

A Salmon is A Salmon

In fact, all over the world, a salmon is a salmon; that simple, stupid! This is still the impression you get when you read the latest aquaculture papers, even in top scientific journals. Laboratories working with Atlantic salmon, in North America, South America, Australia, Europe, or Asia, for example, always identify their study object as *Salmo salar* – and advanced authors add the naming authority in its Latin form, 'Linnaeus', and, for the brave, even the year of publication, '1758'. So simple!

However, nature is more complex and provides much more diversity and information, even within a single taxon, than many research efforts, especially those aimed at human food production, have anticipated. Genetic diversity may satisfy biologists, but it puzzles aquaculturists interested in the safe (mass) production of proteinaceous foods. But even at the non-genetic level, the epi-genetic level, significant diversifications are possible. Animals, whether protists, invertebrates, or vertebrates, respond very rapidly and – most importantly – directionally to environmental cues; otherwise they could not build and maintain persistent populations. For example, Ryu et al. (2020) show in reef fish populations under global warming that DNA methylation, currently the best understood epigenetic mechanism, is an important mechanism associated with buffering adverse effects of elevated temperature within a generation. Such responses can be passed on to subsequent generations as specific acclimations (Wang et al., 2016), at least as long as the environmental challenge persists.

Stimuli may be abiotic factors, such as temperature, oxygen levels, current, or biotic factors, such as food, predation, disease, or parasites. Animals can respond to all of these factors with epigenetic changes. That is, the genetic equipment remains unchanged; however, the readability of the genes or the intracellular fate of the gene transcripts changes, for example, due to the action of non-coding RNAs.

When these factors are applied to aquaculture, there are striking changes in both abiotic and biotic factors that are easy to identify when compared to the natural environment. Biotic factors in aquaculture include both the absence of predators and a constant supply of food. A little thought experiment: Who can guarantee that the feed in different aquacultures in various parts of the world is identical and will remain identical over time? Nobody can! For this reason alone, salmon can have identical genotypes, but not identical epi-genotypes. Epimutations (persistent changes in DNA methylation) are to be expected. And they do occur. As the first fish physiologists, Anastasiadi and Piferrer (2019) report that the farming environment affects the genome of sea bass in the initial stages of domestication by inducing epimutations. These epimutations are established already during early life and involve genes related to developmental processes that are expressed in embryonic structures including the neural crest. The epimutations persist until adulthood in different tissues and some result in measurable changes in gene expression when compared with wild counterparts.

Epimutations can even be triggered by micronutrients as recently identified in Atlantic salmon. Saito et al. (2021) find that micronutrient supplementation suppresses liver gene expression in the pathways related to lipid metabolism and increases the methylation rates in a gene, which is involved in the upstream regulation of the lipid biosynthetic pathway.

With breathtaking speed, epigenetic changes alter the phenotype during the process of domestication. A study of Nile tilapia provides evidence that such changes occur even within a single generation. Konstantinidis et al. (2020) show for the first time that muscle DNA hydroxymethylation differs significantly between wild fish and their captive-bred offspring. In addition, epigenetic modification can be

quite extensive: Many of the differentially methylated sites are associated not only with genes involved in muscle growth, immunity, autophagy, and diet response but also related to epigenetic mechanisms, such as RNA methylation and histone modifications. This bottom-up approach shows that the phenotypic traits often related to domestic animals (e.g., higher growth rate and different immune status) may be regulated epigenetically and even prior to artificial selection on gene sequences (Podgorniak et al., 2022).

A salmon is still a salmon?

In addition to epigenetics, there are a number of other causes that lead to individual variability and phenotypic plasticity. However, the given example may suffice to illustrate the inexcusable gap that arises when aquatic species are treated as a uniform 'monolith' and the study material is not further characterized. Hints for further characterization are available and some are listed in Steinberg (2018, 2022). However, meta-studies of phenomena in aquatic animals will inevitably find that many studies cannot be compared with each other (among many others: Hua and Bureau (2012)), if the study material is not further characterized according to criteria that are yet to be defined. This limits the overall applicability of the findings, and the generalizability of the results remains low.

The salmon is not the salmon of the world, stupid!

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