



AQUA-FAANG

ADVANCING EUROPEAN AQUACULTURE BY GENOME
FUNCTIONAL ANNOTATION

ISSUE 1 • AUGUST 2020



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

TABLE OF CONTENTS

EDITORIAL	2
NEWS	3
JOB POSITIONS	7
IN THE SPOTLIGHT	8
EVENTS	12
CONTACT	12



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, DAN MACQUEEN

Key progress in the Project

Major progress has been made in the first year of the AQUA-FAANG project across all work packages (WP), with most of the milestones and deliverables submitted on time. Functional annotation protocols have been developed and partners are currently working towards generating standardized DevMaps (WP1), BodyMaps (WP1) and ImmunoMaps (WP3, WP4) in their own facilities on their particular species of interest. The six fish genomes targeted in AQUA-FAANG have been annotated using the latest version of the Ensembl gene build pipeline (WP2), applying comparative approaches to classify all genes into families, and to define orthology and paralogy relationships with other vertebrates (WP6). The AQUA-FAANG website has been launched (www.aqua-faang.eu/), project brochures have been developed and the project identity is well established (WP7). Strong links between the two other projects funded under the same H2020 call – BovReg and GeneSWitCH - have been established and formalized as the European node of the FAANG initiative (“EuroFAANG”). This was largely achieved by a very successful workshop co-hosted by EMBL-EBI and AQUA-FAANG called the “FAANG Shared Workshop: Foundation for the Future” held at the Wellcome Genome Campus, Hinxton, Cambridge, UK 25-27th Feb 2020 (WP7), which explored possibilities for collaboration, knowledge exchange and coordination between the three projects.



Kick-off meeting AQUA-FAANG



SIGBJØRN LIEN, DAN MACQUEEN

Impacts of COVID-19

The COVID-19 pandemic has had a considerable negative impact on AQUA-FAANG. The shutting down of labs across European partners began in March 2020 as part of international lockdown measures, at a time when a large amount of lab-based activities were occurring across different work packages, including fish sampling and testing of functional annotation protocols across all six species in the project. While some partners have regained partial access to their labs since May 2020, others (including those in the UK) remain in full lockdown even in July. As a consequence, several key activities in the project have been substantially delayed, with knock-on effects for the timing of downstream milestones and deliverables.

The first annual meeting of the AQUA-FAANG general assembly, which was set to occur in Santiago de la Compostela in May 2020, also had to be cancelled. Instead, we held a video conference (with 55 attendees) to summarize progress across the project work packages, and fully capture the impacts of COVID-19 lockdown, allowing us to map out strategies for project timelines to a more realistic schedule. The overall impact of COVID-19 cannot yet be fully determined, but we have already concluded there will be an unavoidable delay in meeting several project deliverables. Similar negative impacts of COVID-19 are shared by many H2020 projects, including AQUA-FAANG's sister projects BovReg and GeneSWitCH. The global research community is adapting to these challenges rapidly, and AQUA-FAANG continues to make progress in many areas.





EuroFAANG - Joint Dissemination Strategy

A FAANG Joint Dissemination Strategy operating under the name EuroFAANG, has been established including coordinators from the genome annotation projects AQUA-FAANG, GENE-SWitCH and BovReg. The platform has already met several times, both physically and via teleconferences, and invited each other to respective project kick-off meetings. The platform aims to have the three H2020 projects and FAANG meet regularly to coordinate on its direction through calls and a shared development roadmap, thereby shaping decisions on priorities. The first version of a shared FAANG H2020 development roadmap has already been published in December 2019. EuroFAANG functions to maximize knowledge exchange, encourage collaboration, and facilitate standardization of functional annotation. This knowledge exchange platform enables communication between relevant EU projects and initiatives, and coordinates knowledge and data exchange. Additionally, EuroFAANG aims to organize joint communication and dissemination events to increase the uptake of results by joint stakeholders outside the projects. The co-development of the joint-functional annotation workshop, which took place in February 2020, was the first of many dissemination events to come.

AQUA-FAANG brochure

The introductory brochure of the AQUA-FAANG project is now available, providing brief information on the project aim, structure, partners, expected outputs and impact.

Partners

Universities: University of Aberdeen, University of Exeter, University of Liverpool, University of Stirling, University of York, Imperial College London, USC, etc.

Research Institutes: IMB, INRA, MRC, etc.

SMEs and International Organisations: etc.

Stakeholders

A key strength of AQUA-FAANG is industrial engagement across a portfolio of the six most important European farmed fish species. This engagement will allow co-development of commercially relevant outputs with long lasting impacts in European aquaculture.

Evolution Working Group (EWG): The EWG is a platform for cooperation and collaboration between AQUA-FAANG and relevant stakeholder groups including the aquaculture breeding companies (SMIs) and other relevant industry that would update the results of the project.

Knowledge Exchange Platform (KEP)

The KEP consists of project coordinators leading the three H2020 projects funded in the same call as AQUA-FAANG. This includes GENE-SWITCH, focused on chicken and pig, and BovReg, focused on cattle. This group will focus with broader initiatives, including the main FAANG consortium, and aims to enhance coordination of relevant activities across the different projects to maximize knowledge exchange, encourage collaboration, and facilitate standardization of functional annotation.

Are you interested in the AQUA-FAANG project?

You can visit us at <https://www.aqua-faang.eu/> and on Twitter @AQUA_FAANG. Are you a stakeholder and do you want to know more about AQUA-FAANG? Please subscribe to our stakeholders mailing list on our website!

Contact

Please send all your inquiries to aqua.faaang@gmail.com.

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Advancing European Aquaculture by Genome Functional Annotation

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 sea bass, Gilthead sea loach, 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.

The project brings together world-leading interdisciplinary scientific expertise with industry, providing direct pathways to commercial exploitation. An important aim is to enhance phenotype prediction using genomic information, paving the way for precision breeding to improve disease resistance and other commercial traits in aquaculture.

Why?

A new phase of research, in close collaboration with end users, is needed to build on the recent advances in genomics for a sustainable, competitive and profitable European aquaculture. That the well-annotated reference genomes have a fundamental importance as a resource for the research community in both academic and industry.

The application of functional genomics is needed to improve genomic selection, including traits like disease resistance in farmed fish stocks to address the economic impact of infectious diseases and welfare problems.

How?

- Development of standardized functional annotation protocols and implement them to generate functional annotation maps
- Establishment and coordination of standardized bioinformatics tools and data processing to identify and characterize functional genome elements
- Generation of standardized immunopeptides in the six selected AQUA-FAANG species to help understanding fish immune responses and disease resistance mechanisms
- Enhancement of accuracy of genomic prediction for disease resistance by incorporation of functional genomic data
- Exploitation of comparative analyses to enhance the impact of functional annotation maps
- Translation of AQUA-FAANG results into aquaculture practice and increase the uptake of tools and expertise by scientific and commercial communities

Figure: Overall concept of AQUA-FAANG

The figure illustrates the project's workflow: Six main farmed fish in Europe (Atlantic salmon, Rainbow trout, European sea bass, Gilthead sea loach, Turbot, and Common carp) are sequenced. The AQUA-FAANG project focuses on functional annotation of genome sequences and expression. This leads to the identification of functional elements and the generation of immunopeptides. The overall objectives include the development of standardized functional annotation protocols, the establishment of bioinformatics tools, and the generation of immunopeptides. Specific objectives include the development of functional annotation maps, the identification of functional genome elements, and the generation of immunopeptides. The project aims to enhance the accuracy of genomic prediction for disease resistance and to improve the uptake of tools and expertise by scientific and commercial communities.

Impact

AQUA-FAANG has created an international leading consortium for excellence and innovation in farmed fish genome biology. The creation of world experts from both academia and industry, combined with intensive training and dissemination activities, will create a long-term interactive hub expected to influence the duration of the project. Main impact of the project will be the release of all the data produced openly to facilitate academic and commercial research across Europe and around the world.



FAANG Shared Workshop: Foundation for the Future

From 25-27th of February, the “FAANG Shared Workshop: Foundation for the Future”, took place at the Wellcome Genome Campus in Hinxton, Cambridge, UK. The event was co-hosted by EMBL-EBI and AQUA-FAANG. The workshop brought together the three H2020 projects linked to FAANG (AQUA-FAANG, Gene-SWitCH, and BovReg) to build new expert networks, discuss the implementation of shared coding standards, and scrutinize the possibility of collaborative comparative analyses across the three projects. The workshop lasted three days and included a range of presentations from participants in the three projects in addition to external speakers from FAANG partners based in the USA, breakout sessions, and networking activities. At the start of the workshop, participants gained an improved mutual understanding of the three projects, especially in areas relevant to broader FAANG initiative objectives, i.e. their plans for data analysis, coding standards, management of bioinformatic workflows, and comparative analysis. Subsequently, a broad dissection of the possibilities and constraints concerning shared coding standards and practises across the three projects were discussed, in addition to cross-project collaborations on comparative analyses. Progress was made in planning shared dissemination and communication activities across the three projects, building towards a joint dissemination and communication plan. The workshop finalised by having the experts proceed with plans for the future direction of the global FAANG initiative, coined ‘FAANG 2.0’, ensuring the views of AQUA-FAANG were well represented. With this shared workshop, a remarkable amount of ground was covered, surrounding the key themes of the FAANG Joint Dissemination Strategy. We thank all participants for joining and sharing their expertise during all meetings that took place during the course of this successful workshop.



AQUA-FAANG Annual General Assembly

The first annual general assembly of AQUA-FAANG took place on the 7th of May via a Virtual Zoom Meeting. A total of 55 participants were present, representing all 9 Work Packages and the Project Officer (P.O) Germán Valcarcel. Sigbjørn Lien started the meeting with a short introduction and warm welcome to all participants. In the morning session, an overview of WP1, WP3 and WP4 were presented, followed by WP2, WP5, WP6 and WP7 in the afternoon. Progress and results of each of the work packages were discussed as well as the challenges they faced due to Covid-19. The biggest challenge was the fact that the Covid-19 outbreak stopped or strongly reduced the lab work for all partners, thereby eventually delaying the outcomes of the project. Other points that were discussed in these WP meetings concerned budgeting and work description amendments. Additionally, lab protocols were clarified to improve protocol development. By the end of the meeting, the P.O. ensured the consortium to receive full support from the European Commission and not to worry about project delays or deviations. We look back at a fruitful (online) annual general assembly which we can hopefully follow up with the second general assembly in person, in 2021.



JOB POSITIONS

Post-doctoral position in comparative functional genomics of fishes (AQUA-FAANG project)

15-month post-doctoral position available in the lab of Prof. Dan Macqueen at The Roslin Institute, University of Edinburgh. The position is funded by AQUA-FAANG.

The position: You will lead the generation and analysis of ChIP-Seq, ATAC-Seq, and RNA-Seq libraries in two salmonid species using material that has already been sampled. You will contribute to comparative and evolutionary analyses aiming to identify conserved and divergent functional genomic elements (e.g. enhancers) in different fish species.

The candidate: You will have or be close to completing a PhD in a relevant area, for example: functional or comparative functional genomics. You will have wet-lab experience in all steps needed to generate reliable next-generation sequencing libraries, e.g. ChIP-Seq, ATAC-Seq or methods with a similar level of complexity. You will have experience in bioinformatic analyses of functional genomics data e.g. sequence alignment, feature calling, and statistical analysis. Ideally you will have experience in comparative or evolutionary genomics. A record of publication in high quality peer-reviewed journals is desirable. You will have good person skills and contribute to the training of other members of the lab, while also engaging with the wider external community of AQUA-FAANG researchers. There will be broad scope for collaboration, training and mentorship from leading scientists in the field, as well as an expectation for you to present your findings at leading international conferences.

The position is available immediately for 15 months in the first instance. More information can be found on [the website of the University of Edinburgh](#).



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of EDINBURGH



IN THE SPOTLIGHT - WORK PACKAGE

WP1 - Functional Annotation Assays

MATTHEW PETER KENT

Work Package 1 seeks to reveal the many thousands of currently unidentified functional regions of the genome driving gene expression. These regions are only detectable when a gene is being actively regulated meaning that multiple tissues and a series of fish developmental stages must be sampled to build a comprehensive regulatory atlas. Activity in WP1 is firmly rooted in the wet-lab and is focused on the development of standardized lab protocols, that can be freely disseminated and that when applied by multiple groups on different species will generate consistent data. Detailed protocols exist for documenting and collecting samples representing a series of comparable embryonic stages, and from a selection of mature and immature fish tissues. After sampling, biological material must be processed to physically isolate the tiny fraction of the genome behaving as a regulatory region. Protocols of varying complexity (ATAC-seq, ChIP-seq) used to detect functional regions in mammalian cell cultures have been adapted to work in fish embryo and tissue samples. Each reveals a different facet of gene regulation, and when combined with gene expression data (RNA-seq) allow us to generate a comprehensive picture of a particular samples' gene regulatory landscape. Guidelines outlining the collection of mandatory and recommended metadata related to samples and lab activity have been developed. These metadata will ensure that all lab data representing multiple species and developmental stages can be properly contextualized to the benefit of this project and, upon public release, the wider scientific community and experiments beyond the scope of this project. At this time, project partners across Europe are performing sampling and implementing the protocols in their own labs, and metadata fields are being incorporated into the public databases that will host the final data sets.



IN THE SPOTLIGHT - INDUSTRY PARTNER

Xelect Ltd - Genetic Solutions for Aquaculture

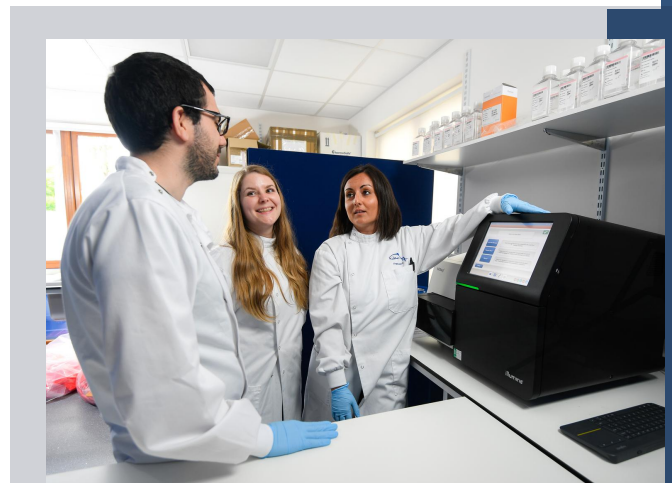
IAN A. JOHNSTON, CHIEF EXECUTIVE OFFICER

Xelect started life as a spin-out from the University of St Andrews in 2012 and has since grown rapidly to become one of the world's leading aquaculture genetics companies (see www.xelect-genetics.com).

Our core business is providing expert genetics support together with the laboratory and data management services to some of the world's best known aquaculture companies. This allows companies to maintain their own broodstock and breeding programmes. Xelect has experience with a wide range of fish species including salmonids, bass, bream, tilapias, amberjacks and barramundi. We currently manage and support breeding programmes for customers in Australia, Canada, Chile, Croatia, France, Greece, Kenya, Malaysia, New Zealand, Spain, United Kingdom, Uganda and Vietnam.

Xelect maintains an active internal R & D programme and was excited to join the AQUA-FAANG consortium. We use amplicon sequencing on an Illumina Mi-Seq as our main genotyping platform and we have extensive experience in the discovery, design and validation of genetic marker panels. Our main role in the AQUA-FAANG project is to develop multifunctional low-density genetic marker panels (<1,000 SNPs) that can be used for parentage assignment, imputation for low cost genomic selection and marker assisted selection. The backbone of the first panel, for gilthead sea bream, is currently under development and will be enriched with functional markers for disease resistance coming from the AQUA-FAANG project.

This is a valuable step towards the democratisation of genome-assisted approaches to selective breeding and promises to bring significant commercial benefits to all our customers.



IN THE SPOTLIGHT - MEET AQUA-FAANG

SIGBJØRN LIEN - COORDINATOR

Professor Sigbjørn Lien is leader of the Genome Biology research group at Faculty of Biosciences, Norwegian University of Life Sciences (NMBU), currently including more than 40 people. His main research interests are functional and comparative genomics, genome evolution and genetic variation related to the genetic architecture of complex traits. His main interest is on the family of salmonid fishes, both for fundamental research as well as on applied explorations directed towards improving the sustainability of salmon aquaculture.



I work as a Professor in genetics and genome biology at the NMBU. Over the last 15 years I have devoted much of my time to the development of Centre for Integrative Genetics (CIGENE, www.cigene.no) at NMBU, which has grown from a small molecular biology lab to Norway's foremost SNP genotyping facility and an internationally important fish genomics research lab devoted to understanding mechanisms and genetic architecture underlying important phenotypes. Outside work, I enjoy spending time with family, jogging and cross-country skiing at our cabin in the Norwegian mountains.

DAN MACQUEEN - DEPUTY COORDINATOR



Professor Dan Macqueen holds a Personal Chair in Integrative Fish Genomics at the Roslin Institute, University of Edinburgh (United Kingdom). His primary research interests are focussed on the genomics, evolution, and physiology of fishes, particularly the salmonid family, both for fundamental discovery science, as well as applied research directed at improvements in the aquaculture sector.

I completed a PhD at the University of St Andrews in Scotland in 2008, investigating the molecular and cellular mechanisms of muscle development in Atlantic salmon. I gained a love for fish at this time, especially the functional and evolutionary complexity of their duplicated genomes. After remaining in St Andrews for post-doctoral positions until 2012, I moved to an Assistant Professor position at the University of Aberdeen in 2013. I moved to my current role as Group Leader at the Roslin Institute in 2018 and was recently promoted to a Personal Chair. Outside work, I enjoy spending time with my wife and two children, running, the odd bit of fishing, and a dram of fine whisky from time to time.



IN THE SPOTLIGHT - MEET AQUA-FAANG

LISE MARIE FJELLSBØ – PROJECT MANAGER

Lise Marie Fjellsbø is the administrative coordinator in AQUA-FAANG and in the Genome Biology group at Faculty of Biosciences, Norwegian University of Life Sciences (NMBU).



My role in the project is to ensure project delivers its tasks on time, arrange meetings, assist with solving unexpected challenges, facilitate internal communication and platforms, and generally assist Sigbjørn and Dan with managing the project. I also have a role in WP7 and assist with dissemination and exploitation of results. I have worked as a scientist for 9 years, within the fields of nanotoxicology and in vitro cell culturing. During this time I was also project manager for an EU FP7 project as well as other internal and external projects. I find genomics truly fascinating and I've learned a lot since working with this group. Outside work, I spend most of my time with my family, do yoga, and when I have time I enjoy hiking in the mountains during summer and cross country in the winter.





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EVENTS



17-18 February 2021: Aqua Farm Conference - Venice, Italy

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