Ceftobiprole Activity against Pathogens Causing Bacterial Skin and Skin Structure Infections in the United States from 2016 through 2018

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Introduction

- Ceftobiprole medocaril is an advanced parenteral cephalosporin prodrug that is approved in 17 European countries, Argentina, Canada, Jordan, Peru, and Saudi Arabia for the treatment of adults with community (CAP)- and hospital-acquired pneumonia (excluding ventilator-associated pneumonia)
- Ceftobiprole was specifically designed to inhibit penicillin-binding protein 2A (encoded by *mecA*), which confers methicillin (oxacillin) resistance in *Staphylococcus aureus*
- Ceftobiprole exhibits potent *in vitro* antimicrobial activity against many important Gram-positive pathogens like *S. aureus* (including methicillin-resistant [MRSA] isolates) and *Streptococcus pneumoniae*
- Additionally, ceftobiprole exhibits antimicrobial activity against *Enterobacteriaceae* and *Pseudomonas aeruginosa* isolates that is similar to other advanced cephalosporins like cefepime
- Ceftobiprole is not approved in the United States (USA) but has qualified infectious disease product status for the potential treatment of acute bacterial skin and skin structure infections (ABSSSIs), *S. aureus* bacteremia, and CAP
- Ceftobiprole is being evaluated in 2 phase 3 clinical trials for patients with
  - ABSSSIs (expected completion in 2019)
  - *S. aureus* bacteremia, including infective endocarditis (expected completion in 2021)
- In this study, the *in vitro* activity of ceftobiprole and comparators was evaluated against recent clinical isolates collected in the USA from patients with skin and skin structure infections (SSSIs)

Materials and Methods

Bacterial isolates

- A total of 7,354 clinical isolates were collected from patients with SSSIs at 32 US medical centers from 2016 through 2018
- Bacterial species were identified by the submitting laboratories and confirmed by JMI Laboratories using standard microbiology methods and matrix-assisted laser desorption ionization-time of flight mass spectrometry (Bruker Daltonics, Bremen, Germany)
- The extended-spectrum β-lactamase (ESBL) phenotype was defined for *Escherichia coli*, *Klebsiella pneumoniae*, *Klebsiella oxytoca*, and *Proteus mirabilis* as an MIC value ≥2 mg/L for ceftriaxone, ceftazidime, and/or aztreonam (CLSI, 2019)
- The major SSSI species and pathogen groups included *S. aureus* (53%), *Enterobacteriaceae* (23%), *P. aeruginosa* (7%), β-hemolytic streptococci (BHS; 6%), *Enterococcus* spp. (4%), and coagulase-negative staphylococci (CoNS; 2%) (Figure 1)

Susceptibility testing

- Susceptibility to ceftobiprole and comparator agents was tested using current Clinical and Laboratory Standards Institute (CLSI) methods
- CLSI and European Committee on Antimicrobial Susceptibility Testing (EUCAST) interpretive criteria were applied according to current guidelines
  - US Food and Drug Administration criteria were used as an alternative breakpoint source for tigecycline
- JMI Laboratories followed current CLSI quality assurance practices when performing the susceptibility tests
  - MIC values were validated by concurrently testing CLSI-recommended (M100, 2019) ATCC quality control (QC) strains
  - QC ranges for tested reference strains were those approved or published by CLSI (M100, 2019)
  - The inoculum density during susceptibility testing was monitored by bacterial colony counts
- The susceptibilities of pathogen groups without specific published interpretive criteria for ceftobiprole were evaluated using the EUCAST non-species-specific breakpoint of 4 mg/L (EUCAST, 2019); further studies are required to evaluate the full clinical utility of ceftobiprole against such organisms

Results

- Ceftobiprole was highly active against *S. aureus* from SSSIs (MIC$_{50/90}$, 0.5/1 mg/L); 99.7% susceptible at the EUCAST breakpoint of 2 mg/L) (Table 1)
  - Ceftobiprole activity against *S. aureus* was virtually identical when the data were stratified by year (Figure 2)
  - Against the MRSA subset (41.9% of all *S. aureus*), the MIC$_{50/90}$ values increased by only 2-fold (99.4% susceptible) (Table 2)
  - All MRSA isolates were susceptible to daptomycin, tigecycline, and vancomycin (Table 2)
  - 97.1% of the MRSA isolates were susceptible to ceftaroline (Table 2)

- Ceftobiprole also exhibited potent activity against the other major groups of Gram-positive cocci associated with SSSIs, including
  - BHS (MIC$_{50/90}$, 0.015/0.03 mg/L; 100% inhibited at ≤0.12 mg/L [4 mg/L is the EUCAST pharmacokinetic/pharmacodynamic non-species-related breakpoint]) (Table 1)
  - *Enterococcus faecalis* (MIC$_{50/90}$, 0.5/2 mg/L; 99.6% inhibited at ≤4 mg/L) (Table 1)
    - Ceftaroline (MIC$_{50/90}$, 2/8 mg/L) was 4-fold less potent than ceftobiprole (Table 2)
  - CoNS (MIC$_{50/90}$, 0.5/1 mg/L; 100% inhibited at ≤4 mg/L) (Table 1)
    - Ceftobiprole was only 2-fold less potent against the methicillin-resistant CoNS subset (MIC$_{50/90}$, 1/2 mg/L; data not shown)
- The overall susceptibility of all *Enterobacteriaceae* SSSI isolates to ceftobiprole was 84.8% (Table 3)
  - *Enterobacteriaceae* susceptibility to ceftobiprole was similar to other expanded-spectrum cephalosporins like cefepime (89.7%) and ceftazidime (85.0%) (Table 3)
  - The majority of *E. coli* and *K. pneumoniae* isolates exhibited a non-ESBL phenotype (coincidentally 77.6% for both species)
  - Ceftobiprole exhibited potent activity against *E. coli* (MIC$_{50/90}$, 0.03/0.06 mg/L; 99.7% susceptible) and *K. pneumoniae* (MIC$_{50/90}$, 0.03/0.06 mg/L; 99.3% susceptible) isolates that exhibited a non-ESBL phenotype (Table 3)
  - Ceftobiprole also exhibited potent activity against *P. mirabilis*, *Serratia marcescens*, and *Enterobacter cloacae* species complex isolates from SSSIs (Table 1)
- A total of 74.4% of *P. aeruginosa* isolates were inhibited by ceftobiprole at ≤4 mg/L (Table 1)
  - 85.9% were susceptible to cefepime and 84.3% were susceptible to ceftazidime (Table 3)
- As expected, ceftobiprole was largely inactive against *Enterococcus faecium* (MIC$_{50/90}$, >4/>4 mg/L; data not shown) and *E. coli* and *K. pneumoniae* isolates that exhibited an ESBL phenotype (Table 1)
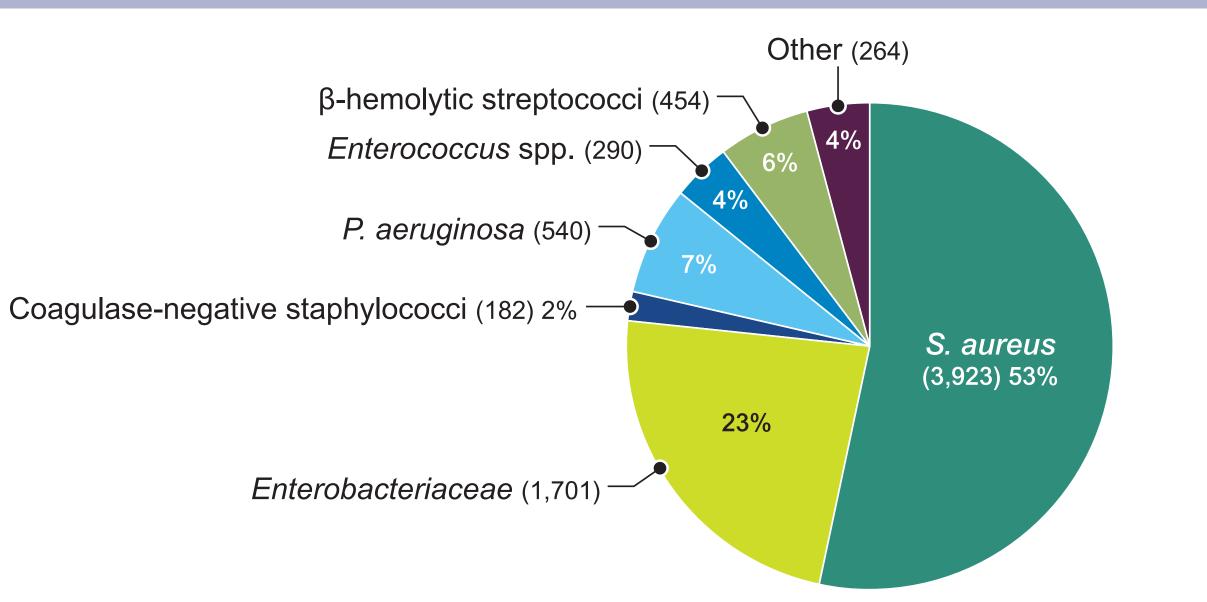
Figure 1 Species and groups (number of US isolates) that were isolated from skin and skin structure infections

Other (264) 4%
β-hemolytic streptococci (454) 6%
Enterococcus spp. (290) 4%
P. aeruginosa (540) 7%
Coagulase-negative staphylococci (182) 2%
S. aureus (3,923) 53%
Enterobacteriaceae (1,701) 23%

Conclusions

- Ceftobiprole was highly active *in vitro* against a large percentage of the clinical isolates from the major Gram-positive and Gram-negative SSSI pathogen groups collected at US medical centers during 2016–2018
- 76% of the SSSI pathogens was composed of *S. aureus* and *Enterobacteriaceae* isolates
  - Overall, the *S. aureus* SSSI isolate set was 99.7% susceptible to ceftobiprole
  - The *Enterobacteriaceae* SSSI isolate set was 84.8% susceptible to ceftobiprole
- The broad-spectrum activity of ceftobiprole, including potent activity against MRSA, supports its further evaluation for this potential indication

Acknowledgements

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Figure 2 Ceftobiprole activity against US *S. aureus* SSSI isolates by year

Table 2 Activity of ceftobiprole and comparator agents when tested against the major groups of Gram-positive bacteria from SSSIs (USA; 2016–2018)

Species or group (no. of isolates) Antimicrobial agent	MIC$_{50}$	MIC$_{90}$	Range	CLSI[a] %S	CLSI[a] %I	CLSI[a] %R	EUCAST[a] %S	EUCAST[a] %I	EUCAST[a] %R
MRSA (1,643)									
Ceftobiprole	1	2	0.25 to 4				99.4		0.6
Ceftaroline	0.5	1	0.25 to 2	97.1[b]	2.9		97.1[c]	2.9	0.0
Ceftriaxone	>8	>8	4 to >8	0.0		100.0			
Clindamycin	≤0.25	>2	≤0.25 to >2	80.8	0.3	18.9	80.7	0.1	19.2
Daptomycin	0.25	0.5	≤0.12 to 1	100.0			100.0		0.0
Erythromycin	>8	>8	≤0.06 to >8	14.2	2.9	82.8	14.5	0.9	84.6
Gentamicin	≤1	≤1	≤1 to >8	97.5	0.2	2.3	97.4		2.6
Levofloxacin	4	>4	0.06 to >4	40.4	1.3	58.3	40.4		59.6
Linezolid	1	2	≤0.12 to >8	99.9		0.1	99.9		0.1
Tetracycline	≤0.5	≤0.5	≤0.5 to >8	93.2	1.1	5.7	91.8	0.9	7.2
Tigecycline	0.06	0.12	≤0.015 to 0.5	100.0[d]			100.0		0.0
Trimethoprim-sulfamethoxazole	≤0.5	≤0.5	≤0.5 to >4	97.3		2.7	97.3	0.0	2.7
Vancomycin	1	1	0.25 to 2	100.0		0.0	100.0		0.0
MSSA (2,280)									
Ceftobiprole	0.5	0.5	≤0.03 to 1				100.0		0.0
Ceftaroline	0.25	0.25	≤0.06 to 0.5	100.0		0.0	100.0[c]	0.0	0.0
Ceftriaxone	4	8	0.5 to 8	100.0		0.0			
Clindamycin	≤0.25	≤0.25	≤0.25 to >2	96.3	0.0	3.7	96.1	0.1	3.7
Daptomycin	0.25	0.5	≤0.12 to 1	100.0			100.0		0.0
Erythromycin	0.25	>8	≤0.06 to >8	66.9	6.3	26.8	67.5	2.2	30.3
Gentamicin	≤1	≤1	≤1 to >8	99.0	0.2	0.8	98.9		1.1
Levofloxacin	0.25	2	0.06 to >4	90.0	0.6	9.5	90.0		10.0
Linezolid	1	2	0.25 to 4	100.0		0.0	100.0		0.0
Tetracycline	≤0.5	≤0.5	≤0.5 to >8	96.4	1.5	3.2	93.8	0.3	6.0
Tigecycline	0.06	0.12	0.03 to 0.5	100.0[d]			100.0		0.0
Trimethoprim-sulfamethoxazole	≤0.5	≤0.5	≤0.5 to >4	99.5		0.5	99.5	0.0	0.5
Vancomycin	1	1	≤0.12 to 2	100.0		0.0	100.0		0.0
β-hemolytic streptococci (454)[e]									
Ceftobiprole	0.015	0.03	0.002 to 0.12				100.0		0.0
Ceftaroline	≤0.008	0.015	≤0.008 to 0.03	100.0			100.0		0.0
Ceftriaxone	0.03	0.06	≤0.015 to 0.12	100.0			100.0		
Clindamycin	≤0.25	>2	≤0.25 to >2	84.6	0.7	14.8	85.2		14.8
Daptomycin	≤0.06	0.25	≤0.06 to 0.5	100.0			100.0		0.0
Erythromycin	0.03	>16	≤0.015 to >16	71.6	0.9	27.5	71.6	0.9	27.5
Levofloxacin	0.5	1	0.12 to >4	99.8	0.0	0.2	99.8		0.2
Linezolid	1	2	0.5 to 2	100.0		0.0	100.0		0.0
Meropenem	≤0.008	0.06	≤0.008 to 0.06	100.0			100.0		0.0
Penicillin	0.015	0.06	≤0.008 to 0.06	100.0			100.0	0.0	0.0
Tetracycline	0.5	>4	≤0.25 to >4	59.4	1.3	39.3	58.7	0.7	40.6
Vancomycin	0.5	0.5	0.12 to 1	100.0			100.0		0.0
Enterococcus faecalis (223)									
Ceftobiprole	0.5	2	≤0.03 to >4						
Ampicillin	1	1	≤0.5 to 2	100.0		0.0	100.0		0.0
Ceftaroline	2	8	≤0.06 to >8						
Daptomycin	1	1	≤0.25 to 4	98.2[f]	1.8	0.0			
Levofloxacin	1	>4	≤0.03 to >4	75.8	0.0	24.2	75.8[f]		24.2
Linezolid	1	2	0.5 to 2	100.0	0.0	0.0	100.0		0.0
Teicoplanin	≤0.5	≤0.5	≤0.5 to >16	97.3	0.0	2.7	96.9		3.1
Tigecycline	0.06	0.12	≤0.015 to 0.12	100.0[d]			100.0		0.0
Vancomycin	1	2	0.25 to >16	96.9	0.0	3.1	96.9		3.1
Coagulase-negative staphylococci (182)[g]									
Ceftobiprole	0.5	1	≤0.03 to 4						
Ceftaroline	0.25	0.5	≤0.06 to 2						
Ceftriaxone	4	>8	≤0.25 to >8	67.6		32.4			
Clindamycin	≤0.25	>2	≤0.25 to >2	82.4	2.2	15.4	81.3	1.1	17.6
Daptomycin	0.25	0.5	≤0.12 to 1	100.0		0.0	100.0		0.0
Erythromycin	0.12	>8	≤0.06 to >8	57.7	0.5	41.8	58.2	0.0	41.8
Gentamicin	≤1	2	≤1 to >8	90.1	0.5	9.3	89.6		10.4
Levofloxacin	0.25	>4	≤0.03 to >4	83.0	0.5	16.5	83.0		17.0
Linezolid	0.5	1	≤0.12 to 2	100.0		0.0	100.0		0.0
Oxacillin	1	>2	≤0.25 to >2	67.6		32.4	68.1		31.9
Tetracycline	≤0.5	1	≤0.5 to >8	92.9	1.1	6.0	90.1	2.7	7.1
Tigecycline	0.06	0.12	≤0.015 to 0.5				100.0		0.0
Trimethoprim-sulfamethoxazole	≤0.5	>4	≤0.5 to >4	83.0		17.0	83.0	7.1	9.9
Vancomycin	1	2	≤0.12 to 2	100.0		0.0	100.0		0.0

SSSIs, skin and skin structure infections; S, susceptible; I, intermediate; R, resistant; MRSA, methicillin-resistant *S. aureus*; MSSA, methicillin-susceptible *S. aureus*
[a] Criteria as published by CLSI 2019 and EUCAST 2019.
[b] Intermediate interpreted as susceptible-dose dependent.
[c] Using other than pneumonia breakpoints.
[d] FDA breakpoints accessed January 2019.
[e] Organisms include: *Streptococcus agalactiae* (142), *S. canis* (3), *S. dysgalactiae* (41), *S. pyogenes* (268).
[f] Uncomplicated urinary tract infection only.
[g] FDA breakpoints accessed January 2019 applied to all *E. faecalis* but approved for vancomycin-susceptible isolates only.
[h] Organisms include: *Staphylococcus epidermidis* (3), *S. capree* (2), *S. epidermidis* (63), *S. haemolyticus* (7), *S. hominis* (1), *S. intermedius* (1), *S. lugdunensis* (90), *S. pseudintermedius* (5), *S. saprophyticus* (1), *S. schleiferi* (1), *S. simulans* (5), *S. warneri* (1), *S. xylosus* (1)

Table 3 Activity of ceftobiprole and comparator agents when tested against the major groups of Gram-negative bacteria from SSSIs (USA; 2016–2018)

Species or group (no. of isolates) Antimicrobial agent	MIC$_{50}$	MIC$_{90}$	Range	CLSI[a] %S	CLSI[a] %I	CLSI[a] %R	EUCAST[a] %S	EUCAST[a] %I	EUCAST[a] %R
Enterobacteriaceae (1,701)[b]									
Ceftobiprole	0.03	>16	≤0.008 to >16				84.8		15.2
Ampicillin-sulbactam	16	>32	≤0.5 to >32	44.9	17.4	37.7	44.9		55.1
Aztreonam	0.12	16	≤0.03 to >16	87.6	1.6	10.8	85.6	2.0	12.4
Cefepime	≤0.12	2	≤0.12 to >16	90.8[c]	2.2	7.0	89.7	2.4	7.9
Ceftaroline	0.12	>16	≤0.03 to >16	75.9	6.0	18.1	75.9		24.1
Ceftazidime	0.25	16	0.03 to >32	88.7	1.2	10.1	85.0	3.8	11.3
Ceftriaxone	0.12	>8	≤0.06 to >8	83.7	1.5	14.8	83.7	1.5	14.8
Colistin	0.25	>8	≤0.06 to >8				67.3		32.7
Gentamicin	0.5	2	≤0.12 to >8	92.5	0.6	6.8	91.7	0.9	7.5
Imipenem	0.25	2	≤0.12 to >8	84.6	11.8	3.6	78.0	21.6	0.5
Levofloxacin	0.06	>4	≤0.03 to >4	79.7	1.8	18.5	79.7	1.8	18.5
Meropenem	0.03	0.06	≤0.015 to 0.06	99.4	0.0	0.6	99.4	0.5	0.2
Piperacillin-tazobactam	2	8	≤0.5 to >64	94.0	2.1	3.9	91.5	2.5	6.0
Tigecycline	0.5	2	≤0.06 to 8	91.7[d]	7.4	0.9			
Trimethoprim-sulfamethoxazole	≤0.5	>4	≤0.5 to >4	79.9		20.1	79.9	0.6	19.4
Non-ESBL-phenotype Escherichia coli (388)									
Ceftobiprole	0.03	0.06	0.015 to 0.5				99.7		0.3
Ampicillin-sulbactam	8	>32	0.5 to >32	52.8	21.6	25.5	52.8		47.2
Aztreonam	0.12	0.25	≤0.03 to 1	100.0	0.0	0.0	100.0	0.0	0.0
Cefepime	≤0.12	≤0.12	≤0.12 to 1	100.0[c]	0.0	0.0	100.0	0.0	0.0
Ceftaroline	0.12	0.5	≤0.03 to 8	95.6	2.1	2.3	95.6		4.4
Ceftazidime	0.25	0.5	0.06 to 1	100.0	0.0	0.0	100.0	0.0	0.0
Ceftriaxone	0.06	0.12	≤0.06 to 0.5	100.0	0.0	0.0	100.0	0.0	0.0
Colistin	0.12	0.25	≤0.06 to 1				100.0		0.0
Gentamicin	1	2	0.12 to >8	92.5	0.0	7.5	92.3	0.3	7.5
Imipenem	≤0.12	≤0.12	≤0.12 to 0.5	100.0	0.0	0.0	100.0	0.0	0.0
Levofloxacin	0.03	>4	≤0.03 to >4	75.8	1.0	23.2	75.8	1.0	23.2
Meropenem	≤0.015	0.03	≤0.015 to 0.06	100.0	0.0	0.0	100.0	0.0	0.0
Piperacillin-tazobactam	2	4	≤0.5 to >64	99.2	0.3	0.5	98.7	0.5	0.8
Tigecycline	0.12	0.25	≤0.06 to 1	100.0[d]	0.0	0.0			
Trimethoprim-sulfamethoxazole	≤0.5	>4	≤0.5 to >4	73.1		26.9	73.1	0.5	26.4
Non-ESBL-phenotype Klebsiella pneumoniae (149)									
Ceftobiprole	0.03	0.06	0.015 to 0.5				99.3		0.7
Ampicillin-sulbactam	8	16	≤0.5 to >32	82.6	12.1	5.4	82.6		17.4
Aztreonam	0.06	0.12	≤0.03 to 0.5	100.0	0.0	0.0	100.0	0.0	0.0
Cefepime	≤0.12	≤0.12	≤0.12 to 0.5	100.0[c]	0.0	0.0	100.0	0.0	0.0
Ceftaroline	0.12	0.25	≤0.03 to 1	99.3	0.7	0.0	99.3		0.7
Ceftazidime	0.12	0.5	0.03 to 1	100.0	0.0	0.0	100.0	0.0	0.0
Ceftriaxone	0.06	0.12	≤0.06 to 1	100.0	0.0	0.0	100.0	0.0	0.0
Colistin	0.12	0.25	≤0.06 to >8				98.6		1.4
Gentamicin	0.25	0.5	≤0.12 to >16	99.3	0.0	0.7	99.3	0.0	0.7
Imipenem	≤0.12	0.25	≤0.12 to 1	100.0	0.0	0.0	100.0	0.0	0.0
Levofloxacin	0.06	0.25	≤0.03 to >8	95.9	2.7	1.4	95.9	2.7	1.4
Meropenem	0.03	0.03	≤0.015 to 0.06	100.0	0.0	0.0	100.0	0.0	0.0
Piperacillin-tazobactam	2	8	≤0.5 to 16	100.0	0.0	0.0	91.9	8.1	0.0
Tigecycline	0.5	1	≤0.06 to 8	97.3[d]	2.0	0.7			
Trimethoprim-sulfamethoxazole	≤0.5	≤0.5	≤0.5 to >4	94.6		5.4	94.6	0.0	5.4
Pseudomonas aeruginosa (540)									
Ceftobiprole	2	16	0.25 to >16						
Amikacin	4	8	≤0.25 to >32	98.7	0.4	0.9	94.6	4.1	1.3
Ampicillin-sulbactam	>32	>32	≤0.25 to >32						
Aztreonam	8	>16	0.06 to >16	68.3	13.0	18.7	81.3		18.7
Cefepime	2	16	0.25 to >16	85.9	10.7	3.3	85.9		14.1
Ceftaroline	16	>16	0.5 to >16						
Ceftazidime	2	32	0.12 to >32	84.3	5.6	10.2	84.3		15.7
Colistin	1	1	0.12 to >8	99.4		0.6	99.4		0.6
Gentamicin	2	4	≤0.12 to >8	90.6	5.7	3.7	90.6		9.4
Imipenem	1	8	0.12 to >8	81.9	3.5	14.6	85.4		14.6
Levofloxacin	0.5	>4	≤0.03 to >4	69.4	8.7	21.9	69.4		30.6
Piperacillin-tazobactam	4	64	≤0.5 to >64	80.5	9.8	9.6	80.5		19.5
Tigecycline	8	>8	0.5 to >8						
Trimethoprim-sulfamethoxazole	>4	>4	≤0.5 to >4						

S, susceptible; I, intermediate; R, resistant; ESBL, extended-spectrum β-lactamase
[a] Criteria as published by CLSI 2019 and EUCAST 2019.
[b] Organisms include: *Citrobacter amalonaticus* (1), *C. amalonaticus/farmeri* (3), *C. farmeri* (1), *C. freundii* (8), *C. freundii species complex* (43), *C. koseri* (31), *Cronobacter sakazakii* (1), *Edwardsiella tarda* (1), *Enterobacter aerogenes* (57), *E. cloacae* (115), *E. cloacae species complex* (129), *Escherichia coli* (500), *E. hermannii* (1), *Klebsiella oxytoca* (90), *K. aerogenes* (1), *K. pneumoniae* (192), *Leclercia adecarboxylata* (1), *Lelliottia amnigena* (1), *Morganella morganii* (7), *Morganella morganii* (73), *Pantoea agglomerans* (2), *P. calida* (1), *P. eucrina* (1), *Pluralibacter gergoviae* (1), *Proteus mirabilis* (258), *P. vulgaris* group (16), *Providencia rettgeri* (14), *P. stuartii* (7), *Serratia fonticola* (1), *S. liquefaciens* (7), *S. liquefaciens complex* (1), *S. marcescens* (135), unspeciated *Pantoea* (2), unspeciated *Providencia* (1), unspeciated *Raoultella* (2)
[c] Intermediate interpreted as susceptible-dose dependent.
[d] FDA breakpoints accessed January 2019.

Table 1 Antimicrobial activity of ceftobiprole tested against the main species and groups from skin and skin structure infections

Organism/organism group (no. of isolates)	≤0.001	0.002	0.004	0.008	0.015	0.03	0.06	0.12	0.25	0.5	1	2	4	8	16	>a	MIC$_{50}$	MIC$_{90}$
Staphylococcus aureus (3,923)							1	0	13	572	1,758	1,215	354	10			0.5	1
							<0.1	<0.1	0.4	14.9	59.8	90.7	99.7	100.0				
Methicillin-susceptible (2,280)							1	0	13	570	1,688	8					0.5	0.5
							<0.1	<0.1	0.6	25.6	99.6	100.0						
Methicillin-resistant (1,643)							0	0	2	70	1,207	354	10				1	2
							0.0	0.1	4.4	77.8	99.4	100.0						
Enterobacteriaceae (1,701)				16	48	862	394	83	40	27	22	18	12	4	4	171	0.03	>16
				0.9	3.8	54.4	77.6	82.5	84.8	86.4	87.7	88.8	89.5	89.7	89.9	100.0		
Escherichia coli (500)				10	291	83	10	6	4	2	1	1	2			90	0.03	>16
				2.0	60.2	76.8	78.8	80.0	80.8	81.2	81.4	81.6	82.0			100.0		
ESBL-phenotype (112)				0	3	4	2	0	1	2	1	1	2			90	>16	>16
				0.0	2.7	6.2	8.0	11.6	14.3	16.1	17.0	17.9	17.9			19.6	100.0	
Non-ESBL-phenotype (388)				10	288	79	8	2	1								0.03	0.06
				2.6	76.8	97.2	99.2	99.7	100.0									
Proteus mirabilis (258)				0	23	195	30	2	0	1	0	0	0			6	0.03	0.06
				0.0	8.9	84.5	96.1	96.9	96.9	97.3	97.3	97.3	97.3			97.7	100.0	
ESBL-phenotype (8)						0	0	0	0	1	1	1	1			6	>16	
						0.0	0.0	0.0	0.0	12.5	12.5	12.5	12.5	12.5	12.5	25.0	100.0	
Non-ESBL-phenotype (250)				0	23	195	29	2	0	1							0.03	0.06
				0.0	9.2	87.2	98.8	99.6	99.6	100.0								

Organism/organism group (no. of isolates)	≤0.001	0.002	0.004	0.008	0.015	0.03	0.06	0.12	0.25	0.5	1	2	4	8	16	>a	MIC$_{50}$	MIC$_{90}$
Klebsiella pneumoniae (192)				0	4	108	32	5	0	2	4	2	1	0		34	0.03	>16
				0.0	2.1	58.3	75.0	77.6	77.6	78.6	80.7	81.8	82.3	82.3	82.3	100.0		
ESBL-phenotype (43)						0	0	0	0	2	3	2	1	0		34	>16	>16
						0.0	2.3	2.3	2.3	4.7	14.0	18.6	20.9	20.9	20.9	100.0		
Non-ESBL-phenotype (149)				0	4	108	31	5	0	1							0.03	0.06
				0.0	2.7	75.2	96.0	99.3	99.3	100.0								
Serratia marcescens (135)				0	2	91	30	7	1	2	2	0	0				0.06	0.12
				0.0	1.5	68.9	91.1	96.3	97.8	99.3	99.3	99.3	100.0					
Enterobacter cloacae species complex (244)				0	100	90	14	1	4	4	5	4	8	1		8	0.06	2
				0.0	41.0	77.9	83.6	84.0	85.7	87.7	91.4	94.7	96.3	96.7	100.0			
Pseudomonas aeruginosa (540)				0	0	1	13	109	191	88	57	56	25				2	16
				0.0	0.0	2.6	22.8	58.1	74.4	85.0	95.4	100.0						
β-hemolytic streptococci (454)	0	5	7	198	142	98	1	3									0.015	0.03
	0.0	1.1	2.6	46.3	77.5	99.1	99.8	100.0										
Streptococcus pyogenes (268)	0	5	5	187	68	1	2										0.008	0.015
	0.0	1.9	3.7	73.5	98.9	99.6	100.0											
Streptococcus agalactiae (142)				0	43	96	2	1									0.03	0.06
				0.0	30.3	97.9	99.3	100.0										
Enterococcus faecalis (223)					4	17	41	101	21	30	4					1	0.5	2
					1.8	3.6	11.2	29.6	74.9	84.3	97.8	99.6				100.0		
Coagulase-negative staphylococci (182)						3	2	27	28	63	48	8	3				0.5	1
						1.6	2.7	17.6	33.0	67.6	94.0	98.4	100.0					

ESBL, extended-spectrum β-lactamase
[a] Greater than the highest concentration tested.