

Case Report

# Digital Infrastructure for Antimicrobial Susceptibility Testing and Surveillance: A CLSI and EUCAST-Based Model for Resource-Limited Settings

Djibril Mbarushimana<sup>1</sup>, MM, MD; Taofeek Tope Adegboyega<sup>2</sup>, PhD; Gatera Jean Damascene<sup>1</sup>, BSc; Muritala Issa Bale<sup>2</sup>, PhD; Buregeya Jean Damascene<sup>1</sup>, MSc; Kayitesi Marie Francoise<sup>1</sup>, MM, MD; Itangishaka Innocent<sup>1</sup>, BSc; Rugamba Alexis<sup>2</sup>, PhD; Rasheed Omotayo Adeyemo<sup>2</sup>, PhD; Bagirinshuti Issa<sup>1</sup>, BACY; Saheed Adekunle Akinola<sup>2</sup>, PhD; Ahmed Adebawale Adedeji<sup>2</sup>, Prof Dr; Mushuru Evariste<sup>1</sup>, MM, MD; Busumbigabo Albert<sup>1</sup>, PharmB, MSc; Mukamana Felicite<sup>1</sup>, MM, MD; Habarurema Sylvain<sup>1</sup>, MM, MD; Felix Habarugira<sup>1</sup>, MSc; Jean Paul Sinumvayo<sup>2</sup>, PhD; Rutambika Noel<sup>1</sup>, PharmB, MSc; Twagirumugabe Theogene<sup>1</sup>, Prof Dr Med; Ndoli Minega Jules<sup>1</sup>, MM, MD; Ngarambe Christian<sup>1</sup>, MM, MD

<sup>1</sup>University Teaching Hospital of Butare, Huye, Rwanda

<sup>2</sup>Department of Microbiology and Parasitology, School of Medicine and Pharmacy, University of Rwanda, Kigali, Rwanda

## Corresponding Author:

Djibril Mbarushimana, MM, MD  
University Teaching Hospital of Butare  
P.O. Box 254, Hospital Avenue, Mamba Ngoma  
Huye  
Rwanda  
Phone: 250 788575656  
Email: [djidji01@gmail.com](mailto:djidji01@gmail.com)

## Abstract

**Background:** Antimicrobial resistance (AMR) poses a significant global health threat, requiring effective antimicrobial susceptibility testing (AST) and surveillance systems. At the University Teaching Hospital of Butare (CHUB) in Rwanda, a baseline Laboratory Assessment of Antibiotic Resistance Testing Capacity (LAARC) identified critical gaps in the Laboratory Information System (LIS), including low capture rates for culture observation (60%) and AST data (25%), no standardization of AST panels (0%), and limited cumulative antibiogram generation (17%). Existing AMR surveillance platforms, such as the Information System for Monitoring Antimicrobial Resistance by the World Health Organization (WHO) Collaborating Center for Surveillance of Resistance to Antimicrobial Agents (WHONET), and the District Health Information System, operate as standalone systems separate from clinical workflows, which limits their real-time clinical utility.

**Objective:** This study aimed to develop an enhanced, web-based LIS integrated within routine clinical care to improve AST reliability, enable real-time AMR surveillance at CHUB, and provide a scalable model for subnational and national surveillance networks in resource-limited settings, supporting antimicrobial stewardship.

**Methods:** We developed an enhanced LIS using the OpenClinic GA, the current open-source hospital information system at CHUB, integrating Clinical and Laboratory Standards Institute (CLSI) and European Committee on Antimicrobial Susceptibility Testing (EUCAST) guidelines, and leveraging metadata from the AMR for R package, WHONET resources, and EUCAST Expert Rules. An agile development approach was used, incorporating a custom database schema, Java-based application programming interfaces (APIs), and web-based user interfaces. The system was designed to support minimum inhibitory concentration (MIC) and disk diffusion (DD) methods, automate result interpretation with color-coded outputs, WHO Access, Watch, Reserve (AWaRe)-based cascade reporting, and enable data export to WHONET for global surveillance.

**Results:** The enhanced LIS improved AST data capture and standardization, providing reliable, automated result interpretation and real-time AMR surveillance capabilities. The system's web-based architecture enables scalability through centralized deployment, allowing multiple facilities simultaneous access. Unlike standalone surveillance tools, the enhanced LIS integrates AST within electronic medical records, maintaining clinical information continuity from specimen registration through result reporting. The system supports immediate clinical decision through AWaRe-based cascade reporting, and automated resistance phenotype detection, followed by standardized WHONET-compatible exports for public health surveillance.

**Conclusions:** This scalable, LIS model demonstrates the feasibility of implementing standards-based AMR informatics in resource-limited settings. By embedding surveillance within clinical workflows rather than treating it as a separate downstream activity, the system maximizes data quality and clinical relevance while minimizing staff burden. The centralized web-based architecture provides inherent scalability from facility to national levels, eliminating data fragmentation and ensuring metadata consistency across networks. Long-term sustainability requires continuous user training, designated personnel for metadata maintenance, local IT capacity building, and funding mechanisms beyond donor dependency. This model provides a practical roadmap for national digital stewardship programs, supporting both immediate patient care and long-term public health surveillance goals.

*JMIR Form Res* 2026;10:e82727; doi: [10.2196/82727](https://doi.org/10.2196/82727)

**Keywords:** antimicrobial susceptibility testing; CLSI; EUCAST; Laboratory Information System; antimicrobial stewardship; resource-limited settings; openClinic GA; University Teaching Hospital of Butare; WHONet

Introduction

Antimicrobial Resistance (AMR) Surveillance Challenges in Resource-Limited Settings

Antimicrobial Resistance (AMR) is a global health emergency, with the World Health Organization (WHO) estimating 10 million annual deaths by 2050 if unchecked [1]. Effective antimicrobial susceptibility testing (AST) and robust surveillance systems are fundamental to combating AMR. AST guides appropriate therapy at the patient level, while surveillance aggregates resistance data to monitor trends and inform evidence-based treatment guidelines [2, 3]. Resource-limited settings, particularly in Sub-Saharan Africa, face significant barriers to implementing reliable AST and surveillance infrastructure, including inadequate laboratory information systems, inconsistent adoption of standardized guidelines (Clinical and Laboratory Standards Institute [CLSI] and European Committee on Antimicrobial Susceptibility Testing [EUCAST]), [4] limited access to quality-assured testing protocols, and fragmented data

management that impairs interoperability with national and global surveillance networks [5-8], undermine antimicrobial stewardship efforts and exacerbate AMR.

Baseline Deficiencies at the University Teaching Hospital of Butare

The University Teaching Hospital of Butare (CHUB), a tertiary referral center in Rwanda, exemplifies these challenges. CHUB’s LIS (Laboratory Information System), built on the OpenClinic GA open-source hospital information system [9], exhibited critical deficiencies in microbiology services. A baseline Laboratory Assessment of Antibiotic Resistance Testing Capacity (LAARC) [10], identified critical deficiencies: 60% capture rate for culture observation, 25% for AST data, 0% standardization of AST panels, and 17% generation of cumulative antibiograms, reflecting systemic issues in resource-limited settings. The assessment revealed several qualitative deficiencies in the LIS that compromised bacteriology services at CHUB (Table 1) [11], which reflect systemic issues, where LIS platforms lack specialized microbiology functionality necessary for standards-compliant AST and surveillance.

**Table 1.** Qualitative LIS<sup>a</sup> deficiencies identified by the LAARC baseline assessment.

Deficiency	Impact
Does not record AST <sup>b</sup> method: Minimum Inhibitory Concentration (MIC) or Disk Diffusion (DD)	Hinders traceability of test methods
Cannot hide individual antibiotic results	Prevents cascade/selective reporting [12]
Only Susceptible, Intermediate, or Resistant (S/I/R) interpretations entered	Limits data granularity for analysis
Lacks automated interpretation	Manual processes, increasing error risk
EUCAST <sup>c</sup> Expert Rules not integrated	Limits clinical decision support
Inconsistent antibiotic panels	Results in data unsuitable for reliable cumulative antibiogram generation
Original results deleted during corrections	Compromises audit trails

<sup>a</sup>LIS: Laboratory Information System.

<sup>b</sup>AST: antimicrobial susceptibility testing.

<sup>c</sup>EUCAST: European Committee on Antimicrobial Susceptibility Testing.

Study Rationale and Objectives

Addressing the revealed gaps requires an enhanced LIS that integrates international AST standards, automates result interpretation, standardizes testing panels, and enables seamless data export to surveillance networks. This study

aimed to develop such a system at CHUB leveraging the OpenClinic GA platform and integrating CLSI and EUCAST guidelines [2,3], incorporating metadata from the AMR for R package [13], and from the Information System for Monitoring Antimicrobial Resistance by World Health Organization

(WHO) Collaborating Center for Surveillance of Resistance to Antimicrobial Agents (WHONET) [6,14,15], as well as EUCAST Expert Rules and expected phenotypes [16].

The enhanced LIS was designed to resolve all LAARC-identified deficiencies, standardize AST processes, enable real-time AMR surveillance, and facilitate data interoperability with the WHO Global Antimicrobial Resistance Surveillance System (GLASS) and national platforms. By building on OpenClinic GA’s established infrastructure, the system provides a scalable, open-source model tailored to resource-limited settings, improving data quality, supporting evidence-based antimicrobial stewardship, and contributing to global AMR monitoring efforts. This approach offers a replicable blueprint for tertiary hospitals and reference laboratories in Sub-Saharan Africa and similar contexts, demonstrating how standards-based digital infrastructure can address critical surveillance gaps with minimal resource requirements and sustainable, locally adaptable solutions.

Methods

Study Design and Setting

This technical implementation study was conducted at CHUB, a key microbiology center in Rwanda, from January 2024 to June 2025. The study focused on upgrading the

CHUB LIS, built on the OpenClinic GA open-source hospital information system [9], to address LAARC-identified deficiencies, leveraging metadata from the AMR for the R package and EUCAST Expert Rules.

System Development Approach

An agile methodology facilitated iterative development, incorporating feedback from laboratory staff, clinicians, and public health experts. Requirements targeted improved data capture, AST panel standardization, antibiogram generation, and interoperability with global surveillance systems, extending the capabilities of the OpenClinic GA platform. The agile approach was chosen based on its proven effectiveness in developing health information systems in low-resource settings [17,18].

Data Analysis and Metadata Integration

Metadata from the AMR for R package, including microbial taxonomy, antimicrobial profiles, and clinical breakpoints, were analyzed to standardize AST processes. EUCAST Expert Rules and expected phenotypes guided automated interpretations and dynamic testing panel generation. Nine metadata files, all in tab separated values (TSV) format, were integrated, each mapped to specific database tables within the OpenClinic GA system (Table 2).

**Table 2.** Integrated metadata files for LIS enhancement. The integration of these metadata files was based on their reliability and global compatibility [6,19-21].

File content	Purpose	Key fields
Clinical breakpoints	Stores CLSI/EUCAST <sup>ab</sup> breakpoint data defining S/R thresholds	Guideline, test method, pathogen, antimicrobial, breakpoint values
Microorganisms	Provides taxonomic and characteristic data for microbial identification	Pathogen identifier, kingdom, genus, species, prevalence, clinical codes (SNOMED <sup>c</sup> )
Antimicrobials	Details antimicrobial agents with Access, Watch, Reserve (AWaRe) classifications	Antibiotic name, class, potency, administration routes, standardized codes (WHONET <sup>d</sup> )
Antimicrobial screening rules	Defines screening rules for specific pathogens	Antimicrobial, target pathogen, screening criteria
Testable Antimicrobials	Lists antimicrobials with standardized AST <sup>e</sup> breakpoints	Group, name, abbreviation, AWaRe classification
Expected Phenotypes	Incorporates EUCAST Expert Rules for expected phenotypes	Antimicrobial, pathogen, phenotype (susceptible/resistant)
Site-Sample Mapping	Maps clinical sites to sample types	Site, specimen type (eg, Respiratory → Sputum)
WHONET Specimen Mapping	Standardizes specimen codes for WHONET interoperability	Local codes, WHONET specimen type codes
AWaRe Classification	Classifies antibiotics into AWaRe categories	Antibiotic name, AWaRe category

<sup>a</sup>CLSI: Clinical and Laboratory Standards Institute.

<sup>b</sup>EUCAST: European Committee on Antimicrobial Susceptibility Testing.

<sup>c</sup>SNOMED: Systematized Nomenclature of Medicine.

<sup>d</sup>WHONET: World Health Organization (WHO) Collaborating Center for Surveillance of Resistance to Antimicrobial Agents.

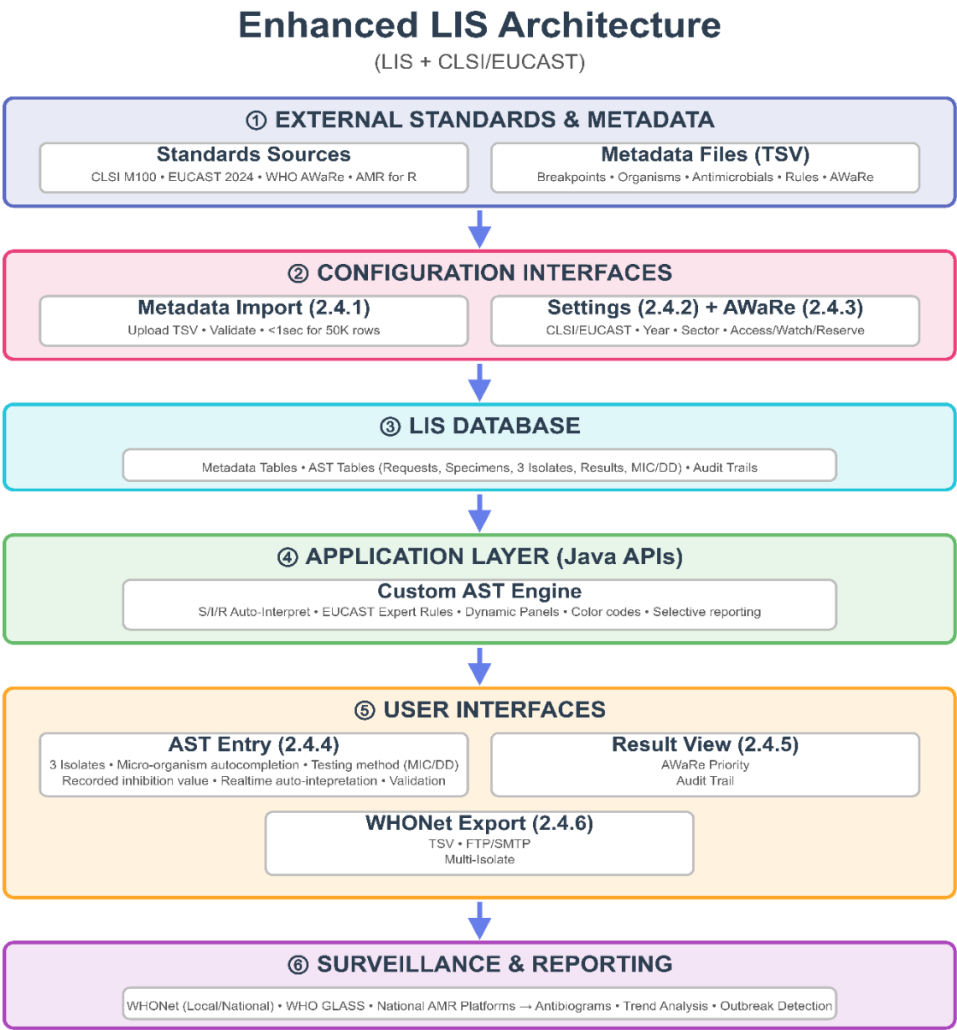
<sup>e</sup>AST: antimicrobial susceptibility testing.

System Architecture and Functionalities

The LIS was developed by extending the OpenClinic GA open-source web-based hospital information system, incorporating a custom database schema, Java-based APIs,

and a web-based interface, optimized for resource-limited settings. The system comprises five key user interfaces, each designed for usability and compliance with CLSI, EUCAST, and WHO GLASS standards (Figure 1).

**Figure 1.** High-level schematic representation of the enhanced LIS architecture and end-to-end data flow. Circled numbers (①-⑥) denote the six architectural layers of the system. Numbers in parentheses refer to subsections in section 2.4 (system architecture and functionalities) where detailed technical descriptions are provided. AST: antimicrobial susceptibility testing; API: application programming interface; AWaRe: Access, Watch, Reserve; CLSI: Clinical and Laboratory Standards Institute; DD: disk diffusion; EUCAST: European Committee on Antimicrobial Susceptibility Testing; LIS: Laboratory Information System; MIC: Minimum Inhibitory Concentration; TSV: Tab Separated Values; WHONET: World Health Organization Collaborating Center for Surveillance of Resistance to Antimicrobial Agents.

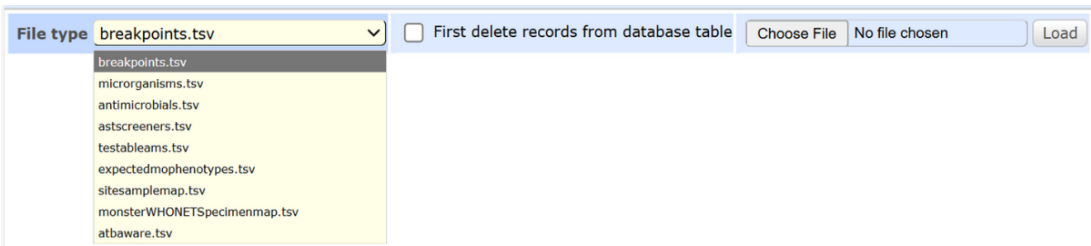


**Metadata Import Interface**

A web-based tool simplifies the import and update of metadata files within the OpenClinic GA. Users select a file type from a dropdown menu, upload TSV files, and optionally clear existing data. The system validates file headers, provides real-time feedback on errors (eg, invalid

format), and deletes temporary files to optimize storage. This interface leverages OpenClinic GA’s robust file-handling capabilities to ensure efficient data management by enabling nontechnical users to update metadata with minimal training (Figure 2).

**Figure 2.** Screenshot of the metadata import interface, showing the dropdown menu for selecting file types, the file upload button, and the feedback panel for validation status.



## Configuration Interface

A web-based tool allows users to configure the AST guideline (EUCAST/CLSI), guideline year, and sector (human or animal) to adapt the system to local needs (Figure 3).

**Figure 3.** Screenshot of the configuration interface, displaying dropdown menus for selecting AST guideline (CLSI/EUCAST), guideline year, and sector (human/animal), with multilingual support options. AST: antimicrobial susceptibility testing; CLSI: Clinical and Laboratory Standards Institute; EUCAST: European Committee on Antimicrobial Susceptibility Testing.

Labo		
ASTguideline	CLSI	EUCAST
ASTguidelineYear		2024
ASTsector	human	human

## AWaRe Classification Management Interface

A dedicated tool manages the AWaRe classification of testable antibiotics. It displays a sortable table of antibiotics

with their group, name, abbreviation, and AWaRe status or Not Available. Users update classifications via dropdown menus, with changes tracked client-side using JavaScript and submitted asynchronously to the server for database updates (Figure 4).

**Figure 4.** Screenshot of the AWaRe classification management interface, showing a sortable table of antibiotics with dropdown menus for updating AWaRe status and real-time feedback indicators. AST: antimicrobial susceptibility testing; AWaRe: Access, Watch, Reserve.

Group	Name	Ab	AWaRe	Status
Aminoglycosides	Amikacin	AMK	Access	Unchanged
Aminoglycosides	Gentamicin	GEN	Access	Unchanged
Aminoglycosides	Gentamicin-high	GEH	Access	Unchanged
Aminoglycosides	Kanamycin	KAN	Watch	Unchanged
Aminoglycosides	Kanamycin/cephalexin	KAC	Watch	Unchanged
Aminoglycosides	Neomycin	NEO	Watch	Unchanged
Aminoglycosides	Netilmicin	NET	Watch	Unchanged
Aminoglycosides	Plazomicin	PLZ	Reserve	Unchanged
Aminoglycosides	Streptoduoicin	STR	Watch	Unchanged
Aminoglycosides	Streptomycin-high	STH	Watch	Unchanged
Aminoglycosides	Tobramycin	TOB	Watch	Unchanged
Amphenicols	Chloramphenicol	CHL	Access	Unchanged

## AST Result Entry Interface

Integrated into worklist management, this modal dialog supports manual entry and validation for up to three isolates per specimen, aligning with CLSI/EUCAST recommendations. Key features include: standardized pathogen identification via WHONET/EUCAST/CLSI taxonomy with autocompletion; dynamic antibiotic panels that expand based

on whether to include screened antibiotics and/or those with expected phenotypes; real-time color-coded validation (green=Susceptible, yellow=Intermediate, red=Resistant) for inhibition zones or MIC values; icons indicating related antimicrobials and administration-route-dependent interpretations; alerts for invalid inputs, and incomplete method specification (Figure 5).



**Figure 5.** Screenshot of the AST result entry interface, showing the modal dialog with isolate panels, dynamic antimicrobial table, color-coded result fields, and autocompletion for pathogen identification. MIC: minimum inhibitory concentration.

**Antibiogram**

Germ 1 Moraxella catarrhalis			Germ 2 Streptococcus pneumoniae			Germ 3 Staphylococcus aureus		
Test screened <input type="checkbox"/> Test expected <input type="checkbox"/>			Test screened <input type="checkbox"/> Test expected <input type="checkbox"/>			Test screened <input type="checkbox"/> Test expected <input type="checkbox"/>		
Antimicrobial	Method	Result	Antimicrobial	Method	Result	Antimicrobial	Method	Result
Amoxicillin/Clavulanic acid	DISK(20/10µg) MIC <input type="radio"/>	23	Chloramphenicol	DISK(30µg) <input checked="" type="radio"/> MIC <input type="radio"/>	23	Cefoxitin	DISK(30µg) <input checked="" type="radio"/> MIC <input type="radio"/>	12
Cefotaxime	MIC <input checked="" type="radio"/>	1	Clindamycin	DISK(2µg) <input checked="" type="radio"/> MIC <input type="radio"/>	12	Chloramphenicol	DISK(30µg) <input checked="" type="radio"/> MIC <input type="radio"/>	13
Ceftazidime	MIC <input checked="" type="radio"/>	2	Erythromycin	DISK(15µg) <input checked="" type="radio"/> MIC <input type="radio"/>	32	Clindamycin	DISK(2µg) <input checked="" type="radio"/> MIC <input type="radio"/>	14
Ceftriaxone	MIC <input checked="" type="radio"/>	1	Oxacillin	DISK(1µg) <input checked="" type="radio"/> MIC <input type="radio"/>	24	Erythromycin	DISK(15µg) <input checked="" type="radio"/> MIC <input type="radio"/>	25
Chloramphenicol	MIC <input checked="" type="radio"/>	9	Rifampin	DISK(5µg) <input checked="" type="radio"/> MIC <input type="radio"/>	22	Gentamicin	DISK(10µg) <input checked="" type="radio"/> MIC <input type="radio"/>	12
Rifampin	MIC <input checked="" type="radio"/>	6	Tetracycline	DISK(30µg) <input checked="" type="radio"/> MIC <input type="radio"/>	13	Rifampin	DISK(5µg) <input checked="" type="radio"/> MIC <input type="radio"/>	23
Tetracycline	DISK(30µg) <input checked="" type="radio"/> MIC <input type="radio"/>	17	Trimethoprim/Sulfamethoxazole	DISK(1.25/23.7 5µg) <input checked="" type="radio"/> MIC <input type="radio"/>	14	Tetracycline	DISK(30µg) <input checked="" type="radio"/> MIC <input type="radio"/>	34
						Trimethoprim/Sulfamethoxazole	DISK(1.25/23.7 5µg) <input checked="" type="radio"/> MIC <input type="radio"/>	14

Save Add Close

**AST Result View Form**

Integrated into laboratory results view, this interface displays finalized AST results for clinicians, infection control staff, and surveillance teams, aligning with CLSI, EUCAST guidelines [12,22-24]. Results appear in modal dialogs grouped by patient and request time, showing up to three isolates with organism names, antimicrobials, S/I/R interpretations, and phenotype indicators. AWARe-based selective display prioritizes Access antibiotics when susceptible or

intermediate, then Watch, then Reserve. Read-only format ensures data integrity; edit history icons track corrections with timestamps and user details. Any pathogen isolated triggers red danger icons in the laboratory results overview that corresponds to automated SMS notifications at result validation sent to the patient informing result availability and to the requesting clinician alerting to urgently review results and take clinical action (Figure 6).

**Figure 6.** Screenshot of the AST result view form, showing the modal dialog with a grouped results table, color-coded isolate data, AWARe-filtered antibiotic display, and tooltips for phenotypic comments. AST: antimicrobial susceptibility testing; AWARe: Access, Watch, Reserve.

**Antibiogram**

Germ 1 Moraxella catarrhalis		Germ 2 Streptococcus pneumoniae		Germ 3 Staphylococcus aureus	
Test screened <input type="checkbox"/> Test expected <input type="checkbox"/>		Test screened <input type="checkbox"/> Test expected <input type="checkbox"/>		Test screened <input type="checkbox"/> Test expected <input type="checkbox"/>	
Antimicrobial	Result	Antimicrobial	Result	Antimicrobial	Result
Amoxicillin/Clavulanic acid	I	Chloramphenicol	S	Cefoxitin	R
Chloramphenicol	R	Clindamycin	R	Chloramphenicol	I
Tetracycline	R	Erythromycin	S	Clindamycin	I
		Oxacillin	S	Erythromycin	S
		Tetracycline	R	Gentamicin	I
		Trimethoprim/Sulfamethoxazole	R	Tetracycline	S
				Trimethoprim/Sulfamethoxazole	I

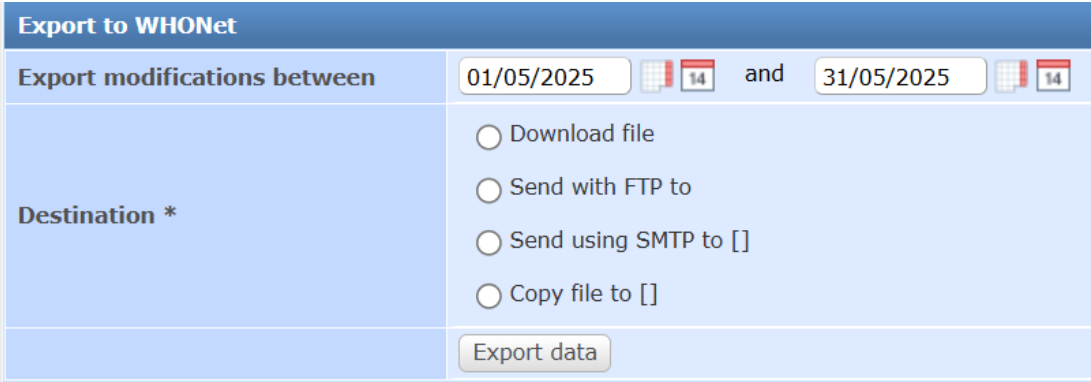
**WHONET Export Interface**

This interface enables seamless export of AST results to WHONET for global AMR surveillance, complying with WHONET’s data formatting requirements. A web form with calendar widgets allows date range selection and export

destination choice (download, FTP, SMTP, or directory). The system queries finalized AST records within the selected range, supporting multi-isolate reporting with patient demographics (ID, sex, age, WHO/CLSI age categories), specimen type (WHONET-mapped), pathogen identification,

test method, antimicrobial codes, result values, S/I/R interpretations, guideline, sector, and workflow timestamps. Output generates TSV files matching WHONET import specifications, with legacy CSV support (Figure 7) [25,26].

**Figure 7.** Screenshot of the WHONET export interface, displaying the web form with calendar widgets for date range selection, a dropdown for export destination, and feedback on export status. WHONET: World Health Organization Collaborating Center for Surveillance of Resistance to Antimicrobial Agents.



**Ease of Integration and Interoperability**

The enhanced LIS incorporates interoperability features tailored for resource-limited settings, supporting structured data formats (TSV, CSV, JSON, HL7, FHIR) for direct mapping of organism codes, test results, and interpretations. Plug-and-play API endpoints enable the LIS to integrate with other systems with minimal development effort. Direct export to WHONET, WHO GLASS, and national platforms includes automated local-to-surveillance code mapping.

**User Verification, Training and Deployment**

Structured user verification and training were conducted before hospital-wide go-live. A dedicated User Acceptance testing was carried out by a team composed of the Laboratory Quality Manager, Microbiology Section Lead, and Information Communication Technology (ICT) staff under the supervision of the Head of Pathology. Nineteen detailed test cases covering system configuration, metadata import, AST result entry (disk diffusion and MIC), dynamic panel generation, EUCAST Expert Rules application, AWaRe-based cascade reporting, audit trails, WHONET export, data integrity, performance, and multilingual support were executed on 10 prospective samples, as per the laboratory standard operating procedure on user verification of LIS. All 19 test cases passed (100 % pass rate). Minor adjustments, mainly related to character encoding compatibility, were applied iteratively.

The six bacteriology laboratory staff received a full day of hands-on training. A 30-minute hospital-wide flash presentation of the new AST reporting features was delivered during clinical grand rounds, and finally, a 5-minute video tutorial covering the entire workflow was produced and disseminated via the hospital’s official WhatsApp groups

The enhanced AST module fully replaced the legacy entry workflow for all new microbiology requests. For backward compatibility and data integrity, the previous (legacy) AST entry and viewing functionality was not removed or disabled. All AST results entered before enhancement remain fully accessible, searchable, and viewable in their original format without any modification or migration issues.

**Ethical Considerations**

The project received ethical approval from the CHUB Research-Ethics Committee (REC/UTHB/91/2023 renew, October 20th, 2024); individual informed consent was waived as the study was a quality-improvement intervention using routine clinical data. Patient confidentiality and data protection fully comply with hospital policy through role-based user authentication, display of patient identifiers and clinical information only to authorized clinical users, secure hosting within the hospital’s firewalled data center with twice daily backups, and complete removal of identifiers from all shared data and aggregate datasets.

**Results**

The enhanced LIS, built on OpenClinic GA, significantly improved CHUB’s bacteriology services, addressing LAARC-identified deficiencies (Multimedia Appendix 1). The system resolved qualitative gaps identified in the baseline LAARC audit, as detailed below.

**Resolution of Qualitative Deficiencies**

The enhanced LIS addressed the qualitative deficiencies identified in the LAARC audit (Section 1.4), all fully resolved. The following Table 3 summarizes the resolution status, referencing relevant system functionalities:

**Table 3.** Resolution status of LAARC qualitative deficiencies.

LAARC deficiency	Status	Evidence and notes
Does not record AST method	Fully Resolved	Captures MIC/DD methods in the AST Result Entry Interface (Section 2.4.4) and includes them in WHONET exports (Section 2.4.5).
Cannot suppress antibiotic results for cascade reporting	Fully Resolved	AST Result View Form (Section 2.4.6) implements AWARe-based cascade reporting.
Only S/I/R entered, not inhibition zone	Fully Resolved	AST Result Entry Interface (Section 2.4.4) captures inhibition zones/MIC values with automated S/I/R interpretation.
Cannot automatically interpret zone sizes	Fully Resolved	Automates S/I/R interpretation using CLSI/EUCAST breakpoints (Section 2.4.4).
Expert rules not integrated	Fully Resolved	Integrates EUCAST Expert Rules for phenotypic predictions (Sections 2.3, 2.4.4, 2.4.6).
Inconsistent antibiotic panels	Fully Resolved	Achieves 100% panel standardization (Section 3) via metadata-driven panels (Section 2.3) and AWARe Classification Management Interface (Section 2.4.3).
Original results deleted during corrections	Fully Resolved	Tracks corrections via edit history icons in the AST Result View Form (Section 2.4.6), logging edited results with timestamps, reason and user details.

<sup>a</sup>LAARC: Laboratory Assessment of Antibiotic Resistance Testing Capacity.

<sup>b</sup>AST: antimicrobial susceptibility testing.

<sup>c</sup>MIC: minimum inhibitory concentration.

<sup>d</sup>DD: disk diffusion.

<sup>e</sup>WHONET: World Health Organization (WHO) Collaborating Center for Surveillance of Resistance to Antimicrobial Agents.

<sup>f</sup>AWARe: Access, Watch, Reserve.

<sup>g</sup>S/I/R: Susceptible, Intermediate, or Resistant.

<sup>h</sup>CLSI: Clinical and Laboratory Standards Institute.

<sup>i</sup>EUCAST: European Committee on Antimicrobial Susceptibility Testing.

## Key Functionalities

The system offers comprehensive AST functionality supporting both MIC and DD methods with automated interpretation based on the selected guideline. Results are displayed using color-coded outputs: green for Susceptible, yellow for Intermediate, red for Resistant, and pink for out-of-range values. The system provides real-time notifications for critical isolates to ensure timely clinical intervention.

Dynamic testing panels automatically adjust based on breakpoints, local antimicrobial stock availability, and clinical context, incorporating EUCAST Expert Rules and expected phenotypes. The cascade reporting feature prioritizes WHO AWARe “Access” antibiotics, thereby reducing inappropriate use of “Watch” and “Reserve” categories.

For surveillance purposes, data export aligns with WHONET variable definitions, enabling seamless integration with WHO GLASS and national surveillance systems through robust interoperability features. The web-based interfaces, including the AST Result View Form, require minimal training and incorporate real-time feedback and tooltips to enhance usability for nontechnical staff.

## Discussion

The enhanced LIS, built upon the OpenClinic GA open-source hospital information system, addresses critical gaps in CHUB’s microbiology services, offering a robust, standards-compliant solution for AST and surveillance in

resource-limited settings. By integrating CLSI and EUCAST guidelines with metadata from the AMR for R package and EUCAST Expert Rules, the system ensures reliable AST results and real-time surveillance capabilities. The agile development approach, coupled with stakeholder engagement, resulted in a user-friendly system accessible to laboratory staff with minimal technical expertise.

The metadata-driven design, particularly the use of WHO AWARe classifications and EUCAST Expert Rules, optimizes antimicrobial testing and supports stewardship by prioritizing “Access” antibiotics and flagging critical resistance mechanisms. The WHONET export interface enhances interoperability with global surveillance networks, contributing to AMR monitoring and policy development [1].

## Comparison With Existing AMR Surveillance Platforms

The enhanced LIS offers distinct advantages over other popular AMR surveillance platforms by providing comprehensive, integrated laboratory workflow management within a clinical care context. Unlike WHONET, which operates as a standalone desktop on Windows environments and focuses exclusively on bacteriology data [27,28], the enhanced LIS is fully web-based, supports comprehensive clinical laboratory operations across all departments (hematology, biochemistry, immunology, microbiology) and accessible from any device with a standard browser, enabling real-time data entry, validation, and clinical decision support at the point of care. Integrated within the electronic medical record system,



the enhanced LIS maintains continuity of clinical information flow from specimen registration through result reporting, directly supporting antimicrobial stewardship through features such as AWaRe-based cascade reporting, automated resistance phenotype detection via EUCAST Expert Rules, and critical alerts that prompt immediate clinical review. While District Health Information System (DHIS2) excels at aggregate health program reporting across multiple domains [29,30], the enhanced LIS provides specimen-level granularity essential for individual patient management, combining automated CLSI/EUCAST-based AST interpretation and quality-assured data validation within a single platform. This integrated approach ensures data serves dual purposes: immediate clinical utility for patient care and antimicrobial stewardship at the facility level, followed by standardized WHONET-compatible exports for public health surveillance at subnational, national, and global levels [6, 15]. By embedding AMR surveillance capabilities within routine clinical workflows rather than treating surveillance as a separate downstream activity, the enhanced LIS maximizes data quality, clinical relevance, and public health impact while minimizing the burden on laboratory staff.

### **Scalability to Subnational and National AMR Surveillance Networks**

The web-based architecture of the enhanced LIS provides inherent scalability for subnational and national AMR surveillance networks through centralized deployment models. The system can be hosted on centralized servers, enabling simultaneous access by multiple testing facilities through standard web browsers without requiring local software installation or high-specification hardware at peripheral sites. This approach ensures real-time data visibility across the network: facility-level users enter AST results through the web interface, while supervisory-level surveillance teams access aggregated data from the same system. From any supervisory level, the WHONET export interface generates standardized data files compliant with WHO GLASS requirements, enabling seamless reporting to global surveillance networks. The centralized model eliminates data fragmentation common in resource-limited settings, reduces infrastructure costs by avoiding multiple server deployments, and ensures metadata consistency (breakpoints, antimicrobial panels, AWaRe classifications) across all participating facilities.

### **Sustainability Considerations**

Long-term sustainability of the enhanced LIS requires attention to three critical areas. First, continuous user

training programs must be established to maintain laboratory staff competency in system use, AST interpretation, and data quality assurance. Second, metadata updates require sustainable mechanisms, including periodic review of CLSI/EUCAST guideline updates, AMR for R package datasets, WHONET resources and taxonomies, local antimicrobial availability changes, and emerging resistance patterns, with designated personnel responsible for metadata maintenance and validation. Third, ongoing technical support requires a multifaceted approach: capacity building for local information technology staff to handle routine troubleshooting, system upgrades, and eventually instrument integration; and sustainable funding mechanisms beyond donor-dependent models to ensure long-term system functionality and relevance.

### **Limitations and Future Directions**

This study primarily describes the technical development and the qualitative resolution of LIS deficiencies identified in the baseline LAARC audit. Quantitative evaluation of key performance indicators was intentionally deferred to allow sufficient post-implementation observation time. Additional limitations include dependency on manual metadata updates and import, which may be challenging in resource-limited settings. Ongoing training is required to sustain system adoption and ensure data quality. Future enhancements could include automatic metadata updates, mobile app integration, and machine learning for predictive resistance modeling, which have shown promise in other AMR surveillance systems [23,31,32].

### **Conclusion**

The enhanced LIS, built on OpenClinic GA and leveraging CLSI, EUCAST, and AMR for R metadata, demonstrates the feasibility of implementing standards-based AMR informatics in resource-limited settings. By significantly improving AST reliability, integrating clinical decision support, and enabling seamless integration with global surveillance networks, this model provides a practical roadmap for national digital stewardship programs. The system's scalability from facility to national levels, combined with its open-source foundation and standards-compliant architecture, offers a replicable blueprint for addressing AMR challenges, supporting both immediate patient care and long-term public health surveillance goals. Widespread adoption of such standards-based digital surveillance systems could significantly contribute to reducing AMR burden through earlier detection of resistance trends and evidence-based policy interventions.

### **Acknowledgments**

We thank the CHUB laboratory staff, clinicians, and public health experts for their invaluable feedback. The authors declare the use of Generative Artificial Intelligence (GAI) in the development of code for the LIS and manuscript writing process. According to the GAIDeT taxonomy (2025), the following tasks were delegated to GAI tools under full human supervision: code generation, code optimization, proofreading and editing, summarizing text, and reformatting. The GAI tools used were Grok 3, Gemini 3, GitHub Copilot, and Claude 4. Responsibility for the final manuscript lies entirely with the authors, and GAI tools are not listed as authors and do not bear responsibility for the outcomes [33].

### **Funding**

This study was funded by Pfizer through Grant Award Number 89814477 as part of the project on Capacity Building for Implementation of AMS Program and AMR surveillance at the University Teaching Hospital of Butare (CHUB).

### Data Availability

Metadata files, system documentation, and deidentified sample data are available at [https://archive.org/download/metadata\\_LIS\\_CLISI\\_EUCAST/Imetadata\\_LIS\\_CLISI\\_EUCAST.zip](https://archive.org/download/metadata_LIS_CLISI_EUCAST/Imetadata_LIS_CLISI_EUCAST.zip) under a Creative Commons Attribution 4.0 International License.

### Authors' Contributions

- DM (Senior Consultant Pathologist, CHUB): Conceptualized the study, developed the model, served as principal investigator, and manuscript writing.
- ATT (Microbiologist, UR): Co-principal investigator, led the Research team, and contributed to manuscript drafting.
- GJD (IT expert, CHUB): Led user acceptance test and integration of new functionalities on production.
- MIB (Microbiologist, UR): Led the Diagnostic Stewardship team, contributed to metadata integration, and reviewed the manuscript.
- BJD (Laboratory Scientist, CHUB): Trained staff on microbiology processes, contributed to system testing, and reviewed the manuscript.
- KMF (Ear Nose and Throat Surgeon, CHUB): Served as General Secretary, coordinated administrative tasks, and reviewed the manuscript.
- II (Laboratory Scientist, CHUB): Facilitated training on Quality Management Systems (QMS) and contributed to system validation.
- RAI (Biochemist, UR): Coordinated events and public outreach, and reviewed the manuscript.
- ARO (Microbiologist, UR): Managed cumulative antibiogram generation and contributed to data analysis.
- BI (Finance Manager, CHUB): Handled financial and administrative logistics, and reviewed the manuscript.
- ASA (Microbiologist, UR): Managed AMR isolate biobanking and contributed to system testing.
- AAA (Pharmacologist, UR): Led the Clinical Stewardship team, contributed to antimicrobial stewardship strategies, and reviewed the manuscript.
- ME (Internist, CHUB): Managed data collection and analysis, and reviewed the manuscript.
- BA (Pharmacist, CHUB): Served as AMS and AMR surveillance liaison, and contributed to system integration.
- MF (Ophthalmologist, CHUB): Facilitated concept note writing and reviewed the manuscript.
- HS (Internist, CHUB): Managed clinical treatment guidelines and contributed to manuscript review.
- FH (Public Health Specialist, CHUB): Served as secretary for the Clinical Stewardship team and reviewed the manuscript.
- JPS (Microbiologist, UR): Trained staff on antimicrobial stewardship and contributed to system testing.
- RN (Pharmacist, CHUB): Monitored antibiotic prescriptions and reviewed the manuscript.
- NMJ (Anesthesiologist, CHUB): Coordinated project teams, facilitated stakeholder engagement, and reviewed the manuscript.
- TT (Anesthesiologist, CHUB): Oversee project implementation, and reviewed the manuscript.
- CN (General surgeon, CHUB): Led administrative logistics, oversee stakeholder engagement, and reviewed the manuscript.

### Conflicts of Interest

None declared.

### Multimedia Appendix 1

Demo of new AST (antimicrobial susceptibility testing) reporting.

[[MP4 File \(MP4 video File\), 11375 KB-Multimedia Appendix 1](#)]

### References

1. Antimicrobial resistance: global report on surveillance. World Health Organization. 2014. URL: <https://iris.who.int/handle/10665/112642> [Accessed 2025-08-04]
2. EUCAST: Clinical breakpoints and dosing of antibiotics. URL: [https://www.eucast.org/clinical\\_breakpoints](https://www.eucast.org/clinical_breakpoints) [Accessed 2025-08-04]
3. EM100 Connect - CLSI M100 ED35:2025. URL: <https://em100.edaptivedocs.net/GetDoc.aspx?doc=CLSI%20M100%20ED35:2025&scope=user> [Accessed 2025-08-04]
4. Clinical & Laboratory Standards Institute: CLSI Guidelines. URL: <https://clsi.org/> [Accessed 2024-08-22]
5. Turner P, Rupali P, Opintan JA, et al. Laboratory informatics capacity for effective antimicrobial resistance surveillance in resource-limited settings. *Lancet Infect Dis*. Jun 2021;21(6):e170-e174. [doi: [10.1016/S1473-3099\(20\)30835-5](https://doi.org/10.1016/S1473-3099(20)30835-5)] [Medline: [33865461](#)]
6. Global antimicrobial resistance and use surveillance system (GLASS). WHO. URL: <https://www.who.int/initiatives/glass> [Accessed 2025-08-04]

7. Tools of the trade: data management software in AMR surveillance. Fleming Fund. URL: <https://www.flemingfund.org/publications/tools-of-the-trade-data-management-software-in-amr-surveillance/> [Accessed 2025-08-04]
8. Aboushady AT, Sujan MJ, Pham K, et al. Key Recommendations for Antimicrobial Resistance Surveillance: Takeaways From the CAPTURA Project. *Clin Infect Dis*. Dec 20, 2023;77(Suppl 7):S581-S587. [doi: [10.1093/cid/ciad487](https://doi.org/10.1093/cid/ciad487)] [Medline: [38118016](https://pubmed.ncbi.nlm.nih.gov/38118016/)]
9. Karara G, Verbeke F, Ndabaniwe E, Mugisho E, Nyssen M. OpenClinic GA Open Source Hospital Information System Enabled Universal Health Coverage Monitoring and Evaluation in Burundian Hospitals. *Stud Health Technol Inform*. 2017;245:738-742. [Medline: [29295196](https://pubmed.ncbi.nlm.nih.gov/29295196/)]
10. CDC. Laboratory assessment of antibiotic resistance testing capacity. Antimicrobial Resistance. Jun 2, 2025. URL: <https://www.cdc.gov/antimicrobial-resistance/php/toolkit/index.html> [Accessed 2025-08-04]
11. Muritala Bale I, Mbarushimana D, Buregeya D, Itangishaka I, Rasheed Omotayo A, Saheed Adekunle A. Findings of Baseline Laboratory Assessment of Antibiotic Resistance Testing Capacity (LAARC). University Teaching Hospital of Butare; URL: <https://archive.org/details/laarc-findings-report> [Accessed 2025-08-04]
12. Wu H, Lutgring JD, McDonald LC, et al. Selective and Cascade Reporting of Antimicrobial Susceptibility Testing Results and Its Impact on Antimicrobial Resistance Surveillance-National Healthcare Safety Network, April 2020 to March 2021. *Microbiol Spectr*. Jan 31, 2023;11(2):e0164622. [doi: [10.1128/spectrum.01646-22](https://doi.org/10.1128/spectrum.01646-22)] [Medline: [36719248](https://pubmed.ncbi.nlm.nih.gov/36719248/)]
13. Berends MS, Luz CF, Friedrich AW, Sinha BNM, Albers CJ, Glasner C. AMR. An R Package for Working with Antimicrobial Resistance Data. *Journal of Statistical Software*. 2022;104:1-31. [doi: [10.18637/jss.v104.i03](https://doi.org/10.18637/jss.v104.i03)]
14. O'Brien TF, Stelling JM. WHONET: an information system for monitoring antimicrobial resistance. *Emerg Infect Dis*. 1995;1(2):66-66. [doi: [10.3201/eid0102.950209](https://doi.org/10.3201/eid0102.950209)] [Medline: [8903165](https://pubmed.ncbi.nlm.nih.gov/8903165/)]
15. WHONET software. URL: <https://whonet.org/software.html> [Accessed 2024-08-22]
16. EUCAST: Expert rules and expected phenotypes. URL: [https://www.eucast.org/expert\\_rules\\_and\\_expected\\_phenotypes](https://www.eucast.org/expert_rules_and_expected_phenotypes) [Accessed 2025-08-04]
17. Boppana V. Implementing Agile Methodologies in Healthcare IT Projects. *GRRBE*. Oct 2024;10(5):172-182. [doi: [10.56805/grrbe.24.10.5.71](https://doi.org/10.56805/grrbe.24.10.5.71)]
18. Goodison R, Borycki EM, Kushniruk AW. Use of Agile Project Methodology in Health Care IT Implementations: A Scoping Review. *Stud Health Technol Inform*. 2019;257:140-145. [Medline: [30741186](https://pubmed.ncbi.nlm.nih.gov/30741186/)]
19. AWaRe classification of antibiotics for evaluation and monitoring of use. 2023. URL: <https://www.who.int/publications/i/item/WHO-MHP-HPS-EML-2023.04> [Accessed 2025-08-04]
20. Luz C. Data Science for Infection Management & Antimicrobial Stewardship. University of Groningen; 2021. [doi: [10.33612/diss.192486375](https://doi.org/10.33612/diss.192486375)]
21. Berends M. A New Instrument for Microbial Epidemiology: Empowering Antimicrobial Resistance Data Analysis. University of Groningen; 2021. [doi: [10.33612/diss.177417131](https://doi.org/10.33612/diss.177417131)]
22. Kahlmeter G, Thilly N, Pulcini C. Selective reporting of antibiotic susceptibility testing results: less is more. *Clin Microbiol Infect*. Apr 2021;27(4):503-505. [doi: [10.1016/j.cmi.2020.11.017](https://doi.org/10.1016/j.cmi.2020.11.017)] [Medline: [33253937](https://pubmed.ncbi.nlm.nih.gov/33253937/)]
23. Moran E, Robinson E, Green C, Keeling M, Collyer B. Towards personalized guidelines: using machine-learning algorithms to guide antimicrobial selection. *J Antimicrob Chemother*. Sep 1, 2020;75(9):2677-2680. [doi: [10.1093/jac/dkaa222](https://doi.org/10.1093/jac/dkaa222)] [Medline: [32542387](https://pubmed.ncbi.nlm.nih.gov/32542387/)]
24. Munting A, Damas J, Viala B, Prod'homme G, Guery B, Senn L. Impact of selective reporting of antibiotic susceptibility testing results on meropenem prescriptions for the treatment of *Pseudomonas aeruginosa* infections after 2020 EUCAST criteria update: an observational study in a university hospital. *Antimicrob Resist Infect Control*. Dec 30, 2022;11(1):165. [doi: [10.1186/s13756-022-01203-x](https://doi.org/10.1186/s13756-022-01203-x)] [Medline: [36585736](https://pubmed.ncbi.nlm.nih.gov/36585736/)]
25. World health organization collaborating centre for surveillance of antimicrobial resistance. BacLink: Exporting Data from an LIS (Laboratory Information Systems). World Health Organization; 2022. URL: [https://whonet.org/WebDocs/BacLink.4\\_Data\\_exports\\_Exporting\\_data\\_from\\_Laboratory\\_information\\_systems.pdf](https://whonet.org/WebDocs/BacLink.4_Data_exports_Exporting_data_from_Laboratory_information_systems.pdf) [Accessed 2025-08-04]
26. World health organization collaborating centre for surveillance of antimicrobial resistance. BacLink: Data Conversion and Code Mapping. World Health Organization; 2022. URL: [https://whonet.org/WebDocs/BacLink.9\\_BacLink\\_and\\_data\\_conversion\\_and\\_code\\_mapping.pdf](https://whonet.org/WebDocs/BacLink.9_BacLink_and_data_conversion_and_code_mapping.pdf) [Accessed 2025-08-04]
27. Dikkatwar M, Vaghasiya J. Development and application of WHONET software in hospital antibiogram. *Clin Epidemiol Glob Health*. Nov 2023;24:101424. [doi: [10.1016/j.cegh.2023.101424](https://doi.org/10.1016/j.cegh.2023.101424)]
28. Maharjan S, Gallagher P, Gautam M, et al. Barriers and perceptions of WHONET/BacLink adoption in Nepal: A qualitative study of clinical microbiology laboratories. *PLOS ONE*. 2025;20(7):e0326658. [doi: [10.1371/journal.pone.0326658](https://doi.org/10.1371/journal.pone.0326658)] [Medline: [40591673](https://pubmed.ncbi.nlm.nih.gov/40591673/)]
29. Asaduzzaman M, Mekonnen Z, Rødland EK, Sahay S, Winkler AS, Gradmann C. District health information system (DHIS2) as integrated antimicrobial resistance surveillance platform: An exploratory qualitative investigation of the one

- health stakeholders' viewpoints in Ethiopia. *Int J Med Inform.* Jan 2024;181:105268. [doi: [10.1016/j.ijmedinf.2023.105268](https://doi.org/10.1016/j.ijmedinf.2023.105268)] [Medline: [37972481](https://pubmed.ncbi.nlm.nih.gov/37972481/)]
30. Sahay S, Rashidian A, Doctor HV. Challenges and opportunities of using DHIS2 to strengthen health information systems in the Eastern Mediterranean Region: A regional approach. *E J Info Sys Dev Countries.* Jan 2020;86(1):e12108. [doi: [10.1002/isd2.12108](https://doi.org/10.1002/isd2.12108)]
  31. Pascucci M, Royer G, Adamek J, et al. AI-based mobile application to fight antibiotic resistance. *Nat Commun.* Feb 19, 2021;12(1):1173. [doi: [10.1038/s41467-021-21187-3](https://doi.org/10.1038/s41467-021-21187-3)] [Medline: [33608509](https://pubmed.ncbi.nlm.nih.gov/33608509/)]
  32. Ibrahim AM, Ahmed MM, Musa SS, et al. Harnessing artificial intelligence for predictive modeling in combating antimicrobial resistance: a call for integration and innovation. *BMC Artif Intell.* 2025;1(1):1. [doi: [10.1186/s44398-025-00001-w](https://doi.org/10.1186/s44398-025-00001-w)]
  33. GAIDeT (Generative AI Delegation Taxonomy): A taxonomy for humans to delegate tasks to generative artificial intelligence in scientific research and publishing: Accountability in Research. URL: <https://www.tandfonline.com/doi/full/10.1080/08989621.2025.2544331> [Accessed 2025-12-25]

## Abbreviations

**AMR:** antimicrobial resistance  
**API:** application programming interfaces  
**AST:** antimicrobial susceptibility testing  
**AWaRe:** Access, Watch, Reserve  
**CHUB:** University Teaching Hospital of Butare  
**CLSI:** Clinical and Laboratory Standards Institute  
**DD:** disk diffusion  
**EUCAST:** European Committee on Antimicrobial Susceptibility Testing  
**GLASS:** Global Antimicrobial Resistance Surveillance System  
**LAARC:** Laboratory Assessment of Antibiotic Resistance Testing Capacity  
**LIS:** Laboratory Information System  
**MIC:** minimum inhibitory concentration  
**TSV:** tab separated values  
**WHO:** World Health Organization  
**WHONET:** World Health Organization Collaborating Center for Surveillance of Resistance to Antimicrobial Agents

*Edited by Amy Schwartz, Matthew Balcarras; peer-reviewed by Annabella Bensusan Osafo, Karen Triep; submitted 28.Aug.2025; final revised version received 25.Dec.2025; accepted 29.Dec.2025; published 21.Jan.2026*

### *Please cite as:*

Mbarushimana D, Adegboyega TT, Jean Damascene G, Bale MI, Damascene BJ, Marie Françoise K, Innocent I, Alexis R, Adeyemo RO, Issa B, Akinola SA, Adedeji AA, Evariste M, Albert B, Felicite M, Sylvain H, Habarugira F, Sinumvayo JP, Noel R, Theogene T, Jules NM, Christian N

*Digital Infrastructure for Antimicrobial Susceptibility Testing and Surveillance: A CLSI and EUCAST-Based Model for Resource-Limited Settings*

*JMIR Form Res* 2026;10:e82727

URL: <https://formative.jmir.org/2026/1/e82727>

doi: [10.2196/82727](https://doi.org/10.2196/82727)

© Djibril Mbarushimana, Taofeek Tope Adegboyega, Gatera Jean Damascene, Muritala Issa Bale, Buregeya Jean Damascene, Kayitesi Marie Françoise, Itangishaka Innocent, Rugamba Alexis, Rasheed Omotayo Adeyemo, Bagirinshuti Issa, Saheed Adekunle Akinola, Ahmed Adebawale Adedeji, Mushuru Evariste, Busumbigabo Albert, Mukamana Felicite, Habarurema Sylvain, Felix Habarugira, Jean Paul Sinumvayo, Rutambika Noel, Twagirumugabe Theogene, Ndoli Minega Jules, Ngarambe Christian. Originally published in *JMIR Formative Research* (<https://formative.jmir.org>), 21.Jan.2026. This is an open-access article distributed under the terms of the Creative Commons Attribution License (<https://creativecommons.org/licenses/by/4.0/>), which permits unrestricted use, distribution, and reproduction in any medium, provided the original work, first published in *JMIR Formative Research*, is properly cited. The complete bibliographic information, a link to the original publication on <https://formative.jmir.org>, as well as this copyright and license information must be included.