Segregation and WASPLab™ automation impact on MRSA screening at LTHT

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Introduction

Methicillin Resistant Staphylococcus *aureus* (MRSA) is an increasing problem in Healthcare settings. It is a well-established cause of Hospital acquired infections and is also increasingly seen in community outbreaks. With emerging resistance to antibiotics, MRSA infections result in longer and more intensive hospital stays and post-operative complications . Healthcare institutes in the UK are already suffering from stretched finite resources and seasonal pressures, so (preventable) outbreaks would further stress an already struggling system.

Active screening to identify carriers and manage individuals accordingly, is recommended by PHE guidelines. At the Leeds Teaching Hospitals Trust (LTHT) targeted screening is conducted on high risk individuals prior to or on admission of elective surgery and certain procedures; screening of inpatients is also carried out monthly and where clinically indicated. Therefore there is a need for a rapid reliable screening method for MRSA, capable of screening a large number of samples. Screening benefits to healthcare institutes include better infection control measures, shorter hospital stays,!! prevention of auto-infection, bacteraemia and ward outbreaks, monetary gains for meeting targets, !! and better overall patient care.

Methods and Materials

Retrospective study compared traditional manual reading to the use of Copan® WASPLab™ WebApp and the use of Chromogenic Detection Module Analysis software (CDM), referred to locally as Segregation software.

Specimen processing: MRSA screening swabs usually consist of triplicate swabs of anterior nares, axilla and groin swabs In all cases MRSA screening samples taken within 48 hours using Copan® Eswabs were processed on the Walk Away Specimen Processor (WASP); Ten microliters of each specimen were seeded on Brilliance MRSA II (Oxoid, UK) by WASP® automation.

Screening:

Automated WASPLab™ WebApp and Segregation (CDM Analysis): a total of 5000 surveillance swabs for MRSA screening were enrolled in the study, collected between October 2016 to October 2017. After 18 hours incubation at 35°C ±2 in the integrated incubator, digital images were acquired by WASPLab™ and examined both by a trained operator and by the Segregation software.

Traditional screening method: Inoculated MRSA screening plates were ejected from the front of the WASP for 18 hour manual incubation in O_2 at 35-37°C in a walk-in incubator. Numerically sequential racks held plates in three stacks of 10 plates with the time of incubation written at the front of each rack. Plates were reviewed and reported by a trained BMS with preliminary bench tests conducted during the course of screening throughout the day.

Reporting: Negative reports were issued immediately after review by an operator in all three methods, however the timing between methods differed which again impacted on laboratory workflow.

Figure 1: Traditional Manual Screening

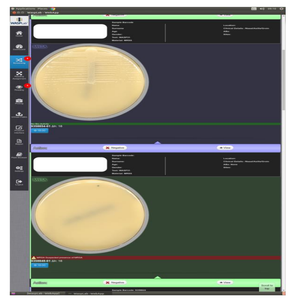


Figure 2: WASPLab WebApp Screening

Figure 3: Segregation Software Screening (Negative samples)

Results

Segregation (CDM) Software analysed each individual pixel per image (48 million pixels per image) against a HSV score determined by Copan® CDM programming. HSV measured Hue (Colour), Saturation (intensity of Colour) and Value (Brightness of Colour). On Brilliance MRSA II media, denim blue colonies highlighted potentially positive growth. Other pigmentation was classed as negative for MRSA.

Method of Screening	Results (% concordance with Traditional Manual Reading)				Average time taken for Screening (Seconds per plate)	Sensitivity %	Specificity %
	True Positives	True Negatives	False Positives	False Negatives			
WASPLab™ WebApp	100	100	0	0	15-20	100	99.9
WASPLab™ Segregation (CDM)	100	99.6	0.4	0	1	100	99.6

Table 1: Comparison of WASPLab WebApp and Segregation Screening vs. Traditional manual reading

The classification of 99.6 % of images studied by Segregation software corresponded with those read on the WASP-Lab manually. Upon review of the discrepant images (False Positives), Segregation (CDM) software was found to be valid and the images were “potentially not negative” requiring further investigation.

Although Segregation (CDM) appeared slightly less specific (99.6% **Specificity**), **Sensitivity** was still 100%. Segregation (CDM) software had 0 **false negatives**, therefore no positive plates were lost Furthermore Segregation’s (CDM) rapid review of negative screens as 30 thumbnails per page, reduced screening times vastly, as the software reliably segregated negative media plates.

Reporting of Negative results was also a key indicator in workflow improvement. Traditional manual reading required each report to be individually recorded and released. This process required multiple repeated movements and alternating between plate examination and manipulation and reporting results on the LIS using a keyboard. Although not a lengthy task for a single report, repetition for several hundred samples a day would accumulate and had the potential to cause strain and fatigue and potential errors. The laboratory benchmark for release of clear-cut Negatives to the LIS was to complete the task by mid-day. With the introduction of WebApp reading, (prior to the implementation of Segregation Software), the day’s negative reporting could be completed by mid-morning. With a simple scroll and click Negative results were reported to the LIS. The implementation of Segregation software further enhanced negative reporting as each set of 30 thumbnail images segregated as Negative samples were released to the LIS with one click. This meant that the majority of negative results were released by 9am coinciding with patient ward rounds and better patient management.

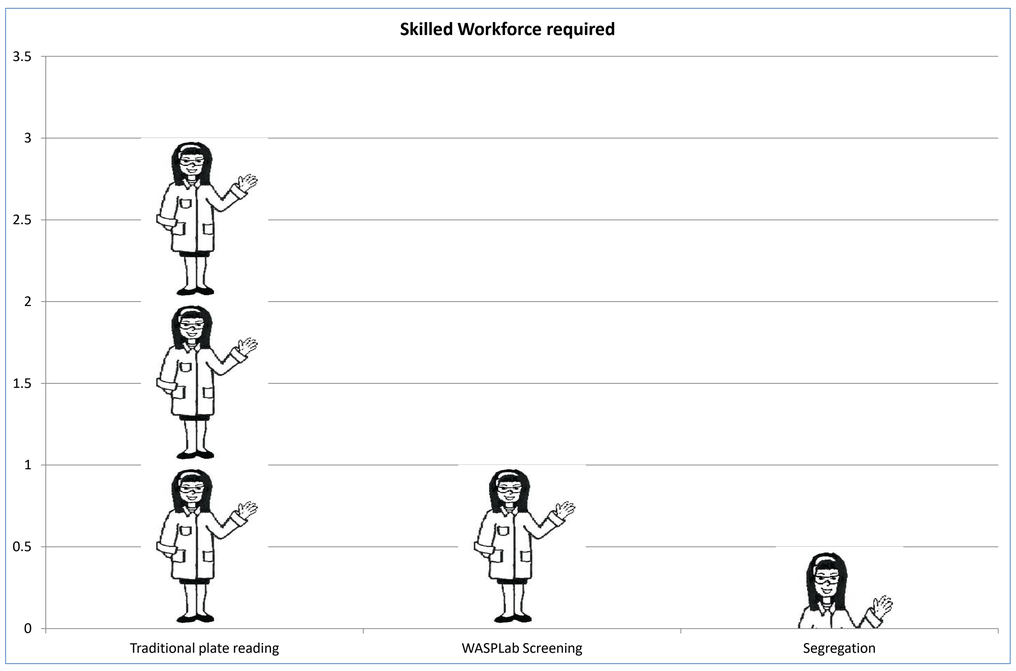
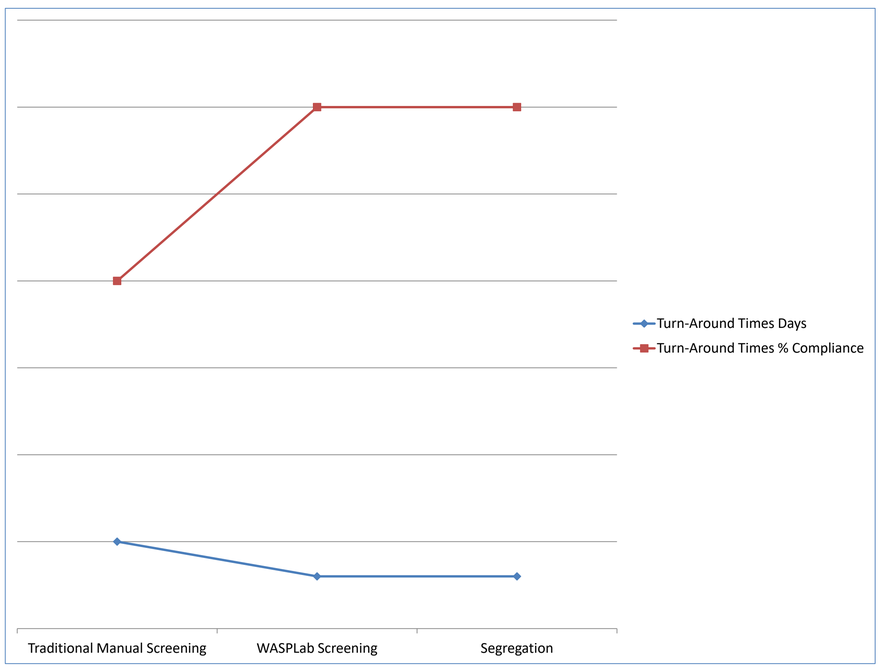


Figure 4 (Left): Skilled workforce required to screen MRSA swabs over a 24 hour period at LTHT.

With the implementation of Segregation (CDM) software the amount of time and therefore the number of BMSs required reduced to half a BMS i.e. the BMS was able to screen MRSAs on WASPLab and complete other work on the same day

Figure 5 (Right): Trend analysis of Turn-Around Times and % compliance

Rapid screening allowed published TAT to be reduced from 5 to 3 days as compliance was better with the introduction of WASPLab and Segregation.



Conclusion

Copan® Segregation (CDM) Software has shown to be a reliable tool for easy isolation and identification of potential target organisms on MRSA Chromogenic media. The use of automation to inoculate, incubate and image plates has improved the standardisation of screening methods at LTHT using the WASPLab™. Segregation (CDM) Software, developed in house by Copan® ® for use on WASPLab™, has shown to reliably segregate work, thus has allowed a reduction in skilled workforce to conduct the same task in a shorter space of time providing greater skilled capacity and time availability for workflow purposes.

Segregation software is an excellent screening tool particularly where large sample numbers are screened and positivity rate is low (1.6% average at LTHT for MRSA screens). It has given LTHT the ability to provide results in less than 24 hours for negative results, reducing turn-around times from 5 to 3 days and has transformed the way in which the Microbiology/Pathology CSU is able to operate. The wider impact is contribution to reduced waiting times, referral times and hospital stays, better infection control, improved workflow and better patient care at the LTHT.

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