# OU Sewage Surveillance Team

<table>
<thead>
<tr>
<th>Multi-Disciplinary Team</th>
<th>Working with 5 Oklahoma Municipalities</th>
</tr>
</thead>
<tbody>
<tr>
<td>Only Group in Oklahoma Monitoring Sewage</td>
<td>Monitoring at Different Scales</td>
</tr>
</tbody>
</table>
Sewage Surveillance Benefits

- Timely
- Geographically, Functionally Representative
- Unbiased by Individual Testing
- Cannot Isolate an Individual
Overview: Sewage Surveillance

Discharged → Sampling → Epidemiological correlations & predictions → Metabolism & Excretion → Found in Sewage → Analysis → Sequencing

Sewage Surveillance Process
The quest for representative samples

Sample Collection
Monitoring is Scalable

Wastewater Treatment Facilities

Sub-Sewer Shed
*e.g. Zip Code Level*

OU Norman Dormitories
Sewage Surveillance Process

Sample Collection

Concentrations of SARS CoV-2

Sample Analysis

Extrapolation to Population

Population Level Extrapolation

Modeling / Predictions

Concentrations of SARS CoV-2

Extrapolation to Population

Modeling / Predictions
Sewage predicts community COVID cases

7 days

before they are reported
Sewage Predicts COVID Cases

- Observed (reported) cases
- Predicted cases

COVID-19 cases

- October
- November
- December
- January
- February
## Comparison of Molecular Approaches

<table>
<thead>
<tr>
<th>Who is monitored?</th>
<th>Individual Testing</th>
<th>Wastewater Testing</th>
<th>Individual Sequencing</th>
<th>Wastewater Sequencing</th>
</tr>
</thead>
<tbody>
<tr>
<td>One Person</td>
<td>Group of People</td>
<td>One Person</td>
<td>Group of People</td>
<td></td>
</tr>
<tr>
<td>Detection Output</td>
<td>Yes / No Answer</td>
<td>Concentration</td>
<td>Strain Type</td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
<td>Virus Copies per Liter</td>
<td></td>
<td></td>
</tr>
<tr>
<td>What is amplified?</td>
<td></td>
<td></td>
<td>Multiple Strain Types</td>
<td></td>
</tr>
</tbody>
</table>
Sequencing SARS-CoV-2 genomes from sewage

- Population genomics of SARS-CoV-2
- Composite picture of mutations in ALL genomes in sample
- Monitor prevalence of variants of concern
- Identify areas of Oklahoma experiencing outbreaks of certain variants
Detected mutations in the Spike protein

- **D614G** early mutation, common
- **Q677P** “Pelican” lineage, mainly U.S.
- **Q677H** 6 other U.S. variants, globally distributed
- **E484K** South Africa, Brazil, and New York variants
Detected mutations in the Spike protein

- D614G  early mutation, common
- Q677P  "Pelican" lineage, mainly U.S.
- Q677H  6 other U.S. variants, globally distributed
- E484K  South Africa, Brazil, and New York variants

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<thead>
<tr>
<th>Sample</th>
<th>D614G</th>
<th>Q677P</th>
<th>Q677H</th>
<th>E484K</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>99.4%</td>
<td>33.7%</td>
<td>-</td>
<td>-</td>
</tr>
<tr>
<td>2</td>
<td>98.4%</td>
<td>37.9%</td>
<td>-</td>
<td>25%</td>
</tr>
<tr>
<td>3</td>
<td>98.5%</td>
<td>51%</td>
<td>-</td>
<td>-</td>
</tr>
<tr>
<td>4</td>
<td>99.3%</td>
<td>42.8%</td>
<td>8.3%</td>
<td>3.8%</td>
</tr>
<tr>
<td>5</td>
<td>99.2%</td>
<td>51.2%</td>
<td>24.4%</td>
<td>-</td>
</tr>
<tr>
<td>6</td>
<td>100%</td>
<td>-</td>
<td>-</td>
<td>-</td>
</tr>
<tr>
<td>7</td>
<td>100%</td>
<td>-</td>
<td>-</td>
<td>-</td>
</tr>
<tr>
<td>8</td>
<td>99.4%</td>
<td>51.9%</td>
<td>-</td>
<td>-</td>
</tr>
<tr>
<td>9</td>
<td>99.5%</td>
<td>26.9%</td>
<td>-</td>
<td>-</td>
</tr>
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Sewage Surveillance Utility

Traditional COVID 19 Sewage Surveillance

- Monitor Infection Rates over Time
- Monitor Infection Trends for Different Areas
- Predict Cases

Sewage Surveillance COVID 19 Sequencing

- Detect New Variants
- Direct Follow Up Sequencing
- Monitor Virus Evolution
Thank you for your contributions

The OU Sewage Surveillance Team
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Variant Strains of SARS-CoV-2 Virus – new US Variants

• At least 7 different variants have been identified in the US.
• Some common mutations that may affect spread of the virus.
• Often local spread of the variant strain

https://www.medrxiv.org/content/10.1101/2021.02.12.21251658v1
# Key Variant Strains Identified in the US*

<table>
<thead>
<tr>
<th>Variant Strain</th>
<th>Characteristics</th>
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| United Kingdom (UK) variant known as B.1.1.7 | - Higher rate of transmission which could lead to more cases  
- May be associated with an increased risk of death  
- A recent mutation of the spike protein that could limit the effectiveness of current vaccines |
| South Africa variant known as B.1.351 | - Vaccines currently used in the US may be less effective against this variant (studies pending)  
- More resistant to neutralization by convalescent plasma or by monoclonal antibodies used to treat COVID-19 |
| Brazil variant known as P.1 (1 case identified in Oklahoma) | - Repeat COVID-19 infections reported in Brazil for people who have recovered from prior COVID disease  
- Effectiveness of the current vaccines against this variant is unknown |

*Cases in the US:*

- B.1.1.7 – 1,881 cases (45 states)
- B.1.351 – 46 cases (14 states)
- P.1 – 5 cases (4 states)