
Genetic Biodiversity: a network cross-cutting themes (RMP 4.1)

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Today, ecological information is available for most keystone species of marine environments while we certainly lack information on the genetic variation of even the most important species and populations, in particular at a European scale. There is a need to resolve the genetic structure of a set of species at a level of detail suitable to make predictions on how global and local perturbations will influence the structuring and the phylogeography of species and their populations.

The main objective of the project is to build a network permitting analysis of the factors influencing the genetic structure of populations of marine taxa to explain the establishment and the evolution of patterns of biodiversity at different scales, local to European (themes 1+2). Such a network is necessary to assess the genetic responses of taxa to short term perturbations and global change (theme 2). Distribution areas are often so wide that a network is the only means to perform the necessary sampling, especially when repeated sampling is required (*e.g.* to study temporal effects in relation to environment changes). This will provide a better understanding of the impact of current biological and anthropogenic processes on the maintenance and sustainability of natural populations and of the processes determining how population structures vary according to ecological and biological traits (life history, reproductive mode, behaviour). It will also provide insights on how the interactions of these traits with physical processes influence population structures (enhancing or restricting gene flow between populations. *e.g.* fragmentation of populations, spatiotemporal compartmentalization over gradients [salinity, temperature], artificial selection due to contaminants, effects of various stresses) and hence the evolution of these populations. The strength of a particular interaction or process (*i.e.* mechanisms underlying functional biodiversity) may vary from one location to another. Such an approach will also permit to detect the signature of historical changes that may explain the present distribution of some taxa, especially the impact of past climate changes on marine life.

The collaborations inside the network will allow comparisons among taxa, which are necessary for a general study of marine communities. Using a multi-species approach across Europe will permit, for the first time, to link the population-species level with the ecosystem function. A European-scale network will also provide the opportunities for using complementary molecular techniques, and also opportunities for training in a context of rapid technical and theoretical progresses.