

European Commission

6th Framework programme [Priority 8: Policy-oriented research]

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

« **AQUAFIRST** »

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Participants

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Introduction

* **Overall aim:** Provide the physiological and genetic basis for marker-assisted selective breeding in fish and shellfish.

* Possibility to characterise stress-responsive genes as potential candidate gene markers for selective breeding.

* **Working hypothesis:** Stress and disease responsive genes might be genetically linked to Quantitative Trait Loci (QTL) which control genetic variation in stress and disease resistance.

→ Take advantage of tools and material from BRIDGEMAP, BASSMAP and STRESSGENES projects.

Objectives and expected achievement.

♦ Four species: Oyster, seabream, seabass and trout.

♦ Situations: confinement stress (fish), resistance to summer conditions (oysters), resistance to pathogen (fish and shellfish).

♦ Main objectives:

♦ Characterisation of stress and disease-responsive genes in the four species.

♦ Determination of genetic parameters of stress and disease resistance by seeking associations between (i) variations in phenotypic response to stress and disease response and (ii) selected candidate genes and microsatellites markers (QTL analysis).

♦ Provide specific protocols for selection and Marker Assisted Selection.

Part 1: Characterisation of genes involved in the functional response to stress and pathogen exposure

- Relevant EST collections in oyster, seabream, seabass (trout: cf. *Stressgenes*).
- Construction of species specific microarrays (microarray technical platform, West Genopole, Brittany).
- Gene expression profiles in relevant tissues during responses to stress and pathogen exposure (seabream, sea bass, trout selected for resistance to confinement stress, oyster exposed to hypoxia or bacterial challenge).

Part 2: Characterisation of SNP in stress/disease-sensitive genes

- In trout and oyster.
- From previously selected EST or genes (part 1)
- Analysis carried out within coding sequences and also promotor region.

Part 3: Identification of QTLs and candidate genes related to stress and disease resistance.

- **Production of biological material:**
 - Trout and oysters: F1 and F2 segregating families for QTL
 - Seabream and sea bass: F1 and F2 families selected for growth (already available)

- **Phenotyping and genotyping:**
 - High resolution mapping of sea bass and seabream genome (continuation of Bassmap and bridgemap project).
 - Radiation hybrid (RH) panel for seabream.
 - QTL characterisation and mapping.

Part 4: Protocols for selection in seabream, sea bass, trout and oyster

Provide sustainable breeding programs for:

- **Marker Assisted Selection (MAS)**
- **Marker Assisted Introgression (MAI)**

Expected achievements.

- ◆ Completion of molecular tools and biological material previously developed in oysters, seabream, sea bass and trout (genome map, functional candidate genes, selected families....)
- ◆ Molecular markers (functional candidate genes) for stress and disease diagnostic.
- ◆ Genetic markers related to stress and disease resistance traits.
- ◆ Protocols for selections.