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Detection of *Stx2* Gene of *Escherichia coli* and Elevated Levels of Fecal Bacteria in the Cattle Farming Regions of Lake Oconee

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ABSTRACT

The presence of Total coliform, *Escherichia coli* and enterococci were enumerated in the cattle farming areas of the Oconee Watershed using colilert™ and enterolert™ IDEXX plates, respectively. Microbial Source Tracking (MST) using *Bacteroidales* molecular markers for ruminant (RuBac) and human (HuBac) specific bacterial groups were used to determine the source of the fecal pollution in the watershed. In the cattle farming regions of the watershed higher levels of fecal bacteria were detected compared to the levels of fecal bacteria at the forested and residential sites. MST indicated that the cattle farming regions (except DC2) of the lake was impacted by fecal pollution from a ruminant source such as cattle. In addition, qPCR for the *tuf* gene of *E. coli* and the *Stx2* gene that is commonly found in enterohemorrhagic *E. coli* O157:H7 were used to evaluate the presence of these bacteria in the study area. *E. coli* O157:H7 (*Stx2* gene) was detected only in the beef cattle regions of the watershed. The presences of *E. coli* and *Stx2* gene in the Oconee Watershed represent a potential public health risk because Lake Oconee and its tributaries are used for recreational activities as well as crop irrigation.

KEYWORDS

 Fecal Bacteria; Oconee Watershed; qPCR; *Escherichia coli*; *Tuf* Gene; Bacteroidale

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