NEXT-GENERATION SEQUENCING OF DNA APPEARS TO IDENTIFY BIOFILM AND ANTIMICROBIAL SENSITIVITIES/RESISTANCES ON PENILE PROSTHESES BETTER THAN TRADITIONAL CULTURE METHODS IN-VIVO: THE NEW GOLD STANDARD?

ABSTRACT

Introduction

- Previous studies have used traditional culture methods to identify microbial species present at removal and replacement of penile prostheses.
- Next generation sequencing of microbial DNA, which is compared to known bacterial and fungal taxonomies to identify isolates and microbial susceptibilities, is considered the gold standard in other medical specialties.
- The purpose of this study was to compare biofilm compositions and antimicrobial sensitivities/ resistances at penile prosthesis removal/replacement using next generation DNA sequencing to traditional culture methods.

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- 101 patients had both traditional and next generation sequencing results to compare.
- Some of the bacteria identified using both methods were known prosthetic infectious pathogens, with the next generation DNA sequencing producing more isolates (average of 9) than traditional culture methods (p < 0.01) (figure 1).
- Many of the next generation sequencing isolates had sensitivities/resistances to 34 unique antimicrobial agents, enabling the physician to accurately tailor treatments for each patient and was significantly higher in the number of unique antimicrobial agents than traditional culture methods with an average of 7.3 (p < 0.05).

Next generation sequencing of DNA has proven to be beneficial in its thorough analysis of biofilm composition and antimicrobial sensitivities/resistances on penile prosthesis in vivo. It appears to be more sensitive and gives more antimicrobials sensitivities than traditional culture methods.

Methods

Two intraoperative penile prosthesis pump fluid / biofilm specimens were submitted at the time of revision surgery: one for each traditional culture and next-generation sequencing: these were randomly sent for the two methods. For the next generation DNA sequencing methods, the pathogens' genetic signatures and the relative abundances of organisms present in each specimen with any biofilm pathogens evaluated against unique antimicrobial agents.

Results



Conclusions