

Performance of the VITEK 2 Advanced Expert System (AES) as a Rapid Tool for Reporting Antimicrobial Susceptibility Testing (AST) in *Enterobacterales*

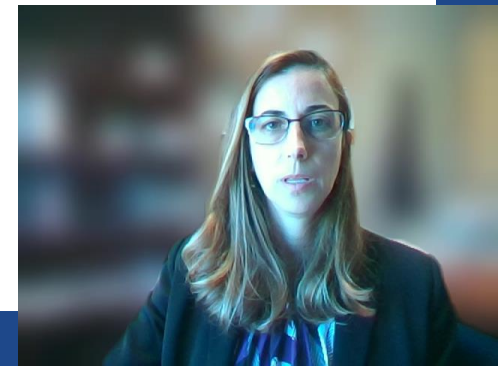
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Objective

To evaluate the performance of the VITEK 2 AES in comparison to the reference broth microdilution on a challenging set of whole genome sequenced *Enterobacterales* isolates of North and Latin American origin.

Methods

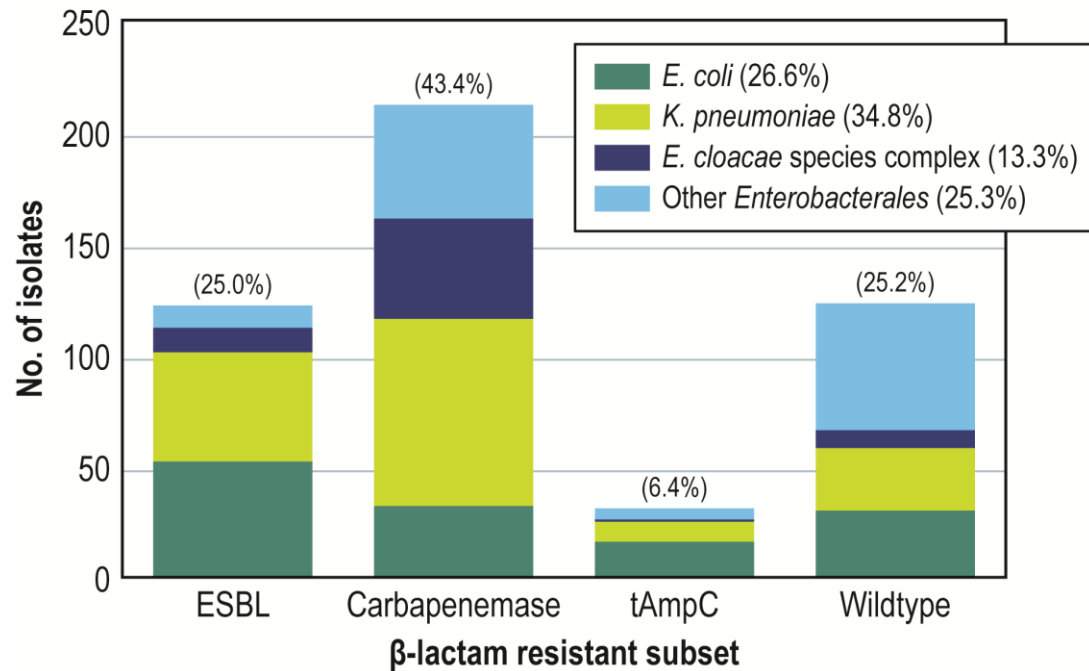
- 488 unique, molecularly characterized *Enterobacterales* isolates were selected from 2015-2019 SENTRY Antimicrobial Surveillance program (384 isolates) and CDC AR Bank (104 isolates).
- Isolates from North America (61 medical centers in the US) and Latin America (11 medical centers in 6 countries) were included.
- Isolates were tested by reference broth microdilution (BMD; CLSI) and VITEK 2 using N802 and XN15 AST cards and AES (v.9.02) in the CLSI-based + Natural Resistance (NATR) mode.
- BMD and VITEK 2 results for 29 antimicrobial agents were compared and discordant results were repeated by both methods using the same inoculum.
- The AES phenotypes were compared to resistant genotypes, while AES levels of confidence (green, yellow, and red) were compared to BMD results for accuracy.



Results

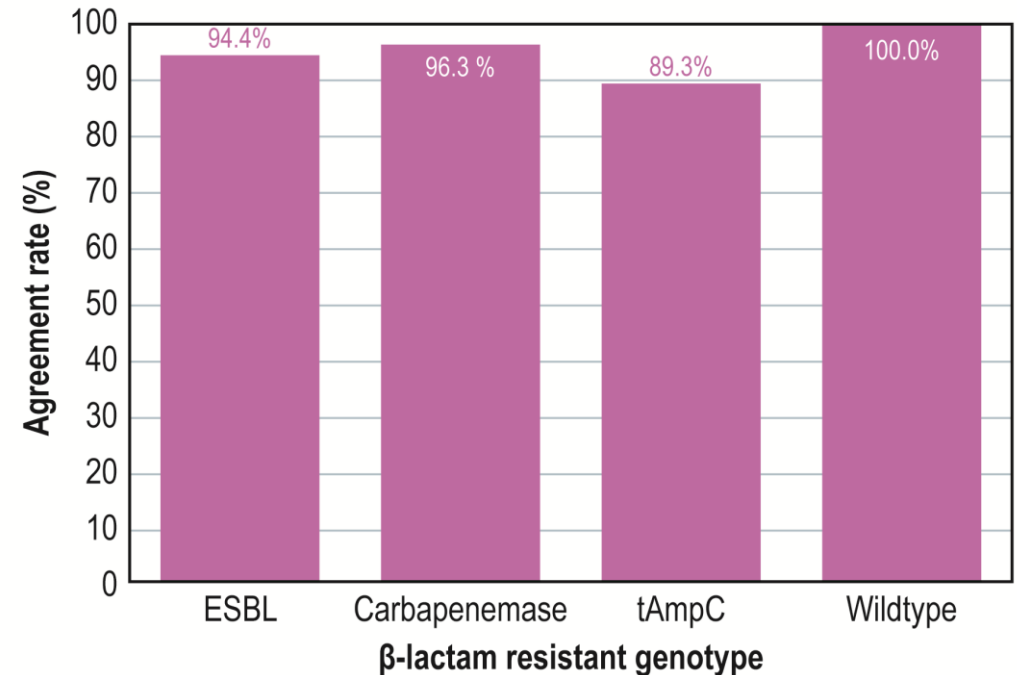
- A total of 365 (74.8%) isolates harboured β -lactam resistant genes and 123 (25.2%) were wildtype.
- An AES phenotype was reported for 447 (91.6%) isolates, and 431/447 (94.6%) results agreed with the genotype.

Figure 1. Distribution of *Enterobacterales* isolates by species and β -Lactam resistant genotype



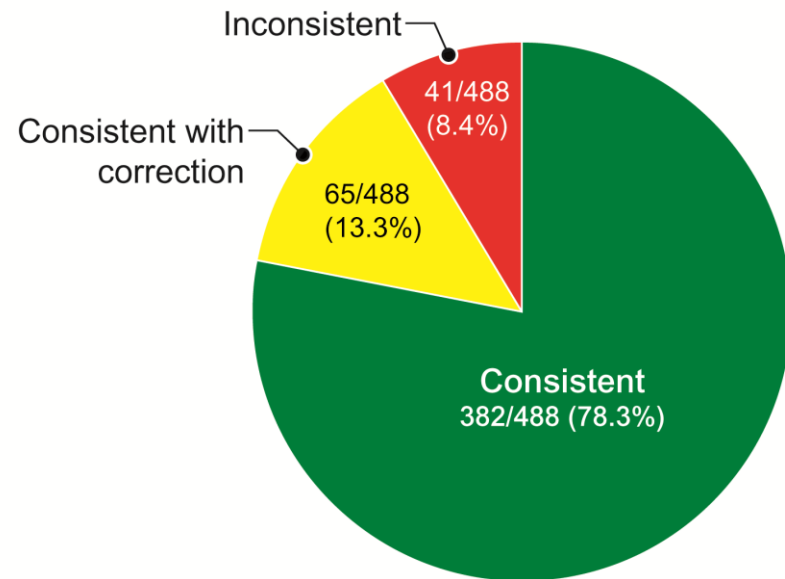
Other *Enterobacterales* included: *C. freundii* species complex (21), *C. koseri* (13), *Klebsiella aerogenes* (7), *K. oxytoca* (15), *Kluyvera ascorbata* (1), *Morganella morganii* (5), *Pluralibacter gergoviae* (1), *Proteus mirabilis* (18), *Providencia rettgeri* (5), *P. stuartii* (3), *Serratia marcescens* (34).

Figure 2. Agreement rates between VITEK 2 phenotype disposition and β -lactam resistant genotype



Results

Figure 3. Distribution of VITEK 2 AES labeling colors



Recommended label based on BMD results

	Green	Yellow
AES - Green	360	22
AES - Yellow	16	49
Total	376	71

Green Reports: 360/382 (94.2%) isolates could have been automatically reported without further review.

- 337 (88.2%) agreed to BMD with no ME or VME.
- 23 (6.0%) displayed at least 1 ME or VME that may not be detected by further review.
- The remaining 22 isolates displayed discrepancies that could be corrected by the AES by implementing additional corrections.

Yellow Reports: AES corrections were acceptable for 45/65 (69.2%) isolates.

- For 16 (24.6%) isolates, the initial result agreed with BMD and could be released as green.
- The 4 remaining isolates had a mismatch between phenotype and genotype.

Red Reports: 41 isolates were not a match for VITEK 2 AES phenotypes.

- Isolates displayed the following genotypes: 20 carbapenemase, 15 ESBL, 4 tAmpC, and 2 wildtype.
- 32/41 (78.0%) isolates displayed no ME or VME.



Results

Proposed corrections to improve the VITEK 2 AES report based on broth microdilution results.

Error Observed	No. of occurrences	Correction proposed
Cefepime VME	13	Call cefepime resistant if a carbapenemase phenotype is detected
Aztreonam VME	6	Call aztreonam resistant when a high level cephalosporinase (AmpC) phenotype is detected
Meropenem-vaborbactam ME	2	Call meropenem-vaborbactam susceptible if meropenem is susceptible
Piperacillin-tazobactam VME	1	Call piperacillin-tazobactam resistant if a carbapenemase phenotype is detected

Conclusions

- Compared to WGS, AES reports displayed accurate phenotypes for >90% of this challenge collection *Enterobacterales* isolates.
- Out of all green AES reports, >94% of *Enterobacterales* isolates could be confidently and rapidly auto-released, which could significantly aid antimicrobial stewardship initiatives and generate better patient outcomes.

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