

AQUA-FAANG Abstract

Recent developments in genomics have advanced innovation in European aquaculture. However, despite the creation of reference quality genome sequences for the main species, our understanding of genome functions remains limited. AQUA-FAANG will deliver a step improvement in understanding of genome function and exploitation of genotype-to-phenotype prediction in the six most important European farmed fish species.

The project brings together world-leading interdisciplinary expertise and industry partners providing direct pathways to commercial exploitation. AQUA-FAANG will functionally annotate the genomes of all six species, employing standardized experimental assays and analysis pipelines defined by the FAANG initiative. AQUA-FAANG datasets will be shared and coordinated with other FAANG initiatives via the FAANG data coordination centre, and made available through the Ensembl genome browser.

As infectious disease is of paramount concern for sustainable aquaculture, the project focuses on understanding functional genomic regions in both healthy and immune-challenged fish. This will improve knowledge of the genomic basis for disease resistance and is complemented by novel approaches to increase understanding of immune cell heterogeneity. Standardized comparative analyses will provide essential insights into genome functions that cannot be gained from study of single species. Functional assays will be used to study intermediate phenotypes and prioritise causative genetic variants in trait-associated genomic regions to accelerate selection of disease-resistant stocks. Functionally-enriched marker panels will be developed to improve accuracy of genomic selection. An active programme of stakeholder engagement and dissemination will ensure uptake of project outputs by industry, academia, the public and in policy. The outputs will enhance precision breeding, drive competitiveness within the aquaculture sector, and enhance food and nutrition security in Europe.