



FISHBOOST

The next level of aquaculture breeding

In this edition:

- [FISHBOOST announcements](#)
- [Breeding program for gilthead seabream profitable after five years](#)
- [Adaptation of rainbow trout genotypes to simultaneous changes in multiple plant-based diet ingredients](#)
- [Genomic selection selection methods in aquaculture breeding programmes](#)
- [WCGALP conference](#)
- [In the spotlight: Pierrick Haffray](#)

This newsletter updates you on recent developments in aquaculture breeding and the FISHBOOST project.

This is FISHBOOST:

FISHBOOST is an FP7 EU resesarch project that works on improving the main components of breeding programmes for the main six fish species produced in Europe:

Atlantic salmon, common carp, European seabass, gilthead seabream, rainbow trout and turbot.

www.fishboost.eu

FISHBOOST announcements

FISHBOOST organizes a **Farmer's Day** for producers and breeders on August 26. The event will take place during the joint event of WAS and EAS (25-29 August) in Montpellier. EAS is a global aquaculture event with participation from more than 60 countries. The targeted topics include disease resistance, production efficiency, benefits of genomics in aquaculture breeding, inbreeding and software tools, economics, and future challenges. Finally, there will be a round table discussion focusing on "Research needs and future challenges of aquaculture breeding". The Farmer's Day is organized by EFFAB, Luke, NMBU, Nofima, WUR and UEDIN. Registration details will soon be shared from <http://www.fishboost.eu/>

FISHBOOST is organizing a 2 day training on **advanced aqua breeding technologies** in Montpellier on November 6-8, 2018. EFFAB, LUKE, IFREMER, INRA, NMBU, Nofima, SYSAAF, WUR and UEDIN are the responsible partners for this event. The program includes an introduction into aquaculture breeding in Europe and specific results from the FISHBOOST project. The training will, among others, target breeding programs, disease resistance, production efficiency, genotyping/RAD sequencing, and improving European aquaculture efficiency by genomic selection. Finally, there will be a ½ day technical visit to the research facility of IFREMER in Palavas-les-flots. The training will be given by 10 lecturers, and there

will be space for maximum 40 course participants. Applications will be accepted as "First come first served". More details on registration will soon be given at www.fishboost.eu

Successful FISHBOOST webinar on feed efficiency

FISHBOOST organised an **interactive webinar on feed efficiency** for breeders and researchers on June 12. The two-hour lasting webinar was organized by EFFAB, LUKE, INRA and WUR and gathered many specialists. The scope of the webinar was on "prospects on selection of feed efficiency in aquaculture". The targeted topics were *i)* general principles of improving feed efficiency, *ii)* economics and impact management, and *iii)* practical experiments on feed intake. The final panel discussion was on "Can we do more than select for fat percentage". The webinar was well attended and the interactive atmosphere brought up some interesting discussions. We want to thank all attendees for their valuable input.

Breeding program for gilthead seabream profitable after five years

Kasper Janssen (WUR)

Cost-benefit analysis in a recent [study](#) revealed that a breeding program for gilthead seabream can reach a positive net present value five years after its start. After ten years, the net present value of the studied breeding program was 2.9 million euro. For an integrated company with an annual production of 5000 tons, a breeding program can thus be highly profitable investment. A breeding program improves the genetic level of the animals used in production and thereby increases farm profit. Benefits of a breeding program depend on the rate of increase of the genetic level of animals used in production and production output of the company. The current study compared multiple alternative breeding program designs to a baseline breeding program that was based on the breeding program of Andromeda, Greece. A comparison between breeding program designs demonstrated that the profitability of a breeding program can be improved when production is supplied directly between the nucleus and producers instead of from the multiplier tier. Thus a multiplier tier delays the benefits of genetic improvement, analysis of the relation between the number of selection candidates and profitability revealed that. The optimum number of selection candidates increases with the length of the time horizon and production output. Using too many selection candidates relative to the optimum leads to less reduction in profitability than using too few selection candidates.

<https://gsejournal.biomedcentral.com/articles/10.1186/s12711-018-0372-3>

Adaptation of rainbow trout genotypes to simultaneous changes in multiple plant-based diet ingredients

*A Kause, M Janhunen, A Nousiainen, H Koskinen, J Koskela
(Natural Resources Institute Finland, Luke)*

Feed composition is one of the fastest changing environmental factors for farmed fish. For carnivorous fish like Atlantic salmon, European seabass, gilthead seabream, rainbow trout and turbot, fishmeal produced from wild-caught small pelagic fish species is considered as the superior protein source in feeds. Due to the depletion of wild fish populations and the consequent economical and environmental pressure, feed companies have replaced a major part of fishmeal with protein of plant-origin. The number of potential plant protein sources for farmed fish is large, and most nutritional research has focused on ingredients with security of supply, such as soybeans, wheat, corn and pea. However, some genotypes or fish strains may be less capable of adapting to these novel diets with protein of plant-origin.

Selective breeding makes fish adapted to novel diets

FISHBOOST results on one-year old rainbow trout show that indeed sires differ in their sensitivity to cope with challenging diets. Nevertheless, breeding programmes selecting for fish performance on the current on-growing feeds will make rainbow trout better adapted to the future feeds that use even more plant-protein concentrates to replace fish meal. With the availability of genetic variation and the limited amount of adverse genotype-by-diet interactions in rainbow trout, breeding programmes are aided to make fish more adapted to the novel feeds.

Plant-based ingredients compromise fish performance

Although the genotype-by-diet interactions are generally not of concern, there is high pressure to improve fish performance and welfare specifically on the new plant-based diets. Fish performance, measured as economically important traits such as growth, feed conversion ratio (FCR) and protein retention efficiency, is compromised when large amounts of plant-protein are added to fish feeds.

The use of a mixture diet design in this study allowed the identification of diet mix combinations that support good fish performance. In contrast to the one-ingredient-at-a-time experiments, interactions between the ingredients could be observed and clearly showed benefits when including several plant protein mixes. Simultaneously the multiple ingredients support fish performance better than on their own, likely because they compensate for each other's limitations.

Future needs

These results emphasise the further need for genetically improving the feed utilisation traits of rainbow trout on new plant-based feeds, and simultaneously, to tailor-make feeds specifically for the genetically superior farmed fish with their unique nutritional needs.

This FISHBOOST study has linked animal genetics, the main focus on the FISHBOOST project, with the development of novel more sustainable fish feeds. Such information highlights the power of selective breeding to support sustainable development in other areas such as feed development.

Methodology in detail

To assess the degree to which genotypes are adapted to multiple diet ingredients, genetic variation in the sensitivity of one-year-old rainbow trout against multiple diet ingredients was quantified.

Rather than using two alternative diets, rainbow trout were fed with the currently used diet (diet FM with 300 g kg⁻¹ of fish meal), and on a range of commercially potential future diets with decreasing fish meal content. A total of seven different diets were used in which the concentrations of three commercially viable raw material concentrate mixes varied: fish meal (FM), soya protein-wheat gluten concentrate (S-MIX) and pea protein-wheat gluten concentrate (P-MIX).

The implemented mixture diet design to quantify fish responses as a surface along several changing diet ingredient mixes allowed the identification of diet mix combinations that support good fish performance, identified as the area on the response surface at which fish performance is at least 95% of the maximum observed performance. This area identifies any combination of the three ingredient mixes that produces almost the same fish performance.

As expected, fishmeal diet was the most optimal diet supporting high growth for all progenies of sires. However, the progenies of sires differed in the extent of the area with at least 95% of the maximum growth. The fast-growing genotypes on FM diet generally had very small 95% optimal response area, i.e., they were more specialists (Sire 1 in Fig 1.), whereas the slow-growing genotypes on FM diet had much larger 95% area (more generalist genotype) (Sire 10 in Fig. 1).

This is the reflection that there is among-family variation in the sensitivity of rainbow trout to plant protein concentrate mixes, and that the fast growing genotypes have their unique physiological needs for maintaining their high genetic potential.

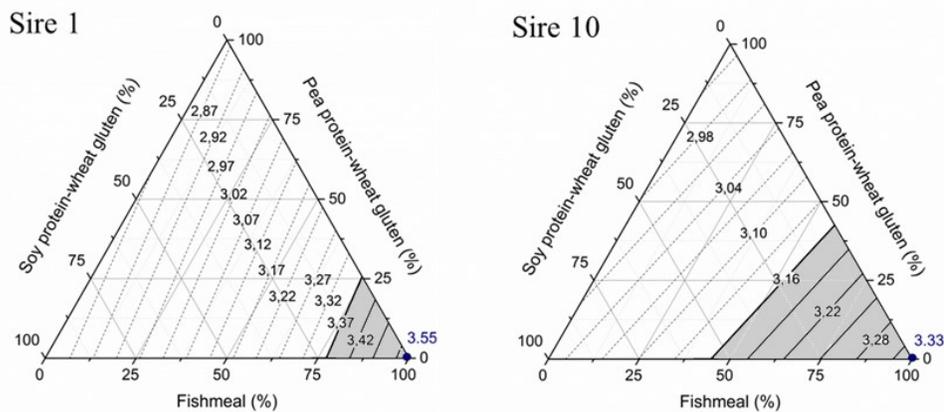


Fig. 1. Tertiary plots showing daily growth coefficient (DGC) as a function of concentrations of fishmeal, pea protein-wheat gluten concentrate-mix, and soy protein-wheat gluten concentrate-mix for the progeny of two extreme sires. The feed component axes are given in percentages of ingredient concentrates. Grey area confine the diet combinations that produces at least 95% of the maximum DGC for each sire. For sire 1 (fast grower), the area with at least 95% DGC is small, yet DGC at 100% FM diet is much higher than DGC for sire 10. For sire 10 (slow grower), the area with at least 95% DGC is large, about 25% of the diet ingredient combinations support high growth.

The mixture diet design aids in determining the most potential combinations of feed ingredient concentrations for practical feed formulae.

The response surfaces produced via the mixture diet design allow dynamic determination of suitable feeds when multiple diet ingredients need to be considered. Production of industrial aquafeeds is a dynamic process in which the amounts of raw materials or their concentrates vary between batches, depending on the availability and price of the ingredients. There is not a single fixed diet formula, but rather many different combinations of several ingredients that can be used to produce a feed with more or less the same proximate feed composition (energy, protein, lipid, carbohydrates).



The experiment was performed with the families originating from the Finnish national breeding programme for rainbow trout. In addition to feed utilization, the trait recording included non-destructive measuring of fillet lipid percentage.

Genomic selection methods in aquaculture breeding programmes

Theo Meuwissen (NMBU)

The showcase for genomic selection is dairy cattle, but aquaculture breeding programmes also yield substantial opportunities for genomic selection. Many traits of interest to fish breeders are not directly recorded on the candidates for selection for elite breeding, such as disease resistance traits and carcass traits. The recording of the former traits is performed in disease challenge tests on sibs of the candidates in order to avoid a disease outbreak amongst elite breeding animals, and the recording of the latter requires slaughtering of the fish. In addition, the large family sizes that are typical to fishbreeding schemes make it possible to set up reference populations within the families and apply the genomic selection

technology within the families, i.e. the so-called within family genomic selection. Within families, the associations between genetic markers and genes are strong, so we do not need such high marker density as in traditional population-wide genomic selection, and the number of within family reference individuals can be relatively small. Theoretical developments show that within family genomic selection can reach an accuracy of 100% in fishbreeding because of the potentially large family sizes. This implies a substantial increase in accuracy of selection compared to the traditional family selection based fish breeding schemes, which reach a theoretical maximum accuracy of 70%. This is because e.g. a traditional challenge test for disease resistance reveal only which family has best disease resistance, whereas genomic selection also predicts which individual within a family has the best genes for disease resistance.

Within family and the more traditional population wide genomic selection were compared by UMB in computer simulation studies. The computer simulation studies showed that at very low marker densities, within family genomic selection yielded higher selection accuracies, but within family genomic selection was more sensitive to small family sizes. In analysis done by Nofima, UEDIN and UMB of common carp, European seabass, gilthead seabream and turbot, population wide genomic selection gave 1-2 percent point higher accuracy than within family genomic selection. The results also seemed to depend on whether there were large genes affecting the trait and markers that are associated to these genes, since in this situation population-wide genomic selection may successfully find these associations by combining data across families. Generally, both population-wide and within family genomic selection were clearly more accurate than traditional pedigree based selection (10-22 percent points).

DNA pooling strategies were investigated by Nofima where DNA of e.g. the survivors of a challenge test is pooled and similarly the DNA of the diseased fish is pooled. Next, the marker testing or sequencing of these DNA pools was performed instead of genotyping individual fish. This may reduce genotyping costs by a factor 100 or more, whilst the accuracy of genomic selection was still high, although not as high as when marker genotypes on individual was used. Moreover, INIA compared methods to estimate inbreeding and genetic diversity based on genomic data, as well as alternative mating strategies based on genetic (dis)similarities. In the absence of genomic data, associative mating was shown to increase genetic progress in fish breeding schemes.

Fishboost researchers present results at the World Congress of Genetics Applied to Livestock Production conference

Several researchers from FISHBOOST partners presented outputs from the project at the leading animal breeding conference which took place in Auckland, New Zealand this February. The conference, called the World Congress of Genetics Applied to Livestock Production (WCGALP) occurs every four years, and is generally considered premier event for researchers and professionals involved in genetic improvement of livestock (including fish). Scientists from INIA (Spain), The Roslin Institute (UK), Nofima (Norway) and Wageningen University (Netherlands) are amongst those who made FISHBOOST presentations.

Dr. Luqman Aslam from Nofima presented a paper on the genetic basis of host resistance

to the parasite *S. chrysoophrii* in farmed gilthead sea bream originating from the breeding company Andromeda. He showed that resistance to this parasite has a significant but low heritability, and also a strong negative genetic correlation with growth related traits, suggesting indirect selection. He presented a significant quantitative trait locus (QTL) on chromosome 17, and discussed that genomic selection using all markers can improve trait prediction by up to 23 % compared to pedigree-based methods. The research also involved scientists from Andromeda, HCMR in Greece and University of Padova in Italy.

Dr. Maria Saura from INIA discussed how new genomic information obtained in FISHBOOST for turbot has been used to refine the genetic and physical maps of this species. She presented about how genomic data also allowed us to evaluate the potential use of within-family genomic selection in turbot to improve disease resistance. She discussed the estimates of heritabilities for resilience, resistance and tolerance to the ciliate disease scuticulociliatosis, genetic correlations between these traits (all positive). Finally, she presented the identification of a QTL region for resilience that explains 33% of the genetic variance of the trait. This research also involved scientists from CETGA and GeneAqua in Spain, and The Roslin Institute, UK.

Dr. Christos Palaiokostas from The Roslin Institute discussed the use of genotyping by sequencing methods to improve disease resistance in farmed fish, taking the case studies of viral nervous necrosis in sea bass and koi herpes virus in common carp. He presented data which show convincing evidence for heritability of resistance to both these diseases, as measured by fish survival during an experimental challenge. Further, he presented the identification of genome-wide significant QTL on several chromosomes, and talked about the advantage of using the genotyping by sequencing data to improve accuracy of prediction of breeding values. These research projects also involved scientists from University of South Bohemia and the Veterinary Research Institute in the Czech Republic (carp), and Ferme Marine de Douhet, Ifremer and INRA in France (bass).

Dr. Kasper Janssen from Wageningen University presented recent work on the economic value of R_0 for macroparasitic diseases, including sea lice. R_0 is a disease trait that accounts for the dynamics of disease transmission and is thereby more appropriate as a breeding goal trait than measures of disease prevalence, for which the response to selection cannot be predicted from quantitative genetic theory. Costs of a disease are the sum of production losses induced by the parasites and expenditures on their control. By relating the value of R_0 to losses or expenditures of a disease, its economic value can be calculated from algebraic expressions.

Dr. Osvaldo Anacleto from the Roslin Institute presented the first empirical evidence that individuals not only vary in their genetic risk of becoming infected, but also in spreading infections. This evidence was obtained from the FISHBOOST turbot disease challenge experiment, which was specifically designed to disentangle how differences in genetic resistance, tolerance and infectivity contribute to mortality rates in disease outbreaks. This research also involved scientists from INIA and CETGA in Spain.

Dr. Andrea Doeschl-Wilson from the Roslin Institute presented in her talk new opportunities for implementing resistance, tolerance and infectivity as novel disease traits into more effective breeding programmes to reduce infectious disease spread in livestock populations.



In the spotlight: Pierrick Haffray (SYSAF)

SYSAF organisation is involved in FISHBOOST concerning two major aspects: 1) technically supporting French breeding company FMD, Les Poissons du Soleil and Les Aquaculteurs Bretons partners to perform their tasks (production of experimental families, data and sample collection for DNA parentage assignment or genomic approaches and analysis) and 2) identification of predictors of carcass or fillet yields and estimation of their heritability (resistance to VNN in sea bass and pasteurellosis in sea bream; indirect predictors of processing yields) and genetic correlations with production traits.



SYSAF was also directly involved in the testing on real data the new genetic softwares developed by other partners to manage inbreeding or optimise breeding programs or in providing technical information to perform simulations.

Personally, I manage our team of geneticist in order to make the different tasks successful. I participate in the extensive phenotyping on quality traits in bass, bream and trout (> 6500 fish processed), the organisation of the challenges to VNN or pasteurellosis in France, the data treatment and the dissemination of results in e.g. scientific publications. I was also member of the Board where I worked with other Board members to plan the General Assemblies and communication or dissemination strategies (EAS or WAS workshop events, Technical training session).

Major results achieved by FISHBOOST with our participation were the estimation of the resistance to the diseases reported above. We know now that progress can be achieved on

these traits and will not impair gain on other production traits for pasteurellosis but may decrease genetic gain on growth when selecting for resistance to VNN. We also know that these resistances are polygenic. The genomic investigations developed in FishBoost also showed that an improvement until 37 % can be expected in efficiency when compared with family-based selection. This may justify future investment in genomic selection. Another major result achieved was the demonstration that selection to improve fillet or carcass yields works efficiently in trout (+0.5 % gain per generation) and should work also in the other species according to simulations done by INRA in using data collected from French breeding programs. In order to demonstrate and quantify this potential gain, the "Les Aquaculteurs Bretons" breeding company performed the experience during two generations and processed nearly 4000 individuals of large rainbow trout.

Genotypes and phenotypes created in FISHBOOST were used by the breeding companies in order to create progress that will benefit the whole European industry in the future. SYSAAF also participated as co-authors to several scientific publications, some still being in progress to submission. Results were also presented during public events organised by EAS in Edinburgh or in Dubrovnik or will be presented at the next WAS event in Montpellier in September.

SYSAAF is the professional organisation in charge by the French Ministry of Agriculture to support poultry and aquaculture breeding companies (42 in 2018). Our main objective is to advise them in breeding, to train their staff, to estimate genetic breeding values and to propose optimal mating to manage and limit inbreeding. This work is done in aquaculture in fishes (trout, bass, bream, turbot, meagre, sturgeons, tilapia...), molluscs (oysters, abalone and clam) and in blue shrimp. We also provide some expertise as in Thailand or in Mexico in shrimp breeding (vannamei or monodon). SYSAAF developed a data base software to collect and manage performances and pedigree. We employed 13 geneticists and 4 PhD students. By nature, SYSAAF also participates or coordinates research projects to improve practices, to develop or adapt methods (artificial vision, ultrasound, MRI...) to measure new traits (40 % of our budget). Since several years, SYSAAF and aquaculture breeding companies extensively developed application of DNA parentage assignment to include new traits in breeding programs in order to improve disease resistance, fillet yield, fillet colour and lipid contents or reproductive traits. The collective approach allow to share R&D cost and to transfer innovation rapidly from one species to another. The new challenge is to move aquaculture breeding to genomic selection as already done in poultry breeding in the last 2 years.



Share

Tweet

Forward



The research leading to these results has received funding from the European Union's [Seventh Framework Programme](#) for research, technological development and demonstration under grant agreement n° 613611 - FISHBOOST.

Copyright © 2014 [FISHBOOST](#) Project, All rights reserved.

You receive this newsletter because you are on the FISHBOOST contact list or on the contact list of one of our project partners and we sincerely think you might be interested in the FISHBOOST project news. Do you wish not to receive further newsletters of FISHBOOST, please click the unsubscribe button.

[unsubscribe from this list](#) [update subscription preferences](#)

Contact information EFFAB

EFFAB is an independent European forum representing farm animal reproduction and selection organisations. Our membership includes cattle, pigs, poultry and aquaculture.

T: +31 317412006
E: effab@effab.info
W: www.effab.info

Office: Dreijenlaan 2, 6703 HA Wageningen, the Netherlands
Postage: P.O. Box 76, 6700 AB Wageningen, the Netherlands



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.

