

# Evaluation of the Becton Dickinson Phoenix and bioMérieux VITEK Legacy Automated Microbiology Identification and Antimicrobial Susceptibility Systems.

K.G. Snow et al.

Walter Reed Army Medical Center and Armed Forces Institute of Pathology

## REVISED ABSTRACT

The Phoenix (Becton Dickinson, Sparks, MD) and the VITEK Legacy (bioMérieux, Durham, NC) are designed as automated, “walk-away” instruments, and promise rapid results for both identification (ID) and antimicrobial susceptibility testing (AST). We compared the Phoenix against our VITEK Legacy for accuracy of bacterial ID and AST using clinical isolates from our institution and a set of known challenge isolates with complex identification and/or susceptibility phenotypes. We tested a total of 200 Gram-positive and Gram-negative isolates for ID and AST. Accuracy of results was defined as agreement between the two systems or individual agreement to the known reference phenotype if available. Identification discrepancies were resolved by restriction enzyme digestion and fingerprint analysis on the Qualicon RiboPrinter (DuPont, Wilmington, DE). Where applicable, AST discrepancy resolution was performed by Etest (AB Biodisk, Solna, Sweden). Identification was confirmed for 182 of 200 isolates tested on each system with a final resolved accuracy of 91% and 82% for Phoenix and VITEK, respectively. For those same 200 isolates, AST yielded a total of 28 discrepant results from a total of 15 isolates. Twelve of the 28 AST discrepant results were tested by Etest with 8 and 4 results in agreement with Phoenix and VITEK, respectively. Five of the 28 AST discrepant results involved system software expert rule implementation. Two discrepancies involved ESBL interpretation, with arbitration resulting in 1 isolate in agreement with VITEK and 1 isolate in agreement with Phoenix. The final 9 AST discrepant results were unresolved due to a lack of confirmatory test capability. In this study the BD Phoenix was more accurate than the VITEK Legacy for both ID and AST of bacteria commonly isolated in our laboratory and a set of previously characterized challenge isolates.

## INTRODUCTION

Automated methods for identifying bacterial isolates and testing antimicrobial susceptibility have, in recent years, become the de facto norm in most clinical laboratories. Laboratories seeking to combine ease of use, rapid turnaround time, and cost savings have driven the demand for new generations of instrumentation. The Phoenix System (Becton Dickinson, Sparks, MD) is the most recent addition to the list of available diagnostic instruments for the clinical microbiology laboratory, and promises greater ease of use, greater reliability, and faster turnaround time, compared to other currently available instruments. The Phoenix system utilizes a combination of fluorogenic and chromogenic substrates for its identification algorithms, a broth-based AST method that utilizes a redox indicator to enhance detection (at 20 minute intervals), and a robust data processing application (the Phoenix EpiCenter).

We compared the Phoenix against our VITEK Legacy (bioMérieux, Durham, NC) for accuracy of bacterial ID and AST using clinical isolates from our institution and a set of known challenge isolates with complex identification and/or susceptibility phenotypes. We tested a total of 200 Gram-positive and Gram-negative isolates for ID and AST. Accuracy of results was defined as agreement between the two systems or individual agreement to the known reference phenotype if available. Identification discrepancies were resolved by ribotyping and AST discrepancies by MIC determination.

## METHODS

Two hundred isolates were submitted for identification (ID) and susceptibility testing (AST) on both the VITEK Legacy instrument and the BD Phoenix instrument. Isolates were obtained from either clinical specimens collected at Walter Reed Army Medical Center (86 isolates), or from reference collections submitted by the instrument manufacturers (90 isolates provided by Becton Dickinson, 24 isolates provided by bioMérieux). Isolates were tested concurrently on both instruments, using identical colonies. Instrument quality control was performed and recorded according to the manufacturers' instructions. Isolates were cultured from frozen stock or from lyophilized material onto 5% sheep blood agar plates, and frozen (after testing) at -70°C in 10% Trypticase Soy Broth.

Identification results that did not match between instruments were identified as discrepant (regardless of previous characterization). These discrepancies were resolved at the Armed Forces Institute of Pathology (AFIP) using an automated restriction enzyme digestion and fingerprint analysis on the Qualicon Riboprinter system (DuPont, Wilmington, DE). Thirty-seven isolates were flagged as ID discrepant, with 18 tested at the AFIP; 19 flagged isolates were not tested due to the inability of the Qualicon system to resolve certain genera in its installed configuration.

## METHODS continued

Discrepant AST results (any isolates exhibiting differences between systems in measured susceptibility results) were resolved using the E-test epsilometer assay (AB Biodisk, Solna, Sweden). Sixteen isolates were flagged as discrepant, with a total of 33 discrepant results. Of the 16, 6 were not tested due to the unavailability of E-tests for the antibiotics in question. Of the tested isolates, 14 of 27 were resolved (the remaining 13 discrepancies were either the result of expert rule interpretations or represented antibiotics for which E-tests were unavailable).

Both test systems include assays for the presence of extended-spectrum beta-lactamases (ESBL). ESBL discrepant results were resolved using Kirby Bauer disk diffusion methodology.

Quality control procedures for the RiboPrinter (ID discrepancy analysis), for the E-test assay (AST discrepancy analysis), and for Kirby Bauer disk diffusion (ESBL discrepancy analysis) were performed and recorded according to manufacturers' instructions or according to CLSI recommendations.

## RESULTS

### IDENTIFICATION

- One hundred and five Gram-negative isolates and 95 Gram-positive isolates (200 total) were tested on both the Phoenix and VITEK systems. Fourteen Gram-negative isolates and 23 Gram-positive isolates were identified as different organisms by the two systems and were flagged as ID discrepant. Discrepancies also included three Gram-positive isolates that were submitted as previously characterized challenge isolates (by the instrument manufacturers), but which were identified differently from the "known" result (with the instruments in agreement). Isolates that were identified in agreement with previous characterization (i.e. were part of a submitted challenge set), but were not verified by 16s characterization (due to limitations of the RiboTyper system) were considered correctly identified by the system in agreement.
- Isolates that were characterized as "coagulase negative *Staphylococcus*" in a submitted challenge set, but were identified to species level by a particular instrument, were considered discrepant if the species identification did not match arbitration.
- Of the 37 flagged discrepant, 17 were unresolved, due to problems with organism viability or limitations of the Qualicon RiboPrinter system. Of the resolved discrepancies (either by 16s characterization or by comparison to previous characterization), 19 were in agreement with the Phoenix system, and 1 was in agreement with the VITEK Legacy system.
- Of the 200 tested isolates, the Phoenix system correctly identified 182 (91%) and the VITEK Legacy system correctly identified 164 (82%). Of the 183 arbitrated isolates, the percentage of correct identification was 99% and 90% for the Phoenix and VITEK Legacy systems respectively.

### ANTIMICROBIAL SUSCEPTIBILITY TESTING

- Of the 200 isolates tested, antimicrobial susceptibility results were in agreement (identical MICs for drugs tested on both instruments) in 124 instances. Sixty-one of the discrepant results resulted from differences of one dilution (that did not alter interpretation) or were considered minor errors, and were not flagged for arbitration.
- Of the 15 isolates flagged for further testing, two involved discrepancies in testing for the presence of extended-spectrum beta-lactamases. Arbitration favored VITEK in one case and the Phoenix system in the second.
- Three of the tested isolates (with a total of 5 flagged discrepancies) were flagged for discrepant interpretations, resulting from application of system expert rules. Arbitration was not performed in these cases. One of these isolates (Study #63) exhibited 3 of the flagged discrepancies (with 1 discrepancy flagged as a MAJOR interpretation error). These discrepancies resulted from ESBL expert rule interpretation. In this case, ESBL arbitration favored the VITEK system. In the other two flagged isolates (Study #65 and #66), both discrepancies involved expert rule interpretations of sulfamethoxazole-trimethoprim (SXT) results of *Acinetobacter* isolates by the Phoenix system.
- Four of the unresolved discrepant AST results (four discrepant isolates) involved interpretation of nitrofurantoin. These discrepancies were unresolved due to the unavailability of nitrofurantoin E-test strips. The discrepancies were notable, though, in that they represented MAJOR errors of interpretation, and in that they reflected an observed pattern of the two systems with regard to nitrofurantoin (of the 105 Gram-negative isolates, 25 exhibited discrepant nitrofurantoin results, with the Phoenix system interpretations generally averaging 1 dilution higher than the both the VITEK system and predicted Phoenix values).
- Of the 12 flagged results (from 8 isolates), arbitration favored the Phoenix in 8 cases (66%), and the VITEK system in 4 (33%).

## CONCLUSIONS

- Bacterial ID on the BD Phoenix system was more accurate than the bioMérieux VITEK Legacy System with final arbitration yielding 91% vs 82% correct identification, respectively.
- Susceptibility testing on the Phoenix system was more accurate than the VITEK Legacy with final arbitration of isolates yielding 66% vs 33% AST errors, respectively.
- Determination of antimicrobial phenotypic characteristics, specifically the presence of extended-spectrum beta-lactamases, was comparable (based on accuracy) between the two systems.
- The Phoenix system demonstrated unresolved interpretations of nitrofurantoin ASTs in Gram-negative isolates. Results were generally one dilution higher than the known result and occasionally resulted in major errors of interpretation.
- Overall, the Phoenix system was considered to be more accurate than the VITEK Legacy system for both ID and AST.