Data Article

Whole transcriptome data of zebrafish exposed to chronic dose of depleted uranium

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A B S T R A C T

The concentration of depleted uranium (DU) in the environment is expected to increase due to anthropogenic activities, posing potential risks on ecosystems. The effects of chronic exposure to DU at concentration close to the environmental standards (0.3–30 μg DU/L) are scarcely characterised. Genomic alterations caused by low doses of pollutants can potentially propagate over generations, but how these effects may affect the health of the progeny remain uncertain for the vast majority of toxicants. The present dataset describes the transcriptomic effects of a chronic exposure to 20 μg DU/L during 10 days on adult zebrafish (*Danio rerio*) organs, the brain, the testis and the ovaries. The potential multigenerational effects of DU were assessed on the progeny of the adult exposed fish at the two-cells stage and after four days of development. We describe in this article the summary statistics of the differential gene expression analysis and focus on key molecular pathways affected by an exposure to a low concentration of DU. The data presented in this study supports the observation made in Armant et al. (2017) [1] (https://doi.org/10.1016/j.dib.2016.05.007) that DU can induce a molecular stress in both adult zebrafish and their progeny. The raw dataset has been deposited at the Gene Expression Omnibus (GEO) repository under the accession number *GEO:* GSE96603.

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Specification Table

Subject area	Biology
More specific subject area	Bioinformatics and toxicogenomics
Type of data	Figures, tables
How data was acquired	High-throughput RNA sequencing
Data format	Filtered and analysed with statistical tests
Experimental factors	Wild type versus exposed to depleted uranium
Experimental features	Comparison of the transcriptomic response from adult zebrafish tissues (brain, ovaries and testis) exposed to depleted uranium and their progeny (at two times of development) to their respective controls. Triplicates were used for each condition. Directional libraries were sequenced on Illumina HiSeq. 15000 in paired-end reads
Data source location	Institut de Radioprotection et de Sureté Nucléaire (IRSN), PRP-ENV/SERIS/LECO, Cadarache, Saint-Paul-lez-Durance 13115, France.
Data accessibility	Data are available with this article, and via NCBI's GEO accession number GEO: GSE96603 http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE96603

Value of the data

- Depleted uranium is a heavy metal posing potential environmental risks due to its increasing release from anthropogenic activities.
- This dataset presents the differentially expressed genes in adult brain and gonads (testis and ovaries) from zebrafish exposed to 20 μg/L depleted uranium for 10 days.
- It also provides the potential multigenerational effects of a parental exposure to depleted uranium in the progeny of exposed fish at both the two-cells stage and on four-days larvae.
- The analysis of the biological pathways impacted by a chronic depleted uranium exposure will help to understand the molecular mechanisms of toxicity of this toxicant or other heavy metals.
- The identification of the depleted uranium (DU) de-regulated genes could lead to the development of biomarkers of DU and other heavy metals.

1. Data

This data consists of 35 high-throughput sequencing samples of adult brain, testis and ovaries obtained from adult zebrafish exposed to 20 μg/L of depleted uranium (DU) for 10 days, as well as their progeny both at the two-cells stage and four-days larvae (96 h post-fertilization, hpf) [1,2]. The data are deposited under the Gene Expression Omnibus (GEO) number GEO: GSE96603 at http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE96603. The list of samples collected in this study is provided in Table 1. The principal component analysis on the regularized log transformed (rlog) expression data shows at the global level that the biological replicates group by stage and tissue (Fig. 1). A selection of 22 samples with low biological variability was made for the differential expression analysis (Table 2, Fig. 1B). The summary statistics of the deregulated genes obtained after pairwise differential analysis is provided in Table 3. The expression of a selection of genes involved in diverse biological processes (such as cell adhesion, response to oxidative stress, ATPase activity, protein chaperons, lipid metabolism, hatching and tissue regeneration) altered after DU-exposure is displayed in Fig. 2. The gene ontology analysis (GO) was applied to classify the most significantly affected pathways in each condition (Table 4).