# **Using Molecular Methods to Improve Metal Mixture Risk Assessment at Mining-Impacted Sites**

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#### Hypotheses

- The Cd only exposed group and the Zn-Cd mixture exposed group will have DEGs in common indicative of bioavailable Cd in the presence of Zn
- Transcriptional analysis will reveal key physiological mechanisms indicative of toxicity in the Cd only exposed group that will be nullified in the Zn-Cd mixture exposed group of *D. magna*.

# **INTRO**

- Mining waste impacts human and environmental health
- Metal mixtures are common in mining effluent
- Metals behave differently in mixtures
- One behavior observed is a less-than-additive (protective) effect of Zn for Cd toxicity in *D. magna* at some doses
- Physiological response plays a role in this protective effect

## METHODS

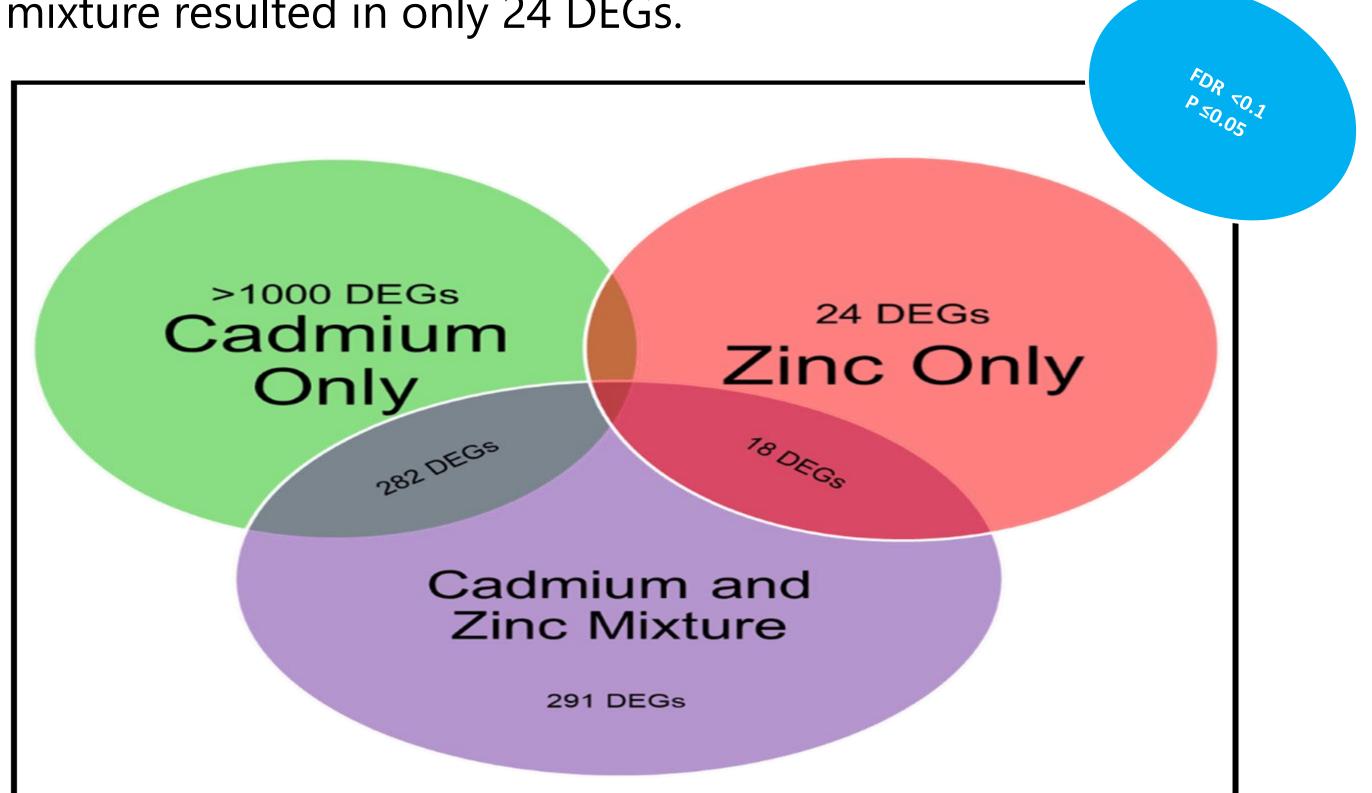
- 1. Exposure: Acute Zn, Cd, and Zn-Cd mixtures using D. magna
- 2. RNA extraction: TRIzol/Chloroform with a Qiagan RNEasy Mini Kit, Converted to cDNA
- 3. Library Prep and QC: Novagene, Inc.
- 4. Gene expression: using an Illumina Novaseq 6000
- 5. Physiological Effects: Differentially Expressed Gene (DEG) counts and gene ontology analysis using Blast2Go





#### RESULTS

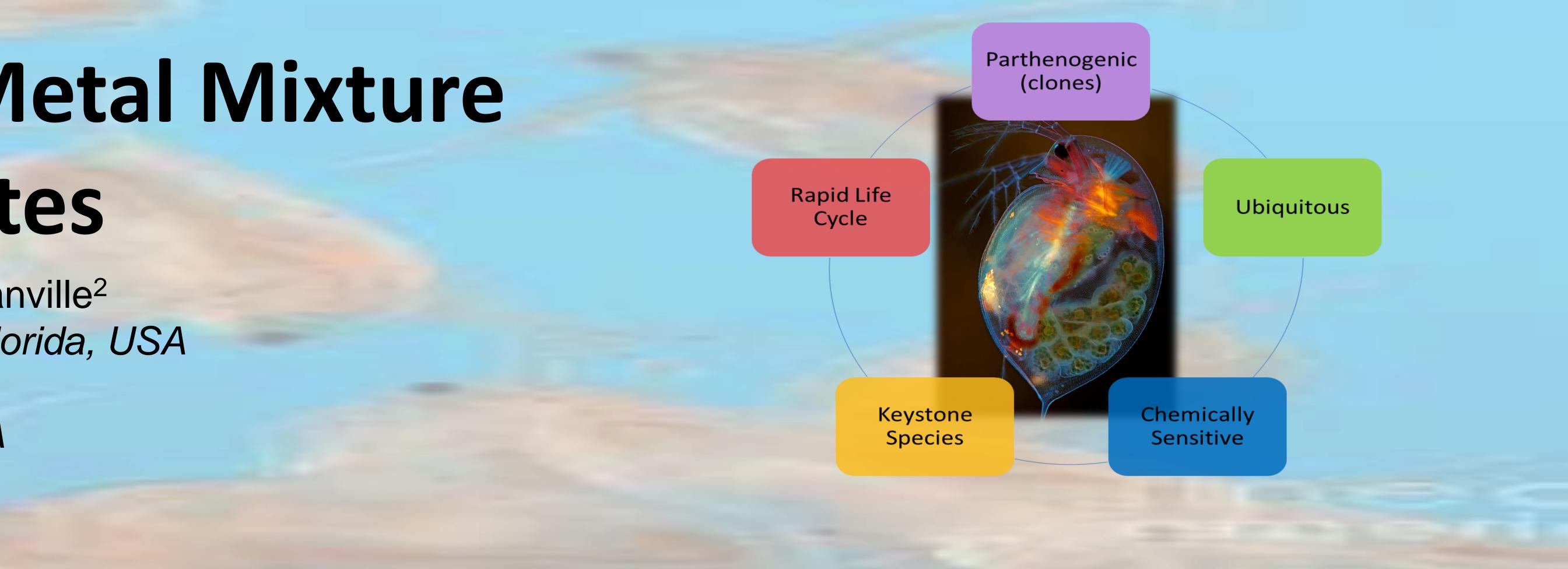
- *D. magna* exposed to toxic doses of Cd alone differentially expressed over 1000 genes (DEGs)
- In the Cd-Zn mixture at the same Cd concentration, the number of DEGs decreased to 291. 282 of those DEGs were shared between the two groups.
- Exposure to Zn alone at the same Zn concentration as in the mixture resulted in only 24 DEGs.

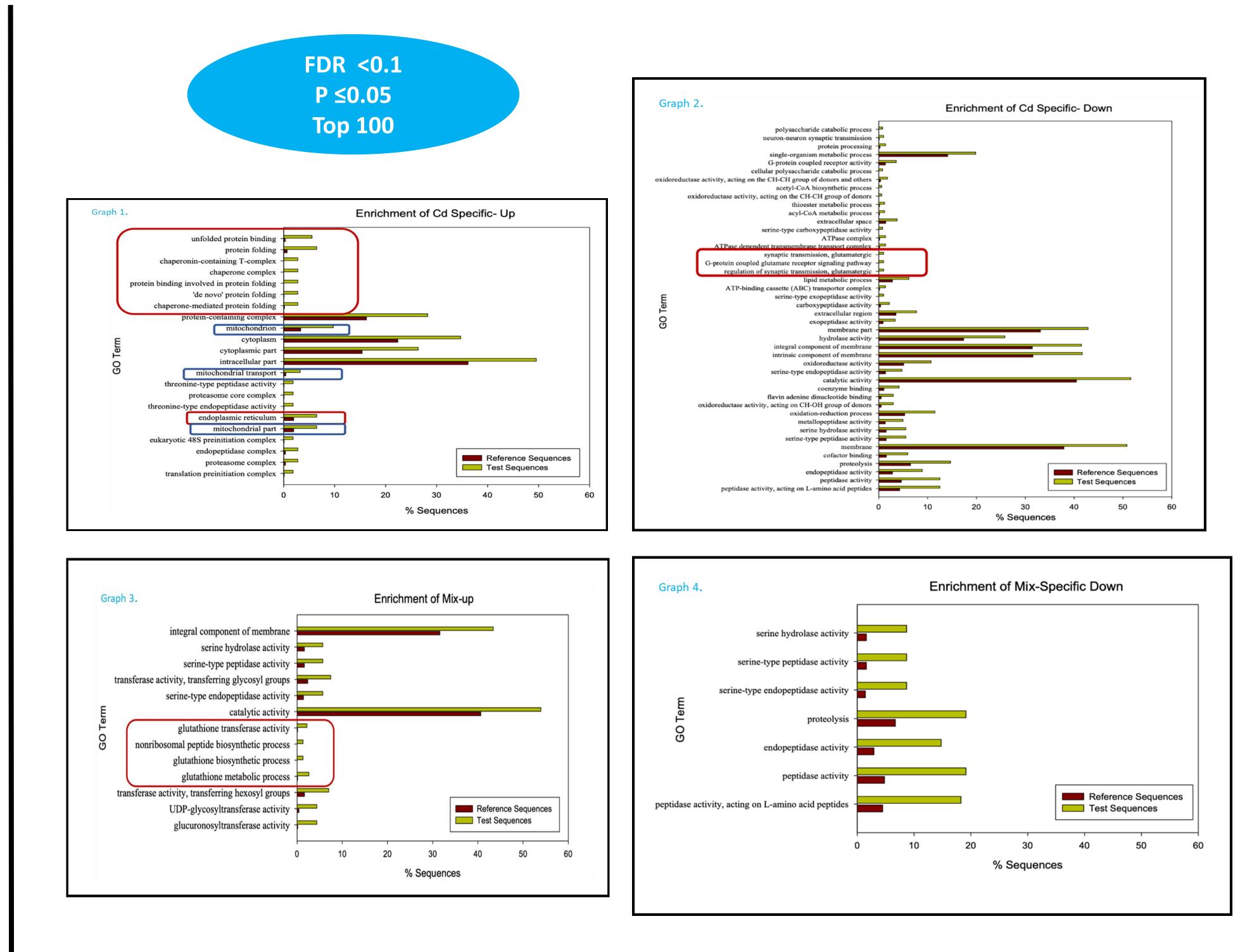


### DISCUSSION

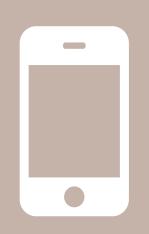
- These findings are consistent with a model in which Cd is still bioavailable in the mixture, but Zn may prevent deleterious physiological effects
- Overall, this work indicates an important role for an internal physiological interaction in the presence of metal mixtures. More work is required to better understand that role.

# **Toxicogenomic** methods may provide a more accurate way to assess the effects of metal mixtures.





Key differentially expressed genes as gene functional groups for each treatment group of D. magna. Graph 1 shows the DEGs for upregulated genes in Cd only treated D. magna. 2 shows the DEGs for downregulated genes in Cd only treated *D. magna*. Graph 3 shows the DEGs for upregulated genes in Cd and Zn mixture treated *D. magna*. Graph 4 shows the DEGs for downregulated genes in Cd and Zn mixture treated *D. magna*.



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