OFFRE DE STAGE MASTER 2

Characterization of the variations in mitochondrial genome linked to fitness traits in various rainbow trout lines

BACKGROUND AND AIM OF THE STUDY

Rainbow trout (*Oncorhynchus mykiss*) is a worldwide cultured salmonid species with numerous breeding programs implemented over the last 50 years in closed populations. Rainbow trout is a freshwater species originally from the Pacific coast of North America which is widely spread to the rest of the world due to its particularly good adaptation to farming conditions. It is the main fish production in France.

Our GenAqua team in GABI unit is mainly dedicated to research in the genetics of this species. While we did a lot of research over the last 10 years dedicated to the nuclear genome of this species, we are now willing to better characterize the variations observed in its mitochondrial genome. Indeed, mitochondria are involved in numerous cellular functions, which can impact traits of interest for animal productions. Generally, variability of mitochondrial genome is not well studied in animals and fish in particular. In fish, the contribution of mitochondrial activity to phenotypes has only received little attention. A few studies have started to show the role of mitochondrial genome on the early development and oxygen consumption (Brown et al. 2006) or the ability to response to stressors (Bermejo-Nogales et al. 2014). It is hence important to better characterize the mitochondrial genome variability and its functional impact in rainbow trout.

As for any other vertebrate species, the rainbow trout mitochondrial DNA (mtDNA) encodes 13 protein-coding genes, 2 ribosomal RNA (rRNA), and 22 transfer RNAs (tRNA) and a large 1 kb- non-coding control region also called the D-loop region (Zardoya et al. 1995). These 37 genes are coded in a covalently closed circular DNA molecule whose total length is 16,660 bp. The organization of vertebrate mitochondrial genomes is highly conserved and extremely compact (Attardi 1985). Despite its highly conserved gene organization, mtDNAs evolve very rapidly, accumulating differences in their nucleotide sequences, and therefore are particularly valuable for phylogenetic studies (Brown et al. 1979).

We have already sequenced the mitochondrial genomes of our 19 INRAE isogenic (double haploids) lines; among them 6 isogenic lines were challenged to both acute hyperthermia and acute hypoxia stresses. We also get the genotypes for 28 mitochondrial SNPs (mtSNP) for a set of reproducers coming from 3 distinct French rainbow trout lines: 15 dams from the INRAE synthetic line whose reproduction traits were recorded; 75 dams from a first commercial population were also genotyped for these mtSNPs and their progeny were challenged to acute hyperthermia; 190 dams from a second commercial line were also genotyped for these mtSNPs and their progeny were challenged to acute hypoxia.

Recent nuclear GWAS indicated that some QTL regions for both acute stresses included nuclear genes that are well-known to interact with the mitochondrial genome (as they initially were part of it as ancient bacteria integrated into host cells by a process of endosymbiosis). In addition, significant maternal effects were estimated on responses to both challenges. Therefore the question arises whether or not those maternal effects may be linked to mtDNA variations and interactions between nuclear and mitochondrial genomes

ASSIGNEMENTS

The aim of the internship will be to answer this question by:

1) characterizing the mtDNA diversity observed in all the 4 studied populations
2) performing the mitochondrial genome association studies for the phenotypic traits recorded depending on the studied population
3) assessing potential interactions between nuclear and mitochondrial genomes on these phenotypic variations.

This is an activity of statistical and genetic analysis based on the genotypes and phenotypes already available in various projects of the team.

LOCATION AND CONDITIONS

Working place: INRA, UMR1313 GABI, équipe de Génétique en Aquaculture, Jouy-en-Josas (78 350)
Training period: 6 months between January to June 2023.

CV and cover letter are to be sent before the 15th of November to

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PROFILE

M2 population genetics or quantitative genetics, bioinformatics;
Knowledge in animal genetics and / or aquaculture appreciated
Good knowledge and taste for programming and statistics
Mastery of office software and statistical software (R, SAS)
Capacities of synthesis, writing, listening, rigor, organization, relational ease, availability and autonomy.