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Letter

POM-1 metallo- β -lactamase-producing *Pseudomonas* otitidis isolate from a patient with chronic otitis media^{$\frac{1}{12}$}

Sir,

Pseudomonas otitidis is a new species designated by Clark et al. (2006). Roland and Stroman (2002) reported 33 *Pseudomonas "otitidis*" otic infections in the USA. Recently, 2 isolates of *P. otitidis* were identified by molecular characterization among 104 phenotypically identified *Pseudomonas aeruginosa* isolates from otic infections in Japan (Motoshima et al., 2007). We report a case of chronic otitis media due to *P. otitidis*.

A 53-year-old man presented to a Korean hospital in 2005 with a chief complaint of ear discharge. Examination of his right ear showed erosion of the tympanic membrane with purulent discharge, and a culture yielded an isolate of Gramnegative bacilli. Treatment included oral trimethoprim–sulfamethoxazole (80–400 mg twice a day for 2 weeks), topical ofloxacin (3 mg/mL solution applied twice a day for 4 weeks), and boric acid plus carbol-fuchsin dressings for 4 weeks. The otic discharge subsided and the *P. otitidis* isolate was no longer cultivable.

Our isolate was presumptively identified as *P. aeruginosa*, but it was negative for pyocyanin and fluorescein. Species identification using ID 32 GN test strips (bioMérieux, Marcy l'Etoile, France) yielded ambiguous results: *P. aeruginosa* (ID = 1.5%). Analysis of the 16S rRNA gene sequence revealed 100% identity of our isolate (GenBank accession no. HQ615871) with the *P. otitidis* type strain (GenBank accession no. AY953147).

Susceptibility testing by the CLSI (2011) methods showed that the *P. ottitidis* isolate had an unusual susceptibility as an MBL producer, i.e., resistant to carbapenems but susceptible to piperacillin, ceftazidime, and cefepime (Table 1). MICs of piperacillin, ceftazidime, and aztreonam were slightly higher than those tested by Etest (AB bioMérieux, Solna, Sweden) (Thaller et al., 2011). The results of an imipenem-disk Hodge test and a double-disk synergy test using disks of imipenem and EDTA + sodium mercaptoacetic acid were positive, indicating production of a metallo- β -lactamase (MBL) (Lee et al., 2010), but *bla*_{IMP-1}-, *bla*_{VIM-2}-, or *bla*_{SIM-1}-like, present in Korea at that time, was not detectable by polymerase chain reaction. An investigation resulted in finding a new MBL, POM-1 (Thaller et al., 2011).

A GenBank search showed 12 isolates of P. otitidis, including the type strain and our isolate. The source of the other isolates included plant, water, and an environmental sample. Clinical microbiologists should be able to differentiate intrinsically MBL-gene possessing P. otitidis from P. aeruginosa. After 24-h incubation of a blood agar plate at 35 °C, the colonies of our P. otitidis isolate were large (mean diameter, 1.6 mm) with incomplete hemolysis. A stained smear showed slender, Gramnegative, regular bacilli similar to those of P. aeruginosa. The isolate was oxidase positive, grew at 42 °C, and oxidized glucose, but not mannose, mannitol, and xvlose. We suggest that Pseudomonas isolates with no bluegreen pigment and with unusual *β*-lactam susceptibility should be identified by analyzing the 16S rRNA gene sequence. It was suggested that detection of bla_{POM-1} could be used for identification of P. otitidis isolates (Thaller et al., 2011).

In conclusion, *P. otitidis* is difficult to identify by phenotypic tests. The organism has an intrinsic bla_{POM-1} gene, but shows unusual β -lactam susceptibilities that can potentially misguide antimicrobial therapy.

Table 1

MICs of antimicrobial agents determined by the CLSI agar dilution method for a *P. otitidis* isolate

Antimicrobial agent	MIC (µg/mL)	Susceptibility
Ampicillin	128	R ^a
Ampicillin-sulbactam	128	R ^a
Piperacillin	4	S
Cephalothin	>128	R ^a
Cefotaxime	4	R ^a
Ceftazidime	4	S
Cefepime	4	S
Aztreonam	8	S
Imipenem	>32	R
Meropenem	>32	R
Amikacin	0.5	S
Gentamicin	0.12	S
Tobramycin	0.12	S
Ciprofloxacin	1	S
Trimethoprim-sulfamethoxazole	2/38	S

R = resistant; S = susceptible.

^a Based on breakpoints for Enterobacteriaceae; others are based on breakpoints for *P. aeruginosa*.

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