**REVIEWED ABSTRACT**

Background: Automated systems are commonly used to identify bacterial pathogens seen in veterinary practice although performance limitations are recognized. We evaluated the sensitivity and specificity of the Sensititre ARIS 2X (TREK Diagnostic Systems) and Vitek 2 (bioMérieux) systems compared with existing laboratory methods on a contemporary collection of bacterial isolates.

Methods: Bacterial isolates (459 total) recovered in 2010 from companion and other animals were tested using Sensititre® (GFP) and GNID, and Vitek 2 (G2 and GN) identification panels. Results were compared with existing laboratory biochemicals. Consensus was defined as ≥2 systems producing matching results; other results were considered discordant.

Results: A total of 1373 identifications were analyzed (see Table). Overall, 83.5% and 85.1% of isolates were identified to the correct genus and species levels, respectively; genus- and species-level accuracy was 93.5% and 83.4%, respectively. Genus and species of isolates included Escherichia coli, Klebsiella spp., Proteus mirabilis, and Enterococcus spp. (27 species from both systems). Species-level identifications were problematic for Pseudomonas aeruginosa, Actinobacillus equuli, and other 35 genera.

Conclusions: The Sensititre ARIS 2X and Vitek 2 systems produced a high level of accurate identification at the genus level (both systems 93.5%) but less well at the species level (83.4% compared with Vitek 2 (97.4%)).

**MATERIALS & METHODS**

**Isolation & Species Groups**

<table>
<thead>
<tr>
<th>Isolate Species/Groups</th>
<th>n</th>
<th>Sensititre ARIS 2X</th>
<th>Vitek 2</th>
<th>No Agreement Between Methods</th>
</tr>
</thead>
<tbody>
<tr>
<td>Actinobacillus pleuropneumoniae</td>
<td>90</td>
<td>99.2</td>
<td>70.8</td>
<td>97.8</td>
</tr>
<tr>
<td>Actinobacillus pleuropneumoniae</td>
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<td>85.2</td>
<td>40.7</td>
<td>96.3</td>
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<tr>
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<td>90.2</td>
<td>62.5</td>
<td>96.3</td>
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<tr>
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<td>100</td>
<td>100</td>
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<tr>
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<td>37</td>
<td>95.8</td>
<td>95.8</td>
<td>100</td>
</tr>
<tr>
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<td>95.0</td>
<td>95.0</td>
<td>100</td>
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<tr>
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<td>92.9</td>
<td>92.9</td>
<td>100</td>
</tr>
<tr>
<td>Proteus mirabilis</td>
<td>100</td>
<td>100</td>
<td>100</td>
<td>97.0</td>
</tr>
</tbody>
</table>

**RESULTS**

- **Bacterial isolates**: A total of 459 veterinary pathogen isolates (all from year 2010) were recovered from companion and other animals. These included Escherichia coli (20 isolates), Klebsiella spp. (24 isolates), Proteus mirabilis (33 isolates), Pseudomonas aeruginosa (38 isolates), and other genera.

- **Sensitivity and Specificity**: The Sensititre ARIS 2X and Vitek 2 systems provided very acceptable species-level identifications for E. coli (95.8% and 100%, respectively), Klebsiella spp. (95.0% and 100%), Proteus mirabilis (89.2% and 98.3%), and other genera.

- **Discordance**: There was greater discordance at the genus level (93.5%) compared with the species level (83.4%). The Vitek 2 system was better able to identify P. aeruginosa (97.4%) at the species level than was the Sensititre ARIS 2X (86.8%). Vitek 2 produced a better level of agreement between Systems (93.5%) compared with Vitek 2 alone (89.2%).

- **Implementing automated systems for identification of bacterial pathogens**

**CONCLUSIONS**

- The Sensititre ARIS 2X and Vitek 2 systems produced an acceptable level of identification of bacterial pathogens overall at the genus level (both systems 93.5%) but less well at the species level (83.4% and 85.1%) when compared with each other and the standard laboratory identification algorithm (Table 1).

- **Limitations**:
  - **Discordance**: There was greater discordance at the genus level (93.5%) compared with the species level (83.4%). The Vitek 2 system was better able to identify P. aeruginosa (97.4%) at the species level than was the Sensititre ARIS 2X (86.8%). Vitek 2 produced a better level of agreement between Systems (93.5%) compared with Vitek 2 alone (89.2%).
  - **Species identifications**: The Sensititre ARIS 2X and Vitek 2 systems were most problematic for other Enterobacteriaceae (79.3% and 74.1%, respectively), non-fermentative bacilli (54.5% and 57.6%), and coagulase-negative staphylococci (40.7% and 51.9%, Tables 1 and 2).

**SELECTED REFERENCES**


**ACKNOWLEDGMENTS**

This investigation was supported in part by TREK Diagnostic Systems and bioMérieux, Inc.