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A total of 304 (1.1%) CREs were observed in the study period; 45 (14.8%) isolates did not carry carbapenemases (Figure 1).

- These isolates mainly were Klebsiella aerogenes, Enterobacter cloacae species complex, and Klebsiella pneumoniae (11, 11 and 10 isolates, respectively).

Five other species also were included.

Acquired β-lactamase genes, including ESBLs and transferable cephalosporinases, were detected among 18 isolates (Figure 1).

- bla_{CTX-M-15} was the most common gene and was detected among 14 isolates.
- bla_{CTX-M-15} was accompanied by bla_{CXA-1} in 11 isolates.
- bla_{CTX-M-14}, bla_{CTX-M-2}, and bla_{SHV-12} each were observed in 1 isolate.
- One P. mirabilis carried 2 ESBLs, bla_{TFM-155}, and bla_{TEM-2}.
- One E. coli isolate harbored bla_{CMY 2}.

All *K. aerogenes*, 1 *K. oxytoca*, and 10 of 11 *E. cloacae* did not carry acquired β-lactamase genes (Figure 1).

- Among the 2 *C. freundii* species complex isolates analyzed, one carried bla_{TEM-1}, but neither harbored ESBLs or transferable cephalosporinases (Figure 1).

Analysis of outer membrane proteins (OMPs) demonstrated that 18 isolates had both OmpC/OmpK36 and OmpF/OmpK35 disrupted (nonsense or insertions and deletions), including 10 isolates with nonsense mutations in both OMPs (Figure 1). Isolates with both OMPs disrupted were detected among 7 species.

- 3 and 17 isolates had either OmpF/OmpK35 or OmpC/OmpK36 disrupted, respectively.

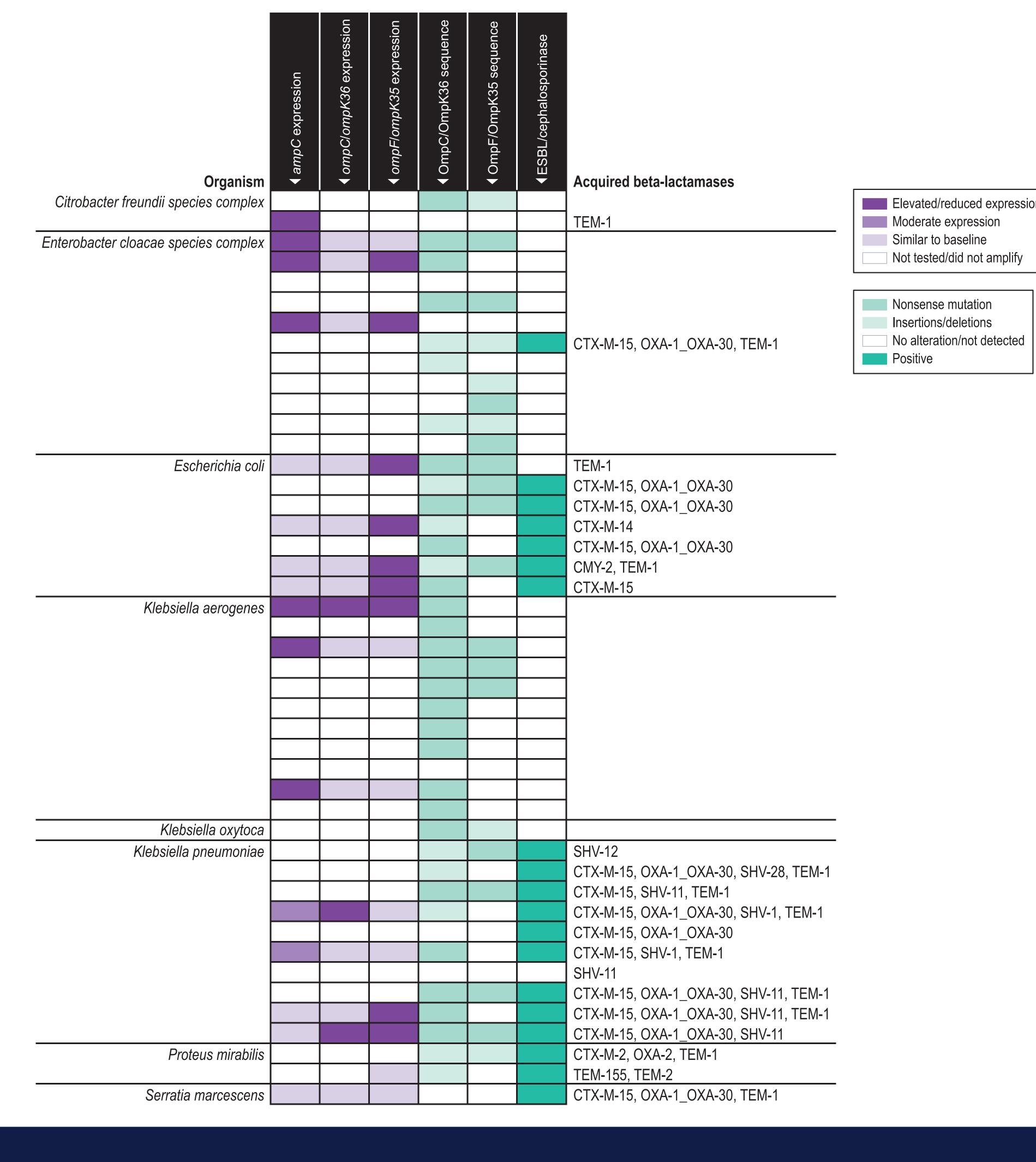
AmpC was overexpressed among 7 of the 17 isolates tested.

- Among the 17 isolates tested for expressions, 3 and 7 isolates had reduced expression of OMPs.

Ceftazidime-avibactam (100% susceptible) inhibited all isolates at the current CLSI breakpoint (Figure 2).

- β-lactam agents had limited activity, inhibiting 11.1% to 24.4% of these isolates.
- Tigecycline and amikacin inhibited 88.9% and 95.6% of the isolates at the current breakpoint, respectively.
- A total of 93.3% had intermediate MIC values for colistin (CLSI breakpoints).
- Other comparators inhibited 44.4% to 77.8% of the non-carbapenemaseproducing CRE isolates.





Meropenem-vaborbactam inhibited 71.4% of the 35 meropenem-resistant isolates (Figure 2).

Non-carbapenemase-

producing CRE isolates were

resistant to most β-lactams.

Most comparator agents had

limited activity against these

- Ceftazidime-avibactam was active against all meropenem-resistant isolates.

CRE isolates that did not produce

carbapenemase had multiple

resistance mechanisms that

included acquired β-lactamases,

changes in permeability, and

overexpression of intrinsic enzymes.

- Meropenem-resistant isolates were more resistant to other β-lactams, except for imipenem and gentamicin, when compared to the 45 non-carbapenemase-producing CRE isolates.

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Ceftazidime-avibactam demonstrated in vitro

activity against all carbapenemase-negative CRE

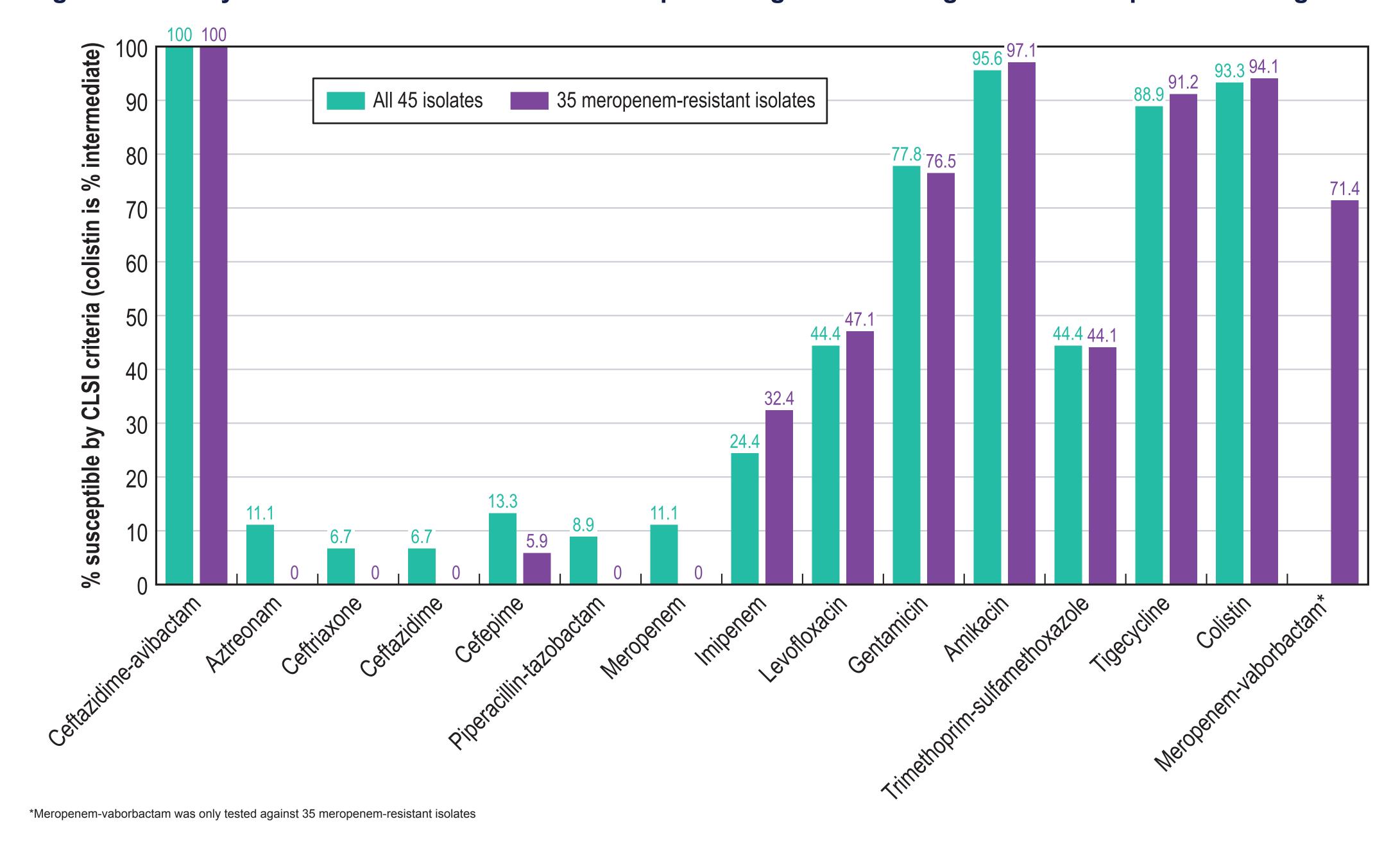
carrying multiple resistance mechanisms.

Meropenem-vaborbactam inhibited 71.4% of

the 35 meropenem-resistant carbapenemase-

negative CRE isolates.

Figure 2. Activity of ceftazidime-avibactam and comparator agents tested against 45 carbapenemase-negative CRE



Carbapenem-resistant *Enterobacterales* isolates emerged worldwide. Most of these carry carbapenemases, such as metallo β-lactamases (MBLs), oxacillinases with carbapenemase activity (OXA-48-like), and KPCs.

Carbapenem-resistant isolates that do not carry carbapenemases are not perceived as widespread as carbapenemase producers, but they remain a challenge for treatment with carbapenem agents. These isolates usually have elevated expression β-lactamases associated with permeability alterations and/or penicillin-binding protein (PBP) alterations.

Ceftazidime-avibactam is active against ESBLs, cephalosporinases, serinecarbapenemases, and some oxacillinases. Despite being affected by nonenzymatic resistance mechanisms, these resistance mechanisms against ceftazidime might be different from those mechanisms affecting carbapenems.

We investigated the prevalence, resistance mechanisms, and activity of ceftazidime-avibactam and comparator agents against CRE that did not carry carbapenemase genes from US hospitals.

Meropenem-resistant isolates were tested for meropenem-vaborbactam.

A total of 28,904 Enterobacterales isolates were collected in 70 US hospitals during 2016–2018.

- Isolates were identified as the cause of infection.
- Isolates were limited to 1 per patient per infection episode.

Isolates were susceptibility tested using the reference broth microdilution method described by the Clinical and Laboratory Standards Institute (CLSI).

- Categorical interpretations for all comparator agents were those criteria found on CLSI M100 document.
- Quality control (QC) was performed according to CLSI guidelines (M07, 2018). All QC minimal inhibitory concentration (MIC) results were within acceptable ranges as published in CLSI documents.
- Meropenem-vaborbactam was tested using lyophilized broth microdilution panels (ThermoFisher Scientific) according to manufacturer instructions. Carbapenem-resistant *Enterobacterales* (CRE) isolates were defined as any

isolate exhibiting imipenem and/or meropenem MIC values of ≥2 µg/mL. These isolates were submitted to whole genome sequencing (WGS).

 Proteus mirabilis and indole-positive Proteeae were categorized as CRE if doripenem and/or meropenem MIC values were at ≥2 μg/mL due to intrinsically elevated imipenem MIC values.

WGS was performed on a MiSeq (Illumina, San Diego, California, USA) instrument targeting a 30X coverage.

- Sequences were de novo assembled.
- Analysis of β-lactam resistance mechanisms and MLST was performed
- Genes encoding resistance were searched using a curated library and a criteria of >94% sequencing identity and 40% minimum length coverage

Selected isolates were evaluated for expression levels of intrinsic resistance \sim genes associated with resistance to β -lactams.

- Expression levels were determined by in triplicate quantitative real-time PCR using high quality RNA samples.
- Genes tested were the chromosomal ampC, ompC, and ompF (non-Klebsiella species) and ompK35 and ompK36 (Klebsiella spp.).
- Transcription levels were considered different if at least a 10-fold for AmpC and a 5-fold for other genes increase was noted compared to the baseline susceptible isolate.

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