

Report as of FY2006 for 2006PA64B: "Identification and Enumeration of Pathogenic Bacteriophages in the Waters Surrounding Presque Isle State Park"

Publications

- Conference Proceedings:
 - Smith, Cody and Steven Mauro (2007). Distribution and abundance of shiga toxin indicators in beach waters, in final program of the American Society for Microbiology General 107th Meeting, American Society for Microbiology, Washington, DC, N-202.

Report Follows

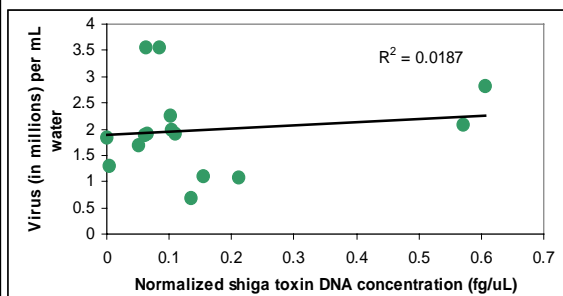
Principal findings and significance

In the summer, fall, and winter months of 2006, our work utilized molecular techniques to identify and enumerate indicators of pathogenic bacteriophages in the waters of and surrounding Presque Isle State Park. The main body of our work focused on utilizing real-time PCR on DNA isolated from beach and stream water samples to quantify the shiga toxin gene, a common indicator of bacteriophages that reside in enterohaemorrhagic *E. coli* responsible for food and water related dysentery.

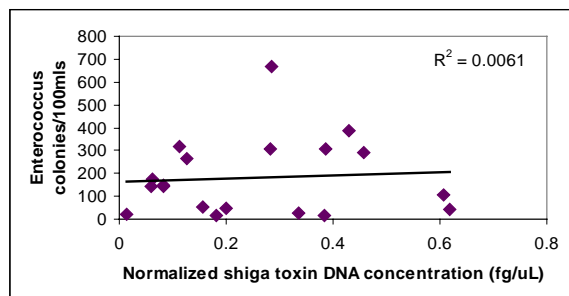
An overall summary of our results finds that a surprisingly large percentage of samples tested positive for the presence of shiga toxin DNA. Specifically, 26% of the over 100 water samples screened contained the shiga toxin marker indicative of the bacteriophages responsible for causing dysentery. However, no sample location continually tested high for shiga toxin DNA, and there was no predictable pattern in the temporal or spatial distribution of this pathogenic bacteriophage indicator. Together, these results suggest that pathogenic bacteriophages are present in our waterways, but are originating and distributed through a currently unknown mechanism.

The high percentage of samples that tested positive for shiga toxin DNA prompted us to examine how the abundance of this indicator of pathogenic bacteriophages relates to numbers of common indicators of microbial pollution, such as total viral and bacterial counts. Our results find no correlation between the amount of shiga toxin DNA in a sample to the number of virus (Figure 1A below) or bacteria (Figure 1B below) in a sample.

Figure One- Abundance of shiga toxin DNA in water samples do not correlate with viral or bacterial numbers



(A.) The total number of viruses present in water samples do not correlate with stx gene frequency (the r-squared value of a linear regression is shown in the upper right corner). Each circle is one of the samples that tested positive for the stx gene.



(B) The total number of *Enterococci* bacteria present in water samples do not correlate with stx gene frequency (r-squared value of a linear regression is shown in the right corner). Each diamond represents one of the samples that tested positive for the stx gene. Other studies not shown demonstrate that total number of *E. coli* or three other bacteria tested also do not correlate with levels of shiga toxin DNA.

These results provide evidence that levels of bacteria that harbor shiga toxin positive bacteriophages will not be adequately accounted for through the use of common assays currently utilized to judge microbial quality in recreational waters. Our results highlight the need for further study that better define the source(s) and pathogenic potential of shiga toxin bacteriophages that we have shown already exist in our heavily

utilized beach and stream waters surrounding Presque Isle and to similarly test these waters for other pathogenic microbial agents.

Students Supported: Cody Smith (Biology major, Bachelor of Science, conferred 2007) and Jayme Dylewski (Biology major, Bachelor of Science, conferred 2007).

Presentations and other information transfer activities: Oral Presentations at: Regional Science Consortium 2nd Annual Meeting (Erie, PA, Fall, 2006), Pennsylvania Academy of Sciences 83rd Annual Meeting (Monroeville, PA, March 2007), Sigma Xi Annual Undergraduate Research Conference (Erie, PA, April, 2007), Our Lake Our Future conference on *E.coli* pollution (Erie, PA, May, 2007), Mercyhurst College Academic Celebration (Erie, PA, May, 2007),

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