Detection of plasmid-mediated tigecycline-resistant gene $tet(X4)$ in *Escherichia coli* from pork, Sichuan and Shandong Provinces, China, February 2019

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The plasmid-mediated high-level tigecycline resistance gene, $tet(X4)$, was detected in seven *Escherichia coli* isolates from pork in two Chinese provinces. Two isolates belonged to the epidemic spreading sequence type ST101. $Tet(X4)$ was adjacent to IS*Vsa3* and concurrent with *floR* in all seven isolates. In addition to IncFIB, the replicon IncFII was found to be linked to $tet(X4)$. This report follows a recent detection of $tet(X3)/(X4)$ in *E. coli* from animals and humans in China.

It has been speculated that one in five resistant human infections are caused by antibiotic resistant bacteria originating from food and animals [1]. China is the world’s biggest producer and consumer of pork and has trade links with many countries [2]. In May 2019, He et al. reported the finding of two transferable plasmid-mediated tigecycline resistance genes, $tet(X3)$ and $tet(X4)$ [3]. These genes were detected in numerous Enterobacteriaceae and *Acinetobacter* from animals and meat for consumption (chicken and pork) in three representative provinces of China located in different geographical areas, as well as from patients originating from 20 hospitals in 20 different cities of the country [3]. Both genes conferred clinically-significant levels of tigecycline resistance (minimum inhibitory concentration, MIC ≥ 32 mg/L) [3]. The newly emerging, rapid and widespread dissemination of $tet(X3)$ and $tet(X4)$ illustrated a flux mediated by horizontal gene transfer representing a paradigm shift in tigecycline resistance, which until now had only been found to be spread by vertical transmission mechanisms [3]. This currently poses a further threat to public health, as the emergence of these transferable tigecycline resistance genes in food-producing animals could potentially lead to an increased risk of infection by strains harbouring these genes and treatment failure in humans [3].

*Escherichia coli* harbouring transferable $tet(X4)$ obtained in this study

In this study, we sought bacteria harbouring the newly reported tigecycline resistance genes in two provinces in China using the method reported by He’s study [3]. Seven $tet(X4)$ positive isolates (20.6%, 95% confidence interval (CI): 8.7–37.9), were recovered from 34 retail pork samples taken in Sichuan (8.7%, 2/23, 95%CI: 1.1–28.0) and Shandong (45.5%, 5/11, 95%CI: 16.7–76.6) Provinces in February, 2019. The $tet(X4)$ sequences in all seven isolates were identical to that reported by He et al. [3]. No $tet(X3)$ was detected. All isolates were identified as *Escherichia coli* by VITEK 2 and 16S rDNA-based sequencing. The MICs against tigecycline ranged from 16 to 32 mg/L, with all isolates expressing resistance to the majority of antimicrobial agents tested for in this study except meropenem (Table). All isolates were multidrug-resistant (MDR), in that they were resistant to three or more different classes of antimicrobials and two were confirmed as extended spectrum beta-lactamase (ESBL)-producing (denoted as 2019XSD9 and 2019XSD11). S1-pulsed-field gel electrophoresis (PFGE) profiling showed that...
Table

Characteristics of tet(X4) positive *Escherichia coli* isolated from pork samples and their serotypes, sequence types, antimicrobial resistance profiles and resistance determinants along with their minimum inhibitory concentrations to tigecycline, Sichuan and Shandong Provinces, China, February 2019

<table>
<thead>
<tr>
<th>Isolates</th>
<th>Serotypes</th>
<th>Sequence types</th>
<th>Antimicrobial resistance profiles</th>
<th>Tigecycline MIC (mg/L)</th>
<th>Additional resistance determinants identified by WGS</th>
</tr>
</thead>
<tbody>
<tr>
<td>2019XSD6</td>
<td>O82:H8</td>
<td>ST101</td>
<td>AMP-CHL-SXT-TET-TGC</td>
<td>32</td>
<td>qnrS1, aadA2, blaTEM12, dfrA14, floR, inu(F), tet(X4)</td>
</tr>
<tr>
<td>2019XSD8</td>
<td>O5:H32</td>
<td>ST761</td>
<td>AMP-CHL-SXT-TET-TGC</td>
<td>16</td>
<td>qnrS1, blaTEM12, dfrA5, floR, mef(B), sul3, tet(A), tet(M), tet(X4)</td>
</tr>
<tr>
<td>2019XSD9</td>
<td>O109:H40</td>
<td>ST101</td>
<td>AMP-CAZ-CHL-CTX-SXT-TET-TGC</td>
<td>16</td>
<td>aadA2, blaTEM12, floR, inu(F), strA, strB, sul2, blaTEM12, tet(X4)</td>
</tr>
<tr>
<td>2019XSD10</td>
<td>O126:H2</td>
<td>ST30</td>
<td>AMP-CHL-GEN-SXT-TET-TGC</td>
<td>16</td>
<td>qnrS1, aac(3)-IId, aadA2, aadA22, blaTEM12, dfrA12, erm(42), floR, mef(B), mph(A), sul3, tet(A), tet(M), tet(X4)</td>
</tr>
<tr>
<td>2019XSD11</td>
<td>ONT:H25</td>
<td>ST847_similar</td>
<td>AMP-CAZ-CHL-CTX-TET-TGC</td>
<td>16</td>
<td>qnrS1, aadA22, blaTEM12, dfrA12, floR, fosA, strA, strB, sul2, tet(A), tet(X4)</td>
</tr>
<tr>
<td>2019XSC8</td>
<td>O5:H11</td>
<td>ST48</td>
<td>AMP-CHL-CHL-CTX-SXT-TET-TGC</td>
<td>16</td>
<td>qnrS2, aph(3’)-Ia, blaTEM12, floR, sul2, sul3, tet(A), tet(M), tet(X4)</td>
</tr>
<tr>
<td>2019XSC9</td>
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<td>AMP-CHL-CHL-CTX-SXT-TET-TGC</td>
<td>16</td>
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</tr>
</tbody>
</table>

AMP: ampicillin; CAZ: ceftazidime; CHL: chloramphenicol; CIP: ciprofloxacin; CTX: cefotaxime; GEN: gentamicin; MIC: minimum inhibitory concentration; SXT: trimethoprim/sulfamethoxazole; TET: tetracycline; TGC: tigecycline; WGS: whole genome sequencing.

Figure 1

A heat-map showing the comparison of the *Escherichia coli* donors and the resultant transconjugants, characterised on the basis of their origins, plasmid profiles; ESBL-types; replicon types; susceptibility profiles and MIC of tigecycline, China, February 2019

AMP: ampicillin; CAZ: ceftazidime; CHL: chloramphenicol; CIP: ciprofloxacin; CTX: cefotaxime; ESBL: extended spectrum beta-lactamase; GEN: gentamicin; IMP: imipenem; MIC: minimum inhibitory concentration; SXT: trimethoprim/sulfamethoxazole; TET: tetracycline; TGC: tigecycline.

The MIC for tigecycline in each group combination is also shown. In the first column, the letters ‘TC’ typify the transconjugants. Black and white squares denote the presence and absence, respectively of a particular feature.

* The size of the plasmids was determined according to the S1-pulsed-field gel electrophoresis results.

* The plasmid profile of 2019XSD11-TC2 is due to a fusion in the transconjugant of two plasmids originating from the donor strain (data not shown).
cases and a >64-fold increase was recorded, compared to the plasmid-less recipient (E. coli J53, 0.125 mg/L).

Plasmids harbouring tet(X4) have been reported to be related to IncFIB replicon types in E. coli. In this study, identification of types IncFI1, IncFIA, IncHIA and IncHIB now appear to expand this repertoire of tet(X4)-associated plasmids (Figure 1).

**Discussion**

In this study, we detected tigecycline resistant E. coli (20.6%), positive for tet(X4), from pork in two provinces in China 2019. Most tet(X3) or tet(X4)-positive strains reported by He et al. also originated from pigs, and among bacteria positive for such genes, E. coli was the predominant species [3]. Taken together, the results suggest that E. coli strains positive for tet(X3) and tet(X4) might exhibit a broad geographical distribution having already spread in some areas of China. Interestingly, tet(X4) was located on various conjugative plasmids of diverse replicon types. These observations suggested that tet(X4) could be captured by a range of mobile genetic elements circulating among bacterial strains (Figure 1), a scenario reminiscent of mcr-1 [6].

In silico MLST analysis enabled us to identify two isolates belonging to ST101. This ST was reported earlier to be common among ESBL-producing E. coli recovered from meat products imported into the European Union (EU) from non-EU countries [7], a finding potentially suggesting that the international trade of food products, which is expanding, could present a route for dissemination of antibiotic-resistant food-borne pathogens. ST101 has been reported previously in 15 countries, and is also frequently associated with NDM-1 [8,9]. In this context, and given the finding of tet(X4)-positive E. coli in the current study, it is interesting to speculate that ST101 might represent a convenient and efficient way of spread for the tet(X4)-mediated resistance mechanism, thereby posing a serious challenge to public health.

The other two tet(X4)-positive isolates reported here (2019XSC8 and 2019XSC9) belonged to ST48. These
were cultured from two samples obtained at the same retail outlet on the same day in Sichuan province and had 20 hqSNPs difference. Given this difference, it is unlikely that the isolates originated from cross-contamination of meat products at the outlet. This could rather point to a possible origin by clone-like transmission either within a given live animal (if samples originated from the same pig) or among different pigs following cross-colonisation. Under the scenario of transmission within one single animal, the SNP-based genomic differences identified would suggest that intra-host variation [10] was stable. Colonisation/adaptation in the animal host, however, remains to be confirmed.

Tigecycline is not licensed for veterinary use. However, the production and use of tetracyclines are highest among all of the antimicrobial compounds in China [11,12]. It has been predicted that Tet(X) might become the most problematic future Tet determinant given its weak intrinsic tigecycline-resistance activity [13] concomitant with the historical selective pressure exerted by large scale use of earlier generations of this class of antibiotics.

Our findings demonstrate that high-level tigecycline resistant *E. coli* from pork harbouring the tet(X4) gene were associated with promiscuous plasmid types, resulting in a diverse range of clones. With international trade of food-producing animals and products derived from them, along with travel, tet(X4) -positive tigecycline resistant *E. coli* could represent the emergence of an additional antimicrobial mechanism of concern. Understanding the transmission mode of these genes allied to active surveillance of plasmid-mediated tet(X3)/(X4) variants in bacteria based on a one health approach is urgently recommended to support improvements in infection control practices to limit its further dissemination.

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Conflict of interest

None declared.

Authors’ contributions

LB and PCD performed the research and drafted the manuscript. PCD, HHS, YJD, PZ, YPW, QL, SF and SHC analysed and interpreted these data. LB and YNW designed the study, supervised the whole project, analysed the data and wrote the manuscript. All authors reviewed, revised, and approved the final report.

References


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