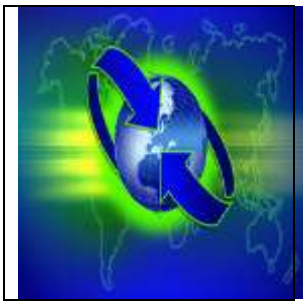


Data-Quality Audit of Bacteriology Electronic Medical Records at a Nigerian Tertiary Hospital

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Abstract

In low- and middle-income countries (LMICs), routine microbiology data from clinical laboratories make up most of the data used for antimicrobial resistance (AMR) surveillance. Most of these data are stored in the electronic medical records (EMRs) of clinical and public health laboratories. However, these data are rarely evaluated for quality. We audited EMR data for all cultures and susceptibility tests from the Department of Medical Microbiology and Parasitology, University of Calabar Teaching Hospital (UCTH), Nigeria, from 2021 to 2025. The authors assessed the data for conformance, completeness, plausibility, uniqueness, and timeliness. They also checked antimicrobial susceptibility test results against CLSI and EUCAST intrinsic resistance and reporting rules. The change from year to year was analyzed using the Cochran–Armitage test. A total of 222,620 rows (including missing data) of information were analyzed in the bacteriology export for the five years under study. The bacteriology export included 2,250 culture-positive requests and 2,704 organism records. Of the 19,476 reported susceptibility test results for bacteria, 2,427 (12.5%) were either invalid or not reported. Of the reported susceptibility information for bacteria tested against antibiotics, 180 susceptible results were reported for intrinsically resistant bacteria. Also, 16 disk diffusion tests for vancomycin susceptibility were reported as resistant for *S. aureus*. Clinical diagnosis information was missing for 61% of the bacteriology requests analyzed in this study. Information on the pathologist's verification of identity for organisms in the bacteriology requests analyzed in this study increased from 0% to 26% for three consecutive years (2019 to 2023) and increased to 99% for the two years (2024 to 2025) analyzed in this study. The inbuilt demographic and date fields of the UCTH EMR were found to be captured appropriately; however, the manner in which susceptibility test results were stored in the system for various organisms allowed for the entry of inappropriate values. Organism-specific antibiotic panels, rule-based entry validation, and mandatory coded clinical fields are required to enable the use of the data for AMR surveillance.

Keywords: data quality; electronic medical records; antimicrobial resistance; laboratory surveillance

Introduction

The increasing adoption of electronic medical records (EMRs) in tertiary hospitals for quality assurance has improved the documentation, storage, retrieval, and exchange of patient

information, including bacteriology laboratory results. Bacteriology services are essential for identifying bacterial pathogens, determining antimicrobial susceptibility, supporting the diagnosis of infectious diseases, and guiding appropriate treatment. The reliability of these functions depends not only on the accuracy of laboratory procedures but also on the quality of the information entered, processed, stored, and communicated through electronic systems. Data quality audit refers to the systematic examination of recorded information to determine whether it is complete, accurate, consistent, valid, timely, and fit for its intended purpose (Kahn, et al., 2016; Clinical and Laboratory Standards Institute, 2022; Lewis, et al. 2023).

Ghalavand et al. (2024), and An et al. (2025) reinforced the importance of systematic data quality assessment in electronic health systems. McGinnis et al. (2023) cited in An, et al. (2025) reviewed 103 publications and identified completeness, correctness, concordance, plausibility, and currency among the frequently assessed dimensions of electronic health record data quality. Their findings highlighted the absence of a universally standardized approach to data quality assessment. Similarly, Ghalavand et al. (2024), in their systematic review of common data quality elements for health information systems, examined 58 papers and identified 14 dimensions, with accuracy, completeness, and timeliness among the most frequently emphasized. More recently, An et al. (2025), in challenges for data quality in the clinical data life cycle: systematic review of105 papers and emphasized the need for standardized quality management across the planning, construction, operation, and utilization stages of clinical data (Clinical and Laboratory Standards Institute, 2024).

Despite advances in electronic medical record systems and laboratory information management, the availability of electronic records does not automatically guarantee that bacteriology data are complete, accurate, consistent, or timely. Missing specimen details, incorrect patient identifiers, duplicate records, incomplete culture reports, inconsistent organism names, omitted antimicrobial susceptibility findings, and delays in entering or releasing results are potential problems that a systematic audit should investigate rather than assume. Such

deficiencies may impair clinical interpretation, compromise antimicrobial treatment decisions, weaken infection surveillance, and reduce the reliability of hospital data used for research and management. Although existing literature provides useful frameworks for electronic health record quality assessment and laboratory quality management, there remains a need to establish how these principles apply to bacteriology electronic medical records in the specific tertiary hospital being studied (Federal Ministries of Agriculture, Environment & Health, 2017; Collins, 2024).

Weiskopf and Weng (2013) identified completeness, correctness, concordance, plausibility, and currency as important dimensions for assessing electronic health record data. In bacteriology, these dimensions can be applied to patient identification, specimen type, specimen collection date, laboratory accession number, bacterial identification, antimicrobial susceptibility results, interpretation, and the date and time of result reporting. Consequently, auditing bacteriology electronic medical records is important for maintaining reliable laboratory information, supporting clinical decision-making, improving patient safety, and strengthening hospital quality assurance. Furthermore, Weiskopf and Weng (2013), in Methods and dimensions of electronic health record data quality assessment: Enabling reuse for clinical research, conducted a review of approaches used to assess the quality of electronic health record data. Their work identified five major dimensions of data quality: completeness, correctness, concordance, plausibility, and currency.

The authors also examined methods used to evaluate these dimensions and highlighted inconsistencies in the terminology and approaches adopted by researchers. Their findings provided a useful foundation for auditing bacteriology electronic medical records because laboratory information must be sufficiently complete, accurate, internally consistent, clinically plausible, and up to date. For instance, an audit could determine whether a patient's identifier matches the laboratory accession number, whether bacterial identification agrees with the recorded laboratory findings, and whether the final antimicrobial susceptibility result is available

in the patient's electronic record. The relevance of this study lies in its provision of a structured approach to electronic record quality assessment. However, its focus was electronic health records generally rather than the specific data requirements and reporting processes of bacteriology laboratories in tertiary hospitals (International Organization for Standardization, 2022).

Kahn et al. (2016), in a study on harmonized data quality assessment terminology and framework for the secondary use of electronic health record data, developed a framework for standardizing data quality terminology, assessment procedures, and reporting practices. Their work drew on published literature, expert contributions, and operational experiences from established electronic health record research networks. The authors emphasized the importance of using clearly defined and consistent criteria to determine whether electronic health data are suitable for their intended uses. This framework is relevant to bacteriology record audits because inconsistent terminology, missing fields, duplicated laboratory entries, and discrepancies between laboratory information systems and hospital medical records can compromise data reliability.

Iskandar, et al. (2021) posited that applying a harmonized framework would enable auditors to establish explicit criteria for assessing completeness, conformance to recording standards, consistency between related data fields, and the plausibility of laboratory results. It would also improve the comparability of audit findings across laboratory units and hospital departments. Nevertheless, the study did not specifically evaluate bacteriology records in tertiary hospitals, creating an opportunity to adapt its framework to laboratory-specific information and reporting requirements.

In a study by the World Health Organization (WHO, 2011) in its laboratory quality management system Handbook, cited in Lewis, et al. (2023) presented a comprehensive approach to maintaining quality in clinical and public health laboratories. The handbook addresses essential components of laboratory quality management, including personnel, equipment, process control, information management, documents and records, occurrence management, assessment,

and continual improvement. It emphasizes the importance of accuracy, timeliness, and reliability in the production and management of laboratory results. These principles are directly applicable to bacteriology electronic medical records because errors may occur at several stages, including specimen registration, result entry, verification, authorization, transmission, and retrieval. A systematic audit could therefore examine whether patient and specimen identifiers are correctly recorded, whether bacterial culture and antimicrobial susceptibility findings are completely documented, whether amended reports are traceable, and whether results are communicated within appropriate timeframes (Okeke , et al. 2020; Fadahunsi, et al., 2021; Ghalavand, et al., 2024).

The WHO handbook provides an important operational foundation for developing laboratory audit checklists and corrective-action procedures. However, it is a laboratory quality management guide rather than a study measuring the prevalence or magnitude of data quality problems in electronic bacteriology records. Collectively, these studies support the use of structured audit criteria, reproducible assessment procedures, and continuous quality improvement. However, their broad focus on electronic health records and clinical data leaves the specific quality of bacteriology information, including culture results, organism identification, antimicrobial susceptibility records, and electronic reporting, requiring further investigation in individual tertiary hospitals.

In order to describe the pattern and distribution of antimicrobial resistance (AMR), clinical and microbiological data from individual patients can be systematically collected, stored, processed, and analyzed in electronic medical records (EMRs). Electronic medical records (EMRs) are electronic versions of patients' medical files and charts, including laboratory and radiology information. Laboratory information systems are integrated into patient-oriented EMRs in a manner that links clinical data with corresponding microbiological culture data and antimicrobial susceptibility testing (AST) results. In this way, resistant bacteria found in patients can be monitored, and resistance development over time and between different departments or

even hospitals can be assessed. Despite some investment in EMRs in health care settings in sub-Saharan Africa to capture clinical, laboratory, and other patient information, several challenges must be addressed before they can be used for health research. These include a lack of necessary infrastructure to support the systems, insufficient user training, and systems' inability to support research using clinical information from patients' electronic health records because of EMR errors (Choy, et al.2025; An et al., 2025).

While errors in laboratory medicine have long been measured, the vast majority occur before the analytical phase, i.e., while requesting tests, labeling samples, transcribing, and reporting results (Penev, et al., 2024; An et al., 2025). In addition to these pre-analysis errors, antimicrobial susceptibility testing can also produce specific errors. Errors can occur in the organism–drug combinations tested and reported, as well as in reporting biologically impossible results. Software programs, such as WHONET (Adaran, et al., 2025), have been designed to apply rules to improve the quality of routine antimicrobial susceptibility test results. However, few studies on data quality have been conducted in hospital laboratories in sub-Saharan Africa using their EMR for bacteriology culture and susceptibility testing.

The central problem, therefore, is the need for empirical evidence on the completeness, accuracy, consistency, validity, and timeliness of bacteriology data documented in the hospital's electronic medical record system. A focused data quality audit should compare electronic entries with authoritative laboratory source records, assess the frequency and types of discrepancies, identify the stages of the laboratory information pathway where errors occur, and recommend corrective measures. Such an investigation would provide evidence for improving laboratory documentation, strengthening information governance, and supporting safer, more reliable patient care.

Research design and methods

Research design

This was a retrospective audit of laboratory records from a single center, following the RECORD extension of the STROBE statement for observational studies (Benchimol et al., 2015; von Elm et al., 2007).

Study area and settings

The University of Calabar Teaching Hospital (UCTH) is a tertiary health care center in Calabar, Cross River State, in southern Nigeria. The Department of Medical Microbiology and Parasitology at UCTH is equipped to perform microscopy, culture, antibiotic sensitivity testing, serology, and molecular testing. All requests and results are entered into the hospital's EMR by the laboratory staff and verified by the staff before they are finalized. This study audited the bacteriology culture and susceptibility information from the Department's laboratory information system over five years (2021–2025). The objective of the audit was to evaluate the records of bacteriology cultures and susceptibility for conformance, completeness, plausibility, uniqueness, and timeliness.

Data sources

Bacteriology requests and results for 5 years (2021 to 2025) were extracted from the Department of Medical Microbiology and Parasitology EMR in spreadsheets. Each row represented results for one organism on one request, including all antibiotics tested for that organism. All rows were included in the analysis. Patients' telephone numbers and hospital numbers were removed from the data set as required by the Nigeria Data Protection Act, 2023.

Audit framework

All 5 aspects of the harmonized framework for assessing the quality of clinical data by Kahn et al. (2016) were evaluated, complemented by two additional aspects previously described by Wang & Strong (1996) and Weiskopf & Weng (2013). The respective evaluation criteria for each of the 5 aspects are shown on Table 1.

Table 1. Data-quality dimensions and checks applied

Dimension	Definition	Checks applied
Conformance	Values and structure match the expected format	File label against content; column sets across years; naming of tests, wards, organisms, and antibiotics; result formats in free text
Completeness	Expected values are present	Missing age, sex, hospital number, ward, clinical diagnosis, and specimen per request; isolates with no AST result
Plausibility	Values are believable	Age range; sex against specimen; organism identification; intrinsic resistance and reporting rules for each organism–drug pair; internally inconsistent AST patterns
Uniqueness	Each event is recorded once	Exact duplicate rows; repeat isolates per patient, species, and year
Timeliness	Events are recorded in a plausible order and time	Collection-to-result interval; collection year against export year; pathologist verification rate and delay

Validation rules for susceptibility results

The results from each organism–drug combination were validated using the intrinsic-resistance data from the tables and the reporting guidance from CLSI M100 (Clinical and Laboratory Standards Institute, 2024) and the EUCAST expert rules for susceptible reporting (Leclercq et al., 2013). Thus, results from organisms that are intrinsically resistant to a drug were classified as invalid if they were reported as susceptible or intermediate. Results from drug–organism combinations for which a particular drug is not reported for a group of organisms (e.g. beta-lactams other than penicillin, oxacillin, and cefoxitin for *S. aureus* isolates and aminoglycosides for enterococci) and results from methods for which the results for a particular drug–organism combination are not reported (e.g. vancomycin disk diffusion for staphylococci) were also classified as invalid. However, resistant results for intrinsically resistant organisms were classified as uninformative, not as an error. We defined the first isolate(s) from a patient, species, and year using CLSI M39 (Clinical and Laboratory Standards Institute, 2022). Multidrug

resistance was defined as non-susceptibility to at least one agent in three or more antimicrobial categories (Magiorakos et al., 2012).

Analysis

We carried out these data imports and analyses in Python (using the pandas library for data manipulation). Frequency counts and proportions of resistance were determined for each year of surveillance and overall. The Cochran–Armitage test for trend (Armitage, 1955) was used to assess the significance of changes in the proportion of resistant isolates over time. We also created derived tables showing the effect of data-quality problems on surveillance outputs, which are reproducible from the completed workbook containing the cleaned data.

Results and discussions

Dataset profile

The five exports listed in Table 2 contained 222,620 rows. The 2021 export was partial and covered results received from 19 July 2021 to 5 October 2021.

Table 2. Profile of the bacteriology EMR exports, 2021–2025

Measure	Value
Raw rows	222,620
Exact duplicate rows	688 (0.3%)
Rows analyzed	221,932
Requests (invoices)	2,250
Organism records	2,704 (2,644 first isolates)
Rows with a usable result	19,476 (8.8%)
Distinct test names	29

Only culture-positive requests appear in the bacteriology exports, so the denominator of all cultures performed could not be determined. Nine in ten exported rows were empty placeholders, and 12.5% of the remaining susceptibility results were removed by validation. Figure 1 traces the bacteriology records from export to analysis.

Conformance

The five bacteriology export files changed from year to year, with 34 columns in total, but 26 to 31 were present in any given year. Some fields, such as specimen, were missing in certain years (e.g., 2022 and 2024), while others, such as Gram stain and smear, were missing in other years (e.g., 2023 and 2025). The pathologist-verification date field appeared only in the bacteriology information from 2024 onward. Most of the coding was free text.

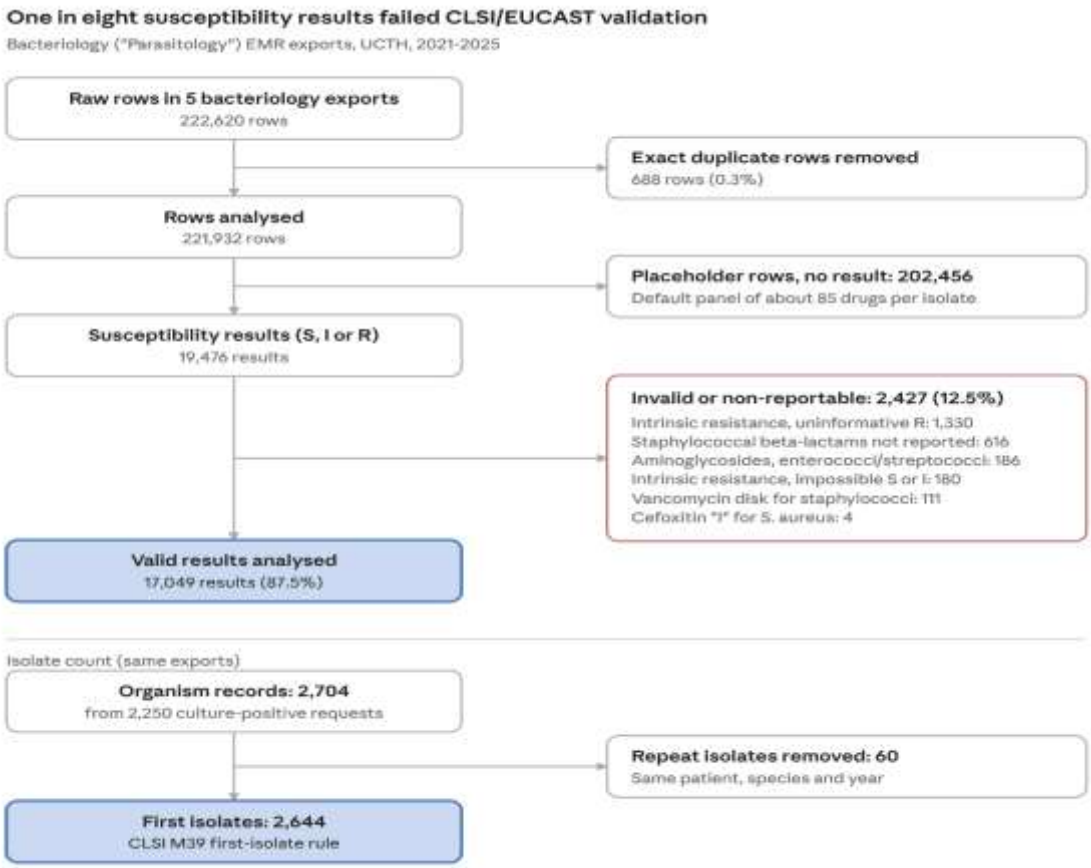


Figure 1. Flow of bacteriology records from export to analysis, UCTH, 2021–2025

Completeness

Almost all demographic and date fields were complete (Table 3). However, important clinical information to help interpret the cultures was frequently missing or listed as “NA”for not available This data was missing for 61.2% of the bacteriology requests for clinical diagnosis for the years listed above. However, this improved to 42% in 2025 (Fig. 2). There were also 64 organism records (2.4%) with no susceptibility result.

Table 3: Missing values per request, 2021–2025

Field	% missing (range by year)
Age	0.0 (0.0–0.0)
Sex	0.5 (0.0–1.7)
Hospital number	2.0 (1.5–3.2)
Ward or clinic	2.1 (1.7–3.2)
Clinical diagnosis	61.2 (42.3–72.8)
Specimen	68.6 (18.7–100.0)

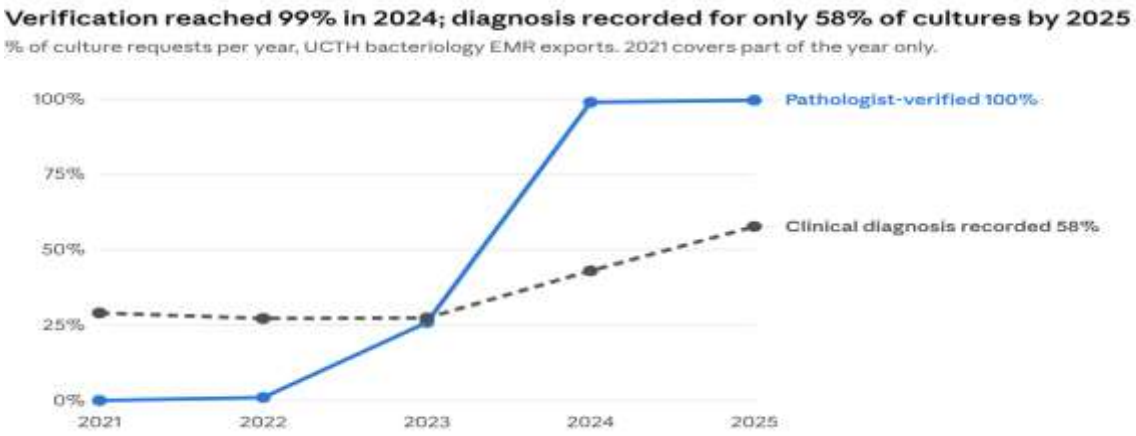


Figure 2: Pathologist verification and recorded clinical diagnosis by year, UCTH bacteriology EMR, 2021–2025 (2,250 culture requests)

Plausibility

Among 19,476 susceptibility test results (Table 4), 12.5% (2,427/19,476) were listed as 'Invalid' or 'Non-reportable' according to CLSI and EUCAST guidelines. These impossible results included gentamicin-susceptible *Providencia stuartii*, ampicillin-susceptible *Citrobacter freundii* and *Proteus vulgaris*, and ceftriaxone-susceptible *Pseudomonas aeruginosa*. Of 50 tested *S. aureus* isolates, 16 were reported as vancomycin-resistant using a 30 µg vancomycin disk. However, vancomycin-resistant *S. aureus* is extremely rare, and disk diffusion cannot accurately detect such organisms. Linezolid-resistant *S. aureus* was found in 25 out of 229 tested *S. aureus* isolates.

Table 4: Invalid and non-reportable susceptibility results

Category	Results	Example
Intrinsically resistant combination reported resistant (uninformative)	1,330	Penicillin tested on *Escherichia coli*
Beta-lactam not reported for *S. aureus*	616	Meropenem or cefepime reported for *S. aureus*
Intrinsically resistant combination reported susceptible or intermediate (impossible)	180	Gentamicin "susceptible" for *P. stuartii*
Aminoglycoside reported for enterococci or streptococci	186	Gentamicin for Enterococcus species
Vancomycin by disk diffusion for staphylococci	111	16 "vancomycin-resistant" *S. aureus*
Cefoxitin screen reported intermediate for S. aureus	4	No intermediate category exists
Total excluded	2,427	

Uniqueness

Duplicated records: 688 out of 222,620 (0.3%) records were exact duplicates of previous records. After applying the CLSI M39 rule for the first isolate, we removed 60 of 111 duplicate isolate requests for the same organism from the first-isolate list (2.2%), leaving 2,644 first isolates (Table 1).

Timeliness

The median time to result from specimen collection for culture requests was 3.9 to 5.2 days per year. However, for 115 (5.1%) culture requests, results were reported within 12 hours of collection, while for 18 (0.8%) requests, results were reported more than 30 days after collection (maximum 545 days). There were 16 bacteriology requests for which the collection date was in a different year from the file in which they were reported. In 2024, a collection date was in August 2022. The pathologist's verification of results was not recorded until 2023. After that, it was

recorded 99% of the time for the following 2 years, with a median time to verification of 4 hours after results entry (Figure 2).

Discussion

While the UCTH laboratory EMR collects the information on who was tested and when they were tested in a very complete manner, the information on what was found in the tests is collected in a manner that permits the inclusion of impossible values. Therefore, one in eight susceptibility test results was invalid or non-reportable; most lacked clinical context for cultures; and results fields were collected as free text. Consequently, the antibiogram generated from these records would incorrectly report tests for some organisms, e.g., vancomycin-resistant *S. aureus*, include impossible values, and produce artifact-averaged susceptibility and resistance information based on selective testing.

The problems identified with field completeness in secondary clinical data sources for analysis corresponding to those previously published (Weiskopf & Weng, 2013). Applying the broader framework for assessing clinical data (Kahn et al., 2016; Lewis et al., 2023) reinforces the primary finding that conformance and plausibility problems relate to secondary clinical data completeness rather than missing data. For laboratory error, most problems are reported to arise in the pre- and post-analytical stages of testing, i.e., test requesting, result transcription, and result reporting (Lewis, 2023; Ghalavand, et al. 2024; Plebani, 2006). The impossible susceptibility test results reported here represent a class of post-analytical error. Although the individual laboratory tests may have been performed correctly, the design of the default panels, together with how results are recorded, has allowed reporting test results that are biologically, and therefore analytically, impossible for the organism in question.

The main structural causes for these errors were (i) the default-designed panel of around 85 antibiotics for each isolate, resulting in over 200,000 rows of empty data for various combinations of organism, isolate and antibiotic, which would never be tested or reported by CLSI and EUCAST (Clinical and Laboratory Standards Institute, 2024; An, et al.2025); and (ii)

application of expert rules for defining antibiograms at analysis time as opposed to entry time. Many countries apply the same rules when AMR surveillance is conducted using software such as WHONET (O'Brien & Stelling, 1995 cited in Basil, 2026). CLSI M39 outlines the rules for designing antibiograms for routine use (Clinical and Laboratory Standards Institute, 2022).

This category of errors needs special focus because some organisms are considered public health threats. Misidentification of such organisms, or entry of erroneous results for them by frontline health workers, would lead to erroneous notifications for AMR surveillance. Such notifications in unconfirmed EMRs would distort estimates on which AMR policies are based. Thus, structural barriers to quality laboratory data systems in health care as highlighted by Tadesse and colleagues (2017); Podolsky , et al. (2023); Li, et al. (2026); Saengpattrachai , et al. (2026) for AMR surveillance in particular, persist in some health care systems in Africa, including Nigeria. Although health care systems in Nigeria are embracing health information technology for Electronic Medical Records (EMRs) and other systems, programs must be strengthened to equip health care laboratories with information technology and improve data quality for AMR surveillance.

Conclusion

This study on data quality auditing of bacteriology medical records in tertiary hospitals in Nigeria demonstrates that the quality, accuracy, completeness, consistency, timeliness, and reliability of electronic medical records are fundamental to effective bacteriological diagnosis, patient management, infection prevention, antimicrobial stewardship, and evidence-based healthcare delivery. Deficiencies in recording, processing, storing, and retrieving bacteriology test results may contribute to diagnostic errors, delays in treatment, inappropriate antibiotic prescriptions, compromised surveillance of antimicrobial resistance, and poor clinical decision-making. Although electronic medical records offer opportunities to improve laboratory information management, their effectiveness depends on standardized data-entry procedures,

competent personnel, functional information technology infrastructure, routine data quality assessments, and strong institutional accountability mechanisms.

The outcome of this study therefore highlights the need for tertiary hospitals to institutionalize systematic data quality audits that identify errors, assess compliance with established standards, and promote continuous improvement in laboratory information management. Strengthening these measures through evidence-informed policies, staff capacity development, effective monitoring, and secure digital record management will improve the integrity of bacteriology data, enhance patient safety, and support more efficient and accountable healthcare delivery.

Recommendations

i. Hospital management, in collaboration with medical laboratory departments and health information management units, should establish a formal policy requiring periodic audits of electronic bacteriology medical records. The audits should assess data completeness, accuracy, consistency, validity, timeliness, and traceability. Quarterly audits, supplemented by annual comprehensive reviews, should be considered to identify recurring deficiencies and guide corrective action.

ii. Tertiary hospitals should develop and enforce standardized operating procedures for documenting, validating, storing, and reporting bacteriology test results. These procedures should cover specimen identification, patient demographics, specimen collection dates, culture findings, organism identification, antimicrobial susceptibility results, and report authorization. Standardized electronic templates, mandatory data fields, and automated validation rules should be incorporated into laboratory information systems to minimize missing, inconsistent, and inaccurate records.

iii. Hospital administrators and relevant professional regulatory bodies should support regular training for medical laboratory scientists, microbiologists, health information managers, clinicians, and information technology personnel on electronic record

management, data quality assurance, confidentiality, and error prevention. Clearly defined responsibilities, performance indicators, and reporting mechanisms should be introduced to strengthen accountability while encouraging staff to report and correct errors without fear of unjustified punishment.

iv. Federal and state governments, hospital governing boards, and healthcare development partners should prioritize adequate funding for reliable electronic medical record systems, laboratory information management systems, secure data storage, dependable electricity, network connectivity, and routine system maintenance.

v. Tertiary hospitals should establish multidisciplinary data quality audit committees responsible for reviewing audit findings, recommending corrective measures, and monitoring implementation. Measurable indicators, including record completeness, transcription error rates, turnaround time for reporting results, frequency of corrected records, and compliance with audit recommendations, should be used to evaluate progress.

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