Data Article

Draft genome sequence data of a tigecycline-resistant *Enterobacter cloacae* ST93 clinical strain isolated from bloodstream infection

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**A B S T R A C T**

Here we report data on the draft genome sequence of a tigecycline-resistant *Enterobacter cloacae* ST93 clinical isolate TREC1 producing KPC-2 carbapenemase from China. The draft genome sequence of *E. cloacae* TREC1 consisted of 74 contigs that comprised 5,322,835 bp, and the overall GC content of this strain amounted to 54.63%. In total, 57 tRNA genes, 5 rRNA operons and 5108 protein-coding sequences were identified in the genome. TREC1 belongs to sequence type ST93. Nineteen antimicrobial resistance genes were confirmed. Antimicrobial susceptibility testing revealed that besides colistin this isolate is resistant to all antibiotics including tigecycline. This Whole Genome Shotgun project has been deposited at DDBJ/EMBL/GenBank under the accession number PJZE00000000. (http://www.ncbi.nlm.nih.gov/nuccore/PJZE00000000).

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Specifications table

| Subject area          | Biology                                      |
|----------------------|----------------------------------------------|
| More specific subject area | Genomics, tigecycline-resistant *Enterobacter cloacae* |
| Type of data         | Figure, table                                |
| How data was acquired | The data was acquired on HiSeq™ 4000 (Illumina) sequencing platform |
| Data format          | Analysed                                     |
| Experimental factors | Genomic DNA from pure culture               |
| Experimental features| Isolation of bacteria, genome sequencing, draft genome assembly and annotation |
| Data source location | Hangzhou, China                              |
| Data accessibility   | Data is with this article, also this Whole Genome Shotgun project has been deposited at DDBJ/EMBL/GenBank under the accession number PJZE00000000. (http://www.ncbi.nlm.nih.gov/nuccore/PJZE00000000) |

Value of the data

- This data may help us to understand the genomic feature and molecular characteristic of this bacterial pathogen.
- This data may help us to understand the resistance gene diversity of this bacterial pathogen.
- The genome sequence of *Enterobacter cloacae* TREC1 can be used as a reference sequence for comparative analysis of tigecycline-resistant *E. cloacae* aimed to reveal the mechanism of tigecycline-resistance in CRE.

1. Data

The draft genome sequence of *Enterobacter cloacae* TREC1 consisted of 74 contigs that comprised 5,322,835 bp, and the overall GC content of this strain amounted to 54.63%. In total, 57 tRNA genes, 5 rRNA operons and 5108 protein-coding sequences were identified by the RAST server, respectively. According to the MLST scheme of *E. cloacae*, TREC1 belongs to sequence type ST93. The genome also contains one intact and one incomplete prophage sequences, three CRISPR sequences and several IS elements: the majority belonging to the IS3 and IS5 families. The resistance genes present in the genome of the isolate are presented in Table 1. We identified the aminoglycoside resistance genes *armA*, *aadA5*, *strA* and *aph(6)-Id*; the beta-lactam resistance genes *bla*<sub>CTX-M-14</sub>, *bla*<sub>ACT-7</sub>, *bla*<sub>KPC-2</sub> and *bla*<sub>CTX-M-3</sub>; the fluoroquinolone resistance genes *qnrS1* and *qnrA1*; the fosfomycin resistance gene *fosA*; the macrolide, Lincosamide and Streptogramin B resistance genes *msr(E)* and *mph(E)*; the phenicol resistance gene *catA2*; the sulphonamide resistance genes *sul1* and *sul2*; the trimethoprim resistance genes *dfrA1* and *dfrA14*; and the tetracycline resistance gene *tetA*. Ceftazidime, cefepime, imipenem, meropenem, piperacillin/tazobactam, cefoperazone/sulbactam, fosfomycin, amikacin, ciprofloxacin, trimethoprim/sulfamethoxazole, minocycline, tigecycline and colistin were used in the susceptibility testing. The isolate was resistant to all antimicrobials above except colistin. The MIC values are presented in Table 2. Isolate *E. cloacae* TREC1 not only produce KPC-2 carbapenemase, but are also resistant to tigecycline bringing a great challenge to clinical treatment. The relative expression level of efflux pump genes (*acrA*, *acrB*, *oppXa* and *oppXB*) in the tigecycline-resistant isolate TREC1 were examined by qRT-PCR. Relative expression of each target gene was calibrated against the corresponding expression of a tigecycline-susceptible isolate *E. cloacae* TSEC (expression = 1), which was served as the control. According to the results (Table 3), the expression level of efflux pump AcrAB was increased 2–3 fold relative to the susceptible isolate. The expression level of efflux pump OqxAB...
### Table 1
Antimicrobial resistance genes in isolate E. cloacae TREC1.

| Resistance gene          | %Identity | HSP length/query | Contig  | Position in contig | Predicted phenotype                          | Accession number |
|--------------------------|-----------|-----------------|---------|--------------------|----------------------------------------------|------------------|
| **Aminoglycoside**       |           |                 |         |                    |                                              |                  |
| armA                     | 99.87     | 774/774         | contig_57 | 1189.1962          | Aminoglycoside resistance                     | AY220558         |
| aadA5                    | 100       | 789/789         | contig_58 | 150.938            | Aminoglycoside resistance                     | AF137361         |
| strA                     | 100       | 804/804         | contig_59 | 54016204           | Aminoglycoside resistance                     | M96392           |
| aph(6)-Id                | 100       | 837/837         | contig_59 | 6204.7040          | Aminoglycoside resistance                     | M28829           |
| **Beta-lactam**          |           |                 |         |                    |                                              |                  |
| blาCTX-M-14              | 100       | 876/876         | contig_85 | 1618.2493          | Beta-lactam resistance                        | AF252622         |
| blаACT-7                 | 99.56     | 1146/1146       | contig_8 | 19,282.20427       | Beta-lactam resistance                        | FJ237368         |
| blаKPC-2                 | 100       | 882/882         | contig_54 | 3990.4871          | Beta-lactam resistance                        | AYO34847         |
| blαCTX-M-3               | 100       | 876/876         | contig_73 | 413.1288           | Beta-lactam resistance                        | EF437434         |
| **Fluoroquinolone**      |           |                 |         |                    |                                              |                  |
| qnrS1                    | 100       | 657/657         | contig_7 | 23,019.23675       | Quinolone resistance                          | AB187515         |
| qnrA1                    | 99.85     | 657/657         | contig_70 | 54.710             | Quinolone resistance                          | AYO70235         |
| **Fosfomycin**           |           |                 |         |                    |                                              |                  |
| fosA                     | 98.12     | 426/426         | contig_27 | 322,842.323267     | Fosfomycin resistance                         | AEXB01000013     |
| **MLS - Macrolide, Lincosamide and Streptogramin B** | | | | | | |
| msr(E)                   | 100       | 1476/1476       | contig_57 | 4261.5735          | Macrolide, Lincosamide and Streptogramin B resistance | EU294228         |
| mph(E)                   | 100       | 885/885         | contig_57 | 5792.6676          | Macrolide resistance                          | EU294228         |
| **Phenicol**             |           |                 |         |                    |                                              |                  |
| catA2                    | 96.11     | 642/642         | contig_97 | 749.1390           | Phenicol resistance                           | X53796           |
| **Sulphonamide**         |           |                 |         |                    |                                              |                  |
| sul1                     | 100       | 840/840         | contig_71 | 2179.3018          | Sulphonamide resistance                       | AY2241685        |
| sul2                     | 100       | 816/816         | contig_36 | 3828.4643          | Sulphonamide resistance                       | GQ421466         |
| **Tetracycline**         |           |                 |         |                    |                                              |                  |
| tetA                     | 100       | 1200/1200       | contig_83 | 1471.2670          | Tetracycline resistance                       | AJ517790         |
| **Trimethoprim**         |           |                 |         |                    |                                              |                  |
| dfrA1                    | 100       | 474/474         | contig_58 | 1455.1928          | Trimethoprim resistance                       | JQ690541         |
| dfrA14                   | 99.59     | 483/483         | contig_7 | 30.512             | Trimethoprim resistance                       | DQ388123         |
between TREC1 and TSEC was not significant. Tetracycline resistant gene tetA was found in TREC1, but no mutation was detected.

2. Experimental design, materials and methods

Isolate *E. cloacae* TREC1 was recovered from a blood sample of a male hospitalised patient in Hangzhou, Zhejiang province, China, in 2017. The isolate was preliminarily identified using the VITEK 2 system (bioMérieux, France) and was further confirmed by 16S rRNA gene sequencing. Antimicrobial susceptibility testing was performed according to the guidelines of the Clinical and Laboratory Standards Institute (CLSI). The MICs of tigecycline and colistin were determined using standard broth microdilution tests with fresh (<12 h) Mueller-Hinton broth (Cation-adjusted, Oxoid LTD, Basingstoke, Hampshire, England). The MICs of other antimicrobial agents were determined using the agar dilution method and Etest method. Whole genome sequencing has increasingly being applied to clinical practice server [1]. The genome of *E. cloacae* TREC1 was sequenced using the Illumina HiSeq™ 4000 platform (Illumina Inc., San Diego, CA, USA) following the paired-end 2 × 150 bp protocol. The whole genome sequence was assembled using CLC Genomics Workbench 10.0 software (Qiagen, Valencia, CA) and annotated by the Rapid Annotation System Technology (RAST) server [2]. The pie chart demonstrated the counts for each subsystem feature and the subsystem coverage (Fig. 1). In silico Multilocus sequence typing (MLST) analysis was performed using the PubMLST database. Resistance-related genes were analysed using ResFinder 3.0 [3]. Further bioinformatics analysis, such as identification of insertion elements (IS), prophage sequences and clustered

Table 2

| Antibiotics                                 | MIC (mg/L) |
|---------------------------------------------|------------|
| ceftazidime                                 | 256        |
| cefepime                                    | > 256      |
| imipenem                                    | 256        |
| meropenem                                   | 128        |
| piperacillin/tazobactam                     | > 256      |
| ceferazone/sulbactam                       | > 256      |
| fosfomycin                                  | > 256      |
| amikacin                                    | > 256      |
| ciprofloxacin                               | > 32       |
| trimethoprim/sulfamethoxazole               | > 32       |
| minocycline                                 | 16         |
| tigecycline                                 | 8          |
| colistin                                    | 0.25       |

* a Tested by agar dilution method.

* b Tested by Etest method.

* c Tested by standard broth microdilution tests.

Table 3

Expression level of *acrA*, *acrB*, *oqxA* and *oqxB* in TREC1 compared with a tigecycline-susceptible isolate *E. cloacae* TSEC.

| Isolate | Relative expression a | MIC (mg/L)b |
|---------|------------------------|-------------|
|         | *acrA* | *acrB* | *oqxA* | *oqxB* |
| TSEC    | 1      | 1      | 1      | 0.25   |
| TREC1   | 2.86 ± 0.25 | 3.07 ± 0.29 | 1.24 ± 0.18 | 1.06 ± 0.21 | 8    |

* a Relative expression compared with tigecycline-susceptible isolate TSEC (expression = 1). Results are means of 3 runs ± standard deviation.

* b MIC of tigecycline.
regularly interspaced short palindromic repeat (CRISPR) sequences were predicted by application of ISfinder, PHASTER and CRISPRFinder, respectively [4–6].

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Transparency document. Supporting information

Transparency data associated with this article can be found in the online version at https://doi.org/10.1016/j.dib.2018.10.004.

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