Supplemental Digital Content 5

Characterization of β-lactamase genotypes

Gram-negative pathogens meeting specific drug susceptibility criteria indicating the presence of a b-lactamase[1] underwent further evaluation for genotypic identification. Characterization of β-lactamase genotypes was completed using total genomic DNA extracted by a fully automated Thermo Scientific™ KingFisher™ Flex Magnetic Particle Processor (Cleveland, OH, USA).[1] Extracted DNA was used as input material for library construction. DNA libraries were prepared using the Nextera™ library construction protocol (Illumina, San Diego, CA, USA) according to the manufacturer's instructions and were sequenced on a MiSeq Sequencer (JMI Laboratories, North Liberty, IA, USA). FASTQ format sequencing files for each sample set were assembled independently using de novo assembler SPAdes 3.9.0. Screening of β-lactamase genes was performed by an in-house designed software that aligned the assembled sequences against a curated database containing known β-lactamase genes. In addition, the quantitative expression of the chromosomal AmpC gene was performed as previously described.[1]

1. Mendes RE, Castanheira M, Woosley LN, et al. Molecular beta-lactamase characterization of Gram-negative pathogens recovered from patients enrolled in the ceftazidime-avibactam phase 3 trials (RECAPTURE 1 and 2) for complicated urinary tract infections: Efficacies analysed against susceptible and resistant subsets. *Int J Antimicrob Agents*. 2018;52:287–292.