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Multi-laboratory evaluations of the performance of *Catellicoccus marimammalium* PCR assays developed to target gull fecal sources

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ABSTRACT

This manuscript reports results from a multi-laboratory (n = 11) evaluation of four different PCR methods targeting the 16S rRNA gene of *Catellicoccus marimammalium* originally developed to detect fecal contamination from gulls in coastal environments. The methods included conventional end-point PCR, a SYBR® Green qPCR method, and two TaqMan® qPCR methods. Different techniques for data normalization and analysis were also tested. Data analysis methods had a pronounced impact on assay sensitivity and specificity calculations. Across-laboratory standardization of metrics including the lower limit of quantification (LLOQ), target detected but not quantifiable (DNQ), and target not detected (ND) significantly improved results compared to results submitted by individual laboratories prior to definition

standardization. The unit of measure used for data normalization also had a pronounced effect on assay performance. Data normalization to DNA mass improved quantitative method performance as compared to enterococcus normalization. The MST methods tested here were originally designed for gulls, but they also detected feces from other birds, particularly feces from pigeons found at the coast. Some pigeon feces from California were found to contain sequences similar to *C. marimammalium* from gull feces. However, the prevalence, geographic scope, and ecology of *C. marimammalium* in host birds other than gulls are unclear and still require further investigation. This study represents an important first step in the multi-laboratory assessment of these methods and highlights the need to broaden and standardize additional evaluations, including environmentally relevant target concentrations in ambient waters from diverse geographic regions.

Full Text

http://ftp.sccwrp.org/pub/download/DOCUMENTS/AnnualReports/2013AnnualReport/ar13_523_539.pdf