MO031 Historical mercury contamination in Belgian rivers; screening for suitable biomarker genes of the three-spined stickleback (Gasterosteus aculeatus). V. Delahaut, University of Antwerp / Biology SPHERE; R. Blust, University of Antwerp; R. Blust, Systemic Physiological and Ecotoxicological Research SPHERE University of Antwerp / Biology; G. De Boeck, University of Antwerp / Biology SPHERE. Historical metal contamination of the Belgian surface waters dates back to the nineteenth century. In recent decades, regulatory implementations and increased sanitation efforts did contribute to an overall better water quality. Yet, traces of past contamination events are still detectable. Amongst others, there is the presence of mercury in aquatic sediments and biota, a reminder of historical metal smelting activities. The overall goal of this project is to discover whether there is a significant inheritability of the adaptive traits of populations towards the presence of sub-lethal mercury concentrations. The three-spined stickleback, *Gasterosteus aculeatus*, has been selected as a sentinel species for this research because of its wide dispersion, and tolerance towards contaminated environments. During a first field campaign, two rivers known for their historical mercury contamination and one near-to-pristine stream, were sampled at four different trophic levels; water, sediment, invertebrates and fish. All samples were subjected to an optimized protocol for the determination of the exact concentration of the following metals; As, Cd, Cr, Cu, Hg, Ni, Pb, and Zn. First, we wanted to have an estimation of the metal concentration which is still present at these four levels of the food web. These results were then used to calculate site-specific bioaccumulation and biomagnification factors for the analyzed metals. In addition, some of the stickleback caught at each site were dissected and their liver was collected. A set of biomarkers for oxidative stress was selected and used to evaluate the effect of contamination in each river at a molecular level. Therefore, the expression of the following genes was determined; *catalase, metallothionein, heat shock protein 70, glutathione peroxidase* and *superoxide dismutase.* Novel primer pairs were developed, and have now been evaluated suitable for real time qPCR analysis. First results suggest an overall higher expression of catalase in comparison to the four other genes of interest, while the difference among sites was less pronounced.