



## Conference Report

# Report on the 6th Genomics in Aquaculture (GIA) Symposium Held in Granada, Spain, 4–6 May 2022

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## 1. Stress and Immune Response

### Conservation of Pro-inflammatory Transcriptomic Responses in Two Salmonid Species Sharing a Recent Whole Genome Duplication

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### Summary

Infectious diseases represent one of the most pressing threats to modern aquaculture at a global scale. Control of disease outbreaks is essential for maintaining fish health and welfare, which is crucial for sustainable and profitable aquaculture production. The work presented here is part of the EU Horizon 2020 project, AQUA-FAANG, which aims to understanding the relationship between genotype and phenotype by the improvement of genome annotation in European farmed fish species.

The early innate immune response is critical to the outcome of infection and many previous studies have examined the transcriptomic response at this time. Here, we extend such work to profile both responses in vivo and in vitro within head kidney leukocytes. We used a bacterial infection (heat killed *vibrio*) as the inducer in both Atlantic salmon and rainbow trout, two closely related salmonids that are extensively used in European aquaculture. Our aim was to determine the commonalities and differences in response to *vibrio* stimulation between these species through gene expression analysis considering gene evolutionary relationships, including with respect to an ancestral salmonid-specific whole genome duplication (WGD) event.

A total of 48 in vivo and in vitro Atlantic salmon and rainbow trout *vibrio* stimulated, and control libraries were sequenced (~30 M paired end 150 bp reads per sample). The number of differentially expressed genes was measured using DESeq2 (salmon in vivo up = 1609, down = 2013; in vitro up = 3210, down = 4329; trout in vivo up = 1184, down = 1914; in vitro up = 2931, down = 3752) (adjusted  $p < 0.05$ , Log2Fold change  $> 1$  or  $< -1$ ). Differentially expressed genes common between in vivo and in vitro stimulations were assessed (salmon up = 594, down = 890; trout up = 558, down = 640). Pathway and gene set enrichment analyses using DAVID indicated a strong immune response from all the stimulated groups. We are examining the conservation of expression responses for key pro-inflammatory gene families between Atlantic salmon and rainbow trout, taking into account orthology and paralogy relationships across species. These data will inform our understanding of the evolution of the innate immune response in salmonid species in relation to their lineage-specific WGD.

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### Mapping for Males: Sustainable Sex Control in Nile tilapia

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#### Summary

Sexual dimorphism of aquaculture traits is common for farmed fish. The Nile tilapia is the second most important farmed species with a production 6 million tons in 2020. Intensive farming relies on the production of all-males due to males’ higher growth rate, and as a way to avoid uncontrolled reproductions. Currently the large majority of the all-male productions are obtained through androgen treatments. We aim to use more sustainable procedures to produce all-males such as the use of YY males. Until now, the use of YY males has not been reliable. This is because sex determination in Nile tilapia is complex and controlled by several factors. Although sex determinism follows an XX/XY system, the linkage group (LG) carrying the major sex determinant gene has been assigned to either LG1 or LG23, depending on the domesticated strain. Minor parental factors can also be implicated and in addition, high temperatures can override the genetic determinism. It is not clear to what extent these differences in sex determination are due to natural diversity in the mechanisms of sex determination or due to processes of domestication. It is therefore necessary to better understand the genetic basis of sex determinism in order to use this approach to generate all-males. For this, we decided to work on wild populations in Africa that have not suffered domestic manipulations. We underwent a study of sex determination in several wild populations from West (Lake Volta, Lake Kou) and East Africa (Lake Koka and Lake Hora). We used complementary genomic approaches of ddRAD, whole genome sequencing and long Nanopore reads. We were able to determine that the *amh* region present on LG23 is the major sex-determining region in most of these populations. Nevertheless, our results also show that there is high polymorphism in this SD region. Furthermore, there are populations that lack the male-specific *amh* duplication on LG23. Hence, there are no universal Y markers for Nile tilapia. It is necessary to work at the population level to identify and validate sex markers, in order to allow the local production of YY males.