Sewage contamination of our ground and surface waters is a major public health concern. Current indicator bacteria, such as *Escherichia coli* and enterococci, can naturalize in subtropical and tropical environments, ergo better indicator organisms are needed. Furthermore, current indicator bacteria do not discriminate between contamination sources, and hence the application of microbial source tracking (MST) tools is needed for meaningful management decisions.

Several approaches to identify contamination sources exist. Although in theory library-independent molecular PCR marker based methods are applicable worldwide, recent studies have indicated limited host specificity of several bacterial markers. As no marker validation study has been conducted in Hawaii, caution should be used when interpreting results based on source specific bacterial markers developed elsewhere. Application of both molecular and cultivation based techniques and a multi-tiered approach is recommended in many situations. While the application of selected markers is useful, next-generation sequencing based microbial community analysis methods, which have vastly improved over the last years, can now be used to establish more detailed and comprehensive microbial fingerprints associated with potential contamination sources (e.g. wastewater treatment plants, septic systems) and integrated into water quality monitoring programs. Furthermore, the effects of pollution on the environment, or environmental change in general, can be assessed using this type of data as well. This is highly important as our waterways and coastal environments face many challenges today due to population growth, ocean acidification and climate change.