



BALTGENE

BALTIC SEA GENETIC BIODIVERSITY

Genetic diversity is crucial for ecosystem function and sustainability. BALTGENE provides new genetic data on ecologically and socio-economically important species and shows that many authorities treat genetic diversity suboptimal with negative consequences on aquaculture and wild populations. BALTGENE shows how the information can be readily used in sustainable management, and designs studies that will fill part of current information gaps.

KEY RESULTS

- Current conservation policy lacks implementation for genetic biodiversity in the Baltic Sea
- Large gaps in knowledge on genetic biodiversity in the Baltic Sea have been identified with a very few species having acceptable levels of genetic data for proper management
- Species are in general genetically heterogeneous in the Baltic Sea which means that each species is divided into several more or less independent populations
- Commonly used methods over-estimate loss of genetic diversity in the presence of gene flow and many fish populations are not that seriously threatened than earlier thought
- Connectivity (dispersal) is a major factor for sustainability of most Baltic populations, being more important than habitat quality, and models are developed that can be used to predict optimal designs of Marine Protected Areas
- Genetic diversity support ecosystem function and resilience for seaweeds, indicating direct values of genetic diversity in addition to long-term values
- Release of fishes can compromise genetic diversity and local adaptation which should be taken into account during restocking

WHO NEEDS THE INFORMATION

The authorities responsible for developing the management plans. Such plans are needed for all ecologically and/or commercially important species to support long-term survival, and these must be based on information about genetic structure within and among populations, and on patterns of connectivity among populations.

PROJECT PARTNERS

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