Improving European aquaculture by advancing selective breeding to the next level for the six main finfish species

Reporting

Project Information

FISHBOOST

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Project closed

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Periodic Report Summary 4 - FISHBOOST (Improving European aquaculture by advancing selective breeding to the next level for the six main finfish species)

Project Context and Objectives:
Ca 70% of today's European aquaculture production use genetically improved stocks. In Europe, some breeding programmes consist of only the basic components of a breeding scheme. Hence, there is large potential to increase efficiency and profit by domestication and genetic improvement of farmed finfish. Acknowledging the different capacities of the species, the aim of FISHBOOST was 'To improve the efficiency and profitability of European aquaculture by advancing selective breeding to the next level for each of the six main finfish species through collaborative research with industry'. FISHBOOST considered the main components of breeding programmes for Atlantic salmon, common carp, European seabass, gilthead seabream, rainbow trout and turbot, thereby reaching 90% of the finfish production in Europe. 14 well-recognised RTD participants on aquaculture breeding collaborated from February 2014 until January 2019 in this comprehensive research project with 7 SMEs, 4 large industries and 1 NGO. A mixture of low- and high-technological advances depending on current capacities of the species was developed to move each species' breeding program to the next level.

For the European aquaculture breeding industry and RTD, FISHBOOST has delivered:
- recording protocols for defining new traits and breeding objectives, e.g. to select for improved resistance to diseases, fillet% and feed efficiency;
- trait-heritabilities and genetic relationships between traits, estimated from pedigree and genomic relationships, showing the potential for selective breeding programs in the investigated fish species;
- genomic architecture for disease resistance traits enabling the choice of optimum selection strategies;
- QTL (Quantitative Trait Loci) and Estimated Breeding Values (EBV; either pedigree, genomic or combined) for the studied production and disease resistance traits, enabling the selection of superior stocks;
- software tools to set up base populations, select parents for the next generation, estimate genomic breeding values and optimize breeding programmes;
- RAD sequencing protocols and ca 20,000 verified single nucleotide polymorphisms (SNP) for common carp, European seabass, gilthead seabream and turbot, somewhat fewer for rainbow trout, to be used in

future genotyping activities of these species;
- alternative cost-efficient genomic selection methods;
- optimized breeding strategies for each of the six species;
- information on the views of producers and representative organization on prioritsations for breeding programmes;
- economic assessments of the benefits of aquaculture breeding programmes.

FISHBOOST has had extensive dissemination and training activities: 87 popular articles, 32 published scientific articles, five educative movies, 9 newsletters which were sent to ca 300 persons, presentations at industry specific events, 91 contributions at scientific conferences and one exhibition participation. We have also organized three scientific sessions at the Aquaculture Europe meetings and three training sessions for industry and RTD. Four PhD students have been connected to FISHBOOST.

The EU science base has gained significant knowledge in the genomics and comparative genomics of the six most important finfish species in European aquaculture; optimised genotyping-by-sequencing protocols and dense SNP marker sets for genome-wide genotyping for each species; genetic architectures and marker-based genetic predictors of host resistance to infectious disease; knowledge of in vivo strategies adopted by populations for reducing the impact of epidemics – resistance, infectivity, and tolerance; the biology of feed efficiency; validation of genomic selection techniques; basic knowledge on fish biology (disease resistance and production efficiency). The EU science base has also benefitted from strengthening of collaborations across Europe promoting cross-fertilisation of ideas, exchange of knowledge, better use of resources to test innovations, and developing best RTD practice throughout Europe.
Project Results:
WP6. In collaboration with AQUATRACE, a survey showed the market share of selectively bred genetic material of the species. It varied between 0 and 100%. The types and technological level of the breeding programmes also differed to a large extent.
WP1. FISHBOOST performed genetic studies of major diseases in five European aquaculture species: KHV in common carp, VNN in European Seabass, Pasteurellosis and Sparicotyle chrysophrii in gilthead Seabream, Flavobacteriosis in rainbow trout, and Scuticociliatosis in turbot. Moderate-high heritability for disease resistance traits were obtained. Results of a GWAS and linkage analysis experiment show genome-wide significant QTL for every experiment. However, overall results show polygenic inheritance of the diseases.
WP1. Overall, no significant genetic correlation between the disease resistance traits and production efficiency traits were found.
WP2. FISHBOOST has developed indicators that can be used for indirect selection of feed efficiency or fillet%. FISHBOOST results showed that different lipid% and fillet% showed the strongest relationships to feed efficiency. Indirect morphological (2D and 3D) predictors have been developed for fillet%.
WP2. FISHBOOST has also developed a method to select for a combination of increased winter survival and increased winter growth in common carp and gilthead seabream.
WP2. A method has been developed to optimise feeds for fish with different genetic background.
WP3. Restriction-site-Associated DNA (RAD) sequencing is a method of simultaneous SNP discovery and genotyping by sequencing of multiplexed, barcoded samples. Re-sequencing was done of fish that had been disease challenged, using RAD, ddRAD and 2bRAD libraries. 19-25 kSNPs panels were developed

for common carp, European seabass, gilthead seabream, and turbot, and one panel with fewer SNPs for rainbow trout.
WP3. Alternative cost-efficient genomic selection methods were developed and tested in the populations with genomic data. Multitrait genomic selection were resulted in higher selection accuracies than single trait genomic selection. DNA pooling and within-family genomic selection resulted in somewhat lower accuracy of selection, but at a lower cost.
WP3. Except for common carp and one gilthead experiment, results show that the developed SNP panels result in similar heritability estimates as conventional methods, showing the ability of the SNP panels to pick up the existing genetic variation.
WP3. Overall, estimated effective population sizes are lower than the recommended 50 in the populations that were re-sequenced in FISHBOOST.
WP4. Four software tools have been developed to set up base populations, select parents for the next generation, estimate genomic breeding values and optimize breeding programmes.
WP4. Minimum coancestry-mating of parents results in higher genetic gains than random mating, but assortative or disassortative mating has no effect on genetic gains.
WP4. Next level breeding designs have been optimized for all populations in FISHBOOST.
WP5. FISHBOOST interviewed representative organisations from the aquaculture sector and one animal welfare organisation. A survey was also conducted amongst producers. The results were combined into recommendations in relation to the optimisation of breeding programmes, the economic assessment of breeding programmes and training, communication and dissemination.
WP6. Bio-economic models have been developed for the derivation of economic values of traits in Atlantic salmon, European seabass, gilthead seabream, rainbow trout and turbot breeding programmes.
WP6. Costs and benefits of running breeding programmes were estimated by simulating breeding programmes combined with production data.
WP6. The effects of alternative selection indices on the net present value of breeding programs were tested.

Potential Impact:
The realized impact of FISHBOOST is generally as anticipated in the DoW.
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- genomic architecture for disease resistance traits enabling the choice of optimum selection strategies;
- QTL (Quantitative Trait Loci for traits of interest) and Estimated Breeding Values (EBV; either pedigree, genomic or combined) enabling the selection of superior stocks;
- software tools to set up base populations, select parents for the next generation, estimate genomic breeding values and optimize breeding programmes;
- RAD sequencing protocols and ca 20,000 verified single nucleotide polymorphisms (SNP) for common carp, European seabass, gilthead seabream and turbot, somewhat fewer for rainbow trout, to be used in future genotyping activities of these species;
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Further impact of FISHBOOST to European aquaculture industry is still expected to come as the knowledge base and implemented tools mature.

List of Websites:
www.fishboost.eu

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Permalink: https://cordis.europa.eu/project/id/613611/reporting