OPEN PEER REVIEW

Open Peer Review (OPR)

As a new feature for progressing towards transparency, we decided to open a new window for all of our editors as well as authors titled "**Open Peer Review**". We hope by this new facility, our reviewers will be more motivated and authors will be more satisfied with the review process. We believe that publishing our peer review reports could make a transparent and clear environment for all our efforts within a journal, but not all reviewers tend to publish their comments.

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

- More transparency, constructiveness and tactful comments of the peer review process: leads to an increase in the quality of reviews
- More motivations for all involved roles in the review process
- Authors' satisfactions from the review process: Increases honesty between authors and reviewers
- Education of both authors and new students
- Prevents reviewers from following their individual agendas and leading to the detection of reviewers' conflicts of interests

You can find out more at:
https://brief.land/briefland/knowledgebase/category/tree.html#opr.html

Gene, Cell and Tissue
Article DOI: 10.5812/gct.102700
Published in: Gene, Cell and Tissue: 7(2); e102700

Peer Review Report for "Prevalence of *bla*$_{CTX-M}$, *bla*$_{SHV}$, and *bla*$_{TEM}$ Genes in *Escherichia coli* Strains Isolated From Urinary Tract Infection Samples of Patients in the Intensive Care Unit in Qom, Iran"

Author(s): Shima Sadat Lesani , Mohammad Soleimani , Pegah Shakib, Mohammad Reza Zolfaghari

Review Timeline:

Submit Date: 16 Mar 2020
Revised Date: 22 Apr 2020
Accepted Date: 25 Apr 2020

Revision (0)

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

REFEREE: Reviewer | **Revision** (0) 17 Mar 2020

Dear AE,
This research article seeks to characteristics of blaCTX-M, blaSHV, and blaTEM genes in Escherichia coli strains obtained from the intensive care unit in three different hospitals in Qom. The subject of the article is interesting. Although the topic is of interest for Gene, Cell, and Tissue journal, the manuscript and study have some serious flaws. In this situation, some points could be considered by the authors:
1. The manuscript, however, has extensive grammatical errors that could be fixed by consultation with an editor. As a result of such errors, there are frequent paragraphs where it is not clear what the authors are trying to say.
2. Keywords arranged alphabetically and selected from the mesh.

3. The Objectives of the study are different in the main text and abstract section. Please write something similar, highlighting the purpose of the study in the abstract section.
4. The manuscript could have provided more descriptive information on the isolates (colonization vs infection), outbreaks during the sampling period, infection measure controls...etc.
5. Start the discussion by presenting your main findings.
6. Conclusion: at large non-congruent with the manuscript. In Conclusions: in this section, you should conclude what you have found in the study, not repeat what you have done.
Thanks.

REFEREE: Reviewer | **Revision (0)** 1 Apr 2020

Dear AE,
The authors aimed to determine the prevalence of blaCTX-M, blaSHV, and blaTEM genes in Escherichia coli strains, which were isolated from urinary tract infection patients. The work lacks novelty. Still, it would be reconsidered for publication in GCT Journal after some revision.
1) The text has some typo-errors. For example, “Escerichia coli”. Besides, the manuscript does not have a consistent font.
2) Some sentences need rewording to improve the readability. Avoid repeated use of structures with “One of the.” or “therefore.”
3) Which oxidase test was used as a biochemical measurement? Please clarify.
4) How did the authors confirm the quality and quantity of extracted DNAs? Please explain.
5) The NCBI primer blast (available at https://www.ncbi.nlm.nih.gov/tools/primer-blast) does not find target genes for the designed primers in Table 1. How do the authors explain this matter?
6) The authors did not mention the limitations of their study by comparing their methods and findings with similar works. For this purpose, check these publications;
https://www.ncbi.nlm.nih.gov/pubmed/25149062
https://www.ncbi.nlm.nih.gov/pmc/articles/PMC6613628
Thanks.

Azam Asemi Rad: Reviewer | **Revision (0)** 4 Apr 2020

Dear AE,
Concerning the manuscript entitled “Prevalence of blaCTX-M, blaSHV, and blaTEM genes in Escherichia coli Strains isolated from urinary tract infection in Intensive Care Unit (ICU) Qom, Iran " for Gene, Cell and Tissue Journal.
With respect to the authors, the article is recommended to accept after major revision. Rewriting or adding more findings could improve the study.
However, I have the following specific concerns about this particular study:
1. There is a lot of articles related to this topic, what is the novelty of this manuscript?
2. Authors mentioned that" Biochemical and microbiological standard tests such as gram stain, IMViC, oxidase, catalase and fermentation/oxidation test were used to identify isolates", why results of this part have not presented in results?
3. Discussion section should be revised with more focus on possible hypothesis about findings.

4. English editing is highly recommended
Thanks.

Bita Moudi: Associate Editor | **Revision** (0) 4 Apr 2020

Dear EIC,
The manuscript is studied, and there are some comments which should be addressed by the author. According to the comments, the document needs major revision.
Kind regards,

Zahra Heidari: EIC | **Revision** (0) 5 Apr 2020

Dear Authors,
Based on the reviewers' and AE comments and as I read, this manuscript needs major revision and a point by point reply to the comments.
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.

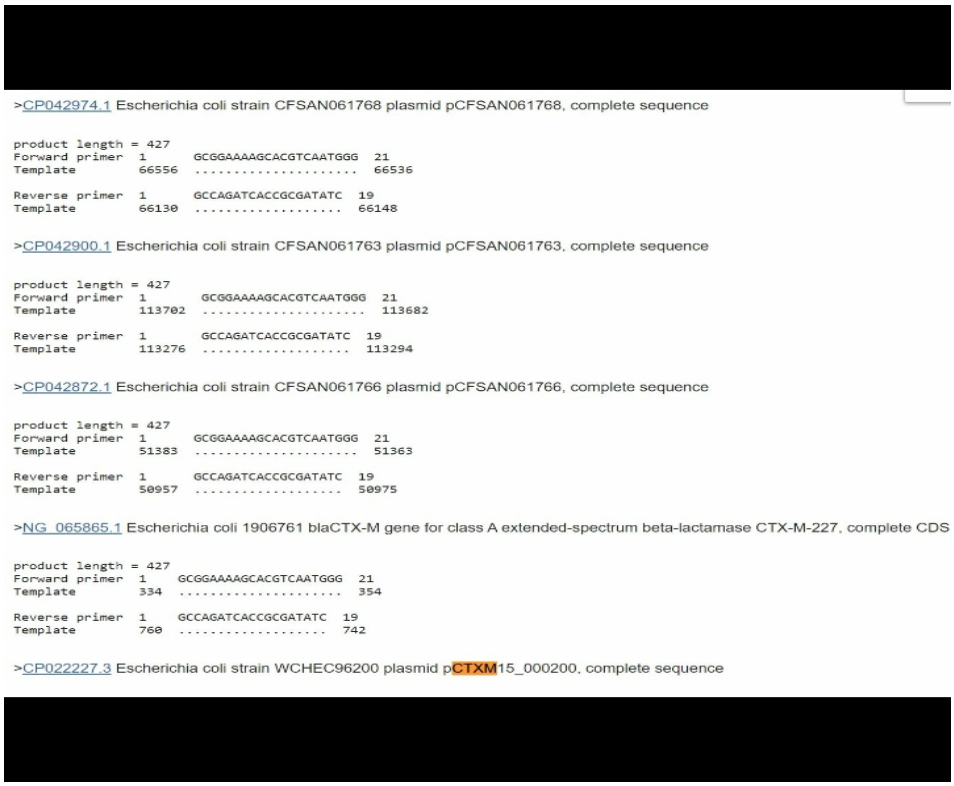
Dear reviewer

I would like to thank you for your kind attention to the study. We have tried to edit the manuscript according to your comments and we hope that we will be able to satisfy you.
Reforms include:
1.Our manuscript was edited grammatical errors

.Key words arranged alphabetically and selected from the mesh .2
.The abstract section written again .3
.Start the discussion by presenting your main findings .5
Conclusion was edited .6
.Novelty and limitation of this manuscript *written in* discussion *section* .7
The result of Biochemical and microbiological standard tests such as gram stain, IMViC, .8 oxidase, catalase and fermentation/oxidation test were used to identify isolates written in .method section
.The quality and quantity of extracted DNAs explained .9
I re-examined the primers and found that they were correct. The file I sent you probably had a .10 .problem. Below is a table of primers. Please check the following primers

Best Regards

Genes	Primer sequences (5′ to 3′)	Temperature	Length (bp)	References
bla SHV	Forward: GCTTTCCCATGATGAGCACC- Reverse: AGGCGGGTGACGTTGTCGC-	60 61	292	Primers were designed by the authors
bla TEM	Forward: GGTGAAAGTAAAAGATGCTGAAG- Reverse: AACTTTATCCGCCTCCATC-	59 60	559	
bla CTX-M	Forward: GCGGAAAAGCACGTCAAT GGG- Reverse: GCCAGATCACCGCGATATC-	62 61	427	



>CP042974.1 Escherichia coli strain CFSAN061768 plasmid pCFSAN061768, complete sequence

```
product length = 427
Forward primer  1      GCGGAAAAGCACGTCAATGGG  21
Template        66556  .....................  66536

Reverse primer  1      GCCAGATCACCGCGATATC  19
Template        66130  ...................  66148
```

>CP042900.1 Escherichia coli strain CFSAN061763 plasmid pCFSAN061763, complete sequence

```
product length = 427
Forward primer  1       GCGGAAAAGCACGTCAATGGG  21
Template        113702  .....................  113682

Reverse primer  1       GCCAGATCACCGCGATATC  19
Template        113276  ...................  113294
```

>CP042872.1 Escherichia coli strain CFSAN061766 plasmid pCFSAN061766, complete sequence

```
product length = 427
Forward primer  1      GCGGAAAAGCACGTCAATGGG  21
Template        51383  .....................  51363

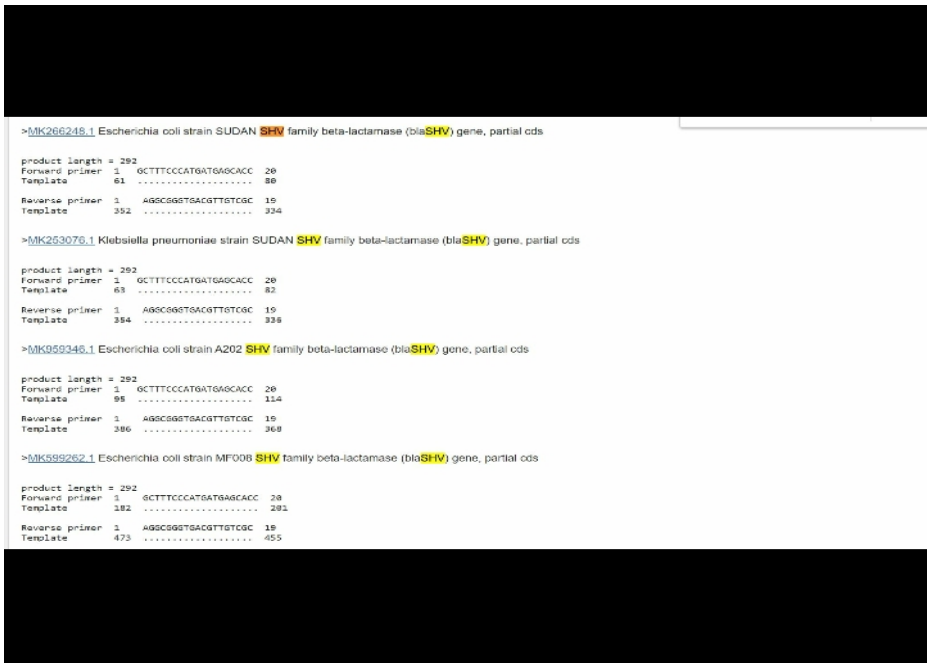
Reverse primer  1      GCCAGATCACCGCGATATC  19
Template        50957  ...................  50975
```

>NG_065865.1 Escherichia coli 1906761 blaCTX-M gene for class A extended-spectrum beta-lactamase CTX-M-227, complete CDS

```
product length = 427
Forward primer  1    GCGGAAAAGCACGTCAATGGG  21
Template        334  .....................  354

Reverse primer  1    GCCAGATCACCGCGATATC  19
Template        760  ...................  742
```

>CP022227.3 Escherichia coli strain WCHEC96200 plasmid pCTXM15_000200, complete sequence



>MK266248.1 Escherichia coli strain SUDAN SHV family beta-lactamase (blaSHV) gene, partial cds

```
product length = 292
Forward primer  1    GCTTTCCCATGATGAGCACC  20
Template        61   ....................  80

Reverse primer  1    AGGCGGGTGACGTTGTCGC  19
Template        352  ...................  334
```

>MK263076.1 Klebsiella pneumoniae strain SUDAN SHV family beta-lactamase (blaSHV) gene, partial cds

```
product length = 292
Forward primer  1    GCTTTCCCATGATGAGCACC  20
Template        63   ....................  82

Reverse primer  1    AGGCGGGTGACGTTGTCGC  19
Template        354  ...................  336
```

>MK959346.1 Escherichia coli strain A202 SHV family beta-lactamase (blaSHV) gene, partial cds

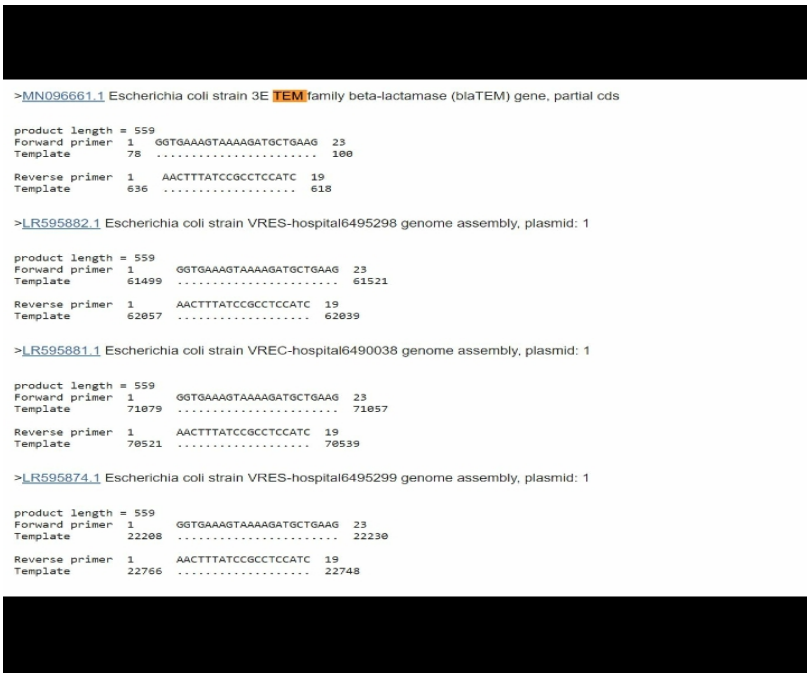
```
product length = 292
Forward primer  1    GCTTTCCCATGATGAGCACC  20
Template        95   ....................  114

Reverse primer  1    AGGCGGGTGACGTTGTCGC  19
Template        386  ...................  368
```

>MK599262.1 Escherichia coli strain MF008 SHV family beta-lactamase (blaSHV) gene, partial cds

```
product length = 292
Forward primer  1    GCTTTCCCATGATGAGCACC  20
Template        182  ....................  201

Reverse primer  1    AGGCGGGTGACGTTGTCGC  19
Template        473  ...................  455
```



>MN096661.1 Escherichia coli strain 3E TEM family beta-lactamase (blaTEM) gene, partial cds

```
product length = 559
Forward primer  1   GGTGAAAGTAAAAGATGCTGAAG  23
Template        78  ......................  100

Reverse primer  1    AACTTTATCCGCCTCCATC  19
Template        636  ...................  618
```

>LR595882.1 Escherichia coli strain VRES-hospital6495298 genome assembly, plasmid: 1

```
product length = 559
Forward primer  1      GGTGAAAGTAAAAGATGCTGAAG  23
Template        61499  ......................  61521

Reverse primer  1      AACTTTATCCGCCTCCATC  19
Template        62057  ...................  62039
```

>LR595881.1 Escherichia coli strain VREC-hospital6490038 genome assembly, plasmid: 1

```
product length = 559
Forward primer  1      GGTGAAAGTAAAAGATGCTGAAG  23
Template        71079  ......................  71057

Reverse primer  1      AACTTTATCCGCCTCCATC  19
Template        70521  ...................  70539
```

>LR595874.1 Escherichia coli strain VRES-hospital6495299 genome assembly, plasmid: 1

```
product length = 559
Forward primer  1      GGTGAAAGTAAAAGATGCTGAAG  23
Template        22208  ......................  22230

Reverse primer  1      AACTTTATCCGCCTCCATC  19
Template        22766  ...................  22748
```

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: Reviewer | **Revision** (1) — 23 Apr 2020

Dear AE,
Revisions were done as demanded. The article is now acceptable for publication.
Thanks.

Abbas Farahani: Reviewer | **Revision** (1) — 24 Apr 2020

Dear AE,
The study is reviewed carefully. According to comments and revisions by the author, this manuscript is accepted.
Thanks

Azam Asemi Rad: Reviewer | **Revision** (1) — 24 Apr 2020

Dear AE,
Thanks for giving the opportunity of peer review to me. I have read the manuscript entitled “Prevalence of blaCTX-M, blaSHV, and blaTEM genes in Escherichia coli Strains isolated from urinary tract infection in Intensive Care Unit (ICU) Qom, Iran”.
Considering that this manuscript had a peer review in the previous version, I read the manuscript and reviewed the sections modified by the author in response to the reviewers. I must point out that this version is suitable for accepting.
Sincerely,

Zahra Heidari: Associate Editor | **Revision** (1) — 25 Apr 2020

Dear EIC,
Based on the reviewers' comments and as I read revisions were done well thus this manuscript can be accepted for publication in GCT.
Thanks.

Zahra Heidari: EIC | **Revision** (1) — 25 Apr 2020

Dear Author,
The document is reviewed carefully by the reviewers. According to their comments and your revisions as requested, this manuscript is accepted.

Thanks.