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# Original article

## Emergence of *Klebsiella pneumoniae* carbapenemase-producing *Proteus mirabilis* in Hangzhou, China

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**Keywords:** *enterobacteriaceae*; *proteus mirabilis*; carbapenem; *Klebsiella pneumoniae* carbapenemase

**Background** Carbapenems are used to treat severe infections caused by multi-drug-resistant organisms, however, the emergence of carbapenem-resistant bacterial isolates is becoming an increasing therapeutic challenge. Since the first *Klebsiella* (*K.*) *pneumoniae* carbapenemase (KPC)-producing *K. pneumoniae* was reported in 2001, KPC-producing isolates have been found increasingly, specially in *Enterobacteriaceae*. The aim of this study was to characterize the mechanisms of a carbapenem-resistant *Proteus* (*P.*) *mirabilis*.

**Methods** A carbapenem-resistant *P. mirabilis* isolate was recovered from pleural drainage fluid of a patient admitted to surgical intensive care unit. Antimicrobial susceptibility testing of the isolate was performed by disk diffusion according to Clinical and Laboratory Standards Institute guidelines, and subsequent minimal inhibitory concentrations were determined with the E-test. Amplification of the *bla*<sub>KPC</sub> gene generated a positive band and the PCR products were sequenced subsequently. The plasmid of the isolate was extracted and was successfully transformed into *Escherichia* (*E.*) *coli* DH5 $\alpha$ .

**Results** The *P. mirabilis* isolate was resistant to all detected antimicrobial agents except tigecycline. KPC-2 was confirmed by DNA sequence analysis. The transformant *E. coli* was resistant to carbapenems. Further study demonstrated that upstream and downstream regions of *bla*<sub>KPC-2</sub> were identical to that observed in *K. pneumoniae* submitted to GenBank from China in 2007.

**Conclusion** Carbapenem resistance in the *P. mirabilis* isolate in this study is mainly due to production of KPC-2.

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Carbapenems are used to treat severe infections caused by multi-drug-resistant organisms, especially by extended-spectrum  $\beta$ -lactamase-producing pathogens. However, the emergence of carbapenemase is becoming an increasing therapeutic challenge because this enzyme hydrolyzes not only carpaenems but also penicillins, cephalosporins, and monobactams.<sup>1</sup> The carpaenem-resistant *Klebsiella* (*K.*) *pneumoniae* was first reported to produce *K. pneumoniae* carbapenemase (KPC)-1 in US in 2001. Since then, KPC-type  $\beta$ -lactamases have been found in *Klebsiella oxytoca*,<sup>2</sup> *Escherichia coil* (*E. coli*),<sup>3</sup> *Citrobater spp.*,<sup>4</sup> *Pseudomonas aeruginosa*,<sup>5</sup> *Salmonella spp.*,<sup>6</sup> *Serratia marcescens*,<sup>4</sup> as well as *Proteus mirabilis* (*P. mirabilis*).<sup>7</sup>

*P. mirabilis* are clinical isolates which barely have  $\beta$ -lactamase activity under usual growth conditions. However, carbapenem resistance in *Proteus spp.* mediated by OXA-23 (a class D  $\beta$ -lactamase) and VIM-1 (a class B metallo- $\beta$ -lactamase) has been identified.<sup>7</sup> Changes in penicillin-binding proteins or outer membrane proteins could result in carbapenem resistance in *Proteus pp.*<sup>8,9</sup> Carbapenem resistance in *P. mirabilis* caused by a class A  $\beta$ -lactamase, KPC-2, firstly reported by Tibbetts et al<sup>7</sup> in 2008. In this study, we characterized a clinical carbapenem-resistant isolate of *P. mirabilis* carrying *bla*<sub>KPC-2</sub> gene in Hangzhou, China.

### METHODS

#### Bacterial strains

In December 2009, a carbapenem-resistant *P. mirabilis*

strain BP1 was isolated from pleural drainage fluid of a patient with esophageal carcinoma, in surgical intensive care unite (SICU) in the First Affiliated Hospital of Zhejiang University (Hangzhou, China). Prior to the isolation, the patient was repeatedly treated with antimicrobial agents including penicillins, cephalosporins, carbapenems, and aminoglycosides for 2 months. The isolate was identified with the Vitek-2 system (bioMe'rieux, France).

#### Antimicrobial susceptibility testing

Antimicrobial susceptibility of *P. mirabilis* BP1 was assayed using disk diffusion according to guidelines of Clinical and Laboratory Standards Institute.<sup>10</sup> *E. coli* ATCC 25922 and *E. coli* DH5 $\alpha$  were used as quality control in the assay.

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### PCR amplification for *bla* genes

The primers used to amplify *bla*<sub>KPC</sub>, *bla*<sub>TEM</sub>, *bla*<sub>SHV</sub>, *bla*<sub>IMP-1</sub>, *bla*<sub>IMP-2</sub>, *bla*<sub>VIM-1</sub>, *bla*<sub>VIM-2</sub>, *bla*<sub>SPM-1</sub> were described previously.<sup>11,12</sup> Prepared bacterial DNA of the *P. mirabilis* BP1 was used as the template for PCR amplifications.

### Conjugal transfer experiment and analysis of plasmid

The conjugation experiment was carried out in mixed broth cultures and rifampicin-resistant *E. coli* 600 was used as the recipient strain. Plasmids of *P. mirabilis* BP1 were prepared with a QIAprep Spin Miniprep Kit (QIAGEN, Hilden, Germany) according to the manufacturer's protocol. The plasmids were transformed into competent *E. coli* DH5 $\alpha$ . The transformants, *E. coli* BP001T, were selected on a Mueller-Hinton Agar (MHA) plate containing 1  $\mu$ g/ml of meropenem. *E. coli* BP1 T contained a plasmid with the size greater than 50 kb (data not shown). Amplification of *bla*<sub>KPC</sub> gene of the *E. coli* BP1T by PCR with the same primer described above was positive. Additional antimicrobial susceptibilities of the *P. mirabilis* BP1 and *E. coli* BP1T were assayed by E-test (AB Biodisk, Solna, Sweden).

## RESULTS

*P. mirabilis* BP1 was resistant to all the tested agents. The presence of *bla*<sub>KPC</sub> was confirmed while the other *bla* genes mentioned above were not detected. And the DNA sequencing of the PCR products identified the gene as *KPC-2*.

The conjugation experiments failed. DNA sequencing analysis of *KPC-2* and its adjacent regions was performed using traditional Sanger method. An approximately 3-kb fragment including *bla*<sub>KPC</sub> gene was analyzed by sequencing. Subsequent BLAST search showed that the *KPC-2* gene in this study had 100% identity at the nucleic acid level with the *KPC-2* gene sequence submitted to GenBank from Hangzhou, China (GenBank accession number DQ897687). Furthermore, the regions flanking *bla*<sub>KPC-2</sub> in *P. mirabilis* BP1 were identical to that observed in *K. pneumoniae* by Wei et al in China.<sup>13</sup> Minimal inhibitory concentrations of *E. coli* BP1T were lower than those for *P. mirabilis* BP1 (Table). This may contribute to the mutation of porins which results in the decreased membrane permeability.

In addition, because a prospective study on the relationship between gut flora and nosocomial infection pathogens was performing in our laboratory, the carpaenem-resistant isolates of *P. mirabilis* were also found in fecal specimens of the patient in the week the *P. mirabilis* BP1 was isolated from pleural drainage fluid.

## DISCUSSION

In this study, we described a clinical *KPC-2*-positive *P. mirabilis* isolate in China. Reports on carpaenem-resistant

**Table.** Minimal inhibitory concentrations ( $\mu$ g/ml) of *P. mirabilis* BP1, *E. coli* BP1T, and *E. coli* DH5 $\alpha$

Antimicrobial agents	<i>P. mirabilis</i> BP1 (parent)	<i>E. coli</i> BP1T (transformant)	<i>E. coli</i> DH5 $\alpha$ (host strain)
Imipenem	$\geq 32$	12	0.125
Ertapenem	$\geq 32$	4	0.016
Meropenem	8	6	0.016
Aztreonam	$\geq 256$	$\geq 256$	0.023
Ampicillin	$\geq 256$	$\geq 256$	2.000
Cefotaxime	$\geq 32$	$\geq 32$	0.125
Cefepime	24	16	0.023
Gentamicin	4	0.380	0.380
Amikacin	2	0.750	0.750
Ciprofloxacin	12	0.023	0.023
Colistin E	$\geq 256$	0.750	0.750
Tigecycline	1.500	0.250	0.190

microbes carrying *bla*<sub>KPC</sub> gene have been increasing,<sup>14,15</sup> since the initial discovery of KPC-producing *K. pneumoniae* in China.<sup>13</sup> This may contribute to the wide use of carpaenems and cephalosporins. In addition, what alarming is that several infections caused by KPC-producing *K. pneumoniae*, *E. coli*, *Enterobacter cloacae*, and *P. aeruginosa* have occurred during the past 6 months in the hospital (data unpublished). Because there is potential prevalence for those KPC-positive bacteria in the clinic, further study on the epidemiological relationship between these organisms is needed.

It has already been known that higher mortality rates associated with infection were caused by *bla*<sub>KPC</sub>-carrying bacteria.<sup>16</sup> Therefore, it is essential to establish strict resistance surveillance and drug administration for avoiding the epidemic KPC-producing organisms in this country.

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