

Effects of Volume on Acute Toxicity and the Transcriptome in **Fathead Minnow Exposures** M. Le¹, K. Flynn², D. Villeneuve², A. Biales², D. Bencic², R. Flick², J. Martinson²

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Background

A core mission of the U.S. Environmental Protection Agency (USEPA) is to assess the effect of anthropogenic chemicals on freshwater ecosystems using data gathered from standardized tests across many biological taxa. One common species used for testing is the Fathead minnow (FHM), also known as Pimephales promelas. These tests measure chemical induced mortality and vary in observable endpoints.

- Traditionally, these tests employ long time frames and large amounts of chemical to conduct exposures.
- A modern alternative to this involves a high-throughput format of testing to costeffectively and efficiently collect large amounts of toxicological data.

We hypothesize container volume in relation to controls in multi-well plates should not significantly affect transcriptomic response nor LC50 values in this type of screening assay compared to traditional methods of testing and thus, facilitate a high-throughput approach to future chemical risk assessment.

Objective

To evaluate the effect that differences in exposure volume and associated loading density could have on both survival and the transcriptome-level response in a highthroughput format

Exposures

- 24-hour static exposures to FHM larvae were conducted with 12 concentrations of CuSO4, NiSO4, and ZnSO4
- Three exposure volumes were tested, specifically: 96-well plates (96WP), 24-well plates (24WP), and single 15mL cups (CUP)
 - 96WP: 1 FHM/well; 700uL exposure media/well; 8 replicates
 - 24WP: 1 FHM/well; 2.5mL exposure media/well; 4 replicates
 - CUP: 1 FHM/cup; 15mL exposure media/cup; 3 replicates



96-well plate (96WP)



24-well plate (24WP)



(CUP)

LC50s, with 95% confidence interval, were assessed with 96WP exposures in full concentrationresponse with 12 concentrations of half-log dilutions corresponding to each chemical starting at high concentrations of 2, 15.8, & 4 mg/L of CuSO4, NiSO4, & ZnSO4, respectively

Cher CuSO4 NiSO4 ZnSO4

RNA-seq data was collected from all 12 concentrations of the 96WP and only 3 concentrations of CuSO4 from 24WP and CUP formats ^{2, 3}

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U.S. Environmental Protection Agency Office of Research and Development

BMDExpress2

BMDExpress2, <u>https://www.sciome.com/bmdexpress/</u>), is a desktop application that enables analysis of dose/concentration-response data produced in differential gene expression experiments • Transcriptomic response using RNA-Seq data was assessed in pairwise comparisons between container volumes using control data only ^{1,2,3}

• Points of Departure (POD) were calculated from Differentially Expressed Genes (DEGs) in each volume independently ^{1, 2}

• Volume-specific LC50 values were calculated with BMDExpress2 and were compared with published LC50s from ECOTOX knowledgebase, https://cfpub.epa.gov/ecotox/index.cfm⁴

Survival

	BMDExpress2	Published Literature	
	96WP (24h)	Traditional (24h)	Traditional (96h)
mical	LC50	LC50	LC50
l (mg/L)	0.57 (0.47 - 0.69)	0.74	0.25
(mg/L)	11.3 (9.2 – 13.7)	N/A	6.2
(mg/L)	3.8 (3.3 – 3.9)	2.46	2.19

RNA Seq Data

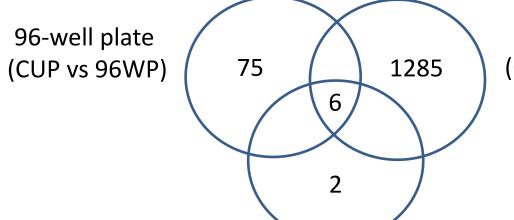
RNA-Seq raw reads were assembled into transcript models, aligned with annotations, counted, normalized, and log2 transformed for each transcript

• Low count feature filtering: any given feature had to have a count of 10 or more in a minimum of 4 samples or that feature was filtered out

• The impact of exposure volume on the transcriptome of controls was explored by comparing lists of DEGs from pairwise comparisons

Transcriptomic-derived PODs from each volume were compared to determine the impact exposure volume may have on the analysis

of Differentially Expressed Genes (DEGs) in Controls Across Volumes³



24-well plate (CUP vs 24WP) **#DEGs**

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• Survival across the different exposure formats was similar in all three chemicals, and LC50 values calculated from the these were similar to published 24-hour LC50's. For instance, the LC50 for CuSO4 from exposure in a 96-well plate was 0.57 mg/L, comparable to 0.74 mg/L, the median value from several published tests documented in the EPA's ECOTOX knowledgebase. Comparable results were also observed for NiSO4 and ZnSO4

Results of pairwise comparisons between controls across volumes suggests negligible biological response related to volume format

- Expand volume comparisons to other chemical modes of action



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POD Calculation for CuSo4 in each Volume					
BMDExpress2 Results	Volume Format				
	CUP ²	24WP ²	96WP		
#DEGs via ANOVA	53/32996	11/32996	4139/32548		
via Williams Trend Test + 2-Fold Change	369	159	208		
#DEGs passing NTP filters ¹	128/369	52/159	108/208		
Median POD (mg/L)	0.0445	0.045201	0.025		
edian POD lower limit (mg/L)	0.028027	0.028289	0.017		
edian POD upper limit (mg/L)	0.101045	0.106327	0.046		

Highlights

• PODs calculated for CuSO4 from each volume were similar indicating final POD calculations were not impacted by volume

Future Recommendations

- Analyze full concentration-response data for 24WP and CUP formats for a complete comparison to 96WP format
- Compare water quality parameters (ex. pH, DO, etc) across volumes

¹ Due to COVID restrictions, data for NiSO4 and ZnSO4 is pending

² A full 12 concentration-response was calculated for the CuSO4 96WPs, however only 3 concentrations were analyzed for the 24WP and CUP formats

³ DEGs calculated by pairwise comparisons using One-Way Analysis of Variance (ANOVA) ⁴ Follows National Toxicology Program (NTP) Approach to Genomic Dose-Response Modeling, https://ntp.niehs.nih.gov/ntp/results/pubs/rr/reports/rr05 508.pdf?utm source=direct&ut m medium=prod&utm campaign=ntpgolinks&utm term=rr05