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

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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%).

Objective: This study aimed to develop an enhanced LIS to improve AST reliability and enable real-time Antimicrobial Resistance (AMR) surveillance at CHUB, addressing challenges in resource-limited settings to support antimicrobial stewardship and improve patient care.

Methods: We developed an enhanced LIS using the OpenClinic GA open-source hospital information system, 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 and EUCAST Expert Rules. An agile development approach was employed, 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, prioritize WHO AWaRe “Access” antibiotics, 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 user-friendly interface and compatibility with WHONet facilitated seamless data integration and reporting, addressing previous deficiencies in data capture and antibiogram generation.

Conclusions: This scalable, open-source LIS model enhances antimicrobial stewardship by improving AST reliability and surveillance in resource-limited settings. By addressing critical gaps at CHUB, the system supports better patient outcomes and contributes to global AMR monitoring efforts.

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

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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%). This study aimed to develop an enhanced LIS to improve AST reliability and enable real-time Antimicrobial Resistance (AMR) surveillance at CHUB, addressing challenges in resource-limited settings to support antimicrobial stewardship and improve patient care.

Methods

We developed an enhanced LIS using the OpenClinic GA open-source hospital information system, 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 and EUCAST Expert Rules. An agile development approach was employed, 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, prioritize WHO AWaRe “Access” antibiotics, and enable data export to WHONet for global surveillance.

Findings

The enhanced LIS improved AST data capture and standardization, providing reliable, automated result interpretation and real-time AMR surveillance capabilities. The system's user-friendly interface and compatibility with WHONet facilitated seamless data integration and reporting, addressing previous deficiencies in data capture and antibiogram generation.

Interpretation

This scalable, open-source LIS model enhances antimicrobial stewardship by improving AST reliability and surveillance in resource-limited settings. By addressing critical gaps at CHUB, the system supports better patient outcomes and contributes to global AMR monitoring efforts.

Funding

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Keywords: Antimicrobial susceptibility testing; CLSI; EUCAST; Laboratory Information System; Antimicrobial stewardship; Resource-limited settings; OpenClinic GA; University Teaching Hospital of Butare. WHONet.

1. Introduction

1.1 Background on Antimicrobial Resistance

Antimicrobial resistance (AMR) is a global health emergency, with the World Health Organization (WHO) estimating 10 million annual deaths by 2050 if unchecked. [1] Multidrug-resistant pathogens, such as methicillin-resistant *Staphylococcus aureus* (MRSA) and extended-spectrum beta-lactamase (ESBL)-producing *Enterobacteriaceae*, compromise treatment efficacy, particularly in resource-limited settings where alternative therapies are scarce. [2]

1.2 Role of Antimicrobial Susceptibility Testing and Surveillance

Antimicrobial susceptibility testing (AST) determines pathogen susceptibility to guide effective therapy, while surveillance systems aggregate data to monitor resistance trends and inform evidence-based treatment guidelines. [3,4] In resource-limited settings, inadequate laboratory infrastructure, limited access to standardized guidelines, and fragmented data management hinder these processes, exacerbating AMR. [5–8]

1.3 Study Context

Sub-Saharan Africa, including Rwanda, faces significant barriers to robust AST and surveillance, such as inconsistent guideline adoption and poor data interoperability [5]. The University Teaching Hospital of Butare (CHUB), a tertiary referral center in Rwanda, exemplifies these challenges. CHUB's LIS, built on the OpenClinic GA open-source hospital information system, has been used to support patient administrative and health insurance data management, as demonstrated in Burundian hospitals for universal health coverage (UHC) monitoring. [9] However, a baseline Laboratory Assessment of Antibiotic Resistance Testing Capacity (LAARC), [10] identified critical deficiencies in CHUB's LIS for microbiology services: 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. These metrics were derived from a comprehensive audit of laboratory workflows and data systems conducted prior to the study intervention. [11]

1.4 Baseline LAARC Deficiencies

The LAARC audit revealed several qualitative deficiencies in the LIS that compromised bacteriology services at CHUB: [11]

- The LIS does not record the method used to obtain AST results (e.g., MIC or Disk Diffusion), hindering traceability.
- It cannot suppress individual antibiotic results in patient reports without deleting them from the database, preventing cascade/selective reporting. [12]
- Only Susceptible, Intermediate, or Resistant (S/I/R) interpretations are entered, without capturing raw inhibition zone or MIC values, limiting data granularity.
- The system lacks automated interpretation of zone sizes or MIC values into S/I/R, relying on manual processes that increase error risk.
- There is no input for descriptive responses, such as morphologies, quantities of colonies, or biochemical test results, restricting qualitative data capture.
- EUCAST Expert Rules or similar decision-support tools are not integrated, limiting automated detection of resistance phenotypes.
- Antibiotic panels are inconsistent, resulting in extractable data unsuitable for reliable cumulative antibiogram generation.
- When corrections to patient results are made, original results are deleted from the records, compromising audit trails and data integrity.

These gaps, combined with the quantitative metrics, underscore the need for an enhanced LIS to improve AST reliability, standardization, and surveillance capabilities.

1.5 Problem Statement

The LAARC findings underscore compromised bacteriology services at CHUB due to low data capture rates, lack of standardized AST panels, and inadequate antibiogram generation within the OpenClinic GA-based LIS. These deficiencies impair reliable AST and surveillance, undermining antimicrobial stewardship and increasing the risk of resistance spread.

1.6 Study Goal

This study aimed to enhance CHUB's LIS, leveraging the OpenClinic GA platform, by integrating CLSI and EUCAST guidelines, [3,4] incorporating metadata from the AMR for R package, [13] and from WHONet, [6,14] as well as EUCAST Expert Rules and expected phenotypes, [15] to address LAARC-identified gaps, standardize AST processes, and enable real-time AMR surveillance.

1.7 Significance

The enhanced LIS aligns CHUB with global surveillance networks, such as WHO GLASS, offering a scalable model for resource-limited settings. By building on OpenClinic GA's established infrastructure, the system improves data management, standardization, and interoperability, enhancing patient outcomes and supporting evidence-based antimicrobial stewardship.

2. Materials and Methods

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

2.2 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. [16,17]

2.3 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 were tailored to support the LIS design, each mapped to a specific database table within the OpenClinic GA system:

1. **Clinical Breakpoints File** (breakpointstsv): Stores CLSI and EUCAST breakpoint data, defining susceptibility (S) and resistance (R) thresholds for antibiotics. Fields include guideline, test method, pathogen, antimicrobial, and breakpoint values, ensuring automated, standardized AST interpretations.
2. **Microorganisms File** (microrganismstsv): Provides taxonomic and characteristic data for microbial identification, with fields like pathogen identifier, kingdom, genus, species, prevalence, and clinical relevance codes (e.g., SNOMED). This file supports accurate pathogen identification and surveillance.
3. **Antimicrobials File** (antimicrobialstsv): Details antimicrobial agents, incorporating WHO AWaRe classifications (Access, Watch, Reserve), [18–20] and standardized codes (e.g., WHONET). Fields include antibiotic name, class, potency, and administration routes, enabling dynamic panel generation.
4. **Antimicrobial Screening Rules File** (amscreenerstsv): Defines screening rules for specific pathogens, with fields for antimicrobial, target pathogen, and screening criteria, optimizing testing efficiency in resource-constrained settings.
5. **Testable Antimicrobials File** (testableamstsv): Lists antimicrobials with standardized AST breakpoints defined by CLSI or EUCAST irrespective of pathogen, including fields for group, name, abbreviation, and AWaRe classification.
6. **Expected Phenotypes File** (expectedmophenotypestsv): Incorporates EUCAST Expert Rules for expected phenotypes (susceptible/resistant), with fields for antimicrobial, pathogen, and phenotype, supporting rapid clinical decision-making.
7. **Site-Sample Mapping File** (sitesamplemaptsv): Maps clinical sites to sample types (e.g., meningitis => CSF), ensuring accurate specimen association for AMR analysis.
8. **WHONet Specimen Mapping File** (monsterWHONETSpecimenmaptsv): Standardizes

specimen codes for interoperability with WHONet, mapping local codes to WHONet specimen type code.

9. **AWaRe Classification File** (atbawaretsv): Classifies antibiotics into Access, Watch, and Reserve categories, [20] to guide selective reporting.

The integration of these metadata files based on their reliability and global compatibility. [6,20–22]

2.4 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:

2.4.1 Metadata Import Interface

A web-based tool simplifies the import and update of metadata files within the OpenClinic GA framework. Users select a file type from a dropdown menu, upload tab-separated values (TSV) files, and optionally clear existing data. The system validates file headers, provides real-time feedback on errors (e.g., 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 non-technical users to update metadata with minimal training.

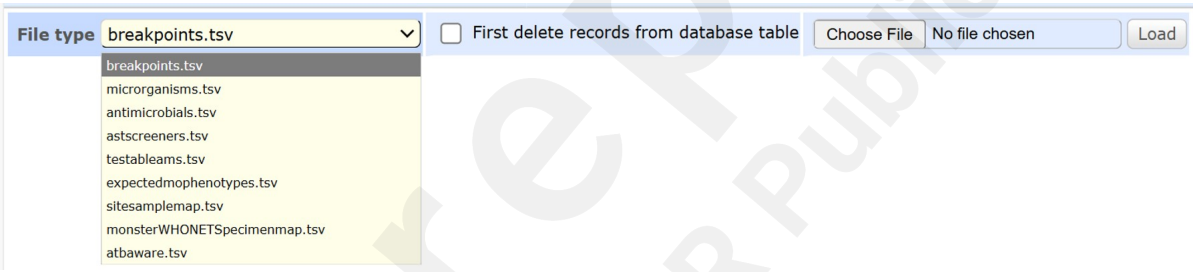

Figure1: Screenshot of the Metadata Import Interface, showing the dropdown menu for selecting file types, file upload button, and feedback panel for validation status.

2.4.2 Configuration Interface

A web-based configuration tool, allows users to adapt the system to local needs. It includes three configurable parameters:

- **AST Guideline**: A dropdown menu for selecting EUCAST (default) or CLSI, ensuring appropriate breakpoint application.
- **Guideline Year**: A text input for specifying the guideline year (default: 2024), validated for integer values, accommodating updates to standards.
- **Sector**: A dropdown menu for human (default) or animal protocols for adapting human or veterinary testing, tailoring protocols to the relevant context.

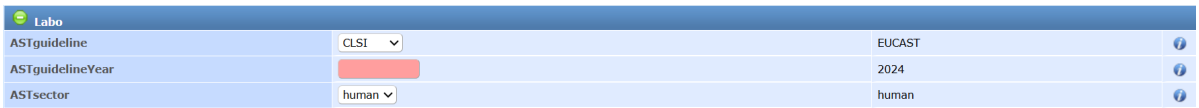

Figure2: Screenshot of the Configuration Interface, displaying dropdown menus for selecting AST guideline (CLSI/EUCAST), guideline year, and sector (human/animal), with multilingual support options.

2.4.3 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 (Access, Watch, Reserve, or Not Available). Users update classifications via dropdown menus, with changes tracked client-side using JavaScript and submitted via AJAX to a server-side for database updates.

Manage antibiotics for susceptibility testing (AST)

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	Streptoduocin	STR	Watch	Unchanged
Aminoglycosides	Streptomycin-high	STH	Watch	Unchanged
Aminoglycosides	Tobramycin	TOB	Watch	Unchanged
Amphenicols	Chloramphenicol	CHL	Access	Unchanged

Figure3: Screenshot of the AWaRe Classification Management Interface, showing a sortable table of antibiotics with dropdown menus for updating AWaRe status (Access, Watch, Reserve, Not Available) and real-time feedback indicators.

2.4.4 AST Result Entry Interface

The AST result entry interface, integrated into the worklist management, provides a robust tool for entering, validating, and managing AST results. Launched as a modal dialog, it supports manual entry, review, and technical validation for up to three isolates per specimen, aligning with CLSI and EUCAST recommendations for digital AST data capture.

Functionalities:

- **Isolate Management:** Supports up to three isolates with strict autocompletion for pathogen identification based on a standardized microorganisms' taxonomy (WHONET/EUCAST/CLSI) for consistency. Includes comment icon if clicked reveals list of antibiotic on which the isolate has expected phenotype, as well two checkboxes "screened" and "expected" for epidemiological tracking as well as If checked, the antibiotic testing panel dynamically expands:
    - Screened: Includes antibiotics directly tested, as well as additional agents inferred or suggested based on screening results.
    - Expected: Includes antibiotics associated with expected phenotypic profiles based on known resistance or susceptibility patterns for the identified pathogen.
- **AST Data Capture**: Displays a dynamic table for each isolate, listing relevant antimicrobials based on the configured testable antimicrobials, guideline, sample type, local availability, Antimicrobial Screening/inference rules as well as expected phenotype of the isolate. Columns include:

- Antimicrobial name (standardized via WHONET/EUCAST/CLSI codes).
- Test method (radio buttons for DISK(concentration) and MIC).
- Result entry (numeric input for inhibition zones or MIC values, with real-time validation and color-coding: green for Susceptible, yellow for Intermediate, red for Resistant).
- Clickable icon, shown only if the current antibiotic has one or more related agents, when clicked reveals list of antibiotic screened or inferred by the displayed one if any.
- Clickable icon, displayed only if AST interpretations may vary based on the route of administration for the current antibiotic. When clicked, it presents these interpretation variations.

- **Real-Time Validation**: Alerts users to invalid inputs mainly non-numeric values, duplicate isolate entries and measurements entered without specifying a method.
- **Data Submission**: Serializes results into structured JSON, capturing method, breakpoints, interpretations, and comments, with technical validation checkboxes for quality assurance.

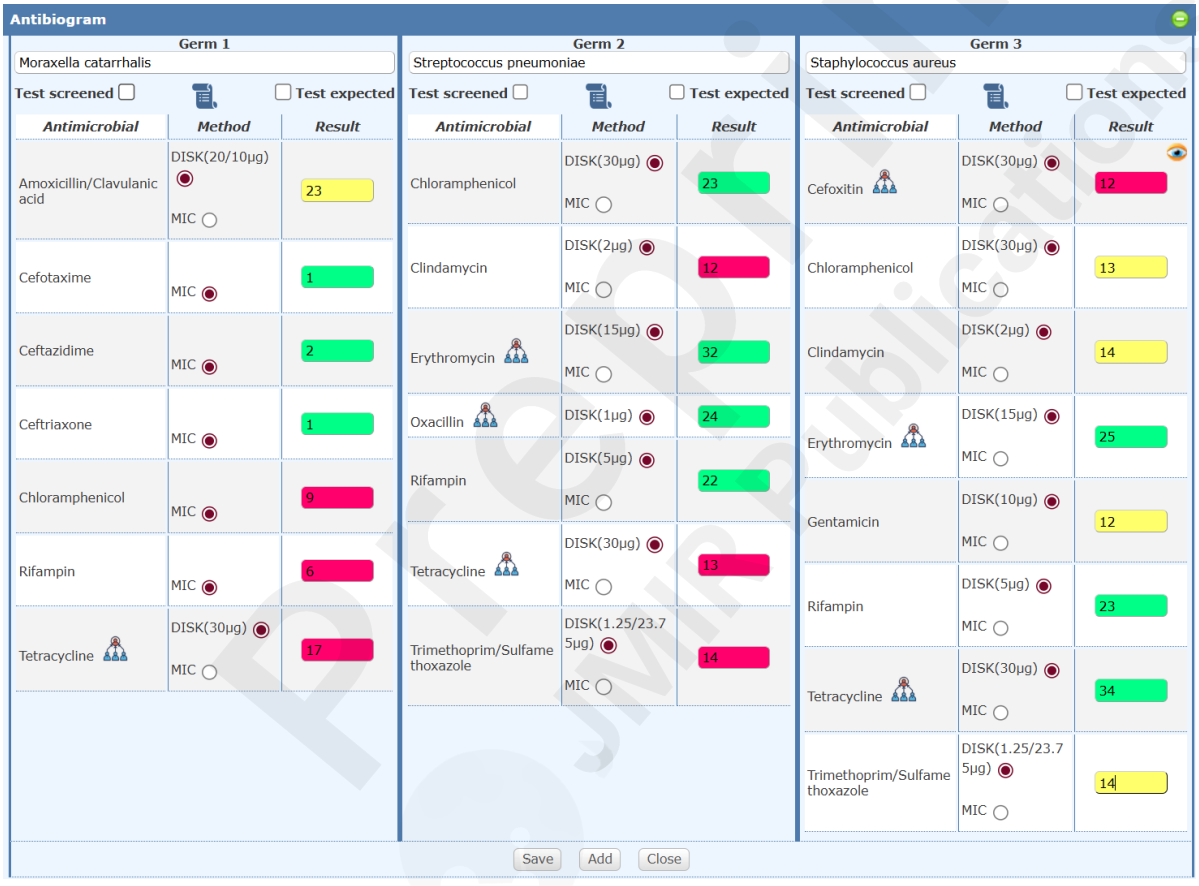

Figure4: Screenshot of the AST Result Entry Interface, showing the modal dialog with isolate panels, dynamic antimicrobial table, color-coded result fields, and autocompletion for pathogen identification.

2.4.5 AST Result View Form

The AST result view form, integrated into the laboratory results view, renders finalized AST results. This interface provides a selective, user-friendly, and standards-driven display for clinicians, infection control staff, and surveillance teams, ensuring results are traceable, interpretable, and actionable. It aligns with CLSI, EUCAST, and WHO GLASS guidelines for harmonized data

presentation. [12,23–25]

Functionalities:

- **Entry Point and Context**: Results are displayed within a lab request context, grouped by request time and patient. A link opens a modal dialog showing only finalized results.
- **Result Rendering**:
  - AST data supports up to three isolates per specimen, displaying organism names, tested antimicrobials, S/I/R interpretations, an icon for expected phenotypes, screening/inferred status, expected phenotype testing status, and clickable icons for screened/inferred antibiotic details and interpretation variability.
  - **Selective Display**: Prioritizes antibiotics based on WHO AWaRe classification, displaying Access antibiotics if susceptible/intermediate, then Watch, then Reserve, to guide treatment decisions.
  - **Read-Only Display**: Ensures data integrity by preventing modifications to finalized results.
  - **Audit Trails for Corrections:** Tracks changes to patient results via edit history icons, logging updated results with timestamps, reason and user details, ensuring traceability and supporting quality assurance.

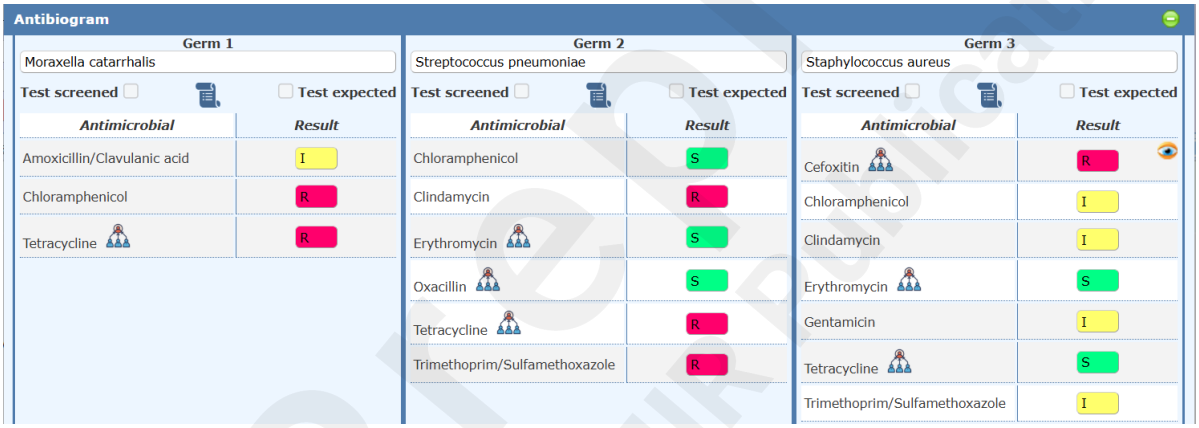

Figure5: Screenshot of the AST Result View Form, showing the modal dialog with a grouped results table, color-coded isolate data, AWaRe-filtered antibiotic display, and tooltips for phenotypic comments.

2.4.6 WHONet Export Interface

The WHONet export interface enables seamless export of AST results to the WHONet platform, supporting global AMR surveillance. It provides a web form for selecting a date range and export destination (download, FTP, SMTP, or directory). The export functionality was designed to comply with WHONet's strict data formatting. [26,27]

Functionalities:

- **User Interface**: Offers a web form with calendar widgets for date range selection and a dropdown for export destination, with an export button to initiate the process.
- **Export Logic**:
  - **Download Mode**: Generates a TSV file via a client-side for immediate download.

- **Remote Modes**: Transfers files via FTP, SMTP, or directory using server-side methods with feedback on success or failure.

- **Data Extraction**: Queries the database for finalized AST records within the selected date range, supporting multi-isolate reporting. Each row includes:
  - Patient demographics (ID, sex, age, age category per WHO/CLSI guidance).
  - Specimen type (mapped via the WHONet Specimen Mapping File).
  - Pathogen identification.
  - Test method, antimicrobial name/code, result value, interpretation (S/I/R), guideline, sector, and workflow timestamps.
- **Data Formatting**: Outputs a TSV file matching WHONet import requirements, with legacy CSV support. [26,27]

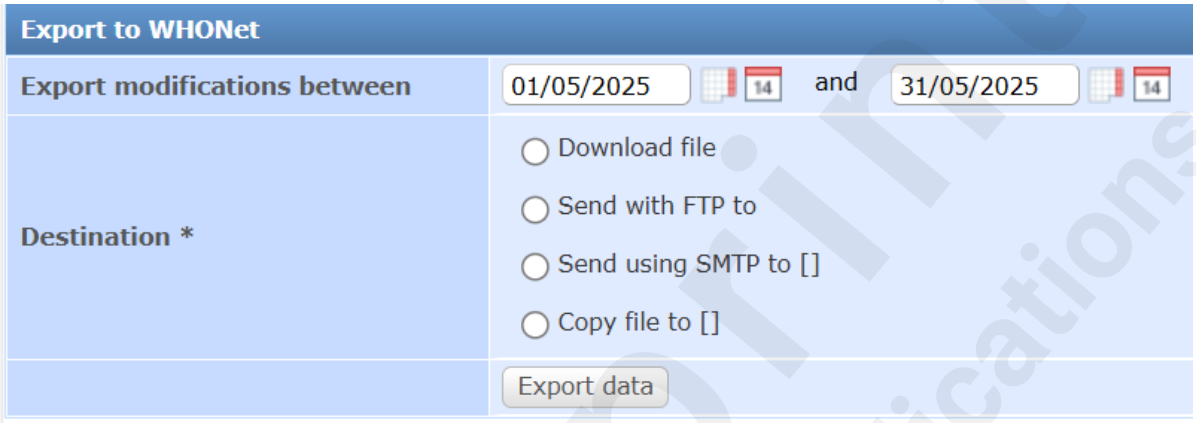

Figure6: Screenshot of the WHONet Export Interface, displaying the web form with calendar widgets for date range selection, dropdown for export destination, and feedback on export status.

2.5 Ease of Integration and Interoperability

To ensure seamless integration of automatic identification and AST workflows with laboratory instruments, LIS, and external surveillance platforms, the enhanced LIS incorporates robust interoperability features tailored for resource-limited settings.

Functionalities:

- Supports **structured data formats** (TSV, CSV, JSON, HL7, FHIR) for direct mapping of organism codes, test results, and interpretations.
- Offers plug-and-play API endpoints for LIS vendors to integrate AST and identification modules with minimal development effort, supporting real-time or scheduled data synchronization.
- Enables direct export to WHONet, WHO GLASS, and national reporting platforms with automated mapping of local codes to surveillance codes.

3. Results

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

3.2 Resolution of Qualitative Deficiencies

The enhanced LIS addressed the qualitative deficiencies identified in the LAARC audit (Section 1.4), with most fully resolved and one partially addressed. The following table summarizes the resolution status, referencing relevant system functionalities:

Table 1: Resolution Status of LAARC Qualitative Deficiencies

LAARC Deficiency	Resolution 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 selective display without deleting data, supporting 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.

3.3 Key Functionalities

- **AST Functionality**:
  - Supports MIC and DD methods with automated interpretation based on selected guideline.
  - Provides color-coded result outputs (green for Susceptible, yellow for Intermediate, red for Resistant, pink for out-of-range).

    - Delivers real-time notifications for critical isolates.
- **Dynamic Testing Panels**: Panels adjust based on breakpoints, local antimicrobial stock, and clinical context, incorporating EUCAST Expert Rules and expected phenotypes.
- **Selective Reporting**: Prioritizes WHO AWaRe “Access” antibiotics, reducing inappropriate use of “Watch” and “Reserve” categories.
- **Surveillance Integration**: Data export aligns with WHONet standards, enabling seamless integration with WHO GLASS and national surveillance systems, enhanced by robust interoperability features.
- **User Experience**: Web-based interfaces, including the AST Result View Form, require minimal training, with real-time feedback, tooltips, and selective display enhancing usability for non-technical staff.

4. 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]. Leveraging OpenClinic GA’s established infrastructure, previously validated for UHC monitoring in Burundian hospitals [9], the system extends its capabilities to support microbiology-specific workflows, demonstrating its versatility in resource-limited settings.

The study focused solely on addressing qualitative deficiencies in the LIS, such as improving data capture, standardization, and user interface functionality, and reserved quantitatively evaluating improvements against baseline metrics (e.g., culture observation capture rate of 60%, AST data capture rate of 25%, or antibiogram generation of 17%) for future assessment after a period of implementation and use. 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.[24,28,29]

5. Conclusion

The enhanced LIS, built on OpenClinic GA and leveraging CLSI, EUCAST, and AMR for R metadata, provides a scalable, user-friendly solution for resource-limited settings. It significantly improves AST reliability, supports antimicrobial stewardship, and enables integration with global surveillance networks. This model, extending an established open-source platform, offers a blueprint for addressing AMR challenges in low-resource environments, with potential for broader adoption in Sub-Saharan Africa and beyond.

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Author Contributions

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- **Gatera Jean Damascene** (IT expert, CHUB): Led user acceptance test and integration of new functionalities on production.
- **Muritala Issa Bale** (Microbiologist, UR): Led the Diagnostic Stewardship team, contributed to metadata integration, and reviewed the manuscript.
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- **Kayitesi Marie Francoise** (Ear Nose and Throat Surgeon, CHUB): Served as General Secretary, coordinated administrative tasks, and reviewed the manuscript.
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All authors approved the final manuscript.

Competing Interests

The authors declare no competing interests.

Data Availability

Metadata files, system documentation, and de-identified sample data are available at [Repository Link] under a Creative Commons Attribution 4.0 International License.

Supplementary Information

Supplementary materials, including detailed database schemas, user interface screenshots, and metadata file structures, are available online at [Journal Website].

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Supplementary Files