ADVANCING FISH BREEDING IN AQUACULTURE THROUGH GENOME FUNCTIONAL ANNOTATION:

THE AQUA-FAANG WHITE PAPER

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Classical genetic selection techniques using pedigree relationships have resulted in transformative gains in aquaculture production and sustainability over the last 40-50 years. More recently, advances in genomics have seen improved methods of aquaculture breeding, including marker-assisted selection and genomic selection, resulting in accelerated rates of genetic progress.

However, incomplete assemblies of genomes at the chromosome level and an almost complete lack of understanding of how the millions of letters of the genetic code relate to characteristics of importance to aquaculture remain a barrier to further progress.

AQUA-FAANG CONTRIBUTION TO SOLUTIONS

The EU Horizon 2020 project AQUA-FAANG:

Advancing European Aquaculture by Genome Functional Annotation, which finishes in October 2023, brought together 13 leading academic groups and ten companies involved in fish breeding to address these bottlenecks. The research focused on the six species (Atlantic salmon, rainbow trout, common carp, gilthead seabream, European seabass and turbot), which account for 90% of European farmed fish production. There was a particular emphasis on immune responses and resistance mechanisms to some important diseases that threaten the sustainability and profitability of fish farming.

An enormous effort was put into developing standardised state-of-the-art methodologies, protocols, and training across the network to have a persistent impact on research progress beyond the project's life. Thousands of genomics datasets were collected representing samples from embryos to mature adults, sex, and following exposure of cells and animals to agents which mimic bacterial and viral infection. Functional activity across the genome (i.e. complete genetic sequence) of each species was characterised, revealing regions that were expressed or involved in controlling gene expression regions. These annotations of functional regions have been shared as open data through the Ensembl genome browser.

APPLICATIONS AND POTENCIAL IMPACT

The potential impact of this step change in knowledge for breeding practices is explored in a new **White Paper** with the perspective of commercial and academic partners within the AQUA-FAANG consortium. AQUA-FAANG data can be used to rapidly identify the overlap between genetic variants and regulatory elements in fish genomes. Such *functional variants* have scope to impact gene expression and maybe be exploited to enable more accurate selection of the best individuals for breeding and to potentially reduce animal use in disease challenge trials.

The data also provides numerous novel targets for gene editing to validate causal genetic variants going forwards. Future research is required to determine how much adding functional information will improve the effectiveness of selection methods. Since aquaculture sectors and businesses are highly diverse in terms of scale and technological readiness, cost-benefit analyses will be needed to determine the most profitable use of genomic tools in breeding for each species and production system.