AQUAFIRST

Complete Title: **Combined genetic and functional genomic approaches for stress and disease resistance marker assisted selection in fish and shellfish**

Duration : November 2004-May 2008

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Summary

The overall aims of the project is to identify, in sea bream, sea bass, oyster, and rainbow trout, genes of which expression is associated with disease and stress resistance and, from this information, to develop genetic approaches that allow characterisation of genetic markers for marker-assisted selective breeding of disease and/or stress resistant individuals.

For such project, the following main objectives will have to be reached:

- Characterisation in sea bream, sea bass, trout and oyster, stress- and disease-responsive genes as potential candidate gene markers for desirable traits;

- Seeking associations between (i) variations in response to stress and resistance to pathogen and (ii) selected candidates genes and microsatellites markers by segregation analysis in appropriate families (QTL analysis);

- Mapping of these genes in linkage and gene maps.

In order to characterize disease and stress-responsive genes in seabream, sea bass, trout and oyster, a common strategy using microarray technology have been developed. During the first year of the project, construction of relevant cDNA collection using an SSH approach have been initiated and will provide large dedicated EST collections to be spotted on glass slides. Moreover, in order to provide to partners access to microarray facilities, a management structure is accessible: this includes a microarray platform devoted to the construction and analysis of microarrays for the project and a bioinformatic resource centre for gene expression data management. These tools will be further used to analyze gene expression profiles in animals exposed to stress or to pathogen.

During the first year of the project, we have also started several tasks devoted to characterization of genetic markers associated with stress or disease resistance. This includes search for SNP in stress or disease-resistant genes, production of relevant biological material (oyster and trout) on which a QTL analysis would be developed, development of new genetic markers (microsatellites) which would be later used for genotyping individuals in QTL protocols, construction of a radiation hybrid panel for sea bass. These tasks initiated during the first year will continue and expand during the second year.