



AQUA-FAANG

ADVANCING EUROPEAN AQUACULTURE BY GENOME
FUNCTIONAL ANNOTATION

ISSUE 5 • AUGUST 2023

Final AQUA-FAANG Conference

11-13 October 2023. Edinburgh, UK



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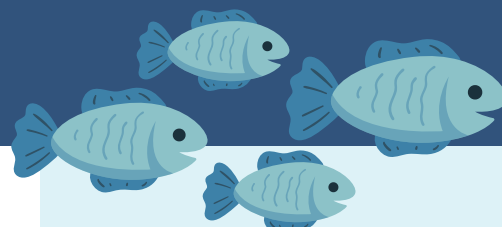
The AQUA-FAANG project has received funding from the European Union's Horizon 2020 research and innovation program under Grant Agreement No 817923.

DAN MACQUEEN & SIGBJØRN LIEN

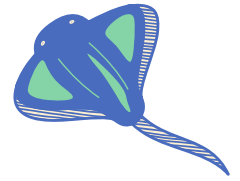
We are entering an exciting and busy phase for AQUA-FAANG, with just six months of the project remaining. The team is working hard to deliver new genomic resources and biological insights from the extensive data generated, while also disseminating findings through conferences and publications. A headline achievement is that 4,300 functional annotation libraries have been sequenced across the six AQUA-FAANG project species. This is broken down into approximately 1,000 mRNA-Seq, 300 small RNA-Seq, 2,250 ChIP-Seq and 700 ATAC-Seq datasets. This is a unique resource for functional genomics in farmed fish species, and a foundation for years of downstream analysis and exploitation. Our datasets have been shared on the Ensembl genome browser, including ATAC-Seq peaks in the most recent release for Atlantic salmon, European seabass, Rainbow trout and turbot. In future Ensembl releases, more developed regulatory annotations will be available, with elements like promoters and enhancers predicted using both ATAC-Seq and ChIP-Seq data.

Findings are pouring in across the project, more than can be detailed here. A few examples include the first demonstration of regulatory regions activated in response to immune stimulation, enriched in predicted binding sites for immune transcription factors. Novel cell lines have been produced where many genes involved in the antiviral response have been knocked-out for functional studies of responses to viral infections. *A major quantitative trait loci for resistance to viral nervous necrosis in European seabass has been fine-mapped using functional genomics data, revealing a candidate regulatory variant responsible for disease resistance* through alteration of the expression of an antiviral gene. Comparative analyses of functional annotation data are progressing, for example, investigating changes in gene expression and regulatory elements following whole genome duplication events in salmonids and common carp.

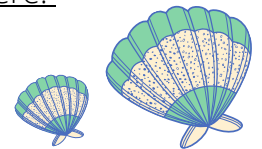
In the last period, AQUA-FAANG participants have disseminated their findings extensively in 2022 and 2023, including at the International Symposium on Genetics in Aquaculture (ISGA), the Genomics in Aquaculture Symposium (GIA), the World Congress on Genetics Applied to Livestock Production (WCGALP), and the International Society for Animal Genetics (ISAG) annual meeting, among others. To accelerate impact and knowledge transfer, AQUA-FAANG has been working with another Horizon 2020 project called AquaIMPACT to deliver joint outreach and dissemination activities, including a series of webinars targeting industry exploitation. AQUA-FAANG has contributed to the wider EuroFAANG initiative through a range of activities, and the project leadership team will be contributing to a recently funded Horizon Europe Infrastructure for EuroFAANG running across the next three years. Looking ahead, we are planning **the AQUA-FAANG final meeting, a 3-day event in Edinburgh between 11-13 October 2023**. This meeting will be in person for participants and selected industry representatives, with the major sessions promoted and streamed live online to reach and influence broader project stakeholders. The final meeting will include an industry-facing day, where results from the project will be considered from the perspective of both academia and industry, to *critically appraise the role of functional genomics in the future of selective breeding and genetic improvement in aquaculture*.



Using genetics to support sustainable aquaculture: results from 20 years of breeding rainbow trout by Marc Vandeputte, UMR Marbec (Marine Biodiversity, Exploitation & Conservation)

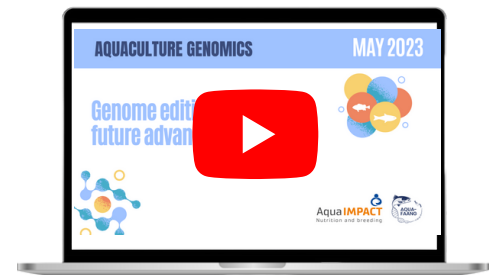


The Aqualande group, INRAE, Les Sources de l'Avance, and the French Poultry and Aquaculture Breeders Technical Center (SYSAAF) have conducted a 20-year rainbow trout breeding program, comparing the growth and nutrition needs of selected trout with unselected trout. The results show that selected trout need 17% to 20% less feed to achieve the same growth as unselected trout, reducing the environmental impacts of fish farming. A locally produced feed without fish oil, fishmeal, or soy was tested on both groups, and the fish fed this "future" feed achieved similar growth performance. The study demonstrates that selective breeding and sustainable feeds are crucial for reducing the environmental impact of farmed fish production and accelerating the transition to more sustainable aquaculture. Read the full article [here](#).

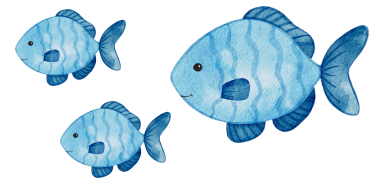


Aquaculture Genomics Webinars

In the spring of 2023, AQUA-FAANG and AQUAIMPACT hosted a webinar series on aquaculture genomics that covered significant subjects. Pedigree-based and genomic selection, functional annotation and precision breeding, disease resistance and immune response, genome editing, and upcoming developments were all topics of discussion. The notable speakers were Antti Kause, Sigbjørn Lien, Luca Bargelloni, Sara Faggion, Diego Robledo, and Sigrid Bratlie. Adrian Millan, Romain Morvezen, Isabel Ana Ferreiro Garcia, and Alan Tinch all contributed to stakeholder feedback. 284 people from Europe, Asia, Africa, South America, North America, and Oceania attended the webinars. Participants represented the fields of research, business, aquaculture, policy, and the food industry. The series promoted cooperation among various stakeholders in the industry while offering insightful information about the potential uses of genomics in aquaculture.



EuroFAANG Animation video

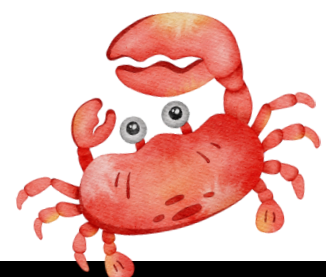


We are happy to introduce you to our animated movie!

Animals possess remarkable phenotypic variation in different climates, which allows them to adapt to diverse environmental challenges. This variation is influenced by both coding and non-coding regions of their DNA. While coding regions consist of genes and constitute only a small portion of the genome, the non-coding regions, comprising 95% of the genome, play a crucial role in regulating essential traits such as milk production and disease resistance. Understanding these non-coding regions and their regulatory elements through functional genome annotation is vital for effectively selecting and breeding animals with desired traits, enhancing productivity and resilience in agriculture.

The EuroFAANG initiative, part of the FAANG consortium, focuses on three H2020-funded projects: AQUA-FAANG, BovReg, and GENE-SWitCH. These projects are dedicated to unravelling the functional aspects of fish, cattle, chicken, and pig genomes. By advancing our functional genomics knowledge, EuroFAANG aims to drive innovation in animal breeding, sustainable farming systems, and agricultural practices to meet economic and societal demands. To stay updated on the groundbreaking advancements in functional genomics and contribute to a more efficient and sustainable future for animal agriculture, visit the project websites or follow EuroFAANG on social media.

Functional annotation of farmed animal genomes is crucial to fully comprehend these regulatory elements and their interactions. Functional annotation creates a comprehensive map of genome features, acting as a navigational reference for geneticists.



AquaFarm

During the 15th and 16th of February, the Department of Comparative Biomedicine and Food Science of the University of Padova drew attention to the AQUA FAANG project during the congress Aquafarm2023 held in Italy.

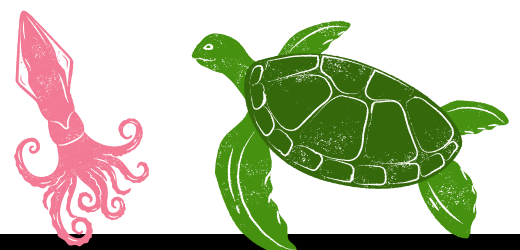
This year, the congress's main theme was “sustainable aquaculture production”, which is one of the fundamental and global goals of AQUA FAANG. The close collaboration between researchers, aquaculture farms and stakeholders was highlighted, as it is peculiar to achieve the sustainable development goal of the project.

Working together for sustainable aquaculture!



AQUA-FAANG Training Workshop Enhances Genome Function Understanding and Genotype-to-Phenotype Prediction

On April 17–18, the UK hosted an insightful AQUA-FAANG Training Workshop under the direction of renowned researcher Peter Harrison from EMBL. The workshop's main objective was to use AQUA-FAANG data and ensemble resources as effectively and as efficiently as possible to advance scientific research. The objective was to deepen our understanding of how the genome works and investigate the use of genotype-to-phenotype prediction of the most important six farmed fish species in Europe. Participants gained useful skills from the training that will allow them to reuse and use AQUA-FAANG data effectively in their respective fields, maximising the potential of genomics. The workshop aided in the ongoing development of aquaculture genomics and its potential for scientific advancement by encouraging group learning and sharing knowledge.



KEY RESULTS FROM THE AQUA-FAANG PROJECT'S RECENT PROGRESS

We have some exciting updates on the progress of the AQUA-FAANG project! In Work Package 3 (WP3), our team diligently assesses the data obtained from analyzing and interpreting RNA sequences. Simultaneously, we have successfully completed the functional annotation data for clonal lines, which underwent processing through the WP2 bioinformatics pipeline. Moving on to Work Package 4 (WP4), we have recently evaluated the efficiency of the transient expression CRISPR-Cas9 protocol, a groundbreaking technique with immense potential for advancing our breeding practices. Additionally, WP5 has been making remarkable strides in various areas. Notably, we are nearing completion of the analyses of our main European sea bass experiment, where we have integrated genetic and functional genomics data.



This integration has led to a significant discovery—identifying a potential causative mutation for the major QTL associated with resistance to Viral Nervous Necrosis. We also actively refine and annotate disease resistance QTL in other species, including turbot, common carp, and gilthead seabream. Lastly, we are working on testing and optimizing selective breeding algorithms to prioritize functional information, as we believe they will play a vital role in enhancing aquaculture practices. Thanks to the incredible dedication and teamwork exhibited by our partners, individuals, and teams, we are on track, and substantial progress has been achieved in the project activities.



IN THE SPOTLIGHT

JOSEPH ROBERTSON (NMBU)



Joe received his PhD in Cell Biology from the University of Manchester, UK, after which he moved to Norway for a postdoc position at the University of Oslo. More recently, he has worked in a range of science communication and research administration/project management roles, including positions at the Centre for Molecular Medicine Norway (NCMM) and the National Advanced Proteomics Infrastructure in Norway (NAPI).

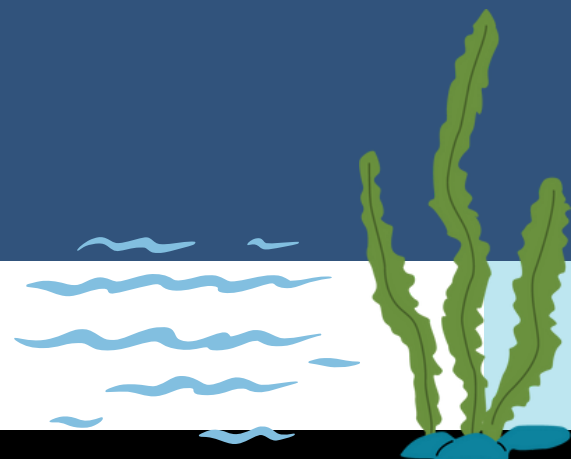
He started his role as Project Manager at AQUA-FAANG in January 2023, where he has been working with various project partners to oversee progress during the final 10 months of the project.

PETER HARRISON (EMBL)

Peter Harrison is Ensembl's Genome Analysis Team Leader at [EMBL's European Bioinformatics Institute](#). Ensembl is a world-renowned genome browser that has served the genomic interpretation requirements of the scientific community for more than twenty years.



In AQUA-FAANG, Peter leads the work package on Bioinformatics and data analysis, whose role in the project is to establish and coordinate standardised bioinformatics tools and data processing to identify and characterise functional genome elements in the six AQUA-FAANG species. This included updated Ensembl gene annotations, homology predictions for all species, and the first Ensembl regulatory builds in Salmon, Turbot and European seabass. EMBL also lead the projects data management and visualisation of data through the FAANG Data Coordination Centre and the development of [the AQUA-FAANG component of the FAANG data portal](#). This gives the community access to the wealth of data the project generates.



IN THE SPOTLIGHT - INDUSTRY PARTNER

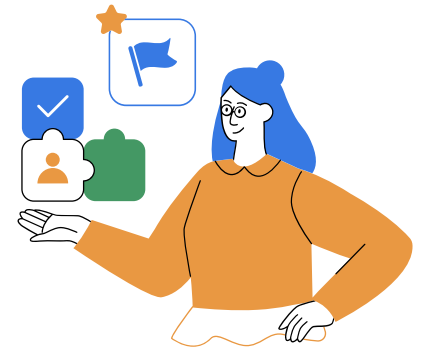
EFFAB

**EFFAB**European Forum of
Farm Animal Breeders

The team members: Ana Granados, Çağla Kaya, Noraly van Hemert, Bárbara Barbosa, María Ramírez and Geena Cartick

About your company

The European Forum of Farm Animal Breeders (EFFAB) represents animal breeding and reproduction organisations across Europe. EFFAB has a diverse membership, including experts engaged in the genetic improvement of various farm animal species. Ruminants, pigs, poultry, aquaculture and insects are the main species covered by EFFAB members.



In collaboration with FABRE-TP and guided by the code of good practices for farmed animals, the Code EFABAR, we are at the forefront of promoting responsible and balanced animal breeding practices for the above-mentioned species. Together we advocate for sustainable breeding, animal welfare, and environmental stewardship

EFFAB recognizes the challenges faced by the aquaculture sector, and we address them together with our diverse membership of aquaculture breeders and experts. We collaborate to develop and implement standards namely, the Aquaculture Code EFABAR, to ensure responsible balanced aquaculture breeding. EFFAB and FABRE-TP contribute to aquaculture breeding practices' long-term success and sustainability by facilitating collaboration, knowledge exchange, and linking industry with research.

Role in AQUA-FAANG

EFFAB is the main representative organization for Europe's animal breeding and reproduction sector in the AQUA-FAANG project. EFFAB facilitates knowledge exchange and transfer between market and research through its extensive stakeholder network, including sectoral experts, scientists, and policymakers.



EFFAB serves as the primary link between aquaculture breeding companies and project researchers and actively engages with governing bodies and other stakeholders. Its knowledge and experience ensure the project's objectives align with long-term sectoral and stakeholder needs. EFFAB works closely with sectoral partners, particularly in dissemination, exploitation, and communication, to deliver project objectives, exploit outputs for economic and societal impact, and bring forward critical sectoral challenges.

IN THE SPOTLIGHT - INDUSTRY PARTNER

EFFAB

**EFFAB**European Forum of
Farm Animal Breeders

How can the AQUA-FAANG results be implemented /applied

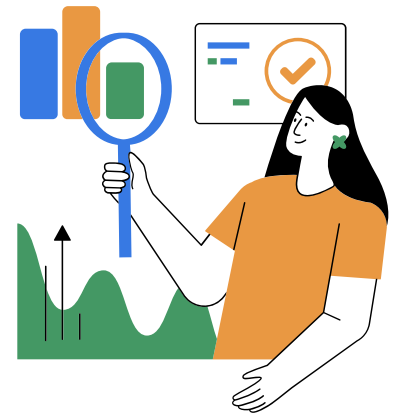
The AQUA-FAANG project has made significant strides in aligning its research results with the needs of the aquaculture breeding sector, thereby contributing to the goals outlined in the EC's Strategic Guidelines for a more sustainable and competitive EU aquaculture. EFFAB's aquaculture breeding companies will benefit from the functional annotation maps, and genomic data generated for important commercial fish species.



By improving genomic prediction of disease resistance and refining the annotation of disease resistance QTL, the project provides valuable insights for selective breeding programs. Furthermore, the integration of genetic and functional genomics data aids in identifying causative mutations for disease resistance.

Expected short and medium-term impacts of new knowledge

The new knowledge generated from the AQUA-FAANG project is expected to have significant short and medium-term impacts on the aquaculture breeding sector. The project's research results directly address crucial areas such as disease resistance, flesh quality, growth, metabolism, nutrition, and reproductive traits by aligning with the needs outlined in the Strategic Guidelines for EU aquaculture. The standardized lab protocols, functional annotation maps, and genomic data provide valuable tools and insights for aquaculture breeding companies associated with EFFAB.



These advancements will enable more precise and efficient selective breeding programs, leading to improved disease resistance in fish populations, enhanced flesh quality, optimized growth and metabolism, and better nutritional profiles. The outcomes will contribute to the sustainability and competitiveness of the EU aquaculture sector by promoting animal welfare, reducing negative environmental impacts, and meeting the demands of a growing market. In the short and medium term, the aquaculture industry can leverage this new knowledge to enhance their breeding practices and make informed decisions based on genetic predictions and functional information, ultimately leading to improved economic viability and environmental stewardship.

More information about our work can be found at www.effab.info , www.fabretp.eu , and www.responsiblebreeding.eu



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EVENTS



EAAP Lyon 2023 - EuroFAANG session - 31 August, Lyon, France

EuroFAANG Summer School - 11-15 September, Paris, France

EAS Aquaculture 2023 - 18-21 September, Vienna, Austria

Aquafaang Final Conference - 11. 13 October, Edinburgh, UK

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