Whole genome sequencing (WGS) update/part II

Martin Wiedmann, Dr. med. vet., Ph.D.
Gellert Family Professor of Food Safety
Department of Food Science
Cornell University, Ithaca, NY
E-mail: mw16@cornell.edu
Phone: 607-254-2838
**Take home messages**

- Make sure someone in your organization knows how to use the NCBI Pathogen Detection database
- Have a serious discussion about use of subtyping as part of your environmental monitoring programs
  - Can be WGS or another **reliable** approach
- Consider WGS for root cause analysis of microbial pathogens (beyond *Listeria*, *Salmonella*, and *E. coli*) and spoilage issues
- Do a WGS pilot to test potential partners (labs etc.)
Outline

• NCBI Pathogen Detection database
• Listeria tracking example
• WGS-based characterization of bacteria
COVID-19 is an emerging, rapidly evolving situation.
Get the latest public health information from CDC: https://www.cdc.gov/
Get the latest research from NIH: https://www.nih.gov/coronavirus.

Pathogen Detection BETA

To assist the National Database of Antibiotic Resistant Organisms (NDARO), NCBI Pathogen Detection identifies the antimicrobial resistance, stress response, and virulence genes found in bacterial genomic sequences. This enables scientists to track the spread of resistance genes and to understand the relationships between antimicrobial resistance and virulence.

NCBI Pathogen Detection integrates bacterial pathogen genomic sequences originating in food, environmental sources, and patients. It quickly clusters and identifies related sequences to uncover potential food contamination sources, helping public health scientists investigate foodborne disease outbreaks.

Learn More

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Antimicrobial Resistance Factsheet
Antimicrobial Resistance
Contributors
Help

NCBI Pathogen Detection database

• Industry can do WGS without submitting isolates to NCBI
  • But, FDA may request WGS data if they are aware that WGS is being performed
### Explore the Data

<table>
<thead>
<tr>
<th>Species</th>
<th>New Isolates</th>
<th>Total Isolates</th>
</tr>
</thead>
<tbody>
<tr>
<td>Salmonella enterica</td>
<td>76</td>
<td>271,920</td>
</tr>
<tr>
<td>E. coli and Shigella</td>
<td>10</td>
<td>105,597</td>
</tr>
<tr>
<td>Campylobacter jejuni</td>
<td>4</td>
<td>51,310</td>
</tr>
<tr>
<td>Listeria monocytogenes</td>
<td>8</td>
<td>34,345</td>
</tr>
</tbody>
</table>

See more organisms...
Summary of *L. monocytogenes* data on NCBI (release 1382, August 16, 2019)

<table>
<thead>
<tr>
<th>Total number of isolates</th>
<th>Number of clusters</th>
<th>Number of unclustered isolates (&gt; 50 SNPs to any other isolate in the DB)</th>
<th>Number of human clinical isolates</th>
<th>Number of environmental/food isolates</th>
</tr>
</thead>
<tbody>
<tr>
<td>28,285</td>
<td>2,492</td>
<td>5,508</td>
<td>9,857</td>
<td>18,428</td>
</tr>
</tbody>
</table>

Isolates in the same SNP cluster differ from at least one other isolate in the cluster by at most 50 SNPs.
CONSUMER ALERT: Listeria Monocytogenes Contamination in High Point Dairy Monterey Jack Raw Milk Cheese
2017 DKH Cheese Recalls (Listeria monocytogenes contamination)

Deutsch Kase Haus, LLC of Middlebury, Ind. has announced a voluntary nationwide recall on various cheese products due to the potential for it to be contaminated with Listeria monocytogenes. Deutsch Kase Haus’ action has resulted in several additional product recalls of brands that received cheese from the firm. Below is a list of the recalls that identify Deutsch Kase Haus as their supplier.

Please note this list only includes recalls of FDA-regulated products from brands that named Deutsch Kase Haus as their supplier in their press release. Additionally, some recalled cheeses may not have been supplied by Deutsch Kase Haus, but were further processed in common facilities. For the most complete recall information, consult FDA’s recall page https://www.fda.gov/Safety/Recalls/ and search “cheese.” For USDA-regulated products under recall, see https://www.fsis.usda.gov/wps/portal/fsis/topics
WGS-based characterization of isolates obtained from a single facility over 17 years.
**Reduced quat sensitivity in *L. monocytogenes* strains obtained from a seafood processing plant**

<table>
<thead>
<tr>
<th>Strains</th>
<th>Cluster</th>
<th>&quot;Quat resistance&quot; genes (based on WGS)</th>
<th>MIC* for</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td></td>
<td></td>
<td>BC</td>
</tr>
<tr>
<td>FSL H1-0506</td>
<td>1</td>
<td>None</td>
<td>1 mg/L</td>
</tr>
<tr>
<td>FSL M6-0204</td>
<td>1</td>
<td>qacH</td>
<td>3 mg/L</td>
</tr>
<tr>
<td>FSL H1-0322</td>
<td>2</td>
<td>bcrABC</td>
<td>4 mg/L</td>
</tr>
<tr>
<td>FSL T1-0027</td>
<td>3a</td>
<td>bcrABC</td>
<td>3 mg/L</td>
</tr>
<tr>
<td>FSL T1-0077</td>
<td>3b</td>
<td>bcrABC</td>
<td>3 mg/L</td>
</tr>
</tbody>
</table>

BC = benzalkonium chloride, BZT = benzethonium chloride, CPC = cetylpyridinium chloride; MIC value indicates conditions for which no growth was detected (at the detection threshold OD$_{600nm}$ 0.15) after 24 h of incubation.
Rapid, High-Throughput Identification of Anthrax-Causing and Emetic Bacillus cereus Group Genome Assemblies via BTyper, a Computational Tool for Virulence-Based Classification of Bacillus cereus Group Isolates by Using Nucleotide Sequencing Data

Laura M. Carroll, Jasna Kovac, Rachel A. Miller, Martin Wiedmann
Department of Food Science, Cornell University, Ithaca, New York, USA

Production of hemolysin BL by Bacillus cereus group isolates of dairy origin is associated with whole-genome phylogenetic clade

Jasna Kovac, Rachel A. Miller, Laura M. Carroll, David J. Kent, Jiahui Jian, Sarah M. Beno and Martin Wiedmann
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