Building a Freshwater Bacterial Flora Database for Remote Sensing Applications

Daniel Zimmerman  
*St. John Fisher College*, djz03192@students.sjfc.edu

Laura Moore  
*St. John Fisher College*, lam04586@students.sjfc.edu

J. A. Concha  
*Rochester Institute of Technology*

N. Raqueño  
*Rochester Institute of Technology*

Maryann Herman  
*St. John Fisher College*, mherman@sjfc.edu

*See next page for additional authors*

How has open access to Fisher Digital Publications benefited you?

Follow this and additional works at: https://fisherpub.sjfc.edu/undergraduate_ext_pub

Part of the Biology Commons

Publication Information

https://fisherpub.sjfc.edu/undergraduate_ext_pub/10

Please note that the Publication Information provides general citation information and may not be appropriate for your discipline. To receive help in creating a citation based on your discipline, please visit http://libguides.sjfc.edu/citations.

This document is posted at https://fisherpub.sjfc.edu/undergraduate_ext_pub/10 and is brought to you for free and open access by Fisher Digital Publications at St. John Fisher College. For more information, please contact fisherpub@sjfc.edu.
Building a Freshwater Bacterial Flora Database for Remote Sensing Applications

Abstract
The identification and classification of microbial flora in bodies of fresh water has the potential of enhancing our understanding of this ecosystem and improving water management and bioremediation. This effort may be facilitated by the use of remote sensing technologies. For the last 3 years our undergraduate students have collected water samples in the Lake Ontario Rochester Embayment and Irondequoit Bay with the goal of constructing a database of bacterial species and water parameters (e.g. organic matter and chlorophyl content). Such a database is necessary to establish potential correlations between the presence of certain bacterial species and water parameters that can be measured using satellite imagery collected by the Landsat 8 OLI and TIRS sensors. In the past we reported initial efforts at mapping the distribution of bacterial species using 16S rRNA. Here we present our results for the summer of 2015 and present a compounded analysis of 3 consecutive summers. Of approximately 450 bacterial isolates, we have cultured and identified more than 40 different species spanning over 20 genera. Several fish and human pathogens were identified, and antibiotic-resistance profiles determined. Year to year variation of the flora's composition at individual locations has emerged as the main challenge in establishing reproducible patterns that may be linked to satellite measurements.

Keywords
fsc2016

Disciplines
Biology

Comments
Presented at American Society for Microbiology 116th General Meeting. Boston, MA.

Authors
Daniel Zimmerman, Laura Moore, J. A. Concha, N. Raqueño, Maryann Herman, and Fernando Ontiveros

This poster presentation is available at Fisher Digital Publications: https://fisherpub.sjfc.edu/undergraduate_ext_pub/10
Building a Freshwater Bacterial Flora Database for Remote Sensing Applications

D. Zimmerman*, L.A. Moore*, J.A. Concha†, N. Raqueño†, M.A.B. Herman, PhD*, F. Ontiveros, PhD*
†Rochester Institute of Technology, 1 Lomb Memorial Dr., Rochester, NY 14623 *St. John Fisher College, 3690 East Ave, Rochester, NY 14618

The identification and classification of microbial flora in bodies of fresh water has the potential of enhancing our understanding of this ecosystem and improve water management and isolating candidate organisms for bioremediation. This effort may be facilitated by the use of remote sensing technologies. For the last 3 years we have collected water samples in the Lake Ontario Rochester Embayment & Irondequoit Bay with the goal of constructing a database of bacterial species and water parameters (e.g. organic matter and chlorophyll content). Such a database is necessary to establish potential correlations between the presence of certain bacterial species and water parameters that can be measured using satellite imagery collected by the Landsat OLI and TIRS sensors. In the past we reported initial efforts at mapping the distribution of potential correlations between the presence of certain bacterial species and water parameters (e.g. chlorophyll, total suspended solids (TSS) or erythromycin). We are currently in the process of building meaningful correlations between the presence of individual locations has emerged as the main challenge in establishing reproducible patterns that may be linked to satellite measurements.

**Results**

Given the goal of building a database that would provide statistical support for establishing useful correlations between water parameters (e.g. chlorophyll, total suspended solids (TSS)), we set to isolate and identify a large number of samples over a long period of time at different locations. We collected the samples at the water surface on the same days that the LANDSAT 8 carrying the OLI sensors flew over the sampled area. This was with the objective of being able to compare satellite imagery with ground-truth data. The water samples were filtered and the resulting colonies were isolated, grown in pure cultures and stored for future sequencing/identification. A simple analysis in which the concentrations of water particles and pigments are compared between species of the same genus is shown in Fig. 1. Member of the Acinetobacter genus mostly appear in samples with overall low concentrations. Members of the Pseudomonas, Bacillus and Chryseobacterium genera mostly appear in samples with overall high concentrations (red arrows).

**Methods**

Water samples were collected at the water surface from 12 locations on the Lake Ontario-Rochester Embayment. Water samples were filtered through a 0.2 µm Milipore membrane to separate bacteria. Membranes were placed on R2A plates and incubated at room temperature for 24 hours. Bacterial colonies were then streak plated onto fresh R2A plates and allowed to grow for 24 hours. Bacterial colonies were sub-cultured until pure colonies were obtained. Pure cultures were isolated from samples showing a wide range of concentrations, while members of the Pseudomonas and Exiguobacterium genera mostly appear in samples with overall low concentrations of the parameters measured. Figure 2 displays the sites of collection and the genera found at different locations on different years. Our bacterial library is composed of approximately 450 bacterial isolates, spanning 23 genera and over 80 distinct species. Several plant and animal pathogens have been found, including members of Aeromonas, Enterobacter, Pasteurella, Bacillus, Erwinia, and Pantoea. Among these, strains of Pantoea agglomerans and Pseudomonas azotothrophicus showed resistance to ampicillin and erythromycin. We are currently in the process of building meaningful correlations between the presence of specific species and the parameter that satellite’s sensors can measure. Table 1 displays a real-data example of the database under construction.

**Acknowledgements**

This project was funded by the School of Arts and Sciences at St. John Fisher College, the National Geographic Society and the Chester F. Carlson Center for Imaging Science at the Rochester Institute of Technology.

---

**Table 1. Database Example**

<table>
<thead>
<tr>
<th>Chlorophyll a (mg/m³)</th>
<th>TSS (mg/l)</th>
<th>Species/Genus</th>
</tr>
</thead>
<tbody>
<tr>
<td>&lt;1.00</td>
<td>&lt;2.00</td>
<td>Enterobacter, Aeromonas</td>
</tr>
<tr>
<td>1.00</td>
<td>1.40</td>
<td>Bacillus, Pseudomonas</td>
</tr>
<tr>
<td>1.00</td>
<td>1.72</td>
<td>Rheinheimera, Acinetobacter</td>
</tr>
<tr>
<td>1.00</td>
<td>0.87</td>
<td>Brevundimonas, Exiguobacterium</td>
</tr>
<tr>
<td>3.43</td>
<td>6.60</td>
<td>Planomicrobium, Planomicrobium, Planomicrobium</td>
</tr>
<tr>
<td>8.02</td>
<td>39.10</td>
<td>Bacillus, Exiguobacterium</td>
</tr>
<tr>
<td>9.36</td>
<td>10.80</td>
<td>Streptomyces, Streptomyces</td>
</tr>
<tr>
<td>10.70</td>
<td>4.80</td>
<td>Pantoea, Pantoea</td>
</tr>
<tr>
<td>20.10</td>
<td>5.11</td>
<td>Enterobacter, Enterobacter</td>
</tr>
<tr>
<td>20.10</td>
<td>6.30</td>
<td>Pasteurella, Pasteurella, Pantoea</td>
</tr>
<tr>
<td>38.10</td>
<td>16.70</td>
<td>Aeromonas, Aeromonas, Pantoea</td>
</tr>
<tr>
<td>38.10</td>
<td>21.40</td>
<td>Pseudomonas, Pasteurella</td>
</tr>
<tr>
<td>44.10</td>
<td>22.60</td>
<td>Exiguobacterium, Exiguobacterium</td>
</tr>
<tr>
<td>44.86</td>
<td>154.29</td>
<td>Bacillus, Bacillus</td>
</tr>
</tbody>
</table>

Lake Ontario

- Aeromonas
- Enterobacter
- Rheinheimera
- Pseudomonas
- Bacillus
- Fluvicola

Irondequoit Bay

- Aeromonas
- Enterobacter
- Rheinheimera
- Pseudomonas
- Bacillus
- Fluvicola

Rochester, NY

- Acinetobacter
- Bacillus
- Pseudomonas
- Chryseobacterium
- Curtobacterium
- Exiguobacterium
- Planomicrobium
- Pantoea

Genesee River

- Acinetobacter
- Bacillus
- Exiguobacterium
- Pantoea

Landsat 8 Image

- 2013
- 2014
- 2015
- REPEAT