

AQUALEAP: INNOVATION IN GENETICS AND BREEDING TO ADVANCE UK AQUACULTURE PRODUCTION

PARTNERS

The Roslin Institute (University of Edinburgh), University of Aberdeen, University of Exeter, Institute of Aquaculture (University of Stirling), Xelect Ltd, Scottish Aquaculture Innovation Centre (SAIC), Centre for Environment, Fisheries and Aquaculture Science (Cefas), Hendrix Genetics, Otter Ferry Seafish Ltd, National Lobster Hatchery

FUNDERS

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BACKGROUND

Genomics is transforming aquaculture by offering cutting-edge solutions to enhance the productivity and sustainability of a growing number of farmed aquatic species, such as Atlantic salmon. Sustainable aquaculture relies on high-quality stock and breeding approaches that impart desirable traits like disease resistance, rapid growth, and environmental resilience.

Sources of stock for aquaculture species range from wild animals to commercial lines managed using advanced methods. Well-managed domestication and breeding programmes can prevent infectious disease outbreaks. However, knowledge gaps in the genetic basis of economically important traits and a lack of genetic tools and expertise within the industry have hindered progress for many target species.

Moreover, the application of some genomic tools faces challenges: ethical concerns, regulatory hurdles, and potential ecological impacts require consideration for gene editing, a technology that allows target traits to be modified precisely.

This case study explores the AquaLeap project's aims to develop and uptake genomics technologies in support of stock enhancement for four species of existing or potential economic importance to UK aquaculture, including a large, advanced industry (Atlantic salmon) and smaller, emerging industries (European lobster, European flat oyster, and lumpfish). Overall, this research sought to tackle existing and emerging disease threats, while also addressing animal welfare concerns.

AquaLeap was a very productive project that achieved its original goal of pushing forward the respective boundaries of genomic technologies in each of the target aquaculture species, generating a wealth of new methods, open datasets and applications in support of breeding and conservation goals.

Professor Dan Macqueen, The Roslin Institute

The research was led by the University of Edinburgh's Roslin Institute, a world-leading centre of farmed animal bioscience and genetics, and the core academic team included the University of Aberdeen, which specialises in fish physiology and immunology; the University of Exeter, a leading institution in aquatic biology; and the Institute of Aquaculture at the University of Stirling, an international centre specialising in sustainable aquaculture and food security. Commercial partners were Xelect Ltd, Hendrix Genetics, The National Lobster Hatchery, and Otter Ferry Seafish Ltd. Furthermore, the project benefitted from collaboration with scientists from the Centre for Environment, Fisheries and Aquaculture Science.

AIMS

AquaLeap aimed to overcome barriers to selective breeding and domestication of aquaculture species by:

1. Developing novel genomic tools and resources for genetic improvement of four species: European lobster, European flat oyster, lumpfish and Atlantic salmon;
2. Investigating the genetic and epigenetic basis of critical commercial traits, including growth, robustness and disease resistance;
3. Improving gene editing techniques and identifying the causative factors underlying disease resistance in salmon;
4. Addressing skill gaps in key areas, including quantitative genetics, bioinformatics and gene editing, through training opportunities and knowledge exchange;
5. Engaging societal stakeholders in aquaculture genetics, including consumers.

SPOTLIGHT ON TARGET SPECIES

European lobsters are a high-value species with potential for diversifying UK aquaculture. AquaLeap sought to inform selective breeding methods, hatchery conditions, and choice of juveniles for on-growing, and to improve the performance of lobsters at sea.

Native oysters (European flat oysters) have declined dramatically in recent years, and there is significant interest in restocking oyster populations. A major barrier to hatchery-based restocking and production is the parasitic disease Bonamia.

Lumpfish are used extensively as cleaner fish to remove sea lice in salmon farming. Hatchery reproduction is now possible; the next step is selective breeding for traits to enhance robustness and performance.

Salmon breeding is highly advanced, using established genomic approaches to enhance trait improvement and control inbreeding via genomic selection (GS).

Across the target species, consortium partners conducted sequencing and assembly of reference genomes and created single nucleotide polymorphism (SNP) marker panels. SNPs are molecular variants at single base positions in the DNA, analysed by scientists to understand genetic relatedness and to explore the genetic basis traits of interest. AquaLeap also sought to identify and exploit other genetic variations, focusing on structural variants (SV), which are expected to strongly influence aquaculture traits including disease resistance.

RESULTS

This project successfully generated reference genomes for two species ([European lobster](#) and [European flat oyster](#)) and developed SNP and SV panels across the target species. Innovative approaches were applied to improve the cost-efficiency of GS and test this approach on the three emerging aquaculture species.

[Gene-editing technology will potentially lead to breakthroughs in addressing common aquaculture problems](#). Therefore, project partners developed techniques to modify a specific gene in salmon that drives resistance to viral disease, supporting future gene editing for infectious disease resilience.

Scientists involved in the project led the writing and publication of a [seminal review on aquaculture genetics](#), published in the top journal in the field, Nature Reviews Genetics. AquaLeap created significant training and engagement activities, including a workshop with industry, academic and funding representatives on the future of genetic improvement in aquaculture.

EUROPEAN LOBSTER:

The [European lobster genome was sequenced and assembled](#), leading to the identification of genes for distinctive characteristics of the species, such as longevity, resistance to disease, and genetic and epigenetic determinants of growth. Heritability for growth and survival traits were estimated, while the relative contribution of genetics and epigenetics to these traits were assessed.

Genetic data for lobster breeding was used to analyse the success of breeding techniques regarding which animals survive past the juvenile stage. These outcomes will further support partner organisations to inform their practices and management of hatcheries and fisheries.

EUROPEAN FLAT OYSTERS:

A reference genome assembly for the European flat oyster was generated and has supported ongoing research [within and beyond the consortium](#), particularly to identify genes associated with disease resistance. The genome continues to support research in flat oyster population restoration.

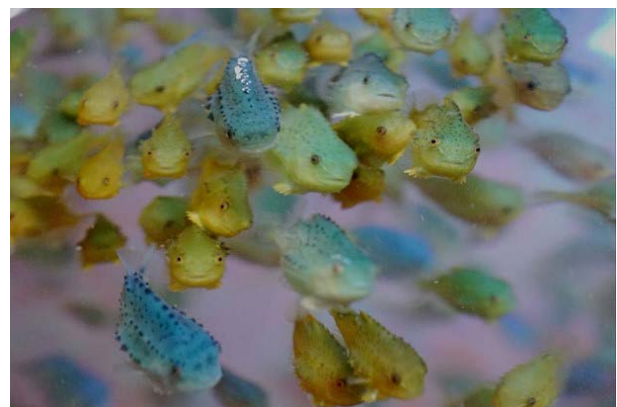
For instance, external partners working with the AquaLeap team [identified a genomic region](#) potentially associated with host resistance to the parasite Bonamia ostreae. The results suggest that marker-assisted selection could be applied to breed strains of flat oysters resilient to bonamiosis if certain conditions are met.

Experimental data from the laboratory and field studies demonstrated that [growth and disease resistance are heritable traits](#) and that methods of GS are likely to benefit the production of faster-growing animals.

Lumpfish:

In lumpfish, the research team assessed stock diversity using RAD-Sequencing to inform the choice of animals for base populations, followed by the heritability of production traits and identification of genomic regions potentially associated with growth rate. [Genomic regions were identified for sex, weight and standard length](#).

Lumpfish production has been reduced substantially in recent years due to changes in salmon husbandry methods. Nevertheless, the tools developed in this project would be valuable if demand for lumpfish production were to increase again.



ATLANTIC SALMON:

In salmon, the research team [identified a novel set of SV](#) and developed methods to genotype these variants in large populations suitable for applications in aquaculture breeding. Work continues at Hendrix Genetics to explore options for incorporating SV genotyping into existing Atlantic salmon breeding

programmes. Team members have overcome barriers in analysing SVs and generated new resources to support SV discovery and analysis in other species.

Furthermore, the team concluded that [ribonucleoprotein complexes are highly efficient at genome editing of salmon cell lines](#), and researchers can effectively transfer this technique from cell lines to animals and provide the basis for studying gene function in vivo.

IMPACT

Partners of this research have generated and shared a wealth of genetic and epigenetic information on key farmed aquatic species. This data will continue to inform research on resistance to disease and selective breeding, as well as the management practices of industry partners. The impact of this project will be far-reaching and continue to support the growth of the British aquaculture sector.

The dissemination of results through roadshows, workshops, conference presentations, seminars and digital content has already informed policymakers, regulatory frameworks, the scientific community and the general public about the significance of gene editing within aquaculture. This project has the potential for a long-term positive impact on aquaculture production, improving the sustainable production of high-quality food products with reduced environmental impact.