Nosocomial outbreak of carbapenem-resistant *Pseudomonas aeruginosa* carrying bla_{VIM-2} in burn wards, China

Dear Editor,

We reported the outbreak of a *Pseudomonas aeruginosa* strain producing VIM-2 type MBLs in burn wards, which happened after the transfer of a patient with *P. aeruginosa* infection.

The outbreak of carbapenem-resistant *P. aeruginosa* occurred in four different burn wards of the Jilin Factory Hospital in China during the period of July to September 2006. The first carbapenem-resistant *P. aeruginosa* strain was isolated from the burn culture of a 6 year-old child at admission. The patient was transferred from a local hospital for burn injury on the leg. He had received broad-spectrum antibiotics, including ampicillin-sulbactam and piperacillin-tazobactam at the local hospital. His antibiotic was switched to impenem for pneumonia coverage, admitted to the general burn ward. After one week, blood and burn cultures yielded *P. aeruginosa* isolates susceptible only to aztreonam and he died from sepsis and multiple-organ failure soon thereafter. Subsequently, the carbapenem-resistant *P. aeruginosa* strain was recovered in seven other patients hospitalized in the general burn ward.

A total of eight clinical isolates of carbapenem-resistant *P. aeruginosa* were consecutively recovered from patients hospitalized at the burn wards. Routine antibiograms were performed by the disk diffusion method according to the guidelines of the Clinical and Laboratory Standards Institutes.[1] The resistance patterns of the eight strains are illustrated in Table 1. Among the antimicrobial agents tested, four isolates were only susceptible to ciprofloxacin and aztreonam. Metallo-β-lactamases production was evaluated using the imipenem-EDTA disk method.[2] All isolates were positive in the EDTA disc synergy test indication the presence of an MBL.

PCR analyses were performed with whole genomic DNA from all case isolates. Primers used for analysis of bla_{VIM} /bla_{IMP} genes were Vim F/R, Imp F/R respectively. PCR primers were designed and PCR conditions were performed as previously described.[3] Association of integrons with MBL genes was confirmed by PCR using combination of bla- and integron-specific primers as described previously.[4]

PCR products of bla_{VIM}/bla_{IMP} were electrophoresed on a 1.5% agarose gel. Nucleotide sequencing was performed directly on cloned fragments using an ABI Prism 377 DNA sequencer. Sequence homology was performed using the BLAST program available at the website of the National Center of Biotechnology Information.

PCR using the VIM forward and VIM reverse yielded an internal fragment of approximately 650 bp suggesting the presence of a bla_{VIM} gene, and sequencing of its PCR product was consistent with bla_{VIM-2}, while no other metallo-β-lactamases was detected. Furthermore, by combining the primer attI1 with VIM-R and attI1 with VIM-F, colinearity of bla_{VIM-2} genes with class 1 integrons was detected in all isolates.[5]

Genomic DNA, prepared as described previously and digested with SpeI was subjected to PFGE with the CHEF DRIII. Comparison of the PFGE profiles with those strains isolated in burn wards indicated that the epidemic strains were identical (data not shown).[6]

The emergence of the bla_{VIM-2} gene at the hospital was rapid, and the patients had strong epidemiological links. In addition, the bla_{VIM-2} – carrying isolates, which were recovered from the eight patients during the single hospitalization, were the same strain, suggesting a nosocomial transmission. The spreading of car-

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We declare no conflict of interest.

Table 1. Antimicrobial susceptibility patterns of MBL-producing* Pseudomonas aeruginosa *(PA) isolates

Strain No.	MIC (μg/mL)							Disc diffusion test					
	TIC	TCC	ATM	CAZ	IMP	CTX	FEP	GEN	TOB	AMK	CIP	CHL	SXT
PA 1	> 256	> 256	64	> 256	64	> 128	> 128	R	R	R	R	R	R
PA 2	> 256	> 256	64	> 256	64	> 128	> 128	R	R	R	R	R	R
PA 3	> 256	> 256	64	> 256	64	> 128	> 128	R	R	R	R	R	R
PA 4	> 256	> 256	64	> 256	64	> 128	> 128	R	R	R	R	R	R
PA 5	> 256	> 256	8	> 256	32	> 128	> 128	R	R	R	S	R	R
PA 6	> 256	> 256	8	> 256	32	> 128	> 128	R	R	R	S	R	R
PA 7	> 256	> 256	8	> 256	32	> 128	> 128	R	R	R	S	R	R
PA 8	> 256	> 256	8	> 256	32	> 128	> 128	R	R	R	S	R	R

CTX, cefotaxime; CAZ, ceftazidime; FEP, cefepime; ATM, aztreonam; IMP, imipenem; TIC, ticarcillin; TCC, ticarcillin plus clavulanic acid; CHL, chloramphenicol; GEN, gentamycin; TOB, tobramycin; AMK, amikacin; CIP, ciprofloxacin; SXT, sulfamethoxazole-trimethoprim; S, susceptible, R, resistant.

bapenem resistance, mediated by VIM-2 MBL in *P. aeruginosa* isolates in burn wards, is largely due to clonal expansion of a VIM-2-carrying strain throughout the burn wards, which was carried on a mobile gene cassette inserted into a class 1 integron located on the bacterial chromosome.

Contaminated hands of health personnel and colonized or infected patients are sources of infection. Therefore, constant glove changing between patients and proper hand sanitization should be enforced.[7]

Follow-up testing did not reveal the presence of the epidemic strains in burn wards as well as in the hospital settings studies for the following half year.

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