In vitro antibacterial effect of fosfomycin combination therapy against colistin-resistant Klebsiella pneumoniae

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Objectives: Colistin is still a “last-resort” antibiotic used to manage human infections due to multidrug-resistant (MDR) Klebsiella pneumoniae. However, colistin-resistant K. pneumoniae (CR-Kp) isolates emerged a decade ago and had a worldwide distribution. The purpose of this study was to evaluate the genetic data of CR-Kp and identify the antibacterial activity of fosfomycin (FM) alone and in combination with amikacin (AMK) or colistin (COL) against CR-Kp in vitro.

Methods: Three clinical CR-Kp isolates from three patients were collected. Whole-genome sequencing and bioinformatics analysis were performed. The Pharmacokinetics Auto Simulation System 400, by simulating human pharmacokinetics in vitro, was employed to simulate FM, AMK, and COL alone and in combination. Different pharmacodynamic parameters were calculated for determining the antimicrobial effect.

Results: Whole-genome sequencing revealed that none of the three isolates contain mcr gene and that no insertion was found in pmrAB, phoPQ, or mprB genes. We found the antibacterial activity of AMK alone was more efficient than FM or COL against CR-Kp. The area between the control growth and antibacterial killing curves of FM (8 g every 8 hours) combined with AMK (15 mg/kg once daily) was higher than 170 LogCFU/mL·h⁻¹. In addition, the area between the control growth and antibacterial killing curves of FM (8 g every 8 hours) combined with COL (75,000 IU/kg every 12 hours) was higher than that of monotherapies (>100 LogCFU/mL·h⁻¹ vs <80 LogCFU/mL·h⁻¹).

Conclusion: FM (8 g every 8 hours) combined with AMK (15 mg/kg once daily) was effective at maximizing bacterial killing against CR-Kp.

Keywords: Pharmacokinetics, pharmacodynamics, monotherapy, combination therapy, colistin-resistant Klebsiella pneumoniae

Introduction
The continuing worldwide emergence of multidrug-resistant Enterobacteriaceae, especially carbapenem-resistant and/or tigecycline-resistant isolates, is becoming an urgent public health threat.1,2 Polymyxin, one of the last resorts in the treatment of multidrug-resistant Gram-negative bacteria, is an old antibacterial drug that was recently reintroduced in human medicine. Polymyxin E (colistin) is used most widely and interacts with anionic lipopolysaccharide (LPS) molecules and covalently bonds to a fatty acid chain to enhance antimicrobial activity against Gram-negative bacteria.3

Klebsiella pneumoniae, a major concern in the clinic, causes a wide range of infections, from urinary tract infections to pneumonia. Highly resistant K. pneumoniae is emerging worldwide and has become an urgent public health threat. Colistin-resistant
K. pneumoniae (CR-Kp) was reported not only on account of the plasmid-mediated colistin resistance gene – mcr – but also due to chromosome mutation of the related genes mgrB or the PmrAB and PhoPQ two-component systems.4–6 MgrB alteration is a common resistance mechanism of colistin among KPC-producing K. pneumoniae (KPC-Kp).5 PmrAB and PhoPQ two-component systems, which are associated with lipopolysaccharide (LPS) modification, play a significant regulatory role in colistin resistance among K. pneumoniae isolates.6

Therapeutic options for multidrug-resistant (MDR) K. pneumoniae are extremely limited, a situation made worse by exhaustion of new drug development for anti-infective agents. Combination therapy is gaining increasing attention to combat the MDR K. pneumonia due to the synergistic effect and breadth of the antibacterial spectrum.7 However, robust evidence of antimicrobial combination therapy used in clinical practice due to CR-Kp infections is lacking. Our previous studies indicated that fosfomycin (FM) enhanced the antibacterial activity of imipenem, ertapenem, tigecycline, colistin (COL), and amikacin (AMK) against 136 KPC-Kp strains, and further in vitro pharmacokinetics/pharmacodynamics (PK/PD) evaluation showed the combination of FM plus AMK or COL tended to show more prominent bacterialidal effect and suppressed the emergence of resistance.8,9 Hence, in this study, the genetic data of CR-Kp were investigated and human drug metabolism of FM, AMK, and COL alone and in combination against CR-Kp infections were simulated in vitro.

Methods

Bacterial strains and antibiotic susceptibility test

Three clinical CR-Kp strains were used in this study, including 2887, 3155, and 18253, recovered from urine, sputum, and blood, respectively, as part of routine hospital laboratory procedure.

The antimicrobial susceptibility testing of isolates was determined using Mueller–Hinton agar dilution for 21 antibiotics according to the Clinical and Laboratory Standards Institute guidelines.10 Escherichia coli ATCC 25922 and Pseudomonas aeruginosa ATCC27853 were used as reference isolates.

Whole-genome sequencing (WGS) and data analysis

WGS was carried out for the three CR-Kp, with further analyses of gene–environment interaction. Genomic DNA was extracted using the QIAamp DNA Mini Kit (Qiagen, Hilden, Germany) and sequenced using HiSeq 2000 (Illumina, San Diego, CA, USA) by constructing 2×125 bp pair-end libraries. De novo assembly was done using the CLC Workbench v8.0 (QIAGEN). The resistance genes were identified with BLASTn against the ResFinder 2.1 database (https://www.genome.jp/databases/ResFinder). The bioinformatics tools used in this study are available on the following web platforms: National Center for Biotechnological Information, Sequence Manipulation Suite, and European Bioinformatics Institute.

This Whole-Genome Shotgun BioProject for the three CR-Kp has been deposited at GenBank under the accession numbers NRJC00000000, NRJD00000000, and NRJE00000000.

Antibiotic dosing

The human serum concentrations of FM, AMK, and COL were referenced based on previous PK data (Table S1 shows the PK parameters of three drugs and Figure S1 shows the simulated time–concentration curves).11–13 The following regimens were simulated over 24 hours: FM 8 g every 8 hours (FM 8 g q8h),11 AMK 15 mg/kg once daily (AMK 15 mg/kg qd),12 COL 75,000 IU/kg every 12 hours (COL 75,000 IU/kg q12h),13 FM (8 g q8h)/AMK (15 mg/kg qd), and FM (8 g q8h)/COL (75,000 IU/kg q12h).

In vitro PK model and PD analysis

The dynamic model of human PK simulation in vitro was performed using the Pharmacokinetics Auto Simulation System 400 (PASS 400), a product of Dainippon Seiki (Kyoto, Japan) (as shown in Figure S2). The working mechanism and PD parameter calculations were performed as previously described.9

A two-compartment model was used for all experiments. Growth curves without antibiotic were regarded as control. There were 1.5 mL samples collected for CFU determination at predetermined time points (0, 1, 2, 4, 6, 8, 10, 12, 14, 17, 20, and 24 hours) and diluted with 0.9% normal saline before plating on Mueller–Hinton agar plates. All counting plates were incubated at 37°C overnight. The limit of detection was 30–300 colonies. Each dosing regimen was simulated in triplicate.

A total of 13 PD parameters were calculated, including maximum kill down, maximum kill time, area above kill curve, bacterial growth recovery time (RT), –1Log kill time, –2Log kill time, –3Log kill time, regrowth recovery time (SRT), +1Log growth time, Total –1Log kill time, Total –2Log kill time, Total –3Log kill time, and the area between the control growth and antibacterial killing curves (IE). One
Characteristics and treatment of CR-Kp

Diagram is provided as an illustration to help understand the relationship between different PD parameters (Figure 1). RT and IE were regarded as the most comprehensive parameters for determining the antibacterial activity.14

Results
Antibiotic susceptibility test and drug-resistant characteristics
Antimicrobial susceptibilities for the three CR-Kp isolates are presented in Table 1. All isolates were resistant to COL with high minimum inhibitory concentration (MIC) level (＞32 mg/L). Isolate 18253 was multidrug resistant. Isolate 2887 was resistant to trimethoprim–sulfamethoxazole and 3155 was resistant to piperacillin–tazobactam, while both isolates were susceptible to other test antibiotics. WGS of these three COL-resistant isolates indicated that they all had β-lactamase genes (Table 1). Isolate 2887 contains blaSHV-11 and blaSHV-75. Isolate 3155 contains blaSHV-28, while isolate 18253 contains blaSHV-11, blaSHV-12, and blaKPC-2. WGS also revealed that none of the three isolates contained the mcr gene. In addition, no insertion was found in pmrAB, phoPQ, or mgrB genes. Other mechanisms of COL resistance of these isolates are conceivable.

Time–kill antibacterial effect
The time–kill assays showed that the antibacterial activity of FM/AMK or FM/COL combination was superior to monotherapies against CR-Kp, while regrowth was found as well (Figure 2). AMK monotherapy showed more antibacterial effect than FM and COL. It is of note that FM (8 g q8h) alone had little discernible bactericidal effect.

For AMK monotherapy, increasing MIC showed less bactericidal effects against susceptible strains (Figure 2A, C, and E). However, FM/AMK combination enhanced the bactericidal effect, resulting in substantial improvements in bacterial killing (up to >5 Log10 CFU/mL) over 24 hours for 2887 (Figure 2A). Also, this combination reduced the population of 3155 and 18253 to >3 Log10 CFU/mL compared with the initial count at 14 hours (Figure 2C and E). Thus, FM/AMK was the most potent combination against both test strains.

FM/COL demonstrated synergistic activity as well, although the three isolates were COL resistant. It is noteworthy that more rapid bacterial killing activity was observed for the combination of FM (8 g q8h)/COL (75,000 IU/kg q12h) against CR-Kp than FM and COL monotherapies (Figure 2B, D, and F). FM/COL combination resulted in a reduction in bacterial count >3 Log10 CFU/mL against 3155 at 24 hours.

PD parameters of different dosages against CR-Kp
The PD parameters were calculated using the built-in Analyze Bactericidal Activity software of PASS 400 (Table 2). In the FM (8 g q8h) monotherapy time–kill assays, RT of 2887 and

Figure 1 The sketch of PD parameters.

Abbreviations: –1KT, –1Log kill time; –2KT, –2Log kill time; –3KT, –3Log kill time; SRT, regrowth recovery time; +1RT, +1Log growth time; AAKC, area above kill curve; AST, analysis start time; MKD, maximum kill down; MKT, maximum kill time; PD, pharmacodynamics; RT, bacterial growth recovery time; TAAKC, total area above kill curve; T–1KT, total –1Log kill time.
In this study, three CR-Kp with high MIC level (>32 mg/L) were selected to evaluate the effect of FM, AMK, and COL monotherapies. AMK (15 mg/kg qd) monotherapy showed longer RT (>16 hours) and –3Log Kill Time T (>12 hours), higher maximum kill down (>6 LogCFU/mL), and larger IE (>130 LogCFU/mL·h⁻¹). Although the three strains were resistant to COL, IE of FM/COL combination was still greater than 100 LogCFU/mL·h⁻¹ and RT exceeded 13.8 hours. Importantly, the IEs of FM (8 g q8h)/AMK (15 mg/kg qd) against 2887, 3155, and 18253 were 219.9, 201.1, and 173.72 LogCFU/mL·h⁻¹, respectively.

**Discussion**

In order to counteract the COL-resistant strains, recent studies have shifted to studying drugs in combination. As previously reported, COL alone or in combination in the study showed rapid killing activity during the first hour in the time–kill experiments, but subsequent regrowth was observed in most combinations. Against COL-susceptible KPC-Kp strains, FM/COL combination was shown to be synergistic in chequerboards and time–kill experiments. The same was true for hollow-fiber infection model experiments and the dynamic model of PASS 400 simulation. Michalopoulos et al demonstrated that intravenous administered FM/COL had better bacteriological and clinical outcome for six patients with carbapenem-resistant *K. pneumoniae*.
In this study, FM/COL combination showed more rapid bacterial killing than monotherapies, consistent with our previous reports.\(^8\)\(^,\)\(^18\) FM/COL combination prolonged the time of antibacterial effect, but unfortunately, regrowth was still present against CR-Kp isolates. Although the IE of FM/COL combination was still greater than 100 LogCFU/mL h\(^{-1}\) for CR-Kp isolates, it was still significantly lower compared to COL-susceptible strains (>200 LogCFU/mL h\(^{-1}\)).\(^5\) This may be associated with the synergistic mechanism of COL permeabilizing the outer bacterial membrane.

In the present study, the bacterial killing of AMK monotherapy at 10 hours was almost similar to FM/AMK
Table 2 PD parameters of different regimens against the three KPC-producing Klebsiella pneumonia

<table>
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<tr>
<th>Isolates</th>
<th>Dosage regimen</th>
<th>MKD (ΔLogCFU/mL)</th>
<th>MKT (h)</th>
<th>AAKC (ΔLogCFU/mL)</th>
<th>RT (h)</th>
<th>–1KT (h)</th>
<th>–2KT (h)</th>
<th>–3KT (h)</th>
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<th>T–2KT (h)</th>
<th>T–3KT (h)</th>
<th>IE (LogCFU/mL h⁻¹)</th>
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<td>9.1</td>
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<td>2.4</td>
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<td>NA</td>
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<td>8.5</td>
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<td>NA</td>
<td>NA</td>
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<td>11.16</td>
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Abbreviations: –1KT, –1Log kill time; –2KT, –2Log kill time; –3KT, –3Log kill time; +1RT, +1Log growth time; AAKC, area above kill curve; AMK, amikacin; COL, colistin; FM, fosfomycin; MKD, maximum kill down; MKT, maximum kill time; IE, the area between the control growth and antibacterial killing curves; NA, Not Applicable; PD, pharmacodynamics; q8h, every 8 hours; q12h, every 12 hours; qd, once daily; RT, bacterial growth recovery time; SRT, regrowth recovery time; T–1KT, Total –1Log Kill Time; T–2KT, Total –2Log Kill Time; T–3KT, Total –3Log Kill Time.
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Author contributions
WY and QXL developed the concept and designed the experiments. WY, QXL, CH, and XY performed the experiments. QXL, TSN, and KZ performed statistical analysis. WY gave conceptual advice. WY and QXL wrote the paper. All authors discussed the results and implications and commented on the manuscript at all stages. All authors contributed toward data analysis, drafting and critically revising the paper and agree to be accountable for all aspects of the work.

Disclosure
The authors report no conflicts of interest in this work.

References
Supplementary materials

Figure S1 (A–F) The time–concentration curves of antibiotics in the Pharmacokinetics Auto Simulation System 400.

Abbreviations: FM, fosfomycin; AMK, amikacin, COL, colistin; q8h, every 8 hours; q12h, every 12 hours; qd, once daily.

Figure S2 Pharmacokinetics Auto Simulation System 400.

Table S1 PK parameters of different regimens

<table>
<thead>
<tr>
<th>Regimens (11–13)</th>
<th>t1/2(β) (h)</th>
<th>AUC (mg h/L)</th>
<th>CL (mL/min)</th>
<th>V (L)</th>
<th>Cmax (mg/L)</th>
</tr>
</thead>
<tbody>
<tr>
<td>AMK 15 mg/kg once daily</td>
<td>2.4±0.5</td>
<td>154.5±29.9</td>
<td>112.8±9.2</td>
<td>11.2±1.8</td>
<td>76</td>
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<tr>
<td>COL 2.5 mg/kg every 12 hours</td>
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<td>17.6±8.80</td>
<td>10.5±4.1</td>
<td>94.9±30.2</td>
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<tr>
<td>FM 8 g every 8 hours</td>
<td>3.7±2.2</td>
<td>1,330±609</td>
<td>126±68</td>
<td>28.6±9.9</td>
<td>443.6</td>
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</table>

Note: Data presented as mean ± SD.

Abbreviations: AMK, amikacin; AUC, area under the plasma concentration–time curve; Cmax, maximum plasma concentrations; CL, body clearance; COL, colistin; FM, fosfomycin; t1/2, elimination half-life; PK, pharmacokinetics; V, volume of distribution.