

## Nutrigenomics in Aquaculture Research

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### Editorial

Research on aquatic animal nutrition has demonstrated that the expression of related genes can be modified with different feeding components. From the nutrigenomics point of view, nutrients are feeding signals, which are detected by the cellular system of sensors and which influence the expression of genes and proteins and in consequence, the production of metabolites. Therefore, today, it is generally accepted that feeding components have a substantial impact in the expression of related genes, as well as in the welfare of reared aquatic animals. As fish have similar stress responses and sense of nociception to mammals, standards of fish welfare are rapidly emerging in the field of aquaculture. New fish welfare measures can dramatically improve farming outcomes, but a sustainable balance between implementation costs and their benefits must first be reached.

With this continuous expansion of aquaculture industry, a worldwide requirement for a reduction of full-dependence from natural harvested populations (depletion of fish stocks) for the production of fish meals and fish oil, inevitably dominates. A sufficient amount of research studies exist in the bibliography that have investigated transcriptional responses with the replacement of plant originated oil in fish feed. Often, when such replacements reach maximum (~100%) in experimental conditions, limited growth are recorded. Nevertheless, the reasons for these changes could have a combined result of reduction of the requisite fatty acids, and/or changes in the profile of amino-acids.

The intestine is the main tissue with a direct contact with any components of feed and for this reason can be very sensitive in feeding changes and habits. The intestine has been recorded as the tissue with the highest regulated transcriptional response for both the number of genes that are expressed in different standards and for the extent of differential expression of such genes that are described in the bibliography. A lot of biological processes could be significantly diverse in various fish feed ratio schemes, that do relate with intestinal functionality like immunogenic and/or stress related processes, with

the metabolism of proteins, with the mitochondrial energy and activity and with the metabolism and transport of lipids. Moreover, genes that encode the proteins that are related with immunogenic response have been already recorded, illustrating differential expression related with various nutritional modifications.

Consequently, a need is emerging on examining the biochemical physiology of fish growth (growth compensation phenomenon) with the aid of novel transcriptomics [i.e. Illumina sequencing-Next Generation Sequencing (NGS)] in the medium intestine, in liver and in muscle tissue of intensively reared and commercially important fish with appropriate rotation periods of issuing nutrients along with intervals of starvation. Such examined tissues (not only the aforementioned above) could reveal the different physiological roles in fish, while at the same time could record their interlock from the nutritional modifications, as illustrated in the differential transcriptomic response profiles observed in these tissues in question. Jointly, with a series of other screenings of various *gene transcriptomics*-based assays regarding nutritional effects (where extreme handlings were avoided), fish response in variant feed ratio schemes appear to have resulted in alterations of the physiological and metabolic pathways. Genes that are related with metabolism of proteins, energy metabolism, apoptosis and immunogenic functionality, protein synthesis, stress and digestion of proteins are subjects to be thoroughly evaluated in the near future.

Such orientated results will optimize the comprehension of mechanisms and biochemical pathways that are activated at the increase of growth compensation. More specifically, carefully scheduled rotated periods of food intake and starvation could mean that such techniques and targeted fish feed diets can yield considerable profits for the viability and competitiveness of the intensive aquaculture industry. Conclusively, such results could help in the choice of suitable molecular bio-markers useful for the formation of new alternative fish diets in worldwide aquaculture enterprises.