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Comparison of gull feces-specific assays targeting the 16S rRNA gene of *Catellibacillus marimammalius* and *Streptococcus* spp.

Hodon Ryu¹, John F. Griffith, Izhar U.H. Khan², Stephen Hill², Thomas A. Edge², Carlos Toledo-Hernandez³, Joel Gonzalez-Nieves³ and Jorge Santo Domingo¹

¹National Risk Management Research Laboratory, Cincinnati, OH

²National Water Research Institute, Environment Canada, Burlington, Canada

³University of Puerto Rico, Department of Biology, San Juan, Puerto Rico

ABSTRACT

Two novel gull-specific qPCR assays were developed using 16S rRNA gene sequences from gull fecal clone libraries: a SYBR-green-based assay targeting *Streptococcus* spp. (gull3) and a TaqMan qPCR assay targeting *Catellibacillus marimammalius* (gull4). The objectives of this study were: to compare the host specificity of a previous *C. marimammalius* qPCR assay (gull2) with that of the new markers; to examine the presence of the three gull markers in environmental water samples from different geographic locations. Of the 255 gull fecal samples tested, 86% were positive for gull2 and gull4, whereas only 28% were positive with gull3. Low prevalence and abundance of tested gull markers were observed in fecal samples from six non-avian species (n = 180), whereas the assays cross-reacted to some extent with other (non-gull) avian fecal samples. The gull3 assay was positive against fecal samples from 11 of 15 avian species including gull, suggesting that it has a potential to be a general avian marker. Of the presumed gull-impacted water samples (n = 349), 86, 59, and 91% were positive for the gull2, the gull3, and the gull4 assays, respectively. Approximately 5% of 239 non-gull impacted waters were positive with the gull2 and the gull4 assays, whereas 21% were positive for the gull3 assay. While the relatively high occurrence of gull markers in waters impacted by gull feces suggests that these assays could be used in environmental monitoring studies, the data also suggest that multiple avian-specific assays will be needed to accurately assess the contribution of different avian sources in recreational waters.

Full Text

http://ftp.sccwrp.org/pub/download/DOCUMENTS/AnnualReports/2012AnnualReport/ar12_309_322.pdf