Short- and long-term effects of environmental mercury exposure on three-spined stickleback (*Gasterosteus aculeatus*) populations.

A multitude of anthropogenic activities have left a legacy of mercury pollution in the region of Flanders (Belgium). As a consequence, mercury levels in certain aquatic habitats are currently still exceeding environmentally safe limits. The three-spine stickleback is a well-known model species in environmental monitoring and evolutionary biology. It is a fish species that is inhabiting most of the low-land rivers in Flanders, which makes it a promising sentinel species for environmental monitoring and risk assessment. The overall goal of our research is to identify how stickleback populations, being exposed for multiple generations to elevated Hg-levels, developed strategies to increase their success of survival.

In a first study we identified 21 stickleback populations distributed all over the Scheldt- and Meuse basin. The degree of mercury exposure was characterized, and each population was genotyped by sequencing. The results were combined in a genome wide association study (GWAS), in order to identify single nucleotide polymorphisms (SNPs) that potentially have played a role in adaptation to mercury. In a second study, invertebrate samples were taking at 3 unpolluted and 3 polluted locations. Additionally, a suit of biochemical and organismal endpoints was tested to identify biomarkers that correlate robustly with environmental mercury contamination.

A wide variation of mercury accumulation was observed between the 21 distinct stickleback population, ranging from 18.4 ± 2.3 ng/g DW to 374.2 ± 45.5 ng/g DW and there was a significant correlation between length and Hg-level in the muscle tissue. Hepatic enzyme activities and metabolites related to oxidative stress pathways were elevated in those populations which are continuously being exposed to higher mercury levels in their diet. The GWAS resulted in 2 SNPs that were significantly associated with increased mercury levels measured in the fish. No genes were annotated at the exact position of these SNPs in the genome. However, potentially relevant causal genes were found down- and upstream of the particular locus. Additionally, alignments with genomes of other species did result in sequences of known genes. It is currently being investigated whether this is of any significance or not, and what the role of the mutation might be.