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### THESIS/DISSERTATION INFORMATION

Author (last name, first name): Rodriguez, Sergio

Title: Microbial Source Tracking: Determination of Animal Sources of Enterococci in Oso Creek, Nueces County, Texas

Keywords (please provide at least three keywords that identify the topic of your work): Microbial Source Tracking, MST, Microbiology, Enterococci, Enterococcus, Bacteria, Environmental, Animal Source, Oso Creek, Sergio, Rodriguez, Carbon Source Utilization, Antibiotic Resistance Analysis, Random Forests, Linear Discriminant Analysis, Oso Bay, Waste Water Treatment, Environment, Biolog, Antibiotic Resistance, Toolbox Approach, Fecal Bacteria, Coastal Watershed, Kirby Bauer, Biomic, Animal Hosts, Fecal Contamination, Fecal Pollution, Fecal Indicator, Water Quality, Microbial Identification

Abstract: Enterococci are a genus level group of gram-positive facultative anaerobes found primarily in the intestinal tract of mammals and birds. This characteristic, and their role as fecal indicator bacteria for water quality standards, makes them ideal for use in microbial source tracking (MST) studies. An MST study conducted in a south Texas coastal watershed, involved the creation of a library of carbon source utilization (CSU) and antibiotic resistance profiles (ARP) of enterococci from multiple animal hosts. A total of 1,369 enterococci were isolated from sewage, livestock, domestic, and wild animal fecal samples for the library, and 824 isolates were filtered from creek water and sediments via EPA Method 1600. The MicroLog™ (Biolog Inc.) Microbial Identification System (MIS) was used to create CSU profiles, while ARPs were created using 21 antibiotics through the Kirby-Bauer disk diffusion method and the Biomic™ Microbiology Analyzer. Profiles of animal and creek isolates were compared using two statistical techniques - linear discriminant analysis (LDA) and random forests (RF). Speciation using the MicroLog™ MIS showed certain animals harbored fewer species than others and some Enterococcus spp. were only associated with particular hosts. Combining CSU profiles and ARPs in a toolbox approach, allowed for source identification of creek and sediment enterococci. Both avian (inland species) and non-avian wildlife were found to be responsible for the majority of contamination within the creek using LDA and RF analysis. Models developed using LDA outperformed RF when using both CSU profiles and ARPs. This study demonstrated that using multiple laboratory and statistical methods in a "toolbox" approach, could both characterize and identify animal fecal sources of enterococci from within the environment. These results provide valuable source information for use in developing remediation plans to reduce the levels of contamination in a rural coastal watersheds.

Description (optional, enter any other description or comments here): This research project represents the culmination of over 11 years of graduate student microbial research into indicators, markers, and sources of contamination within the Oso watershed. Sara Heilman, Katie Crysap, Zeke Campbell, Marc Carpenter, Michelle Lindsey, and myself have all labored towards the common goal of microbiologically understanding the Oso watershed within Nueces County, Texas. We have followed the lead of several diligent environmental investigators such as: Joanna Mott, Richard Hay, Roy Lehman, and Brien Nicolau. Their examples have ultimately led us, the students, to utilize science as a tool to discover, examine, and identify microbial contamination within Oso Creek. The conclusion of this project is as much their accomplishment, as is it is mine. Our hope is that one day, this waterway, that hosts numerous human developments as well as both animal and plant habitat, may yet be reclaimed, and that our research may further lead to understanding and development of global water quality.

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