

Evaluating Potential Nonpoint Source Pollution Impacts in the Upper Reaches of the Horse Creek Watershed in Aiken County, SC

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The Horse Creek Watershed (03060106-02) is located in Edgefield and Aiken Counties of South Carolina. The major force of development along Horse Creek was textile mills and mill villages, the first of which was built in 1828, in Vacluse, SC. This community, along with others built downstream, thrived until the collapse of the U.S. textile industry in the late twentieth century. Most Horse Creek Valley textile operations are now closed, resulting in several mill villages with aging or abandoned water and sewer infrastructure. A major target of public health concern within this watershed is Langley Pond, a 285-acre reservoir fed by Horse Creek (Figure 1). This reservoir is extensively used for recreation (e.g., fishing, swimming, and boating) by local residents, most of whom represent a disproportionately impacted low-income, minority population (i.e., a community receiving Environmental Justice consideration).

There have been indicators that this watershed received significant nonpoint source pollutants in the past, and the presence of excess fecal coliform bacteria resulted in its inclusion on SC's 303(d) list of impaired waters beginning in 1998. As a further consequence, the watershed was placed under a TMDL plan for reducing fecal coliform bacteria from nonpoint sources in 2005 (SC DHEC, 2005). It was suspected that the old mill villages within the watershed were experiencing failures with their aging sewer and septic systems; therefore, SC DHEC issued a nonpoint source management grant (a 319 grant) to the Clemson University Extension Service for public outreach and numerous septic repairs within the Horse Creek community. This was followed by a Clean Water State Revolving Fund ARRA project in 2010 to install green infrastructure improvements in downtown Aiken that would reduce stormwater flow and nonpoint source pollution into Horse Creek. The most recent SC DHEC water quality assessment for this area indicated that water quality standards had been attained at all but one monitoring station on Horse Creek (SC DHEC, 2010).

The University of South Carolina Aiken began an undergraduate student monitoring and assessment program in the upper reaches of Horse Creek in January 2011. The goals for this project were as follows:

1. to begin frequent and regular assessment of the number of coliform bacteria (both total and fecal coliforms) in Horse Creek;
2. to implement strategies for microbial source identification of fecal coliforms; and
3. to evaluate and compare phytoplankton community structure in upstream and downstream reservoirs of this portion of the watershed.

Four locations within the watershed were selected for the bacterial study. Two of the sampling locations were in Horse Creek, and two were located in the Sand River tributary (Figure 1). Samples were collected bi-weekly for one year for the enumeration of total coliforms using 3M Petrifilm plates. One milliliter of sample was incubated on each 3M Petrifilm plate for 24 hours at 37°C. It should be noted that this method is not approved for regulatory environmental testing, although studies have illustrated its usefulness as a screening tool and its comparability to standard membrane filtration techniques (Vail et al., 2003; Schraft and Waterworth, 2005; Stepenuck et al., 2011). Observations indicated that Sand River, the tributary draining the Aiken/Hitchcock Woods area of the watershed, contributed the majority of the total coliform bacteria to the upper Horse Creek watershed with averages of 17,400 cfu/100 mL and 15,200 cfu/100 mL for the Dibble Road and Gregg Park sampling locations, respectively.

In 2012, the source tracking study focused on Sand River alone, and the 3M Petrifilm plates were incubated at 44°C for the specific enumeration of fecal coliforms. Using this technique, fecal coliform counts in Sand River averaged 1,200 cfu/100 mL during periods of dry weather. Significant spikes in fecal coliform counts

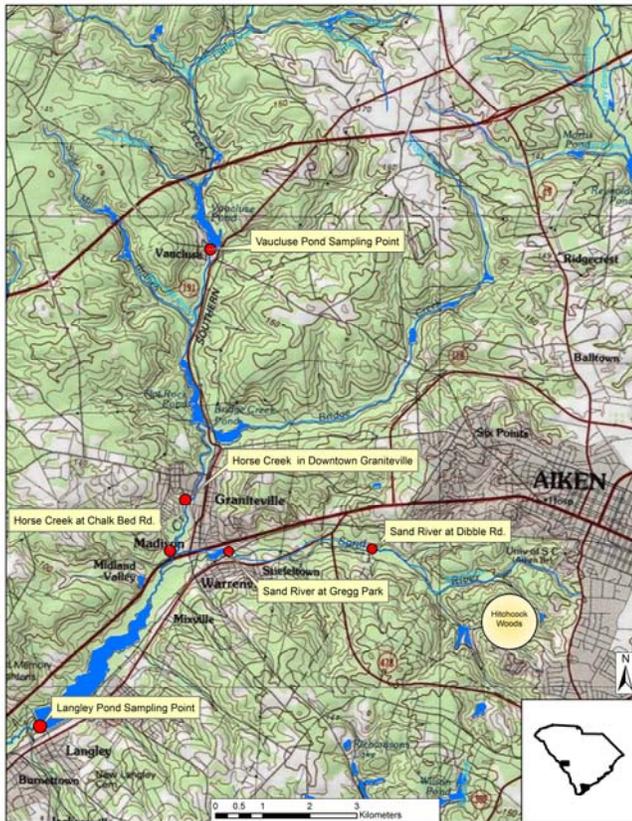


Figure 1. Sampling points in the upper reaches of the Horse Creek watershed are indicated above.

(10,000 - 49,000 cfu/100 mL) were observed after rain events. Based on the 3M Petrifilm technique, the data indicated that fecal bacteria were entering the Horse Creek watershed through Sand River, especially during periods of wet weather. While SC DHEC reports that the issue of excess fecal coliforms in Sand River has been greatly improved since issuing the TMDL in 2005 (SC DHEC, 2010), our results raise interesting questions regarding the source(s) of the pollution which remains.

Sand River has its headwaters in the downtown area of Aiken, SC, before it flows through Hitchcock Woods, a 2100-acre urban forest. The stream then joins Horse Creek immediately upstream of Langley Pond (Figure 1). While the headwater area is within the city limits, a number of older homes in the area still depend upon septic systems. In addition, Aiken boasts a thriving horse industry, with numerous stables in the downtown area, and the major recreational activities within Hitchcock Woods are equestrian in nature. This makes humans and/or horses the most likely sources for fecal pollution in Sand River.

Antibiotic resistance profiles of fecal coliforms isolated from Sand River were evaluated and statistically compared to a library of known fecal sources from the watershed. The known sources included feces from horses, dogs, and waterfowl, as well as untreated sewage

from the Horse Creek Wastewater Treatment Plant (Aiken County Public Service Authority, Beech Island, SC). Approximately 140 isolates from each source were exposed to three concentrations of six antibiotics. When fecal coliform bacteria was isolated from Sand River during July and August 2012 and compared to the library, the majority (>70%) of fecal coliform isolates statistically grouped with sewage, with the remainder grouping with either waterfowl or horses (West et al. 2012). In addition, our lab has isolated genomic DNA from fecal coliform isolates. Using PCR to examine molecular makers, isolates from Sand River have been identified as *Escherichia coli* (Steen et al., 2012). Host-specific molecular makers will be used to determine the source (i.e., human or animal).

The effects of nonpoint source pollutants on the phytoplankton community were evaluated by comparing phytoplankton biomass and makeup in the upstream reservoir (Vaucluse Pond) to the reservoir downstream of the two mill villages and the drainage from Aiken (Langley Pond). The goals were to monitor for the most obvious signs of pollutant effects (algal blooms followed by eutrophication), as well as the more subtle changes in the community structure of the phytoplankton.

The phytoplankton study consisted of bi-weekly sampling from June through October 2011. Basic water chemistry parameters were measured, along with nutrient and chlorophyll *a* concentrations. Functional groups within the phytoplankton community were determined by separating pigments with High Performance Liquid Chromatography (HPLC), and applying the data to a ChemTax software analysis. Nutrients were less than 1 mg/L in all cases throughout the summer, and dissolved oxygen ranged from 4.5 to 9.4 mg/L with no obvious trends other than a typical correlation with temperature.

Chlorophyll *a* concentrations in Langley Pond (downstream) were generally higher than that of Vaucluse Pond during the June to October 2011 study period. There were significant differences between chlorophyll *a* concentrations in the two reservoirs in August through October, with Langley Pond, the downstream reservoir, showing the highest concentrations. The phytoplankton community remained stable in both reservoirs with no indication of nuisance algal blooms or eutrophication.

In summary, phytoplankton biomass, as determined by chlorophyll *a* concentration, was significantly higher in Langley Pond when compared to Vaucluse Pond, but there were no actual differences in the structure of those communities. Sand River was the major contributor of fecal coliform bacteria in the upper reaches of the watershed. Most of the fecal coliform isolates (>70%) from Sand River match the antibiotic resistance profile for sewage. Using genetic markers, fecal coliform isolates from Sand River have been identified as *E. coli*.

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