

## KEY OUTPUT

### NEW ONLINE BIOINFORMATIC TOOL (FISH AND CHIPS) ADAPTED TO ENABLE META-ANALYSIS OF FISH GENOMIC DATA



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**SUMMARY:** “Fish and Chips” is an online resource that contains all the public gene expression data related to fish species in various physiological conditions. This tool has been used to select genes which are relevant for characterising welfare and health status in farmed fish species.

#### AT A GLANCE

**FULL TITLE:** New online bioinformatic tool (Fish and Chips) adapted to enable meta-analysis of microarray data obtained in fish to determine if particular identified genes are relevant to welfare and health characteristics of three species of farmed fish (salmon, trout and sea bream)

**KNOWLEDGE TYPE:** Report

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

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**PATENTS OR OTHER IPR EXPLOITATIONS:** No

#### INTRODUCTION

The bioinformatic tool “Fish and Chips” aims to develop a meta-analysis of several sets of existing gene expression data coming from different independent experiments and published in a public database. This tool has been used to select genes which are relevant for characterising welfare and health status in three farmed fish species: salmon, trout and sea bream. The tool was initially developed by medical researchers for human health disease questions.

#### KEY INFORMATION

In this study, clusters of differentially expressed genes

from muscle tissues of sea bream facing a nutritional stress (reduced ration size) were used for a meta-analysis across experiments in Fish and Chips. This approach highlighted the role of mitochondria-related genes and Gene Ontology (GO) terms in a diverse array of sea bream tissues and stress conditions. These results confirmed the role of mitochondria as key responders to environmental and nutritional stress in gilthead sea bream, and indicate the importance of mitochondria genes as reliable subcellular markers of stress phenotyping in fish.

To develop the Fish and Chips tool, the following were completed and are included in the tool:

- 1. Development of fish data sets:** This included development of a database containing all available information Expressed Sequence Tags (ESTs) from several fish species (sea bream, salmon, trout, sea bass) and also genome information of four model species (fugu, zebrafish, stickleback, medaka) using data from public repositories (UniGene, National Centre for Biotechnology Information (NCBI)).
- 2. Gene annotation for each fish species:** This was carried out on four species: sea bream, sea bass, salmon and trout. For each identified cluster, functional annotation was performed using GO.
- 3. Integration of microarray data:** Collection and integration of fish microarray data from approximately 400 data sets.
- 4. Development of program for data re-normalisation and clustering:** Normalisation of microarray data and standardisation of each entry to the database. Then, hierarchical classification was used to allow investigation of relationships between samples and genes.
- 5. Development of a program allowing the set-up of orthology relationships between distant fish species.**

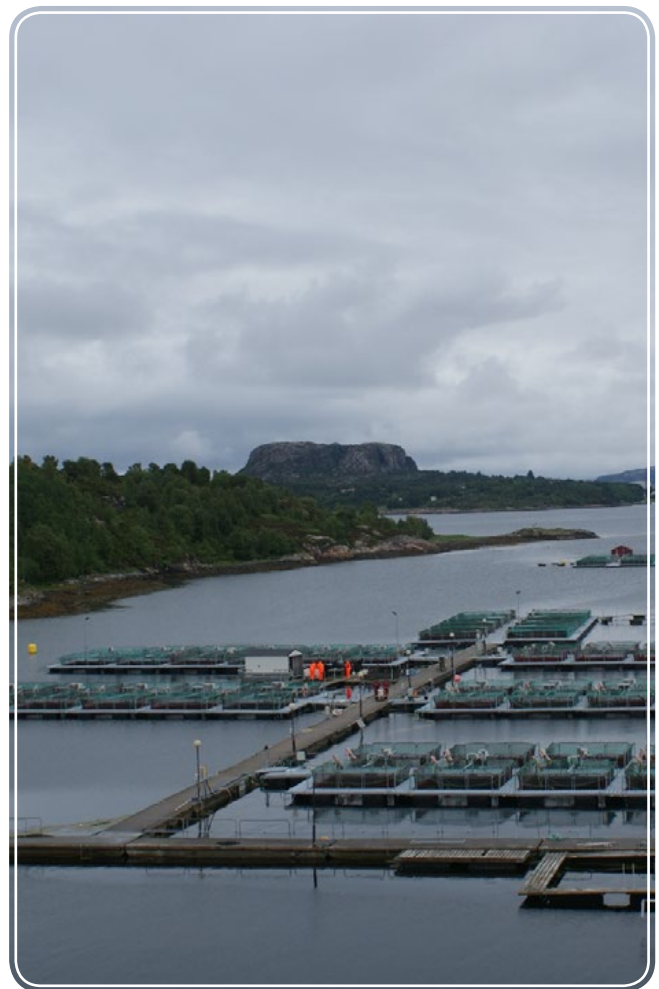
This tool was implemented on the West Genopole bioinformatics platform and access will become public through the [AQUAEXCEL](#) website where instructions for log-on and use will be provided.

#### END-USER & APPLICATION

- ➔ **END-USER 1:** Scientific Community - marine genomics.  
**APPLICATIONS:** Researchers (from basic or applied research) who are interested in comparing and analysing improved transcriptomic data sets related to stress and welfare of the species chosen.
- ➔ **END-USER 2:** Scientific Community - marine biodiversity.  
**APPLICATIONS:** Researchers (from basic or applied

research) can use this tool to collect genomic knowledge on individual species and increase their biodiversity knowledge.

- ➔ **END-USER 3:** Aquaculture industry.  
**APPLICATIONS:** Salmon, trout, sea bass and sea bream breeding companies could use this tool to analyse and compare the genetic information of their stock in order to develop different selective breeding programmes helping breed better farmed fish leading to increased production.



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#### IMPACT

The impact will primarily be increasing the knowledge of the connections between gene expressions and characteristics as well as highlighting conserved gene expression signatures between multiple independent studies. Impact on the European aquaculture industry could be the ability to increase selectivity of breeding based on characteristics such as ability to deal with stress and so breed better farmed fish leading to increased fish production.