Clinical exposure–response relationship of cefepime/taniborbactam against Gram-negative organisms in the murine complicated urinary tract infection model

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Objectives: Complicated urinary tract infections (cUTIs) are frequently encountered in hospitals and ICUs. Increasingly, the causative pathogens harbour enzymatic resistance mechanisms. Taniborbactam is a novel β -lactamase inhibitor with activity against Ambler class A, B, C and D β -lactamases. Herein, we assessed the efficacy of cefepime alone and the combination cefepime/taniborbactam in a neutropenic murine cUTI model.

Methods: Eighteen cefepime-resistant clinical isolates (9 Enterobacterales, 3 Pseudomonas aeruginosa and 6 Stenotrophomonas maltophilia; cefepime MIC = 32 to >512 mg/L) were assessed. Cefepime/taniborbactam MICs ranged from 0.06 to 128 mg/L. Human-simulated plasma regimens (HSRs) of cefepime alone and in combination with taniborbactam were developed in the murine cUTI model. The efficacy of cefepime HSR and cefepime/taniborbactam HSR was determined as the change in log_{10} cfu/kidney at 48 h compared with 48 h controls.

Results: Mean \pm SD initial bacterial burden was $5.66 \pm 0.56 \log_{10}$ cfu/kidney, which increased to $9.05 \pm 0.39 \log_{10}$ cfu/kidney at 48 h. The cefepime HSR was ineffective, as bacterial burden was similar to untreated controls $(-0.14 \pm 0.40 \text{ change in } \log_{10} \text{cfu/kidney})$. In contrast, cefepime/taniborbactam exhibited substantial killing, with log_{10} cfu/kidney changes of -5.48 ± 1.3 , -4.79 ± 0.3 and -5.04 ± 0.7 for ESBL/AmpC-, KPC- and OXA-48harbouring Enterobacterales, respectively. Cefepime/taniborbactam also exhibited robust killing of P. aeruginosa (-6.5 ± 0.26) and S. maltophilia (-5.66 ± 0.71).

Conclusions: Humanized exposures of cefepime/taniborbactam achieved robust killing of Enterobacterales, P. aeruginosa and S. maltophilia harbouring ESBL, AmpC, KPC and/or OXA-48. These data support the role of cefepime/taniborbactam for cUTI treatment for cefepime/taniborbactam MICs up to 32 mg/L.

Introduction

Urinary tract infections (UTIs) continue to be one of the most common bacterial diseases globally, resulting in substantial clinical and financial burden among outpatients and hospitalized patients.^{1–3} β -Lactam antibiotics are an important option for treating bacterial infections, including UTIs, due to their wellestablished safety profile and effectiveness; however, the rising incidence of β -lactamase-harbouring pathogens is reducing the clinical utility of these agents. $4,5$ Taniborbactam is a novel cyclic boronic acid-based β -lactamase inhibitor with potent in vitro activity against many clinically relevant Ambler class A, C and D β -lactamases and select class B MBLs (e.g. NDM and VIM). $6-8$ Taniborbactam is being developed in combination with cefepime as a broad-spectrum option for the treatment of serious Gramnegative infections and is currently being evaluated for safety and efficacy in a Phase III randomized complicated UTI (cUTI), includ-ing acute pyelonephritis, clinical trial (NCT03840148).^{6,[9](#page-4-0)}

In the preclinical arena, the evaluation of dose–response relationships in a variety of infection types (thigh, lung, kidney and sepsis animal models) using clinically relevant exposures has been instrumental for bridging in vitro data to clinical efficacy. To that end, this study sought to develop a human-simulated exposure of cefepime/taniborbactam in the neutropenic murine complicated kidney infection model and assess in vivo efficacy against a variety of clinical isolates.

Methods

Ethics

All murine experiments were conducted in concordance with the National Research Council of the National Academy of Sciences standards. The

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protocol was approved by the Institutional Animal Care and Use Committee of Hartford Hospital (Assurance #A3185-01).

Isolates and antimicrobial susceptibility testing

Eighteen clinical isolates [9 Enterobacterales and 9 non-fermenting Gramnegative pathogens (Pseudomonas aeruginosa and Stenotrophomonas maltophilia)] were included in this study. Respective isolate genotypes are provided in Table 1. Enterobacterales isolates harboured acquired AmpC, KPC or OXA-48/OXA-48-like enzymes, while P. aeruginosa isolates harboured acquired AmpC or KPC. Notably, two isolates (EC 773 and EC 774) had 4 amino acid insertions in PBP3 (the target of cefepime), in addition to b-lactamase-mediated resistance. WGS analysis was performed using Geneious Prime version 2021.1.1 (Biomatters Inc., CA, USA). DNA extraction, Illumina library preparation and raw WGS data from Illumina HiSeq 2×150 bp were provided by Genewiz (NJ, USA).

Cefepime, cefepime/taniborbactam, meropenem/vaborbactam and ceftazidime/avibactam MICs were determined in at least triplicate by broth microdilution.^{10,11}

Neutropenic cUTI model

Female, specific-pathogen-free, CD-1 mice (weight = 20–22 g) were obtained from Charles River Laboratories, Inc. (NC, USA). All animals were allowed to acclimatize for 48 h. During acclimatization, animals were housed in groups of six mice at controlled room temperature in HEPAfiltered cages (Innovive, CA, USA). Cages were supplemented with nesting material for enrichment purposes. Study rooms were maintained with diurnal cycles (12 h light/12 h dark). Food and water was provided ad libitum. Monitoring was conducted at least three times per day for signs of morbidity. A 48h cUTI model using a direct kidney inoculation technique was conducted as previously described (Figure [S1,](https://academic.oup.com/jac/article-lookup/doi/10.1093/jac/dkab405#supplementary-data) available as [Supplementary](https://academic.oup.com/jac/article-lookup/doi/10.1093/jac/dkab405#supplementary-data) [data](https://academic.oup.com/jac/article-lookup/doi/10.1093/jac/dkab405#supplementary-data) at JAC Online).^{12,13}

Pharmacokinetic studies

Dosing regimens were developed that resulted in murine exposures similar to Phase I healthy volunteer mean plasma exposures of cefepime 2 g administered over 2 h every 8 h and cefepime/taniborbactam 2/0.5 g administered over 2 h every $8 h¹⁴$ To guide regimen development, 48 h pharmacokinetic studies ($n = 4$ studies) of cefepime (6.5 ma/kg at 0 h and 3.5 mg/kg q8h thereafter; 8 mg/kg at 0 h and 4.5 mg/kg q8h thereafter; 10 mg/kg at 0 h and 5.5 mg/kg q8h thereafter; and 15 mg/kg at 0 h and 7.5 mg/kg q8h thereafter) were conducted in the cUTI model. Similarly, pharmacokinetic studies ($n = 2$) with concomitant administration of cefepime and taniborbactam (i.e. cefepime/taniborbactam) were conducted: (10/5 mg/kg at 0 h and 5.5/2.5 mg/kg q8h thereafter; and 15/7.5 mg/kg at 0 h and 7.5/3.75 mg/kg q8h thereafter). Blood was collected at eight sampling points over a 48 h period (1, 2, 4, 7.5, 25, 26, 28 and 31.5 h) by cardiac puncture following $CO₂$ asphyxiation. Blood samples were placed in K₂EDTA vials and centrifuged at 10000 rpm for 10 min at 8°C. Plasma samples were collected and stored at -80°C until drug concentration analysis.

Cefepime and taniborbactam concentrations were analysed using a qualified LC-MS/MS method (AB SCIEX Triple Quad™ 5500 System, Keystone Bioanalytical, PA, USA). Intra-batch precision (coefficient of variation) and accuracy (relative error) for all quality control (QC) plasma samples for both cefepime and taniborbactam ranged from 3.18% to 5.05% and -8.14% to 7.15%, respectively. Inter-batch precision and accuracy for all QC plasma samples for both compounds ranged from 3.88% to 9.21% and $-4.83%$ to 4.02%, respectively. Pharmacokinetic parameters were calculated and regimens were simulated using Phoenix 64 (WinNonlin 6.4; Pharsight Corp., CA, USA). Human and murine drug concentrations were

Table 1. Isolates included in neutropenic murine direct kidney infection model studies and corresponding MICs of tested agents (in mg/L)

EC, Escherichia coli; KP, Klebsiella pneumoniae; ECL, Enterobacter cloacae; PSA, Pseudomonas aeruginosa; STM, Stenotrophomonas maltophilia. ^a α No additional β -lactamase detected by WGS and genome analysis.

bBroth microdilution conducted at International Health Management Association (IHMA).

^cBroth microdilution reported by the Centers for Disease Control (CDC).

corrected for cefepime (humans, 20%; mice, 0%) and taniborbactam (humans, 0%; mice, 19.4%) protein binding[.15](#page-4-0)

In vivo efficacy studies

Three hours after inoculation, one group of six mice was sacrificed via $CO₂$ asphyxiation followed by cervical dislocation and their kidneys ($n = 12$) harvested aseptically (0 h control group). The remaining groups (six mice per group) were administered one of the following interventions: vehicle (saline), cefepime human-simulated plasma regimen (HSR) or cefepime/ taniborbactam HSR. After 48 h of treatment, the mice were sacrificed and their kidneys were harvested aseptically. All kidneys were homogenized in 0.9% normal saline and serially diluted onto 5% sheep's blood agar plates and incubated overnight for enumeration. For consistency with previous murine cUTI studies, $12,13$ efficacy was assessed by the change in log₁₀ cfu/kidney from 48 h controls and reported as mean ± SD. To compare antimicrobial efficacy between cefepime and cefepime/taniborbactam, a Student's t-test was used and a P value \leq 0.05 was considered statistically significantly different.

Results

All isolates were cefepime resistant and cefepime/taniborbactam MICs ranged from 0.06 to 128 mg/L (Table [1\)](#page-1-0). Ceftazidime/avibactam and meropenem/vaborbactam MICs ranged from 1 to >128 mg/L and \leq 0.06 to >64 mg/L, respectively, spanning their clinical breakpoints.

Pharmacokinetic studies

A one-compartment model was used to fit the data (Table [S1\)](https://academic.oup.com/jac/article-lookup/doi/10.1093/jac/dkab405#supplementary-data). The cefepime and cefepime/taniborbactam combination murine concentration–time profiles, as well as % f 7>MIC and f AUC_{0–8} values, were comparable to the human profiles (Figure [S2](https://academic.oup.com/jac/article-lookup/doi/10.1093/jac/dkab405#supplementary-data) and Table [S2\)](https://academic.oup.com/jac/article-lookup/doi/10.1093/jac/dkab405#supplementary-data). When the cefepime and taniborbactam murine HSRs were administered concomitantly, cefepime elimination was enhanced and the plasma exposure was observed to be slightly reduced, which necessitated a cefepime dose modification for animals receiving the combination, in order to attain the target human plasma exposure. As a result, the cefepime HSR dosing regimen was as follows: 8 mg/kg at 0 h followed by 4.5 mg/kg every 8 h. For the combination HSR therapy, the cefepime doses utilized were: 15 mg/kg at 0 h followed by 7.5 mg/kg every 8 h thereafter when co-administered with taniborbactam (7.5 mg/kg at 0 h followed by 3.75 mg/kg every 8 h thereafter).

In vivo efficacy studies

Enterobacterales

A composite graph of in vivo efficacy in Enterobacterales ($n = 9$ isolates; cefepime/taniborbactam MIC range = 0.06–16 mg/L) is presented in Figure $1(a)$ $1(a)$ (Figure $S3$). The average bacterial density was 5.67 ± 0.59 log₁₀ cfu/kidney at 0 h, increasing to 9.16 ± 0.29 log_{10} cfu/kidney in untreated control animals after 48 h. Among all Enterobacterales isolates evaluated, cefepime/taniborbactam resulted in a statistically significant bacterial density reduction $(P< 0.001)$, i.e. >4 log₁₀ cfu/kidney reduction compared with 48 h controls. In addition, cefepime/taniborbactam exhibited profound average $-4.79 \pm 0.94 \log_{10}$ cfu/kidney reduction against the two isolates of Escherichia coli with OXA-48/OXA-48-like blactamases, ESBLs and PBP3 variants associated with an elevated cefepime MIC.^{[16](#page-4-0)}

Non-fermenting Gram-negative bacteria

More profound cefepime/taniborbactam activity was observed amongst the non-fermenting isolates (Figure [1](#page-3-0)b and Figure [S3\)](https://academic.oup.com/jac/article-lookup/doi/10.1093/jac/dkab405#supplementary-data). Cefepime/taniborbactam resulted in an average bacterial burden change of -6.50 ± 0.26 log₁₀ cfu/kidney among all P. aeruginosa isolates (MIC range = $4-16$ mg/L) ($P < 0.001$). For five out of the six S. maltophilia isolates studied (cefepime/taniborbactam MIC range = 1–32 mg/L), cefepime/taniborbactam resulted in an average bacterial burden reduction of -6.47 ± 0.65 log₁₀ cfu/kidney (P < 0.001). Against S. maltophilia isolate STM 111 (MIC = 128 mg/ L), cefepime/taniborbactam resulted in expectedly poor activity relative to 48h controls given its cefepime concentration-time profile (f T>MIC₁₂₈ = 0%).

Discussion

The ability of taniborbactam to prevent cefepime degradation via reversible covalent inhibition of a variety of clinically relevant serine b-lactamases influenced the isolates and genotypes selected for evaluation in this current animal study. Using clinical exposures of cefepime and taniborbactam, this study demonstrated the enhanced efficacy of this novel β -lactam/ β -lactamase inhibitor combination against a variety of cefepime-resistant Gram-negative bacteria harbouring a range of enzyme (ESBL, AmpC, KPC and OXA-48/OXA-48-like)- and cefepime target (PBP3 insertion) mediated resistance mechanisms in the neutropenic murine cUTI infection model.

Bacterial killing with cefepime/taniborbactam was observed among cefepime-resistant Enterobacterales, P. aeruginosa and S. maltophilia clinical isolates with cefepime/taniborbactam MICs \leq 32 mg/L. This finding is likely due to the optimization of the β -lactam backbone [i.e. maximum approved cefepime dose (2 g q8h) and prolonged infusion regimen (2 h)] and taniborbactam's high potency of β -lactamase inhibition.¹⁵ Notably, the observed bacterial growth (i.e. therapeutic failure of the cefepime/taniborbactam HSR) with the S. maltophilia isolate having an elevated cefepime/ taniborbactam MIC (128 mg/L) further validates the UTI model as it demonstrates strong correlation between loss of in vitro activity and in vivo efficacy.

There are study limitations worth considering. We acknowledge that the cUTI model required administration of different cefepime doses (mg/kg), but this was necessary to maintain suitable plasma exposures over the range of MICs. While plasma exposures were consistent with human exposures for both regimens, we did not assess urine or kidney tissue drug concentrations. Further studies should be conducted to assess implications of urine or kidney tissue drug concentrations, which may be variable among and within mice over the 48 h dosing period. Secondly, cefepime/taniborbactam has demonstrated in vitro activity against both clinically important serine b-lactamases and MBLs; however, isolates in this current study were limited to serine β -lactamase-harbouring isolates only. This is as a result of β -lactam in vitro-in vivo discordance against MBL-harbouring isolates in the mouse model, necessitating a different study design to appropriately determine that

Figure 1. In vivo efficacy comparison of 48 h control, cefepime HSR and cefepime/taniborbactam HSR against individual (a) Enterobacterales isolates and (b) P. aeruginosa and S. maltophilia isolates. Each bar represents the average bacterial density (±SD) of 12 infected kidneys from six mice. An asterisk indicates a statistically significant decrease in cfu/kidney compared with cefepime HSR. The y-axis starts at the lower limit of detection $(2.00 \log_{10} c$ fu/kidney). This figure appears in colour in the online version of JAC and in black and white in the print version of JAC.

any antimicrobial activity observed in vivo is due to the combination of cefepime and taniborbactam against MBLs. $17-19$ Resistance development was not assessed in this study and is warranted in future animal studies. Notably, extensive resistance development studies have been performed with cefepime/taniborbactam, including a 7 day hollow fibre model, with no emergence of resistant subpopulations.^{[6,20](#page-4-0)}

In summary, these translational data support the current clinical regimen being evaluated in the cUTI Phase III clinical trial and provide insights into the in vivo potency and spectrum of cefepime/taniborbactam antimicrobial activity over an extended treatment period in the kidney infection model. Ultimately, assessing antimicrobial activity across multiple infection models enhances confidence in the clinical dose required to achieve the pharmacokinetic/pharmacodynamic targets.

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Transparency declarations

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The sponsor provided support and did not exercise control over the conduct or reporting of the research except with WGS and genome analysis of S. maltophilia isolates.

Supplementary data

Figures [S1](https://academic.oup.com/jac/article-lookup/doi/10.1093/jac/dkab405#supplementary-data) to [S3](https://academic.oup.com/jac/article-lookup/doi/10.1093/jac/dkab405#supplementary-data) and Tables [S1](https://academic.oup.com/jac/article-lookup/doi/10.1093/jac/dkab405#supplementary-data) and [S2](https://academic.oup.com/jac/article-lookup/doi/10.1093/jac/dkab405#supplementary-data) are available as [Supplementary](https://academic.oup.com/jac/article-lookup/doi/10.1093/jac/dkab405#supplementary-data) [data](https://academic.oup.com/jac/article-lookup/doi/10.1093/jac/dkab405#supplementary-data) at JAC Online.

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