Comparative Evaluation of the BD Phoenix Yeast ID Panel and Remel RapID Yeast Plus System for Yeast Identification

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Becton Dickinson Phoenix Yeast ID Panel was compared to the Remel RapID Yeast Plus System using 150 recent clinical yeast isolates and the API 20CAUX system to resolve discrepant results. The concordance rate between the Yeast ID Panel and the RapID Yeast Plus System (without arbitration) was 93.3% with 97.3% (146/150) and 95.3% (143/150) of the isolates correctly identified by the Becton Dickinson Phoenix and the Remel RapID, respectively, with arbitration.

1. Introduction

Epidemiology of invasive fungal infections is evolving. Fungemia is now the fourth leading cause of bloodstream infections [1–3] with an increasing number of Candida yeast infections from non-albicans species [4–6]. These infections may be associated with high morbidity and mortality rates [7–10]; however, enhanced preventive measures, earlier detection, and implementation of proper treatment [4, 11] have slowly improved disease outcomes. Nevertheless, the increasing development of candidemia and cryptococcal infection resistance to fluconazoles and other azoles [1, 2, 6, 11–14] underscores the urgent need for accurate and rapid detection methods. New identification platforms like matrix-assisted laser desorption/ionization time of flight mass spectrometry (MALDI-ToF MS) and DNA sequence based methods are promising solutions [15], but their high cost and limited organism databases have kept traditional commercial phenotypic tests as the main identification method for yeast and in most clinical laboratories. These tests range from labor-intensive manual panels to newer automated detection systems.

The purpose of this study was to compare the performance of the automated Becton Dickinson (BD, Sparks, MD) Phoenix Yeast ID Panel (Phoenix) to a manual Remel RapID Yeast Plus System (RYP, Remel, Thermo Fisher Scientific, Lenexa, KS). The BD Yeast ID Panel, first introduced in 2011, is for use on the Phoenix Microbiology System. The BD Yeast ID Panels are self-inoculating molded polystyrene trays containing 3 control wells (1 negative fluorescent control and 2 positive fluorescent control) and 47 wells with dried biochemical substrates that use traditional qualitative microbiology methods such as fermentation, oxidation, degradation, and hydrolysis in combination with chromogenic and fluorogenic substrates along with carbon sources for identification. Previous studies demonstrated an accuracy of 94.4% and 84% [16, 17]. The RYP is a qualitative micromethod that uses 18 conventional and chromogenic substrates for identification. In previously published studies, RYP has demonstrated accuracies within 77–97% [18–22].
2. Methods

150 yeasts and isolates encompassing 11 species were tested. Isolates were obtained from clinical samples (blood, urine, tissue, CSF, pleural fluid, and bronchial aspirate) collected from patients at Temple University Hospital, in Philadelphia, PA, over a 6-month period. Specimens were subcultured to Sabouraud-Emmons dextrose agar plates (Remel, Thermo Fisher Scientific, Lenexa, KS) and incubated at 30°C for 24 or 48 hours as required by Phoenix and RYP, respectively. All study isolates were simultaneously tested with the BD Phoenix and RYP systems, according to the instructions of each ID panel. While the BD Phoenix result was automated, the RYP system required reaction interpretation based on color changes that were used to obtain a numeric code for a computer database of yeast. This analysis was performed by 2 individuals simultaneously. Both systems produced a result with a confidence indicator. A result was accepted for the Phoenix if the confidence value was >90%, while results listed as implicit, satisfactory, or adequate were accepted for RYP. If an unacceptable result was obtained for either test, both tests were repeated and the results from the additional run were used if they met the criteria. If the Phoenix and RYP results were in agreement, the isolate was considered correctly identified. Where Phoenix and RYP systems disagreed, the isolate was further analyzed by the API 20C AUX system, which utilized corn meal morphology and colorimetric tests for conventional assimilation substrates, actidione resistance, and phenoloxidase production. The identification made by two of the three systems was considered correct.

3. Results

Table 1 shows species identified by the two systems. The four most common species were C. albicans (27%), C. glabrata (26%), C. tropicalis (19%), and C. parapsilosis complex (13%). Overall, the Phoenix and RYP agreed for 140 of the 150 isolates (93.3%). Of the 10 discrepancies, the reference test (API) agreed with the Phoenix for 6 isolates and the RYP for 3 isolates. These results were not statistically significant (Z-score 0.948; approximate \( P = 0.1736 \)) and are similar to a recently published study by Gayibova et al. who demonstrated 88% concordance with API ID 32C AUX system [23]. Neither study utilized molecular or proteomic identification of the yeast isolates; therefore, determinative sensitivity, specificity, and positive and negative predictive values were not appropriate for this evaluation.

Phoenix incorrectly identified 3 frequently encountered clinical yeast isolates (2 Candida spp. and 1 Cryptococcus sp., Table 2). Two isolates of C. glabrata (accuracy for C. glabrata 94.9%) and 1 isolate of C. tropicalis (accuracy for C. tropicalis 96.4%) were misidentified and a Cryptococcus laurentii was identified by the Phoenix as a Trichosporon asahii. Two C. glabrata were misidentified by the Phoenix as C. firmetaria, and one C. tropicalis was misidentified as

### Table 1: Identification results obtained with the Phoenix and RYP systems for 150 clinical yeast isolates.

<table>
<thead>
<tr>
<th>Species (number tested)</th>
<th>Number (%) of isolates with indicated result</th>
<th>Identified</th>
<th>Misidentification</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td></td>
<td>Phoenix</td>
<td>Phoenix</td>
</tr>
<tr>
<td></td>
<td></td>
<td>RYP</td>
<td>RYP</td>
</tr>
<tr>
<td>C. albicans (41)</td>
<td></td>
<td>41</td>
<td>0</td>
</tr>
<tr>
<td>C. glabrata (39)</td>
<td></td>
<td>37</td>
<td>2</td>
</tr>
<tr>
<td>C. tropicalis (28)</td>
<td></td>
<td>27</td>
<td>1</td>
</tr>
<tr>
<td>C. parapsilosis (19)</td>
<td></td>
<td>19</td>
<td>0</td>
</tr>
<tr>
<td>C. krusei (8)</td>
<td></td>
<td>8</td>
<td>0</td>
</tr>
<tr>
<td>C. neoformans (8)</td>
<td></td>
<td>8</td>
<td>0</td>
</tr>
<tr>
<td>C. lipolytica (1)</td>
<td></td>
<td>1</td>
<td>0</td>
</tr>
<tr>
<td>C. albida (1)</td>
<td></td>
<td>1</td>
<td>0</td>
</tr>
<tr>
<td>C. laurentii (1)</td>
<td></td>
<td>0</td>
<td>1</td>
</tr>
<tr>
<td>T. asahii (1)</td>
<td></td>
<td>1</td>
<td>0</td>
</tr>
<tr>
<td>Total (150)</td>
<td></td>
<td>146 (97.3)</td>
<td>4 (2.7)</td>
</tr>
<tr>
<td></td>
<td></td>
<td>143 (95.3)</td>
<td>7 (4.7)</td>
</tr>
</tbody>
</table>

*After arbitration using API 20C AUX.

### Table 2: Discrepant identifications by Phoenix and RYP systems for 10 yeast isolates.

<table>
<thead>
<tr>
<th>Reference*</th>
<th>Identification method</th>
<th>(number misidentified)</th>
</tr>
</thead>
<tbody>
<tr>
<td>C. glabrata</td>
<td>Candida glabrata</td>
<td>Candida firmetaria (2)</td>
</tr>
<tr>
<td>Cryptococcus laurentii</td>
<td>Trichosporon asahii (1)</td>
<td>Trichosporon beigelli (1)</td>
</tr>
<tr>
<td>C. parapsilosis</td>
<td>Candida guilliermondii (1)</td>
<td></td>
</tr>
<tr>
<td>C. tropicalis</td>
<td>Candida lumbica (2)</td>
<td></td>
</tr>
<tr>
<td>T. asahii</td>
<td>Candida lusitaniae (1)</td>
<td></td>
</tr>
<tr>
<td>T. pelliculosa</td>
<td>Candida zeylanoides (1)</td>
<td></td>
</tr>
</tbody>
</table>

*Identifications were confirmed by using API 20C AUX.
a *C. pelliculosa*. Repeat testing of the *C. glabrata* isolates (by the Phoenix) was identified correctly while *C. tropicalis* remained incorrect. Previous studies demonstrated 100% accuracy when identifying *C. glabrata* but only 93.3–100% with *C. tropicalis* [16, 17]. The initial misidentification of *C. glabrata* by the Phoenix may be of some concern since it is the second most common cause of fungemia in the USA [4] whose susceptibility to commonly used therapies fluconazole and amphotericin B is decreasing [3].

In this evaluation, the RYP misidentified 3 yeast isolates into 7 yeast organisms (Table 2). *Candida parapsilosis* was identified by the RYP into five yeast isolates representing four *Candida* spp. (*C. guilliermondii, C. lamberca, C. lusitaniae,* and *C. zeylanoides*) resulting in 73.7% accuracy for the identification of *C. parapsilosis* using this system. After repeat testing, the misidentified isolates were correctly identified in 3 of the 5 isolates. This rate of misidentification for *C. parapsilosis* was not reported previously [18–22]. The remaining misidentifications by the RYP consisted of a *Cryptococcus laurentii* identified as a *Trichosporon beigelii* and a *Trichosporon asahii* identified as a *Trichosporon beigelii*.

Both the Phoenix and the RYP systems were unable to identify one isolate of *Cryptococcus laurentii* but instead speciated it into a *Trichosporon* species. As per manufacture instructions, the BD Phoenix requires growth on blood agar to identify *C. laurentii* and no recommendations were made for RYP. Therefore, the isolate was subcultured on blood agar and retested in parallel. Both the Phoenix and the RYP correctly identified the isolates that were grown on blood agar. Although *C. laurentii* is known as a biopesticide, clinical infections from it have been reported most commonly in immunosuppressed patients [24]. Therefore, the use of media not recommended by the manufacturer could result in erroneous identification of this unusual organism. Won et al. tested *C. laurentii* isolates with the Phoenix using both media (Sabouraud and blood agars) and the Phoenix was able to identify each one correctly [16]. The significance of the media for certain isolates of *C. laurentii* needs to be further elucidated.

**4. Conclusion**

In summary, the automated Phoenix is comparable to the manual RYP system with a concordance rate of 93.3%. Posteraro and Won demonstrated accuracies for the Phoenix of 94.4% and 84% (using 250 and 351 yeast isolates, resp.). These combined results support the reliability of the Phoenix system. However, it should be noted that if the yeast isolates from the previous two studies were divided into common yeast species and the rare yeast species the accuracy of the Phoenix varied significantly: 98–98.2% for commonly encountered species and 70–76% for rarely encountered species [16, 17]. This suggests that larger databases may be needed to improve discrimination among rarely encountered yeast species. Previous studies also demonstrated quicker turnaround times when compared to other manual and automated systems. The Phoenix required 4–15 hours for identification after growth for 24 hours [17], while the manual RYP and API systems require a minimum of 52 hours (RYP) and 96 hours (API). Therefore, the Phoenix system appears to be a comparable yeast identification system while requiring less incubation time, ultimately allowing for quick and reliable results.

**Disclosure**

A part of this study was presented at the 102nd Annual Meeting of the United States and Canadian Academy of Pathology (USCAP), March 2–8, 2013, Abstract number 1561, Modern Pathology 26: Supp. number 2, p 373A, February 2013.

**Competing Interests**

The authors declare that they have no competing interests.

**Acknowledgments**

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**References**


[8] M. Morrell, V. J. Fraser, and M. H. Kollef, “Delaying the empiric treatment of *Candida* bloodstream infection until positive


