Prevalence of and risk factors associated with faecal carriage of CTX-M \(\beta\)-lactamase-producing Enterobacteriaceae in rural Thai communities

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Objectives: To determine the prevalence of CTX-M \(\beta\)-lactamase-producing Enterobacteriaceae and to study the risk factors associated with faecal carriage in asymptomatic rural Thai people.

Methods: In all, 417 stool samples were obtained from rural Thai people and screened for extended-spectrum \(\beta\)-lactamases (ESBLs) using MacConkey agar supplemented with 2 mg/L cefotaxime. Results were confirmed using cefotaxime and ceftazidime with and without clavulanic acid. The \textit{bla}_{CTX-M} genes were identified and genotyped using PCR with bacterial DNA samples. Multivariate analysis was performed to investigate risk factors associated with the faecal carriage of CTX-M producers.

Results: The prevalence of CTX-M-type ESBL-producing Enterobacteriaceae was 65.7%. The CTX-M-9 group (60.6%) was dominant, followed by the CTX-M-1 group (38.7%). Most of the bacteria were \textit{Escherichia coli} (85.4%) and \textit{Klebsiella pneumoniae} (4.7%). Of a total of 234 \textit{E. coli} strains, 48.7% belonged to phylogenetic group A, 28.6% to group B1, 15.8% to group D and 6.8% to group B2. Most CTX-M producers were susceptible to carbapenems and amikacin, but resistant to tetracycline and gentamicin. In a multivariate logistic regression model, better education status (OR 2.245; 95% CI 1.297–3.884), history of hospitalization (OR 1.643; 95% CI 1.036–2.603) and the use of antibiotics within the last 3 months (OR 1.883; 95% CI 1.221–2.903) were independently associated with faecal carriage.

Conclusions: Faecal carriage of CTX-M-type ESBL-producing Enterobacteriaceae among asymptomatic individuals in rural Thailand remains alarmingly high, and previous antibiotic use and a history of hospitalization may contribute to its dissemination.

Keywords: extended-spectrum \(\beta\)-lactamases, ESBLs, asymptomatic

Introduction

Extended-spectrum \(\beta\)-lactamases (ESBLs), which hydrolyse expanded-spectrum cephalosporins and monobactams but not cephamycins and carbapenems, are being increasingly found among Enterobacteriaceae.\textsuperscript{1,2} Recent studies have noted high levels of ESBL-producing Gram-negative bacilli in the Asia-Pacific region, particularly in India, China and Thailand.\textsuperscript{3–5}

In Thailand, high rates of the ESBL phenotype (26% of Enterobacteriaceae clinical isolates) were reported as early as 1994–96,\textsuperscript{3} and the CTX-M-type ESBLs were first detected during 1998–99.\textsuperscript{6} The emergence of community-onset infection with ESBL-producing \textit{Escherichia coli} in Thailand was reported after an analysis of specimens collected in 2003–04.\textsuperscript{7} In 2004–05, the prevalence of ESBL-producing \textit{E. coli} and \textit{Klebsiella pneumoniae} causing healthcare-associated infections was 13.2% and 12.7%, respectively, and most strains harboured the \textit{bla}_{CTX-M} gene.\textsuperscript{8} ESBL producers continue to be widely disseminated in Thailand, and recent data from 2005–07 showed that the prevalence of ESBL-producing isolates in different clinical specimens had increased to include 30.0%–40.1% of \textit{E. coli} and 27.1%–39.2% of \textit{K. pneumoniae} strains.\textsuperscript{9}

The problem of ESBL production is no longer limited to community-onset or hospital-acquired infections. Faecal carriage
of ESBL-producing Enterobacteriaceae, particularly the CTX-M producers, by asymptomatic individuals has been noted in many parts of the world.\textsuperscript{10–14} The highest levels of ESBL were found in the people of Thailand and China.\textsuperscript{15,16} We previously reported significantly high levels of faecal carriage of CTX-M-type ESBL-producing Enterobacteriaceae in asymptomatic volunteers in three provinces in the northern, southern and central regions of Thailand in 2008–09.\textsuperscript{15} Among the three provinces, Kanchanaburi province had the highest number of \textit{bla}_{CTX-M} carriers (58.2\%).\textsuperscript{17} and this high number may have been linked to antibiotic abuse.\textsuperscript{15} Therefore, to identify factors contributing to the high prevalence of ESBL producers in asymptomatic people, we investigated a possible link between CTX-M ESBL-producing Enterobacteriaceae and previous antibiotic use or hospital admittance.

**Materials and methods**

**Specimen collection and questionnaires**

The study was conducted in two randomly selected districts of Kanchanaburi province, Thailand: Thong Pha Phum district, which borders Burma; and Tha Maka district, located close to the capital city Bangkok. The volunteers were selected by random door-to-door sampling. A total of 450 people aged >18 years were approached to participate in the study, of whom 33 people refused.

Single stool samples from 417 adult volunteers from both districts were collected in November 2010 and analysed. Participants were interviewed using a standardized questionnaire, and the following data were recorded for each participant: age; gender; education; employment; number of persons in the household; monthly household income; consumption of raw meat and vegetables; household water supply and toilet conditions; possession of animals; antibiotic usage in the previous year; and invasive procedures during the previous year. Significant age or gender differences between participants from the two districts. However, participants from Tha Maka district had significantly better education and employment status, and more frequent use of antibiotics.

**Screening for and confirming the presence of ESBLs**

Fresh stool samples were plated on MacConkey agar supplemented with 2 mg/L cefotaxime (‘CTX-M-MacConkey’) and incubated at 37°C for 24 h. ESBL expression was confirmed by the disc diffusion method on Mueller–Hinton agar using cefotaxime (30 μg) and ceftazidime (30 μg) with and without clavulanic acid (10 μg), as recommended by the CLSI, and each set of samples was tested with CLSI quality control strains \textit{E. coli} ATCC 25922 and \textit{K. pneumoniae} ATCC 700603.\textsuperscript{18} Positive isolates were identified using conventional biochemical tests and the API 20E system (Systmex-Biome’rieux, Tokyo, Japan).

**\textit{bla}_{CTX-M} gene identification and genotyping**

The \textit{bla}_{CTX-M} genes were identified and genotyped by PCR using DNA extracted by boiling suspensions of positive isolates. DNA samples at a concentration of 0.1 ng/μL were used as PCR templates and \textit{bla}_{CTX-M} genes were amplified using the universal primers CTX-M-U1 (5’-ATG TGC AGG AGC AGT AAR GTK ATG GC-3’) and CTX-M-U2 (5’-TGG GTR AAR TAR GTS ACC AGA AYC AGC GG-3’), as described previously.\textsuperscript{19} DNA from a reference \textit{E. coli} \textit{bla}_{CTX-M}-positive strain was used as a positive control. For genotyping of the \textit{bla}_{CTX-M} genes, four primer sets were used to amplify group-specific \textit{bla}_{CTX-M} genes, as described elsewhere,\textsuperscript{20} including the CTX-M-1, CTX-M-2, CTX-M-8 and CTX-M-9 groups.

Phylogenetic grouping of the identified \textit{E. coli} isolates was determined by triplex PCR, using a combination of two genes (\textit{chuA} and \textit{yjaA}) and the DNA fragment TSP4E.C2, as described elsewhere.\textsuperscript{21} PCR products were visualized by 2% agarose gel electrophoresis and staining with GelRed nucleic acid gel stain (Biotium, Hayward, CA, USA).

**Antimicrobial susceptibility testing**

All ESBL-producing Enterobacteriaceae isolates were tested for susceptibility to imipenem, meropenem, amikacin, gentamicin, ciprofloxacin and tetracycline by the disc diffusion method using an SN Disc (Nissui Pharmaceutical Co., Ltd, Tokyo, Japan) according to the manufacturer’s instructions.

**Statistical analysis**

Data were analysed using SPSS version 16 software. Categorical data were compared using the \( \chi^2 \) test, and continuous data were compared using the Mann–Whitney \( U \) test. Univariate and multivariate logistic regression analyses were used to determine risk factors associated with the faecal carriage of ESBL-producing Enterobacteriaceae. Factors identified as statistically significant in the univariate analysis were included in a multivariate logistic regression model, and the results are presented as ORs with 95% CIs. Statistical significance was set at \( P < 0.05 \).

**Results**

In all, we analysed 417 stool samples, 232 of which were collected from Thong Pha Phum district and 185 of which were collected from Tha Maka district. Data on demographics, history of hospitalization, recent visits to doctors or health officers, and antibiotic use are shown in Table 1. There were no significant age or gender differences between participants from the two districts. However, participants from Tha Maka district had significantly better education and employment status, and more frequent use of antibiotics.

**Genotypes of CTX-M ESBL producers**

Phenotypic screening and confirmation tests showed that 289 of 417 (69.3\%) samples contained ESBL-producing bacteria (Table 2). All the 289 isolates were identified from different participants. After PCR analysis, 65.7% (274 of 417) of the isolates were found to be positive for the \( \textit{bla}_{CTX-M} \) gene. The prevalence of CTX-M-type ESBL-producing Enterobacteriaceae was significantly higher in Tha Maka district than in Thong Pha Phum district (\( P < 0.001 \)). Genotyping of \( \textit{bla}_{CTX-M} \) revealed that most CTX-M producers harboured genes belonging to the CTX-M-9 group (60.6\%), followed by the CTX-M-1 group (38.7\%). Only two (0.7\%) of the \( \textit{bla}_{CTX-M} \) gene-positive isolates belonged to the CTX-M-8 group, and no samples belonged to the CTX-M-2 group.

Among the CTX-M ESBL-producing Enterobacteriaceae, 85.4\% (234 of 274) were identified as \textit{E. coli} and 4.7\% (13 of 274) were identified as \textit{K. pneumoniae}. The remainder of the CTX-M-type ESBL producers were \textit{Citrobacter}, Enterobacter and other bacteria. Phylogenetic group analysis of the \textit{E. coli} strains showed that the highest proportion (114 of 234, 48.7\%) of isolates belonged to phylogenetic group A and the next highest proportion belonged to group B1 (67 of 234, 28.6\%) (Table 3).
All CTX-M-type ESBL-producing isolates were susceptible or intermediate to imipenem, meropenem and amikacin, except for two isolates: one was resistant to imipenem, meropenem, tetracycline and gentamicin, and the other was resistant to amikacin and tetracycline. Moreover, 88.0% (241 of 274) of them were resistant to tetracycline, 63.1% (173 of 274) to gentamicin and 19.7% (54 of 274) to ciprofloxacin. Of CTX-M ESBL-producing bacteria, 56.4% (75 of 133) from Thong Pha Phum district and 70.2% (99 of 141) from Tha Maka district were resistant to two or more of the antibiotics tested. The prevalence of such multidrug-resistant CTX-M ESBL producers was significantly higher in Tha Maka district than in Thong Pha Phum district ($P = 0.018$).

### Table 1. Characteristics of the study participants

<table>
<thead>
<tr>
<th>Characteristic</th>
<th>District</th>
<th>P valuea</th>
</tr>
</thead>
<tbody>
<tr>
<td>Age (years), median (range)</td>
<td>Thong Pha Phum, n = 232</td>
<td></td>
</tr>
<tr>
<td></td>
<td>Tha Maka, n = 185</td>
<td></td>
</tr>
<tr>
<td>Male gender</td>
<td>48 (20–84)</td>
<td>46 (20–85)</td>
</tr>
<tr>
<td>Unemployed</td>
<td>87 (37.5%)</td>
<td>71 (38.4%)</td>
</tr>
<tr>
<td>No formal education</td>
<td>60 (26.0%)</td>
<td>12 (6.5%)</td>
</tr>
<tr>
<td>Unemployed</td>
<td>67 (29.0%)</td>
<td>28 (15.1%)</td>
</tr>
<tr>
<td>Visited a doctor or health officer within the last year</td>
<td>155 (68.0%)</td>
<td>116 (64.4%)</td>
</tr>
<tr>
<td>Admitted to a hospital within the last year</td>
<td>98 (42.4%)</td>
<td>62 (34.8%)</td>
</tr>
<tr>
<td>Was prescribed antibiotics within the last year</td>
<td>145 (63.9%)</td>
<td>140 (76.5%)</td>
</tr>
<tr>
<td>Used antibiotics within the last year</td>
<td>159 (68.8%)</td>
<td>142 (78.0%)</td>
</tr>
<tr>
<td>Used antibiotics within the last 3 months</td>
<td>114 (50.0%)</td>
<td>122 (68.2%)</td>
</tr>
<tr>
<td>Used antibiotics without a prescription within the last year</td>
<td>120 (53.1%)</td>
<td>116 (64.1%)</td>
</tr>
</tbody>
</table>

Missing data were excluded from the analysis.

aCalculated by $\chi^2$ test or Mann–Whitney $U$-test as appropriate.

### Table 2. Detection of CTX-M-type ESBL-producing Enterobacteriaceae

<table>
<thead>
<tr>
<th>District</th>
<th>Participants</th>
<th>ESBL phenotypea</th>
<th>CTX-M geneb</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>CTX-M groupc</td>
<td>CTX-M-1d</td>
<td>CTX-M-2e</td>
</tr>
<tr>
<td>Thong Pha Phum</td>
<td>232</td>
<td>148 63.8%</td>
<td>133 57.3%</td>
</tr>
<tr>
<td>Tha Maka</td>
<td>185</td>
<td>141 76.2%</td>
<td>141 76.2%</td>
</tr>
<tr>
<td>Total</td>
<td>417</td>
<td>289 69.3%</td>
<td>274 65.7%</td>
</tr>
</tbody>
</table>

aESBL phenotype was determined according to CLSI recommendations.
bCTX-M gene was determined by PCR.
cGenotype of CTX-M genes was determined by PCR.
dCTX-M-1 group includes CTX-M-1 and several other variants, such as CTX-M-3 and CTX-M-15.
eCTX-M-2 group includes CTX-M-2 and several other variants.
fCTX-M-8 group includes CTX-M-8 and other variants.
gCTX-M-9 group includes CTX-M-9 and several other variants, such as CTX-M-14.

### Table 3. Phylogenetic groups of the CTX-M ESBL-producing E. coli isolates

<table>
<thead>
<tr>
<th>Phylogenetic group</th>
<th>Thong Pha Phum</th>
<th>Tha Maka</th>
</tr>
</thead>
<tbody>
<tr>
<td>A</td>
<td>66</td>
<td>48</td>
</tr>
<tr>
<td>B1</td>
<td>34</td>
<td>33</td>
</tr>
<tr>
<td>B2</td>
<td>4</td>
<td>12</td>
</tr>
<tr>
<td>D</td>
<td>17</td>
<td>20</td>
</tr>
<tr>
<td>Total</td>
<td>121</td>
<td>113</td>
</tr>
</tbody>
</table>

### Antibiotic susceptibility

All CTX-M-type ESBL-producing isolates were susceptible or intermediate to imipenem, meropenem and amikacin, except for two isolates: one was resistant to imipenem, meropenem, tetracycline and gentamicin, and the other was resistant to amikacin and tetracycline. Moreover, 88.0% (241 of 274) of them were resistant to tetracycline, 63.1% (173 of 274) to gentamicin and 19.7% (54 of 274) to ciprofloxacin.

### Risk factors for faecal carriage

Using univariate logistic regression models, we found that the following factors were associated with a risk of carrying CTX-M-type ESBL-producing Enterobacteriaceae: (i) enrolment in formal education (OR 2.095; 95% CI 1.251–3.508; $P = 0.004$); (ii) a history of hospitalization within the last year (OR 1.550; 95% CI 1.009–2.381; $P = 0.045$); (iii) use of antibiotics within the last year (OR 1.592; 95% CI 1.018–2.491; $P = 0.041$); (iv) use of antibiotics within the last 3 months (OR 1.879; 95% CI 1.194–3.014; $P = 0.004$).
A recent study in healthy people of China showed findings of community and clinical isolates from Thai-
(60.6%) and CTX-M-1 (38.7%) groups is consistent with previous
that have been reported among healthy subjects in the commu-
the highest prevalences of ESBL-producing Enterobacteriaceae
variables significantly predicted carriage of CTX-M ESBL producers. The three vari-
biotics within the last 3 months (OR 1.883; 95% CI 1.221–2.903;
However, the final multivariate logistic regression model identi-
3.884; 
P 
¼
0.004), a history of hospitalization within the last
year (OR 1.569; 95% CI 1.015–2.424; 
P 
¼
0.042).
Phum district (Table 2). To the best of our knowledge, these are
higher prevalence of CTX-M ESBL producers than did Thong Pha
province shows a rapid spread of CTX-M ESBLs in the community.
The current finding of 65.7% (274 of 417
samples) carriage of CTX-M ESBL producers in Kanchanaburi
was lower (19.7%) in CTX-M ESBL producers isolated from asymp-
tomatic people than in those isolated from clinical samples.
Our findings are similar to those of hospital studies in Thailand, where all ESBL-producing
E. coli strains isolated from clinical speci-
cmens were susceptible to carbapenems, but 57.8% were resistant
to gentamicin, 81.0% were resistant to ciprofloxacin and 89.1%
were resistant to tetracycline. However, quinolone resistance
was lower (19.7%) in CTX-M ESBL producers isolated from asym-
tomatic people than in those isolated from clinical samples.

Discussion

Genotypes of CTX-M ESBL producers

The results of this study confirmed our previous findings of a high
prevalence (29.3%–50.6% faecal carriage15) of CTX-M-type
ESBL-producing Enterobacteriaceae among asymptomatic indivi-
duals in rural Thailand. The current finding of 65.7% (274 of 417
samples) carriage of CTX-M ESBL producers in Kanchanaburi
province shows a rapid spread of CTX-M β-lactamases compared
with our previous finding of 51.3% (82 of 160) prevalence in
2008.17 Moreover, we observed variations in the prevalence of
ESBLs within the Kanchanaburi province: Tha Maka district,
which had a better education and employment status and
higher use of antibiotics (Table 1), also had a significantly
higher prevalence of CTX-M ESBL producers than did Thong Pha
Phum district (Table 2). To the best of our knowledge, these are
the highest prevalences of ESBL-producing Enterobacteriaceae
that have been reported among healthy subjects in the commu-
nity to date.

Prevalent identification of ESBLs belonging to the CTX-M-9
(60.6%) and CTX-M-1 (38.7%) groups is consistent with previous
findings of community and clinical isolates from Thai-
land.8,15,17 A recent study in healthy people of China showed
50.5% faecal carriage of E. coli producing ESBLs, mainly of the
CTX-M-type, among which also the CTX-M-9 and CTX-M-1
groups were dominant (74.5% and 29.1%, respectively).16
Other Asian countries may soon follow the same pattern of
rapidly spreading CTX-M ESBLs in the community.
In the current study, most ESBL producers were identified as
E. coli belonging to phylogenetic groups A and B1. In China,
phylogenetic groups D and A were found to be prevalent
among ESBL-producing E. coli strains in asymptomatic carriers.16
A report on the population genetics of E. coli stated that commensal
E. coli strains isolated from Asia mainly belonged to phylogenetic
groups A and B2,23 whereas a recent worldwide dis-
semination of bla genes encoding CTX-M-14 and CTX-M-15 was
considered to be driven by epidemic E. coli strains belonging to
phylogroup B2 (ST131).24–26 However, of the 234 CTX-M ESBL-
producing E. coli strains in this study, only 16 isolates belonged
to phylogroup B2. After multilocus sequence typing, 11 of
these were identified as strain ST131, with 7 samples belonging
to the CTX-M-9 group and 4 to the CTX-M-1 group (data not
shown). This indicates that horizontal plasmid transfer has
played a more important role than clonal expansion in the
current massive community spread of CTX-M-type ESBLs in Asia.

Antibiotic susceptibility

Our findings are similar to those of hospital studies in Thailand,
where all ESBL-producing E. coli strains isolated from clinical speci-
cmens were susceptible to carbapenems, but 57.8% were resistant
to gentamicin, 81.0% were resistant to ciprofloxacin and 89.1%
were resistant to tetracycline. However, quinolone resistance
was lower (19.7%) in CTX-M ESBL producers isolated from asym-
tomatic people than in those isolated from clinical samples.

Risk factors for faecal carriage

Our risk factor analyses show that even in the community
setting, previous healthcare contact and antibiotic exposure
have a major contribution to the faecal carriage of resistant bac-
teria. A history of hospitalization within the last year and anti-
biotic use within the last 3 months indicated higher risks of
carrying CTX-M ESBL-producing Enterobacteriaceae. However,
these factors may be specific to countries where antibiotic man-
agement programmes are uncommon and antibiotics can be
purchased over the counter without a prescription, which is the
case in Thailand.17,19

Previous antibiotic use and a history of hospitalization have
been identified as risk factors for community-onset urinary
tract infections (UTIs) caused by ESBL-producing bacteria,27–29
but have rarely been found to be risk factors for the faecal car-
rriage of ESBL producers. Only one report, to our knowledge,

Table 4. Antibiotic susceptibility of CTX-M-type ESBL-producing Enterobacteriaceae

<table>
<thead>
<tr>
<th>Antimicrobial agent</th>
<th>Susceptible zone diameter breakpointsa, mm</th>
<th>Intermediate zone diameter breakpoints, mm</th>
<th>Resistant zone diameter breakpoints, mm</th>
</tr>
</thead>
<tbody>
<tr>
<td>Imipenem</td>
<td>≥16</td>
<td>14–15</td>
<td>≤13</td>
</tr>
<tr>
<td>Meropenem</td>
<td>≥16</td>
<td>14–15</td>
<td>≤13</td>
</tr>
<tr>
<td>Gentamicin</td>
<td>≥15</td>
<td>13–14</td>
<td>≤12</td>
</tr>
<tr>
<td>Amikacin</td>
<td>≥17</td>
<td>15–16</td>
<td>≤14</td>
</tr>
<tr>
<td>Ciprofloxacin</td>
<td>≥21</td>
<td>16–20</td>
<td>≤15</td>
</tr>
<tr>
<td>Tetracycline</td>
<td>≥15</td>
<td>12–14</td>
<td>≤11</td>
</tr>
</tbody>
</table>

aSusceptibility results were interpreted according to SN Disc (Nissui Pharmaceutical Co., Ltd, Tokyo, Japan) zone diameter breakpoints.
has found a strong association between the use of antibiotics in the previous 3 months and the rectal carriage of ESBL-producing E. coli in elderly people in community settings.30 In contrast, most other studies showed that prior hospitalization or previous use of antimicrobial drugs was irrelevant for the faecal carriage of ESBL-producing Enterobacteriaceae in healthy people.31,32 Neither have studies on faecal carriage of patients attending health centres or at admission to hospitals found association with prior antibiotic use.13,33 Thus, although our results regarding risk factors for faecal carriage differ from previous findings, they are similar to factors associated with community-onset UTIs caused by ESBL producers. This similarity may be explained by the fact that faecal carriage of ESBL-producing E. coli contributes substantially to the development of UTIs and that almost half of these infections are caused by the same strains found in the faeces of patients before the development of UTIs.34

Interestingly, we found a significant association between the faecal carriage of CTX-M producers and enrolment of the participants in formal education. Since the study was conducted in rural areas, enrolment in formal education may be a proxy for socio-economic status. Therefore, it may indicate that those who have better socio-economic status can also afford and/or have better access to medical services, including over-the-counter antibiotics.

Furthermore, different factors, such as acquisition of ESBL-producing E. coli from food or by person-to-person transmission from faecal carriers, dissemination of ESBL-producing E. coli in the environment and carriage by domestic and wild animals, have been proposed to explain the extensive spread of ESBL-producing E. coli in community settings.35 However, our findings did not show any association between the faecal carriage of CTX-M producers and household conditions, food habits or animals possessed by the participants.

Finally, it is important to recognize that the current study was conducted only in one province of Thailand and the findings may not be representative of the whole country. In addition, the study was conducted in community settings among asymptomatic individuals and risk factor analysis for faecal carriage of ESBL producers was therefore based on the participants’ self-reporting, which may have potential for recall bias with regard to factors such as previous antibiotic use. Despite these limitations, our data indicate that faecal carriage of CTX-M family is endemic. Antimicrob Agents Chemother 2008; 52: 2818–24.


15 Luvsansharav UO, Hirai I, Niki M et al. Analysis of risk factors for a high prevalence of extended-spectrum β-lactamase-producing E. coli in elderly people in community settings.30 In contrast, most other studies showed that prior hospitalization or previous use of antimicrobial drugs was irrelevant for the faecal carriage of ESBL-producing Enterobacteriaceae in healthy people.31,32 Neither have studies on faecal carriage of patients attending health centres or at admission to hospitals found association with prior antibiotic use.13,33 Thus, although our results regarding risk factors for faecal carriage differ from previous findings, they are similar to factors associated with community-onset UTIs caused by ESBL producers. This similarity may be explained by the fact that faecal carriage of ESBL-producing E. coli contributes substantially to the development of UTIs and that almost half of these infections are caused by the same strains found in the faeces of patients before the development of UTIs.34

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Finally, it is important to recognize that the current study was conducted only in one province of Thailand and the findings may not be representative of the whole country. In addition, the study was conducted in community settings among asymptomatic individuals and risk factor analysis for faecal carriage of ESBL producers was therefore based on the participants’ self-reporting, which may have potential for recall bias with regard to factors such as previous antibiotic use. Despite these limitations, our data indicate that faecal carriage of CTX-M family is endemic. Antimicrob Agents Chemother 2008; 52: 2818–24.


15 Luvsansharav UO, Hirai I, Niki M et al. Analysis of risk factors for a high prevalence of extended-spectrum β-lactamase-producing E. coli in elderly people in community settings.30 In contrast, most other studies showed that prior hospitalization or previous use of antimicrobial drugs was irrelevant for the faecal carriage of ESBL-producing Enterobacteriaceae in healthy people.31,32 Neither have studies on faecal carriage of patients attending health centres or at admission to hospitals found association with prior antibiotic use.13,33 Thus, although our results regarding risk factors for faecal carriage differ from previous findings, they are similar to factors associated with community-onset UTIs caused by ESBL producers. This similarity may be explained by the fact that faecal carriage of ESBL-producing E. coli contributes substantially to the development of UTIs and that almost half of these infections are caused by the same strains found in the faeces of patients before the development of UTIs.34

Interestingly, we found a significant association between the faecal carriage of CTX-M producers and enrolment of the participants in formal education. Since the study was conducted in rural areas, enrolment in formal education may be a proxy for socio-economic status. Therefore, it may indicate that those who have better socio-economic status can also afford and/or have better access to medical services, including over-the-counter antibiotics.

Furthermore, different factors, such as acquisition of ESBL-producing E. coli from food or by person-to-person transmission from faecal carriers, dissemination of ESBL-producing E. coli in the environment and carriage by domestic and wild animals, have been proposed to explain the extensive spread of ESBL-producing E. coli in community settings.35 However, our findings did not show any association between the faecal carriage of CTX-M producers and household conditions, food habits or animals possessed by the participants.

Finally, it is important to recognize that the current study was conducted only in one province of Thailand and the findings may not be representative of the whole country. In addition, the study was conducted in community settings among asymptomatic individuals and risk factor analysis for faecal carriage of ESBL producers was therefore based on the participants’ self-reporting, which may have potential for recall bias with regard to factors such as previous antibiotic use. Despite these limitations, our data indicate that implementation of antimicrobial stewardship interventions, such as limitation of over-the-counter antibiotics, prescribing the proper antibiotics for the proper duration, and proper hospital infection control, can assist in the prevention of further spread of resistant bacteria among healthy people in rural communities.

Conclusions

Faecal carriage of CTX-M-type ESBL-producing Enterobacteriaceae among asymptomatic individuals in the Kanchanaburi province of Thailand remains alarmingly high. Public health efforts should focus on educating rural Thai communities and healthcare professionals on the proper use of antibiotics.

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