Evaluation of WASPLab® Growth Detection Algorithm for Analysis of Urine Cultures with CLED Agar

Teresa Vicente-Rangel, María José Goyanes, Roberto Alonso*, Emilio Bouza, Patricia Muñoz

Servicio de Microbiología Clínica y Enfermedades Infecciosas. Hospital General Universitario "Gregorio Marañón". Madrid. Spain.

BACKGROUND

Urine cultures are among the most common specimen received by clinical laboratories and generate a major share of the laboratory workload. CLED plates, a specific and differential agar, has been used to expedite urine culture results, but technologists are still needed to review every plate.

We incorporated to our laboratory a robotic system for sample processing which automatically transfers the streaked plates to an intelligent incubator for periodically recording of bacterial growth (Figure 1). Up to now, the recorded images had to be analyzed and interpreted by a qualified operator. Recently, we have introduced a new software for detection and quantification of bacterial colonies.

OBJECTIVES

In this study, we evaluated the *Segregation* WASPlab® software (Copan Wasp s.r.l., Brescia, IT) to interpret urine specimens plated to BD CLED agar (BD, Franklin Lakes NJ, US).

METHODS

Urine specimens submitted for bacterial culture were enrolled durind a one-month period mid-October to mid-November), 2017. All urines were plated on CLED agar using a 1µl loop on the WASP® system. Images of each plate were taken after 0 and 16h of incubation.

Each image was read by both a technologist and the WASPLab®. Software results were reported as negative if <10 colonies were detected (10,000 CFU/mL). Results were compared to manual reading using the same images on an HD-monitor (Figure 2) and all testing was blinded from the software's results.

RESULTS

A total of 5205 urine cultures were enrolled and tested. Raw sensitivity and specificity of the software was 100.0% and 74.5% respectively, which included 988 Manual Negative/Automation Positive (MN/AP) results (Table I A).

The 988 MN/AP specimens were further classified as:

- 45 caused by microcolonies missed by the technologist.
- 778 caused by the technologist not entering a POS results although the final report was >10,000 CFU/mL: most of them with multiple morphotypes corresponding to contaminated urines.
- 165 caused by artifacts on the agar surface.

In total, all these "non-negative" urines accounted for 83.3% of the MN/AP results and if correctly recorded the specificity would raise to 94.6% (Table I B).

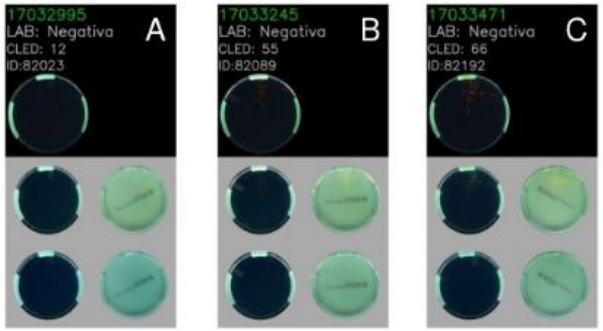

Figure 3: Some examples of MN/AP samples. A, microcolonies, B & C, multiple morphotypes.

A	MANUAL READING (REFERENCE)			
AUTOMATED READING		+	-	
	+	1331	988	2319
	-	0	2886	2886
		1331	3874	5205

Sensitivity: 100
Specificity: 74.5
Positive predictive value: 57.4
Negative predictive value: 57.4

B	CORRECTED MANUAL READING (REFERENCE)			
AUTOMATED READING		+	-	
	+	2154	165	2319
	-	0	2886	2886
		2154	3051	5205

Sensitivity: 100
Specificity: 94.6
Positive predictive value: 92.9
Negative predictive value: 100

Table I: Comparison of methods, automated *vs.* manual reading. A) Raw data, B) Corrected data.

CONCLUSIONS

Although human intervention is still necessary to review plates with bacterial growth, the use of *Segregation*, the highly performance WaspLab® software, could save much human time by automatically segregating the vast majority of the negative plates. The high sensitivity of the software could also improve the quality of the results.

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