Gene expression profiling in zebrafish embryos (*Danio rerio*) for detection of sediment-borne pollution

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Contaminants bound to fluvial or marine sediment pose a risk to biota and to man. Usually, a battery of standardised sediment toxicity tests and chemical analysis are applied to assess the toxicity of sediment. However, given the complex nature of these environmental samples, the identification of parameters causing specific toxicity (e.g. cytotoxicity, developmental impairment, genotoxicity, etc.) are difficult to elucidate. Here, we aim to identify genes, which can serve as markers for exposure of zebrafish embryos to sediment extracts with the aim to support identification and classification of sediment-borne toxicity. Specifically, we address the questions whether (1) specific responses to complex environmental samples can be identified, (2) there are common expression profiles induced by different sediment extracts, and whether (3) single chemical exposure correlates with sediment extract induced profiles. The different sediments caused fingerprint-like gene response patterns. Despite this, a substantial number of genes were clearly regulated by all sediment exposure scenarios. The 20 significantly regulated genes fell into several gene ontology classes including cell cycle and proliferation, phase I detoxification, antioxidant defence, phase II metabolism, developmental regulators, general stress response and immune response. Cluster analysis of sediment and single chemical exposure revealed subclusters reflecting the gene ontology classes of the 20 marker genes as well as varying correlation of sediments to single chemical expression data. Comparison of sediment to single chemical gene expression data remains ambiguous suggesting that many confounding factors influence the effect of a single chemical present in the mixture of a sediment extract. This set of marker genes may facilitate the use of gene expression analysis in sediment risk assessment and may allow classification of sediment contamination.