AquaMax – sustainable aquafeeds

AquaMax, the EU Framework 6 Project "Sustainable Aquafeeds to Maximize the Health Benefits of Farmed Fish for Consumers", involves 32 participants from universities, research institutes, industry and commerce in 12 European countries and India and China. AquaMax is a four year programme, started in March 2006, costing around 10 million Euros.

The strategic goal of the AquaMax is to replace as much as possible of the fish meal and fish oil used in fish feeds with sustainable, mainly terrestrial, alternative feed resources that are as free of undesirable contaminants as possible, consistent with maximising the growth performance, feed conversion efficiency, health and welfare of the farmed fish, and maximising the health-promoting properties, safety, quality and acceptability of the final product to the consumer. AquaMax will focus on Atlantic salmon, rainbow trout, sea bream and carp.

Dr. Gordon Bell, Dr. Douglas Tocher and Prof. Alan Teale of the Nutrition Group are participating, looking particularly at feeds development and contaminant risks. The Stirling research will be based heavily on molecular genetics, involving advanced "DNA chips" capable of defining and assessing the genetic capability of different strains of salmon to respond to the new diets and generate suitably high levels of health promoting long chain n-3 PUFA in their flesh. The research will be carried out in different strains of salmon, provided by Landcatch Natural Selection and Marine Harvest Ltd, that have already been selected for differing characteristics of oil deposition in their flesh.

EU Marie Curie Fellowship Awards to the Nutrition Group

During the last year, the Nutrition Group were successful in obtaining two new post-doctoral research posts through the award of two European Union Marie Curie Intra-European Fellowships in association with Dr Douglas Tocher. Each award is for two years with the fellows taking up their posts in February 2006.

Dr Laure Villeneuve's project, entitled "Microarray Analysis of Salmon Transcriptome (MAST)" is investigating gene expression in Atlantic salmon tissues using the salmon 17K cDNA microarray recently developed as part of the TRAITS project coordinated by Prof Alan Teale and Dr John Taggart. The overall goal of this project is to develop a novel molecular tool that will monitor health and performance of Atlantic salmon. The tool will take the form of an oligonucleotide array for probing key elements of the transcriptome involved in polyunsaturated fatty acid metabolism, protein catabolism, responses to bacterial and viral challenge, and the process of freshwater to seawater adaptation (smoltification). These aspects of the biology/metabolism of salmon were selected on the basis that fatty acid synthesis and storage, food conversion efficiency, infectious disease and adaptation to seawater present the greatest challenges in salmon rearing systems at the present time. Laure's Marie Curie project focuses specifically on fatty acid metabolism with the challenge being salmon grown on fish oil (FO) and vegetable oil (VO) diets.

Dr Christian Schlechtriem is also investigating the ability of Atlantic salmon to adapt to diets containing VO. Specifically his project, "Transcriptome and Proteome Analysis of Salmon (TAPAS) is investigating inter-individual variation in the ability of salmon to maintain high levels of flesh omega-3 fatty acids when fed diets low in these essential fatty acids. The study is testing three hypotheses; that changes in liver gene and protein expression and phenotype are associated; that gene expression in non-lethally obtained samples can be related to gene expression in liver; and that variation within any population can be related to variation in expression of specific genes. The specific objectives are: 1.To determine effects of replacing dietary FO with VO on gene and protein expression in liver of salmon, 2.To determine associations between gene expression, protein expression and phenotype (as measured by flesh omega-3 fatty acid content), 3.To compare gene expression pattern in non-lethally sampled tissues (blood) with that of liver, 4.To determine levels of variation in gene and protein expression and phenotype within the population sampled.