

**BRIDGING GENOMES: AN INTEGRATED GENOMIC APPROACH TOWARDS  
GENETIC IMPROVEMENT OF AQUACULTURED FISH SPECIES". BRIDGE-MAP  
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BRIDGEMAP consortium (<http://www.bridgemap.tuc.gr>):

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### **Objectives**

The aim of the project is to produce important genome resources and tools in gilthead seabream (*Sparus aurata*) in a generic way for marine fish species, which can optimise the investment in genome resources and apply it in a pilot breeding program. This will contribute to the improvement of the gilthead seabream production, including aquaculture and sustainable yield of fisheries, up to the quality control and traceability. The main elements of the project are:

- **transfer** genetic information, by using a comparative genomic approach (based on 1500 genes and ESTs), from model organisms to commercial species and **integrate** genome maps of various ray-finned fish (zebrafish, medaka and fugu) with data from higher vertebrates,
- **bridge** the QTL mapping approach to comparative genomics and the gaps in maps by merging physical and linkage maps (based on 300 microsatellites mapped on linkage map & RH map), also estimating the distribution of recombination rates across the genome, **bridge** the distance between aquaculture research and industry, and **integrate** evolutionary theory and modern technology to generate an applied endpoint
- **demonstrate** in a pilot scale the application of the above by initiating a selective breeding programme in an aquaculture industrial partner and **apply** the developed tools to perform Marker Assisted Selection (MAS)

### **Achievements**

#### ***Radiation Hybrid Panel***

A high quality seabream whole-genome radiation hybrid panel was produced with an average retention rate estimated at about 27%. The panel has improved characteristics compared to other ones (e.g. zebrafish): (a) it has been obtained from primary fibroblast cell culture (not from cell lines), thus avoiding chromosome rearrangements, (b) DNA amplification of hybrid cells is obtained by PCR, leading to less marker loss with parallel gain of several months in developing the tool and leading to practically no limitation of DNA amount. This is a high quality panel, unique among non-model species, that is estimated to be good for mapping of several thousands of genes.

### ***Radiation Hybrid Map (RH map)***

The first radiation hybrid map in any commercial fish ever until now is reality. It comprises 450 markers including both microsatellites and genes (or ESTs) among them, some candidate genes for growth. The analysis of the first 450 vectors gave 28 RH groups (for n=24 chromosomes) with 2 to 19 markers each and 15 unlinked markers.

### ***ESTs***

A total number of 3021 ESTs has been produced from different tissues. Among them, 1812 ESTs are unique and 1209 redundant and have been obtained from several cDNA libraries, as shown in the figure below. Many interesting genes have already been annotated among them, comprising a few of the innate immune system. An additional number of 2500 ESTs is about to be obtained from a normalised headkidney cDNA library, which will bring the available ESTs to more than 5000.

### ***Microsatellites***

More than 200 microsatellites have been produced and optimised and about half of them were used for genotyping the linkage panel (2 parents of wild origin and 48 of their F1 progeny).

### ***BAC library***

A 6x coverage of the genome was obtained with an arrayed BAC library.

### ***Breeding Program and Quantitative Trait Loci mapping (QTL mapping)***

An F1 generation was obtained, initiating a QTL project for growth in a commercial fish farm. Multiplexing of microsatellites has been achieved that will allow rapid parentage assignment.

### ***Database***

A database has been developed which centralises all types of data and analyses.

### **Expected results**

The expected achievements comprise 1500 annotated genes and ESTs mapped on the radiation hybrid panel as well as 300 microsatellites markers. These microsatellites will be used to produce a linkage map and also to merge the two maps. The map of genes will allow producing **comparative maps** with the model fish species and higher vertebrates, giving access to their rich functional information, while microsatellites will link QTL mapping and candidate genes approaches. Furthermore, the BAC library thanks to published genomes, will allow rapid positional cloning of candidate genes, and detailed study of practically most genes of interest. All information will be centralised in the dbBRIDGE-MAP database and will be made available on the web. The breeding program initiated at Nireus Aquaculture will be based on BLUP analysis, partial QTL mapping and candidate genes approach, allowing ambitious follow up.

### **Practical Applications**

The practical applications will be straightforward the selective breeding of Nireus Aquaculture and furthermore to any Aquaculture company that want to start or to optimise a breeding project.

The RH tool has made very easy and fast the mapping of any gene of interest e.g. produced at high rates by running functional projects, and will tremendously enhance the potential of selective breeding for more and more characters in an increasingly precise way.

The BRIDGEMAP consortium is loosely clustered with the BASSMAP consortium to the benefit of both projects.