J Antimicrob Chemother 2011
doi:10.1093/jac/dkr274
Advance Access publication 23 June 2011

Similarities between the genetic environments of \( \text{bla}_{\text{CTX-M-15}} \) in *Escherichia coli* from clinical and food samples from Spain and overseas travellers

Lorena López-Cerero1*, Pilar Egea2, Jesús Rodríguez-Baño1,3 and Alvaro Pascual1,2

1Microbiology and Infectious Diseases Unit, University Hospital Virgen Macarena, Avda Dr Fedriani s/n, 41009 Sevilla, Spain; 2Microbiology Department, School of Medicine, University of Seville, Avda Dr Fedriani s/n, 41009 Sevilla, Spain; 3Medicine Department, School of Medicine, University of Seville, Avda Dr Fedriani s/n, 41009 Sevilla, Spain

*Corresponding author. Tel: +34-955-008138; Fax: +34-955-011587; E-mail: llopez@us.es

Keywords: ESBLs, carriers, IS26, ISEcp1

Sir,

We read with interest the recent article by Dhanji et al.1 on \( \text{bla}_{\text{CTX-M-15}} \) genetic environments. The authors found that up to 17% of overseas travellers returning to the UK with diarrhoea were faecal carriers of CTX-M-15-producing *Escherichia coli* isolates. The extended-spectrum \( \beta \)-lactamase (ESBL) producers detected belonged to phylogenetic group A (40%), group D (32%), group B2 (16%) and, less frequently, group B1 (13%). The majority (62%) of isolates harboured the genetic environment found internationally, with an intact copy of ISEcp1 located 48 bp upstream of \( \text{bla}_{\text{CTX-M-15}} \), and only eight (5%) showed the characteristic 24 bp ISEcp1 remnant of UK strain A. In 22 (15%) isolates a 545 bp ISEcp1 fragment truncated by IS26 in the opposite direction was found upstream of \( \text{bla}_{\text{CTX-M-15}} \), named as the 2c genetic environment in the Dhanji et al.1 study (Figure 1), and 10 of these isolates belonged to phylogenetic group A.

As the authors commented, international travel has been found to be a significant risk for colonization with CTX-M ESBL producers2 and they associated genetic environments of \( \text{bla}_{\text{CTX-M-15}} \) with specific travel destinations. Nevertheless, the unknown previous colonization with CTX-M-15 producers was admitted as a limitation of the study. Recently, we have found CTX-M-15-producing *E. coli* that belonged to group A and sequence type (ST) 410, recovered from five urine samples from community non-related patients and two raw turkey samples between 2005 and 2007 in our area.3 Five of those seven isolates showed 81.2% similarity by PFGE clustering, including clinical and meat isolates. In our study, \( \text{bla}_{\text{CTX-M-15}} \) was co-transferred with other resistance markers in related IncF group plasmids and clustered in the same fragment. Of note, the genetic environment in all these isolates (GenBank accession number GU479916) was identical to that named 2c found in UK travellers (GenBank accession number HQ157353). None of our patients came from the Indian subcontinent, Afghanistan or Egypt, or had travelled to those countries, and the meat samples were purchased fresh in local stores.4

We agree with Dhanji et al.1 that the spread of *E. coli* producing CTX-M-15 is complex and diverse. The emergence of different pulsotypes of highly virulent B2, ST131 producing CTX-M-15 has contributed to international spread5 co-transferred with \( \text{bla}_{\text{OXA-1}}, \text{bla}_{\text{TEM}}, \text{tet}(A), \text{catB3} \) and \( \text{aac(6′)-Ib} \), but, additionally, dissemination within group A strains with low virulence could also occur.

Funding

This work was supported by Ministerio de Ciencia e Innovación, Instituto de Salud Carlos III, Spanish Network for Research in Infectious Diseases (REIPI RD06/0008), and Consejería de Innovación (CTS-5259) and Consejería de Salud (PI-0034) of Junta de Andalucía.

Transparency declarations

None to declare.

References


