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First report of IMP-1 in a clinical isolate of *Escherichia coli* in Latin America

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To the Editor—The emergence of carbapenem-resistant *Enterobacterales* (CRE) is a matter of public health concern that seriously compromises antibiotic treatment for severe infections. Since the first report of acquired IMP-1 in *Pseudomonas aeruginosa* in Japan in 1988,[1] genes encoding IMP enzymes have spread rapidly among *Acinetobacter* spp and *Enterobacterales*.[2] Here, we describe the characteristics of a clinical isolate of *E. coli* harboring $bla_{\text{IMP-1}}$ gene in Latin America.

An *Escherichia coli* (termed *E. coli* 7469F) was recovered from the blood of a patient at Hospital de Clínicas de Porto Alegre in Southern Brazil in May 2019. The *E. coli* 7469F was not susceptible in vitro to meropenem and ertapenem by the disk-diffusion method. The presence of carbapenemase genes ($bla_{\text{NDM-1}}$, $bla_{\text{KPC-2}}$, $bla_{\text{VIM-type}}$, $bla_{\text{GES-type}}$, $bla_{\text{OXA-48-like}}$, and $bla_{\text{IMP-type}}$) was evaluated using multiplex high-resolution melting (HRM) real-time polymerase chain reaction (PCR),[3] which yielded a positive result only for the $bla_{\text{IMP-type}}$ gene. The clinical isolate was submitted to conjugation experiment using *E. coli* J53 as a receptor, and 1 transconjugant (T7469F) was selected for further analysis. The minimal inhibitory concentrations (MICs) of antibiotics representative of β-lactams, aminoglycosides, glycilcycline, and chloramphenicol were evaluated by broth microdilution for the *E. coli* 7469F and its transconjugant (T7469F). The transconjugant T7469F presented significant increase in MICs of the carbapenems and ceftazidime compared with *E. coli* J53 (Table 1). T7469F did not present an increased MIC for aminoglycosides, chloramphenicol, or tigecycline. This whole-genome shotgun project has been deposited at DDBJ/ENA/GenBank under the accession WTVT00000000. The version described here is version WTVT01000000.

The whole genomes of the clinical isolate and its transconjugant were sequenced using the MiSeq platform (Illumina, San Diego, CA), and the data were analyzed using the following tools from the Centre for Genomic Epidemiology website (http://www.genomicepidemiology.org): MLST to characterize sequence typing (ST), ResFinder to characterize antibiotic resistance mechanisms, and PlasmidFinder to characterize plasmid types. Analyses of the whole-genome sequencing (WGS) data confirmed the presence of the $bla_{\text{IMP-1}}$ gene in isolate 7469F and its transconjugant. Other genes related to resistance to β-lactam ($bla_{\text{CTX-M-15}}$ and $bla_{\text{OXA-1}}$) were found in the clinical isolate using in silico data analyses. *E. coli* 7469F presented 4 plasmids, and the $bla_{\text{IMP-1}}$ gene was identified in the plasmid IncA/C_2. In silico data confirmed that the IncA/C_2 was the only plasmid identified in the transconjugant T7469F. Plasmids belonging to the IncA/C incompatibility group are broad host–range vehicles commonly identified among animal and clinical bacterial isolates of *Enterobacterales* worldwide. This plasmid usually harbors different resistance genes, including bla_{CMY}, bla_{NDM}, bla_{VIM}, and bla_{IMP}.[4] The WGS analyses also indicated that the *E. coli* 7469F belonged to the ST648. ST648 is a predominant multidrug-resistant ST observed worldwide; it is increasingly reported in multiple regions.[5-8] In addition, several publications have reported the frequent occurrence of ST648 strains with various β-lactamases (extended-spectrum β-lactamases [ESBLs], New Delhi metallo-β-lactamases [NDMs], and *Klebsiella pneumoniae* carbapenemase [KPCs]),[9,10] as well as the *mcr*-1 gene.[8]

To the best of our knowledge, this is the first report of a clinical isolate of *E. coli* ST648 carrying an IncA/C_2 plasmid with the $bla_{\text{IMP-1}}$ gene in Latin America. Notably, the broad host range

Table 1. Minimal Inhibitory Concentrations (MICs) of Several Antibiotics Used to Treat *Escherichia coli* 7469F, Transconjugant 7469F, and *E. coli* J53

	MIC (mg/L)		
Antibiotics	*E. coli* 7469F	Transconjugant T7469F	*E. coli* J53
Ertapenem	128	8	≤0.03
Imipenem	16	4	0.5
Meropenem	64	8	0.06
Ceftazidime	512	512	0.5
Gentamicin	2	2	2
Tigecycline	0.25	0.5	0.5
Amicacin	8	8	4
Chloranphenicol	8	8	8

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of IncA/C_2 plasmid may contribute to the diffusion and maintenance of bla_{IMP-1} in different groups of bacteria. Considering the concerning spread of carbapenem resistance mediated by plasmids and considering the high prevalence of ST648 *E. coli*, our study highlights the importance of continuous surveillance studies of carbapenemase genes in Latin America.

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Conflicts of interest. All authors report no conflicts of interest relevant to this article.

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The *Legionella* contamination of tap water in a brand-new hospital in Japan before patients move in

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To the Editor—Healthcare facilities are potential settings for *Legionella* infections, and 2%–20% of Legionnaires' disease cases have been estimated to have been acquired at hospitals, long-term care facilities, and clinics.[1,2] The widespread contamination of *Legionella* spp in the water systems of healthcare facilities has recently been recognized.[3,4] The persistent environmental contamination of *Legionella* spp in water systems can often be difficult to eradicate once the organism colonizes because the organism is likely to continue to survive in dead branches of complex plumbing systems. Furthermore, identifying the sources of *Legionella* spp contamination in hospital water systems and determining when colonization occurred can be difficult. Because most studies are performed in operational hospitals, the identified relationships between hospital water systems and *Legionella* are often attributed to old, scaled water pipes.

We evaluated the environmental contamination of *Legionella* spp before patients moved into a brand-new hospital, which was built by a leading Japanese construction company. The study was conducted in June 2019 at Tokyo Medical University Hospital, a 19-story building that has 905 beds and a 3-story basement (completed in March 2019). Overall, 61 sampling points were selected, including 27 manual faucets, 18 touch-free faucets, and 16 showers in inpatient hospital wards. A hot water sample and a cool water sample were obtained at each sampling point. In total, 122 500-mL samples were obtained, starting as soon as the water began to flow, and samples were stored in sterilized bottles. All samples were concentrated on a filtration, followed by treatment at 50°C for 30 minutes. These samples were cultured using Wadowsky-Yee-Okuda-α-ketoglutarate agar culture medium (Eiken Chemical, Tokyo, Japan). Cultures were incubated in a humid environment for 5 days at 36 ± 1°C.

Among the 122 samples taken, 1 sample, from the highest floor, was positive for *Legionella* spp. Matrix-assisted laser desorption/

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