

ABSTRACT

Biofouling is the undesirable growth of living organisms (bacteria, algae, mollusks etc.) on structures submerged in water which causes serious problems for the aquaculture and maritime industries. A number of physical and chemical technologies have been applied in antifouling paints (AF), the most effective of them being the use of tributyltin coatings. However, due to toxicity caused by tributyltin and heavy metals, in September 2008, the International Maritime Organization (IMO) banned the use of self-polishing tributyltin coatings and there is increasing opposition to the use of copper. Preventing the settlement of fouling organisms in a non-toxic manner would be the ideal solution. To this end, there has been a multitude of physical, chemical and biomimetic approaches. Likely, a successful method of AF will need to combine all methods.

Over the past few years several marine metabolites were characterized for their eco-friendly antifouling potential. Among them, a very promising halogenated terpene, bromosphaerol from *S. coronopifolius* isolated by our group. Currently, the major hurdle of the use of marine metabolites is the limited available quantities. To address this limitation, our consortium will approach bromosphaerol biosynthesis in an interdisciplinary manner utilizing all available new tools in biotechnology, genomics, bioinformatics, biochemical and chemical analysis and in-vivo assays. In preliminary work, we have applied Next Generation Sequencing (NGS) to identify several thousands of expressed genes from *S. coronopifolius* including candidate terpenoid biosynthetic genes. In the current project we will expand the NGS approach in additional fresh material, analyze bioinformatically the expressed genes to quantify expression levels, isolate candidate biosynthetic genes, perform enzymatic analysis and metabolic modeling and flux analysis, reconstitute the biosynthetic pathway in heterologous species, refine the chemical analysis tools to identify compounds from tiny amounts of algal material and settlement-inhibition assays of barnacles.

More information can be found on [the COFASP website](#).

CONSORTIUM

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Sector:

- Seafood processing

Topic:

- Explore opportunities for the use of biotechnological tools

Total costs*:

€ 512.400

Funding granted*:

€ 276.100

Duration:

3 years (2017-2019)

* Exact amount may change after completion of national contracts



Antonios Makris, Project Coordinator
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ABSTRACT

Recent biotechnological innovations currently allow the development of new approaches to apply genetic engineering to non-model organisms, including economically important salmonid species. This has been mediated by the introduction of the highly efficient CRISPR-Cas9 methodology, which allows mutating specific DNA sequences in any organism, thus permitting genetic studies on key traits for aquaculture. In recent years several studies have revealed that single SNPs in the genomes of salmonids can explain important traits such as time of maturity and disease resistance. Based on these findings further studies need to aim at elucidating how single nucleotide exchanges can alter important traits for aquaculture such as growth, reproduction and disease resistance. Hence, there is a need to develop technologies that can precisely alter single nucleotides in the genome. This can be obtained by knock in- by a combination of gene editing and homology-directed repair as previously done in zebrafish. So far knock out by gene editing has been established in both rainbow trout and Atlantic salmon. Both species of fish have a long generation time, therefore it will be necessary to perform double allelic knock in by homologous recombination already in the F0, which is challenging considering current low efficiencies of homologous recombination. We have successfully established a methodology using pigmentation as a tracer for double allelic mutations in Atlantic salmon, this methodology can be further explored for knocking in traits. The project will therefore focus on establishing an efficient knock in technology in salmon and rainbow trout. This will be done in combination with exploring the technology further in zebrafish and medaka as efficiency is still low in this species and also since testing out technologies is much faster in these model fish species with their short generation time and fast development. By doing so, we will focus our technology development on genes essential for pigmentation, sex determination, reproduction and egg quality since our groups have been exploring these fields for a long time and results produced can in addition to providing technological improvements explain mechanisms behind some key biological features in fish and other species.

More information can be found on [the COFASP website](#).

Sector:

- Aquaculture

Topic:

- Genome based approach to genetic improvement of aquaculture species

Total costs*:

€ 1.719.200

Funding granted*:

€ 894.100

Duration:

3 years (2017-2019)

** Exact amount may change after completion of national contracts*



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CONSORTIUM

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CHITOWOUND

Biotechnological tools implementation for new wound healing applications of byproducts from the crustacean seafood processing industry



PROJECT FACTSHEET

JOINT CALL COFASP – ERA-MBT
DECEMBER 2016

ABSTRACT

Crustacean shells are an abundant marine biomass containing valuable compounds with unique biological, physical/chemical and mechanical properties. Global aquaculture and catch of crustaceans yield > 10 million tons of biomass annually and the considerable amount of shells from this industry is currently a waste byproduct. The annual global catch the shrimp species *P. borealis* is more than 350 000 MT (FAO), and today only a minor fraction of the available harvested raw material is utilized for chitin/chitosan production. The most important product from crustacean shells is chitosan which is manufactured at about 13 000 tons per year and serve growing multi-sectorial markets. At present the chitosan produced is mainly used for water treatment as a flocculant, and for production of glucosamine for the health food market. However, chitosan is also used as a wound healing promoting component in gels, bandages and dressings for treatment of chronic wounds.

Current bottlenecks for expanded applications relates to the processes for their extraction and recovery which suffer from low yields and batch to batch variations with low reproducibility in the end product. Furthermore, current production processes for chitosan involves use of harsh chemicals and is highly energy consuming. Especially, in Asian countries were production of chitosan mainly takes place, this leads to both an environmental burden and also a significant hazard for the workers at such productions facilities. Thus, there is a great potential and motivation for improving these processes by introducing green chemistry, i.e. exploring the use of biotechnological tools like enzymes.

In the current project we will focus on developing more efficient and environmentally friendly processes for manufacturing of chitosan, and to produce chitosans that are targeting the wound healing market.

More information can be found on [the COFASP website](#).

Sector:

- Seafood processing

Topic:

- Explore opportunities for the use of biotechnological tools

Total costs*:

€ 884.000

Funding granted*:

€ 847.000

Duration:

3 years (2017-2019)

** Exact amount may change after completion of national contracts*



Kjell Morten Varum, Project Coordinator
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CONSORTIUM

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ABSTRACT

The project aims at developing biotechnological tools to improve our understanding of the genomic basis for growth and robustness in European sea bass (*Dicentrarchus labrax*), one of the most intensively farmed teleost species in the Mediterranean. Particular concern will be granted to increase species resistance to diseases, namely vibriosis [*Vibrio (Listonella) spp.*], pasteurellosis [*Photobacterium (Pasteurella) damsela subsp. piscicida*] and Viral Nervous Necrosis (VNN) infection. A family based breeding program, running high quality disease challenge tests on siblings to breeding candidates, can improve resistance by selecting broodstock from genetically best families. Exposing breeding candidates directly to disease to identify superior individuals is not indicated, but genomic analysis can be applied to efficiently discriminate among breeding candidates from the same family that otherwise will be ranked equally if only using family values. Therefore, genetic improvement of European sea bass through advanced selective breeding and molecular tools is expected to reduce production cost in the long term while minimizing production vulnerabilities and risk. In addition, the species shows high susceptibility to stress and displays high basal cortisol concentrations. Preliminary results showed that cortisol responsiveness was a repeated trait and fish with constantly Low (LR) or High (HR) resting and post-stress cortisol concentrations were identified. Interestingly, some quantitative trait loci (QTL) that influence cortisol concentrations seem to be located in the same genomic regions with QTL suggested having an effect on weight. Since stress is being considered as an important co-factor for reproductive dysfunctions and disease outbreaks in this species which in turn hampers production, we aim to investigate more deeply how stress response measured by cortisol level and weight/growth interfere in order to develop a promising selection index in future breeding programmes. Selection based on rigorous phenotype and genotype measurements for increased survival against pathogens and response to acute stress conditions is expected to lead to more robust future generations in the European sea bass populations.

More information can be found on [the COFASP website](#).

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Sector:

- Aquaculture

Topic:

- Genome based approach to genetic improvement of aquaculture species

Total costs*:

€ 1.091.900

Funding granted*:

€ 650.000

Duration:

3 years (2017-2019)

* Exact amount may change after completion of national contracts



Costas Tsigenopoulos, Project Coordinator
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STURGEoNOMICS

Genome-based approaches for improvement of aquaculture
in two marine sturgeon species: Atlantic sturgeon
(*Acipenser oxyrinchus*) and Beluga (*Huso huso*)



PROJECT FACTSHEET

JOINT CALL COFASP – ERA-MBT
DECEMBER 2016

ABSTRACT

This project will use whole genome-based approaches for the improvement of aquaculture in two marine sturgeon species: Atlantic sturgeon (*Acipenser oxyrinchus*) and Beluga (*Huso huso*), characterized by large size, fast growth and relatively compact genomes.

Based on advanced preliminary work, the first common objective is to generate high quality genomes for *H. Huso* and *A. oxyrinchus*. The second objective is to characterize the genetic sex determination, using genomics and gonadal transcriptomics to prepare future molecular biotechnological tools for commercial aquaculture (female-biased breeding, meat, caviar) and species conservation. The third objective is to improve aquaculture breeding and re-stocking using population genomics, specifically elucidating the genomic substructure of native Atlantic sturgeons and re-stocking populations and of the remaining Beluga stocks from the Danube. This will avoid inbreeding in aquaculture and improve genetic make-up and broodstock management for ongoing restoration programs of endangered sturgeons and for sustainable fishery. The fourth objective is to experimentally extract genomics-derived candidate genes related to target traits (growth, disease resistance, sex determination) in captive-bred offspring using whole genome information (positively selected genes) and transcriptome (RNAseq) analyses in order to improve management strategies and breeding for commercial and conservation-related aquaculture.

More information can be found on [the COFASP website](#).

Sector:

- Aquaculture

Topic:

- Genome based approach to genetic improvement of aquaculture species

Total costs*:

€ 1.829.400

Funding granted*:

€ 856.800

Duration:

3 years (2017-2019)

* Exact amount may change after completion of national contracts



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