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OPEN PEER REVIEW

Comprehensive Phenotypic and Molecular Analysis of β-Lactamase Enzymes and Genetic Diversity in *Proteus mirabilis* Clinical UTI Isolates

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About this report

This open peer review (OPR) report shows the public comments made on this article during peer review, by the reviewers, the associate editor and the editor-in-chief, for every revision round, together with the authors' replies. Comments appear only with the consent of the people who wrote them. Reviewers who chose to sign their report are named; the others are shown as "Referee". Comments are edited for language only, and confidential remarks to the editors are not included.

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Contents

1 **Original submission** Referee 1, Referee 2, Associate Editor, Editor-in-Chief 2
2 **Revision 1** Referee 3, Referee 4, Associate Editor, Editor-in-Chief 9
Authors' reply to reviewers 10
Reviewer and editor comments 20
3 **Revision 2** Editor-in-Chief 21
Authors' reply to reviewers 22
Reviewer and editor comments 25

1 Original submission

4 comments · 21 Apr 2026 – 21 Apr 2026

Referee 1 Reviewer

MAJOR REVISION 21 Apr 2026

Dear Authors,

I have reviewed the manuscript, and the comments below are limited to additional scientific-review points that were not already part of the initial editorial screening. The major comments focus on substantive reporting and interpretive issues under the STROBE framework, while the minor comments address clarity, presentation, and editorial refinement.

This manuscript investigates phenotypic and molecular β-lactamase characteristics in 60 clinical urinary *Proteus mirabilis* isolates, combining susceptibility testing, phenotypic enzyme detection, multiplex PCR, and ERIC-PCR genotyping. The topic is clinically relevant and regionally important, particularly given the burden of antimicrobial resistance in urinary pathogens. The combination of phenotypic and genotypic approaches gives the study potential value for infectious-disease surveillance and stewardship-oriented discussions.

The manuscript's main strengths are the clinically relevant organism and setting, the integration of susceptibility, resistance-gene, and genotyping data, and the attempt to link phenotypic resistance patterns with molecular findings. The inclusion of ERIC-PCR diversity analysis also adds epidemiologic interest beyond a purely descriptive antibiogram study.

Major Comments:

1. Sampling framework and representativeness under STROBE (Participants/Setting):

> *The manuscript reports that 60 nonduplicate isolates were collected from two sites, but it does not explain whether these were consecutive isolates, how many urine cultures were screened overall, whether any eligible isolates were excluded, or how the two collection sites contributed to the final dataset (source: Methods 2.1; Results 3.1). This matters because STROBE-based reporting requires readers to understand how the study sample arose and how representative it is of the target clinical population; without this, the external validity of the resistance estimates is difficult to judge (source: Methods 2.1).*
> *Author to-do list:*
>
> ** Clarify whether isolate inclusion was consecutive, convenience-based, or otherwise selected from the eligible culture population (source: Methods 2.1).*
> ** Report the number of urine cultures or *P. mirabilis* candidates assessed before arriving at the final 60 isolates, if available (source: Methods 2.1).*
> ** State how many isolates came from each center and whether any center-specific differences were assessed (source: Methods 2.1).*
> ** Explain why the sample-size formula based on regional UTI prevalence is appropriate for an isolate-based microbiology study, or revise this justification (source: Methods 2.1).*

2. Prespecification and reporting of study variables and outcomes under STROBE (Variables/Outcomes):

> *The manuscript describes many measured variables, including ESBL, AmpC, carbapenemase production, MDR status, individual resistance phenotypes, and β-lactamase genes, but it does not clearly distinguish primary outcomes from secondary outcomes or state which associations were prespecified as the main analytical targets (source: Abstract; Methods 2.4-2.8; Results 3.2-3.5). This weakens analytical transparency because readers cannot readily tell whether the reported comparisons were hypothesis-driven or exploratory, which affects the interpretation of significance testing*

and the emphasis placed on certain findings (source: Results 3.4-3.5).
Author to-do list:

** Define the primary study outcome or primary analytical objective explicitly in the Methods (source: Methods 2.4-2.8).*
** Separate descriptive outcomes from inferential outcomes and state which gene-resistance associations were planned a priori (source: Methods 2.8; Results 3.5).*
** Specify whether MDR prevalence, β-lactamase phenotype prevalence, and gene carriage prevalence were all co-primary descriptive endpoints or secondary endpoints (source: Abstract; Results 3.2-3.5).*
** State clearly whether ERIC-PCR clustering was exploratory epidemiologic typing or part of the main hypothesis-testing framework (source: Methods 2.7; Results 3.6).*

3. Statistical reporting requires strengthening for small-sample molecular association analyses under STROBE (Statistical methods):

The manuscript reports p-values for associations between gene carriage and resistance phenotypes, but it does not provide the underlying contingency counts for each comparison, effect-size estimates, confidence intervals, or any strategy for handling sparse data despite several rare genes being present in very small numbers (for example, blaKPC in 5% and blaAmpC in 6.7%) (source: Methods 2.8; Table 3; Results 3.5). With a total sample of 60 isolates and multiple low-frequency variables, p-values alone are insufficient for robust interpretation, and some comparisons may be unstable or underpowered (source: Table 3; Results 3.3; Results 3.5).
Author to-do list:

** Report the numerator/denominator data underlying each key comparison in Table 3 or a supplementary table (source: Table 3).*
** Add effect-size measures with confidence intervals for the main associations, where feasible (source: Results 3.5).*
** State explicitly which comparisons used Fisher's exact test and why, rather than describing this only in general terms (source: Methods 2.8).*
** Address the issue of multiple comparisons and clarify whether the p-values should be interpreted as exploratory rather than confirmatory (source: Results 3.5).*

4. Interpretation of carbapenemase findings should be more cautious and internally aligned with the actual assay panel under STROBE (Interpretation):

The manuscript concludes that there is circulation of multiple β-lactamase determinants and discusses broad carbapenemase threats, yet the molecular panel assessed only blaKPC among carbapenemase genes and the phenotypic carbapenemase work relied on the Modified Hodge Test, which the Discussion itself acknowledges as limited (source: Methods 2.6.3; Results 3.2-3.3; Discussion). This creates an interpretive gap: the study can support the presence of phenotypic carbapenemase activity in a small subset and blaKPC positivity in a few isolates, but it cannot fully characterize the local carbapenemase landscape or infer the absence or presence of other major carbapenemase families (source: Results 3.2-3.3; Discussion).
Author to-do list:

** Revise the Discussion and Conclusions to distinguish clearly between demonstrated blaKPC positivity and untested carbapenemase mechanisms (source: Results 3.3; Conclusions).*
** Temper broader statements about carbapenemase dissemination in the study setting unless directly supported by the assay panel used here (source: Discussion; Conclusions).*
** Explain more explicitly that carbapenemase-negative PCR results in this study do not exclude other important genes such as blaNDM, blaVIM, blaIMP, or OXA-type enzymes (source: Methods 2.6.3; Discussion).*

> ** Reframe the carbapenemase-related conclusion as preliminary local evidence rather than comprehensive molecular characterization (source: Conclusions).*

Minor Comments:

1. Tables and figures presentation:

> *The manuscript contains 3 main tables and 8 main figures, and each numbered table and figure appears to be cited in the main text; specifically, Tables 1-3 and Figures 1-8 are all referred to in the Results or Methods/Results transitions (source: Table 1-3; Figure 1-8; Results 3.1-3.6). The main presentation issue is not the absence of citations but caption length and redundancy, because several captions repeat methodological detail or interpretation that would be better kept in the text, especially for Figures 6-8 (source: Figure 6-8 captions). Consider shortening captions to identify the content of the display more crisply while moving interpretive detail into the Results text (source: Results 3.3-3.6).*

2. English language and wording quality require careful polishing:

> *Several expressions would benefit from revision for clarity and correctness. For example, "this ourirganism" should be corrected to "this organism," because the current wording is a typographical error that disrupts readability (source: Background). "Supplementory Table S4" should be corrected to "Supplementary Table S4," because the current spelling is inconsistent with standard journal terminology (source: Results 3.3). "P.mirabilis" should be revised to "*P. mirabilis*" with correct spacing and formatting, because the current form is stylistically inconsistent with scientific nomenclature (source: Abstract; Results 3.2). "The high prevalence of multidrug-resistant *P. mirabilis* strains, that harbored diverse β-lactamase genes..." should be revised to remove the unnecessary comma after "strains," because the current sentence is grammatically awkward (source: Conclusions). A full language edit is recommended to improve the article's flow and consistency (source: Abstract; Background; Conclusions).*

3. Numbering and subsection formatting should be standardized:

> *The manuscript contains a numbering inconsistency at "2.5. 3. Modified Hodge Test," which should be formatted consistently with the surrounding subsection structure (source: Methods 2.5. 3). Similar spacing inconsistencies also appear in section and species formatting. Please standardize heading numbering, spacing, and punctuation throughout to improve professional presentation (source: Methods section headings).*

4. Terminology and abbreviation consistency should be improved:

> *Antibiotic abbreviations are not fully harmonized across text, figures, and tables; for example, amikacin appears as "AN" in one place and "AMK" in another figure legend, while ciprofloxacin appears as "CP" in the Methods and "CIP" elsewhere (source: Methods 2.4; Figure 1; Table 2; Table 3). This should be standardized because inconsistent abbreviations make cross-reading harder and may confuse readers comparing datasets across sections (source: Methods 2.4; Figure 1; Table 2-3).*

5. Reference currency should be reviewed selectively:

> *A few references are relatively old and should be reassessed for necessity or replaced with more recent sources where a newer equivalent exists, especially Ref 13 (2000), Ref 14 (1994), and Ref 16 (1996) (source: References 13, 14, 16). These may remain appropriate if they are foundational laboratory texts, but the manuscript would benefit from ensuring that core methodological and clinical statements are supported primarily by up-to-date infectious-disease literature (source: References).*

Best regards,
Scientific Reviewer

Referee 2 Reviewer

MAJOR REVISION 21 Apr 2026

Dear Authors,

Thank you for submitting your manuscript to the journal. Following our initial editorial screening, the issues below must be corrected before the submission can be considered complete for further evaluation.

Please note that references are very important for publication, and all cited sources must be valid, verifiable, cited appropriately in the manuscript text, and suitable for the journal.

2-1- Study period and sampling frame are insufficiently reported:

* What the author wrote: The manuscript reports that 60 non-duplicate *P. mirabilis* isolates were collected from Milad Hospital and Pasargad Research Laboratory and provides inclusion criteria, but does not report the study period or clarify the sampling chronology and source population in sufficient detail. (source: Methods 2.1)
* Why correction is required: This must be corrected because the manuscript is not fully evaluable without a clear study time frame and transparent sampling framework. (source: Methods 2.1)
* To do: Provide the exact sample-collection period and clarify how the final 60 isolates were identified from the eligible clinical population, including whether inclusion was consecutive or based on other selection criteria. (source: Methods 2.1)

2-2- Ethics information is internally inconsistent:

* What the author wrote: The manuscript states that ethical approval was granted under code IR.IAU.ET.REC1402.027, but names Tehran Shargh University in one location and Islamic Azad University, East Tehran Branch in another. (source: Ethics Approval; Methods 2.1)
* Why correction is required: This must be corrected because internal inconsistency currently prevents reliable assessment of ethics approval documentation. (source: Ethics Approval; Methods 2.1)
* To do: Reconcile the approving institution's name across all sections and ensure that the ethics statement is identical wherever it appears. (source: Ethics Approval; Methods 2.1)

2-3- Data availability statement is incomplete:

* What the author wrote: The manuscript contains a Data Availability heading but does not provide a statement under it. (source: Front matter)
* Why correction is required: This must be corrected because the manuscript is not compliant with basic editorial requirements regarding data availability transparency. (source: Front matter)
* To do: Add a complete data availability statement specifying whether data are available, where they can be accessed, and under what conditions. (source: Front matter)

2-4- Supplementary materials are cited but not provided with the submission file:

* What the author wrote: The manuscript refers to Supplementary Figure S1, Supplementary Figure S2, and Supplementary Tables S1-S4, but these files are not present in the uploaded submission material. (source: Results 3.1; Results 3.3)
* Why correction is required: This must be corrected because the manuscript is not fully evaluable without the supplementary materials that are explicitly cited as supporting evidence. (source: Results 3.1; Results 3.3)
* To do: Upload all cited supplementary figures and tables, or revise the manuscript to remove unsupported references to supplementary content. (source: Results 3.1; Results 3.3)

2-5- Reference integrity requires full correction before further processing:

(source: References)
* Why correction is required: This must be corrected because the manuscript is not fully verifiable without a reference list that is current, free of duplicate entries, and bibliographically valid according to basic editorial requirements regarding reference integrity. (source: References)
* To do: Correct every invalid reference, add verifiable DOI and/or PMID information where applicable, remove duplicates, replace outdated references where justified, and submit a fully corrected reference list. (source: References)
* Invalid references:

* Ref 1 - Hassuna et al. — lacks DOI/PMID in the citation entry; duplicate of Ref 10. (source: References 1, 10)
* Ref 2 - Shaaban et al. — lacks DOI/PMID in the citation entry; duplicate of Ref 18. (source: References 2, 18)
* Ref 3 - Pearson et al. — lacks DOI/PMID in the citation entry. (source: References 3)
* Ref 4 - Bedenić et al. — lacks DOI/PMID in the citation entry. (source: References 4)
* Ref 5 - ElTaweel et al. — lacks DOI/PMID in the citation entry. (source: References 5)
* Ref 6 - Joseph et al. — lacks DOI/PMID in the citation entry. (source: References 6)
* Ref 7 - Lombes et al. — lacks DOI/PMID in the citation entry. (source: References 7)
* Ref 8 - González et al. — lacks DOI/PMID in the citation entry. (source: References 8)
* Ref 9 - Fritzenwanker et al. — lacks DOI/PMID in the citation entry. (source: References 9)
* Ref 10 - Hassuna et al. — lacks DOI/PMID in the citation entry; duplicate of Ref 1. (source: References 1, 10)
* Ref 11 - Jamin et al. — lacks DOI/PMID in the citation entry. (source: References 11)
* Ref 12 - Karah et al. — lacks DOI/PMID in the citation entry. (source: References 12)
* Ref 13 - Faddin et al. — lacks DOI/PMID in the citation entry; published in 2000. (source: References 13)
* Ref 14 - Bergey et al. — lacks DOI/PMID in the citation entry; published in 1994. (source: References 14)
* Ref 15 - Tille et al. — lacks DOI/PMID in the citation entry. (source: References 15)
* Ref 16 - Collee et al. — lacks DOI/PMID in the citation entry; published in 1996. (source: References 16)
* Ref 17 - Clinical and Laboratory Standards Institute — lacks DOI/PMID in the citation entry. (source: References 17)
* Ref 18 - Shaaban et al. — lacks DOI/PMID in the citation entry; duplicate of Ref 2. (source: References 2, 18)
* Ref 19 - Al Mamari et al. — lacks DOI/PMID in the citation entry. (source: References 19)
* Ref 20 - Esfandiyari et al. — lacks DOI/PMID in the citation entry; self-citation present in the author list. (source: References 20)
* Ref 21 - Zhang et al. — lacks DOI/PMID in the citation entry. (source: References 21)
* Ref 22 - Hafiz et al. — lacks DOI/PMID in the citation entry. (source: References 22)
* Ref 23 - Anju et al. — lacks DOI/PMID in the citation entry. (source: References 23)
* Ref 24 - Sattler et al. — lacks DOI/PMID in the citation entry. (source: References 24)
* Ref 25 - Alqurashi et al. — lacks DOI/PMID in the citation entry. (source: References 25)
* Ref 26 - Adekanmbi et al. — lacks DOI/PMID in the citation entry. (source: References 26)
* Ref 27 - Amadi et al. — lacks DOI/PMID in the citation entry. (source: References 27)
* Ref 28 - Fattah Hamid et al. — lacks DOI/PMID in the citation entry. (source: References 28)
* Ref 29 - Al-Fahham et al. — lacks DOI/PMID in the citation entry. (source: References 29)
* Ref 30 - Yaseen et al. — lacks DOI/PMID in the citation entry. (source: References 30)
* Ref 31 - Meeprawat et al. — lacks DOI/PMID in the citation entry. (source: References 31)

Please revise the manuscript accordingly and submit a corrected version together with any required supporting material.

Kind regards,
Screening Reviewer

Associate Editor

MAJOR REVISION 21 Apr 2026

Dear Authors,

This original article examines the phenotypic and molecular profiles of β-lactamase-mediated resistance and the genetic diversity of clinical *Proteus mirabilis* urinary isolates. The topic is timely and relevant to antimicrobial resistance surveillance in infectious diseases, and the manuscript presents potentially useful findings. At the same time, the current version requires substantial revision before it can be considered further.

The strongest aspect of the manuscript is its integration of phenotypic susceptibility testing, β-lactamase gene detection, and ERIC-PCR genotyping in a clinically meaningful organism. The regional relevance of the isolate collection and the stewardship-related implications add value to the study.

The scientific review indicates that the manuscript would benefit from clearer reporting of the sampling framework, sharper definition of outcomes and analytical priorities, stronger statistical presentation, and more cautious interpretation of carbapenemase-related findings. In addition, several presentation issues remain, including terminology inconsistency, language problems, and formatting irregularities. Taken together, these concerns do not negate the potential contribution of the work, but they do limit its present scientific and editorial readiness.

Title and abstract: 7/10
Introduction and rationale: 7/10
Methods rigor: 5/10
Results presentation: 7/10
Discussion and interpretation: 6/10
Reporting quality: 5/10
Language and structure: 6/10
Clinical relevance or scholarly value: 8/10
Overall quality: 6/10

The manuscript is promising and addresses a relevant infectious-disease topic, but it should be reconsidered only after major revision. A substantially revised version that resolves the methodological-reporting deficiencies, strengthens analytical transparency, and improves editorial presentation would be needed before further evaluation.

Kind Regards,
Associate Editor

Editor-in-Chief

MAJOR REVISION 21 Apr 2026

Dear Authors,

Thank you for submitting your manuscript entitled “Comprehensive Phenotypic and Molecular Analysis of β-lactamase Enzymes and Genetic Diversity in *Proteus mirabilis* Clinical UTI Isolates.” Following editorial assessment and scientific review, we believe the manuscript addresses a relevant infectious-disease topic with potential value for regional antimicrobial resistance surveillance. However, the current version requires substantial revision before it can be considered further for publication.

The main concerns relate to incomplete reporting of key methodological and submission details, limitations in reference-list integrity and supporting-file completeness, and the need for clearer analytical reporting and

more cautious interpretation of some findings. These issues are potentially correctable, and we would be willing to reconsider a thoroughly revised version if all comments raised during review are addressed carefully and comprehensively.

Please submit a revised manuscript together with any required supplementary material and a clear point-by-point response to the review comments.

Kind Regards,
Editor-in-Chief

2

Revision 1

AUTHORS' RESPONSE TO REVIEWERS

Authors' reply to reviewers

The next pages contain the authors' point-by-point reply to the comments of this revision round, as submitted with the revised manuscript. It is published as the authors wrote it.

Dear Associate Editor,

Thank you very much for your thoughtful and constructive evaluation of our manuscript titled “Comprehensive Phenotypic and Molecular Analysis of β-lactamase Enzymes and Genetic Diversity in *Proteus mirabilis* Clinical UTI Isolates “. We appreciate the time and effort you and the reviewers dedicated to providing such comprehensive feedback. We are encouraged by your recognition of the study’s clinical relevance and the value of integrating phenotypic, genotypic, and ERIC-PCR genotyping in *Proteus mirabilis***.** Following your suggestions, we have performed a major revision of the manuscript. Below is a summary of the key improvements made:

1. Methodological Rigor and Reporting Framework: As suggested, we have significantly clarified the sampling framework. We now provide a more detailed description of the isolate collection period, inclusion/exclusion criteria, and the clinical settings from which the samples were obtained. The definition of outcomes and analytical priorities has been sharpened to ensure greater transparency.
2. Statistical Presentation: We have revised the statistical section to improve clarity and transparency. The associations between specific β-lactamase genes and resistance phenotypes are now more rigorously presented, ensuring that the analytical findings are robust and easy to interpret.
3. Discussion and Interpretation of Findings: Taking your advice, we have adopted a more cautious approach in interpreting the carbapenemase-related findings. We have specifically addressed the limitations of the Modified Hodge Test (MHT) and contextualized our PCR results within the broader molecular landscape, acknowledging that other unscreened determinants could play a role. Furthermore, we have integrated recent scholarly literature to reflect global and regional resistance trends more accurately.
4. Terminology, Language, and Formatting: The entire manuscript has undergone thorough professional editing to correct language inconsistencies, improve flow, and ensure technical terminology is used accurately throughout. Formatting irregularities in the text, tables, and references have been standardized according to the journal’s guidelines.
5. Integration of Suggested Literature: In line with the editorial recommendations, we have carefully reviewed the suggested publications. We have incorporated the most relevant studies to strengthen the Discussion. These additions have helped us better correlate our findings with international and regional data on plasmid-mediated resistance and ESBL-producing Enterobacteriaceae.
6. Enhancement of Molecular Mechanisms Discussion: In response to the reviewer’s brief comment, we have expanded the discussion on the molecular mechanisms of beta-lactamase genes. We have elaborated on how the co-occurrence of these genes facilitates extensive antimicrobial resistance and drives the evolution of multidrug-resistant (MDR) phenotypes in P. mirabilis.
7. Reference Improvement: We have updated the reference list to include recent and highly relevant research as suggested in the peer-review report (Reviewe 1). This has improved the academic rigor and helped contextualize our findings within the current literature on uropathogenic bacteria.

We believe that these substantial revisions have significantly improved the scientific quality and editorial readiness of our work. We hope the revised manuscript is now suitable for publication in your prestigious journal.

Thank you once again for your guidance in improving our manuscript.

Kind Regards,
Corresponding Author

Reply to Reviewer (1)

Major comments:

1. Sampling framework and representativeness under STROBE (Participants/Setting):
> The manuscript reports that 60 non-duplicate isolates were collected from two sites, but it does not explain whether these were consecutive isolates, how many urine cultures were screened overall, whether any eligible isolates were excluded, or how the two collection sites contributed to the final dataset (source: Methods 2.1; Results 3.1). This matters because STROBE-based reporting requires readers to understand how the study sample arose and how representative it is of the target clinical population; without this, the external validity of the resistance estimates is difficult to judge (source: Methods 2.1).
> Author to-do list:>> Clarify whether isolate inclusion was consecutive, convenience-based, or otherwise selected from the eligible culture population (source: Methods 2.1).
> Report the number of urine cultures or *P. mirabilis* candidates assessed before arriving at the final 60 isolates, if available (source: Methods 2.1).> State how many isolates came from each center and whether any center-specific differences were assessed (source: Methods 2.1).
> Explain why the sample-size formula based on regional UTI prevalence is appropriate for an isolate-based microbiology study, or revise this justification (source: Methods 2.1).
Response: We thank the reviewer for highlighting the importance of the sampling framework.
1. Sampling Strategy: The isolates were collected consecutively between November 2023 and May 2024 to ensure a representative clinical sample.
2. Flow of Participants: During the study period, approximately 900 urine cultures were screened. From these, 110 *P. mirabilis* isolates were initially identified. After applying the inclusion and exclusion criteria (e.g., excluding patients with recent antibiotic use or incomplete clinical data), 60 non-duplicate isolates were finally selected for comprehensive molecular and phenotypic analysis.
3. Center Contribution: Of the 60 included isolates, 35 were from Milad Hospital and 25 from Pasargad Research Laboratory. No significant geographical bias in resistance profiles was observed between the two sites.
4. Sample Size: The calculation was used to ensure that the 60 isolates provided sufficient statistical power to reflect the regional prevalence and capture the genetic diversity via ERIC-PCR.
The revised text in Section 2.1 has been highlighted in the manuscript.

2. Prespecification and reporting of study variables and outcomes under STROBE (Variables/Outcomes):
> The manuscript describes many measured variables, including ESBL, AmpC, carbapenemase production, MDR status, individual resistance phenotypes, and β-lactamase genes, but it does not clearly distinguish primary outcomes from secondary outcomes or state which associations were pre-specified as the main analytical targets (source: Abstract; Methods 2.4-2.8; Results 3.2-3.5). This weakens analytical transparency because readers cannot readily tell whether the reported comparisons were hypothesis-driven or exploratory, which affects interpretation of significance testing and emphasis placed on certain findings (source: Results 3.4-3.5).> Author to-do list:
> Define the primary study outcome or primary analytical objective explicitly in the Methods (source: Methods 2.4-2.8).

> Separate descriptive outcomes from inferential outcomes and state which gene-resistance associations were planned a priori (source: Methods 2.8; Results 3.5).
> Specify whether MDR prevalence, β-lactamase phenotype prevalence, and gene carriage prevalence were all co-primary descriptive endpoints or secondary endpoints (source: Abstract; Results 3.2-3.5).
> State clearly whether ERIC-PCR clustering was exploratory epidemiologic typing or part of the main hypothesis-testing framework (source: Methods 2.7; Results 3.6).
Response: We have carefully addressed the reviewer's request for transparency in variable reporting:
1 .Analytical Framework: We have updated Section 2.8 (Statistical Analysis) to clarify that our p-value calculations were focused on pre-specified hypothesis testing (Genotype-Phenotype associations), while ERIC-PCR (Section 2.7) was used for exploratory clustering.
2. Outcome Hierarchy: We have now explicitly labeled the phenotypic results in Section 3.2 as secondary descriptive outcomes to distinguish them from the primary molecular findings.
3. Standard Compliance: These changes ensure that the readers can distinguish between hypothesis-driven results and exploratory observations, fully aligning the manuscript with STROBE recommendations.
According to the modifications made in the Abstract, and as previously noted, the revised text in Sections 2.8 (Methods) and 3.5 (Results) has also been highlighted in the manuscript.

3. Statistical reporting requires strengthening for small-sample molecular association analyses under STROBE (Statistical methods):
> The manuscript reports p-values for associations between gene carriage and resistance phenotypes, but it does not provide the underlying contingency counts for each comparison, effect-size estimates, confidence intervals, or any strategy for handling sparse data despite several rare genes being present in very small numbers (for example blaKPC in 5% and blaAmpC in 6.7%) (source: Methods 2.8; Table 3; Results 3.5). With a total sample of 60 isolates and multiple low-frequency variables, p-values alone are insufficient for robust interpretation, and some comparisons may be unstable or underpowered (source: Table 3; Results 3.3; Results 3.5).> Author to-do list:>> Report the numerator/denominator data underlying each key comparison in Table 3 or a supplementary table (source: Table 3).
> Add effect-size measures with confidence intervals for the main associations, where feasible (source: Results 3.5).> State explicitly which comparisons used Fisher’s exact test and why, rather than describing this only in general terms (source: Methods 2.8).
> Address the issue of multiple comparisons and clarify whether the p-values should be interpreted as exploratory rather than confirmatory (source: Results 3.5).
Response: We appreciate the reviewer’s guidance on strengthening our statistical reporting for small-sample molecular analyses. We have implemented all recommended changes:
1. Transparency of Data: We have added Supplementary Table S5, which reports the raw contingency counts (numerators/denominators) for each key gene-phenotype comparison, allowing for a clear view of the underlying data.
2. Effect Size Estimates: We have now included Odds Ratios (OR) and 95% Confidence Intervals (CI) for the main associations in Section 3.5, providing a measure of effect size beyond simple p-values.

3. Methodological Precision: We have updated Section 2.8 to state explicitly that Fisher's exact test was used for all comparisons involving rare genes (*bla*KPC, *bla*AmpC, and *bla*FOX) where expected counts were <5. These are also marked in Table 3.
4. Inference Level: Following the STROBE guidelines, we have clarified in the Results that these p-values are to be interpreted as exploratory due to the multiple comparisons and small sample size.

4. Interpretation of carbapenemase findings should be more cautious and internally aligned with the actual assay panel under STROBE (Interpretation):
> The manuscript concludes that there is circulation of multiple β-lactamase determinants and discusses broad carbapenemase threats, yet the molecular panel assessed only blaKPC among carbapenemase genes and the phenotypic carbapenemase work relied on the Modified Hodge Test, which the Discussion itself acknowledges as limited (source: Methods 2.6.3; Results 3.2-3.3; Discussion). This creates an interpretive gap: the study can support the presence of phenotypic carbapenemase activity in a small subset and blaKPC positivity in a few isolates, but it cannot fully characterize the local carbapenemase landscape or infer absence/presence of other major carbapenemase families (source: Results 3.2-3.3; Discussion).
> Author to-do list:>> Revise the Discussion and Conclusions to distinguish clearly between demonstrated blaKPC positivity and untested carbapenemase mechanisms (source: Results 3.3; Conclusions).
> Temper broader statements about carbapenemase dissemination in the study setting unless directly supported by the assay panel used here (source: Discussion; Conclusions).
> Explain more explicitly that carbapenemase-negative PCR results in this study do not exclude other important genes such as blaNDM, blaVIM, blaIMP, or OXA-type.
> Reframe the carbapenemase-related conclusion as preliminary local evidence rather than comprehensive molecular characterization (source: Conclusions).
Response: We agree with the reviewer's assessment regarding the interpretive gap. Following the STROBE guidelines, we have revised the Discussion and Conclusion to be more cautious and internally aligned with our methodology. Specifically:
1. Explicit Limitation: We now explicitly state in the Conclusion that our molecular characterization is limited to blaKPC* and does not exclude other major carbapenemase families (e.g., *bla*NDM, *bla*VIM, *bla*IMP**,** or OXA-type enzymes) that were not part of our assay panel.
2. Tempered Language: We have reframed our findings as "preliminary local evidence" of esistance determinants rather than a comprehensive landscape of all carbapenemases.
3. Internal Alignment: The Discussion has been updated to acknowledge the limitations of the Modified Hodge Test (MHT) in light of our specific molecular findings. (Please see the highlighted changes in the Conclusion and Discussion sections).
4. Revised Conclusions: We have clearly distinguished between demonstrated *bla*KPC positivity and untested carbapenemase mechanisms to avoid over-generalization.
(Please see the highlighted changes in the Discussion and Conclusions sections of the revised manuscript).
Minor Comments:
1. Tables and figures presentation:
> The manuscript contains 3 main tables and 8 main figures, and each numbered table and figure appears to be cited in the main text; specifically, Tables 1-3 and Figures 1-8 are all referred to in the Results or Methods/Results transitions (source: Table 1-3; Figure 1-8; Results 3.1-3.6). The

main presentation issue is not citation absence but caption length and redundancy, because several captions repeat methodological detail or interpretation that would be better kept in the text, especially for Figures 6-8 (source: Figure 6-8 captions). Consider shortening captions to identify the content of the display more crisply while moving interpretive detail into the Results text (source: Results 3.3-3.6).

Response: We appreciate this constructive feedback. We agree that several captions contained redundant methodological and interpretive details that are better suited for the main text. In response, we have revised the presentation of our figures as follows:

1. Streamlined Captions: The captions for Figures 6, 7, and 8 have been significantly shortened to provide a crisp identification of the display content. For instance:

In Figure 6, we removed the specific percentages for each gene (e.g., *bla*TEM: 98.3%), as these are already detailed in the Results section (Section 3.3). In Figure 7, we removed the technical specifications of amplicon sizes (bp) and references to BLAST validation, moving these details entirely to the Results text where they are now more appropriately discussed. In accordance with the reviewer's suggestion, we have drastically reduced the length of the caption for Figure 8. The exhaustive list of individual isolates belonging to each of the 15 clusters has been removed from the caption to ensure a crisper presentation. Instead, the general distribution and cluster characteristics are now clearly summarized in the Results section (Section 3.6), and Figure 8 now serves as a focused visual representation of the genetic relatedness and UPGMA clustering.

2. Relocated Details: All interpretive statements and technical nuances previously found in the captions have been integrated into the Results section (Sections 3.3–3.6). This ensures that the text carries the narrative and data, while the figures serve as clear visual aids.

3. Consistency Check: We have also reviewed and adjusted the captions for Tables 1–3 and Figures 1–5 to ensure a consistent, concise style throughout the manuscript.

Example of Revision (Figure 7):

- Original Caption: Included detailed band sizes (747 bp, 489 bp, etc.), descriptions of the BLAST analysis, and interpretive statements regarding assay specificity.
- Revised Caption: Now strictly identifies the panels (A–E) and defines the lane markers (M, +C, and –C) for clarity.

(Please see the revised captions on pages [Insert Page Numbers] and the updated Results text in Section 3.3).

2. English language and wording quality require careful polishing:

> Several expressions would benefit from revision for clarity and correctness. For example, "this ourirganism" should be corrected to "this organism," because the current wording is a typographical error that disrupts readability (source: Background). "Supplementory Table S4" should be corrected to "Supplementary Table S4," because the current spelling is inconsistent with standard journal terminology (source: Results 3.3). "*P.mirabilis*" should be revised to "*P. mirabilis*" with correct spacing and formatting, because the current form is stylistically inconsistent with scientific nomenclature (source: Abstract; Results 3.2). "The high prevalence of multidrug-resistant *P. mirabilis* strains that harbored diverse β-lactamase genes..." should be revised to remove the unnecessary comma after "strains," because the current sentence is grammatically awkward (source: Conclusions). A full language edit is recommended to improve article flow and consistency (source: Abstract; Background; Conclusions).

Response: We appreciate the reviewer's meticulous attention to detail.

1. We have corrected all the specific typographical and formatting errors identified (e.g., correcting "this ourirganism" to "this organism", fixing the spelling of "Supplementary", and ensuring correct spacing and italics for *P. mirabilis*)
2. The unnecessary comma in the Conclusion section has been removed as suggested.
3. Beyond these specific points, the entire manuscript has undergone a thorough English language polishing to improve clarity, grammar, and scientific flow.
(See highlighted changes throughout the manuscript).

3. Numbering and subsection formatting should be standardized:
> The manuscript contains a numbering inconsistency at “2.5. 3. Modified Hodge Test,” which should be formatted consistently with the surrounding subsection structure (source: Methods 2.5. 3). Similar spacing inconsistencies also appear in section and species formatting. Please standardize heading numbering, spacing, and punctuation throughout to improve professional presentation (source: Methods section headings).
Response: We apologize for the inconsistencies in the heading formats.
1. We have standardized the numbering and spacing across all sections of the manuscript.
2. Specifically, the error in the Methods section (previously 2.5.3) has been corrected to a consistent hierarchical format (e.g., 2.5.1).
3. We have also reviewed all section headings, species formatting, and punctuation to ensure a professional and uniform presentation throughout the text.
(See revised headings in the Methods and Results sections).

4. Terminology and abbreviation consistency should be improved:
> Antibiotic abbreviations are not fully harmonized across text, figures, and tables; for example, amikacin appears as “AN” in one place and “AMK” in another figure legend, while ciprofloxacin appears as “CP” in the Methods and “CIP” elsewhere (source: Methods 2.4; Figure 1; Table 2; Table 3). This should be standardized because inconsistent abbreviations make cross-reading harder and may confuse readers comparing datasets across sections (source: Methods 2.4; Figure 1; Table 2-3).
Response: We fully agree with the reviewer that consistent terminology is essential for clarity.
1. We have thoroughly audited the entire manuscript, including all tables, figures, and legends, to harmonize antibiotic abbreviations.
2. For instance, amikacin is now consistently abbreviated as "AK" and ciprofloxacin as "CIP" throughout the text, tables, and figures.
3. We have also added a clear definition for all abbreviations in the footnotes of Table 2 and Table 3, as well as in the legends of Figure 1, to facilitate easier cross-reading of the datasets.
(Please see the updated Tables and Figure legends).

5. Reference currency should be reviewed selectively:
> A few references are relatively old and should be reassessed for necessity or replaced with more recent sources where a newer equivalent exists, especially Ref 13 (2000), Ref 14 (1994), and Ref 16 (1996) (source: References 13, 14, 16). These may remain appropriate if they are foundational laboratory texts, but the manuscript would benefit from ensuring that core methodological and clinical statements are supported primarily by up-to-date infectious-disease literature (source: References).

Response: We have revised the reference list to ensure core methodological and clinical statements are supported by up-to-date literature. As suggested, we have replaced the older foundational texts (Refs 13, 14, and 16) with the following current editions:
Reference 13: Replaced with Manual of Clinical Microbiology (13th Edition, 2023)
Reference 14: Updated to Bergey's Manual of Systematics of Archaea and Bacteria (2015).
Reference 16: Replaced with Bailey & Scott's Diagnostic Microbiology (15th Edition, 2021).
These updates ensure that our laboratory methods and phenotypic identifications are aligned with the most recent international standards.

Reply to Reviewer (2)
2-1- Study period and sampling frame are insufficiently reported:
What the author wrote: The manuscript reports that 60 non-duplicate P. mirabilis isolates were collected from Milad Hospital and Pasargad Research Laboratory and provides inclusion criteria, but does not report the study period or clarify the sampling chronology and source population in sufficient detail. (source: Methods 2.1) Why correction is required: This must be corrected because the manuscript is not fully evaluable without a clear study timeframe and transparent sampling framework. (source: Methods 2.1).
To do: Provide the exact sample-collection period and clarify how the final 60 isolates were identified from the eligible clinical population, including whether inclusion was consecutive or otherwise selected. (source: Methods 2.1).
Response: We sincerely thank the reviewer for this constructive comment. We agree that methodological transparency regarding the study timeframe and sampling framework is crucial for the reproducibility and evaluability of the study. We have thoroughly revised Section 2.1 to address these points. The following modifications were made:
1. Exact Study Period: We have now specified that the study was conducted over a 7-month period, from November 2023 to May 2024.
2. Sampling Framework & Chronology: We have clarified that the isolates were collected consecutively from the source population. To ensure a robust sampling frame, we have detailed the recruitment flow: starting from 900 screened urine cultures, identifying 110 initial *P. mirabilis* candidates, and finally selecting the 60 isolates that met our strict inclusion criteria.
3. Inclusion/Exclusion Clarity: The criteria for inclusion (adults, clinical UTI symptoms, and no prior antibiotic use within 48 hours) have been explicitly stated to show how the final 60 isolates were identified from the eligible population.
4. Logistics and Maintenance: As suggested by the need for better reporting, we added details on sample transport (at 4°C within 2 hours) and long-term storage (-80°C in TSB with 20% glycerol) to ensure the integrity of the isolates for molecular analysis.
5. Statistical Validation: We have also retained the sample size calculation formula to justify that the 60 isolates provide sufficient statistical power for this regional study.
(See highlighted changes in Methods, Section 2.1).

2-2- Ethics information is internally inconsistent: What the author wrote: The manuscript states that ethical approval was granted under code IR.IAU.ET.REC1402.027, but names Tehran Shargh University in one location and Islamic Azad University, East Tehran Branch in another. (source: Ethics Approval; Methods 2.1) Why correction is required: This must be corrected because internal inconsistency currently prevents reliable assessment of ethics approval documentation. (source: Ethics Approval; Methods 2.1)* To do: Reconcile the approving

institutional name across all sections and ensure that the ethics statement is identical wherever it appears. (source: Ethics Approval; Methods 2.1).
Response: We appreciate the reviewer's attention to detail regarding the institutional name. We have carefully re-examined the entire manuscript, including the "Methods" section and the "Ethical Considerations" statement. We have ensured that the name "Islamic Azad University, East Tehran Branch" is used consistently and exclusively throughout the document to refer to the approving institution. Any potential inconsistencies between the manuscript and the submission metadata have also been addressed to ensure full alignment with the ethics approval code (IR.IAU.ET.REC1402.027).

2-3- Data availability statement is incomplete:
What the author wrote: The manuscript contains a Data Availability heading but does not report any actual statement under it. (source: Front matter) Why correction is required: This must be corrected because the manuscript is not compliant with basic editorial requirements regarding data availability transparency. (source: Front matter)
To do: Add a complete data availability statement specifying whether data are available, where they can be accessed, and under what conditions. (source: Front matter).
Response: We apologize for this omission in the initial submission. We have now included a formal Data Availability Statement in the "Front Matter" section of the revised manuscript. As specified, the raw data supporting the findings of this study are available from the corresponding author upon reasonable request, ensuring compliance with the journal's editorial requirements regarding data transparency.

2-4- Supplementary materials are cited but not provided with the submission file:
What the author wrote: The manuscript refers to Supplementary Figure S1, Supplementary Figure S2, and Supplementary Tables S1-S4, but these files are not present in the uploaded submission material. (source: Results 3.1; Results 3.3) Why correction is required: This must be corrected because the manuscript is not fully evaluable without the supplementary materials that are explicitly cited as supporting evidence. (source: Results 3.1; Results 3.3)
To do: Upload all cited supplementary figures and tables, or revise the manuscript to remove unsupported references to supplementary content. (source: Results 3.1; Results 3.3).
Response: We sincerely apologize for this technical oversight during the initial submission process. We have now provided all the missing supplementary materials. Specifically, Supplementary Figures S1-S2 and Supplementary Tables S1-S4 have been uploaded as a separate "Supplementary Material" file alongside the revised manuscript. These files contain the supporting evidence for the results presented in Sections 3.1 and 3.3, ensuring that the study is now fully evaluable.

2-5- Reference integrity requires full correction before further processing:
What the author wrote: The manuscript provides a 31-item reference list, but no entry includes a DOI or PMID in the citation text, 3 references were published in 2011 or earlier, and duplicate entries are present. (source: References) Why correction is required: This must be corrected because the manuscript is not fully verifiable without a reference list that is current, uniquely listed, and bibliographically valid according to basic editorial requirements regarding reference integrity. (source: References)

To do: Correct every invalid reference, add verifiable DOI and/or PMID information where applicable, remove duplicates, replace outdated references where justified, and submit a fully corrected reference list. (source: References) Valid references: None identified**.** Invalid references:
Ref 1 - Hassuna et al. — lacks DOI/PMID in citation entry; duplicate of Ref 10. (source: References 1, 10) Ref 2 - Shaaban et al. — lacks DOI/PMID in citation entry; duplicate of Ref 18. (source: References 2, 18)
Ref 3 - Pearson et al. — lacks DOI/PMID in citation entry. (source: References 3) Ref 4 - Bedenić et al. **—** lacks DOI/PMID in citation entry. (source: References 4)
Ref 5 - ElTaweel et al. — lacks DOI/PMID in citation entry. (source: References 5) Ref 6 - Joseph et al. — lacks DOI/PMID in citation entry. (source: References 6)
Ref 7 - Lombes et al. — lacks DOI/PMID in citation entry. (source: References 7) Ref 8 - González et al. — lacks DOI/PMID in citation entry. (source: References 8)
Ref 9 - Fritzenwanker et al. — lacks DOI/PMID in citation entry. (source: References 9) Ref 10 - Hassuna et al. — lacks DOI/PMID in citation entry; duplicate of Ref 1. (source: References 1, 10)
Ref 11 - Jamin et al. — lacks DOI/PMID in citation entry. (source: References 11) Ref 12 - Karah et al. — lacks DOI/PMID in citation entry. (source: References 12)
Ref 13 - Faddin et al. — lacks DOI/PMID in citation entry; published in 2000. (source: References 13) Ref 14 - Bergey et al. — lacks DOI/PMID in citation entry; published in 1994. (source: References 14)
Ref 15 - Tille et al. — lacks DOI/PMID in citation entry. (source: References 15)
Ref 16 - Collee et al. — lacks DOI/PMID in citation entry; published in 1996. (source: References 16) Ref 17 - Clinical and Laboratory Standards Institute — lacks DOI/PMID in citation entry. (source: References 17)
Ref 18 - Shaaban et al. — lacks DOI/PMID in citation entry; duplicate of Ref 2. (source: References 2, 18) Ref 19 - Al Mamari et al. — lacks DOI/PMID in citation entry. (source: References 19)
Ref 20 - Esfandiyari et al. — lacks DOI/PMID in citation entry; self-citation present in author list. (source: References 20) Ref 21 - Zhang et al. — lacks DOI/PMID in citation entry. (source: References 21)
Ref 22 - Hafiz et al. — lacks DOI/PMID in citation entry. (source: References 22) Ref 23 - Anju et al. — lacks DOI/PMID in citation entry. (source: References 23)
Ref 24 - Sattler et al. — lacks DOI/PMID in citation entry. (source: References 24) Ref 25 - Alqurashi et al. — lacks DOI/PMID in citation entry. (source: References 25)
Ref 26 - Adekanmbi et al. — lacks DOI/PMID in citation entry. (source: References 26) Ref 27 - Amadi et al. — lacks DOI/PMID in citation entry. (source: References 27)
Ref 28 - Fattah Hamid et al. — lacks DOI/PMID in citation entry. (source: References 28) Ref 29 - Al-Fahham et al. — lacks DOI/PMID in citation entry. (source: References 29)
Ref 30 - Yaseen et al. — lacks DOI/PMID in citation entry. (source: References 30)* Ref 31 - Meeprawat et al. — lacks DOI/PMID in citation entry. (source: References 31).
Response: We sincerely apologize for the technical errors in the reference list. We have performed a comprehensive revision of the bibliography to meet the journal's editorial standards:
1. DOI and PMID: We have added verifiable DOI or PMID links to every single reference in the list.
2. Removal of Duplicates: Duplicate entries (previously Ref 1/10 and Ref 2/18) have been

merged, and the entire citation numbering throughout the manuscript has been updated accordingly.
3. Updating Outdated References: We have replaced the outdated references (Ref 13, 14, and 16 from the 1990s/2000) with recent, high-impact literature from 2019-2024 to ensure the clinical and methodological context is current.
4. Consistency Check: The final list now contains 31 unique, valid, and fully verifiable references, all formatted according to the journal's style.

2 Revision 1

4 comments · 31 May 2026 – 15 Jun 2026

Referee 3 Reviewer

ACCEPT 31 May 2026

Dear Author
With regard
I have carefully read your article.
I am pleased to inform you that, based on the method used in the study, your article is approved for publication in this journal.
Thank you

Referee 4 Reviewer

MINOR REVISION 1 Jun 2026

Dear authors,
I appreciate the time and effort you spent preparing a manuscript on the phenotypic and molecular analysis of beta-lactamase enzymes and the genetic diversity of Proteus mirabilis in UTI patients. I believe that your study was well conceptualized and that the data were accurately corrected and analyzed. I suggest publication of your manuscript after minor revision. Please address my comments:
1- Please discuss local publications from Iran on Proteus mirabilis and compare your findings with those of others.
2- Please highlight the clinical implication of your study in the discussion section.
Best regards,

Associate Editor

MINOR REVISION 15 Jun 2026

Minor revision

Editor-in-Chief

MINOR REVISION 15 Jun 2026

Minor revision

3

Revision 2

AUTHORS' RESPONSE TO REVIEWERS

Authors' reply to reviewers

The next pages contain the authors' point-by-point reply to the comments of this revision round, as submitted with the revised manuscript. It is published as the authors wrote it.

Dear Editor,

We are pleased to submit the revised version of our manuscript entitled " **Comprehensive Phenotypic and Molecular Analysis of β-lactamase Enzymes and Genetic Diversity in *Proteus mirabilis* Clinical UTI Isolates** " for further consideration for publication in your esteemed journal.

We would like to express our gratitude to the reviewers for their constructive feedback and the editorial office for their valuable suggestions. Their insights have been immensely helpful in refining our work and strengthening the academic rigor of our findings. We have carefully addressed all the comments provided by Reviewer 2 and the editorial office. Specifically, we have:

1- Expanded the Discussion to include a comprehensive comparison of our results with local publications from Iran, emphasizing the regional trends of antimicrobial resistance.

2- Detailed the Clinical Implications of our study, specifically addressing the necessity of local AST and the challenges associated with MDR strains and β-lactamase determinants in clinical settings.

3- Incorporated the suggested references provided by the editorial office to better contextualize our findings and align our study with the most current literature in the field.

All changes have been implemented in the manuscript and are highlighted in the "Marked Version" of the text. A point-by-point response to the reviewer's and editor's comments is provided below.

We believe that these revisions have significantly improved the quality and comprehensiveness of our manuscript. We hope that the revised version is now suitable for publication.

Thank you for your time and consideration.

Sincerely,

Corresponding Author

Response to Reviewer 2

We sincerely thank the reviewer for the constructive and encouraging comments. We are grateful for the positive evaluation of our study and for the helpful suggestions to further improve the Discussion.

Comment 1: Please discuss local publications from Iran on *Proteus mirabilis* and compare your findings with the others.
Response: We sincerely thank the reviewer for this valuable suggestion. We have now incorporated a detailed comparison between our results and previous studies conducted in various regions of Iran. Specifically, we have highlighted the consistency of our resistance patterns (particularly regarding β-lactams and fluoroquinolones) with other Iranian clinical isolates, suggesting that the observed phenotypes reflect a broader regional trend. This addition can be found in the third paragraph of the Discussion section (Page 17, Line 489).

Comment 2: Please highlight the clinical implication of your study in the Discussion section.
Response: We appreciate the reviewer's insightful comment. We have expanded the discussion to emphasize the clinical implications of our findings. We specifically addressed the need for local antimicrobial susceptibility testing (AST) before initiating empirical therapy, given the high prevalence of MDR strains and the presence of critical determinants like *bla* KPC. We also discussed the necessity of stringent infection control and molecular surveillance to prevent the spread of these resistant strains in healthcare settings. These revisions are detailed in the second-to-last paragraph of the Discussion section (Page 19, Line 578).

Response to associated Editor Comments

Attachment 1) Improve your references:
Please read the comments below and try to improve your references.
As part of the review process, we would like to draw the authors' attention to several recent publications that may be relevant to their study. These references are suggested to help strengthen the manuscript's background, contextualize its findings within the broader literature, and ensure that it reflects the most up-to-date research in the field. These references are provided solely as suggestions, and citing them is not mandatory. The aim is to enhance the academic rigor and comprehensiveness of the manuscript.
These article(s) are as below:

1. Comprehensive Analysis of Urinary Tract Infections: Investigating Risk Factors, Antimicrobial Resistance Profiles, and Beta-lactamase Genotyping for Effective Management Strategies
2. Reason: This study examines similar risk factors and resistance profiles relevant to UTI management in clinical settings. Link: https://doi.org/10.5812/jjm-162976
3. Detection of Extended-spectrum Beta-lactamases (ESBLs), Carbapenemase, Metallo-β-lactamase Production Bacteria and Antibiotic Susceptibility Pattern in Hospitalized Patients with Ventilator-associated Pneumonia
   Reason: The findings discuss antimicrobial resistance patterns, including β-lactamases, that are pertinent to clinical diseases like UTIs. Link: https://doi.org/10.5812/jjm-129434
4. Antimicrobial Resistance Rates and Risk Factors for Extended-Spectrum Beta-Lactamase-Producing Escherichia coli-Associated Urinary Tract Infections in Older Outpatients in East Anatolia from 2011 – 2019.
   Reason: This article elaborates on the resistance mechanisms and features similar demographics pertinent to UTI cases. Link: https://doi.org/10.5812/jjm-132890

Response: The authors are grateful to the editorial office for the suggested references. We have reviewed these articles and incorporated them into the revised manuscript to better contextualize our findings and strengthen the clinical discussion. These additions help to better reflect the current regional resistance patterns and the challenges of effective UTI management. We believe these revisions have enhanced the overall academic quality of the work.

3 Revision 2

1 comment · 17 Jul 2026

Editor-in-Chief

ACCEPT 17 Jul 2026

Accept