

KEY OUTPUT

NEW GENOMIC INFORMATION IDENTIFIED THROUGH GENE EXPRESSION ANALYSIS TO POTENTIALLY CHARACTERISE MARKERS FOR WELFARE AND HEALTH STATUS IN SALMON, TROUT AND SEA BREAM



SUMMARY: This knowledge output compiles a list of candidate genes as markers for stress in salmon, sea bream and trout through analysis of their microarray data sourced from both published and non-published data.

AT A GLANCE

FULL TITLE: New genomic information identified through gene expression analysis to potentially characterise markers for welfare and health status in three fish species: salmon, trout and sea bream

KNOWLEDGE TYPE: Report

WHERE TO FIND IT: fishandchips.genouest.org/index.php (a user guide is included)

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PATENTS OR OTHER IPR EXPLOITATIONS: No

INTRODUCTION

Over the last 20 years, research in aquaculture has been developed based on an integrative knowledge of fish biology as well as information provided by the studies of fish behaviour, physiology, endocrinology etc. Such a multidisciplinary approach is becoming more essential in developing new methodological approaches, using a minimum number of fish, to bring together the maximum

amount of information for characterising specific species markers including those for fish welfare, health and performance. Developing new methodologies or improving existing ones for phenotyping fish in research infrastructures is therefore a priority for fish research.

KEY INFORMATION

This knowledge output compiles a list of candidate genes

as markers for stress in salmon, sea bream and trout through analysis of their microarray data sourced from both published and non-published data.

For sea bream, mitochondrial gene identification was performed using next generation sequencing which highlighted previously unknown mitochondria.

For salmon, candidate genes have been selected based on their involvement in nutritional challenges using gene expression profiles in liver from salmon exposed to diets with fish oil substitution. This generated a list of genes differentially expressed following statistical analysis.

For rainbow trout, potential markers for different types of stress were identified (salinity, nutrition and confinement) using transcriptomic analysis in liver tissue, gill tissue in seawater and gill tissue in freshwater respectively. The common criteria for selecting those genes are that they would be characteristic of the health and welfare status of the fish when exposed to challenging situations.

END-USER & APPLICATION

➔ **END-USER 1:** Scientific Community - marine genomics.

APPLICATIONS: Researchers (basic or applied research) who are interested in comparing and analysing improved transcriptomic data sets related to stress and welfare of the species chosen. The methodology used might also be of interest.

➔ **END-USER 2:** (When data is validated using the Fish and Chips tool) Aquaculture industry.

APPLICATIONS: Salmon, trout and sea bream breeding companies could use this information to increase the genetic selectivity of their stock.



IMPACT

Increased meta-analysis of three important aquaculture species; salmon, trout and sea bream, could allow for more stress resistant stock as a result of selective breeding using the identified genetic markers, helping breed better farmed fish leading to increased production.