Implementation of the VITEK® MS and Its Use in Microbial Identification

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Manager, Scientist, Laboratory Testing Services, ATCC
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About ATCC

- Founded in 1925, ATCC is a non-profit organization with headquarters in Manassas, VA
- World’s premiere biological materials resource and standards development organization
- ATCC collaborates with and supports the scientific community with industry-standard biological products and innovative solutions
- Strong team of 400+ employees; over one-third with advanced degrees
Certification and accreditation

ISO 9001:2008 certification for quality management system
- Demonstrates commitment to quality products, customer service, and continued improvement

ISO 13485:2003 certification for the design, development, production, testing, and distribution of medical devices
- Applies to synthetic molecular standards, the HIV surveillance kit, and other diagnostic and research kits

ISO Guide 34:2009 accreditation for production
- Applies to Certified Reference Materials (CRMs)

ISO/IEC 17025:2005 accreditation for testing
- Applies to all ATCC cultures, derivatives, and bioproducts tested in our laboratories
Deposits come from every continent
- Newly identified species, outbreak strains, type strains, etc.

Grow/expand deposit to a large enough scale to distribute
- Preserve according to the best method for the species
- Some cultures have to be maintained in continuous culture

Confirm identity noted by the depositor
- Minimum test is purity, viability, and sequence
- Goal is two platforms to confirm the item

Worldwide distribution
- Ship frozen/live materials
Identification of microbes – After the 19th century

- What does it look like?
  - Macroscopic
    - Microscopic
- How does it grow?
  - Solid media
  - Suspension
  - Biphasic
  - Temperature
  - Atmosphere
  - Carbon source
    - Metabolic by-products
- What does it smell like?
  - Not recommended
Identification of microbes – After the 19\textsuperscript{th} Century

- How does it stain?
- To name a few:
  - Gram stain
  - Acid-fast stain
  - Gimenez
  - Giemsa
Identification of microbes – Genotypic testing
Identification of microbes – Genotypic testing

- Confirm identity by genotypic methods to the genus and species level
- Sequencing analysis of the 16S rRNA gene
- Fast and reliable, but limited species and strain resolution
- DNA-DNA hybridization
- Ribotyping

There is no concise definition of a species!
Risks of relying on just phenotypic authentication

- Descriptions can be very subjective
- You need to know what tests to apply
- Some genera are biochemically inert
- Time consuming

- Grew anaerobically, 37°C
- Gram-negative rods
- Non-motile
- To differentiate – aerobic growth, catalase, oxidase, motility, variety of carbohydrates, etc.
Risks of relying on just genotypic authentication

Not answered by most genotypic testing:

- Which one is it?
- Does it express the trait I need?
- No consensus on definition of a species at the genetic level. Minimum homology can be from 50% to 70%.

<table>
<thead>
<tr>
<th>Description</th>
<th>Max score</th>
<th>Total score</th>
<th>Query cover</th>
<th>E value</th>
<th>Max ident</th>
</tr>
</thead>
<tbody>
<tr>
<td>Clostridium acetobutylicum strain SS12 16S ribosomal RNA gene, partial sequence</td>
<td>2242</td>
<td>2242</td>
<td>100%</td>
<td>0</td>
<td>100%</td>
</tr>
<tr>
<td>Bacillus anthracis strain R5-331 16S ribosomal RNA gene, partial sequence</td>
<td>2242</td>
<td>2242</td>
<td>100%</td>
<td>0</td>
<td>100%</td>
</tr>
<tr>
<td>Bacillus cereus strain OPP5 3-2 16S ribosomal RNA gene, partial sequence</td>
<td>2242</td>
<td>2242</td>
<td>100%</td>
<td>0</td>
<td>100%</td>
</tr>
</tbody>
</table>

Specimen: BAA-2186_59794805_LuQu
N:Join: 1.0%

- Escherichia coli W3110
- Escherichia coli (ATCC=10536)
- Escherichia coli (ATCC=8739)
- Shigella flexneri (ATCC=29903)
- BAA-2186_59794805
- Escherichia coli O157:H7
ATCC identification – the most robust system possible

ATCC utilizes both classical and modern techniques

- Phenotypic analysis
- Genotypic analysis
- Functional analysis

No single method of identification is sufficient
ATCC identification – Why do we need the most robust system possible?

- Help our customer make the right choice when selecting a catalog item
- Provide the most consistent product possible
- Perform according to the standard
- Comply with local, state, federal, and international regulation

Permits may be required for shipping this product

Distribution requires completion of a Customer Acceptance of Responsibility (CAR) for Commerce Control List Biologicals form.

Customers located in Hawaii will need to contact the Hawaii Department of Agriculture to determine if an Import Permit is required.
Phenotypic testing

Culture Purity and Biochemical Properties

Colony Morphology

Cell Attributes

Biochemical Analysis
Phenotypic testing platforms at ATCC

- API® ID
- Remel RapID™
- Biolog Microbial ID
- VITEK® 2
- Serotyping
- Hundreds of biochemical tests
Functional testing

- Serotype
- Drug Resistance
- Virulence
Functional testing platforms at ATCC

- AST
- Toxin assay
- IFA
- ELISA
- Cytotoxicity assay

Photo credit: James Gathany
Genotypic testing

- Sequencing
- Toxinotyping
- Ribotyping
Genotypic testing platforms at ATCC

- ABI 3500 XL analyzers
  - MicroSeq® database
  - Public databases
  - Sequence provided by the depositor
- PCR
- DuPont™ RiboPrinter®
- Illumina® MiSeq
Steps to the identification of microbes at ATCC

What is the current identification?

Is this a new taxon?

How does it grow?

Is it in a database?

Is it pure?

What tests should we do?

What will this item be used for?

- Culture Purity and Biochemical Properties
- Cell Attributes
- Biochemical Analysis
- Colony Morphology
- Sequeencing
- Toxinotyping
- Ribotyping
- Targeted Gene Sequencing
What is the current identification?
Steps to identification - How does it grow?

How do we grow it?

- Media
- Atmosphere
- Temperature
- Incubation time

- Access to thousands of media formulations
- >15 temperatures available at all times
- Anaerobic chambers
- Cannula system for custom gas mixtures
- Lighted incubators
Steps to identification – Is it pure?

- Contaminants are not tolerated
- We avoid selective media for growth
- We spot check when the material is passaged
- We check all anaerobic cultures for aerobic contaminants
Steps to identification – Is it a new taxon?
Is it described in a database or literature?

- Check depositor information
- Peer reviewed literature
- Text books, such as Bergey’s Manual of Systematic Bacteriology
- Online databases, NCBI, RDP, etc.
- Not every catalog item has been described in depth
- Minimal test is purity, viability, and sequencing
- If we have access, we can confirm 16S rRNA sequence
Steps to identification – What will this be used for?

- Is this a Quality Control strain?
- Can we improve turnaround time?
- What are our customers using?
- Why expand our authentication resources?
How does VITEK® MS compare to current methods?

<table>
<thead>
<tr>
<th>Method</th>
<th>Complexity</th>
</tr>
</thead>
<tbody>
<tr>
<td>API® ID</td>
<td>Moderate</td>
</tr>
<tr>
<td>Biolog Microbial ID</td>
<td>Moderate</td>
</tr>
<tr>
<td>VITEK® 2</td>
<td>Moderate</td>
</tr>
<tr>
<td>Hundreds of biochemical tests</td>
<td>Moderate-Advanced</td>
</tr>
<tr>
<td>ABI 3500 XL analyzers</td>
<td>Advanced</td>
</tr>
<tr>
<td>DuPont™ RiboPrinter®</td>
<td>Moderate</td>
</tr>
<tr>
<td>PCR</td>
<td>Moderate-Advanced</td>
</tr>
<tr>
<td>VITEK® MS</td>
<td>Easy</td>
</tr>
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</table>
## How does VITEK® MS compare to current methods?

<table>
<thead>
<tr>
<th>Method</th>
<th>Turnaround time</th>
</tr>
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<tbody>
<tr>
<td>API® ID</td>
<td>24-48 hours</td>
</tr>
<tr>
<td>Biolog Microbial ID</td>
<td>8 hours</td>
</tr>
<tr>
<td>VITEK® 2</td>
<td>4-6 hours</td>
</tr>
<tr>
<td>Hundreds of biochemical tests</td>
<td>24 hours or longer</td>
</tr>
<tr>
<td>ABI 3500 XL analyzers</td>
<td>1 day</td>
</tr>
<tr>
<td>DuPont™ RiboPrinter®</td>
<td>1 day</td>
</tr>
<tr>
<td>PCR</td>
<td>4 hours</td>
</tr>
<tr>
<td>VITEK® MS</td>
<td>Minutes</td>
</tr>
</tbody>
</table>
How does VITEK® MS compare to current methods?

<table>
<thead>
<tr>
<th>Method</th>
<th>Sample Preparation</th>
</tr>
</thead>
<tbody>
<tr>
<td>API® ID</td>
<td>Fresh, pure</td>
</tr>
<tr>
<td>Biolog Microbial ID</td>
<td>Fresh, pure</td>
</tr>
<tr>
<td>VITEK® 2</td>
<td>Fresh, pure</td>
</tr>
<tr>
<td>Hundreds of biochemical tests</td>
<td>Fresh, pure</td>
</tr>
<tr>
<td>ABI 3500 XL analyzers</td>
<td>Pure</td>
</tr>
<tr>
<td>DuPont™ RiboPrinter®</td>
<td>Pure</td>
</tr>
<tr>
<td>PCR</td>
<td>Pure</td>
</tr>
<tr>
<td>VITEK® MS</td>
<td>Fresh, Pure</td>
</tr>
</tbody>
</table>
How does VITEK® MS compare to current methods?

Sample preparation

- Basic protocol for bacteria:
  - Grow bacteria on a solid surface for isolation
  - Transfer a spot from the colony to the slide
  - Add matrix
  - Allow to dry
  - Read slide
- For fungi, an additional lysis reagent is needed
- Sample prep take less than five minutes
## Interpretation of data

<table>
<thead>
<tr>
<th>Method</th>
<th>Data Output</th>
<th>Ease of Interpretation</th>
</tr>
</thead>
<tbody>
<tr>
<td>API® ID</td>
<td>Genus, species, score</td>
<td>Easy</td>
</tr>
<tr>
<td>Biolog Microbial ID</td>
<td>Genus, species, score</td>
<td>Easy</td>
</tr>
<tr>
<td>VITEK® 2</td>
<td>Genus, species, score</td>
<td>Easy</td>
</tr>
<tr>
<td>Hundreds of biochemical tests</td>
<td>+ or -</td>
<td>Moderate</td>
</tr>
<tr>
<td>ABI 3500 XL analyzers</td>
<td>FASTA File</td>
<td>Complex</td>
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<tr>
<td>DuPont™ RiboPrinter®</td>
<td>Genus, species, score</td>
<td>Easy</td>
</tr>
<tr>
<td>PCR</td>
<td>+ or - / size amplicon</td>
<td>Easy-Moderate</td>
</tr>
<tr>
<td>VITEK® MS</td>
<td>Genus, species, score</td>
<td>Easy</td>
</tr>
</tbody>
</table>
How does VITEK® MS compare to current methods?

## Interpretation of data – Biochemical results

<table>
<thead>
<tr>
<th>Assay</th>
<th>L. grayi</th>
<th>L. innocua</th>
<th>L. ivanovii</th>
<th>L. monocytogenes</th>
</tr>
</thead>
<tbody>
<tr>
<td>Mannitol</td>
<td>+</td>
<td>-</td>
<td>-</td>
<td>-</td>
</tr>
<tr>
<td>L-Rhamnose</td>
<td>-</td>
<td>d</td>
<td>-</td>
<td>+</td>
</tr>
<tr>
<td>Soluble starch</td>
<td>+</td>
<td>-</td>
<td>-</td>
<td>-</td>
</tr>
<tr>
<td>D-xylose</td>
<td>-</td>
<td>-</td>
<td>+</td>
<td>-</td>
</tr>
<tr>
<td>B-hemolysis</td>
<td>-</td>
<td>-</td>
<td>+</td>
<td>+</td>
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</tbody>
</table>
How does VITEK® MS compare to current methods?

Interpretation of data – VITEK® 2 card

<table>
<thead>
<tr>
<th>Identification Information</th>
<th>Card: GN</th>
<th>Lot Number: 241287420</th>
<th>Expires: Oct 27, 2014 13:00 EDT</th>
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<tbody>
<tr>
<td>Completed: Jun 27, 2014 15:48 EDT</td>
<td>Status: Final</td>
<td>Analysis Time: 8.00 hours</td>
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</tr>
</tbody>
</table>

Selected Organism

Klebsiella pneumoniae ssp rhinoscleromatis

96% Probability

Blonumber: 6205710542560200

Confidence: Excellent identification

Analysis Organisms and Tests to Separate:

SRF Organism

Analysis Messages:

Contraindicating Typical Biopattern(s)

Klebsiella pneumoniae ssp rhinoscleromatis

CMT(11).

Biochemical Details

<table>
<thead>
<tr>
<th>2</th>
<th>APPA</th>
<th>3</th>
<th>ADO</th>
<th>+</th>
<th>4</th>
<th>PyrA</th>
<th>+</th>
<th>5</th>
<th>IARL</th>
<th>-</th>
<th>7</th>
<th>dCEL</th>
<th>+</th>
<th>9</th>
<th>BCAL</th>
<th>-</th>
</tr>
</thead>
<tbody>
<tr>
<td>10</td>
<td>H2S</td>
<td>-</td>
<td>11</td>
<td>BNAG</td>
<td>-</td>
<td>12</td>
<td>AGLT</td>
<td>-</td>
<td>13</td>
<td>dGLU</td>
<td>+</td>
<td>14</td>
<td>GGT</td>
<td>-</td>
<td>15</td>
<td>OFF</td>
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<tr>
<td>17</td>
<td>BGLU</td>
<td>+</td>
<td>18</td>
<td>dMAL</td>
<td>+</td>
<td>19</td>
<td>dMAN</td>
<td>+</td>
<td>20</td>
<td>dMNE</td>
<td>+</td>
<td>21</td>
<td>BXYL</td>
<td>-</td>
<td>22</td>
<td>BAlap</td>
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<tr>
<td>23</td>
<td>ProA</td>
<td>-</td>
<td>26</td>
<td>LIP</td>
<td>-</td>
<td>27</td>
<td>PLE</td>
<td>-</td>
<td>29</td>
<td>TyrA</td>
<td>+</td>
<td>31</td>
<td>URE</td>
<td>-</td>
<td>32</td>
<td>dSOR</td>
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<tr>
<td>33</td>
<td>SAC</td>
<td>-</td>
<td>34</td>
<td>dTAG</td>
<td>-</td>
<td>35</td>
<td>dTRE</td>
<td>+</td>
<td>36</td>
<td>CIT</td>
<td>-</td>
<td>37</td>
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<td>+</td>
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<td>5KG</td>
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<tr>
<td>40</td>
<td>ILATk</td>
<td>+</td>
<td>41</td>
<td>AGLU</td>
<td>-</td>
<td>42</td>
<td>SUCT</td>
<td>+</td>
<td>43</td>
<td>NAGA</td>
<td>-</td>
<td>44</td>
<td>AGAL</td>
<td>+</td>
<td>45</td>
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<tr>
<td>46</td>
<td>GlyA</td>
<td>-</td>
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<td>ODG</td>
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<td>48</td>
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<td>53</td>
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<td>-</td>
<td>56</td>
<td>CMT</td>
<td>+</td>
<td>57</td>
<td>BGUR</td>
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<tr>
<td>58</td>
<td>C129R</td>
<td>-</td>
<td>59</td>
<td>GGAA</td>
<td>-</td>
<td>51</td>
<td>IMLTa</td>
<td>+</td>
<td>62</td>
<td>ELM</td>
<td>-</td>
<td>84</td>
<td>ILATa</td>
<td>-</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>
How does VITEK® MS compare to current methods?

Interpretation of data – MicroSeq® database search

<table>
<thead>
<tr>
<th>Specimen</th>
<th>Library</th>
<th>Library Entry Name</th>
<th>% Match</th>
<th>Consensus Length</th>
<th>Library Entry Length</th>
<th>Total Mismatches</th>
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</thead>
<tbody>
<tr>
<td>6908 622520 91_SaLi</td>
<td>AB_BacterialF ullGeneLib_2.0</td>
<td>Klebsiella pneumoniae rhinoscleromatis (ATCC=13884)</td>
<td>100.0</td>
<td>812</td>
<td>1488</td>
<td>0</td>
</tr>
<tr>
<td>6908 622520 91_SaLi</td>
<td>AB_BacterialF ullGeneLib_2.0</td>
<td>Klebsiella pneumoniae ozenzae (ATCC=11296)</td>
<td>99.61</td>
<td>812</td>
<td>1488</td>
<td>4</td>
</tr>
<tr>
<td>6908 622520 91_SaLi</td>
<td>AB_BacterialF ullGeneLib_2.0</td>
<td>Klebsiella pneumoniae (ATCC=10031)</td>
<td>99.48</td>
<td>812</td>
<td>1457</td>
<td>5</td>
</tr>
<tr>
<td>6908 622520 91_SaLi</td>
<td>AB_BacterialF ullGeneLib_2.0</td>
<td>Klebsiella pneumoniae pneumoniae (ATCC=13883)</td>
<td>99.48</td>
<td>812</td>
<td>1488</td>
<td>4</td>
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<tr>
<td>6908 622520 91_SaLi</td>
<td>AB_BacterialF ullGeneLib_2.0</td>
<td>Enterobacter cancerogenus (ATCC=33241)</td>
<td>99.11</td>
<td>812</td>
<td>1488</td>
<td>9</td>
</tr>
</tbody>
</table>
How does VITEK® MS compare to current methods?

Interpretation of data – API® strip

![API LISTERIA V1.2 Identification Result](image)

**Reference**

DATE 7/14

**Comment**

19113_52671205

**Good Identification**

<table>
<thead>
<tr>
<th>Strip</th>
<th>API LISTERIA V1.2</th>
</tr>
</thead>
<tbody>
<tr>
<td>Profile</td>
<td>0 5 10</td>
</tr>
</tbody>
</table>

**Significant taxa**

<table>
<thead>
<tr>
<th>Listeria monocytogenes</th>
<th>% ID</th>
<th>Test value</th>
</tr>
</thead>
<tbody>
<tr>
<td>98.6</td>
<td>1.0</td>
<td>Tests against</td>
</tr>
</tbody>
</table>

**Next taxon**

<table>
<thead>
<tr>
<th>Listeria innocua</th>
<th>% ID</th>
<th>Test value</th>
</tr>
</thead>
<tbody>
<tr>
<td>1.3</td>
<td>0.68</td>
<td>DIM 95%</td>
</tr>
</tbody>
</table>
How does VITEK® MS compare to current methods?

Interpretation of data – VITEK® MS
How does VITEK® MS compare to current methods?

### Database

<table>
<thead>
<tr>
<th>Method</th>
<th>Data Output</th>
<th>Size of database</th>
</tr>
</thead>
<tbody>
<tr>
<td>API® ID</td>
<td>Genus, species, score</td>
<td>&gt;300</td>
</tr>
<tr>
<td>Biolog Microbial ID</td>
<td>Genus, species, score</td>
<td>&gt;1500</td>
</tr>
<tr>
<td>VITEK® 2</td>
<td>Genus, species, score</td>
<td>&gt;400 species</td>
</tr>
<tr>
<td>Hundreds of biochemical tests</td>
<td>+ or -</td>
<td>?</td>
</tr>
<tr>
<td>ABI 3500 XL analyzers</td>
<td>FASTA File</td>
<td>?</td>
</tr>
<tr>
<td>DuPont™ RiboPrinter®</td>
<td>Genus, species, score</td>
<td>&gt;1400</td>
</tr>
<tr>
<td>PCR</td>
<td>+ or - / size amplicon</td>
<td>NA</td>
</tr>
<tr>
<td>VITEK® MS</td>
<td>Genus, species, score</td>
<td>&gt;2000</td>
</tr>
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</table>
How does VITEK® MS compare to current methods?

**Expandability**

<table>
<thead>
<tr>
<th>Method</th>
<th>Size of database</th>
<th>Can we expand the database?</th>
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<tbody>
<tr>
<td>API® ID</td>
<td>&gt;300</td>
<td>No</td>
</tr>
<tr>
<td>Biolog Microbial ID</td>
<td>&gt;1500</td>
<td>No</td>
</tr>
<tr>
<td>VITEK® 2</td>
<td>&gt;400 species</td>
<td>No</td>
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<td>Hundreds of biochemical tests</td>
<td>?</td>
<td>No</td>
</tr>
<tr>
<td>ABI 3500 XL analyzers</td>
<td>?</td>
<td>Yes</td>
</tr>
<tr>
<td>DuPont™ RiboPrinter®</td>
<td>&gt;1400</td>
<td>Yes</td>
</tr>
<tr>
<td>PCR</td>
<td>NA</td>
<td>NA</td>
</tr>
<tr>
<td>VITEK® MS</td>
<td>&gt;2000</td>
<td>Yes</td>
</tr>
</tbody>
</table>
### Summary – Methods

<table>
<thead>
<tr>
<th>Method</th>
<th>Complexity</th>
<th>Turnaround Time</th>
<th>Sample Preparation</th>
<th>Ease of Interpretation</th>
<th>Size of the Database</th>
</tr>
</thead>
<tbody>
<tr>
<td>API® ID</td>
<td>Moderate</td>
<td>24-48 hours</td>
<td>Fresh, pure</td>
<td>Easy</td>
<td>&gt;300</td>
</tr>
<tr>
<td>Biolog Microbial ID</td>
<td>Moderate</td>
<td>8 hours</td>
<td>Fresh, pure</td>
<td>Easy</td>
<td>&gt;1500</td>
</tr>
<tr>
<td>VITEK® 2</td>
<td>Moderate</td>
<td>4-6 hours</td>
<td>Fresh, pure</td>
<td>Easy</td>
<td>&gt;400 species</td>
</tr>
<tr>
<td>Hundreds of biochemical tests</td>
<td>Moderate-Advanced</td>
<td>24 hours or longer</td>
<td>Fresh, pure</td>
<td>Moderate</td>
<td>?</td>
</tr>
<tr>
<td>ABI 3500 XL analyzers</td>
<td>Advanced</td>
<td>1 day</td>
<td>Pure</td>
<td>Complex</td>
<td>?</td>
</tr>
<tr>
<td>DuPont™ RiboPrinter®</td>
<td>Moderate</td>
<td>1 day</td>
<td>Pure</td>
<td>Easy</td>
<td>&gt;1400</td>
</tr>
<tr>
<td>PCR</td>
<td>Moderate-Advanced</td>
<td>4 hours</td>
<td>Pure</td>
<td>Easy-Moderate</td>
<td>NA</td>
</tr>
<tr>
<td>VITEK® MS</td>
<td>Easy</td>
<td>Minutes</td>
<td>Fresh, Pure</td>
<td>Easy</td>
<td>&gt;2000</td>
</tr>
</tbody>
</table>
How does VITEK® MS compare to current methods?

Installation:
- Required only one modification to change an electrical socket
- Reset climate control to 68°F to ensure proper functioning of machine
- Very few moving parts of the machine, can be remotely monitored and manipulated if needed

Training:
We have over ten people trained on the use of the machine. We used a ‘train the trainer approach’ where one of our team members went to the bioMérieux training and is responsible for training our staff in sample preparation and machine usage.
Implementation into the ATCC Process

Receive material

Did we receive the right thing?

- Morphology/Microscopic observation
- Sequence analysis
- VITEK® MS
- VITEK® MS
- Sequence analysis
- API® ID
- Remel RapID™
- Biolog Microbial ID
- VITEK® 2
- Serotyping
- Hundreds of biochemical tests

Grow &Preserve material

Is it pure?

- Morphology/Microscopic observation
- Sequence analysis
- VITEK® MS
- API® ID
- Remel RapID™
- Biolog Microbial ID
- VITEK® 2
- Serotyping
- Hundreds of biochemical tests
- PCR
- DuPont™ RiboPrinter®

Authenticate material

Authenticate the material
Challenges to implementation?

- Developing protocols for broth grown cultures
- Developing protocols for filamentous fungi
- There will always be slash calls

*There is no concise definition of a species!*
Conclusion

- VITEK® MS is a user-friendly platform
- Training is straightforward with some practice required
- Data is easy to interpret
- It has one of the largest, curated databases available
- Sample preparation is comparable to other methods currently being used
- Turnaround time is faster than other methods currently being used
- Installation was simple

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Thank you for joining today!

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- **October 29, 2015**  
  10:00 AM, 3:00 PM EST  
  Barry R. Bochner, Ph.D., CEO & CSO, Biolog, Inc.  
  High Resolution Phenomic Analysis of Microbial and Mammalian Cells

- **November 12, 2015**  
  10:00 AM, 3:00 PM EST  
  Bill Hirt, Ph.D., Director of Accreditation, ANAB  
  How Does ISO 17025 Accreditation Build International Confidence?

Please email additional questions to: tech@atcc.org