

WP2: Integrating evolutionary ecology into coastal and shelf processes (Allan Cembella, Veronika Hellwig)

We define and interpret evolutionary strategies and chemical ecology of temperate and polar marine organisms with respect to adaptation to changing regimes in coastal and shelf seas

Objectives and challenges

Our primary objective is to show how organisms have evolved and adapted to their physical, chemical and biotic environments in coastal and adjacent shelf ecosystems. All coastal regions, but especially in the Arctic and on the Western Antarctic Peninsula, are currently undergoing the greatest and most rapid climate-mediated change of any region on Earth. Comparative investigations in the different climatic regions will broaden our understanding of evolutionary adaptations and acclimation capacities in model organisms. The WP will provide organism-based modules to model response to change in coastal communities from different climatic regions. Challenges implicit in this research are to:

- Link causes and consequences of evolutionary change in species, both in coastal and shelf seas in polar and temperate latitudes to improve conceptual modelling of change in both regions;
- Differentiate the effects of intrinsic (genetic) versus extrinsic (habitat) factors, in shaping physiological processes among coastal model species and populations under different climate conditions along latitudinal gradients;
- Establish the absolute and relative importance of chemical ecology and anthropogenic substances in cellular responses, chemical ecology and population dynamics of model species.

Implementation

The hierarchical systems approach in the WP integrates physiological, metabolic and genetic processes, from the molecular and cellular level to whole organisms and populations. The response to change as expressed via life history stages of *model species* will be combined with analyses of population genetics and dynamics and their capability to archive environmental change. Studies on behaviour, gene flow, and physiological/ metabolic adaptations in response to environmental forcing will be conducted in controlled laboratory experiments and through field research. Comparative research on morphological, ecological, biochemical and molecular stress signals and pathways regulating metabolism and biosynthesis of primary and secondary metabolites will be compared in seaweeds, protists and marine ectoderms (cold-blooded animals) from polar and temperate climates.

In collaboration with other Workpackages and external partners, this WP will target adaptive strategies, such as those employed to evade or respond to stress. This involves cell systems and signalling pathways, as well as physiological and ecological adjustments of single cells and organisms. A functional genomics approach combined with bioinformatics will be employed for gene expression studies and population genetic modelling. Key species will be empirically selected, based upon their evaluated importance in elucidating critical processes and mechanisms. The research is partitioned into the following sub-work packages.

Acclimation & adaptation in changing coastal systems

The hypothesis that polar marine invertebrates and seaweeds are highly specialized and thus of low adaptive capacity when confronting environmental fluctuations will be explored. The extent of adaptive biodiversity and competitive abilities in model species will be studied throughout all reproductive phases, with a particular focus on the “bottleneck” of early life history stages (link to WP1). Investigations will range from developmental shifts in temperature/salinity tolerance of larvae and spores through expression of metabolic enzymes and stress proteins to gene expression patterns. The focus will be on model species of crustaceans, molluscs and seaweeds from polar and temperate coastal environments. Cell, organ and whole-animal models will be developed for standardized studies of natural and anthropogenic stress (link to WP4 on marine mammals). Long lived and locally autochthonous (= staying in place) bivalves from temperate, tropical and polar environments will be studied with respect to energy budgeting, survival strategies and stress response over their lifetimes. Cellular ageing and autophagy will be studied in soft tissues, and trace element accretion into shells will be analyzed as archives for coastal climate change (link to WP4, TO1-WP6).

Chemical ecology and responses of coastal and benthic communities

This element focuses on natural bioactive substances and potential synergistic interactions with man-made toxicants, on allelochemical interactions and molecular ecology of toxic protists. Model organisms will be selected among the marine bacteria, seaweeds, protists, invertebrates and fish. New elements to be incorporated include regulatory aspects of bacterial-protist and grazing interactions in response to chemical signals (link to WP1). Cell model systems will be established from naturally occurring single cells (sea urchin eggs, protists) or primary cell cultures to analyse effects of bioactive substances on cellular regulation. Expression of specific ion channels, receptors and genetic manipulation methods will be explored for defining function of cellular targets.

Molecular tools (e.g. microsatellites, DNA microarrays) for analysis of genetic diversity and gene expression of toxic metabolites will be combined with natural products chemistry for elucidation of biosynthetic pathways. Functional gene hunting for regulatory genes will be pursued by limited genomic studies on selected toxigenic algae and interpreted by bioinformatic analysis. Such diagnostic systems for key chemically mediated metabolic processes are expected to play a future role in biotechnological applications. An integrated study of benthic communities with respect to chemical ecological interactions will incorporate chemical defence and signalling strategies of resident benthic toxic dino-flagellates and seaweeds and associated bacterial and invertebrate grazer assemblages, as well as toxin transfer among benthic and pelagic compartments. This information will help to understand food web relations (WP1).

Functional genetics and population dynamics

High-resolution molecular markers will be employed to determine the adaptive strategies of model organisms from among marine animal ectotherms, seaweeds and protists. For example, related species from the South American Magellan region and from coastal Antarctica will be compared to identify genetic features supporting survival under polar conditions. This will be linked to comparative analyses of population structures and growth dynamics of selected species along the European coastal margins, focussing on the North Sea and Wadden Sea. Genetic proxies selected as model organisms are essential to understand evolutionary and acclimation strategies. The resulting data will be provided as modules for modelling the ecosystem response to different disturbance scenarios (links to WP1 and WP4).

Research will focus on selected marine phytoplankton (e.g., harmful algal species), macroalgae, marine invertebrates and fish. Different dispersal and growth strategies (pelagic larvae, benthic cysts) and abiotic factors including coastal geomorphology and currents, fragmentation of coastal habitats and temperature gradients will be scrutinized for their role as promoters or barriers to gene flow between populations. Integrating molecular techniques for population genetics with functional genomic analysis will yield critical information to predict species responses to coastal change and conservation strategies.

Integration of the three sub-elements of this WP will yield the following deliverables:

- Determination of the interactions and mechanisms of natural bioactive compounds and man-made chemicals in selected marine organisms, including protein expression and their role in defence, growth, toxicity and metabolism;
- Determination of structure, biosynthetic pathways and gene regulation of natural bioactive components, e.g. algal toxins;
- Estimates of adaptive capacity, genetic diversity and gene flow within model coastal species along latitudinal gradients, e.g. comparing North Sea, with Arctic and Southern Ocean populations;
- Identification of cell signalling pathways and proxies for aging and stress responses for bio-archiving of environmental changes in marine species.

Milestones

- Identification of the mode of action and cellular effects of known natural phycotoxins and key anthropogenic compounds (year 2);
- Complete biosynthetic pathways and structural elucidation of polyether algal toxins and other selected bioactive metabolites from marine invertebrates (year 3)
- Demonstration of the utility of cell signalling mechanisms and practical proxies for stress and aging responses in bio-archiving of global and regional change in coastal species (year 4)
- Development of a coupled physiological-genetic conceptual model, comparing polar versus temperate populations of at least one species of seaweed, protist, crustacean, bivalve mollusc and fish, in terms of their adaptive capacity and evolutionary strategies for survival (year 5)