



BONUS-BAMBI

Management recommendations

Improve adaptive potential of Baltic Sea species - include genetic diversity in management

Maintaining biodiversity is a crucial goal for the Baltic Sea. But it cannot be reached without also protecting the diversity within species – the genetic diversity. Increased awareness and recognition of the role of genetic diversity is therefore needed.

Genetic diversity is the biological variation that occurs within species. It forms the basis for all biodiversity and makes it possible for species to adapt when the environment changes. Large genetic diversity within dominant species positively affects ecosystem resilience and function.

The genetic diversity of Baltic Sea species is unique and particularly vulnerable. It has been shaped over thousands of years by natural selection, resulting in local adaptation to the brackish environment.

Populations of marine species in the Baltic show lower levels of genetic diversity than elsewhere and remaining variability needs protection. The most efficient way to counteract loss of genetic diversity is to maintain large and well connected populations.

Small and isolated populations will rapidly lose genetic variation resulting in lower adaptive capacity, loss of resilience and weak potential for long-term survival. Activities such as heavy fishing, stocking, or habitat fragmentation can negatively affect the genetic diversity.

The BONUS BAMBI research project

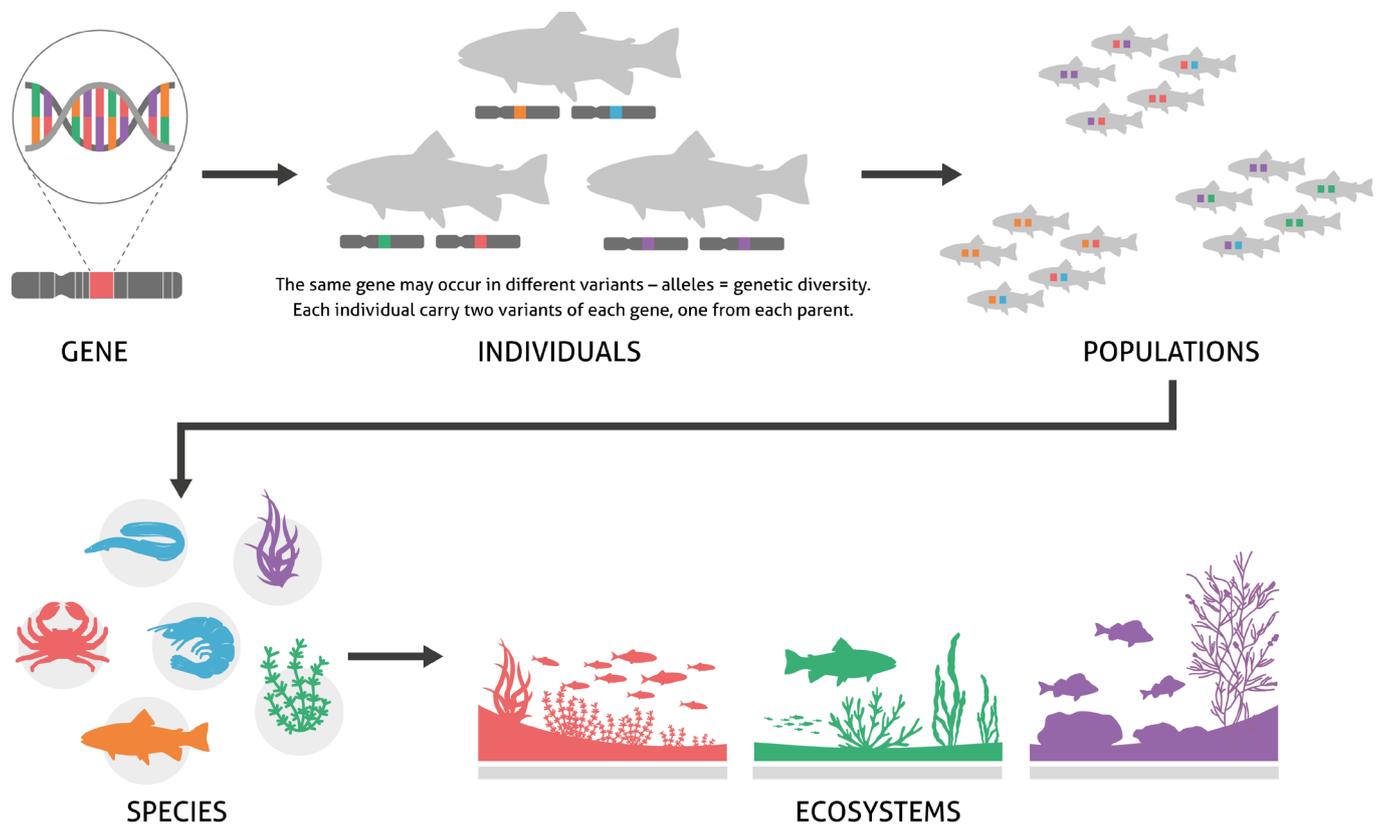
BAMBI is short for Baltic Sea Marine Biodiversity - a project funded by the BONUS EEIG under EU: bonusportal.org

The project ran 2014-2017 and was led by Professor Kerstin Johannesson at University of Gothenburg.

More about BAMBI: www.bambi.gu.se
More about genetic diversity of the Baltic Sea: bambi.gu.se/baltgene



The Baltic salmon is strongly structured genetically. Historically each river harbored at least one genetically unique population. Lost reproduction of separate rivers has resulted in loss of unique biodiversity. BAMBI research shows that such losses also affect the system of salmon populations as a whole; when separate populations are removed, the rate of loss of diversity will increase in remaining rivers. Further, compensatory releases pose genetic threats to wild salmon. Photo: Ingemar Petersson/Azote



Genetic diversity is variation at the DNA level (here symbolized with colors). It forms the basis for all biodiversity. The adaptive potential of species, and the resilience of ecosystems relies on genetic diversity (colors at species and ecosystem levels symbolize diversity at those levels). Illustration: Jerker Lokrantz/Azote

Genetic diversity not considered in MPA management

Halting the loss of biodiversity is a global priority included in the UN Sustainable Development Goals. At EU level, member states are responsible for implementing the Birds and Habitat Directives and ensuring that species and habitats are protected. The European Commission's new **Action plan for nature, people and the economy** consists of 15 actions to be carried out by 2019. By accelerating the member states' implementation of the Birds and Habitats Directives, the Commission hopes to improve the overall protection of Europe's threatened species and habitats. As recognised in the UN Convention on Biological Diversity this cannot be achieved without protecting genetic diversity.

However, new research from the BONUS BAMBI project shows that genetic diversity is insufficiently taken into account in practical management. International and national policy for genetic diversity is not reflected in the management of marine protected areas (MPAs) in the Baltic Sea¹.

Marine policy at international and national level lags behind with respect to genetics; targets and goals from the Convention on Biological Diversity on genetic diversity is clearly reflected in the EU Habitats Directive but not in the EU Marine Strategy Framework Directive. An interview study² with regional managers working with MPAs in the Baltic Sea supports the observation that genetics are not considered, mainly because managers lack clear guidance and knowledge of genetic diversity.

What is genetic diversity?

Genetic diversity is the occurrence of variation at the molecular level of the DNA, resulting in variants (alleles) of separate genes.

Genetic diversity is the basis of all other biological variation. When we drain species of their genetic diversity we destroy their adaptive potential and their long term survival will be jeopardised. Genetic diversity is particularly important under rapid environmental change, such as in the Baltic Sea.

Most species are subdivided into local populations, which are more or less genetically distinct. The reason for the subdivision is often a combination of local adaptation and isolation. If isolation increases for instance due to loss of nearby populations then genetic variation will likely decrease over time.

Knowledge is available

A recent synthesis³ of current knowledge of genetic diversity for Baltic Sea species shows that for over 60 species, we have at least some data on genetic diversity. For around 20 species, we have useful knowledge that can inform management and conservation of these species. This includes ringed, harbour and grey seals and harbour porpoise, eleven of the most common fish species and a number of habitat-forming species such as bladderwrack and blue mussel.

Genetic uniqueness of Baltic Sea populations

Baltic Sea populations of a majority of species are genetically distinct. The uniqueness of the Baltic salmon was recognised already in the 1980s and the cod east of Bornholm is, based on recent genetic data, a separate species. The flounder and the bladderwrack have both diverged in the Baltic Sea and formed new (and endemic) species. The genetic distinction of Baltic Sea populations is coupled with rapid genetic adaptation to the Baltic environment, not least the low salinity.

Strong genetic differences in bladderwrack

The important habitat-forming bladderwrack exhibits strong genetic differences between different parts of the Baltic Sea. This means that if the bladderwrack is lost in one part of the Baltic Sea, unique genotypes and genetic variation are lost. In particular, the bladderwrack in Southwestern Finland and Estonia is genetically very different from other populations.

In the Bothnian Sea and in the Gulf of Finland, bladderwrack and the closely related narrow wrack have evolved asexual reproduction. Along the Swedish coast of the Bothnian Sea one female clone is dominating most populations, resulting in very low capacity for adaptation. The populations in Estonia and western Finland are less clonal and should be in focus for conservation.

Genetics of fish populations needs recognition

The majority of fish species form more or less genetically distinct groupings within the Baltic. Most socio-economically important species, including herring, salmon, cod, trout and pike need management that combines local and large scales. Locally, spawning grounds of genetically different populations need maintenance. Over large scales, naturally occurring genetic exchange among local groups needs safeguarding and total population size kept large.

Many commercial fishes are subjected to strong fishing pressures and release of individuals raised in captivity (stocking) which poses risks of loss of genetic diversity.

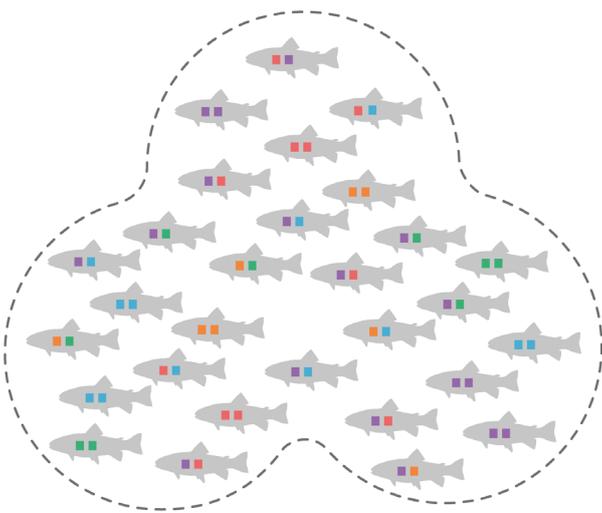
Ensuring connectivity between marine protected areas

To maintain genetic diversity of species, their populations should be large and well connected. Small and isolated MPAs may result in populations rapidly losing genetic diversity, which will jeopardise population persistence and species survival.

Larval transport and drifting of individuals or reproductive parts are crucial to connect populations. Modelling of transport of larvae and individuals shows that the current network of MPAs in the Baltic Sea do not fully ensure genetic exchange between the single MPAs. Also, many MPAs are too small. The models can be used to show how the MPA network can be extended in order to improve connectivity.

HIGH GENETIC DIVERSITY

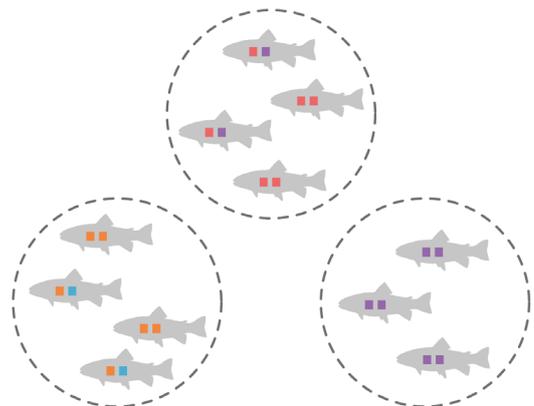
Large populations retain high genetic diversity



- Higher adaptiv capacity
- Potential for long term survival
- High resilience

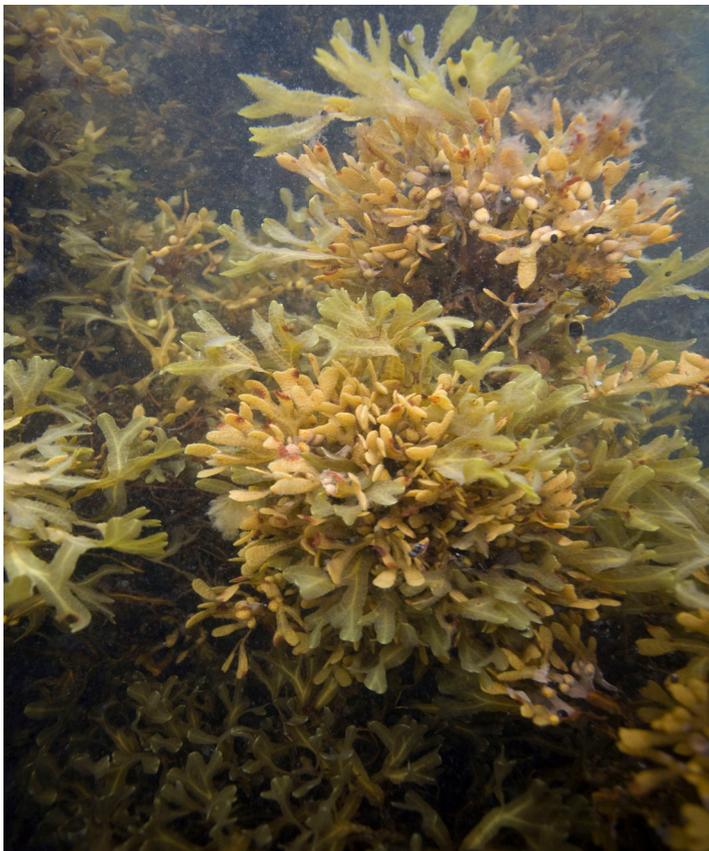
LOW GENETIC DIVERSITY

Small, isolated populations lose genetic diversity



- Lower adaptiv capacity
- Weak potential for long term survival
- Loss of resilience

Large populations can harbour much genetic diversity (illustrated with many colours). Small population cannot do that and will rapidly loose variation. Illustration: Jerker Lokrantz/Azote



Bladderwrack and the closely related narrow wrack are the most important habitat-forming seaweeds in the Baltic Sea, with a wide distribution including the Bothnian Sea, Gulf of Finland, Gulf of Riga and the Baltic Proper. Photo: Hans Kautsky/Azote

Recommendations

Assure that the goals regarding genetic diversity in international and national policy documents are reflected in the regional MPA management plans and goals.

Make effective use of existing scientific knowledge regarding genetic diversity in both fisheries management, and in designing MPAs. Use genetic information in stock assessment of commercially targeted fish species in order to prevent overharvest of local stocks in mixed fisheries. Use information on dispersal and population connectivity in the design of networks of MPAs in order to allow dispersal and genetic exchange between protected populations.

Support the development of genetic mapping and monitoring programs for key ecological species, including habitat-forming species such as bladderwrack, seagrass, mussels and socio-economically important fishes such as salmon, cod, brown trout and pike.

Bridge the gap between researchers and managers by supporting platforms for regular meetings and knowledge transfer concerning genetic diversity so that available knowledge can be used in management.

References

¹Laikre L, Lundmark C, Jansson E, Wennerström L, Edman M, Sandström A. 2016. Lack of recognition of genetic biodiversity: international policy and its implementation in Baltic Sea marine protected areas. [Ambio 45:661-680](#).

²Sandström A, Lundmark C, Jansson E, Edman M, Laikre L. 2016. Assessment of management practices regarding genetic biodiversity in Baltic Sea marine protected areas. [Biodiversity and Conservation 25:1187-1205](#).

³Wennerström L, Jansson E, Laikre L. 2017. Baltic Sea genetic biodiversity: current knowledge relating to conservation management. [Aquatic Conservation: Marine and Freshwater Ecosystems, 2017: 1-22](#).

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