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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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concordance in the degree of overall improvement on PGI-I was poor(n=40), with responses significantly favoring greater improvement after surgery (p<0.001). Both pessary use and surgery were associated with significant improvements in prolapse symptoms from baseline on POPDI-6(both p<0.001) and POPIQ-7(both p<0.001), overactive bladder symptoms on OABSS(pessary p=0.03, surgery p=0.005), and colorectal symptoms on CRAIQ-7(pessary p=0.03, surgery p=0.007). The degree of improvement was larger following surgery on POPDI-6(p<0.001), PFIQ-7(p=0.004), and OABSS(p=0.004), but not the CRAIQ-7(p=0.3).

Conclusion: Both pessary use and surgery significantly improved pelvic floor symptoms from baseline. However, concordance between the degrees of improvement between these treatments was poor, with more favorable outcomes after surgery for prolapse and overactive bladder symptoms.

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Poster #74

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.

Methods: Urine samples were collected from patients presenting with possible UTI to 37 Urology clinics from July 2018 to February 2019. Multiplex polymerase chain reaction (M-PCR) was used to test for 33 ABR genes. Pooled Antibiotic Susceptibility Testing (P-AST) was performed against 14 different antibiotics. The concordance rate between the ABR genes and P-AST results was generated. The concordance rates for each antibiotic between monomicrobial and polymicrobial infection were compared using chi-square analysis.

Results: Urine samples were collected from 2,512 patients. Bacteria were detected in 1,579 (63%). 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. Discordant rate was 40%. **Table 1.** Concordance rates were significantly lower for polymicrobial infections for vancomycin, meropenem, and piperacillin/tazobactam (p<0.05).

Conclusion: The concordance rate of the ABR genes and phenotypic resistance was 60%. In 40%, the reliance on ABR report without the phenotypic sensitivity may lead to inappropriate treatment.



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