OPEN PEER REVIEW

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What is "Open Peer Review" process?

An "Open Peer Review" process is making the details of all review process (including reviewers, associate editors, and EICs comments) as "Public" as it is agreed by EIC, Authors, and reviewers.

Advantages of "Open Peer Review" process

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https://sites.kowsarpub.com/kowsar/knowledgebase/category/tree.html#opr.html

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Peer Review Report for "Phenotypic and Genotypic Evaluation of Antibiotic Resistance of *Acinetobacter baumannii* Bacteria Isolated from Surgical ICU Patients in Pakistan"

Author(s): Nureen Zahra, Basit Zeshan, Muhammad Mubeen Ali Qadri, Musarat Ishaq, Muhammad Afzal, Naveed Ahmed

Review Timeline:

Submit Date: 18 Jan 2021
Revised Date: 22 Jun 2021
Accepted Date: 22 Jun 2021

Revision (0)

Here, you can see the **Reviewers**, **Associate Editors** and **EICs'** comments from the beginning to the end of the revision process.

Ramin Abiri: Reviewer | Revision (0)

20 May 2021

Dear AE,
The manuscript entitled: "Phenotypic Resistance Pattern and Molecular Detection of Carbapenemases in Multidrug-Resistant Acinetobacter baumannii from Surgical ICU" has been submitted for publication in JJM.
The manuscript presents the data concerning antibiotic resistance and the prevalence of some of genes incorporated in antibiotic resistance in the clinical isolate from SICU in a hospital in Lahore. The main problem of the manuscript is the aim of the study which is repeated several times: "Objectives: The aim of the study was to find out the correlation of phenotypic resistance with carbapenemase resistance genes in multidrug resistant clinical isolates isolated from patients admitted in SICUs of a tertiary care hospital in Lahore, Pakistan.
According to this aim the manuscript must be rejected mainly because:
1- Other resistance mechanisms are also assessed
2- There is no need to assess a relationship in a limited area, like a department, specific ward or even in a hospital. The relationships are universal

3- In order to assess this relationship, all the mechanisms must be examined, like the genes involved in multidrug efflux systems
4- There is no statistics available to check these relations
5- There is no conclusion concerning the aim
6- In the introduction part, It is not explained why this relationship is important. We know that antibacterial resistance is an important issue but why the relationship between phenotypic and genotypic traits?
So, the aims are not stratified and answered in the manuscript
If the aim of the study is a simple report of antibacterial resistance rate and genotypes in a specific department of a local hospital, it must be mentioned, while it seems to be necessary to compare antibiotic-resistant rates statistically
Thanks.

Farhad Safarpoor Dehkordi: Reviewer | **Revision (0)** 31 May 2021

Dear AE,
ID: 113008, Phenotypic Resistance Pattern and Molecular Detection of Carbapenems in Multidrug-Resistant Acinetobacter baumannii from Surgical ICU Patients
Well, this is an original paper about the Phenotypic Resistance Pattern and Molecular Detection of Carbapenems in Multidrug-Resistant Acinetobacter baumannii from Surgical ICU Patients in Pakistan. Authors showed that the phenotypic resistance against amikacin was 27.2%, ceftriaxone (100%), ceftazidime (27.2%), cefepime (63.3%), ciprofloxacin & co-trimoxazole (100%), gentamicin (40%), imipenem (22.2%), meropenem (21.1%), piperacillin-tazobactam (27.2%), tigecycline (27.2%) and tetracycline was resistant to 63.3% of isolates. All A. baumannii isolates were found sensitive to colistin (CT), polymixin-B (PB) and tobramycin (TOB). The PCR amplification of carbapenemases genes revealed the prevalence of blaOXA-23, blaOXA-51, blaOXA-40 in 73, 90 and 64.4% isolates. blaNDM1 (92.2%), blaVIM (40%) blaIMP (90%), ISAba1 (85.5%), sul1 (16.6%), sul2 (20%), armA (32.2%) and PER-1 (12%) While blaOXA-24 and blaOXA-58 genes were not detected in the isolates. The sequence analysis of blaOXA-23 and blaOXA-51 genes showed 98% and 95% similarity with previously reported sequences in GenBank database.
This is an interesting work but some major revisions are required to its fully acceptance for publication in JJM by the authors:
MY COMMENTS:
1- Text is full from grammatical and typographical mistakes. Thus, it should check by a native English speaker.
2- Please changed the title as follow:
Phenotypic and genotypic evaluation of antibiotic resistance of Acinetobacter baumannii bacteria isolated from Surgical ICU Patients in Pakistan
3- Please determine the type of study in the method section.
4- Please add the method of sampling.
5- Please add any ethical issues considered by authors.
6- Please add the number of samples collected from each site of infection.
7- Please add the names of hospitals in which samples were collected.
8- Please add the method of bacterial isolation and identification completely.
9- Please add reference for the bacterial isolation and identification.

10- Please add the criteria used for the disk diffusion.
11- Please add the culture explanation for the disk diffusion.
12- How the antibiotic disks were selected.
13- Please add the disk concentrations.
14- Please add valid reference for the disk diffusion.
15- DNA was detected from bacteria or initial samples? Which one? Please add more details.
16- How the quality of extracted DNA was assessed?
17- How the quantity of extracted DNA was assessed?
18- Please add all information need for the PCR in table 1. I mean times and volumes.
19- Please add the electrophoresis completely.
20- As I understand, you made the following procedure in your survey: Samples collection, Isolation and identification of Acinetobacter baumannii, Assessment of antibiotic resistance pattern of isolates, assessment of the antibiotic resistance genes amongst DNA samples extracted from all bacteria or just carbapenem-resistant strains or multi-drug resistant strains? Which one? It is not clear in the text. Please made it clear.
21- Why you didn't present any demographical characters of the targeted population? Please add it.
22- Why you didn't present your data according to the types of infections? Please add it
23- I cannot find any statistical analysis on your tables. Please add them
After these changes, I should assess your paper another time and then, I will present acceptance or maybe some minor revisions.
Cheers
FSD

REFEREE: Associate Editor | **Revision** (0) 5 Jun 2021

Dear EIC
Comments for the authors:
1. Add objectives of study at the end of the introduction in a separate subheading (Objectives).
2. Put CLSI guidelines suitable reference.
3. Add accession numbers in the results section.
Thanks.

REFEREE: EIC | **Revision** (0) 5 Jun 2021

Dear Authors,
Thank you for submitting your manuscript to JJM. I have completed the review of your manuscript and a summary is appended below (Pleases find attached files). The reviewers recommend the reconsideration of your paper following major revision. I invite you to resubmit your manuscript after addressing all reviewer comments. Please answer point by point to reviewer's comments on a separate sheet under WORD format and write your modifications in the revised version (WORD format) in colored or highlighted letters. Your answers to reviewers' queries are not only for the Editorial Board but for the readers and should be included, when appropriate, in the manuscript for improvement and a better

understanding.

When resubmitting your manuscript, please carefully consider all issues mentioned in the reviewers' comments, outline every change made a point by point, and provide suitable rebuttals for any comments not addressed. In addition, JJM INSTRUCTION attached to the mail, Pleases find it.

Note:

Please add ORCID number into you and your collages account, then automatically appear in your published papers in JJM both in HTML and pdf. Pleases follow the below link for the process. https://sites.kowsarpub.com/jjm/knowledgebase/category/tree.html#orcid.html

Thanks.

OPEN PEER REVIEW

Revision (1)

Reply to Reviewers

Ideally, the reviewing process can significantly improve the submitted manuscripts by allowing the authors to take into account the advice of reviewers. Author(s) must reply to all reviewers' comments in a separate Word file, point by point. A "**Reply to Reviewers**" document is submitted along with revised manuscript during submission of revised files, summarizing the changes that the authors made in response to the reviewers' comments. The responses to reviewers' comments specifies how the authors addressed each comment the reviewers made.

You can read the authors' responses to the reviewers' comments in the next page.

RESPONSE TO REVIEWER'S COMMENTS

Dated: 18-06-2021

Dear Editor-In-Chief,
Jundishapur Journal of Microbiology,
Subject: Response to Reviewer's Comments
Manuscript Number: 113008

Dear Sir,

Thank you so much for the consideration of the manuscript entitled "Phenotypic and genotypic evaluation of antibiotic resistance of *Acinetobacter baumannii* bacteria isolated from Surgical ICU Patients in Pakistan".
I have addressed the changes suggested by reviewers and associate editor, and also the changes have been highlighted in the manuscript.

I hope it will be processed as soon as possible.

Thank you and Best Regards

Yours Sincerely,

Reviewer 1:

ID: 113008,

Phenotypic Resistance Pattern and Molecular Detection of Carbapenems in Multidrug-Resistant *Acinetobacter baumannii* from Surgical ICU Patients.

Well, this is an original paper about the Phenotypic Resistance Pattern and Molecular Detection of Carbapenems in Multidrug-Resistant *Acinetobacter baumannii* from Surgical ICU Patients in Pakistan. Authors showed that the phenotypic resistance against amikacin was 27.2%, ceftriaxone (100%), ceftazidime (27.2%), cefepime (63.3%), ciprofloxacin & co-trimoxazole (100%), gentamicin (40%), imipenem (22.2%), meropenem (21.1%), piperacillin-tazobactam (27.2%), tigecycline (27.2%) and tetracycline was resistant to 63.3% of isolates. All A. baumannii isolates were found sensitive to colistin (CT), polymixin-B (PB), and tobramycin (TOB). The PCR amplification of carbapenemases genes revealed the prevalence of blaOXA-23, blaOXA-51, blaOXA-40 in 73, 90, and 64.4% isolates. blaNDM1 (92.2%), blaVIM (40%) blaIMP (90%), ISAba1 (85.5%), sul1 (16.6%), sul2 (20%), armA (32.2%) and PER-1 (12%) While blaOXA-24 and blaOXA-58 genes were not detected in the isolates. The sequence analysis of blaOXA-23 and blaOXA-51 genes showed 98% and 95% similarity with previously reported sequences in the GenBank database.

This is an interesting work but some major revisions are required to its fully acceptance for publication in JJM.

1- Text is full from grammatical and topographical mistakes. Thus, it should check by a native English speaker.

Action: The manuscript has been thoroughly checked for grammatical mistakes by the native English speaker. Also, it has been checked and updated topographically.

2- Please changed the title as follow: “Phenotypic and genotypic evaluation of antibiotic resistance of *Acinetobacter baumannii* bacteria isolated from Surgical ICU Patients in Pakistan”.

Action: The title has been changed as per the suggestion.

3- Please determine the type of study in the method section.

Action: It was a cross-sectional study.

4- Please add the method of sampling.

Action: Simple random sampling technique was used for the current study. The statement has been written in the manuscript.

5- Please add any ethical issues considered by the authors.

Action: The statement about ethical approval of the study has been added to the manuscript.

6- Please add the number of samples collected from each site of infection.

Action: The exact number of samples from each site has been added to the manuscript.

7- Please add the names of hospitals in which samples were collected.

Action: The hospital names, from where we collected the samples, have been added to the manuscript.

8- Please add the method of bacterial isolation and identification completely.

Action: Bacterial isolation and identification protocol have been defined in the manuscript.

9- Please add the reference for the bacterial isolation and identification.

Action: The following reference has been added in the respective section.
Cheikh HB, Domingues S, Silveira E, Kadri Y, Rosário N, Mastouri M, et al. Molecular characterization of carbapenemases of clinical Acinetobacter baumannii–calcoaceticus complex isolates from a University Hospital in Tunisia. 3 Biotech. 2018;8(7):297.

10- Please add the criteria used for the disk diffusion.

Action: The disk diffusion method has been described in the material and methods section of the manuscript.

11- Please add the cultural explanation for the disk diffusion.

Action: The explanation for the disk diffusion method has been added in the respective section of the manuscript.

12- How the antibiotic disks were selected?

Action: The antibiotics were used as per CLSI guidelines 2020. The same statement has been mentioned in the manuscript.

13- Please add the disk concentrations.

Action: Disk concentrations have been written in the manuscript.

14- Please add the valid reference for the disk diffusion.

Action: The following reference has been added in the respective section.

Vrancianu CO, Gheorghe I, Czobor IB, Chifiriuc MC. Antibiotic Resistance Profiles, Molecular Mechanisms and Innovative Treatment Strategies of Acinetobacter baumannii. Microorganisms. 2020;8(6):935.

15- DNA was detected from bacteria or initial samples? Which one? Please add more details.

Action: DNA was extracted from *A. baumannii* bacterial isolates. The sentence has been also added to the manuscript.

16- How the quality of extracted DNA was assessed?

Action: The quality of DNA was assessed using gel electrophoresis.

17- How the quantity of extracted DNA was assessed?

Action: The quantity of DNA was not measured as we check only the quality of DNA, that is either the DNA/genes were present or not.

18- Please add all information need for the PCR in table 1. I mean times and volumes.

Action: PCR conditions and volumes have been added in the material and method section of the manuscript.

19- Please add the electrophoresis completely.

Action: The details of gel electrophoresis have been added to the manuscript.

20- As I understand, you made the following procedure in your survey: Samples collection, Isolation, and identification of *Acinetobacter baumannii*, Assessment of antibiotic

resistance pattern of isolates, assessment of the antibiotic resistance genes amongst DNA samples extracted from all bacteria or just carbapenem-resistant strains or multi-drug resistant strains? Which one? It is not clear in the text. Please made it clear.

Action: All of the 90 *Acinetobacter baumannii* isolates proceeded for molecular identification of genes. It has been described in the material and method section as well.

21- Why you didn't present any demographical characters of the targeted population? Please add it.

Action: Gender-wise distribution has been provided in the manuscript. The other demographical characteristics have not been described as they were not concerned for the manuscript.

22- Why you didn't present your data according to the types of infections? Please add it

Action: The details of data according to the sites of infection have been added in the manuscript.

23- I cannot find any statistical analysis on your tables. Please add them

Action: Statistical analysis has been written in the text (result section), but not in the tables.

Reviewer 2:

Dear Sir

The manuscript entitled: "Phenotypic Resistance Pattern and Molecular Detection of Carbapenemases in Multidrug-Resistant *Acinetobacter baumannii* from Surgical ICU" has been submitted for publication in JJM.

The manuscript presents the data concerning antibiotic resistance and the prevalence of some of the genes incorporated in antibiotic resistance in the clinical isolate from SICU in a hospital in Lahore. The main problem of the manuscript is the aim of the study which is repeated several times: "Objectives: The study aimed to find out the correlation of phenotypic resistance with carbapenemase resistance genes in multidrug-resistant clinical isolates isolated from patients admitted in ICUs of a tertiary care hospital in Lahore, Pakistan.

According to this aim, the manuscript must be rejected mainly because:

Action: Dear valuable reviewer, we are glad for your kind observations. We have made corrections in the study as per your observations and suggestions. Also, we have tried to answer your all queries related to the manuscript. We hope that, after we have answered all of your queries, you will consider our manuscript to be reviewed once again.

1- Other resistance mechanisms are also assessed

Action: The specific objectives have been changed as per the suggestion and also added at the end of the introduction section in the manuscript.

2- There is no need to assess a relationship in a limited area, like a department, specific ward, or even in a hospital. The relationships are universal

Action: The statement about the relationship has been removed from the objectives of the study.

3- To assess this relationship, all the mechanisms must be examined, like the genes involved in multidrug efflux systems

Action: Dear respected reviewer, we are glad for your observation. Furthermore, the statement about the relationship has been removed from the objectives of the study.

4- There are no statistics available to check these relations

Action: Statistical analysis has been written in the text (result section), but not in the tables.

5- There is no conclusion concerning the aim

Action: The conclusion section has been revised accordingly.

6- In the introduction part, It is not explained why this relationship is important. We know that antibacterial resistance is an important issue but why the relationship between phenotypic and genotypic traits?

Action: A paragraph has been added in the introduction section of the manuscript.

7- So, the aims are not stratified and answered in the manuscript If the aim of the study is a simple report of antibacterial resistance rate and genotypes in a specific department of a local hospital, it must be mentioned, while it seems to be necessary to compare antibiotic-resistant rates statistically

Action: The aims of the study have been rewritten and also a statistical analysis has been written in the text (results).

Associate Editor's Comments:

Associate Editor 1:

1. Add objectives of study at the end of the introduction in a separate subheading (Objectives).

Action: The specific objectives have been added at the end of the introduction section in the manuscript.

2. Put CLSI guidelines suitable reference.

Action: Following reference has been added in the respective section.

Geisinger E, Mortman NJ, Dai Y, Cokol M, Syal S, Farinha A, et al. Antibiotic susceptibility signatures identify potential antimicrobial targets in the *Acinetobacter baumannii* cell envelope. Nature Communications. 2020;11(1):1-16.

3. Add accession numbers in the results section.

Action: Accession numbers of the closely related taxa have been provided in the manuscript. Due to high sequence identity with these accession numbers, we did not submit our sequences in the genebank. The detail has been indicated in the phylogenetic tree.

OPEN PEER REVIEW

Revision (1)

Here, you can see the **Reviewers**, **Associate Editors** and **EICs'** comments from the beginning to the end of the revision process.

REFEREE: Associate Editor | **Revision** (1) 22 Jun 2021

Dear EIC
The manuscript is completely revised according to reviewer comments by authors and it is acceptable for publishing.
Thanks.

REFEREE: EIC | **Revision** (1) 22 Jun 2021

Dear Author,
I am pleased to inform you that your manuscript has been accepted for publication in the Jundishapur Journal of Microbiology and sent to the publisher for the next process. Please remember to always include your manuscript number, whenever inquiring about your manuscript. When you receive the proofs for your article, please check all names and affiliations very carefully, as these cannot be corrected once the article is published. Moreover, Please add the ORCID number to you and your collages account as soon as possible. For more details
https://sites.kowsarpub.com/jjm/knowledgebase/category/tree.html#orcid.html
Thanks.