

Fish Toxicogenomics

Identifying and defining the bases of individual and population susceptibility and adaptation to environmental pollutants in fish: An integrated 'omic' approach.



Introduction

This project has been funded by the NERC as part of the **Post-Genomics and Proteomics programme** (<http://www.nerc.ac.uk/research/programmes/proteomics/>).

The identification and assessment of organismal and ecosystem responses to, adaptation to, and selection by multiple pollutants is a major challenge. This project sets out to utilise functional toxicogenomics and metabolomics based upon techniques which place no a priori emphasis on the currently limited knowledge of genotypic and phenotypic responses in marine and freshwater fish to toxic anthropogenic inputs. The aim of the programme is to inform on "what makes species, populations and taxa resistant or vulnerable to environmental change and impact". We wish to identify the key genetic and phenotypic determinants for the resistance and vulnerability of these species and their populations to anthropogenic pollutant impact.

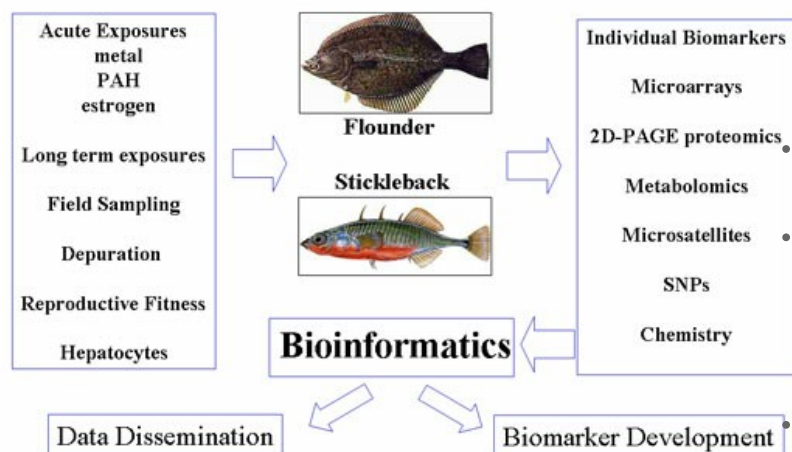
Furthermore the approach addresses another important basic question "does chronic pollution of UK estuaries and rivers reduce the genetic diversity of their fish populations" and will have an important practical "spin off" for end users in that it will enable development of a more appropriate methodology and set of practical tools (including in vitro cell culture systems) to contribute to environmental impact assessment and regulation of discharges by the regulatory authorities. This will provide a more informed knowledge of the health of the aquatic environment thus protecting our aquatic resources and biodiversity.

Aims

The major questions that this project will address are:

- What specific measurable phenotypes are present in UK fish species dwelling in chronically and multiply polluted environments compared to reference sites?
- What are the critical determinants of resistance and vulnerability of fish species to priority pollutants of the UK marine and freshwater environments?
- Are such pollutants, through selective pressure, causing genotypic changes in populations and thus lowering biodiversity?
- What are the male fitness consequences of adaptation to polluted environments?
- Can such information be used to design informative tools for ecological and environmental risk assessment, and ultimately be used to inform policy and assess the effect of regulation?

What makes fish populations resistant or vulnerable to environmental change and impact?



Specific Objectives

To determine the integrated phenotypes (including gene, protein and metabolite global profiles) of individual fish (a) both between and within populations of sentinel fish species from reference and polluted sites, (b) in fish experimentally exposed to single pollutants and a complex mixture of environmental origin, and (c) in one species after laboratory depuration to assess reversibility of phenotypic markers.

To determine genotypes of these fish with respect to polymorphisms in candidate tolerance or susceptibility genes, variations in neutral marker genes and population microsatellite markers.

To establish bioinformatic and statistical protocols for integrating and interrogating the phenotypic and genotypic data in order to derive critical factors determining susceptibility and resistance to complex pollutant mixtures and fitness in the studied natural environments, and to validate this from experimental mesocosms/cages and laboratory exposures. To establish a website to disseminate all the datasets and the bioinformatic tools developed.

To derive a framework (initiated by a workshop and presentations to the CMAs and WGBEC) for the derivation of an integrated, extended set of tools for environmental pollutant impact assessment including the use of generic laboratory procedures.

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