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LETTER TO THE EDITOR

Emergence of *Klebsiella pneumoniae* Coharboring KPC and VIM Carbapenemases in Colombia

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Klebsiella pneumoniae strains coharboring KPC and VIM carbapenemases have been reported, to the best of our knowledge, only in Greece (1–5) and Germany (6). The coexpression of these two resistance determinants poses a major threat to antibiotic utility worldwide. Herein we report, for the first time in the Americas, a *K. pneumoniae* isolate harboring bla_{KPC} and bla_{VIM} genes.

In September 2010, a 74-year-old woman presented to the emergency department after acute onset of an ischemic stroke. During hospitalization she developed nosocomial pneumonia, which resulted in intubation and transfer to an intensive care unit (ICU). In the ICU she received multiple antibiotics, including piperacillin-tazobactam, cefepime, meropenem, and vancomycin. On her 15th day of hospitalization, a tracheostomy was performed due to her inability to be weaned from mechanical ventilation. Five days later, due to the persistence of respiratory distress, a culture of bronchial secretion was taken. The laboratory reported a *K. pneumoniae* isolate (isolate 3359) nonsusceptible to ciprofloxacin, amikacin, β-lactams/β-lactamase inhibitors, expanded-spectrum cephalosporins, imipenem, and ertapenem but susceptible to meropenem, tigecycline, and polymyxin B. The patient was continued on meropenem (2 g intravenously three times a day) with progressive improvement but unfortunately died of ventricular fibrillation after 76 days of hospitalization.

Isolate 3359 was sent to CIDEIM, where the species identification was corroborated using Vitek 2 (bioMérieux, Marcy l'Etoile, France) and antibiotic susceptibility testing was performed using the broth microdilution method (Sensititre panels; TREK Diagnostic Systems, Westlake, OH). According to CLSI 2010 breakpoints (7), the isolate was nonsusceptible to ceftazidime, cefotaxime, ceftriaxone, aztreonam, amikacin, ciprofloxacin, and piperacillin-tazobactam, had reduced susceptibility to imipenem (MIC, 2 μg/ml), and was susceptible to the other carbapenems (MIC ≤ 0.5 μg/ml), tigecycline, and polymyxin B.

PCR-based screening for bla_{CTX-M}, bla_{TEM}, bla_{SHV}, bla_{IMP}, bla_{KPC}, and bla_{VIM} gave positive results for the last two of these genes, which were identified as VIM-24 and KPC-2. S1 nuclease/I-CeuI digestions and probe hybridizations (8, 9) revealed that neither gene was located chromosomally: bla_{KPC-2} was carried by two plasmids of 133 and 23 kb, while bla_{VIM-24} was harbored by a 164-kb plasmid. The genetic environment was determined using previously reported PCR mapping protocols (10–12): bla_{KPC-2} was found within a Tn*4401b*-like structure, whereas bla_{VIM-24} was found to be the first cassette of a class 1 integron, followed by *aacA7*, *catB3*, *arr-3*, and *qacE*Δ1*sulf-1* cassettes, as previously reported (10, 13). Multilocus sequence typing (MLST) performed as published at the *K. pneumoniae* MLST website (www.pasteur.fr/mlst/Kpneumoniae.html) showed that the isolate belonged to ST-20, which according to that database, has been isolated from human blood, urine, and stool samples in Germany, The Netherlands, Spain, and the United States.

This is the first report of a *K. pneumoniae* isolate coharboring bla_{VIM} and bla_{KPC} outside Europe. Given the active propagation of KPC in Colombia (13) and the results of our previous report on VIM-producing *Enterobacteriaceae* (14), the copresence of these two plasmid-encoded carbapenemases is worrisome, due to the possibility of widespread dissemination and the further limitation on therapeutic options.

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