Gene-by-environment interactions and resistance to the embryotoxic effects of PCB-126 and B[a]P in killifish *Fundulus heteroclitus.*

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My research aims to identify the genomic variation underlying the evolved resistance to the embryotoxic effects of dioxin-like compounds and polycyclic aromatic hydrocarbons in populations of killifish, *Fundulus heteroclitus*, living in polluted environments. Identifying the functionally important genetic variation with these compounds will shed light on the wide range of variation in toxicity observed across other vertebrates, and allow for the generation of better hypotheses on the mechanisms of toxicity in early life stage exposures. Resistance to these classes of compounds is associated with the blockade of genes downstream of the aryl hydrocarbon receptor (AHR), an enigmatic pathway that is important for development and response to many environmental contaminants. My goals are to (1) determine if geographically independent populations have evolved compound specific strategies for resistance to dioxin-like-compounds by comparing the phenotypic and gene expression responses to PCB and PAH exposure and (2) Determine the genomic regions that associate with dioxin-like-compound sensitivity using quantitative genetics and transcriptome sequencing of embryological stages of exposure to compare results from population genetic re-sequencing.