Epigenetic mechanisms of toxicity and tolerance to metals in fish

Supervisors

Main supervisor: Dr Eduarda Santos (University of Exeter)
Co-supervisor: Prof Peter Kille (Cardiff University)

Project enquiries - Email: e.santos@exeter.ac.uk **Contact number:** +44 (0) 1392 264607

Supervisory team:
Prof Jonathan Mill (University of Exeter)
Dr Ronny van Aerle (Centre for Environment, Fisheries and Aquaculture Science)
Dr Ioanna Katsiadaki (Centre for Environment, Fisheries and Aquaculture Science)

Host Institution: University of Exeter

Project description

Metal contamination in UK freshwaters is one of the principal reasons for failures of water bodies to meet the Water Framework Directive criteria and for locally reduced or absent fish populations. This is due, at least in part, to contaminated waters originating from historical mining that continue to enter water systems, in particular during flooding events. However, some of these rivers can sustain fish populations, indicating that they are able to tolerate toxic levels of metals (Figure 1). The processes underpinning this extraordinary tolerance are not understood, and may involve genetic, epigenetic and/or physiological adaptation.

There is a significant knowledge-gap in our understanding of the impact of metals on the epigenome of organisms inhabiting metal-polluted environments, the linked implications for population viability and the potential multi-generational responses. Given the substantial body of evidence describing effects of metal exposure on the human epigenome (Salnikow and Zhitkovich 2008, Chem Res Toxicol. 21(1):28-44) and associated population level health impacts (Niedzwiecki et al. 2013, Epigenetics 8,730 738) the lack of environmental data represents a prominent omission. This studentship will address the hypothesis that metal exposure causes significant alterations in the epigenome of exposed fish and that these changes may play a role in the tolerance to metals observed in wild populations.

The student will employ a multidisciplinary approach to investigate the effects of exposure to metals on the epigenome of exposed fish. We will focus on arsenic, nickel and copper, because of known mechanistic links to changes in epigenetic markers, and their environmental relevance (Figure 1). The data will be integrated with effects at the physiological, biochemical and transcriptomics levels to determine the global effects of metals. The student will then investigate if any of the alterations seen persist in the absence of the exposure, and if they are inherited by future generations. Finally, data will be integrated with that for wild populations originating from metal-contaminated rivers to assess the extent to which epigenomic mechanisms contribute to metal tolerance in wild populations.

Three-spined stickleback (*Gasterosteus aculeatus*) will be used as model species because of its environmental relevance, availability of genomics resources, ease of maintenance, short generation time, and suitability for laboratory exposures. The outcomes of the project will contribute significantly to understanding mechanisms of metal toxicity and relationships between exposure history and differential susceptibility in wild fish populations.

Figure 1: Metal accumulation in a population of brown trout originating from the highly contaminated River Hayle, Cornwall (blue), in comparison with a control river (green). The levels of metal recorded are the highest ever recorded for fish demonstrating the extreme tolerance to metals in this population.