Data in Brief 11 (2017) 628–633

Contents lists available at ScienceDirect

Data in Brief

journal homepage: www.elsevier.com/locate/dib

Data Article

The pesticide dieldrin disrupts proteins related to oxidative respiration and mitochondrial stress in the central nervous system

Andrew M. Cowie [a], Kathleena I. Sarty [a], Angella Mercer [a],
Jin Koh [b], Karen A. Kidd [a], Christopher J. Martyniuk [a,*]

[a] Canadian Rivers Institute and Department of Biology, University of New Brunswick, Saint John,
New Brunswick E2L 4L5, Canada
[b] Interdisciplinary Center for Biotechnology Research, University of Florida, Gainesville, Florida 32611, USA

ARTICLE INFO

Article history:
Received 9 February 2017
Accepted 7 March 2017
Available online 11 March 2017

ABSTRACT

Quantitative proteins analysis was carried out in the hypothalamus of zebrafish following dietary exposure to the legacy pesticide dieldrin. Data were collected using iTRAQ labeling methodology and data were acquired using a hybrid quadrupole Orbitrap (Q Exactive) MS system (Thermo Fisher Scientific, Bremen, Germany). There were 3941 proteins identified in the hypothalamus of zebrafish, and these proteins comprised 23 unique expression patterns for proteins based on the three doses of dieldrin. There were 226 proteins that were regulated in one or more doses of dieldrin and 3715 proteins that were not affected. Thus, 5.7% of the proteins detected responded to the treatment. Many proteins that were differentially expressed were those found in, or associated with, the mitochondria. The proteomics data described in this article is associated with a research article, “Transcriptomic and proteomic analysis implicates the immune system and mitochondria as molecular targets of dieldrin in the zebrafish (*Danio rerio*) central nervous system” (A.M. Cowie, K.I. Sarty, A. Mercer, J. Koh, K.A. Kidd,

---

DOI of original article: http://dx.doi.org/10.1016/j.jprot.2017.02.003

[*] Corresponding author. Current address: Department of Physiological Sciences and Center for Environmental and Human Toxicology, University of Florida Genetics Institute, College of Veterinary Medicine, University of Florida, Gainesville, FL 32611 USA.

E-mail address: cmartyn@ufl.edu (C.J. Martyniuk).

http://dx.doi.org/10.1016/j.dib.2017.03.008

C.J. Martyniuk, submitted) [1], and serves as a resource for researchers working in the field of pesticide exposures and protein biomarkers.

Specifications Table

Subject area	*Biology*
More specific subject area	*Pesticide neurotoxicity, proteomics, biomarkers, pathway analysis, zebrafish*
Type of data	*Table, figure, and supplemental file of protein data in excel*
How data was acquired	Mass spectrometry using a hybrid quadrupole Orbitrap (Q Exactive) MS system (Thermo Fisher Scientific, Bremen, Germany).
Data format	*Filtered and analyzed*
Experimental factors	*Samples were subjected to SCX fractionation prior to analysis*
Experimental features	*Female adult zebrafish, 5 months of age were fed dieldrin. There were four treatment groups that included a control, and three doses of dieldrin spiked feed (0.03, 0.15, and 1.8 μg DLD /g d.w. feed). Fish were fed for 21 days.*
Data source location	*Not applicable.*
Data accessibility	*Data are with this article.*

Value of the data

- Characterizes dieldrin-regulated pesticides in the zebrafish central nervous system.
- Identification of biomarker candidates for pesticide induced neurotoxicity that can be tested in further studies.
- Offers a proteomic framework for the relationship between chemical exposures and neurodegenerative diseases.
- Discovery and identification of mitochondrial proteins that are responsive to the organochlorine pesticide dieldrin and which can be compared to other studies investigating pesticide-induced mitochondrial dysfunction.

1. Data

Quantitative proteomics using isobaric tagging for relative and absolute quantitation (ITRAQ) was conducted in the hypothalamus of zebrafish fed the organochloride pesticide dieldrin (Cowie et al., submitted) [1]. Data were collected using iTRAQ labeling methodology and data were acquired using a hybrid quadrupole Orbitrap (Q Exactive) MS system (Thermo Fisher Scientific, Bremen, Germany). There were 3941 proteins identified in the hypothalamus of zebrafish and 226 proteins that were regulated in one or more doses of dieldrin (Supplemental Data 1). These proteins comprised 23 unique expression patterns for proteins based on the three doses of dieldrin (Table 1). The remaining proteins that were not changed (3715) are indicated in group X1.The most dramatic proteomic response in terms of protein number occurred with the high feed dose, and 61 proteins were significantly decreased (Cluster XII) with 1.8 μg DLD/g d.w. feed. Proteins in this group were not changed with the two lower doses of dieldrin. The group that contained the second highest number of proteins