

Chips for Salmon

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The Institute of Aquaculture is leading research to develop a user-friendly genetic tool to monitor the health and performance of Atlantic salmon (*Salmo salar*).

The 'TRAITS' (TRanscriptome Analysis of Important Traits in Salmon), is a four-year, multi-centre collaborative research project between the Universities of Stirling, Aberdeen and Cardiff, together with ARK Genomics at the Roslin Institute and the Norwegian School of Veterinary Science. The project is being coordinated by Alan Teale, Professor of Molecular Genetics in the Institute, and is being carried out under BBSRC's Exploiting Genomics Initiative. The work also involves a number of industrial partners including Operon Biotechnologies GmbH, Marine Harvest and Scottish Quality Salmon.

The aims of the project are to identify the genetic basis of commercially important traits in salmon and to develop DNA microarrays or "chips" as a transcriptomics tool to monitor indicators of health and performance. In the last year, a preliminary deliverable of the project, a 17K feature cDNA trait-targeted microarray was produced based on expressed sequence tag (EST) collections, supplemented with ESTs obtained by suppressive subtractive hybridisations, and candidate genes cloned by the partner institutions. The EST resource was therefore enriched for genes potentially differentially regulated in the systems under study. In essence, DNA chips enable a 'snapshot' of indicator biological processes within the fish to be assessed from small tissue samples. Initial results indicate that the cDNA microarray will prove a valuable research tool. The work is also set to benefit the salmon farming industry, and could also help efforts in the conservation and restocking of wild salmon populations.

To achieve the aims of TRAITS, different aspects of the biology of salmon that are relevant in terms of the constraints on salmon aquaculture, including supply of contaminant-free oils for the salmon diet, protein growth efficiency, infectious disease, and a long and complex lifecycle, were studied. New molecular resources and techniques were used

in order to further dissect the molecular basis of the biology underlying these constraints. In addition to the practical tools in the form of cDNA chips, the project is also advancing our knowledge of basic physiology and its genetic control in salmon, and fish in general. Specifically, the project has identified suites of genes involved in polyunsaturated fatty acid (PUFA) metabolism, protein metabolism, bacterial and viral infection, and freshwater to seawater adaptation. Greater knowledge of these processes will enable us to monitor the health, development and productivity of farmed Atlantic salmon with a depth and precision that has not been possible previously.

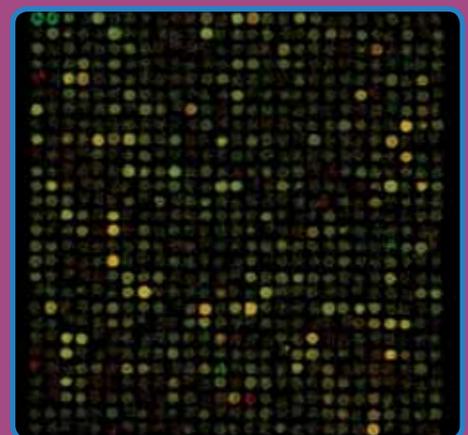
Research in Stirling has focused on the genes controlling synthesis of omega-3 highly unsaturated fatty acids (HUFA) and has been carried out by Drs John Taggart and James Bron, along with Dr Douglas Tocher of the Nutrition Group. Being able to monitor the functioning of these genes in fish will enable precision in dietary formulation and optimisation of feeding levels. It will also enable breeders to select for fish in which these genes are more active than in the majority of the population.

This aspect of TRAITS is driven by the need to make the farming of salmon, and fish in general, sustainable. Atlantic salmon have flesh with a naturally high content of omega-3 HUFA, eicosapentaenoic (EPA) and docosahexaenoic (DHA) acids, that are essential nutrients, important for growth and development in all animals, particularly for the normal functioning of cell membranes of the central nervous system, and for protecting humans against cardiovascular diseases. With traditional fisheries declining, aquaculture supplies an increasing proportion of the fish in the human food basket. However, the current high use of fish oils derived from feed-grade marine fisheries in aquaculture feeds is not sustainable, and will constrain growth of aquaculture activities. Vegetable oils, a sustainable alternative to fish oil, can be rich in short-chain PUFA, but lack the omega-3 HUFA abundant in fish oils. The extent to which fish can convert short-chain PUFA to HUFA varies with species dependent upon their gene complement. The goal is to replace as much as possible of the fish oil used in fish

feeds, consistent with maximising the growth performance, feed conversion efficiency, health and welfare of the farmed fish, but without compromising the flesh omega-3 HUFA content and the health-promoting properties of farmed salmon. To this end, TRAITS has identified genes differentially regulated in fish fed diets formulated with vegetable oil versus standard fish oil based diets.

Similarly, researchers at the University of Aberdeen have analysed gene expression in fish tissue samples, following infection with different pathogens. Several hundred genes were found to be increased or decreased following a bacterial infection in salmon. These genes have different roles in the immune response including bactericidal activity, cytokine functions and involvement in acute phase response. In addition, the Cardiff team has identified a number of genes that appear to be differentially regulated during smoltification in tissues such as gill, brain, pituitary and kidney, which could be useful in determining the readiness of fish for saltwater transfer and would also provide a means of studying the effects of environmental pollutants on smoltification.

With the large-scale gene expression analysis using the 17K cDNA microarray completed and performance indicators (key genes) selected, the final stage of the project is the construction of a "diagnostic" oligonucleotide microarray containing some 1000 – 2000 key indicator gene probes and confirming its suitability for use in the aquaculture industry and for assessing wild salmon stocks.



Gene expression signals from part of a TRAITS microarray