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Concordance Between Antibiotic Resistance Genes by Multiplex Polymerase Chain Reaction and Antibiotic Susceptibility by Pooled Antibiotic Sensitivity Testing in Symptomatic Patients with Urinary Tract Infection

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Table 1. Mean number of clinical findings by number of bacteria detected

Bacterial content of urine specimen	Number of specimens	Mean number of clinic findings (standard deviation, range)
Monomicrobial	683	2.66 (1.25, 0-6)
Consortia polymicrobial	433	2.84 (1.25, 0-6)
2 bacteria within consortia	271	2.77 (128, 0-6)
3 bacteria within consortia	144	2.85 (1.15, 1-6)
4 bacteria within consortia	18	3.72 (1.41, 2-6)

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#BS24 | CONCORDANCE BETWEEN ANTIBIOTIC RESISTANCE GENES BY MULTIPLEX POLYMERASE CHAIN REACTION AND ANTIBIOTIC SUSCEPTIBILITY BY POOLED ANTIBIOTIC SENSITIVITY TESTING IN SYMPTOMATIC PATIENTS WITH URINARY TRACT INFECTION

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Introduction: Studies have shown many genes influence antibiotic resistance, and the relationship between genotypic and phenotypic antibiotic resistance is unclear. We sought to analyze the concordance between the presence of antibiotic resistance (ABR) genes and antibiotic susceptibility results in urine samples collected from symptomatic UTI patients.

Methods: Urine samples were collected from patients presenting with possible UTI to 37 geographically disparate Urology clinics from July 2018 to February 2019. Multiplex polymerase chain reaction (M-PCR) was used to test for 33 different ABR genes. Samples in which at least one organism was identified at a quantity of ≥104 cells per mL, Pooled Antibiotic Susceptibility Testing (P-AST), which involves simultaneously growing all detected bacteria together in the presence of antibiotics and then measuring susceptibility, was performed against 14 different antibiotics. The concordance rate between the ABR genes and the P-AST results was generated for the overall group. The concordance rates for each antibiotic between monomicrobial and polymicrobial infection were compared using chi-square test.

Results: Among the 2,512 patients, bacteria were detected in 1,579. ABR gene genotyping and P-AST analysis was performed for 1,155. ABR genes were detected in 36.3% (419/1155) of specimens. Overall, the presence or absence of ABR genes was 60% concordant with antibiotic susceptibility patterns. Two circumstances accounted for the concordance: ABR gene not present by M-PCR/antibiotic sensitive by P-AST (48.4%) and ABR gene present/antibiotic resistant (11.5%). In the 40% non-concordant cases, 25% were ABR gene not present/antibiotic resistant and 15% were ABR gene present/antibiotic sensitive, **Table 1.** Most antibiotics were associated with similar concordance rates for monomicrobial and polymicrobial infections. However, the concordance rates were significantly lower for polymicrobial for three antibiotics: vancomycin, meropenem, and piperacillin/tazobactam, with absolute differences of 9.3% (p value=0.002), 13.1% (p value<0.0001), and 19.0% (p value = 0.019), respectively.

Conclusion: The concordance rate of the ABR genes as identified by M-PCR and phenotypic resistance as detected by P-AST was 60%. Thus, in 40% of samples, the reliance on the M-PCR antibiotic resistance gene report without the phenotypic data reported by P-AST data may lead to inappropriate treatment.

Table 1. Overall Concordance between Presence of ABR genes by M-PCR and the Antibiotic Susceptibility by P-AST Testing

CONCORDANCE		DISCORDANCE	
ABR detected + Bacteria Resistant based on P-AST	ABR NOT detected + Bacteria Susceptible based on P-AST	ABR detected but Bacteria Susceptible based on P-AST	ABR NOT detected but Bacteria Resistant based on P-AST
11.5%	48.4%	15%	25%
60%		40%	

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