

AQUAFIRST

Enrichment of aquaculture implants by introduction of new marine species from the wild to breeding

The Challenge

Under intensive aquaculture breeding conditions, fish are exposed to various unavoidable stressors. These stressful conditions lead to an overall reduction in performance, including poor acclimatization and growth performance, impaired reproduction and increased susceptibility to disease. These conditions lead farmers to rely on antibiotics and drugs. During the summer months significant mortality of Pacific oysters occurs in several countries. A complex mix of physiological, environmental and pathological causes is the origin of the problem.

Stress factors have a significant effect on the performance of the fish-farming sector. The effects of these factors could be improved if the risk of stress and disease were reduced through targeted, selective breeding.

Project Objective

The AQUAFIRST project sought to identify genes associated with stress and disease resistance in fish (sea bream, sea bass and rainbow trout) and molluscs (oyster) to provide a physiological and genetic basis for marker-assisted selective breeding of disease and/or stress resistant individuals.

Key Points

- Historically experiments were based on extraction of RNA from the most relevant tissues per stressor per species e.g. trout was exposed to the VHS virus and fin and spleen tissues were tested. Based on this, a relevant Expressed Sequence Tag (EST) collection was constructed of cloned genes that are implicated in either confinement stress or pathogen exposure.
- Specific markers, known as SNP markers, were developed, so as to improve the density of the available linkage maps.
- These maps were then used to increase the probability of detecting the desired Qualitative Trait Loci (QTL) - regions of DNA of which the expression is associated with disease and stress resistance. These QTL's were analysed to identify genes associated with stress specific traits and disease resistance traits.
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- Finally, operational genetic protocols were outlined, incorporating identified QTL and traditional breeding approaches in oyster, sea bream and sea bass.

EATiP Thematic Area of Relevance

- TA1:** Product Quality, Consumer Safety and Health
- TA2:** Technology and Systems
- TA3:** Managing the Biological Lifecycle
- TA4:** Sustainable Feed Production
- TA5:** Integration with the Environment
- TA6:** Knowledge Management
- TA7:** Aquatic Animal Health and Welfare
- TA8:** Socio-Economics and Management

Key Words

Genomic, stress resistance, disease resistance

Project Information

Contract number:
513692

Contract type:
Networks of Excellence

Action Line:
POLICIES-1.3 The modernisation and sustainability of fisheries policies

Duration:
42 months (01/11/2004 – 03/04/2008)

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Output Highlights

Genomics resources:

The AQUAFIRST project has increased the number of EST sequences (Expressed sequence Tags) in sea bream, oyster, trout and sea bass databases, all important resources for many genomic studies, including annotation of the genome of these species. The project developed transcriptome analysis in trout, sea bream, sea bass and oyster. These new databases will significantly contribute to the development of genomic tools and approaches within European research laboratories.

Location of functional candidate genes for immune and stress response

These microarrays analyses led to the production of lists of genes of which expression was significantly up or down regulated after exposure to stress. In trout and oyster, comparison of gene profiles obtained in divergent selected lines focused on genes potentially involved in genetically-based expression differences. For oyster and trout selected genes, this information was transferred for Single Nucleotide Polymorphisms (SNP) analysis. Candidate genes for SNP were identified and analysis of these transcriptome data was carried out to identify potential biological processes (molecular or cellular) which could be associated with stress (confinement, pathogen exposure) responses in the test species.

Quantitative Trait Loci (QTL) existence and mapping

QTL mapping protocols were developed for species that exhibit a range of biological and reproductive characteristics. Heritability estimates were provided for growth and morphological traits in both sea bass and sea bream, and QTL were found for both traits in the two species. QTLs were identified for disease resistance (in sea bream and trout) and summer survival (in oyster). For the first time, QTL involved in osmoregulation ability were discovered in trout. Significant or suggestive QTL were mapped for cortisol response to confinement in trout and sea bass, while none could be identified in sea bream. QTL contributed to a substantial part of the variability of the traits under study.

Animal welfare

Information generated in the project can be utilised to improve health and welfare of aquaculture species. The effect of integrating such QTL with various effects in mass selection for aquaculture species led to genetic gain consistent with the results from other species. However, an unexpected behaviour of inbreeding was detected with potential undesirable effects on performances.

Access to new technology

Training sessions open to all partners to learn microarray technology and the bioinformatics tools to be used for analysing microarray data were provided during the course of the project.

The Full Report

For a description of the research project, visit <http://aquafirst.vitamib.com/>

Next Steps – Suggested Actions/Follow On



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- Further studies aimed at understanding the variation of immune and stress response is required. There is an inherent difficulty associated with the analysis of complex traits such as resistance to stress or to pathogens. There is a need to refine the description of complex traits such as stress response and getting a more detailed characterization of phenotypes including functional genomic information.
- Further work is required in the areas of choice of reference populations, and the choice and standardization of phenotyping procedures before genomic selection can be implemented in aquaculture.
- QTL analyses illustrate the benefits which could result from improvements in mapping resolution- the addition of more markers on these maps would contribute to a more precise characterisation of these QTL, and would help to target positional candidate genes.



Knowledge Transfer

- Further discussions involving geneticists and physiologists are needed in order to fully integrate structural and functional information in the first steps of QTL detection.

Related Publications/Projects

- AQUAGENOME (FP6)
INRA-SIGENAE (Toulouse, France 2009 -2010).