



# AQUA-FAANG

ADVANCING EUROPEAN AQUACULTURE BY GENOME  
FUNCTIONAL ANNOTATION

ISSUE 4 • NOVEMBER 2022



## ABOUT AQUA-FAANG

The AQUA-FAANG (Advancing European Aquaculture by Genome Functional Annotation) project aims to greatly improve our understanding of genome function in the six most commercially important European farmed fishes namely Atlantic salmon, Rainbow trout, European seabass, Gilthead seabream, Turbot, and Common carp. Genome-wide functional annotation maps will be generated for each species and used to develop an understanding of their contribution to variation in traits of commercial relevance, exploiting comparative approaches to enhance transferability of findings.

## AQUA-FAANG NEWSLETTER

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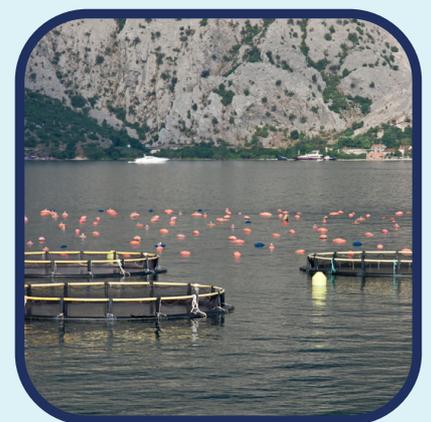
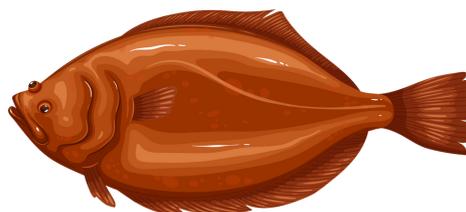
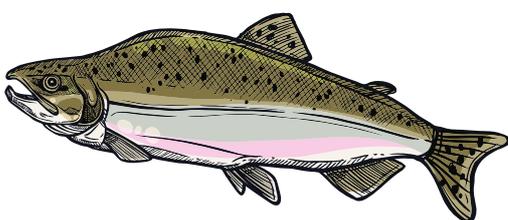
The AQUA-FAANG project has received funding from the European Union's Horizon 2020 research and innovation program under Grant Agreement No 817923.

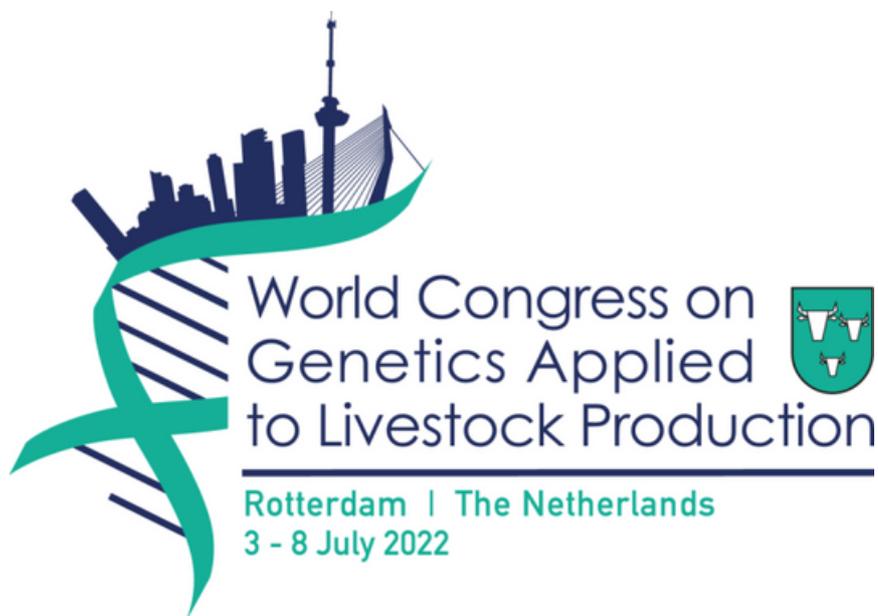
SIGBJØRN LIEN & DANIEL J. MACQUEEN

In the last year, extensive progress has been made across all work packages of AQUA-FAANG, generating many results and contributing greatly towards the project's objectives. We have now completed sequencing for the majority of samples for the key functional annotation maps generated in the project. This is a huge milestone, representing thousands of novel datasets, including extensive RNA-Seq, small RNA-Seq, ATAC-Seq, ChIP-Seq data. All contributing partners are now experienced in generating ATAC-Seq and ChIP-Seq libraries.

Another major achievement was the successful uptake of nf-core pipelines for functional annotation data analysis. These pipelines were rigorously tested and are now routinely used by partners to support standardized comparisons between species and datasets. Also new approaches and resources for comparative genomics in fishes have been established. Improved genome assemblies and annotations for all six AQUA-FAANG species were generated and made publicly available through the Ensembl genome browser. These genomes have also been successfully uptaken to the Genomicus browser. Single cell RNA-Seq has been performed in rainbow trout, revealing novel immune cell heterogeneity and its potential link to disease resistance. Gene edited cell lines has been generated as research tools to understand viral disease resistance mechanisms. A chromosome region responsible for VNN resistance in European sea bass has been fine-mapped to identify underlying causative variants using genome-wide genetic variation and functional annotation datasets. Significant progress has been made on communication, dissemination and knowledge exchange of project outcomes. For example, an animated YouTube movie was created and released in different languages to raise awareness to AQUA-FAANG and its expected impacts.

Finally, the European Commission approved an amendment to the project inclusive of a **6-month extension**, which helps us work around the many lingering challenges caused by the COVID-19 pandemic. According to the amended schedule, we are on track to achieve the project objectives, and deliver a step-improvement in functional annotation of farmed fish genomes.



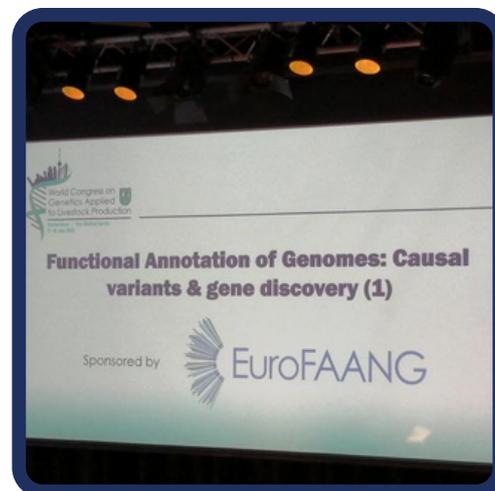


The AQUA-FAANG project presented its results in two scientific sessions during WCGALP 2022 in Rotterdam.

Marie-Odile Baudement (NMBU) presented on **"The epigenetic landscape of Atlantic Salmon with a focus on liver tissue"** during the session focusing on Functional Annotations of Genomes which EuroFAANG sponsored. The BodyMap annotations for all six Finfish species will also be available soon.

Robert Mukiibi (UEDIN) presented the results of **"A major QTL affects resistance to viral nervous necrosis in farmed European seabass"** at the aquaculture-specific session. Selective breeding offers an opportunity to develop seabass strains with increased resistance, thus reducing the impact of the disease on the industry, which causes a significant threat resulting in extensive losses due to mortality and impaired growth of infected fish.

Presenting the research results at the World Congress on Genetics Applied to Livestock Production is considered a significant milestone for the AQUA-FAANG project.



## Join to the AQUA-FAANG training!



This one-and-a-half-day workshop will provide detailed training on methods to use and reuse the wealth of data generated by the AQUA-FAANG project, one of the EuroFAANG projects.

The seminar will primarily focus on the comprehensive and integrated annotation of these six species by the Ensembl genome browser. The course will also dive deeper into gene annotation, regulation, and demonstrations of the specific analyses and research conducted by AQUA-FAANG scientists.

**Register here**



The AQUA-FAANG workshop will take place on the 17th and 18th of April, 2023, in Hinxton, United Kingdom. Registration is open until the 8th of January, 2023.

## New member of EuroFAANG



Holoruminant is a multi-actor project aiming to elucidate the role of ruminant-associated microbiomes and their interplay with the host animal in early life and throughout fundamental life events (e.g. weaning, feed transitions and lactation) that are known to affect health, welfare and environmental efficiency in ruminant production systems.

HoloRuminant will use a holistic multi-omics approach to characterise the establishment and dynamics of microbiomes. This way, HoloRuminant will determine the connectivity between microbiomes from different body sites, their heritability and their influence on the host's key performance indices (KPIs) of efficiency of production, growth, and resistance to disease methane emissions, carbon footprint and phenotypic resilience to changing environmental conditions.

The project's main outputs will be the creation of an expandable benchmark dataset of ruminant-associated microbes, microbiomes and methods for analysis that will be used for answering essential (who, what, where and when) scientific questions and will be the knowledge foundation for innovation.



# IN THE SPOTLIGHT - PROGRESS IN WPS



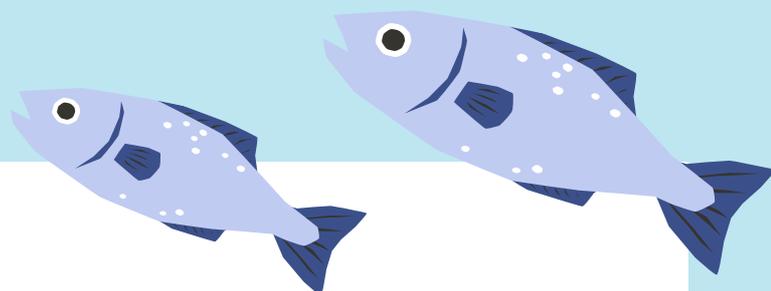
## AM updates - WP1-WP5



In recent months, productive progress has been made across all the AQUA-FAANG work packages (WP) despite the challenges faced by the COVID Pandemic. Standardised lab protocols for DevMap and BodyMap were built using Atlantic Salmon as a sample and disseminated. Currently, 19 publicly available describing sample collection and preservation, RNA preservation and extraction, and ATAC-seq and ChIP-seq library publications.

Furthermore, the team of WP1 also produced standardised protocols for biological sampling and collection and registration of metadata guidelines focused on embryonic stage standardisation and cryopreservation. Our team has provided support and training to partners performing collection and library preparation through 36 FAD on-site meetings since November 2020 with approximately 35 attendees. We are now preparing for the BodyMap and DevMap sequencing libraries through the different protocols' output.

Together with WP 1, 3 and 4, we are generating a genome-wide functional annotation map for the six more important commercial fish species in Europe (EU). We managed to sequence 3,138 functional genomics libraries, which sum up to 36.6 trillion DNA-base pairs of data. Functional annotation maps capture genes and genomic features that control traits relevant to aquaculture's sustainability and profitability, animal welfare, and reducing negative impacts on the environment and wild fish population.



# IN THE SPOTLIGHT - PROGRESS IN WPS

## AM updates - WP1-WP5

The main key target remains a better understanding of disease resistance, but we will also be able to assess flesh quality, growth and metabolism, nutrition, and reproductive traits. Through WP 2 deliverables, we have had our first FAANG aquaculture metadata standards with six richly annotated high-quality AQUA-FAANG genomes and complete homology in the Ensembl genome browser. This data will be available to anyone for research applications through WP2. The outcome of this working package will also help in the primary project target of WP 5, which is the exploitation of these data for enhancing fish breeding through improved genomic prediction of disease resistance in these breeds.

In WP3, the team is currently interpreting the data generated by analysing and interpreting the RNA sequences. The functional annotation data for clonal lines has been completed and processed through the WP2 bioinformatics pipeline. The WP4 team also evaluated the efficiency of the transient expression CRISPR-Cas9 protocol. Meanwhile, WP5 allowed us to separate the causal from non-causal genetic variation. It can be harnessed to enhance the accuracy of genetic prediction in more divergent breeding populations, which can be applied to any trait. Overall, we are on track, and substantial progress has been made. This was due to an incredible team effort from all the partners, individuals and teams that went above and beyond to complete the project activities.



# GLOSSARY



We realise that scientific research can be challenging to understand, especially in a technical project such as AQUA-FAANG that uses various methodologies that are new and developing. To help you, we have defined some important terms mentioned in this newsletter.

**ChIP-seq:** Identifies the binding sites of DNA-associated proteins and can be used to map global binding sites for a given protein.

**ATAC-seq:** (Assay for Transposase-Accessible Chromatin using sequencing) is a technique used in molecular biology to assess chromatin accessibility across the genome. It can help uncover how chromatin packaging and other factors affect gene expression.

**DevMap:** sequence inputs from a pool of Embryos (Developmental Stage).

**BodyMap:** sequence inputs from a single tissue sample grouped by tissue, sex, and sexual maturity.

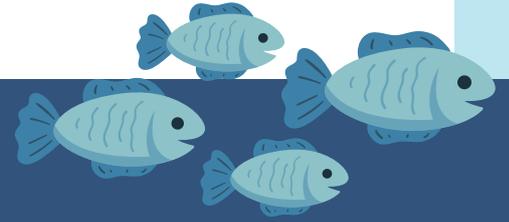
**Functional annotation map:** Information about and describing a region or a gene across a genome. It helps to visualise and interpret a GWAS.

**CRISPR-Cas9:** Edits genes by precisely cutting DNA and then letting natural DNA repair processes take over.



# MEET OUR PARTNERS

## WP3 & WP5



### SAM MARTIN (UNIABDN) - WP3



Sam Martin has over 30 years of research experience in fish genomics, focusing on health and physiology. He is director of the Scottish Fish Immunology Research Centre (SFIRC) and also director of research for the School of Biological Sciences at the University of Aberdeen. Sam's lab has an emphasis on identifying differentially expressed genes related to immune function in both Atlantic salmon and rainbow trout, two major aquaculture species in northern Europe.

His research programs cover both fundamental fish health and how genes respond to both pathogens and during inflammation, many of the projects are directly relevant to aquaculture industry. In the past few years there has been a focus on mucosal health with several live projects investigating intestine, gill and skin mucosal health. He is Co-I on the UK funded Aquaculture Research Collaborative Hub –UK, that is identifying priority areas for future research for both finfish and shellfish aquaculture in UK. His lab has funding from Research Councils UK (BBSRC and NERC), EU, Scottish Aquaculture Innovation Centre (SAIC) and a number of industrial funded projects. Within Aquafaang Sam leads on WP3 on Immunomaps and also contributes several other WPs.

### PIERRE BOUDINOT (INRAE) - WP5

I lead the team Fish Infection and Immunity at the department of Molecular Virology and immunology of INRAE, at Jouy-en-Josas close to Paris. I have been working in fish and comparative immunology for more than 25 years. My group focuses on mechanisms of antiviral immunity in fish (salmonids and zebrafish), immune repertoires in healthy, infected and vaccinated salmonids, and genetic resistance to viral diseases.

We are particularly interested in the mechanisms of the type I IFN response induced by the viral infection in fish, and by the evolution and functions of Interferon stimulated genes using gain and loss of function experiments. We develop in vitro models of mutant fish cell lines through CRISPR/Cas9 genome editing. We are also interested in dissecting the mechanisms of genetic resistance to viral diseases using a combination of approaches. We characterize trout isogenic lines of contrasted resistance to a viral and a bacterial disease using single cell sequencing and comparative (epi)genomics. As part of my research, I also study B and T cell responses using repertoire sequencing, to understand the role of public and private responses in the protection afforded by antiviral vaccines in salmonids.



# IN THE SPOTLIGHT - INDUSTRY PARTNER

**Stolt Sea Farm** 



ISABEL ANA FERREIRO GARCIA

Stolt Sea Farm is an aquaculture company established in 1972, that produces turbot (*Scophthalmus maximus*) and sole (*Solea senegalensis*) in land-based farms in Spain, Portugal, France, Norway and Iceland. For both species, the company manages the whole value chain, from the production of eggs, larval rearing, on-growing, harvesting, processing and commercialization. Stolt Sea Farm is the leading company in Flat Fish production in Europe, and reaches more than 30 countries with its products, and brands, Prodemar, King Sole and King Turbot. Stolt Turbot broodstock has been under a Selective Breeding Program since the early 90s, focusing on the character growth improvement.

## What its role in AQUA-FAANG

Stolt Sea Farm is participating in the project in the WP7, dissemination, exploitation and communication. Communication of project brochure, Project web page and worksheet are shared with Stolt clients, suppliers and general public through the company web pages, and company trademark web pages. Additionally, Stolt Sea Farm is providing this project Turbot biological material, as embryos, larvae and adults, for WP 1, specifically the task 1.4 (DevMaps and BodyMaps). The USC team (partner 10), led by Dr Martínez, is responsible for work with turbot in the project.

## How can the AQUA-FAANG results be implemented in Stolt Sea Farm

After 30 years working on Selective Breeding, we have the ambition on incorporating new characters to the program, focusing in disease resistance, as we consider that such characteristics will increase the robustness of our turbot strain, adapting better to the new challenges, as climate change, and competition for new locations. Genomic tools developed in the project will help our program to obtain more accurate results,

increasing the speed that we will incorporate our genetic gain. An effective transference is expected with the collaboration of scientific partners of this project, in future applied national R&D projects.



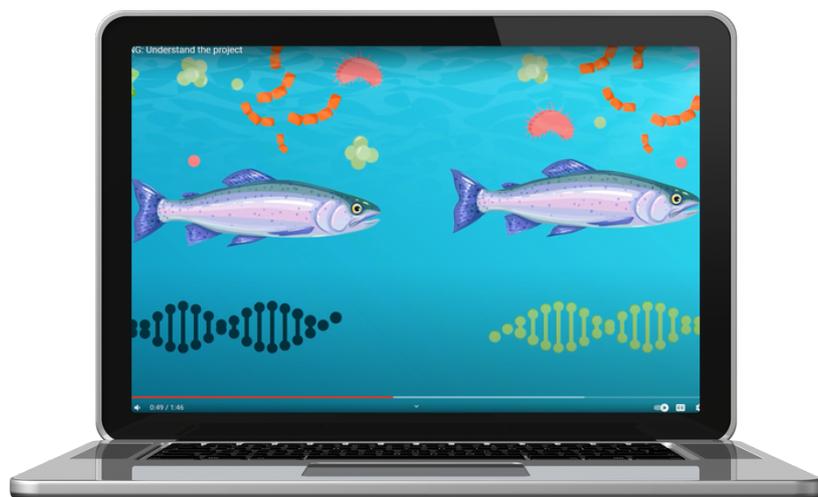


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AND DON'T FORGET TO WATCH OUR ANIMATION VIDEO!



**French version**



**Spanish version**



**Greek version**

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