STRESSGENES PROJECT

Title of the project : A functional genomic approach to measuring stress in fish aquaculture

Duration: November 2001- January 2005

List of participants

Partner 1 (Coordinator) : Institut National de la Recherche Agronomique (INRA UR 1037)
Responsible scientist : Dr. Patrick PRUNET
INRA/SCRIBE, campus de Beaulieu, 35042 RENNES Cédex, France.
Tel : (33)223-48-50-14
Fax : (33)223-48-50-20
Mail : prunet@beaulieu.rennes.inra.fr
Sub-contractor : IRISA/INRIA
Responsible scientist : J. Nicolas
Campus universitaire de Beaulieu, 35042, RENNES Cédex, France

Partner 2 : University of Aberdeen (UNIABN)
Responsible scientist : Professor Chris SECOMBES
Department of Zoology, University of Aberdeen, 2 Tillydrone Avenue, AB24 2TZ Aberdeen, UK
Tel: (44)1224-272872
Fax: (44)1224-272396
Mail: c.secombes@abdn.ac.uk

Partner 3 : National University of Ireland, Galway (NUI, Galway)
Responsible scientist: Dr. Michael CAIRNS
National Diagnostic Centre, University road, Galway, Ireland.
Tel: (353)91-586-559
Fax: (353)91-586-570
Mail: michael.cairns@nuigalway.ie

Partner 4: The University of Liverpool (Liverpool)
Responsible scientist: Professor Andrew COSSINS
University of Liverpool, School of Biological Sciences, Derby Building, Brownlow Street, L69 3BX Liverpool, UK
Tel: (44)151-794-4992
Fax: (44)151-794-5017
Mail: cossins@liv.ac.uk

Partner 5 : The Natural Environment Research Council (NERC)
Responsible scientist: Dr. Tom POTTINGER
Centre for Ecology and Hydrobiology, Windermere Laboratory, Far Sawrey, LA22 0LP
Ambleside, Cumbria, UK
Tel: (44)15394-42468
Fax: (44)15394-46914
Mail: tgp@ceh.ac.uk

Partner 6 : Uppsala University (U.U.)
Responsible scientist: Professor Svante WINBERG
Evolutionary Biology Centre (EBC), Department of Comparative Physiology, Uppsala University, Norbyvaegen 18 A, SE-752 36 Uppsala, Sweden.
Tel: (46)18-471-26-49
Fax: (46)18-471-26-83
Mail: svante.winberg@devbiol.uu.se

Summary

The overall aim of this study was to identify in rainbow trout candidate genes associated with resistance to stress conditions. These information will constitute the physiological and genetic basis for new selection strategies. This study implied to carry out the following tasks: (1) Development of microarray technology which will allow analysis of gene expression at a large scale. (2) Use of this technology to identify those genes of which expression is modified during the application of a stressors (handling/confinement, salinity change, hypoxia, pathogen exposure, temperature change.(3) Carrying out a more complete characterisation of a limited number of genes in relation to physiological responses following exposure to the stressors. The first part of the present study covered construction of a large trout EST collection corresponding to genes involved in the stress response, several stress experiments (hypoxia, confinement, salinity, temperature, pathogen exposure). This was carried out by preparing 36 SSH cDNA libraries made form various tissues (gill, liver, head-kidney, muscle, skin, spleen, brain, intestine, pituitary) collected on trout exposed or not to stressors. From this collection, about 9408 clones corresponding 2820 contigs were spotted on glass-slide microarrays. Analysis by Gene Ontology profilling of the annotated contigs indicated that this Stressgenes collection was enriched in genes involved in macromolecule metabolism, biosynthesis, catabolism, response to biotic stimulus, response to stress and immune response. An important task of last year was to select from this large collection those genes of which expression is regulated after stress exposure. These Stressgenes microarrays have been further used used to analyse gene profile expressions after stressor exposure. Thus, gene expression profillings have been carried out in head-kidney and spleen of trout exposed to bacterial challenge, in gill and of trout exposed to salinity stress, in liver and head-kidney of trout exposed to confinement stress, in the brain of trout receiving feed enriched in tryptophan and exposed to confinement stress, in brain, liver, and muscle of trout exposed to cooling, warming and hypoxia stress. Statistical analysis of these gene expression profiles allowed us to select for each tissue and stressor alist of genes significantly over- or under-expressed after stress exposure. Moreover, Gene Ontology analysis allowed us to identify in each tissue functional features of the stress responsesand revealed sometimes specific expression signatures. This genomic approach allowed us to identify a range of candidate genes involved in the stress response and possibly endowing resistance to stress.