MOLECULAR APPROACH FOR TARGETING SPECIFIC FECAL CONTAMINATION IN THE GRAND BAY

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Abstract: Grand Bay National Estuarine Research Reserve (NERR) is an important ecosystem in the Mississippi Gulf Coast. It serves as important nursery areas for juvenile of many species of fish. The bay also used for fishing, crabbing, oyster tagging, boating as well as recreation. Like in other aquatic environments this bay may be contaminated by microorganisms including pathogenic bacteria which play a significant role in the causation of human diseases. The objective of the present study was to track sources of fecal pollution in the Grand Bay waters using enterococcal surface protein (esp), as a marker of human fecal pollution. To achieve this goal, water samples were collected aseptically every month in Bayou Heron, Bayou Cumbest, Middle Bay, and Bangs Lake. Enterococci were concentrated from water samples by membrane filtration. Filters were incubated for 48 hours on mEI Agar (Difco), according to the methodology outlined in USEPA Method 1600. After incubation, DNA was extracted from bacteria colonies on the membrane filters by using QIAamp DNA extraction kit according to manufacturer’s instructions (Qiagen, Inc.). Primers specific for esp gene in Enterococcus faecium were purchased from DNA Intergrated Technologies (IDT). Water samples were also tested for the presence of traditional indicator microorganisms including: heterotrophic plate count (HPC), total coliforms (TC), fecal coliforms (FC) and enterococcus bacteria (ENT). Esp gene was detected in one site of bayou Cumbest, an area where human resides, in other sites of the Grand Bay it was not detected. No Correlation was observed between the presence of the esp gene and concentration of any indicator bacteria. Lower mean numbers of fecal coliform and enterococcus compared to the maximum recommended by federal and the state of Mississippi, do not suggest that water in the Grand Bay cannot be associated with gastrointestinal infections because esp gene were detected in Bayou Cumbest at the time where the number of indicator bacteria were lower compared to the recommended/acceptable standards. The specificity of esp gene from Enterococcus faecium in detecting the source of human fecal pollution warrants useful tool for prediction of public health risks.

Keywords: Pathogenic, Bayous, Membrane filtration, Human health

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