During recent years ecotoxicology has been an emerging field and its experimental focus has been expanded from using mainly chemical stressors (e.g. cadmium) to assessing the effects of natural or non-chemical stressors (e.g. temperature) as well. Both kinds of stressors are known to influence the fitness of entire populations, but are expected to have different mechanisms of action. Parallel to the latter evolution ecotoxicology has broadened its view on effect assessment by taking a greater amount of parameters on different levels of biological organisation into account. In this context this study investigates effects of both cadmium and temperature in zebrafish (*Danio rerio*) on several levels of biological organisation, ranging from the organismal to the molecular level. Laboratory experiments were conducted in which adult zebrafish were exposed to either cadmium or a rise or drop in temperature and responses were investigated at several time points. Swimming performance and condition factor were chosen as high level parameters. At the biochemical level organ specific energy stores and metal accumulation patterns were assessed. Finally, transcriptomics and proteomics data are being gathered using microarrays and 2D DIGE respectively. This project aims at elucidating the mechanisms of these two stressors separately, prior to the research of combined exposure effects.

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CSS.4
Dissecting the mechanisms of environmental stress adaptation: A systems biology approach

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Adaptation to environmental stress is essential to the survival of all organisms. Temperature stress in particular, has profound effects on biological systems, especially poikilotherms, whose tissues, cells and molecules are exposed to the full effects of any thermal variation. We previously identified a powerful adaptive response to cold stress in the nematode *Caenorhabditis elegans*, with prior cold conditioning (acclimation) leading to acquired protection to chill damage. Membrane adaptation has long been considered the principle mechanism underpinning such phenotypic transitions in cold tolerance. However, our work showed that this mechanism accounted for just 16% of the phenotype. Thus, what other molecular mechanisms underpin the transition from the stress-sensitive to stress-tolerant state? To address this question, and gain a global view of the genetic mechanisms underpinning the cold stress response, we used Affymetrix arrays to identify genes that were cold upregulated, and then downregulated again upon stress recovery (when cold sensitivity returned). Using WormNet, we generated a gene interaction network containing these genes, and also identified further candidates likely to be involved in the cold stress response. Metabolomic analyses were then used to highlight potential genetic mechanisms underpinning the synthesis of cold-induced metabolites. From this systems biology approach we created list of approximately 200 genes, which formed the basis of a targeted RNAi screen. This has allowed us to disseminate key components of the stress response, by knocking down selected gene transcripts and recording the effect on the cold tolerance phenotype.

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CSS.5
Toxicity evaluation of perfluorooctane sulfonate (PFOS) in common carp (*Cyprinus carpio*): A systems biology approach

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Perfluorooctane sulfonate (PFOS) has been manufactured for over 50 years in increasing quantities and has been used for several industrial and commercial aims. Due to the persistence and the bioaccumulation of this pollutant, it can be found worldwide in wildlife and humans. The lack of toxicity data results in an incomplete understanding of the effects and the mode of action of this pollutant. In the present study, common carp (*Cyprinus carpio*) was exposed to PFOS. In parallel with the high throughput technology of microarrays, effects at higher levels of biological organization such as available energy reserves as well as the relative condition factor and the hepatosomatic index were determined. When combining these levels of biological organization, indications of a tradeoff between the metabolic cost of toxicant exposure on one hand and processes vital to the survival of the organism on the other hand were seen. This systems biology approach takes gene expression data to the next level: a biological meaning in a more integrated approach.

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CSS.6
Comparative analysis of gene expression in brain, liver, skeletal muscle and gills of the zebrafish (*Danio rerio*) exposed to environmentally relevant uranium water concentrations

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The effects of uranium (U) waterborne exposure on gene expression were examined in four organs of the zebrafish (*Danio rerio*). After 3, 10, 21, and 28 days of exposure followed by a 8 day depuration period, gene expressions and U bioaccumulations were analysed. Bioaccumulation decreased significantly in liver during the depuration phase, and genes involved in detoxification, apoptotic mechanism and immune response were strongly induced. Among these genes, *tap* which belongs to the ABC transporter family was 4-fold and 24-fold induced in organisms preliminary exposed at 23 and 129.5 μg l^{-1} of U, respectively. These results emphasize the role of liver in detoxification mechanisms. In gills, at the highest U concentration, *gpx*, *cat*, *sod* (Cu/Zn), and *sod* (Mn) genes were upregulated at day 21, indicating the onset of oxidative stress. Mitochondrial metabolism and DNA integrity were also affected since *coxI*, *atpb*, and *rad51* genes were upregulated at day 21 and during the depuration phase. In skeletal muscles, *coxI*, *atpb*, and *cat* were induced at day 3 suggesting an impact on the mitochondrial metabolism and production of reactive oxygen species. In brain, *gls1* was also induced at day 3 suggesting a need in glutamate synthesis involved in neuron transmission. During the depuration phase, U excretion was inefficient in brain and skeletal muscles, and most of the tissue-specific genes expressions were repressed or unchanged.

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