

Legacy Arsenic Contamination and its Effects on Gene Expression of the Heat Shock Protein in Sunfish

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Abstract

In 1888 the ASARCO plant was built in Ruston, WA, and it had served its purpose as a smelter and lead-refining company for just over 100 years until it was shut down in 1993. As a result of the smelting activity, arsenic (As) contamination spread across terrestrial and freshwater ecosystems in the South Puget Sound area. This study aimed to look at the effects of legacy contamination from three different lakes with varying levels of As contamination and the effects it can have on the *hsp-70* gene expression of the liver on Bluegill (*Lepomis macrochirus*) and Pumpkinseed sunfish (*Lepomis gibbosus*). Fish were collected from three lakes, Steel Lake with 48 ppm As, and Lake Killarney with over 200 ppm As sediment concentrations, and Pine Lake, which is located outside of the smelter plume zone and served as a reference. RNA was extracted from the liver tissue, a major site for detoxification in the body. *Hsp-70* was used as a target gene because it assists in the folding of polypeptide chains and repairs altered or damaged proteins, and As is a metalloid contamination which can alter protein conformation and function with other proteins leading to tissue damage. A housekeeping gene (*EFl- α*) was used as well, they were amplified using reverse transcriptase PCR and products were visualized using gel electrophoresis. The lake with the highest contamination (Lake Killarney) was predicted to have a greater *hsp-70* expression than fish with no As exposure from Pine Lake. There was no significant difference between the gene expressions across the three lakes. These results may indicate that sunfish are able to adapt to the contaminated environment. There are still many other studies that can be performed to further study the effects of legacy contamination on fish, including analyzing biomarker responses in other tissues as well as other species.