Comparison of the APAS Independence Automated Plate Reader System with manual standard-of-care for processing urine culture specimens

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BACKGROUND

Urine cultures are amongst the highest volume tests run in clinical microbiology laboratories and usually require considerable manual labor to perform. We analyzed the APAS Independence Automated Plate Reader System's ability to expedite quality results while reducing manual steps required to process urine cultures by comparing its performance to that of the standard-of-care (SOC) for processing urine cultures. The APAS Independence System provides an automated image analysis using artificial intelligence to interpret growth from urine culture plates and sorts them based on the presence or absence of significant growth.

METHODS

Urine cultures were inoculated onto Sheep's Blood Agar and MacConkey Agar Plates using the Copan WASP before being incubated at 37ºC for 18 hours. The incubated plates were loaded onto the APAS Independence to be sorted based on their growth patterns. The plates were then manually reviewed to confirm the APAS's designations. Identification of organisms was performed using the Bruker MALDI-TOF and antibiotic susceptibility testing was performed using the BD Phoenix M50 System. The antibiotic susceptibility data was compared to the SOC. Minimal Inhibitory Concentration (MIC) and SIR interpretations were used to calculate Categorical (CA) and Essential Agreements (EA).

PLATFORMS

Urine culture plates were sorted using the APAS Independence from Clever Culture Systems. The organisms were identified using the Bruker MALDI-TOF and the antibiotic susceptibilities were performed using the BD Phoenix M50. The APAS urine culture results and workflow were compared to the standard-of-care (SOC). Up to 240 plates can be loaded onto the APAS Independence at a time and up to 200 plates can be sorted and imaged per hour.

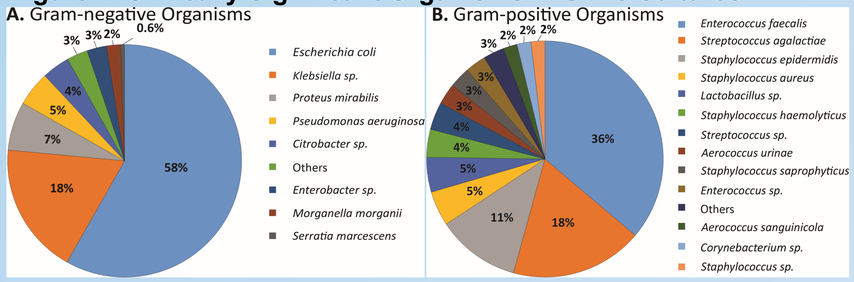
RESULTS

Table 1. Positive and Negative Culture Growth Patterns

Growth Pattern	Number (Percentage of total)
Total Number of Enrolled Specimens	1,519
Total Number of Positive Cultures	993 (65.37%)
Total Number of Negative Cultures	526 (34.63%)
Total Number of Growth Discrepancies Between Positive Cultures	74 (7.45%)
Total Number of Growth Discrepancies Between Negative Cultures	0 (0.00%)

We enrolled 1,519 urine specimens into the study. 993 of the specimens had clinically significant growth and 526 of the specimens showed no significant growth (<5 CFU/mL). We then evaluated the growth and found no discrepancies amongst those with clinically insignificant growth, and 74 amongst those with clinically significant growth. Only 1 discrepancy was clinically significant.

Figure 1. Clinically Significant Organisms In Urine Cultures



We identified a variety of Gram-negative (Panel A) and Gram-positive (Panel B) bacteria from the positive urine cultures. The majority of the Gram-negative bacteria were *E. coli*, followed by high numbers of *Klebsiella sp.*, *Proteus sp.*, and *P. aeruginosa*, amongst others. The Gram-positive bacteria largely consisted of *E. faecalis* followed by *S. agalactiae, S. epidermidis*, and *S. aureus*, amongst others. There were 56 total urine specimens (3.69%), where discrepancies were identified between the SOC and the APAS workflows. 41 (75%) of those discrepancies were in additional pathogens identified via the APAS workflow, and 14 (25%) were in additional pathogens identified via the SOC workflow. We did not identify specimens in which the identification of specific pathogens were inconsistent.

Table 2. ASTs for Gram-positive and Gram-negative Bacteria

	Number of Organisms	Number of Reported Antibiotics	EA	CA	mE	ME	ME
Gram Positive	105	341	341 (100%)	337 (98.83%)	0	0	0
Gram Negative	519	7,604	7,527 (98.99%)	7,388 (97.16%)	136 (1.71%)	41 (0.52%)	36 (0.45%)

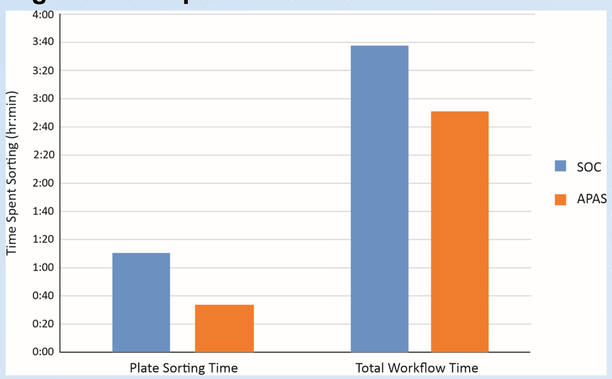
There was high essential (EA) and categorical agreement (CA) between the SOC and APAS workflows for both Gram-positive and Gram-negative bacteria. Of all the ASTs performed, there were 41 ME and 36 VME identified. These errors belonged to relatively few isolates.

Table 3: SOC and APAS Binning Times

		Duration (hr:min:sec)	No. Plates	Time per Plate (sec)
SOC	Day 1	3:30:00	460	46
	Day 2	2:30:00	364	41
	Day 3	3:00:00	480	38
	Mean Binning Time per Plate (sec)			**42**
APAS	Day 1	0:20:22	72	17
	Day 2	0:49:22	171	17
	Day 3	0:20:05	72	17
	Mean Binning Time per Plate (sec)			**17**

We examined urine cultures over 3 days and determined the time it took for a plate to be categorized. On average, the APAS spent 17 seconds to designate a plate into its respective bin (No Growth, Doubtful, Probable, and Review), whereas the SOC required 42 seconds.

Figure 2. Comparison of Work Time



When examining the APAS and SOC workflows, we found that the APAS resulted in 37 fewer minutes of hands-on-time in processing urine plates and an overall difference of approximately 52 minutes from sample to answer for approximately 141 plates.

CONCLUSIONS

- Relatively few urine specimens (7.45%; 74/993) had detectable growth discrepancies when comparing the SOC and APAS workflows. Most of these discrepancies (75%; 42 discrepancies) involved the identification of additional pathogens in the APAS workflow.
- Of the 1,519 specimens evaluated, we identified a number of different Gram-positive and gram-negative bacteria.
- There was significant CA and EA for Gram-positive and Gram-negative bacteria, along with 41 ME and 36 VME. Most of the ME and VME belonged to a small number of bacteria, suggesting that different isolates with differing susceptibilities were found between the APAS and SOC workflows.
- The APAS workflow resulted in reduced hands-on-time for processing urine specimens with the potential for added FTE savings.