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Escherichia coli with bla_{IMP-8} in Singapore

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An imipenem-resistant *Escherichia coli* strain was isolated from the urine of a local 72-year-old female Chinese patient in 2006. The carbapenem MICs by Etest (bioMérieux SA, Marcy l'Etoile, France) were ertapenem at 2 μg/μl, meropenem at 4 μg/μl, and imipenem at >32 μg/μl. A modified Hodge test was weakly positive. The presence of a metallo-β-lactamase (MBL) was suspected because of enhancement of the zone of inhibition around ertapanem, imipenem, and meropenem antimicrobial susceptibility testing disks with the addition of EDTA (1). A multiplex PCR for detection of carbapenemase genes was positive for bla_{IMP} (2). A 2,847-bp partial integron sequence was amplified using the IntA primer described by Rosser and Young (3) and an in-house primer, tniRR (5′-GGC AAG CTT GTG TTC GGT AT-3′). This sequence (GenBank accession number KF534724) contained *intI1*, bla_{IMP-8}, an aminoglycoside 6′-N-acetyltrasferase gene [*aac(6′)-IId*], and *tniR* (a putative resolvase possibly involved in transposition). This result was identical to that determined for *Klebsiella oxytoca* (GenBank accession number HQ651093.1) from Fujian in China, except the *intI1* partial sequence was not disrupted by IS*26*, though we have not excluded the possibility that this could have been inserted further downstream in the sense of *intI1* (4). This structure is carried on a plasmid of approximately 120 kb that was successfully transferred to *E. coli* J53 Az^r by plate mating. This was determined to be Inc A/C by plasmid replicon typing (5). The only other β-lactamase gene identified was bla_{TEM-1}. However, the high imipenem MIC relative to those of the other carbapenems is difficult to explain and it is possible that an undetected mechanism may contribute to the final resistance phenotype. Multilocus sequence typing showed that the isolate belonged to ST410 (ST23 complex). This sequence type has been associated with spread of carbapenem-nonsusceptible, KPC-2-producing *E. coli* strains in Greece (6).

IMP-8 was first described in *Klebsiella pneumoniae* from Taiwan (7), where it has established itself as the dominant MBL among the *Enterobacteriaceae*. It is a variant of IMP-2, from which it differs by 2 amino acids. Until recently, the distribution of bla_{IMP-8} was restricted to Taiwan and China. However, recently it has been reported in *Pseudomonas mendocina* in Portugual (8), *Enterobacter cloacae* in Argentina (9), *K. oxytoca* in Spain (10), and *K. pneumoniae* in Tunisia (11).

Given the close links between Taiwan, China, and Singapore, it is surprising that this is the only IMP-8 producer found so far in Singapore. However, these strains may be difficult to detect because of their low ertapenem and meropenem MICs. Taiwanese researchers have reported that only a third of IMP-8 producers had a positive modified Hodge test result. Furthermore, meropenem combined disk testing detected only 40% in combination with EDTA and 2% in combination with dipicolinic acid (12). The phenotype of our isolate was similarly difficult to recognize because the modified Hodge test result was weak, like that of an NDM-1 producer, and could easily have been dismissed as negative.

Nucleotide sequence accession number. The sequence determined in this work is available in GenBank under accession number KF534724.

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