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Background

- Empiric treatment for patients with bacteremia or UTI caused by MDROs accurately covers the index pathogen in ~50% of patients¹⁻³
- Appropriate empirical antibiotic treatment in septic patients is associated with a significant reduction in all-cause mortality⁴
- An institution antibiogram (ABG) summarizes hospital resistance and incidence of organisms, predicts likelihood of successful antibiotic treatment, and assists clinicians with empiric antibiotic prescribing
- There may be room to improve the accuracy of institution ABGs to inform antibiotic prescribing with inclusion of patient-specific factors
- Patient-specific antibigrams (PS-ABGs) were developed with the University of Pennsylvania Health System (UPHS) using 8 years of clinical data and logistic regression
- Logistic regression factors included inpatient status, prior antibiotic exposure, and prior microbiological susceptibility
- One model was produced for each organism-antibiotic pair in the institution ABG (n=248)

Objective

- Evaluate the performance of predictive patient-specific ABGs against the institutional ABG in an academic health system

Methods

- PS-ABG susceptibilities were calculated for all positive microbiology specimens from 8/2016 to 12/2016 at UPHS
- Exclusion Criteria: (1) PS-ABG organism-antibiotic pairs with n < 10; (2) Pairs with institution ABG susceptibilities ≥98% or ≤2%
- The evaluation metric was the Brier score, a measure of error for probabilistic predictions with binary results
- Paired t-test was used to compare performance of PS-ABG to institution ABG
- Mean Brier score difference assessed for each organism-antibiotic pair with 95% confidence level

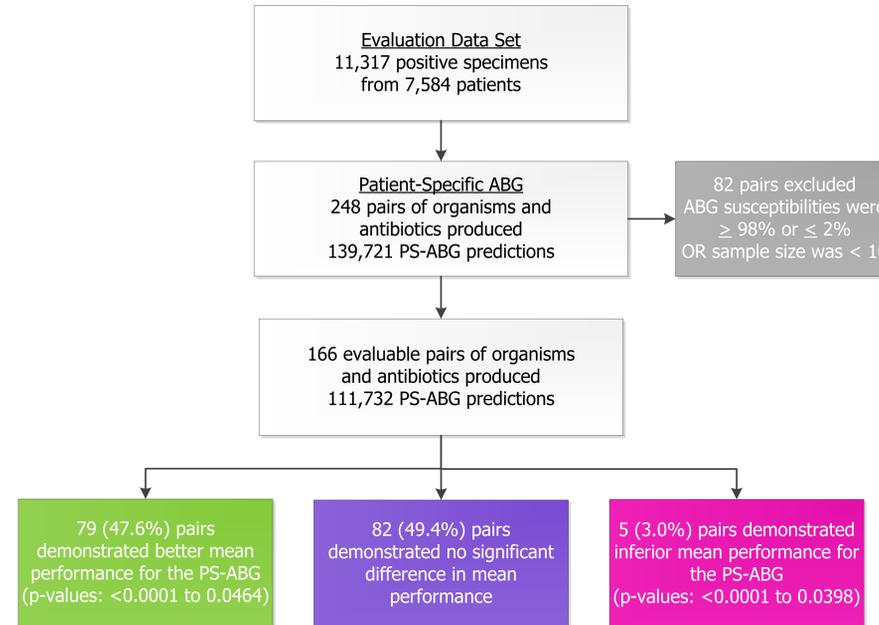
References

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Results

Study Population and Results



Antibiogram Performance Comparison: Gram Negative

	amikacin	amox/clav	ampicillin	amp/sulb	aztreonam	cefazolin	cefepime	ceftazidime	ceftriaxone	fosfomycin	gentamicin	levofloxacin	meropenem	nitrofurantoin	pip/tazo	tetracycline	tobramycin	trim/sulf
<i>A. baumannii</i>																		
<i>C. freundii</i>																		
<i>C. koseri</i>																		
<i>E. aerogenes</i>																		
<i>E. cloacae/asburiae</i>																		
<i>E. coli</i>																		
<i>K. oxytoca</i>																		
<i>K. pneumoniae</i>																		
<i>M. morgani</i>																		
<i>P. mirabilis</i>																		
<i>P. stuartii</i>																		
<i>P. aeruginosa</i>																		
<i>S. marcescens</i>																		
<i>S. maltophilia</i>																		

PS-ABG better than ABG (Green)
 PS-ABG inferior to ABG (Red)
 PS-ABG not significantly different from ABG (Purple)
 Excluded combinations (Grey)

Results (continued)

Antibiogram Performance Comparison: Gram Positive

	amox/clav	ampicillin	amp/sulb	cefazolin	ceftriaxone	clindamycin	daptomycin	fosfomycin	gentamicin	linezolid	oxacillin	penicillin	tetracycline	trim/sulf	vancomycin
<i>E. faecalis</i>															
<i>E. faecium</i>															
<i>Enterococci spp.</i>															
<i>S. aureus</i>															
CoNS															

Antibiogram Performance Comparison: Confidence Intervals with Low/High Sample Sizes



Conclusions

- Incorporation of historic patient data can improve predictions of susceptibility
- Patient-specific ABGs can extend the value of institutional ABGs
- Organism-antibiotic pairs with higher incidence, and therefore more data, generate models with better performance
- Further research is required to evaluate the impact of these predictions on clinical outcomes, the optimal delivery method to clinicians, and generalizability to other settings