



AQUA-FAANG

ADVANCING EUROPEAN AQUACULTURE BY GENOME
FUNCTIONAL ANNOTATION

ISSUE 2 • JUNE 2021



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.

DANIEL MACQUEEN AND SIGBJØRN LIEN

During the last year, great progress has been made to generate genome-wide functional annotation maps for the six fish species targeted in the AQUA-FAANG project (Atlantic salmon, rainbow trout, sea bass, sea bream, turbot and carp). Despite facing continuing operational challenges associated with the COVID pandemic, an impressive amount of functional data (RNA-, ATAC- and CHIP-Seq) has been generated from a wide variety of sample types and tissues; capturing changes during embryo development and in different tissues and organs of juvenile and mature fish, and profiling immunological responses in all six AQUA-FAANG species. Almost 2000 samples have been sequenced, which collectively represent 20 trillion DNA bases!

The data are being uploaded to public databases and represent an unparalleled resource to improve our fundamental understanding of farmed fish biology using functional genomics, while also helping us to predict commercial traits using genetic information. The project has also established infrastructure and computation pipelines towards processing and analysing these data. A bioinformatics training course was recently delivered online to help ensure that partners have the proficiency to conduct bioinformatics analyses.

Another important achievement has been to complete a major disease (Viral Nervous Necrosis) challenge experiment in European seabass. Samples from this experiment have now been genotyped, their parents whole genome sequenced, and analyses of genetic resistance are underway. There has also been recent progress in developing single cell transcriptomic approaches to profile fish immune responses.

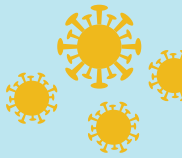
AQUA-FAANG project outcomes are regularly communicated through the AQUA-FAANG website, in addition to social and media channels. In addition, we have, together with the H2020 projects BovReg and Gene-SWitCH, established EuroFAANG to advance knowledge exchange and coordinate project outcomes in alignment with the international FAANG initiative.



THE 2ND ANNUAL MEETING

Active and engaging despite social distancing

LISE FJELLSBØ



Yet another year has passed, and the project is currently in a very busy phase, eager to prepare as many samples for sequencing as soon as possible. During this very hectic period, the project members found the time to meet for a full day online meeting, Friday May 28th. The aim of the meeting was to provide a status update on all the work done in the project, to increase interactions with the exploitation group and initiate the publication strategy and plans. We were also curious for a taste of early results; however, the bulk part of presenting results has been postponed until the Autumn 2021.

At the beginning of the meeting, all participants were encouraged to mark their position on a map of Europe. In a time of distancing, this exercise was a nice way to bring us slightly closer together. We also managed to take a “group photo” (Figure 1).

The morning sessions focused on status and progress in the project overall, presented by deputy coordinator, Dan Macqueen, and in each of the work packages (WPs), presented by their respective WP leaders. The External Expert Advisory Board (EEAB), represented by Prof. Ben Koop, Dr. Sylvie Quiniou and Dr. Shona Wood, was also invited to the meeting. They closed the scientific session by providing useful comments and questions, and were all impressed by the amount of work done despite the pandemic.

The Exploitation Working Group (EWG) is represented by internal industry partners and five external partners. Before the meeting, the EWG were encouraged to provide their thoughts on four specific questions regarding project results, potential barriers, benefits and tools/platforms of interest. This session was very valuable, as well as interesting, and useful points were raised, giving an insight into the industry's point of view for which aspects of our project could be useful to them. For example, SNP panels, VNN resistance and QTL resistance were mentioned by several partners, as well as the importance of cost versus benefits when implementing new genomic selection methods.

As the project is progressing and data are getting available for analysis, it is now time for a more thorough discussion and agreement on a publication strategy and to start feeding information into the publication plan. This session started with a poll, to involve the participants and get some statistics to use as a base for discussion.



Several partners would like to publish within their species, but also be part of the larger papers, with comparative data. We agreed that the best strategy is to arrange several meetings, where the involved participants can share ideas, find potential co-authors within the project, and ensure there are no conflicts of interest. An initial survey will take place in June, followed by followed by a more detailed discussion after the summer holidays.

The final session was dedicated to management and group work. The most lively discussion in this session was whether the participants believe it is possible to arrange a physical meeting in the Autumn. The majority were keen on meeting in a location in Europe, but emphasised that it in any case, this must be a hybrid solution, with the possibility to join in online as well.

In the group work, participants were divided into groups of 5-6 persons. They were instructed to introduce themselves and agree on five words that best describes AQUA-FAANG. The result is illustrated in the word cloud (Figure 2) and can be useful when describing and presenting our project.

Overall, the meeting was filled with lively discussions, both “live” and in the chat. Several good points were raised, that are useful for shaping the directions of the project. The management team is proud of being part of such an engaged group of people and are excited to move into the next phase of the project.

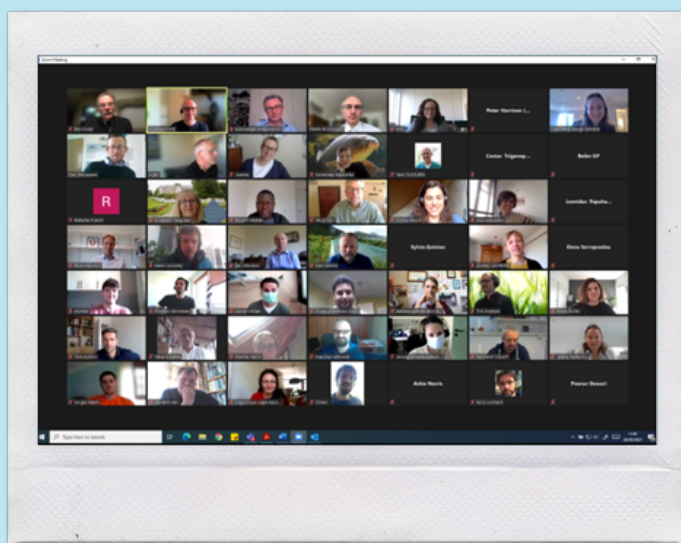


Figure 1 Group photo from the AGM.



Figure 2 This word cloud is the result of the group work, where the participants were asked: “Which word best describes AQUA-FAANG?”



Video interviews with young researchers

AQUA-FAANG has started a new video initiative to create engagement with different level stakeholders as well as the citizens of Europe. One of the objectives within the AQUA-FAANG project is to promote the work of young researchers, thereby also indicating the importance of young researchers for this project. The purpose of these interviews is to introduce PhD students and young researchers that are involved in the AQUA-FAANG project. In each video, the researchers explain their area of research and what they are working on, using language that is also understandable for people outside of the consortium. The videos are also a great way for the PhD students and young researchers to share information about their work, findings and daily life on their social networks.

Shahmir Naseer

In the first video, we meet Shahmir Naseer. Shahmir is a Phd Student at the University of Aberdeen in Scotland, where he is supervised by Professor Sam martin and co-supervised by Professor Dan Macqueen from the Roslin Institute. Shahmir works for the AQUA-FAANG project, mainly in work package 3, where he aims to enhance our fundamental understanding of the genomic basis of the innate immune system in Atlantic Salmon. The results of his research will be helpful to improve fish welfare, fish farm profitability and in general to provide a more sustainable aquaculture industry.

We are very happy and thankful that Shahmir took the time to film his research and explain his PhD. His video gave us insight into his daily routines in the lab and also underlined the importance of Shahmir's research within the AQUA-FAANG project. We are also delighted to see that the European Commission YouTube account CORDIS has shared Shahmir's video on their channel.

[Watch the video here](#)



Annemiek Blasweiler, Joanna Szczygieł and Ada Jimenez-Gonzalez

Our second video is currently being prepared and features Annemiek Blasweiler from Wageningen University & Research, Joanna Szczygieł from the Institute of Ichthyobiology and Aquaculture in Gołysz and Ada Jimenez-Gonzalez, a postdoctoral researcher at the University of Birmingham.

In this video Annemiek, Joanna and Ada will explain how interdisciplinary research can help answer important biological questions, in their case related to the functional genome of the common carp. Their research within the AQUA-FAANG project will improve our understanding of the common carp and how the biological functions within this species are organised, activated and managed.

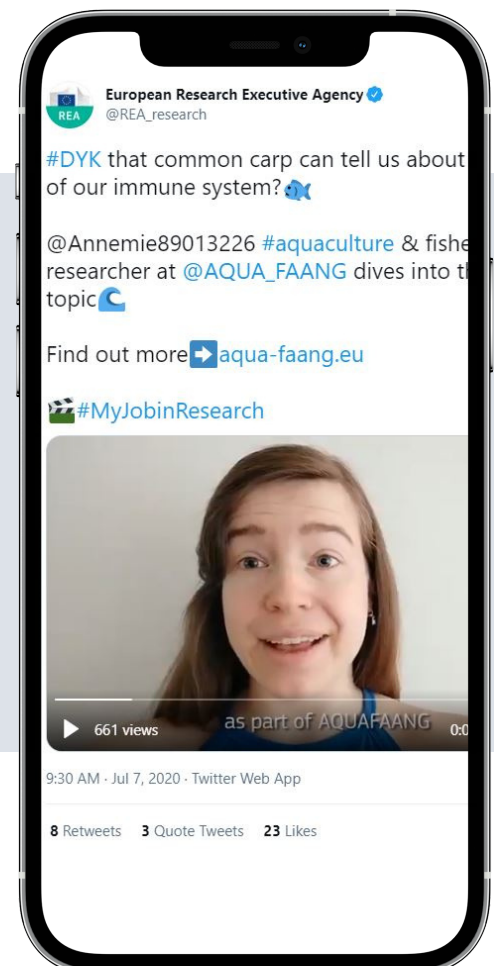
Annemiek featured in REA_research

Annemiek has already created another video that we would recommend to watch and share. The video is a very short pitch, where Annemiek briefly explains about her research work within the AQUA-FAANG project. The video was shared by the European Commission's Research Executive Agency (REA) because they had organised a "My Job in Research" video challenge to promote the work of researchers. Annemiek joined the challenge with her video and as a result of a good effort her video was selected amongst the best ones. Therefore, the video was shared online by REA. We would like to thank Annemiek for her efforts and congratulate her for being featured on the REA_research account.

[Watch the video here](#)

"I study immune gene organisation and function in common to better understand the evolution of our vertebrate immune system and the implications of whole genome duplications"

Annemiek Blasweiler



TRANSLATED FACTSHEETS

AQUA-FAANG aims to support the key objectives of the Green Deal's Farm to Fork Strategy while at the same time aiding the UN Sustainable Development Goals. To increase our communication efforts, a one-page factsheet was created to briefly explain the impact of the AQUA-FAANG project and how our results will benefit these global UN goals and EU strategy's.

The fact sheet is a useful tool to explain the research and projects aims of AQUA-FAANG and more specifically why research in this field is so important. As a result of close collaboration with all the project partners, we managed to translate the factsheet into eight different languages. This is a huge asset in terms of communicating to different stakeholders and gaining more engagement on a national level. The translated fact sheets are also a strong communication tool in terms of interacting with the press and helping to simplify the area of research.

The different fact sheets have already been disseminated through all of our social media channels. We kindly invite everybody to share the factsheet among your network in your preferred language. The fact sheet is currently available in English, Greek, French, Norwegian, Polish, Spanish, Dutch and Italian.

[Find the translations of the factsheet here](#)



AQUA-FAANG

Advancing European Aquaculture by Genome Functional Annotation

www.aqua-faang.eu

AQUA-FAANG er et EU-finansiert forskningsprosjekt innen akvakultur. Prosjektet skal øke vår forståelse av mekanismene som skaper genetiske forskjeller mellom enkeltindivider, med tanke på sykdomsresistens og andre komplekse egenskaper. Prosjektet skal ta for seg de seks viktigste artene innen europeisk akvakultur. Resultatene fra prosjektet vil sette oppdrettsnæringen i bedre stand til å løse problemer knyttet til fiskehelse med mer, for på den måten å bidra til en mer bærekraftig og lønnsom næring.

- 1** UTRYDDE FATTIGDOM
Økt sykdomsresistens vil øke næringens lønnsomhet, slik at næringen kan ekspandere og bidra til økt sysselsetting.
- 2** UTRYDDE SULT
En kostnadseffektiv og bærekraftig oppdrettsnæring vil gi en mer forutsigbar tilgang på sjømat og flere vil få tilgang på et høyverdig, proteinrikt kosthold.
- 3** GOD HEELSE OG LIVSKVALITET
Det er mangel på sjømat i verden, og dette leder til dårligere folkehelse. En mer effektiv oppdrettsnæring vil føre til høyere konsum av sjømat, noe som vil ha gunstige effekter på helse hos forbrukere.
- 9** INDUSTRI, INNOVASJON OG INFRASTRUKTUR
AQUA-FAANG vil gjøre alle data og resultater fritt tilgjengelig, slik at også andre kan dra nytte av dem. Dette vil for eksempel komme aktører som driver oppdrett på andre arter til gode.

- 12** ANSVARLIG FORBRUK OG PRODUKSJON
AQUA-FAANG vil bidra til tillit og åpenhet i verdikjeden, ved å forklare tekniske prosesser for forbrukerne, særlig med tanke på den viktige rollen genetikk spiller.
- 13** STOPPE KLIMAENDRINGENE
Bedret ytelse og fiskehelse vil gi redusert tap av fisk, bedre utnyttning av ressurser og reduserte klimagassutslipp.
- 14** LIVET I HAVET
En bedret forståelse av hvordan genetikken påvirker fiskens egenskaper vil fremme bevaring av villfisk og naturlige økosystemer.
- 17** SAMARBEID FOR Å NÅ MÅLENE
AQUA-FAANG bringer sammen eksperter innen genetikk, genomikk, immunologi og fiskeavl, og bidrar til samarbeid og fremragende innovasjon på tvers av fag og landegrensar.

BETYDNING

AQUA-FAANG støtter opp under Europakommisjonens «Green Deal», som skal kombinere lønnsomhet i bedriftene med et lavere miljøfotavtrykk, uten å gå på bekostning av pris for konsumentene.

AQUA-FAANG vil legge grunnlaget for genetiske løsninger på næringens utfordringer, og slik bidra til bedre fiskelevered, lønnsomhet og bærekraft. Prosjektet støtter dermed opp under **mange av FNs bærekraftsmål**.

BAKGRUNN

Smittsomme sykdommer koster europeiske oppdrettere 18 milliarder kroner i året, og problemet forventes å øke i omfang framover blant annet pga. klimaendringer. Noen av løsningene på problemet kan ligge i fiskens gener, men vi vet ennå for lite til å utnytte denne muligheten maksimalt. Bedre forståelse av hvordan genene reguleres og påvirker hverandre vil hjelpe oss med å finne genetiske løsninger på oppdrettsnæringens utfordringer.

PROSJEKTRESULTATER

De seks artene har alle fått sine genomer (arvestoff) sekvensert, men man vet foreløpig lite om hvilken funksjon hvert enkelt gen har, hvordan ulike gener virker inn på ulike egenskaper (f.eks. resistens mot spesifikke sykdommer), og hvordan genene påvirkes av ytre miljø og fiskens alder og livsfase. Prosjektet skal øke vår kunnskap om disse tingene på en systematisk måte, ved å ta i bruk ny metodikk basert blant annet på helgenomsekvensering.

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

NEWS

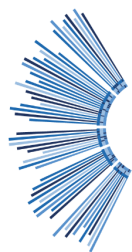
EuroFAANG

By establishing EuroFAANG, the H2020 projects [AQUA-FAANG](#), [BovReg](#) and [GENE-SWitCH](#) have formed a closer relationship to coordinate their objectives within Europe in association with the international FAANG initiative.

[EuroFAANG](#) brings together a wide range of expertise in farmed animal biology and breeding, genomics, bioinformatics, modelling and open data, as well as multiple platforms for dissemination and outreach, with a common goal to discover links between genome and phenome (i.e. G2P) in the frame of the FAANG to Fork strategy. AQUA-FAANG, BovReg and GENE-SWitCH all focus on different groups of animals (respectively farmed fish species, cattle, pigs and chicken).

Although the genomes for most domesticated animals have been successfully sequenced, we have a limited understanding of functional regions in the DNA, including elements that regulate gene transcription under different conditions.

We are very excited about this close collaboration and invite everybody to stay updated on news and other relevant information via the different project's main websites and via social media.



EuroFAANG

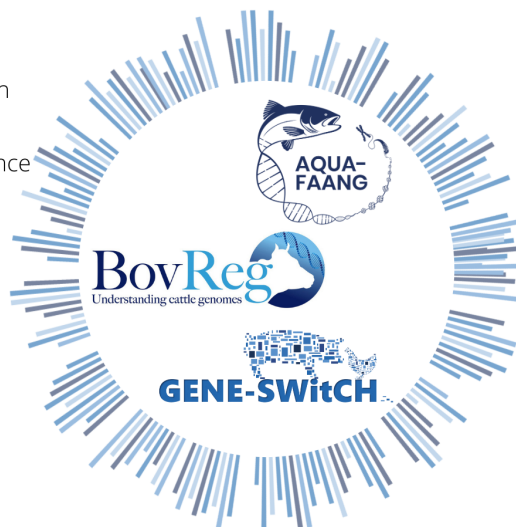
Leveraging functional genomic information to make animal production more robust and sustainable in Europe and beyond

Research aims

- ✓ Increase efficiency through precision breeding
- ✓ Increase disease resistance
- ✓ Minimise environmental impact

Joint strategies

- ✓ Communication & Dissemination
- ✓ Training
- ✓ Research Methodology



IN THE SPOTLIGHT - PROGRESS IN WPS

Data production accelerating in AQUA-FAANG

MATTHEW KENT

AQUA-FAANG seeks to better understand how phenotypes or traits are shaped by specific regulatory features encoded in fish genomes. Regrettably however these specialized features remain largely unknown and are indistinguishable from the billions of DNA bases surrounding them. The first Work Package (WP1) in the project seeks to apply powerful laboratory techniques that will physically isolate these regions allowing researchers to decode their DNA sequences and reveal their locations within chromosomes.

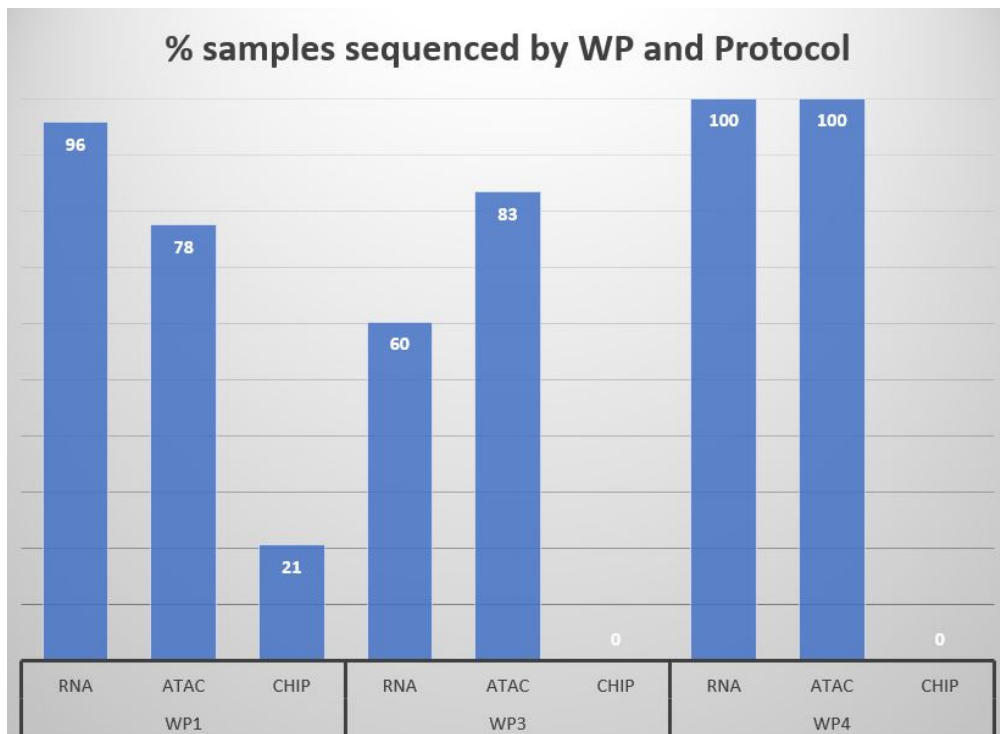
Detailed lab protocols that have been developed in WP1 are now publicly available, allowing researchers to capture open chromatin (regions where supercoiled DNA is relaxed and exposed to gene-expression machinery) and DNA sequences wrapped around histone proteins tagged with chemical modifications that can activate or repress nearby genes.

Described metaphorically, these protocols allow us to observe commuters in a busy city (a biological sample) and can tell us which garage doors are open or closed, and whether the accelerator or the brake is being stepped on, in this representation the “cars” being driven are genes coding for the hundreds or thousands of different proteins.

An embryo, tissue biopsy, or cell culture is highly dynamic and a sample collected at a specific time represents a unique snap-shot of a specific biological state. Using these protocols a single sample weighing a fraction of a gram can be analysed to simultaneously identify open chromatin (ATAC) and DNA associated with histone modifications (ChIP), as well as identify which genes are expressed and at what levels. By merging and interpreting this information, it is possible to build an understanding about how these newly discovered regulatory features affect sample biology.

Since the beginning of 2021 WP1 partners and partners in other WP's (3, 4, and 5) exploring fish immune response have made remarkable progress generating raw data from a wide variety of sample types and experimental tissues. “Remarkable” especially because across Europe the project partners are facing continued fallout from the ongoing COVID pandemic which affected almost every aspect of the sample-to-data pipeline.





To date across 3 WPs, almost 2000 samples have been processed isolating 66 billion regulatory / gene sequences which collectively contain 20 trillion DNA bases. These samples will provide insight into changes during embryo development, tissue and organ specific gene expression patterns, and profile immune response in all six AQUA-FAANG species. Effort is ongoing in all labs to process remaining samples and complete lab processing (especially for ChIP; measuring the accelerator and brake) with an expectation that all remaining work will be complete by mid-Dec 2021.

These data are being swiftly uploaded to public databases and shared with the wider community and represent an unparalleled resource that will improve our fundamental understanding of farmed fish biology and improve our ability to predict commercial traits using genetic information.



IN THE SPOTLIGHT - WORK PACKAGE 2

WP2 – Bioinformatics and Data Analysis

PETER W. HARRISON



Work Package 2 aims to establish and coordinate standardized bioinformatics tools and data processing to identify and characterize functional genome elements across the six commercially important AQUA-FAANG species.

This standardisation in data processing is key to ensure results and analyses are comparable across species and to the wider datasets within FAANG. This includes standardising quality control steps, processing pipelines and tools, and output file formats. To this end the primary bioinformatics analysis for the whole AQUA-FAANG project is being conducted utilising the Ensembl pipelines at the EMBL-European Bioinformatics Institute. Ensembl is a world-renowned genome browser for comparative genomics, evolution, sequence variation and transcriptional regulation, and this will crucially place the AQUA-FAANG species within this wider vertebrate biological context.

Early in the project work package 2 annotated all six of the AQUA-FAANG genomes in the [Ensembl browser](#) for vertebrate genomics. These genomes are a freely available resource required as a foundation for analyses for precision breeding exploitation by industry partners and expanding research into disease resistance, in addition to comparative analyses. The genomes will continue to be updated as new assemblies and transcriptomic data become available.

Work Package 2 is also responsible for the projects Data Coordination and Dissemination. With the assistance from the wider consortium, new rich metadata rulesets were developed to support aquatic species in [FAANG](#) for the first time. A [data portal](#) was developed for AQUA-FAANG that will present all of the samples, datasets, protocols and publications generated by the project within an interactive interface.



The work package is also delivering training to the consortium and wider FAANG projects to ensure competence on computational analysis of functional annotation data. The first of these training courses took place virtually in May 2021 covering ChIP-seq (chromatin immunoprecipitation sequencing) and ATAC-seq (assay for transposase-accessible chromatin sequencing). Participants were trained on the key bioinformatic steps involved in data analysis and interpretation, from raw sequence data through to peak calling, interpretation of data quality, and data integration including by use of genome segmentation methods. Recordings of the training will soon be available from the AQUA-FAANG [YouTube channel](#).

The high-quality Ensembl whole genome regulatory annotation, gene annotation and homology prediction will be a key resource for the consortia to answer its key research questions and a valuable resource to the wider aquatic community.



IN THE SPOTLIGHT - INDUSTRY PARTNER



AquaGen

TIM MARTIN KNUTSEN

AquaGen is a breeding company which develops, produces and delivers genetic material to the global aquaculture farming industry. Through a market-oriented research and development we have achieved a leading position as a provider of fertilized eggs of Atlantic salmon and rainbow trout. Since the 1970's when collection of these fish species began, a continual research and development program has been carried out in cooperation with commercial operators and research institutions. Based on a long-term and systematic breeding work combined with the use of modern breeding technologies, AquaGen offer solutions for many challenges in the aquaculture industry.

AquaGen's role in AQUA-FAANG

AquaGen is part of FAANG Exploitation Working Group (EWG) which we expect will serve as a platform for cooperation and collaboration between AQUA-FAANG key stakeholder groups within the aquaculture breeding industry.



Photo Credit: AquaGen

How would the AQUA-FAANG results be used commercially?

AquaGen is heavily invested in further development of SNP-arrays and refined methods for QTL fine mapping and genomic selection. We therefore have great expectations that improved reference genomes for trout and salmon with state-of-the-art functional annotation will help us further in our search for functional variants so these can be included in our routine genotyping, specialized product development and breeding value calculations.

Photo Credit: AquaGen



IN THE SPOTLIGHT - MEET AQUA-FAANG

PROFESSOR ROSS HOUSTON – PERSONAL CHAIR OF AQUACULTURE GENETICS, THE ROSLIN INSTITUTE, UNIVERSITY OF EDINBURGH

Ross Houston leads WorkPackage 5 of the AquaFAANG project, which is focussed on application of functional genomic data to improve breeding for disease resistance.

Ross is Personal Chair of Aquaculture Genetics at The Roslin Institute, where his team's research focusses on genetics and genome editing technologies in aquaculture species.



His primary research interests include (i) development and application of genomic tools for aquaculture species, including sequencing and functional annotation of genomes; (ii) genomic selection for commercially relevant traits in breeding programmes, with a focus on disease resistance; and (iii) optimising and applying CRISPR/Cas9 genome editing in vitro and in vivo to pinpoint functional disease resistance alleles. You can read more about some of Roslin's Aquaculture team via the [link](#).

Ross has been amongst the first to develop key underpinning genomic tools for several major aquaculture species; for example high density single nucleotide polymorphism arrays for Atlantic salmon, Pacific oyster and Nile tilapia. He has also studied genomic selection for several fish and shellfish species, including studying genotype imputation approaches improve cost-efficiency. His discovery of a major quantitative trait locus explaining almost all the genetic variation in resistance to Infectious Pancreatic Necrosis in salmon has been widely applied in the salmon breeding industry to control this disease. He has led studies to optimise CRISPR/Cas genome editing in salmonid cell lines and embryos, and is applying these tools to understand and improve disease resistance.

Finally, Ross led the writing of a relevant article in Nature Reviews Genetics which addresses the potential of genomics to accelerate genetic improvement in aquaculture species, which is available [here](#).



IN THE SPOTLIGHT - MEET AQUA-FAANG

MATTHEW KENT - SCIENTIST WORKING IN THE GENOME BIOLOGY RESEARCH GROUP AT THE FACULTY OF BIOSCIENCES, NORWEGIAN UNIVERSITY OF LIFE SCIENCES (NMBU)



Dr Matthew Kent is a scientist working in the Genome Biology research group at the Faculty of Biosciences, Norwegian University of Life Sciences (NMBU).

His primary research activities are related to genomics in production species, especially salmonids, and applying state-of-the-art technologies to improve our functional understanding of genotype - phenotype relationships.

I completed my PhD at Lincoln University in New Zealand in 2003 working with livestock and investigating post-mortem biochemical changes occurring in skeletal muscle.

After completing a post-doctoral position at the USDA in Nebraska I moved to Norway and worked for a start-up biotechnology company seeking to develop nanopore based DNA sequencing technologies, it was at this time that my interest in the creative use of technology in genetics and genomics biology was born.

From 2006 I have been employed at NMBU, and have been involved in the adoption of multiple state-of-the-art technology platforms and protocols related to high-throughput genotyping, long-read sequencing, genome-wide CRISPR screening and functional genomics. Outside work, my life revolves around my wife and two active daughters, but I also enjoy exercising and find time to relax with a nice glass of Sauvignon blanc (from NZ of course).



RECENTLY PUBLISHED

A genome-wide association study, supported by a new chromosome-level genome assembly, suggests *sox2* as a main driver of the undifferentiated ZZ/ZW sex determination of turbot (*Scophthalmus maximus*) - April 2021

Martínez P, Robledo D, Taboada X, Blanco A, Moser M, Maroso F, Hermida M, Gómez-Tato, Álvarez-Blázquez B, Cabaleiro S, Piferrer F, Bouza C, Lien S, Viñas AM. A genome-wide association study, supported by a new chromosome-level genome assembly, suggests *sox2* as a main driver of the undifferentiated ZZ/ZW sex determination of turbot (*Scophthalmus maximus*). *Genomics* 113 (2021) 1705-1718

[Read the publication](#)

The European Nucleotide Archive in 2020 - November 2020

Harrison PW, Ahamed A, Aslam R, Alako BTF, Burgin J, Buso N, Courtot M, Fan J, Gupta D, Haseeb M, Holt S, Ibrahim T, Ivanov E, Jayathilaka S, Kadhivelu VB, Kumar M, Lopez R, Kay S, Leinonen R, Liu X, O'Cathail C, Pakseresht A, Park Y, Pesant S, Rahman N, Rajan J, Sokolov A, Vijayaraja S, Waheed Z, Zyoud A, Burdett, Cochrane G. The European Nucleotide Archive in 2020. *Nucleic Acids Research* 2021; Volume 49, Issue D1, 8 January 2021, Pages D82–D85.

[Read the publication](#)

Ensembl 2021 - November 2020

Howe KL, Achuthan P, Allen J, Allen J, Alvarez-Jarreta J, Amode MR, Armean IM, Azov AG, Bennett R, Bhai J, Billis K, Boddu S, Charkhchi M, Cummins C, Fioretto, LDR, Davidson C, Dodiya K, Houdaigui BE, Fatima R, Gall A, Giron CG, Grego T, Gujjarro-Clarke C, Haggerty L, Hemrom A, Hourlier T, Izuogu OG, Juettemann T, Kaikala V, Kay M, Lavidas I, Le T, Lemos D, Martinez JG, Marugán JC, Maurel T, McMahon AC, Mohanan S, Moore B, Muffato M, Oheh DN, Paraschas D, Parker A, Parton A, Prosovetskaia I, Sakthivel MP, Salam AIA, Schmitt BM, Schuilenburg H, Sheppard D, Steed E, Szpak M, Szuba M, Taylor K, Thormann A, Threadgold G, Walts B, Winterbottom A, Chakiachvili M, Chaubal A, Silva ND, Flint B, Frankish A, Hunt SE, Ilesley GR, Langridge N, Loveland JE, Martin FJ, Mudge JM, Morales J, Perry E, Ruffier M, Tate J, Thybert D, Trevanion S, Cunningham F, Yates AD, Zerbino DR, Flicek P. Ensembl 2021. *Nucleic Acids Research* 2021; Volume 49, Issue D1, 8 January 2021, Pages D884–D891.

[Read the publication](#)

From FAANG to fork: application of highly annotated genomes to improve farmed animal production - November 2020

Clark EL, Archibald AL, Daetwyler HD, Groenen MAM, Harrison PW, Houston RD, Kühn C, Lien S, Macqueen DJ, Reecy JM, Robledo D, Watson M, Tuggle CK, Giuffra E. From FAANG to fork: application of highly annotated genomes to improve farmed animal production. *Genome Biol.* 2020; 21:285.

[Read the publication](#)

The European Nucleotide Archive in 2019 - November 2019

Amid C, Alako BTF, Kadhivelu VB, Burdett T, Burgin J, Fan J, Harrison PW, Holt S, Hussein A, Ivanov E, Jayathilaka S, Kay S, Keane T, Leinonen R, Liu X, Martinez-Villacorta J, Milano A, Pakseresht A, Rahman N, Rajan J, Reddy K, Richards E, Smirnov D, Sokolov A, Vijayaraja S, Cochrane G. The European Nucleotide Archive in 2019. *Nucleic Acids Research* 2020; Volume 48, Issue D1, 08 January 2020, Pages D70–D76

[Read the publication](#)





AQUA-FAANG

ADVANCING EUROPEAN AQUACULTURE BY GENOME
FUNCTIONAL ANNOTATION

ISSUE 2 • JUNE 2021

EVENTS



26 - 30 July 2021: ISAG virtual conference (Virtual: [Registration](#))



9 September 2021: AQUA-FAANG 2nd annual meeting - Part 2



4 - 7 October 2021: Aquaculture Europe 2021 (Virtual: [Registration](#))

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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. This publication reflects the views only of the author, and not the European Commission (EC). The EC is not liable for any use that may be made of the information contained herein.