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REVIEWER'S REPORT

Manuscript No.: IJAR-56425

Title: Integrated approach for the detection of bacterial resistance in Mali using chromogenic media

Recommendation:
Accept after major revision ……………..

Rating	Excel.	Good	Fair	Poor
Originality		✓		
Techn. Quality			✓	
Clarity				✓
Significance		✓		

Reviewer's ID: JPR-198

Detailed Reviewer's Report

This is a relevant, field-grounded study tackling a genuinely under-researched problem: using simple chromogenic media for AMR detection in a rural West African setting. The dataset is large for this context (508 blood cultures over nearly four years), the two-site design adds credibility, and the cost analysis is a practical bonus.

That said, the manuscript needs substantial work before it's ready for publication. The main problems are inconsistent numbers across sections, an unclear reference standard, incomplete PCR reporting, weak statistical methods, and language quality that needs professional editing. These are all fixable, and the study is worth fixing.

MAJOR COMMENTS

1. The numbers don't add up — fix the sample flow

This is the most important issue. The manuscript reports 508 blood cultures → 148 positives → 112 isolates → 86 resistant strains, but these steps are never explained. Additionally, PCR analyses use six different denominators (n = 122–133) with no justification. Readers cannot follow the logic of the study as written.

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Please add a clear sample flow diagram (STARD format is ideal) that shows exactly how many samples were included at each step and why numbers decrease. Every denominator used in any table or figure needs to be traceable to this diagram.

2. The reference standard is not clearly defined

Section 3.4 names VITEK 2 as the reference method, but earlier sections describe a combination of MALDI-TOF MS, VITEK 2, and PCR as confirmatory tools. These two descriptions conflict. The 2×2 contingency table used to calculate sensitivity, specificity, PPV, and NPV is never shown.

State clearly what the reference standard was, apply it consistently, and present the underlying contingency table so readers can verify the calculations.

3. PCR results are incomplete relative to the methods

The methods describe amplification of 18 genes, including bla_BEL, bla_ADCb, OXA-1, FOX-1, vanC, icaB, and icaD. None of these appear in the results. This is not a trivial omission — readers need to know whether these genes were tested and not detected, or simply not reported.

For each gene listed in methods, report whether it was detected. If results were grouped or excluded, explain why.

4. The blood culture system changed mid-study

The manuscript acknowledges a switch from Signal™ bottles to BacT/Alert bottles during the study due to supply problems. This is a meaningful methodological change. How many cultures were collected with each system? Did positivity rates differ across the two periods? Was contamination affected?

At minimum, report the proportion of cultures collected under each system and discuss whether this change may have influenced results. If data are insufficient to evaluate this, say so explicitly in the limitations.

5. The statistical methods section is too thin

The methods state only that Excel was used with descriptive statistics and 2×2 tables. For a Q2 journal, this is not enough. The following are missing:

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- How confidence intervals were calculated (Wilson score intervals appear to be used, but this isn't stated)
- Whether sample size was calculated a priori, or this was an observational convenience sample
- How missing data were handled — Table 4 shows variable N across variables without explanation
- Whether any inferential comparisons were made between subgroups

6. Don't draw conclusions from n = 1 or n = 2

Salmonella (n=2) and Acinetobacter (n=1) are reported with diagnostic accuracy values and confidence intervals. You cannot make meaningful statistical claims from samples this small. Label these results as descriptive only, and remove any language that implies they support broader conclusions.

7. The prescribing pattern analysis needs clearer grounding

The antibiotic prescription data in Section 3.2 are interesting but poorly integrated. Were these prescriptions from the same patients whose blood cultures are analyzed? What was the time window for data collection? How many total prescriptions were included?

If this analysis is linked to the study patients, show that connection explicitly. If it is a separate descriptive survey of general prescribing at the facility, say so, and give it its own methods paragraph.

8. Clarify the ethics timeline

The study began in August 2020. Ethics approval (CNESS #2022-138) is dated November 2022 — more than two years later. This requires explanation. Was there an earlier approval that covered the initial data collection? Was the 2022 approval retroactive? This is not a minor detail; it needs to be addressed directly, both for the reader and in accordance with journal policy.

9. The flow diagram on page 6 needs a written description

Figure 1 (sample flow diagram) is present in the manuscript but is never described in the text. The methods section simply says 'according to the following sample flow diagram' without further explanation. Walk readers through the key steps in prose — the figure alone is not sufficient.

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MINOR COMMENTS

Language and formatting

There are consistent grammatical errors, missing spaces between words and citations, and overly long sentences throughout. Two examples that are representative rather than isolated: 'efficiently detectMRSA' (line 113) and 'partialactivity' (line 397). Professional English editing is required before resubmission — not optional.

French-language content

Figure 7 (Salmonella resistance profile) has a French title. Annex Table 2 uses French column headers. All content in the main text and supplements must be in English.

Too many resistance figures

Figures 1–10 show individual resistance profiles for each bacterial species. This creates a cluttered, repetitive results section. Consider consolidating into one or two summary figures (a grouped bar chart or heatmap) that allow cross-species comparison at a glance.

Abstract is too long

The abstract is dense with PCR detection rates, confidence intervals, and diagnostic metrics. It reads like a mini-results section. Cut it to 250 words maximum, keeping only the main findings.

Discussion overstates glycopeptide resistance

The discussion states that '83% of strains are resistant to vancomycin and teicoplanin.' This figure does not correspond to any result clearly reported in the results section — the Enterococcus resistance rate reported is 42.9% (3/7 isolates). Every statement in the discussion must link back to a specific result. Please correct this.

Table 7 is missing denominators

Table 7 reports diagnostic performance parameters, but the n values shown (e.g., n=41 for E. coli) do not match Table 5 isolate counts (49 for E. coli). Explain whether Table 7 reflects only the subset that underwent both CHROMagar and VITEK 2 testing, and why these counts differ.

Reference 1 is a bare URL

Reference [1] is cited throughout the introduction but is listed only as a WHO website URL with no formal citation details. Format all references properly.