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Lab automation

Automated digital quantitation of urine cultures using the WASPLab

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Background: Advances in automation have reduced the time for specimen processing by using robotic systems to inoculate, label, track and incubate plates for culture. However, culture analysis is still a time intensive and costly procedure for the laboratory as technologists have to interpret colony counts to differentiate pathogens from normal flora for several hundred plates a day. Automation that can count and differentiate colony types on blood plates could help to reduce cost of urine cultures by sorting plates based of colony growth. Recently, software was developed for the WASPLab (Copan, Brescia, IT) that reads digital images and provides quantitation of colony forming units (CFU) from blood agar plates (BAP). In this study, we compare the accuracy of this software to manual analysis.

Material/methods: Urine specimens submitted for bacterial culture were enrolled into the study and plated on BAP following standard of care testing. Specimens enrolled were processed by the WASPLab with a 1µL loop and digital images were taken at 0 and 24 hours post inoculation. The software quantitated each plate for colony counts recorded as colony forming units per plate (CFU/plate) and results were compared to manual quantitation. Manual quantitation was performed by a technologist blinded to the results and colonies were counted using the same digital image viewed on a HD monitor. Specimens that contained >1000 CFU/plate were reported manually as 1000 CFU/plate. Results are reported in the following categories: 0 CFU, 1-10 CFU, 11-100 CFU and >100 CFU.

Results: A total of 2,049 urine specimens were enrolled into this study. Manual reading identified 333 (16%) plates negative for growth, 324 (16%) plates containing 1-10 CFU, 487 (24%) plates containing 11-100 CFU and 905 (44%) of plates containing >100 CFU. The software was concordant with manual quantitation in 1,869 (91%) of all cultures tested. Discrepancies occurred in 180 specimens of which 155 specimens resulted in the software reported colony counts in at least one category higher than manual counts. The remaining 25 discrepant specimens resulted in under counting colonies compared to the manual reading. No specimens had growth that was not detected by the software.

Conclusions: Overall the study demonstrated high concordance between the software and manual reading for colony counts. Most of the discordant results involved higher CFU reported by the software than manual quantification, suggesting that either the software is more sensitive compare to manual reading or the software is interpreting large colonies as more than one. Two specimens were reported automatically as 1-10 CFU, but were manual observation counted 11-100 colonies. Technologists have oversight and can review images to override rare underscoring. The reading software is designed to speed workflow and improve turnaround by segregating no growth from cultures that need further work up.