VIM-2-Producing Pseudomonas spp. in Uruguay: Sequence Types, Pulotypos, and Class 1 Integrons Including New Variable Regions Featuring blaVIM-2 and blaGES-7

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Metallo-β-lactamase (MBL) production constitutes a global concern due to its dissemination, its wide spectrum of hydrolysis, and its association with multiple resistance determinants (1). The most frequently detected MBLs in Pseudomonas spp. correspond to VIM and IMP derivatives, usually associated with class 1 integrons (2).

We characterized the MBLs present in the P. aeruginosa and P. putida group, nonredundant clinical isolates obtained from three hospitals in Uruguay from 2011 to 2013. Two of the hospitals were located in our capital city, Montevideo, Uruguay (M1 and M2), and the remaining hospital was in Florida, Uruguay (F1), located 90 km north of the former.

Isolates were identified with the Vitek 2 system (bioMérieux), and their identities were confirmed by matrix-assisted laser desorption ionization–time of flight (MALDI-TOF) mass spectrometry (Bruker). MIC determination was performed by agar dilution and the remaining hospital was in Florida, Uruguay (F1), located 90 km north of the former.

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Pulsed-field gel electrophoresis (PFGE) analysis was performed as previously described (7), albeit using SpeI and running at 14°C with pulse times of 4 to 40 s for 20 h. Multilocus sequence typing (MLST) was performed as previously described (8). Primers trpEnF (CTGGCGGTGTTCACATGGAC) and trpEnR (TCA CGGTTCGGTACCCG) were designed for those isolates belonging to pulsotype 1.

We studied 1,202 P. aeruginosa and 59 P. putida isolates; 289/1,202 (24%) and 32/59 (54.2%), respectively, were resistant to at least one carbapenem. Furthermore, 19/289 (6.6%) and 9/32 (28.1%), respectively, displayed positive synergy tests (antibiotic resistance profiles are depicted in Fig. 1). Three P. aeruginosa isolates and one P. putida isolate could not be recovered for further analysis.

We detected three different P. aeruginosa pulotypos and seven different P. putida pulotypos, six of which were represented by a single isolate (Fig. 1). The most frequent P. aeruginosa pulotype belonged in F1 and was further typed as ST155; on the other hand, M1 and M2 yielded sequence types ST1565 (first described in this work) and ST1195 (Fig. 1). VIM-2-producing P. aeruginosa ST155 isolates have been detected in Spain (9), whereas non-MBL-producing ST155 isolates have been reported in Spain, Australia, Canada, Germany, France, and Brazil (10, 11). Our situation differs from that described in previous reports from Colombia, where VIM-2-producing P. aeruginosa strains belong mainly to ST111 (12).
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REFERENCES


