

Genome Sequence of Multidrug-Resistant Escherichia coli EC302/04, Isolated from a Human Tracheal Aspirate

Wing-Sze Ho, Han-Ming Gan, Kien-Pong Yap, Ganeswrie
Balan, Chew Chieng Yeo and Kwai-Lin Thong
J. Bacteriol. 2012, 194(23):6691. DOI: 10.1128/JB.01804-12.

Updated information and services can be found at:
<http://jb.asm.org/content/194/23/6691>

	<i>These include:</i>
REFERENCES	This article cites 15 articles, 8 of which can be accessed free at: http://jb.asm.org/content/194/23/6691#ref-list-1
CONTENT ALERTS	Receive: RSS Feeds, eTOCs, free email alerts (when new articles cite this article), more»

Information about commercial reprint orders: <http://journals.asm.org/site/misc/reprints.xhtml>
To subscribe to to another ASM Journal go to: <http://journals.asm.org/site/subscriptions/>

Genome Sequence of Multidrug-Resistant *Escherichia coli* EC302/04, Isolated from a Human Tracheal Aspirate

Wing-Sze Ho,^{a,b} Han-Ming Gan,^c Kien-Pong Yap,^{a,b} Ganeswrie Balan,^d Chew Chieng Yeo,^e and Kwai-Lin Thong^{a,b}

Institute of Biological Sciences, Faculty of Science, University of Malaya, Kuala Lumpur, Malaysia^a; Laboratory of Biomedical Science and Molecular Microbiology, UMBIO Research Cluster, University of Malaya, Kuala Lumpur, Malaysia^b; ScienceVision SB, Setia Alam, Seksyen U13, Shah Alam, Selangor, Malaysia^c; Sultanah Aminah Hospital, Johor Bharu, Malaysia^d; and Faculty of Agriculture and Biotechnology, Universiti Sultan Zainal Abidin, Kampus Gong Badak, Kuala Terengganu, Malaysia^e

***Escherichia coli* is an important etiologic agent of lower respiratory tract infections (LRTI). Multidrug-resistant *E. coli* EC302/04 was isolated from a tracheal aspirate, and its genome sequence is expected to provide insights into antimicrobial resistance as well as adaptive and virulence mechanisms of *E. coli* involved in LRTI.**

Lower respiratory tract infections (LRTI) caused by multidrug-resistant bacteria are a common problem worldwide (2, 6), and significant morbidity and mortality associated with LRTI have been reported (5). *Escherichia coli* is one of the common etiologic agents of LRTI among the Gram-negative bacteria (2, 6); it may exist initially as a colonizer but can progress to cause severe infections such as ventilator-associated pneumonia (VAP) in the respiratory tract (6). Patients admitted to intensive care units (ICU) are often at a higher risk of contracting severe LRTI than those in the general wards (15).

E. coli EC302/04 is a multidrug-resistant bacterium isolated from the tracheal aspirate of an ICU patient in 2004 and has been characterized previously (10, 13). Strain EC302/04 was nonsusceptible to ampicillin (10 μg), gentamicin (10 μg), streptomycin (10 μg), kanamycin (30 μg), chloramphenicol (30 μg), amoxicillin-clavulanic acid (30 μg), and cefoperazone (30 μg). Although the genetic makeup of *E. coli* is widely studied, there is limited genomic information for LRTI-associated *E. coli*. Therefore, the genome data harnessed from strain EC302/04 would enhance the understanding of its antimicrobial resistance and adaptive and virulence mechanisms.

The genome sequencing of strain EC302/04 was performed using the Illumina HiSeq 2000 (100-bp read length) with an insert size of 300 bp. The reads were trimmed and assembled *de novo* using CLC Genomics workbench 5.0 (CLC Bio, Denmark). A total of 82 contigs were generated, with an accumulated length of 4,846,195 bp (312-fold coverage) and an average GC content of 51%. The contig *N*₅₀ is 201,460 bp, and the longest assembled contig is 350,759 bp. The genome annotation was performed by the RAST annotation server (3), which led to the identification of 4,738 open reading frames with an average length of 904 bp and a coding percentage of 88.4. Using RNAmmer (12) and tRNAscan-SE (14), 4 rRNAs and 70 tRNAs were found.

Based on *in silico* analysis, the multilocus sequence type and serotype of strain EC302/04 were ST349 and O166:H15, respectively. The genome sequence revealed two multiple antibiotic resistance (*mar*) regulons, *marRAB* and *marC* (1), which have been reported to be involved in resistance to various antibiotics such as chloramphenicol, cephalosporins, and tetracycline (7, 9). Genes encoding other enzymes involved in antimicrobial resistance which were identified in EC302/04 include β-lactamases (*bla*_{TEM-1}, *bla*_{AmpC}) and streptomycin 3'-*O*-adenylyltransferase. It has been demonstrated that biofilm formation on the endotra-

cheal tube facilitates the bacterial entry into the lower respiratory tract, contributing to colonization and LRTI in intubated patients (2, 6, 8). The genome of EC302/04 also possesses genes encoding several biofilm formation-associated proteins such as LuxS, responsible for the production of autoinducer 2 (AI-2) (4), and the YjgK cluster (11). Type 1 pilus FimH adhesin, which has been reported to be critical in *E. coli* biofilm formation and has the ability to bind nonspecifically to abiotic surfaces (4), was also identified in EC302/04.

To the best of our knowledge, this is the first genome sequence of an *E. coli* isolate from human tracheal aspirate, and the availability of this genome data will aid in the understanding of the pathogenesis of the organism.

Nucleotide sequence accession numbers. This whole-genome shotgun project has been deposited at DDBJ/EMBL/GenBank under the accession number AMFM00000000. The version described in this paper is the first version, AMFM01000000. The BioProject designation for this project is PRJNA174602.

ACKNOWLEDGMENTS

This research is supported by the University of Malaya High Impact Research Grant-Molecular Genetics (reference UM.C/625/1HIR/MOHE/-02 [A000002-5000]).

We acknowledge Safwan Jusoh from the ICT department, University of Malaya, for his assistance and for allowing us to use their servers and computational facilities.

REFERENCES

- Alekshun MN, Levy SB. 1999. The *mar* regulon: multiple resistance to antibiotics and other toxic chemicals. *Trends Microbiol.* 7:410–413.
- American Thoracic Society and Infectious Diseases Society of America (ATS/IDSA). 2005. Guidelines for the management of adults with hospital-acquired, ventilator-associated, and healthcare-associated pneumonia. *Am. J. Respir. Crit. Care. Med.* 171:388–416.
- Aziz RK, et al. 2008. The RAST server: rapid annotations using subsystems technology. *BMC Genomics* 9:75.
- Beloin C, Roux A, Ghigo JM. 2008. *Escherichia coli* biofilms. *Curr. Top. Microbiol. Immunol.* 322:249–289.

Received 22 September 2012 Accepted 1 October 2012

Address correspondence to Kwai-Lin Thong, thongkl@um.edu.my.

Copyright © 2012, American Society for Microbiology. All Rights Reserved.

doi:10.1128/JB.01804-12

5. Carroll KC. 2002. Laboratory diagnosis of lower respiratory tract infections: controversy and conundrums. *J. Clin. Microbiol.* **40**:3115–3120.
6. Chastre J, Fagon JY. 2002. Ventilator-associated pneumonia. *Am. J. Respir. Crit. Care Med.* **165**:867–903.
7. Cohen SP, McMurry LM, Hooper DC, Wolfson JS, Levy SB. 1989. Cross-resistance to fluoroquinolones in multiple-antibiotic-resistant (Mar) *Escherichia coli* selected by tetracycline or chloramphenicol: decreased drug accumulation associated with membrane changes in addition to OmpF reduction. *Antimicrob. Agents Chemother.* **33**:1318–1325.
8. Craven DE, Hjalmarson KI. 2010. Ventilator-associated tracheobronchitis and pneumonia: thinking outside the box. *Clin. Infect. Dis.* **51**(S1): S59–S66.
9. George AM, Levy SB. 1983. Amplifiable resistance to tetracycline, chloramphenicol, and other antibiotics in *Escherichia coli*: involvement of a non-plasmid-determined efflux of tetracycline. *J. Bacteriol.* **155**:531–540.
10. Ho WS, et al. 2012. Prevalence and characterization of multidrug-resistant and extended-spectrum beta-lactamase-producing *Escherichia coli* from pediatric wards of a Malaysian hospital. *Microb. Drug Resist.* **18**:408–416.
11. Kim YH, Wang XX, Ma Q, Zhang XS, Wood TK. 2009. Toxin-antitoxin systems in *Escherichia coli* influence biofilm formation through YjgK (TabA) and fimbriae. *J. Bacteriol.* **191**:1258–1267.
12. Lagesen K, et al. 2007. RNAMmer: consistent annotation of rRNA genes in genomic sequences. *Nucleic Acids Res.* **35**:3100–3108.
13. Lim KT, Yasin R, Yeo CC, Putucheary SD, Thong KL. 2009. Characterization of multidrug resistant ESBL-producing *Escherichia coli* isolates from hospitals in Malaysia. *J. Biomed. Biotechnol.* **2009**:165637. doi: 10.1155/2009/165637.
14. Lowe TM, Eddy SR. 1997. tRNAscan-SE: a program for improved detection of transfer RNA genes in genomic sequence. *Nucleic Acids Res.* **25**: 955–964.
15. Tripathi S, Malik GK, Jain A, Kohli N. 2010. Study of ventilator associated pneumonia in neonatal intensive care unit: characteristics, risk factors and outcome. *Internet J. Med. Update* **5**:12–19.