

Functional genomics using marine fish cell lines and embryos

Duration: 36 months

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Abstract

Recent efforts aimed at elucidating genomes of multiple organisms have shown that the number of putative genes for which a likely function can be identified from *in silico* analysis only is at best 50%, based on comparison with other known genes from different organisms. This number can be much lower for genomes from non-mammalian vertebrates such as fish, decreasing in direct proportion to the increasing degree of evolutionary distance from mammals. In addition, the variety of marine environments have led to quite different mechanisms of adaptation that have often resulted in evolutionary related proteins with very different functions. Even when functions are related, expression patterns have often been found to be different both in time and space. For these reasons, genome sequence analysis must be followed by a second level of approaches collectively known as functional genomics, which are required to assign functions to specific genes and their transcripts based upon experimental rather than *in silico* only evidence. The main objective of this project is to develop molecular tools towards the identification of gene function in fish. Genome sequence analysis initiated during the first phase of Marine Genomics Europe NoE must be complemented/ followed by functional genomics to assign a function to specific genes based upon experimental rather than *in silico* only evidences. These functional studies need: (1) *in vitro* cellular models from various tissues to answer specific questions on gene function and regulation, (2) *in vivo* fish models suitable to verify the functional significance of selected genes, and (3) tools for large scale analysis of gene function. *In vitro* studies on specific gene function and regulation will be done through the use of gilthead seabream [*Sparus aurata*] cell lines already available (bone, branchial arch and fin) or developed within the scope of this work package (hepatocyte and adipocyte). Embryos from Atlantic killifish [*Fundulus heteroclitus*] will be used for *in vivo* studies. Large scale analysis of gene function will be done using tissue-specific shRNA libraries to silence gene expression in both *S. aurata* cell lines and *F. heteroclitus* embryos.