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Metallothionein Expression in Yellow Perch Fish

Abstract

It was hypothesized that yellow perch fish that are exposed to higher concentrations would have an increased MT gene expression in their liver. The yellow perch fish was collected from different lakes with different contamination levels. These lakes are located near the ASARCO plume zone, the three lakes are Pine lake (least contaminated), Steel lake (moderately contaminated), and Lake Killarney (most contaminated). Different experimental methods were used such as the Trizol procedure to extract the RNA and the first-strand cDNA which allows it to be amplified with specific primers using PCR which will be used on the target gene (MT gene) and the housekeeping gene (Beta-actin). The gel electrophoresis results indicated brighter bands in the MT gene compared to the beta-actin. The data densitometry results will be obtained through Image J and the fold ratio will be calculated to semi-quantitatively interpret the data densitometry results. The results showed there was no upregulation of the target gene and that there was no statistical significance MT expression between the 3 lakes.