**Escherichia coli** carrying the **bla**<sub>CTX-M-15</sub> gene of ST648

**bla**<sub>CTX-M</sub>-M genes have emerged as the dominant genes encoding extended-spectrum β-lactamases in the world. Among more than 90 **bla**<sub>CTX-M</sub>-M genes that have been identified so far, **bla**<sub>CTX-M-15</sub> is the most widespread variant. Although **Escherichia coli** of O antigen type 25 (O25) and sequence type 131 (ST131) is largely responsible for the intercontinental spread of **bla**<sub>CTX-M-15</sub>, some other sequence types have also been found associated with this gene. During a local surveillance of **bla**<sub>CTX-M</sub>-M genes, an isolate of ST648 carrying **bla**<sub>CTX-M-15</sub> was identified and is reported here. As an ST648 isolate carrying **bla**<sub>CTX-M-15</sub> was found in the USA (Sidjabat et al., 2009) recently, the findings here together with the USA report suggest a possible intercontinental spread of this lineage.

**E. coli** clinical isolate WCE227 was collected from a urine sample and was resistant to cefotaxime (MIC >32 μg ml<sup>-1</sup>) and ceftazidime (MIC >16 μg ml<sup>-1</sup>) as determined by the Phoenix automated microbiology system (BD). The WCE227 was hospital acquired as it was recovered from a patient hospitalized for more than 48 h, although the patient did not receive antimicrobial agents prior to sample collection. The **bla**<sub>CTX-M</sub>-M gene was detected and was subsequently identified as **bla**<sub>CTX-M-15</sub> by PCR and sequencing as described elsewhere (Zong et al., 2008).

WCE227 was identified as being of the O25b subtype by O25b allele PCR. Phylogenetic group typing (Clermont et al., 2000) revealed that WCE227 belonged to group D (subgroup D<sub>1</sub>, having chat<sub>α</sub> but lacking yja<sub>A</sub> and Tspe4.C2). WCE227 was of ST648 as determined by multilocus sequence typing (MLST) following an established scheme based on seven housekeeping genes (adk, fumC, gyrB, icaD, mdh, purA and recA) available through the University College Cork MLST database (http://mlst.ucc.ie/mlst/dbs/Ecoli).

Since **bla**<sub>CTX-M-15</sub> usually co-exists with a few other resistance determinants, **aac**<sup>(3)</sup>-II, **bla**<sub>TEM</sub>, **bla**<sub>OXA-1</sub> (also called **bla**<sub>OXA-30</sub>) and plasmid-encoded quinolone resistance determinants including **qnrA**, **qnrB**, **qnrS** and **qepA**, were screened by PCR, and **aac**<sup>(6)</sup>-Ib-cr was identified by sequencing. WCE227 had **bla**<sub>OXA-1</sub> and **aac**<sup>(6)</sup>-Ib-cr but no others. WCE227 were resistant to trimethoprim (TMP)/sulfamethoxazole and had a class 1 integron with the **dfrA17–aadA5** cassette array that was determined by PCR and sequencing. Class 1 integrons contain **suI**, a sulfonamide-resistance gene, in the 3′-conserved segment. **dfrA17** encodes TMP-insensitive dihydrofolate reductases conferring resistance to TMP. As WCE227 was resistant to ciprofloxacin, the **gyrA** allele was partially sequenced. This revealed Ser83Tyr and Asp87Asn substitutions that have been seen in fluoroquinolone-resistant isolates before (Cagnacci et al., 2008).

Mating was carried out in brain heart infusion broth (Oxoid) with **E. coli** DH5αRf, a spontaneous rifampicin-resistant mutant of DH5α (**ΔΔacZ**) as the recipient strain. WCE227 was sensitive to rifampicin and transconjugants were selected on 4 μg cefotaxime ml<sup>-1</sup> plus 250 μg rifampicin ml<sup>-1</sup>. In WCE227, **bla**<sub>CTX-M-15</sub> was carried by a conjugative plasmid, for which the incompatibility (Inc) group could not be assigned by PCR-based replicon typing (Carattoli et al., 2005). Surprisingly, **aac**<sup>(6)</sup>-Ib-cr and **bla**<sub>OXA-1</sub> were not co-transferred with **bla**<sub>CTX-M-15</sub> in WCE227, in contrast to the findings of reports from elsewhere. The **dfrA17–aadA5** cassette array was also not located on the plasmid carrying **bla**<sub>CTX-M-15</sub> in WCE227.

ST648 isolates carrying **bla**<sub>CTX-M-15</sub> have been seen before, including two isolates carrying **bla**<sub>CTX-M-15</sub> from the USA (Sidjabat et al., 2009) and two carrying **bla**<sub>CTX-M-15</sub> from Spain (Blanco et al., 2009). All of those ST648 isolates like WCE227 belonged to phylogenetic group D. Interestingly, ST648 without **bla**<sub>CTX-M-15</sub> but carrying **aac**<sup>(6)</sup>-Ib-cr had been found in London, UK, prior to the epidemic of **bla**<sub>CTX-M-15</sub> (Jones et al., 2008). The findings from the UK together with the fact that **aac**<sup>(6)</sup>-Ib-cr was not located on the plasmid carrying **bla**<sub>CTX-M-15</sub> in WCE227 suggest that the ST648 lineage acquired the two genes independently. This is in contrast to the ST131 lineage, for which **bla**<sub>CTX-M-15</sub> and **aac**<sup>(6)</sup>-Ib-cr were usually co-transferred on individual plasmids, most of which were FII-like.

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