Aquatic mercury contamination occurs most often as soluble inorganic and insoluble organic compounds. Mercury resistant bacteria detoxify their environments by the enzymatic reduction of soluble Hg(II) to the volatile elemental form Hg(0). The reductase encoded by the *merA* gene of the *mer* operon converts Hg(II) to Hg(0*)*, while the organomercurial lysase encoded by the *merB* gene cleaves organomercury compounds to yield Hg(II).

Because it is important to understand the bioavailability and biological relevance of mercury contamination, a genetic approach will be taken to identify the presence of the mercury reducing genes in microbial communities and to determine if those genes are actively being expressed. *merA* and *B* specific primers will be utilized to amplify samples from a known contamination site, Lavaca Bay, to ascertain the presence of the *mer* operon in bacteria found in aerobic and anaerobic sediments and sea grass epiphytic biofilms. Expression analysis will be conducted by reverse transcriptase polymerase chain reaction (RT-PCR) of the bacterial mRNA to determine the expression level of the *mer* operon genes. Confirmation of expression at a positive control site of expected Hg contamination (Lavaca Bay) will indicate that similar testing at sites of unknown contamination (East Flats and Laguna Madre) is warranted. The addition of the two testing sites may be of particular importance given the expected increase in atmospheric mercury emissions should the proposed construction of the Corpus Christi petroleum coke processing plant, Las Brisas, progress to completion.