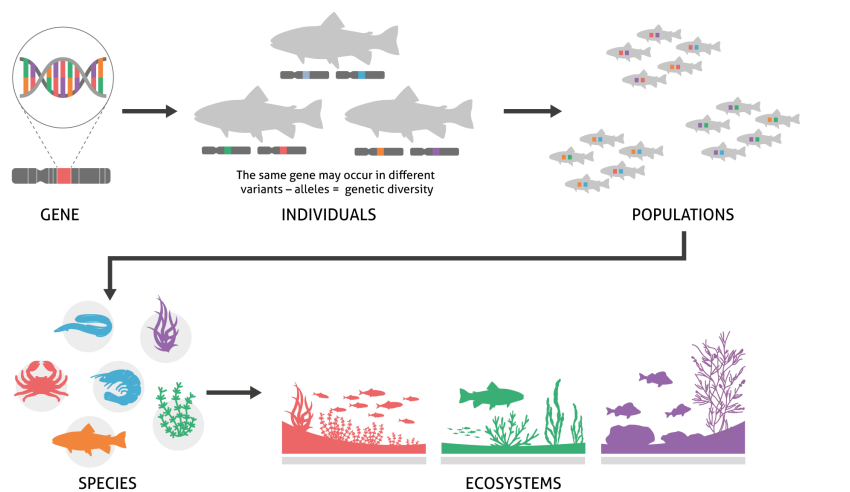


**BONUS BAMBI PROJECT (1.1.2014 to 31.12.2017)**

# The final publishable summary report

February 28<sup>th</sup> 2018



**Project website:** [www.bambi.gu.se](http://www.bambi.gu.se)



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## Project outline of goals and results envisaged at the beginning of the project cycle

A rapidly warming Baltic Sea that will also be impacted by lower salinities than today will put a heavy pressure on all species with marine origin currently living in the Baltic Sea. Already today, the Baltic Sea is extremely species poor with roughly only 10 percent of the number of species found in the North Sea.

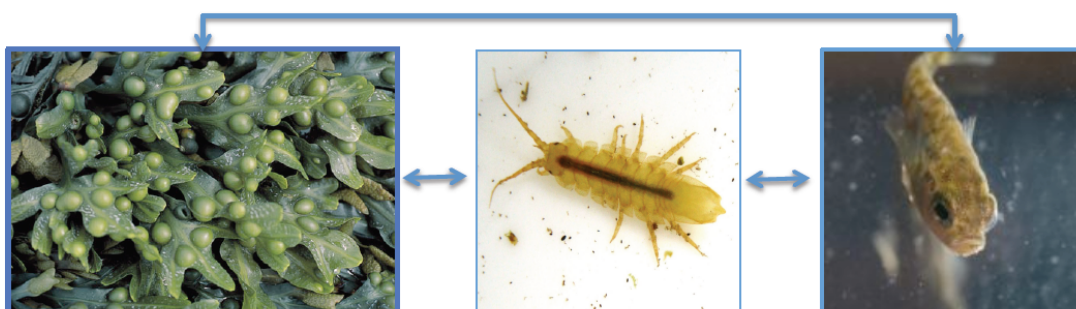
The overall goal of BONUS BAMBI was to generate new knowledge on genetic biodiversity of Baltic Sea populations, in order to understand how the ongoing changes in temperature and salinity will affect key marine species of the Baltic Sea. The project also aimed to assess the degree of management that is currently directed towards genetic diversity. In addition, the goal was to communicate new insights on genetic biodiversity to Baltic Sea managers and policy-makers.

### At start of the project we outlined the following expected contributions from the project:

- ✓ comprehensive descriptions of the genetic variation in four key species
- ✓ mapping of adaptive parts of the genetic variation
- ✓ experimental estimates of demography and inheritance of extreme tolerances
- ✓ suggestions of new policies and governance principles developed together with end-users
- ✓ a framework for modelling distribution and dispersal of species under scenarios of climate change

## Work carried out in the project

A main issue has been to identify the population structures of four key-species; bladder wrack *Fucus vesiculosus*, narrow wrack *Fucus radicans*, Baltic isopod *Idotea balthica* and three-spined stickleback *Gasterosteus aculeatus*. For three of the species this involved the development of new powerful genetic markers, so called RAD markers. These markers are very many (>10,000) and randomly distributed throughout the genome. With the high number of markers, many of them will sit close to genes under selection, while others will signal population genetic structure and gene flow. RAD analysis requires high-quality DNA, and for the two *Fucus* species this turned out to be a challenge. Finally, however, DNA from more than 40 populations of *Fucus vesiculosus*/*F. radicans* and 37 populations of *Idotea balthica* were extracted and sequenced for >10,000 polymorphic sites (SNPs).



*BONUS BAMBI target species. The seaweeds (*Fucus vesiculosus* and *F. radicans*) are grazed upon by the isopod (*Idotea balthica*), that is eaten by the fish (*Gasterosteus aculeatus*), the fish using the seaweed to its nests. This model ecosystem constitutes a dominant part of coastal hard bottom ecosystems of the Baltic Sea. Photos: BONUS BAMBI.*

We used stickleback to assess to what extent environmental change may directly induce genetic differences in terms of changes in gene expression, and if these changes are being transferred to the next generation. The process for this is named "epigenetics" and there are several different mechanisms involved. One is methylation of the DNA of a parent and this methylation will change the regulation of genes and be inherited into the next generation. Six populations of stickleback have been carefully analysed for fixed genome variation, differences in gene expression, and any effects of epigenetic type.

#### **New models for connectivity and distribution**

We have partly developed and used new modelling approaches to map connectivity among populations. Connectivity modelling combines statistical oceanographic data describing directions and dispersal rates of currents, with biological data of larval duration, larval behaviour (depth distribution) and habitat choice. These models can be used to predict how far and in what direction a larva is likely to be transported after release from a certain spot. In our modelling, we typically used multiple release spots and in this way, it was possible to predict connectivity patterns for the whole Baltic Sea environment in the same analysis, for a species with certain characteristics.

We have also mapped the distribution of *Fucus* and *Idotea* from using a combination of new and existing ground-truthing data and climate envelope modelling for the whole Baltic Sea area. This is the first time the complete distribution of these key species is compiled. The current distribution act as a reference to model how the distributions will change upon warming and freshening of the Baltic Sea over coming decades. In the modelling tools we developed, we also included experimental data where tolerance to higher temperature and lower salinity were experimentally assessed.

Maps were produced that summarised the results of the connectivity and dispersal modelling, and these maps were made available to the end users through the BaltGene webpage.

#### **Experimental tests of tolerance levels**

To determine tolerance of *Fucus* and *Idotea* to combined stress from increased temperature and decreased salinity we used experiments. In these experiments, we tested populations from the entrance of the Baltic Sea, from the mid-part and from the innermost (marginal) parts of the species' distributions. These experiments were used both to determine the average tolerance of individuals to stress levels corresponding to future combinations of temperature and salinity, and to find out if the tolerance vary among individuals due to different genotypes. If different genotypes have different tolerances, there is potential for evolution of populations that are more tolerant to future climate than is the present populations.

Tolerance was assessed for fitness parameters such as survival and growth but also to gamete release and fertilization success. The genetic background of tolerance was assessed by sequencing of the transcriptome to see which genes were expressed and not under various environmental conditions.

#### **Studies of knowledge transfer and effects of management measures**

To protect genetic variation (genetic biodiversity) is a major target under the Rio Convention and the Aichi Biodiversity targets. To understand the role genetic biodiversity actually play in management, we used interviews of authority personnel to find out how information on genetic variation is currently used in the design and management of MPAs within the Baltic Sea. In addition, we also assessed currently applied policy and management against the background of existing international agreements, in particular the Strategic Plan of the Convention of Biological Diversity.

We analysed the effectiveness of knowledge transfer to stakeholders comparing lectures and group deliberations, and evaluated both short-term and long-term effects of the transfer on knowledge and beliefs.

Finally, we evaluated the effects of management measures (positions and sizes of MPAs) by both a direct comparison of the genetic variation maintained inside and outside MPAs, and by comparing the location of existing MPAs with the optimal position of Baltic Sea MPAs as generated from a model of connectivity.

We disseminated results from BONUS Bambi and initiated an end-user dialog through the webpage "Baltic Sea Genetics for Managers" (<https://bambi.gu.se/baltgene>) and through a 2-day workshop.

## Main results achieved during the project

In BONUS-BAMBI we show that for the species we have studied, populations of marine origin have changed their genetic composition in a number of different traits to be able to survive and reproduce in the low-saline Baltic Sea. What we also show is that this change has resulted in a highly complex genetic structure with populations locally adapted to different parts of the Baltic salinity gradient. In addition, some species, have acquired completely new traits, such as, cloning in Baltic *Fucus*, which radically change the ways in which genetic variation is maintained and evolving.

In *Fucus*, genetic differences among sites in the Baltic Proper and Gulf of Bothnia, Gulf of Finland and Gulf of Riga are even more pronounced than differences accumulated over the Baltic Sea entrance. All these differences are due to isolation and lack of gene flow, but also to local adaptation.

In both *Idotea* and stickleback we have identified genes under selection, and local adaptation to the low salinity of the Baltic Sea. We expect similar results in *Fucus* (analysis still ongoing). In *Fucus* we see an extremely complex picture with the separation of *F. radicans* from *F. vesiculosus* in some areas, but not in others

### New tools for selecting MPAs and estimate future distributions

Using biophysical modelling to estimate the connectivity between basins and regions within the Baltic Sea we have identified several partial dispersal barriers within the HELCOM area, which may suggest management units and locally adapted subpopulations. Biophysical modelling explained, for example, a large part of the population structure of *Idotea balthica* revealed by our detailed genetic survey. This shows that biophysical modelling is a tool that may be used for a first approximation to identify areas for MPAs.

Results of dispersal modelling of the future *Fucus vesiculosus* populations pointed out that locally adapted genotypes are at a high risk of extinction because *Fucus* are unable to shift their ranges fast enough due to restricted dispersal and long generation time. The worst scenario is that *F. vesiculosus* may disappear from large parts of the Baltic Sea before the end of this century, with large effects on the biodiversity and ecosystem functioning. To reduce this risk, conservation actions like assisted colonization and assisted evolution may be necessary in the future.

### Variation enables future adaptations

We determined tolerance of *Fucus vesiculosus*, *F. radicans* and *Idotea balthica* to future salinity-temperature regimes, for populations from the entrance, central, and marginal Baltic Sea regions. Future conditions hampered growth and survival of the central and marginal Baltic Sea populations of *F. vesiculosus* whereas the entrance populations fared well. We also found that gamete release and fertilization success are highly sensitive to salinity conditions and may be the most critical life-history stage under climate change.

However, we found genetic variation in tolerance and this variation provides the raw material for adaptation to a changing environment. This finding highlights the need for monitoring genetic variation in key ecosystem species. In *Fucus* we also found 72 genes that were differentially expressed between the current and future predicted salinity conditions implying strong genetic background of salinity tolerance.

### Unknown consequences of ecosystem change

The endemic *F. radicans* tolerated better than *F. vesiculosus* the future combination of hyposalinity and warming and phenotypic plasticity occurred even within clonal lineages. From these results, it appears that *F. radicans* is a key-species for the future Baltic Sea environment and may eventually replace *F. vesiculosus* throughout the Baltic Sea. However, our experiments also show that resistance to grazing from *Idotea balthica* decreases in future conditions, and this may be a too great challenge for both species of *Fucus*. In contrast, we can be confident that sticklebacks will be able to adapt and survive future salinity changes in the Baltic Sea. Results from our experiments show that Baltic stickleback has a better tolerance towards decreased than increased salinity. These changes will strongly affect the future Baltic Sea ecosystem, but in what way remains unclear.

### A need for dialogue

Our political science studies clearly show that there is a gap between what the scientific community knows about genetic biodiversity and how it is handled in conservation management. This gap is perhaps more worrying for the Baltic Sea biodiversity than for biodiversity elsewhere, because genetic diversity is of particular importance in this young and species-poor ecosystem. We show that continued information and dialogue between researchers and authorities are necessary to establish and implement management measures protecting critical and/or endangered parts of the genetic diversity. Moreover, we can show that the current distribution of MPAs does not give enough support to important genetic variation or to sites important to maintain a high connectivity among Baltic Sea populations.

**Overall**, the BONUS-BAMBI project has generated new and critical data on genetic variation of Baltic Sea populations. Contrasting earlier beliefs, local adaptation of Baltic Sea populations is the rule rather than the exception, and BONUS-BAMBI has demonstrated this in a number of non-commercial species. With this knowledge at hand, it is worrying that – as documented in BONUS-BAMBI – there is so little focus on genetic biodiversity in management of non-commercial species important to the functioning of the marine ecosystems.

### The continuity plan of the project

Many of the research results generated in the BONUS-BAMBI project are currently being quality checked and made publicly available through publications in open access scientific journals. Already more than 25 scientific papers have been published that had full or partial support from the BONUS-BAMBI project, and another 20 publications are in pipeline as manuscript. During the BONUS-BAMBI project a massive amount of sequencing data has been generated that will be continued to be analysed for the coming 1-2 years and generate publications in the coming years.

Main highlights from our results are currently being made available on the BONUS BAMBI website for managers, <https://bambi.gu.se/baltgene>. An important conclusion from interviews and discussions with managers around the Baltic Sea, is the need for better communications between science and management.

As a direct consequence of the project, a pilot project funded by the Swedish Agency for Marine and Water Management (SWAM) has initiated and is led by Johannesson and Laikre. This project will benefit considerably from the knowledge generated in BONUS-BAMBI. The project will suggest a monitoring program for genetic diversity in Swedish waters. Moreover, the knowledge generated in BONUS-BAMBI is fed into a larger study of genetic variation in northern and western Europe, in the Biodiversa program MARFOR.



End-user conference BaltGene 2017 gathered almost 60 managers, policy-makers and scientists from around the Baltic Sea. For two days, knowledge and experiences was shared on why and how genetic biodiversity should be included in Baltic Sea management. Photos: BONUS BAMBI.