GENOMIC REVOLUTION IN AQUACULTURE: AQUA-FAANG'S BREAKTHROUGH FOR DISEASE-RESISTANT SEA BASS

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The rapid growth of the aquaculture sector has intensified concerns over sustainability and environmental impact. Disease resistance, a pivotal trait, is crucial for both hatchery and on-growing phases. To enhance disease resistance through selective breeding, genomic selection is key.

AQUA-FAANG presents a game-changing solution with its wealth of functional genomic data, leading to the integration of functional genomic annotations into genomic prediction models. Focusing on the European sea bass, the project achieved whole-genome sequencing, QTL detection, and functional element identification, creating powerful genomic prediction models for VNN resistance. These findings not only benefit sea bass but also promise to improve disease management, economic viability, and sustainability across the aquaculture industry.

The rapid expansion of the aquaculture sector over the past two decades (+527% products from aquaculture, +30% supply of aquaculture products intended for human consumption; FAO, 2020) has raised serious concerns regarding sustainability and environmental impact.

© *Adaptation of European Bass* by David Miller, 2018

Genetic selection is considered a useful tool to ensure the sustainable development of intensive aquaculture systems through cumulative and permanent improvement of the traits of interest. **Disease resistance** is one of the most appealing traits both for the hatchery and the on-growing phase, as the spread of diseases represents a serious threat, both economically and in terms of sustainability.

The resistance of the host plays a fundamental role in hindering the spread of the pathogen or limiting the infectious pressure. **Selective breeding** to enhance disease resistance is a powerful approach to prevent and control the negative consequences of disease outbreaks. Due to the complexity of measuring phenotypes for disease resistance, traditional selective breeding based on routine estimation of the genetic merit of the animals directly on selection candidates is not a feasible option.

For this reason, implementing genomic selection procedures is of great interest. However, to fully exploit the potential of genomic selection, we need to improve the accuracy of using the genotype to predict the phenotype, especially across generations and different genetic backgrounds.

Integrating functional genomic information into genomic prediction models has been proposed as a strategy to improve genomic prediction accuracy.

Regulatory genomic regions controlling gene expression can now be identified in different tissues, organs, and cell types. In aquaculture, it's essential to recognize that genetic variations within specific regions, which act as regulators of gene activity, often serve as the primary candidates responsible for developing desirable traits.

These regulatory regions essentially act as control switches for the majority of the valuable traits in aquaculture.

Using functional genomic information is therefore expected to detect causative variants more efficiently and to enhance the prediction accuracy of the genetic merit of future breeding candidates across generations when the reference population is likely to consist of gradually distant relatives of the animals to be predicted.

AQUA-FAANG CONTRIBUTION TO SOLUTIONS

In **AQUA-FAANG**, an unprecedented wealth of functional genomic data has been produced, expressed and regulatory genomic regions have been characterized, and functionally annotated genomes for aquaculture species are now publicly available. Therefore, the stage is set for the integration of functional genomic annotations into genomic prediction models for complex traits such as disease resistance, a further step towards precision breeding.

In the **AQUA-FAANG** project, the target species was the European sea bass (Dicentrarchus labrax L.), which is one of the two most important species for Mediterranean aquaculture. Viral nervous necrosis (VNN) represents a major threat to the sea bass industry. Resistance to VNN in the European sea bass was used as a proof-of-concept to demonstrate the potential of integrating functional data into genomic prediction models.

THE WORK CARRIED OUT IN *AQUA-FAANG* ALLOWED:

1. The whole-genome sequencing of **European Sea Bass**, with the generation of genotypes consisting of over 6 million single nucleotide polymorphisms (SNPs).

2. The detection of a major quantitative trait locus **(QTL)** is significantly associated with VNN resistance; in fact, millions of variants are included in whole-genome sequence data, including potentially causal variants that largely affect the traits of interest but are not present on commercial SNP chips.

3. The detection of regulatory or functional elements in the genome of VNN-infected or mock-infected animals.

4. For the first time, the integration of that information into genomic prediction models for VNN resistance. This can be achieved both by prioritizing the genetic variants characterised by an increased probability of impacting the target trait or by using the functional annotation data as criteria to filter the SNPs.

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APPLICATIONS AND POTENCIAL IMPACT

Research efforts on genome and functional annotation can be effectively made accessible and translated into application, promoting and facilitating the global implementation of genomic selection, either in the sea bass industry to enhance **VNN resistance** or in other aquaculture species for complex traits of economic importance.

In a broader view of precision breeding, these results can be useful to create new, more accurate genetic breeding methods and tools without significant impacts in terms of costs.

The major QTL can be used to design new SNP panels for European sea bass taking into account VNN resistance; once validated, this tool would facilitate the selection of resistant animals.

Functional annotation data may be useful to select those variants that have direct effects on proteins wisely and, in turn, have a phenotypic effect, with the final aim of creating marker panels that could provide higher prediction accuracies for complex traits.

APPLICATIONS AND POTENCIAL IMPACT

In the context of the Strategic guidelines for a more sustainable and competitive EU aquaculture for the period 2021 to 2030, ***AQUA*-*FAANG*** WP5 outputs have major impacts on aquaculture, improving:

1. **Sustainability and resilience**; precision breeding and improved breeding techniques can lead to the development of VNN-resistant sea bass strains, decreasing the impact of VNN on sea bass industry;
2. **Disease management**; precision breeding can reduce the need for pharmaceutical use, improving the overall health of aquaculture stocks;
3. **Economic viability**; improved breeding techniques can enhance the economic viability of aquaculture by increasing production efficiency and product quality.