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

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Disclaimer

- This study was supported by Clever Culture Systems, Inc.

- UC San Diego Health was compensated for their participation in this study.

Goals for this presentation

- Introduce the APAS Independence System.
- Identify how automation might contribute to urine culture processing.
- Provide an overview of our study/feasibility data.
- Identify how the APAS Independence System may fit into laboratory workflow.

APAS Independence Instrument

- Automated interpretation of urine culture plates.
- Uses artificial intelligence to interpret growth patterns.
- Can interpret and bin plates with no growth (don't have to be manually analyzed).
- Interprets No Growth, Probable Growth, and Review.
- Our instrument was not interfaced for this study.

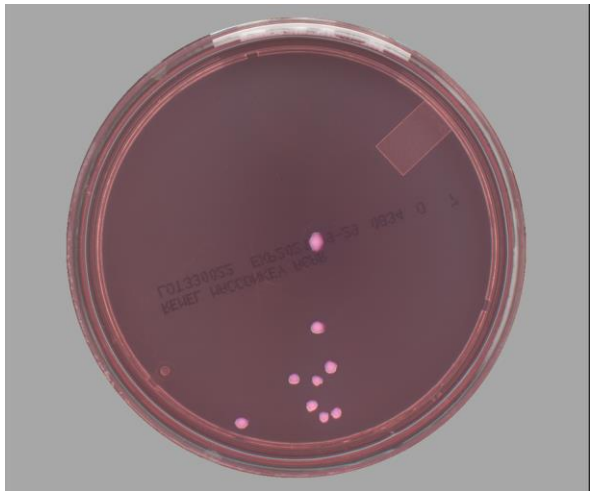
Study Design

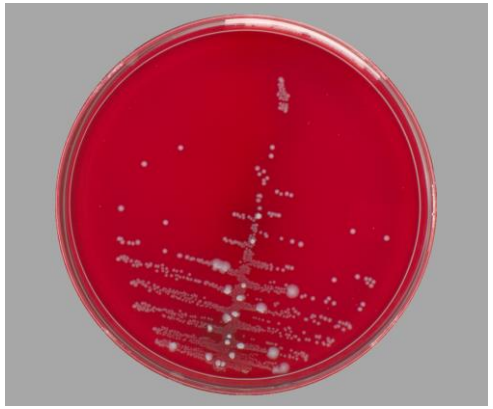
- Performed the study over the course of 4-months in 2021.
- Planted specimens twice using the COPAN Wasp Instrument.
  - Once for our standard-of-care workflow.
  - Once for a workflow including the APAS Independence System.
- Examined growth according to our standard of care and compared that with growth evaluations from the APAS system.
- Identifications performed in both workflows using the Brucker Maldi Biotyper.
- Also performed ASTs using the BD Phoenix M50 in both workflows.
- Examined processing times for both workflows.

In this study

Growth pattern discrepancies	
Growth Pattern	**Number (Percentage)**
Total number of enrolled specimens	1,519
Total number of matching growth patterns	1,445 (95.13%)
Total number of discrepancies	74 (4.87%)
Total number of clinically significant discrepancies	2 (0.13%)

- We identified a high proportion of matching growth pattern evaluations
- There were <5% growth pattern discrepancies
  - Only 2 of the specimens with growth pattern discrepancies resulted in differing pathogen identifications.





APAS designated as Review

- If no growth, is designated as no growth
- If growth, the plate may be designated:
  - Probable or
  - Review

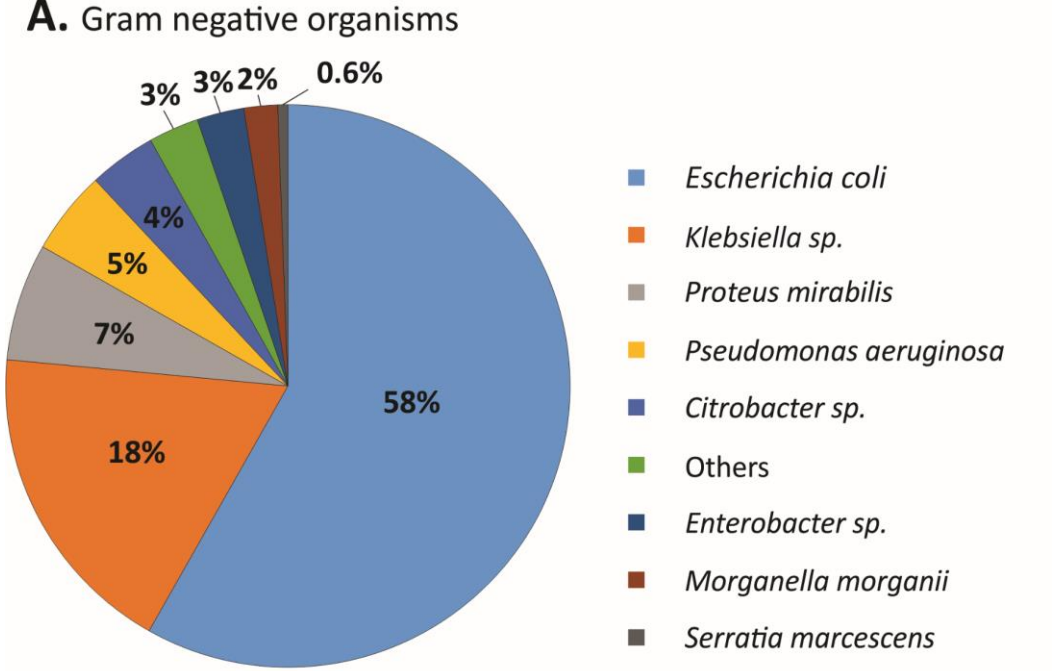
Results

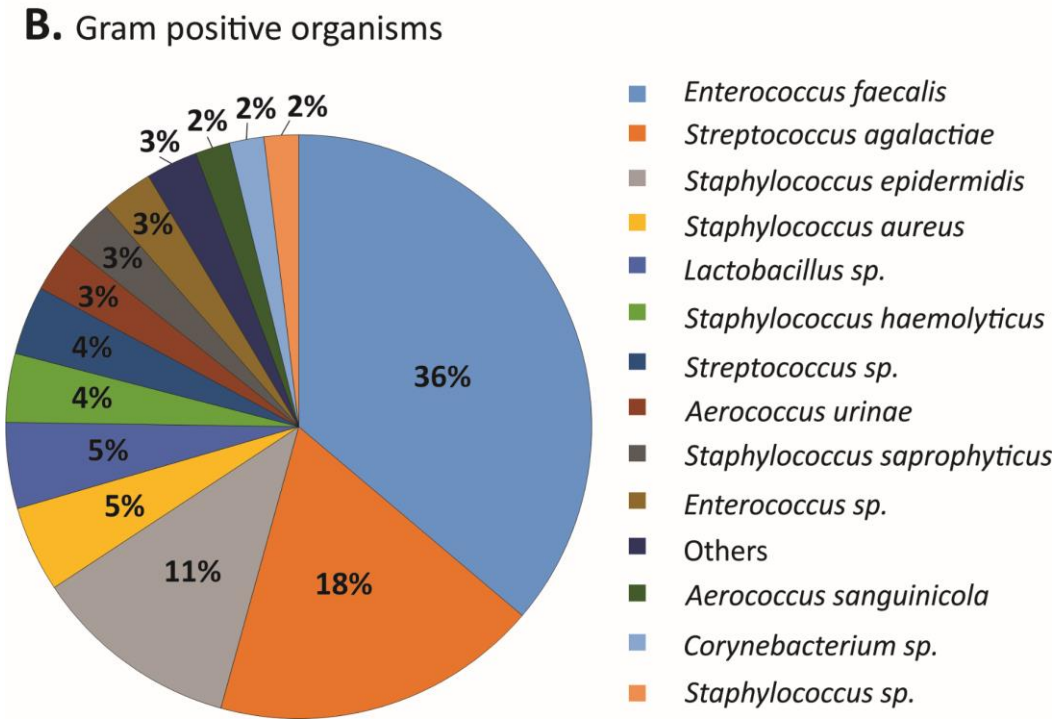
- High percentage of urine culture positives
  - Largely due to our complicated patient population.
  - High numbers of nephrostomies
  - High numbers of neobladders
  - High numbers of catheterized patients
- Found very few discrepancies (3.69%) in bacterial identifications between the workflows.
- Found few discrepancies in antimicrobial resistance (2.69% overall)

Date	Number of Cultures	Number of Positive Cultures	ID Discrepancies	Antibiotics Reported	AST Discrepancies	mE	ME	VME
7/15/2021	73	39	2	349	6	6	0	0
7/23/2021	82	50	4	330	17	8	8	1
7/27/2021	58	25	2	216	12	3	1	8
7/30/2021	79	41	4	396	13	7	3	3
8/4/2021	82	59	2	513	15	14	1	0
8/10/2021	62	42	1	390	8	4	3	1
8/11/2021	80	49	3	410	5	5	0	0
8/12/2021	80	60	4	491	9	4	5	0
8/16/2021	47	25	0	187	6	4	0	2
8/17/2021	55	42	1	416	9	4	1	4
8/18/2021	66	47	0	303	7	6	0	1
8/24/2021	57	34	4	230	9	3	6	0
8/26/2021	56	39	0	328	4	2	2	0
8/31/2021	54	38	2	252	6	3	2	1
9/2/2021	60	40	5	295	3	3	0	0
9/8/2021	53	33	1	223	13	7	6	0
9/21/2021	57	42	2	323	7	6	1	0
9/23/2021	67	46	2	331	7	5	1	1
9/28/2021	51	34	4	302	8	7	0	1
9/29/2021	78	51	2	422	9	7	1	1
10/5/2021	43	35	2	330	13	11	0	1
10/12/2021	58	38	5	217	5	4	0	1
10/13/2021	85	63	3	512	13	10	0	3
10/14/2021	36	21	1	179	10	3	0	7
Total	1519	993	56	7945	214	136	41	36
Percentages	-	65.37%	3.69%	-	2.69%	1.71%	0.52%	0.45%

What bacteria could be identified in this study?

- Were able to identify a wide spectrum of Gram-positive and Gram-negative bacteria.
  - Also identified a small number of yeasts (not shown).
- *E. coli* represented the majority of the Gram-negative bacteria, along with various species of Klesbiella.
- *Enterococcus faecalis*, Group B Streptococcus, *S. epidermidis*, and *S. aureus* represented roughly 70% of the Gram-positive isolates.





Identification discrepancies

- Most discrepancies involved one workflow or the other identifying an additional pathogen.
- For the SOC workflow, we identified 12 specimens with an additional pathogen (21.4% of the discrepancies)
- For the APAS workflow, we identified 40 specimens with an additional pathogen (71.4% of the discrepancies)

Organism ID	SOC Identification	APAS-assisted study Identification
APAS_0043	K. pneumoniae	MUF[a]
APAS_0046	M. morganii, K. pneumoniae	M. morganii
APAS_0081	E. coli, K. oxytoca	E. coli, K. oxytoca, K. pneumoniae
APAS_0083	E. faecalis	E. faecalis, K. pneumoniae
APAS_0104	MUF	E. faecium
APAS_0107	C. glabrata	MUF
APAS_0166	E. faecalis, C. albicans	E. faecalis
APAS_0169	C. glabrata	MUF
APAS_0227	E. coli	E. coli, E. faecalis
APAS_0230	C. lusitaniae	C. albicans
APAS_0241	MUF	E. coli, S. agalactiae
APAS_0337	MUF	E. faecalis
APAS_0362	K. oxytoca, M. odoratimimus, P. rettgeri	K. oxytoca, M. odoratimimus, M. morganii
APAS_0414	MUF	C. tropicalis
APAS_0470	E. coli	MUF
APAS_0476	C. koseri, E. coli	C. koseri, E. coli, E. faecalis
APAS_0512	MUF	S. saprophyticus
APAS_0517	E. coli	E. coli, C. koseri
APAS_0519	MUF	E. faecalis, MUF
APAS_0558	E. coli	E. coli, C. koseri
APAS_0562	P. aeruginosa	MUF
APAS_0668	K. oxytoca, E. coli	K. oxytoca, Enterobacter sp.
APAS_0765	M. morganii	M. morganii, K. pneumoniae
APAS_0778	MUF	K. pneumoniae
APAS_0780	S. epidermidis, S. gallolyticus	S. epidermidis
APAS_0782	S. haemolyticus	S. haemolyticus, Candida sp.
APAS_0902	MUF	E. coli
APAS_0921	S. aureus	MUF
APAS_0932	P. aeruginosa	P. aeruginosa, K. pneumoniae
APAS_0945	E. faecalis	NSG[b]
APAS_0960	C. freundii	C. freundii, E. faecalis, E. coli
APAS_0964	MUF	P. mirabilis
APAS_0983	S. agalactiae	S. agalactiae, E. faecalis, E. coli
APAS_1016	E. coli, P. mirabilis	E. coli, P. mirabilis, K. pneumoniae
APAS_1070	K. pneumoniae	K. pneumoniae, E. coli
APAS_1082	E. coli	E. coli, P. mirabilis
APAS_1146	E. coli	E. coli, E. faecalis
APAS_1152	MUF	E. coli
APAS_1170	C. kefyr	C. kefyr, C. albicans
APAS_1186	MUF	E. faecalis
APAS_1204	NSG	K. pneumoniae
APAS_1206	K. pneumoniae, P. mirabilis	K. pneumoniae, P. mirabilis, K. oxytoca
APAS_1276	P. hauseri	P. mirabilis, E. coli
APAS_1293	E. coli, K. oxytoca	E. coli, P. aeruginosa
APAS_1312	MUF	E. faecalis
APAS_1313	K. variicola, K. pneumoniae	K. variicola
APAS_1341	K. aerogenes	K. aerogenes, E. coli
APAS_1344	E. cloacae	E. cloacae, E. faecalis
APAS_1349	E. coli	E. coli, K. aerogenes
APAS_1350	E. faecalis, E. coli	E. faecalis, E. coli, S. marcescens
APAS_1352	E. coli, C. koseri	E. coli, C. koseri, P. mirabilis
APAS_1353	K. variicola	K. variicola, E. coli
APAS_1400	MUF	E. faecalis
APAS_1445	E. coli, E. faecalis	E. coli
APAS_1478	M. morganii	M. morganii, Citrobacter amalonaticus
APAS_1488	P. mirabilis	P. mirabilis, P. aeruginosa

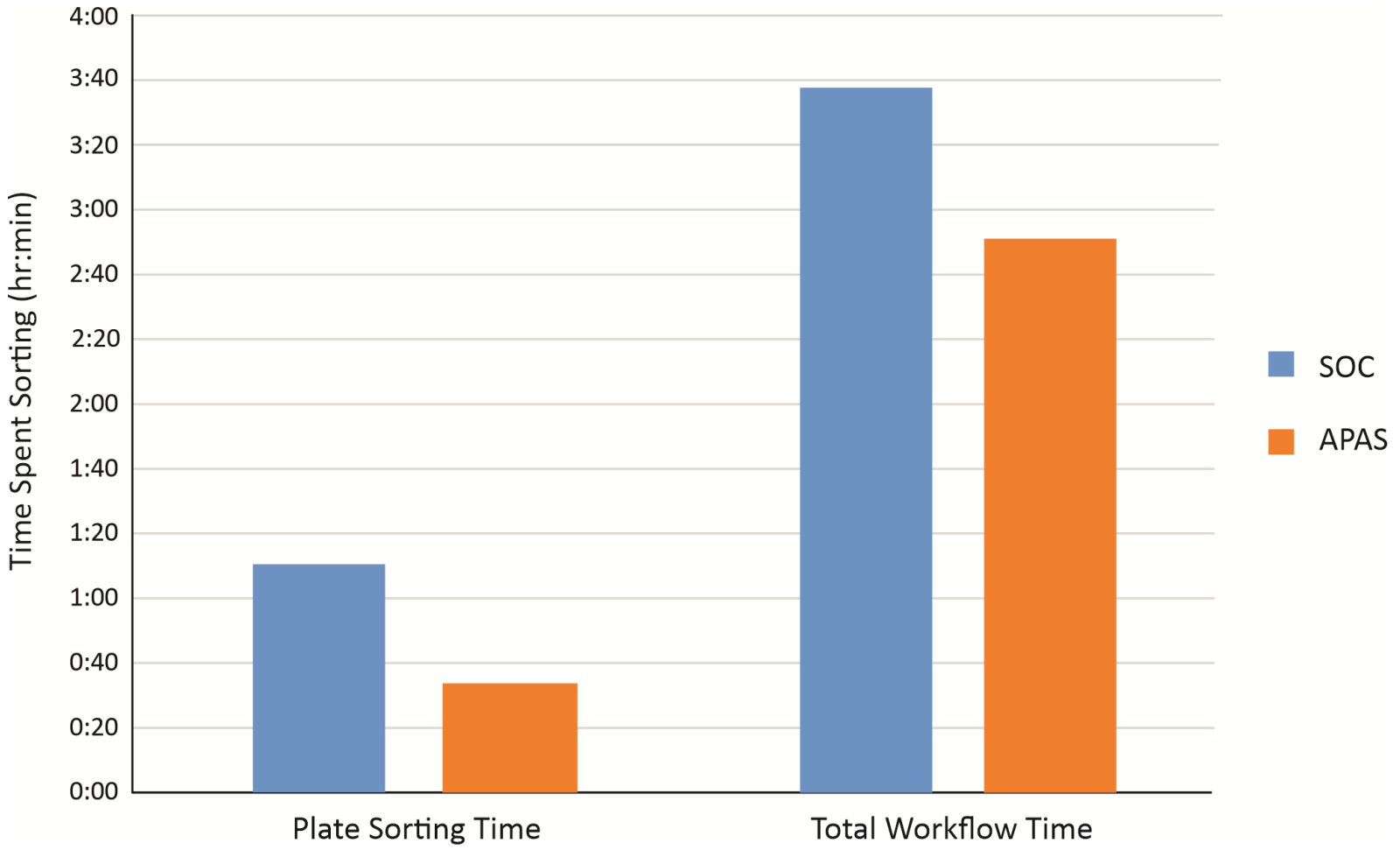
ASTs for Gram-positives and Gram-negatives

	Total Organisms	Total Reported Antibiotics	EA[a]	CA[b]	mE[c]	ME[d]	VME[e]
Gram Positive	105	341	341 (100%)	337 (98.83%)	-	-	-
Gram Negative	519	7604	7527 (98.99%)	7388 (97.16%)	136	41	36

- We had high essential and categorical AST agreement but was higher for Gram-positives than for Gram-negative bacteria.
- Most errors identified were minor, but we identified a number of ME and VME
  - Most of the ME and VME belonged to a small subset of bacteria in the study
  - We believe the MEs and VMEs are more reflective of heterogeneity in antimicrobial susceptibility amongst bacterial strains in each individual, rather than a reflection on the APAS technology.

Differences in workflow times.

- Total workflow times differed between the SOC and APAS workflows.
- The difference in plate sorting times between the APAS and SOC were statistically significant ($p<0.05$).
- There was an approximate time savings of 52 minutes to process on average 62 specimens per day.



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	00:20:22	72	17
	Day 2	00:49:22	171	17
	Day 3	00:20:05	72	17
	Mean binning time per plate (Sec)			17

- We also measured plate sorting times separately to identify differences in the ability of the APAS and SOC to sort plates over the course of a few days.
  - We found that the APAS could perform the same workflow, while reducing approximately 25 seconds for binning each plate.

Conclusions

- The APAS Independence System can be implemented into the standard workflow of most laboratories with relatively minimal modifications.
- Relatively few urine specimens (74/1,519; 4.87%) had detectable growth discrepancies when comparing the SOC and APAS workflows. Most of these discrepancies (42; 75%) involved the identification of additional urinary pathogens in the APAS workflow.
- Of the 1,519 specimens evaluated, we identified a large number of different Gram-positive bacteria, Gram-negative bacteria, and yeasts.
- 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.

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