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JMI Laboratories, North Liberty, Iowa, USA

Introduction

- The rapid detection of -lactam resistant phenotypes such as transferable AmpC (tAmpC), ESBL, and carbapenemase are important for appropriate antimicrobial therapy administration and infection control.
- The VITEK2 Advanced Expert System (AES) provides interpretations of -lactam resistance phenotypes based on an extensive database of MIC distributions and prevalent resistance mechanisms in Enterobacterales isolates.
- In this study, the AES -lactam resistance phenotypes were compared to whole genome sequencing results from 572 European Enterobacterales isolates.

Results

- Figure 2B shows the distribution of the 572 Enterobacterales isolates displaying carbapenemase, ESBL, tAmpC-encoding genes and wildtype genotypes.
- AES provided phenotypic reports for 564 (98.6%) isolates, including isolates harbouring carbapenemase (212; 37.6%), extended-spectrum -lactamase (ESBL; 161; 28.5%), and transferable AmpC (tAmpC; 51; 9.0%) genes as well as wild-type (WT; 140; 24.8%) isolates.
- Eight of 572 isolates (1.4%) failed to report an AES phenotype due to technical error or because the organism expressed a phenotype that was not present in the AES knowledge base.
- Overall, the AES report was accurate for 551/564 isolates (97.7%; Table 1).
- AES accurately reported carbapenemase, ESBL, and tAmpC phenotypes for 96.5%, 98.6%, and 97.9% of isolates, respectively.
- All but 1 (99.8%) WT isolate was correctly categorized by AES, including when isolates displayed intrinsic resistance or an acquired penicillinase.
- AES sensitivity/specificity rates were 99.5%/94.6%, 97.5%/99.0%, 84.3%/99.2%, and 100%/99.8% for reporting carbapenemase, ESBL, tAmpC genes, and WT isolates, respectively (Table 1).
- Table 2 displays the discrepancies between the AES phenotype and genotype, including 8 isolates carrying tAmpC, 1 carbapenemase, and 4 ESBL genes by WGS.
- Additionally, 4 isolates harbouring ESBL were reported as AmpC, and 1 VIM-1–producing *E. coli* isolate was misreported as displaying an ESBL phenotype.

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