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Comparison of gull feces-specific assays targeting the 16S rRNA genes of *Catellicoccus marimammalium* and *Streptococcus* spp.

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ABSTRACT

Two novel gull-specific quantitative PCR (qPCR) assays were developed using 16S rRNA gene sequences from gull fecal clone libraries: a SYBR green assay targeting *Streptococcus* spp. (gull3) and a hydrolysis TaqMan assay targeting *Catellicoccus marimammalium* (gull4). The objectives of this study were to compare the host specificity of a previous *C. marimammalium* qPCR assay (gull2) with that of the new markers and to examine the presence of the three gull markers in environmental water samples from different geographic locations. Most of the gull fecal samples tested (n = 255) generated positive signals with the gull2 and gull4 assays (i.e., > 86%), whereas only 28% were positive with gull3. Low prevalence and abundance of tested gull markers (0.6 to 15%) were observed in fecal samples from six nonavian species (n = 180 fecal samples), whereas the assays cross-reacted to some extent (13 to 31%) with other (nongull) avian fecal samples. The gull3 assay was positive against fecal samples from 11 of 15 avian species, including gull. Of the presumed gull-impacted water samples (n = 349), 86%, 59%, and 91% were positive with the gull2, the gull3, and the gull4 assays, respectively. Approximately 5% of 239 non-gull-impacted water samples were positive with the gull2 and the gull4 assays, whereas 21% were positive with the gull3 assay. While the relatively high occurrence of gull2 and gull4 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.