Analysis of genetic variability of global DNA methylation in response to an early temperature stress in rainbow trout

Delphine Lallias, Edwige Quillet, Nicolas Dechamp, Jean-Michel Le Calvez, Marjorie Bideau, Lionel Goardon, Laurent Labbé, Mathilde Dupont-Nivet

▶ **To cite this version:**

Delphine Lallias, Edwige Quillet, Nicolas Dechamp, Jean-Michel Le Calvez, Marjorie Bideau, et al.. Analysis of genetic variability of global DNA methylation in response to an early temperature stress in rainbow trout. World Aquaculture 2018, European Aquaculture Society (EAS). BEL., Aug 2018, Montpellier, France. 848 p. hal-02734994

HAL Id: hal-02734994
https://hal.inrae.fr/hal-02734994

Submitted on 2 Jun 2020

HAL is a multi-disciplinary open access archive for the deposit and dissemination of scientific research documents, whether they are published or not. The documents may come from teaching and research institutions in France or abroad, or from public or private research centers.

L'archive ouverte pluridisciplinaire **HAL**, est destinée au dépôt et à la diffusion de documents scientifiques de niveau recherche, publiés ou non, émanant des établissements d'enseignement et de recherche français ou étrangers, des laboratoires publics ou privés.

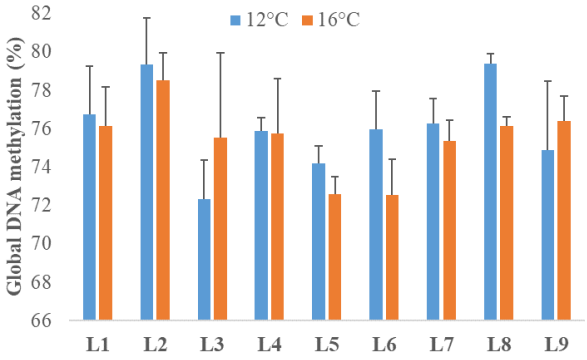
ANALYSIS OF GENETIC VARIABILITY OF GLOBAL DNA METHYLATION IN RESPONSE TO AN EARLY TEMPERATURE STRESS IN RAINBOW TROUT

Delphine Lallias*, Edwige Quillet, Nicolas Dechamp, Jean-Michel Calvez, Marjorie Bideau, Lionel Goardon, Laurent Labbé and Mathilde Dupont-Nivet

GABI, INRA, AgroParisTech, Université Paris-Saclay
78350 Jouy-en-Josas, France
delphine.lallias@inra.fr

We aim to investigate the potential role of epigenetic marks in the expression of phenotypes and their variability in fish, in particular genetic variability of epigenetic marks in response to an environmental stress. In this context, rainbow trout isogenic lines are the material of choice. Within each line, all fish have the same genome i.e. there is no genetic variability. This allows the comparison of epigenetic marks among several individuals with the same genotype. The environmental stress chosen here is temperature because several studies have reported genetic determinism of thermotolerance. Moreover, rainbow trout isogenic lines have recently been characterized for their response to temperature and the existence of a high between-line variability was shown. The aim of this study is to contribute to the understanding of why certain lines are more tolerant to temperature stress than others, by investigating the implication of epigenetic mechanisms in the variability of the response to temperature.

The first objective of this study was to test whether temperature regime experienced during early development leads to epigenetic modifications within and between lines. Nine rainbow trout isogenic lines were chosen. For each line, half of the eggs were incubated at standard temperature (12°C) and the other half at high temperature (16°C), from eyed-stage to hatching. At eyed-stage just before hatching, analysis of global DNA methylation with LUMA (LUminometric Methylation Assay) revealed significant differences between lines but little or no effect of incubation temperature (Figure).



At hatching, no effect of incubation temperature was observed on mortality or malformation rates. After 4 months of rearing at 12°C, mean body weight of batches incubated at 12°C or 16°C was similar.

The second objective of this study was to test whether early temperature regime impacts response to a stress experienced later in life. After tagging fish individually at a mean body weight of 3-4 g, the different batches were grouped into 9 tanks to perform acute temperature stress on 5-month-old juvenile fish. The response was measured in terms of time to equilibrium loss and Upper Thermal Tolerance (UTT). Globally, there was little significant effect of early exposure to high temperatures on the response to a late temperature stress, but tendencies seemed to appear. Thus, in the future, the impact of a longer exposure to high temperatures during early development will be tested.

Funding: This study was carried out within AQUAEXCEL[2020] funded by European Union's Horizon 2020 research and innovation programme under grant agreement No 652831.