

## **FISH PROTEOMICS AND NUTRITION**

Houlihan D.F.<sup>1</sup>,

Martin S.A.M.<sup>1</sup>, Médale, F.<sup>2</sup> & Kaushik, S.<sup>2</sup>.

<sup>1</sup>Department of Zoology, University of Aberdeen,  
Aberdeen AB24 2TZ, UK

<sup>2</sup>Fish Nutrition Laboratory, INRA-IFREMER  
64310, Saint Pée sur Nivelle, France

### **EXTENDED ABSTRACT ONLY- DO NOT CITE**

The proteome is the expressed protein complement of a genome in a tissue. Protein extraction followed by high resolution 2 dimensional electrophoresis, coupled with gel image analysis allows hundreds of protein to be monitored in parallel, permitting a global picture to emerge of changes in protein profile under different metabolic states. Protein spots are then subjected to further analysis leading to protein identification.

A rainbow trout proteome map is being developed in which all proteins are recorded in terms of molecular weight, isoelectric point (pI) and abundance. Protein spots that are found to be of interest are excised from the gel and subjected to trypsin digestion and separation of peptides by mass spectrometry. These peptide mass fingerprints are then used to search the Genbank data base for protein identification. A proteomics approach has been used to study the protein profiles of livers of rainbow trout following different nutritional challenges. Dietary changes will result in a multitude of metabolic and gene expression responses fish, identifying proteins that are altered in their expression pattern will help us have an insight into the biochemical responses of this tissue. Initial experiments were performed on fish that were starved for a period of two weeks, this revealed a panel of proteins that were altered in expression, some of these proteins are directly involved in protein breakdown. This approach supplemented information from transcriptome analysis by showing which proteins were actually increased in amount.

A second project concerns the substitution of fish meal protein with plant derived proteins (soybean); a twelve week growth trial was performed. The growth rate of the fish fed the two diets were not different, however utilisation

of ingested protein was different, with consumption and protein synthesis greater in fish fed the diet with a high proportion of soybean meal (SBM). For both this trial proteomic analysis of the liver has been carried out. During these studies ~800 proteins were analysed for expression pattern, some proteins were up or down regulated as a result of the nutritional change. Currently eighteen proteins have been positively identified from trypsin digest fingerprints using the MASCOT search program.

In conclusion we demonstrate how proteomics coupled with genome characterisation could help understand dietary responses in fish and in the development of alternative feed sources.

### **Acknowledgement**

This research was funded by EU (Q5RS-2000-30068) *PEPPA*

### **References**

- Martin, S.A.M., P.Cash, S. Blaney & D.F. Houlihan 2001. Proteome analysis of rainbow trout (*Oncorhynchus mykiss*) liver proteins during short term starvation. *Fish Physiology and Biochemistry* 24 (3): 259-270
- Carter C, D. Houlihan, A. Kiessling, F. Médale and M. Jobling 2001. Physiological effects of feeding. *In* Food intake in fish (Edited by Houlihan, Boujard & Jobling) Blackwell Science, UK