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

This is FISHBOOST:
FISHBOOST is an FP7 EU research 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

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The holiday season is soon upon us and the FISHBOOST team would like to take this opportunity to wish everyone a merry christmas and a happy new year!

Planned activities for dissemination of FISHBOOST results in 2018

FISHBOOST launches three events in 2018. LUKE, INRA, WUR, and EFFAB will organize a webinar for breeders and researchers on feed efficiency. This event will take place in spring 2018. More details are yet to be confirmed. The second event will be a Farmer's Day organized for producers and breeders. The event will take place during the joint event of WAS and EAS (25-29 August) in Montpellier. The targeted topics include disease resistance, production efficiency, benefits of genomics in aquabreeding, inbreeding and software tools, economics, and future challenges. The Farmer's Day will be organized by UEDIN, LUKE, Nofima, NMBU, WUR, and EFFAB. Finally, a training on advanced aquabreeding technologies will be held in Montpellier in November 2018. SYSAAF, EFFAB, UEDIN, LUKE, Nofima, NMBU, and WUR developed a training that will target disease resistance, production efficiency, genotyping/RAD sequencing, and improvement of European aquaculture efficiency by genomic selection. More details will follow.
How can we select fish to improve fillet yield?
Marc van de Putte (INRA)

Selecting for fillet yield (percent fillet, as a proportion of body weight) is extremely important for species which are sold processed. Using real data from sea bass, sea bream and rainbow trout, as well as simulation approaches, INRA, Ifremer and Sysaaf showed that it is indeed possible to increase fillet yield by selection, to a modest but economically significant level, ranging from 0.4 to 1% per generation.

Why is it important to select for fillet yield?
The objective of aquaculture is to produce edible fish flesh for human consumption. While some species are sold whole, processing is developing, as consumers more and more require easy to prepare fillets. When the commercial product is fillet, improving fillet yield (the ratio of fillet weight to body weight) improves the economic efficiency of production, as more valuable fillet can be sold from the same amount of fish produced at a farm. This also improves the environmental efficiency of farming, as effluents from fish farms are grossly proportional to the quantity of fish produced: thus, producing more fillet from the same amount of fish produced reduces the environmental impact per kg of fillet produced. In addition, less fish waste has to be disposed at the slaughterhouse. Fillet yield is thus a typical production efficiency trait.

Why is it difficult to select for fillet yield?
There are two main reasons that render fillet yield a difficult trait to select for:

- Measuring individual fillet yield requires the killing and processing of fish. Then, a fish cannot be used as a parent for the next generation once it has been measured. This can be solved by “sib selection” approaches, where fillet yield is measured on a number of fish per family, and the remaining live fish of the same families are selected according to the performance of their slaughtered sibs.
- Fillet yield is a ratio of two traits, fillet weight and body weight, which are very highly correlated (typically a correlation of 0.97-0.99, close to the theoretical maximum of 1). Based on this, many breeders consider that it is impossible to improve fillet weight independently of body weight, and thus that selecting for fillet yield will be inefficient. Additionally, ratio traits possess mathematical properties that complicate their use as selection criteria: a higher fillet yield can come from an increase in fillet weight for a given body weight, or a decrease in body weight for a given fillet weight, which obviously does not reflect the same biological variation. Different selection indices combining fillet weight and body weight have been proposed to try to solve this issue.

Which approach did we choose?
We first identified traits that could describe the biological reality of fillet yield but would be less correlated than fillet weight and body weight. Our choice was to propose that a fish is the sum of two fillets and a “waste” component representing head, bones, viscera and fins.

The results show that the (phenotypic) correlation of fillet weight and waste weight was lower, in the range 0.82-0.93. Using family data, we also estimated the heritability and genetic correlations of fillet weight and waste weight in five populations of three species (sea
bass, sea bream and rainbow trout). With these parameters, using genetics theory, we could simulate *in silico* populations of fish (using equations and probabilities in computers), and select them for improved fillet yield over ten generations, using nine different selection indexes that had been proposed to be used for improving fillet yield. Then, we compared the fillet yield of the different populations to evaluate the genetic improvement obtained using the different indexes in the different species.

**What are the results?**

We showed that choosing the fish with the best fillet/waste ratio, the best fillet yield, or the best residual fillet weight\[1\], was efficient at improving fillet yield by 0.4 to 1% per generation (0.66% on average) depending on the population and species. Selecting solely for fillet weight or body weight gave 55-65% less response on fillet yield than selection on the previous indices, while selecting against waste weight could even lead to diminished fillet yield. Thus, we showed that better gain was achievable by selecting for fillet yield or alternate measurements of it (such as residual fillet weight or fillet/waste ratio).

**Where do we go from here?**

The simulations gave interesting results, but are tedious to perform, and we need to evaluate the possibility to predict genetic gains from simple prediction equations using the genetic parameters (heritability, correlations) of the selection indexes tested. This work is ongoing. Additionally, in several species in Fishboost and with industrial partners, indirect predictors of fillet yield using morphological 1,2,3D recordings are being developed in carp, sea bass, sea bream and rainbow trout. These may further facilitate selection for fillet yield by enabling measurements on live fish, and thus selection of individuals taking into account their own performance. This would make selection more effective and could reduce the need for sacrificing fish. Finally, an experimental selection for fillet yield in rainbow trout has been conducted with the industry partners Milin Nevez and Sysaaf. Results of selection response are expected by the end of 2018, and we hope it will confirm the practical feasibility of such an approach, and the real genetic gains to be expected in industry conditions.

[1] which represents the difference between the fillet weight of a fish and the average fillet weight of fish with similar body weight in the population

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**EAAP awarded 'Best Oral presentation' to Kasper Janssen for his work on benefit cost analysis of breeding programs**

Kasper Janssen presented his work on ‘Benefit cost analysis of aquaculture breeding programs’ during the EAAP conference last August in Talinn, Estonia. The commission on Animal Genetics awarded him for the ‘Best oral presentation by a young scientist’.

The presentation was about recent work in FISHBOOST. Kasper estimated benefits and costs of a breeding program for gilthead seabream from data provided by Andromeda SA. Benefit cost analysis demonstrated that the breeding program is profitable from five years onwards. Alternative breeding program designs were compared to the baseline. A key finding from the comparison of breeding program designs is that any delay between the
Timing of costs and benefits should be minimized to maximize profitability. This work is expected to be published soon.

**Genomic selection using pooled DNA sequencing**
Anna Kristina Sonesson (Nofima)

**Great reductions in costs of genotyping**
Genomic selection is a new powerful method to select the best individuals based on DNA data. It estimates the effects of genome-wide dense genetic markers (SNPs) and uses these estimates to select the parents for the next generation. This selection method is today used in Atlantic salmon breeding programs and its accuracies are tested in FISHBOOST on all the species of the project.

In aquaculture, the reference population (the group of fish where the effect of each SNP is estimated) is typically made up of sibs of the selection candidates. However, these populations often contain thousands of fish, which results in high genotyping costs even if the genotyping costs per fish have decreased dramatically over the last years. Hence, ways to further reduce the genotyping costs are being sought.

In this study of the FISHBOOST project, we tested the accuracy of selection when DNA of individuals with extreme phenotypes had been pooled and genotyped either with whole-genome sequence data or with an SNP chip. We compared this accuracy to the accuracy of selection when the reference population is made up of individually genotyped fish.

The typical design for genomic selection schemes in aquaculture species is given in Figure 1. Families are split into two groups: one group of selection candidates that get genotypic records, and one group of test individuals that get genotypic and phenotypic records, e.g. using a disease challenge test. In the latter group, which we call the reference population, the effect of each SNP marker is estimated. These effects are then used to calculate the
genomic breeding values in the genotyped group of selection candidates, and to select parents for the next generation.

The reference population is often large resulting in high genotyping costs, because of the large number of families and individuals per family being genotyped in this group. In this study of the FISHBOOST project, we tested the accuracy of selection when DNA of individuals with extreme phenotypes had been pooled and genotyped either with whole-genome sequence data or with an SNP chip. We compared this accuracy to the accuracy of selection when the reference population is made up of individually genotyped fish.

The reference population originated from the SalmoBreed elite population of Atlantic salmon. It had been tested for pancreas disease (PD), an important viral disease in salmon production, in a controlled challenge test. Individual fish that died during the test were chosen for two mortality (M) pools and similarly, individual fish that survived the test were chosen for two survival (S) pools. Each pool consisted of ca. 200 individuals from 30 families. Equal amount of DNA per fish was collected to form the pools. Three genotyping strategies were compared:

1. Individual genotyping with a 50kSNP chip.
2. Genotyping of 4 pools with a 50kSNP chip
3. Whole genome sequencing of the 4 pools (40x coverage).

Genomic EBVs (using the GBLUP methodology) were calculated for the fish with individual genotypes. The GEBV were correlated to the known individual phenotypes, and accuracy of the genomic breeding values was inferred by scaling the correlation with the square root of the heritability of the trait.

The results of this study show that in this dataset, there were small differences in accuracy of selection when the reference population had been genotyped individually or with the whole genome sequencing of pools of individuals with extreme phenotypes.

In conclusion, genotyping pools of DNA of fish with extreme phenotypes seems to be a cost-effective alternative to individual genotyping of the whole test population in aquaculture genomic selection schemes. In further studies, we will compare the different pooling strategies, size of pools, and other traits.

This study was performed by: Anna K. Sonesson (Nofima), M. L. Aslam (Nofima), M. Baranski (Nofima), T.H.E. Meuwissen (NMBU), G. Malacrida (BMR Genomics) and H. Bakke (SalmoBreed).

In the spotlight: Håvard Bakke (SalmoBreed)
I was asked to be on the operational board of FISHBOOST as representative for the aquaculture industry. I had little experience with EU projects before this, so it has been very interesting to follow this type of research closely.

I feel that I have both an administrative and a “corrective” role in the project. Let me explain: As a board member I feel that it is important to follow the progress of the project, that deadlines are kept and so on. As an industry representative I also want to make sure that the research is relevant for the industry, and aims to answer crucial challenges for the industry. I also have a
small scientific role connected to some of the WPs, but other, more competent people, to most of the research.

The research work in FISHBOOST has been impressive. A lot of good and relevant science has been done, and more will come. I try to follow the scientific work, read the reports and so on. I specially enjoy the scientific discussions we have at the board meetings. The results are relevant on several levels: Some of the work is ground breaking and will have general impact, as a base for more applied research. Some of the work goes directly towards solving important issue for the industry. Examples are the disease resistance experiments in several species resulting in genetic parameters and possibilities for phenotypic and genomic selection.

The results mentioned above will be directly useful for stakeholders. I could also mention the development of computer programs useful for companies who want to start breeding programs, and so on. A lot of the results will, of course, come towards the final stage of the project.

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**FISHBOOST session EAS Dubrovnik: Koi Herpesvirus resistance**

*Christos Palaiokostas*

Cyprinids are the most important farmed fish globally in terms of production volume, being farmed in a wide variety of environments and production systems. Common carp is one of the most valuable species of the group. Koi Herpesvirus (KHV) is one of the main threats to carp production, with disease outbreaks being recorded across the globe. The seriousness of the KHV threat is highlighted by its listing as a notifiable disease both in the European Union and in the World Organization for Animal Health.

Application of selective breeding for improving genetic resistance of farmed fish is one of the main goals of the FISHBOOST project. In a collaborative experiment researchers from the Roslin Institute and Czech Republic partners from University of South Bohemia and the Veterinary Research Institute performed the first wide scale experiment regarding genetic resistance of carp to KHV, utilizing state of the art Next Generation Sequencing technologies. Obtained data strongly suggested that resistance to KHV is highly influenced by genetic factors. Genomic selection approaches demonstrated that breeding values can be estimated with high accuracy allowing selection for KHV resistant carp. Detailed results of the study were presented by Christos Palaiokostas at the Breeding programs and genetics – FISHBOOST session of the European Aquaculture Society meeting in Dubrovnik on 18 October 2017.
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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

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