



# Acknowledgments:

Foremost, we would like to express our sincerest gratitude to the authors whose works have been devotedly arranged in the booklet. They rendered insight and expertise that greatly assisted the prime selection.

Furthermore, we would like to thank all experts throughout the world for the trust placed in our products. Their esteem is the best acknowledgment ever.

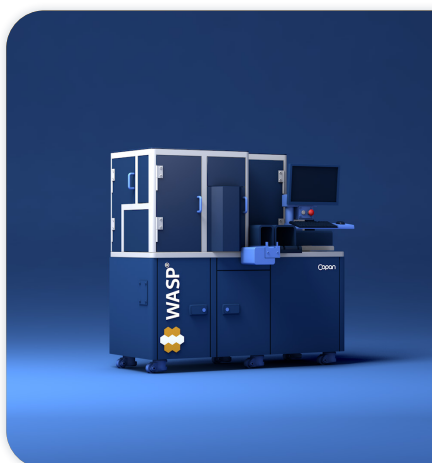
This booklet comprises the last year's studies where our automation solutions are used and integrates our 2020 booklet, offering a valuable collection of the most representative papers and posters from several authors throughout the world.

For the materials other than "open access," we have used a QR code that provides a quick link to the webpage where the original work can be viewed/purchased.

From sample collection to image analysis

## Our comprehensive approach to preanalytics

Automation is only a part of Copan's comprehensive approach to preanalytics; our line of liquid-based microbiology collection and transport systems can be paired with our automation solutions, unlocking your lab's real potential and accompany you from sample collection to data interpretation in the smoothest and more efficient way.



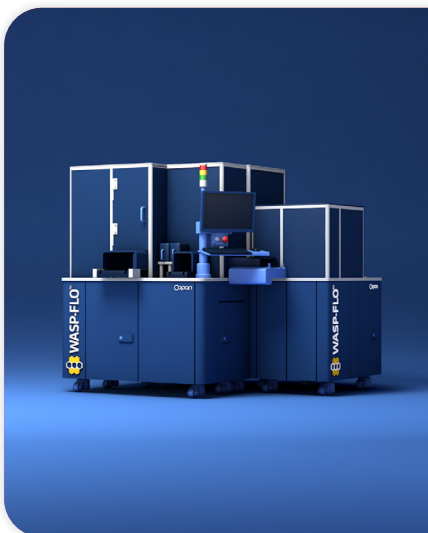
### WASP®

Copan WASP®: Walk-Away Specimen Processor™ is a truly revolutionary instrument for specimen processing for Microbiology. WASP® provides a comprehensive system encompassing all aspects of automated specimen processing, planting and streaking, Gram slide preparation and enrichment broth inoculation.



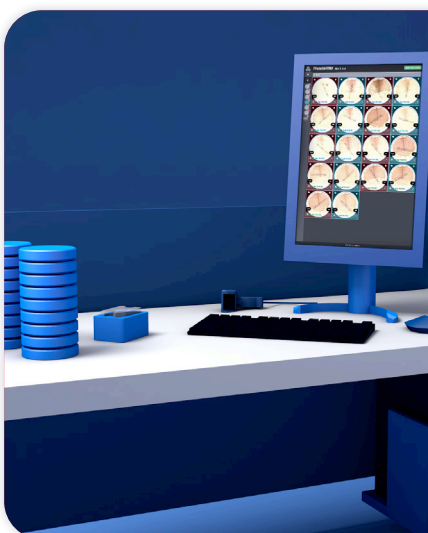
### WASPLab®

WASPLab® is the natural evolution of the WASP® project and Copan philosophy, and it takes care of the incubation/imaging of the plates and brings the customer into the world of Digital Bacteriology. Before and during the incubation, the unique WASPLab® vision system acquires images that will be available in high-quality digital format to the lab technician to perform the reading phase.



### **WASP-FLO™**

WASP-FLO™ is the module we developed for microbiology laboratories with multiple WASP® or WASPLab® lines, to streamline sample loading and unloading. WASP-FLO™ automatically sorts samples[a], drives them to the appropriate WASP®, and batches the tubes in output racks after processing.



### **PhenoMATRIX™**

PhenoMATRIX™ uses artificial intelligence combined with clinical information from the LIS system to automatically read, interpret, and segregate bacterial cultures with the click of a button. Adding PhenoMATRIX™ suite of algorithms to WASPLab® automation system ease the interpretation of patient results and give to microbiology labs the ability to shorten the time to results.



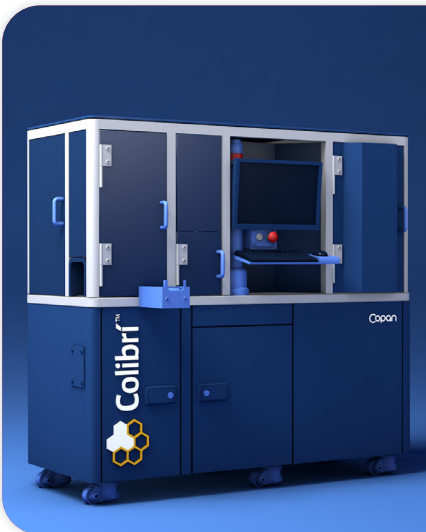
### **MicroHub™**

Connecting WASPLab® to LIS and other instruments, MicroHub® represents the next step into a new way of managing lab data. Think of it as middleware, handling patient data, test orders, results, and the entire lab workload in real-time. Long story short, MicroHub® is the perfect tool to centralize the final validation step and keep lab's productivity under control.



## Radian™

Radian™ is the WASPLab® module dedicated to the full automation and interpretation of Disk Diffusion Antibiotic Susceptibility Testing. It is composed of two modules: Radian™ In-Line Carousel and Radian™ Expert System



## Colibri™

Colibri® is a microbiology system that automatically picks colonies previously selected by PhenoMATRIX™ T.A.G. or by an operator on the WASPLab® reading station. The instrument spots targets for microbial identification through MALDI-TOF technology and prepares microbial suspensions for Antibiotic Susceptibility Testing (AST).



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# Clinical Automation

## Wasp® & WASPLab® Sample Workflow

Benefits Derived from Full Laboratory Automation in Microbiology: a Tale of Four Laboratories

**Karissa Culbreath et al.**

*J Clin Microbiol.* 2021 Feb 18;59(3):e01969-20

8

Multicenter Evaluation of Processing and Analysis of College of American Pathologists (CAP) Proficiency Testing Samples by Laboratory Automation

**N Esther Babady et al.**

*J Clin Microbiol.* 2021 Apr 20;59(5):e03233-20

9

Implementation of the WASPLab™ and first year achievements within a university hospital

**Abdessalam Cherkaoui et al.**

*Eur J Clin Microbiol Infect Dis.* 2020 Aug;39(8):1527-1534

10

## Phenomatrix™ and Image Analysis

Digital Image Analysis for the Detection of Group B Streptococcus from ChromID Strepto B Medium Using PhenoMatrix™ Algorithms

**Justin Baker et al.**

*J Clin Microbiol.* 2020 Dec 17;59(1):e01902-19

11

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**Abdessalam Cherkaoui et al.**

*Front Cell Infect Microbiol.* 2020 Oct 28;10:552122

12

Use of artificial intelligence for tailored routine urine analyses

**Olivier Dauwalder et al.**

*In Press Journal Pre-Proof* 2020 Oct 6

13

# Clinical Automation

## WASPLab® and Antimicrobial Susceptibility Testing

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*Eur J Clin Microbiol Infect Dis.* 2020 Jun;39(6):1063-1070

14

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**Stefano Mancini et al.**

*J Antimicrob Chemother.* 2020 Nov 1;75(11):3218-3229

15

Tentative Breakpoints and Areas of Technical Uncertainty for Early Reading Automated Disc Diffusion for Enterobacterales

**Stefano Mancini et al.**

*J Antimicrob Chemother.* 2020 Jun 1;75(6):1495-1505

16



# Clinical Automation

WASP® & WASPLab® Sample Workflow

## Benefits Derived from Full Laboratory Automation in Microbiology: a Tale of Four Laboratories



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### Keywords

WASPLab®

Efficiency

Laboratory Automation

### Abstract

Automation in clinical microbiology is starting to become more common place and reportedly offers several advantages over the manual laboratory. Most studies have reported on the rapid turnaround times for culture results, including times for identification of pathogens and their respective antimicrobial susceptibilities, but few have studied the benefits from a laboratory efficiency point of view. This is the first large, multi-center study in North America to report on the benefits derived from automation measured in full-time equivalents (FTE), FTE reallocation, productivity, cost per specimen, and cost avoidance. Pre- and post-full automation audits were done at 4 laboratories that have vastly different culture volumes, and results show that regardless of the size of the facility, improved efficiencies can be realized after implementation of full laboratory automation.

# Clinical Automation

WASP® & WASPLab® Sample Workflow

## Multicenter Evaluation of Processing and Analysis of College of American Pathologists (CAP) Proficiency Testing Samples by Laboratory Automation



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### Keywords

CLIA

Automation

Bacteriology

Proficiency testing

### Abstract

No abstract available

# Clinical Automation

WASP® & WASPLab® Sample Workflow

## Implementation of the WASPLab™ and first year achievements within a university hospital



Abdessalam Cherkaoui <sup>1</sup>, Gesuele Renzi <sup>2</sup>, Arnaud Viollet <sup>3</sup>, Mark Fleischmann <sup>4</sup>, Ludovic Metral-Boffod <sup>5</sup>, David Dominguez-Amado <sup>6</sup>, Nicolas Vuilleumier <sup>7,8</sup>, Jacques Schrenzel <sup>2,9</sup>

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### Keywords

WASPLab®

Accuracy

Efficiency

Project management

### Abstract

In essence, automation can be driven by several of the following incentives: increased processing capacity of the laboratory, better costs control through processes standardization, optimized traceability, or improved workflows to reduce turnaround times (TAT). This project aims at presenting an overview of the project management and change management with a focus on the major challenges addressed by lab staff and laboratory leadership during the different phases of the implementation of the WASPLab™ in a routine clinical bacteriology laboratory. This paper reports our experience and reviews changes in the bacteriology laboratory at Geneva University Hospitals when shifting to the WASPLab™. Practically, the whole automation process was segmented into different packages (specimen type-based segmentation) allowing sequential validation, staff training, and routine implementation. Such process allowed reaching 90% of the identified “automatable” samples within 1 year, including personal training, documentation for accreditation supported by publications, without interrupting routine operations. In addition, we implemented a validated automated solution for antimicrobial disk diffusion susceptibility testing. Structured supervision and accurate monitoring of all the activities related to the automation project including key partners such as IT support, technical committee, and after-sales service guaranteed a swift and timely achievement of the project allowing the improvement of the workflow in routine bacteriology within 1 year.

# Clinical Automation

Phenomatrix™ and Image Analysis

## Digital Image Analysis for the Detection of Group B Streptococcus from ChromID Strepto B Medium Using PhenoMatrix™ Algorithms



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### Keywords

Artificial Intelligence

*Group B streptococcus*

Chromogenic Media

Total Lab Automation

### Abstract

Group B Streptococcus (GBS) can be found to colonize about 25% of all healthy, adult women and is the leading infectious cause of early neonatal morbidity and mortality in the United States. This study evaluated the clinical performance of PhenoMatrix (PM) chromogenic detection module (CDM) digital imaging software in detection of GBS from LIM broth plated on ChromID Strepto B chromogenic medium (ChromID) using the WASP® automated processor. The performance of the PM CDM was compared to manual culture review of the digital images and molecular detection of GBS. ChromID alone had a sensitivity and specificity of 84.5% and 94.7%, respectively, after 48 h compared to nucleic acid amplification testing (NAAT). Compared to the composite reference for positivity, when PM CDM was used to detect GBS from ChromID, the sensitivity was 100%, with no true-positive GBS isolates missed by 48 h of incubation. Overall, evaluating all three methods for the detection of GBS, the sensitivities of NAAT, ChromID plus PM CDM at 48 h, and ChromID alone at 48 h were 96.8%, 95.5%, and 90.3%, respectively. The specificities of NAAT, ChromID plus PM CDM, and ChromID alone were 97.7%, 63.0%, and 95.4%, respectively. The sensitivity of ChromID in combination with the PM CDM was similar to the sensitivity of molecular detection. Further, the algorithm never called a culture negative that was determined to be positive by manual reading, and it identified an additional eight true positive specimens that were missed by manual digital image culture reading.

# Clinical Automation

Phenomatrix™ and Image Analysis

## Impact of Total Laboratory Automation on Turnaround Times for Urine Cultures and Screening Specimens for MRSA, ESBL, and VRE Carriage: Retrospective Comparison with Manual Workflow



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### Keywords

TAT Urine

Screening

MRSA-ESBL-VRE

Total Lab Automation

### Abstract

Using computerized time-stamps, we compared the turnaround-times (TAT) for urine samples and screening eSwabs® of MRSA, VRE, and ESBL carriage in the bacteriology laboratory of Geneva University Hospitals between January and December 2017 (period preceding the implementation of the WASPLab®) with the same specimen types analyzed between January and December 2019 (period after the implementation of the automation). During both 1-year periods, a total of 98'380 specimens were analyzed (48'158 in 2017 vs. 50'222 in 2019). On the WASPLab®, all culture plates were imaged at defined intervals each day of incubation, but the processing of the cultures (i.e., pathogen identification and antimicrobial susceptibility testing) was only performed during day shift hours (~8:00 A.M. to 4:30 P.M.). The median TAT for negative reports decreased by almost half for urine samples from 52.1 (2017) to 28.3 h (2019) ( $p < 0.001$ ), and for MRSA screening specimens from 50.7 to 26.3 h ( $p < 0.001$ ). The difference in median TAT for negative reports was less pronounced for screening of ESBL (50.2 vs. 43.0 h) ( $p < 0.001$ ) and VRE (50.6 vs. 45.7 h) ( $p < 0.001$ ). Despite a trend toward shorter result delivery for positive samples, there was no significant change in the median TAT. These results suggest that TAT for negative samples immediately benefit from automation, whereas TAT for positive samples also depend on the laboratory hours of operation and daily human resource management.

# Clinical Automation

Phenomatrix™ and Image Analysis

## Use of artificial intelligence for tailored routine urine analyses



Olivier Dauwalder, Agathe Michel, Cécile Eymard, Kevin Santos, Laura Chanel, Anatole Luzzati, Pablo Roy-Azcora, Jean François Sauzon, Marc Guillaumont, Pascale Girardo, Christine Fuhrmann, Gérard Lina, Frédéric Laurent, François Vandenesch, Chantal Sobas

### Keywords

Algorithms

CHROMIDCPSE

PhenoMATRIX

Urine

### Abstract

**Objectives** - Urine is the most common material tested in clinical microbiology laboratories. Automated analysis is already performed, permitting quicker results and decreasing the laboratory technologist's (LT) workload. These automatic systems have introduced digital imaging concepts. PhenoMATRIX (PHM) is an artificial intelligence software that merges picture algorithms and user rules to provide presumptive results. This study aimed at designing a tailored workflow using PHM, performing its validation and checking its performance in routine practice.

**Methods** - Two data collections including 96 and 135 urine samples from nephrostomy/ureterostomy and artificial bladder (US), 948 and 1257 urine samples from catheter (UC) and 3251 and 2027 midstream urine (MSU) were used to compare LT results with those obtained using two versions of PHM. Another 19 US, 102 UC and 508 MSU were used to monitor performance level 3 months after routine implementation.

**Results** - Before and after revisions, agreement between the first version of PHM and LT results were 83% (95% confidence interval [CI], 74.3–90.2) and 83% (95% CI, 75.3–90.9) (US), 66.7% (95% CI, 63.5–69.5) and 71.7% (95% CI, 68.8–74.4) (UC) and 65.4% (95% CI, 63.8–67.1) and 76% (95% CI, 74.1–77.1) (MSU). The second version improved results, demonstrating 96.2% (95% CI, 91.6–98.8) and 97% (95% CI, 92.6–99.2) (US), 87.5% (95% CI, 85.5–89.2) and 88.9% (95% CI, 87.0–90.5) (UC) and 91% (95% CI, 89.7–92.1) and 92% (95% CI, 91.1–93.4) (MSU) of agreement with LT results before and after revisions. The reliability of PHM results was confirmed by a routine study demonstrating 92% (95% CI, 90.0–94.2) overall agreement.

**Conclusions** - PHM showed high performance, with >90% of results in agreement with LT. PHM could help standardize and secure results, prioritize positive plates during analytical workflow and likely save LT time.

# Clinical Automation

WASPLab® and Antimicrobial Susceptibility Testing

## Rapid Identification by MALDI-TOF/MS and Antimicrobial Disk Diffusion Susceptibility Testing for Positive Blood Cultures After a Short Incubation on the WASPLab®



Abdessalam Cherkaoui<sup>1</sup>, Gesuele Renzi<sup>2</sup>, Nouria Azam<sup>2</sup>, Didier Schorderet<sup>2</sup>, Nicolas Vuilleumier<sup>3,4</sup>, Jacques Schrenzel<sup>2,5</sup>

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<sup>4</sup>Department of Medical Specialities, Division of Laboratory Medicine, Faculty of Medicine, Geneva, Switzerland.

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### Keywords

MALDI-TOF/MS

Short Subcultures

AST by Disk Diffusion

Turn-Around Time

### Abstract

The objectives of this study were to define the shortest incubation times on the WASPLab® for reliable MALDI-TOF/MS-based species identification and for the preparation of a 0.5 McFarland suspension for antimicrobial disk diffusion susceptibility testing using short subcultures growing on solid culture media inoculated by positive blood cultures spiked with a wide range of pathogens associated with bloodstream infections. The 520 clinical strains (20 × 26 different species) included in this study were obtained from a collection of non-consecutive and non-duplicate pathogens identified at Geneva University Hospitals. After 4 h of incubation on the WASPLab®, microorganisms' growth allowed accurate identification of 73% (380/520) (95% CI, 69.1–76.7%) of the strains included in this study. The identification rate increased to 85% (440/520) (95% CI, 81.3–87.5%) after 6-h incubation. When excluding *Corynebacterium* and *Candida* spp., the microbial growth was sufficient to permit accurate identification of all tested species (100%, 460/460) (95% CI, 99.2–100%) after 8-h incubation. With the exception of *Burkholderia cepacia* and *Haemophilus influenzae*, AST by disk diffusion could be performed for Enterobacterales and non-fermenting Gram-negative bacilli after only 4 h of growth in the WASPLab®. The preparation of a 0.5 McFarland suspension for Gram-positive bacteria required incubation times ranging between 3 and 8 h according to the bacterial species. Only *Corynebacterium* spp. required incubation times as long as 16 h. The WASPLab® enables rapid pathogen identification as well as swift comprehensive AST from positive blood cultures that can be implemented without additional costs nor hands-on time by defining optimal time points for image acquisition.

# Clinical Automation

WASPLab® and Antimicrobial Susceptibility Testing

## Evaluation of Standardized Automated Rapid Antimicrobial Susceptibility Testing of Enterobacterales-Containing Blood Cultures: a Proof-of-Principle Study



Stefano Mancini<sup>1\*</sup>, Elias Bodendoerfer<sup>1</sup>, Natalia Kolensnik-Goldmann<sup>1</sup>, Sebastian Herren<sup>1</sup>, Kim Rothlin<sup>1</sup>, Patrice Courvalin<sup>2</sup> and Erik C. Bottger<sup>1</sup>

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### Keywords

Rapid AST

Antibiotic

Blood Cultures

WASPLab® EUCAST

### Abstract

**Background:** Rapid antimicrobial susceptibility testing (RAST) of bacteria causing bloodstream infections is critical for implementation of appropriate antibiotic regimens.

**Objectives:** We have established a procedure to prepare standardized bacterial inocula for Enterobacterales-containing clinical blood cultures and assessed antimicrobial susceptibility testing (AST) data generated with the WASPLab® automated reading system.

**Methods:** A total of 258 blood cultures containing Enterobacterales were examined. Bacteria were enumerated by flow cytometry using the UF-4000 system and adjusted to an inoculum of 10<sup>6</sup> cfu/mL. Disc diffusion plates were automatically streaked, incubated for 6, 8 and 18 h and imaged using the fully automated WASPLab® system. Growth inhibition zones were compared with those obtained with inocula prepared from primary subcultures following the EUCAST standard method. Due to time-dependent variations of the inhibition zone diameters, early AST readings were interpreted using time-adjusted tentative breakpoints and areas of technical uncertainty.

**Results and conclusions:** Inhibition zones obtained after 18 h incubation using an inoculum of 10<sup>6</sup> cfu/mL prepared directly from blood cultures were highly concordant with those of the EUCAST standard method based on primary subcultures, with categorical agreement (CA) of 95.8%. After 6 and 8 h incubation, 89.5% and 93.0% of the isolates produced interpretable results, respectively, with CA of >98.5% and very low numbers of clinical categorization errors for both the 6 h and 8 h readings. Overall, with the standardized and automated RAST method, consistent AST data from blood cultures containing Enterobacterales can be generated after 6–8 h of incubation and subsequently confirmed by standard reading of the same plate after 18 h.



# Clinical Automation

WASPLab® and Antimicrobial Susceptibility Testing

## Tentative Breakpoints and Areas of Technical Uncertainty for Early Reading Automated Disc Diffusion for Enterobacterales



Stefano Mancini<sup>1</sup>, Kim Rothlin<sup>1</sup>, Elias Bodendoerfer<sup>1</sup>, Sebastian Herren<sup>1</sup>, Natalia Kolesnik-Goldmann<sup>1</sup>, Patrice Courvalin<sup>2</sup>, Reinhard Zbinden<sup>1</sup> and Erik C. Bottger<sup>1</sup>

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### Keywords

AST

AUT

Disk Diffusion

WASPLab® EUCAST

### Abstract

**Background:** Disc diffusion is a reliable, accurate and cost-efficient procedure for antimicrobial susceptibility testing (AST) but requires long (18–24 h) incubation times. Reading of disc diffusion after short incubation times (6–8 h) by automated systems is feasible but should be categorized with time-adapted breakpoints to reduce errors.

**Objectives:** This study systematically compared early readings (6 and 8 h) of disc diffusion using an automated system with that of the standard 18 h EUCAST method. Time-adapted tentative breakpoints were proposed to discriminate susceptible from resistant isolates and areas of technical uncertainty were defined to minimize the risk of errors.

**Methods:** A total of 1106 Enterobacterales isolates with a wide variety of resistance mechanisms and resistance profiles were included. All isolates were analysed for susceptibility to amoxicillin/clavulanic acid, ceftriaxone, cefepime, meropenem, ciprofloxacin and gentamicin using the automated WASPLab® system. Part of the collection (515 isolates) was also analysed for susceptibility to an additional 10 antibiotics.

**Results:** Separation between WT and non-WT populations was poorer at early incubation times than following standard incubation. Editing of rapid automated AST results after 6 and 8 h incubation with time-adapted breakpoints resulted in 84.0% and 88.5% interpretable results with assignment to the resistant or susceptible category. Major error and very major error rates for the 6 h readings were only 0.4% and 0.3%, virtually identical to those of 18 h AST reading.

**Conclusions:** Time-adapted clinical breakpoints in disc diffusion testing for Enterobacterales allow for accurate automated AST interpretation after shortened incubation times for a large number of antibiotics, with the additional possibility of subsequent confirmation after 18 h incubation.

### Note

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### Note

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