P0110

Multicenter Evaluation of the WASPLab Digital Image Analysis Software to Segregate Significant Growth of Urine Cultures on Blood and MacConkey Agar

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Introduction

Urine culture interpretation can be complicated by several variables, including the presence of small numbers of colonies and the growth of more than one bacterial type. In general, voided-urine cultures containing ≥10,000 CFU/mL should be reported as potential pathogens if there are not more than 3 pathogens or these organisms are not normal skin flora. In this study, we evaluated the accuracy of the WASPLab (Copan, Brescia, IT) software to differentiate negative and non-negative urine cultures.

Method

Urine specimens submitted for bacterial culture from 3 different sites were plated on sheep blood and MacConkey agars. All specimens were processed by the WASPLab using a 1-µL loop, and images were captured after 0 and 18 h incubation. The software quantitated each plate and reported the specimen as non-negative if any plate contained more than 10 colonies. Results were then compared to manual interpretation as either positive or negative for pathogens based on each laboratory's urine culture policy. These data were also analyzed by separating laboratory-negative specimens depending on site-specific rules no significant growth (skin or fecal contamination). Manual-positive, automation-negative cultures were reviewed by a second technologist.

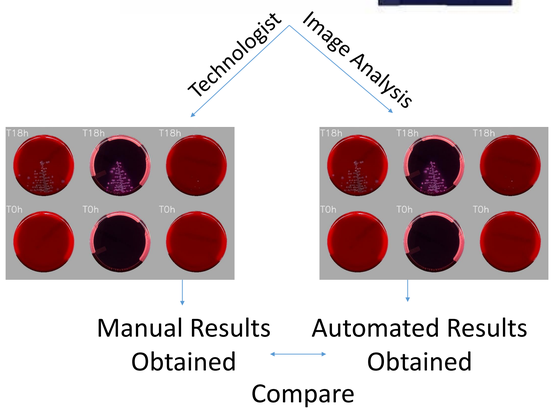

Table 1. Overall Performance of WASPLab segregation software compared to Manual Technologist review.

Site	MP/AP[a]	MN/AN[b]	MN/AP[c]	MP/AN[d]	Total	Sensitivity (95% CI)	Specificity (95% CI)
1	2958	1092	1149	2	5201	99.9 (99-100)	48.7 (47-51)
2	1613	3274	621	5	5513	99.7 (99-100)	84.0 (83-85)
3	1107	1232	410	2	2751	99.8 (99-100)	75.0 (73-77)
Total	**5678**	**5598**	**2180**	**9**	**13465**	**99.8 (99-100)**	**72.0 (71-73)**

Table 1: Reported data was after secondary review of discrepant specimens to remove technologist error. (a) Manual Positive Automation Positive, (b) Manual Negative, Automation Negative, (c) Manual Negative, Automation Positive, (d) Manual Positive, Automation Negative.

Table 2. Site 1/2 Breakout of MN/AP specimens based on laboratory rules

	Lab Negative	NMW/MMO[a]	NSG/MGN[b]	Lab Positive
SW Neg	2941	602	823	7
SW Pos	176	764	830	4571

Table 2: MN/AP specimens were broken out based on the labs expert rules for calling urine specimens as negative. These reasons included (a) NMW/MMO are cultures that are called negative due to potential fecal contamination, (b) NSG/MGN are cultures that contain skin pathogens suggestive of poor collection are reported as negative.

Table 3. site 3 breakout of MN/AP specimens based on Laboratory rules

	Lab Negative	GUF[a]	Lab Positive
SW Neg	706	526	2
SW Pos	17	393	1107

Table 3: MN/AP specimens were broken out based on the labs expert rules for calling urine specimens as negative. These reasons included (a) GUF, which are cultures that contain genital urine flora and are considered negative due to poor collection.

Table 4. Evaluation of 9 remaining MP/AN specimens

Cause of MP/AN	# of specimens	Description
Microcolonies	8	7 colonies and 4 microcolonies
Difference in counts near significant limit	1	8 colonies and 6 microcolonies

Table 4: The vast majority of missed positives by the software were due to growth of microcolonies. The software can detect these colonies, but a limit of 50 microcolonies were needed for positive reporting. Only 1 specimen contained a count difference that impacted results.

Figure 1. Image examples of MP/AN specimens

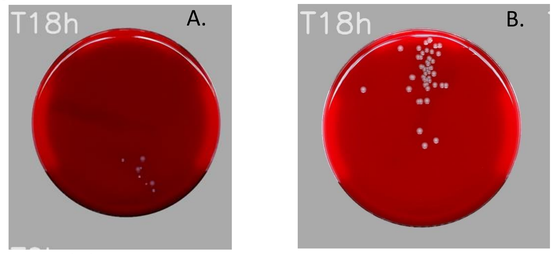

Figure 1. (A) Example of microcolonies not counted consisting of 8 colonies and 6 microcolonies. (B) Colonies near limit that were counted differently by Software and Technologist.

Conclusions

- The segregation software to count colonies is highly accurate and could be used to quickly remove negative urines, which in this study would remove 5,598 cultures.
- Specific laboratory rules could be added to improve MN/AP reporting.
- When specifically evaluating plates that did not need expert rules, sensitivity and specificity of the software increases to 99.8% and 95.0% respectively.
- Machine learning for differentiation will be necessary to create specific rule sets to removal of contaminated urine.