TRANSGENERATIONAL ACTIONS OF FISH FEED AND THE EFFECT ON EPIGENETIC REGULATION OF GENE TRANSCRIPTION

Skjærven, K. H.¹, Dahl, J. A.², Moren, M.¹, Olsvik, P. A.¹, and Hamre, K.¹

National Institute of Nutrition and Seafood Research (NIFES), 5817 Bergen, Norway
Institute of Medical Microbiology, Oslo University Hospital, 0027 Oslo, Norway

E-mail address: ksk@nifes.no

Summary

In the last decade fish feed used by the aquaculture industry has shifted from containing high levels of fish meal to plant based alternatives. High dietary levels of plant proteins and vegetable oils have shown to alter the metabolism of folate, amino acids, and vitamin B12, all of which are important methyl donors (1C) in several biological methylation reactions. Negative effects of plant based ingredients on growth performance and flesh quality have been observed, but how the fish feed composition affect the epigenetic regulation of gene transcription during the different life stages and across generations remains an important and unexplored field. The study of epigenetics encompasses changes in gene expression profiles without alterations in the genomic DNA sequence. These changes arise from the inherited epigenetic regulation of the gene, but are also sensitive to environmental factors like nutrition. We therefore designed a project to study how feed enriched with methyl donors regulates gene expression patterns by DNA methylation, directly and across generations in fish.

A transgenerational (F_0 - F_3) zebrafish feeding trial is ongoing, using diets low and high in 1C. Embryos at 1.5 DPF, larvae, ongrowing and dissected samples of mature zebrafish from each generation are currently being sampled for nutritional status, gene expression and global DNA methylation. Livers from mature fish (F_0 and F_1) will be sampled for methylome and metabolom studies. Preliminary results indicate lower folate concentration in F_0 , a significant decreased weight at 3 months and lower fecundity in the low 1C group, reflecting the general effects observed for plant based diets used in aquaculture settings. qPCR mRNA expression of genes involved in the 1C pathway from F_1 embryos will be presented. To date there are no studies on nutritional epigenetic regulation in fish, and through this project we establish epigenetic procedures and knowledge for nutritional fish studies.