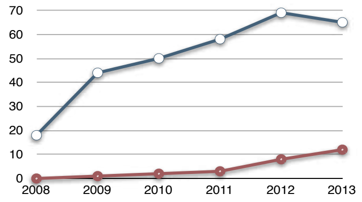
Besides, CeMEB includes associated members from i.e. Chalmers University of Technology in Gothenburg, Södertörn University in Stockholm and Lund University.

CeMEB members (June 2013)



- ● Professors and senior researchers
- ● Younger researchers and postdocs
- ● PhD students
- ● Technical and administrative support

CeMEB members per year



- ○ Total number
- ○ Associated members

Research facilities

CeMEB has access to two marine research stations, Tjärnö and Kristineberg, jointly organized under the Sven Lovén Centre for Marine Sciences at the University of Gothenburg. Situated close to excellent field sites and with lodging and restaurants, these stations offer outstanding opportunities for joint collaborative research activities. Both stations have marine laboratories with through-flow saltwater systems for culturing of organisms and experiments under controlled and manipulated conditions. In addition, state-of the-art DNA and chemical ecology laboratories are available.

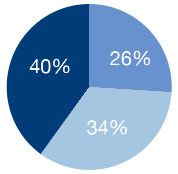
In Gothenburg, there are advanced molecular genetic laboratories and a high-throughput phenotyping facility for unicellular organisms. Besides this, core facilities for genome sequencing and bioinformatics support are available to CeMEB through collaboration with SciLifeLab Stockholm and the Swedish BILS infrastructure.

A Linnaeus Centre of Excellence

CeMEB is funded by a ten year Linnaeus grant from the two Swedish Research Councils, VR and Formas, with the purpose to enhance research of the highest quality. In addition, CeMEB is co-funded by the University of Gothenburg, and gets additional support through grants from i.e. EU, VR, Formas, Hasselblad Foundation and KVA.

CeMEB funding

Total budget 2008-2013: 147 million SEK



- ● Linnaeus grant from VR and FORMAS
- ● Funding from the University of Gothenburg
- ● External support

Organisation

Management

Kerstin Johannesson, director
Anders Blomberg, deputy director
Eva Marie Rödström, coordinator

Steering committee

Prof. Carl André
Prof. Anders Blomberg
Dr. Sam Dupont
Ph.D. Student Mårten Duvetorp
Assoc. Prof. Sanna Eriksson
Prof. Jon Havenhand
Assoc. Prof. Karin Hårding
Prof. Kerstin Johannesson
Prof. Per Jonsson
Prof. Lotta Kvarnemo
Dr. Marina Panova
Prof. Henrik Pavia
Ph.L. Eva Marie Rödström

Advisory board

Prof. Staffan Bensch, Lund University
Prof. Erik Bonsdorff, Åbo Akademy, Finland
Prof. Jeanine Olsen, University of Groningen, The Netherlands
Prof. Stig Omholt, NTNU, Norway

The Linnaeus Centre for Marine Evolutionary Biology, CeMEB, explores the evolutionary mechanisms behind organisms' adaptations under changing environmental conditions. Empirical observations are combined with theoretical models and hypothesis testing. The results provide a basis for a more informed management of marine resources, and potential input in biotechnology and medical research.

This publication, aimed for a nonspecialist audience, presents research and results and gives an introduction to the CeMEB world.

www.cemeb.science.gu.se

UNIVERSITY OF GOTHENBURG
CENTRE FOR MARINE EVOLUTIONARY BIOLOGY

CeMEB is hosted by the University of Gothenburg and is financed by a ten-year Linnaeus grant from the Swedish Research Councils.

Produced by: www.saltkommunikation.se. Cover illustration: Typoform. Photos: Lennart Adler, Carl André, Malin Arnesson, Anders Berglund, Anders Blomberg, Sam Dupont, Mårten Duvetorp, Swantje Enge, Bengt Frizell, Anna Godhe, Mats Grahn, Jon Havenhand, Ola Jennersten, Bo Johannesson, Daniel Johansson, Lena Kautsky, Anna-Sara Krång, Patrik Larsson, Sonja Leidenberger, Lars-Ove Loo, Susanne Liljenström, Torbjörn Lundh, Per Moksnes, Tuuli Mäkinen, Olga Ortega-Martinez, Fredrik Pleijel, Josefin Sagerman, Thron Ullberg, Hannah Wood, Anna-Lisa Wrange, Martin Zackrisson. Language editing: Rowena Jansson. Print: Elanders 2013, 1000 ex.