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Microorganism Profiles of Penile Prosthesis Removed for Infection, Erosion, and Mechanical Malfunction Based on Next-Generation Sequencing.

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- 1 Title: Microorganism Profiles of Penile Prosthesis Removed for Infection, Erosion, And
- 2 Mechanical Malfunction Based on Next-Generation Sequencing
- 3
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14	BACKGROUND: Next-generation sequencing (NGS) is an emerging technology that may
15	allow for more sensitive and sophisticated microbial testing of the microbiota of penile
16	prostheses (PP).
17	
18	AIM: To describe the microorganism profiles of PP explanted for infection, erosion, and
19	mechanical malfunction using NGS.
20	
21	METHODS: All patients who underwent PP removal by two physicians at two institutions
22	were identified. Differences in alpha diversity (i.e., number of species detected, species
23	diversity across samples) and microbiome compositional profiles (Bray-Curtis community
24	dissimilarities) across samples were assessed using ANOVA and PERMANOVA,
25	respectively.
26	
27	OUTCOMES: Number of species detected, species diversity across samples, and microbiome
28	compositional profiles.
29	
30	RESULTS: A total of 83 patients who underwent device removal for infection (n=8, 10%),
31	erosion (n=5, 6%), and mechanical malfunction (n=70, 84%) were included. When
32	considering all studies, 56% (n=48) of NGS and 29% (n=24) of standard cultures resulted
33	positive for presence of microorganisms. Culture only detected the most abundant NGS
34	species in 62.5% (n=5) of infected devices. Species richness and microbiome compositional
35	profiles varied by surgical indication, but not by age, race, diabetes status, or implant
36	duration. Most frequent organisms by surgical indication were Pseudomonas aeruginosa
37	(infection), Staphylococcus epidermidis (erosion), and Escherichia coli (mechanical
38	malfunction). The highest relative abundance organisms were P. aeruginosa (infection),

39	Corynebacterium jeikeium (erosion), and E. coli (mechanical malfunction). GS Vancomycin
40	and gentamicin provide the most comprehensive coverage against these organisms.
41	Minocycline and rifampin do not cover the most abundant organisms for infection and
42	erosion.
43	
44	CLINICAL IMPLICATION: Identifying microbiome profiles of PP removed for infection,
45	erosion, and mechanical malfunction may guide the selection of peri-operative antibiotics and
46	PP antibiotic coatings or hydrophilic dip solutions for each individual scenario.
47	
48	STREGTHS AND LIMITATIONS: While this is the first study to utilize next-generation
49	sequencing to evaluate penile prosthesis biofilm, the clinical significance of these findings
50	has yet to be determined. A prospective, randomized trial aimed at evaluating the clinical
51	significance of NGS in patients with PP infection is currently underway.
52	
53	CONCLUSIONS: NGS testing identified distinct microbiome profiles of PP removed for
54	infection, erosion, and mechanical malfunction.
55	
56	Keywords: Penile prosthesis; penile implant; infection; culture; next-generation sequencing;
57	polymerase chain reaction

INTRODUCTION

60 Penile prosthesis (PP) implantation has emerged as the mainstay surgical treatment 61 for medically refractory erectile dysfunction (ED). Substantial improvements in the efficacy 62 and durability of PP over past decades have allowed a large and growing volume of patients 63 to undergo PP surgery.(1) However, PP infection remains one of the most feared 64 postoperative complications and places a significant economic burden on the healthcare 65 system, with reported cost of management being six times that of the initial placement.(2) Significant efforts, such as infection retardant coatings on implants, better skin prep 66 67 techniques, revision washout, and implementation of the "no-touch" surgical technique, have 68 been utilized to optimize the management and reduce the risk of this complication.(3) 69 As evidence has shown that traditional infection rates of revision surgeries have a 70 much higher rate of infection at 10.0 - 13.3% when compared to virgin cases at 0.5 - 2.0%, 71 surgeons have attempted to use standard culture of the devices to help guide antibiotic 72 therapy for revisions patients.(4) However, recent multi-institutional data evaluating 73 clinically infected device explantations have reported device cultures showing no growth or 74 non-specific growth in up to 33% of cases.(5) This may be attributed to flaws in the culture 75 collection technique, the difficult nature of identifying and growing certain biofilm-76 associated microorganisms, or the administration of antibiotics before culture acquisition.(6) 77 Regardless, this makes tailoring of the antibiotic regimen challenging.

Emerging technology has allowed for more sensitive and sophisticated testing and may be useful in the setting of genitourinary prostheses infections. One of the most promising advances in this realm is rapid molecular sequencing. Polymerase chain reaction (PCR) is the most familiar technology, which is a fast and inexpensive technique that amplifies small segments of DNA targets and may detect a comprehensive group of microorganisms and even resistance genes. This technology is already clinically available for blood cultures, 84 respiratory panels, pneumonia, meningitis, and may play a role in improving patient 85 outcomes and decrease surgical complications in patients with infected PP.(7) Nextgeneration sequencing (NGS), also referred to as high throughput sequencing, is a technology 86 87 which allows for hundreds to thousands of strands of DNA to be sequenced in parallel. 88 Unlike PCR, which is limited to evaluating pre-determined targets, NGS uses bioinformatics 89 to piece DNA fragments together and compare the sequences to reference genome 90 databanks.(8) NGS may help to provide a more global understanding of biofilms and 91 microorganisms found on PP. Herein, we aim to describe the microorganism profiles of PP 92 explanted for infection, erosion, and mechanical malfunction using PCR and NGS molecular 93 techniques.

94

95 MATERIALS AND METHODS

96 <u>Study Design and Patient Population</u>

97 Institutional review board approval was obtained to perform a retrospective review of 98 consecutive patients undergoing PP explant procedures from January 2015 to January 2019 99 by two physicians at two institutions (IRB# TJU 20E.509 & WK 18.0002). Patients 100 undergoing PP explantations were included regardless of indication for surgery (infection, 101 erosion, and mechanical malfunction). Patients undergoing planned device explantation with 102 or without replacement underwent routine preoperative testing, including a urinalysis and if 103 positive, a urine culture. Positive cultures were treated with a seven-day course of culture-104 specific antibiotics preoperatively. Perioperative antibiotics were administered in accordance 105 with the American Urological Association (AUA) Guidelines using vancomycin and 106 gentamicin unless clinically contraindicated.(9, 10) Postoperatively, patients were given 5-7 107 days of trimethoprim/sulfamethoxazole or culture-specific antibiotics based on preoperative

urine cultures. Revision surgery was performed using either the penoscrotal or infrapubic
method, but was not always performed by the same surgeon who performed the initial
placement.(11) The antibiotic impregnated outer layer, InhibiZoneTM, was utilized for the
AMS 700TM inflatable PP, while vancomycin and gentamicin were the hydrophilic solution
of choice for the Titan® Touch inflatable PP. Vancomycin and gentamicin mixed in normal
saline was also the irrigation fluid of choice at the time of implantation.

114

115 Intraoperative Sample Collection and Molecular Testing

At the time of explantation, surgeons minimized device contact with neighboring skin to decrease the potential risk of contamination by normal skin flora. Sterile gauze was used to swab the removed devices. The swabs were stored in sterile containers and shipped overnight at ambient temperature for NGS testing (MicroGenDX, Lubbock, TX). A second specimen or the explanted device was sent to the respective institutional microbiology laboratory for routine aerobic and anaerobic culture.

122 NGS of 16s ribosomal RNA was performed using an Illumina MiSeq sequencing 123 platform (Illumina, San Diego, CA). For this, variable regions 1-2 of 16S rDNA gene were 124 amplified and prepared into libraries for sequencing following molecular methods outlined in Tipton et al. but using primers 28F and 388R.(12, 13) Bioinformatic processing followed that 125 126 reported by Cook et al. and McDonald et al.(8, 14) Generated sequences of microorganisms 127 were compared with an in-house curated species database and an agreement of over 90% 128 between the database and the sequence results as necessary to report a positive result. 129 Bacteria and fungi were reported as relative abundances within each specimen (with 2% 130 being the minimum threshold of reporting). Prior to statistical analysis all NGS sample results were compared to their 131

132 corresponding controls which were a combination of DNA extraction controls and no-

template PCR controls. NGS detection for control samples were first transformed to relative
abundances and then compared to matched samples. If the sample and control both had
detection for a given microbe, the read counts of the sample were depleted proportional to the
relative abundance in the control. Also, any detection of *Pelomonas saccharophila* and *Ralstonia pickettii* were eliminated because they are known common

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138

140 Data and Statistical Analysis

reagent contaminants.

Patient demographics and etiologies for device explantation were abstracted.
Etiologies were broadly classified by infection (e.g. gross infection), erosion (e.g. urethral
erosion, tubing or pump extrusion), or mechanical malfunction (e.g. fluid leak, floppy glans,
impending erosion, cylinder resizing). Standard culture and NGS results were documented as
"yes" for presence of microorganisms, or "no" for absence of organisms. Microorganism
species identifications and relative abundances were documented.

147 Differences in number of species detected (richness) and species diversity (expressed 148 as the exponential function of the Shannon diversity metric, i.e., Hill₁ numbers) across 149 samples explained by age, ethnicity, diabetes status, implant duration, and year of implant 150 removal were assessed using ANOVA with Type III sum of squares and backward stepwise 151 selection. Differences in microbiome compositional profiles among samples were calculated 152 with Bray-Curtis community dissimilarities, and Permutational Analysis of Variance 153 (PERMANOVA) was used to test for the effect of the sample variables mentioned above for 154 ANOVA.(15, 16) An ordination was performed by principal coordinates analysis using Bray-Curtis distances. Tests for differences in the relative abundance of species depending on 155 156 indication classification were conducted using Analysis of Compositions of Microbiomes

with Bias Correction (ANCOM-BC).(17) Chi-squared tests were used to assess relationships
between etiologies and microorganism detection rate. Statistical analyses were performed
using R statistical software.

160

161 RESULTS

162 Patient Demographics

163 From a total of 110 patients, 83 patients, with a median age of 69 (interquartile range: 17) years with both NGS and culture results, were included in this study. Indication for 164 165 device removal included infection (n=8, 10%), erosion (n=5, 6%), and mechanical 166 malfunction (n=70, 84%). The median time from PP implant to explant was 28 (interquartile 167 range: 43.5) months. Of the devices removed, only one was a malleable PP, while the other 168 82 were inflatable PP. At the time of explant, 68 (82%) underwent device replacement, four 169 of which were malleable PP, while the other 64 were inflatable PP. Eight (9.6%) patients had 170 a concomitant artificial urinary sphincter device that was explanted at the time of revision 171 surgery.

172

173 Standard Culture and Rapid Molecular Testing Results

Of the 83 devices, 48 (56%) NGS studies and 24 (29%) standard cultures resulted 174 175 positive for detection of microorganisms (p<0.001). Among the 8 infected cases, all NGS and 176 culture studies tested positive. Focusing specifically on the 8 infected samples there were 14 177 culture positive microorganisms, and 6(42%) of these culture detections were also found in 178 the corresponding patient's NGS result. Making the same comparison at the genus level 179 resulted in 8 (57%) of these culture detections (8 of 14) also occurring in the NGS results. When culture did detect a species and genus reported by NGS, culture detected the most 180 181 abundant NGS species and genus in 5 (63%) of 8 patients.

182 Among the 5 erosion cases, 4 (80%) NGS studies and 4 (80%) cultures studies tested 183 positive (with one instance of NGS being negative and another instance of culture being negative). Among the 70 mechanical malfunction cases, 36 (51%) NGS studies and 12 (17%) 184 185 culture studies tested positive. Considering patients with only mechanical malfunction, NGS 186 and culture were both negative in 29 studies (41%) and both positive in 8 cases (11%). 187 Time for PCR, NGS and standard culture finalized reporting times were assessed 188 specifically in infection and erosion cases from one institution. PCR studies returned at a 189 mean of 1 day, which was significantly faster than NGS and culture (both p<0.01). NGS 190 results returned at a mean 5 days compared to 7 days for finalized conventional culture 191 results (p=0.12). Quantitative PCR also assessed for antibiotic resistance genes, which were 192 detected in 2 cases. Tetracycline resistance was identified in an infected device and 193 methicillin resistance was identified in an eroded device. No resistance genes were detected 194 in devices removed for mechanical malfunction. 195 196 Microorganism Profiles 197 Richness, defined as the number of species present in a sample, was calculated for all 198 NGS positive samples and effect of surgical indication, age, race, diabetes status, and implant duration on observed richness values was assessed (Figure 1). Only surgical indication was 199 200 significant (F=16.01, p<0.01), but time to surgery was the next most influential, albeit not 201 significant (F=3.04, p=0.09). For Hill₁, which is an alpha measure that encapsulates both

richness and evenness of species relative abundances of microbiota profiles, results were
similar to those for observed richness values only with surgical indication being the only
significant variable (F=23.98, p<0.01), and diabetes being the next most influential, albeit not

205 significant (F=2.08, p=0.16).

The most frequent organisms by surgical indication (infection, erosion, and mechanical malfunction) were *Pseudomonas aeruginosa*, *Staphylococcus epidermidis*, and *Escherichia coli*, respectively (Figure 2). The highest relative abundant organisms by infection, erosion, and mechanical indications for revision surgery were *P. aeruginosa*, *Corynebacterium jeikeium*, and *E. coli*, respectively (Figure 3). Common implant antibiotic coatings and dip combinations against the most frequent and abundant organisms were broadly reviewed (Table 1).

213 Fungal elements were identified in two NGS specimens that were not identified in 214 corresponding standard cultures. Verticillium sp. was identified by NGS in one mechanically 215 failed implant from a diabetic patient, while Malassezia restricta was identified by NGS in an 216 infected implant from a non-diabetic patient. Candida parapsilosis was identified by standard 217 culture in one infected implant from a non-diabetic patient that was not detected by NGS. 218 Microbiome compositional profiles varied by surgical indication (F=2.03, p<0.01), 219 but not by age, race, or diabetic status. Each surgical indication was then compared post hoc, 220 revealing that infection and erosion samples did not significantly differ compositionally 221 (p=0.58) but did significantly differ from mechanical malfunction samples (both p<0.01) 222 (Figure 4). Relative abundances of species that were significant through differential 223 abundance testing comparing indication types are exhibited in Figure 5.

224

225 DISCUSSION

Rapid molecular testing is an emerging technology that may allow for more sensitive and sophisticated microbial testing compared to standard techniques. We found that NGS may best play a role in identifying microorganisms in devices explanted due to infection or erosion rather than a mechanical malfunction etiology due to its higher positivity rates for those surgical indications. While it may not seem surprising that infected explants were more likely to yield positive results, Henry et al. previously demonstrated that up to 70% of
patients with clinically uninfected penile prosthesis can grow positive bacteria cultures at the
time of reoperation.(18) Likewise, we found that 51% of NGS and 17% of standard culture
studies of uninfected devices in our cohort detected microorganisms. However, this was a
much lower rate when compared to NGS and standard cultures results of their infected
counterparts (both 100%).

237 When comparing the timings to results reporting in one institution, we found that 238 NGS testing results were reported at a slightly faster rate than culture results, although this 239 difference was not statistically significant. Most notably, PCR results could be returned 240 within hours of receipt of the specimen. Clinically, this may allow for prompt tailoring of 241 antibiotics or antifungals and earlier targeted antimicrobial therapy, and identification of resistance genes. Furthermore, NGS assesses for both bacterial and fungal organisms 242 243 simultaneously, eliminating the long wait for fungal culture results to finalize. Although 244 immediate versus delayed salvage of an implant has not been shown to make a difference, 245 perhaps earlier detection of the causative organisms and assurance that the correct antibiotics 246 are being administered may allow urologists to more confidently proceed with salvage 247 treatments.(19)

248 NGS provides an opportunity to better understand the microbiota on PP and may 249 better described how specific groups may be at risk for infection. The presence of biofilm 250 formation on the implanted device is thought to be a predisposing factor for infection in 251 patients undergoing revision surgery.(18, 20-22) Removal of the primary device may disrupt 252 biofilm and allow previously sequestered bacteria to be released and adhere to the new 253 implant causing clinical infection.(23) In this present study, E. coli was the most frequent and 254 abundant organism on devices replaced for mechanical malfunction, contrary to the historical 255 paradigm of coagulase-negative Staphylococcus being the dominant species of PP

biofilms.(3, 20, 24, 25) The use of antibiotic coated devices and antibiotic irrigation may
have reduced the coagulase-negative *Staphylococcus*, but allowed more virulent organism to
become predominant as a result. Characterizing biofilm on PP is also a clinical imperative
since it may additionally be linked to mechanical failures resulting in decreased device
longevity and increased need for revision surgery.(26)

261 The most conservative treatment of an infected or eroded PP is complete removal 262 with delayed implantation, which may result in corporal fibrosis, decreased penile length, and 263 a potentially challenging replacement surgery. The challenge is that not all eroded devices are 264 infected, even though they may be treated as such. Isolated single component removal and 265 replacement has been described for eroded tubing and pumps in small cases series.(27, 28) 266 Salvage washout with malleable or inflatable PP replacement is also feasible with potential 267 infection-free rates of 93%; however, its use is currently limited to only 17.3% of infected 268 cases.(19, 29)

An improved characterization of microbiota profiles of PPs may help to increase 269 270 utilization and success of salvage treatments by guiding the selection of peri-operative 271 antibiotics for systemic use and PP antibiotic and antifungal coatings or hydrophilic dip 272 solutions. For example, in this study, virulent, Gram-negative Pseudomonas aeruginosa was 273 the most frequent and abundant organisms on infected implants, while skin flora, 274 Staphylococcus epidermidis (most frequent) and Corynebacterium jeikeium (most abundant), 275 were identified predominantly on eroded implants. When common implant antibiotic coatings 276 and dip combinations were broadly reviewed, vancomycin and gentamicin would provide the 277 best coverage for infected and eroded implants which is consistent with a recent large multi-278 center review.(30) Interestingly, the most abundant organisms for infection and erosion were 279 not covered by the combination of minocycline and rifampin, a common infection retardant

coating. Fungal elements were also detected in our study which reiterates the call to identify
the clinical value of incorporating antifungals in PP surgery.(5)

282 NGS detected additional microorganisms not detected on standard cultures and may 283 be more informative. For example, when focusing specifically on infected devices, culture 284 only detected the most abundant NGS species in 62.5% (n=5). Additionally, when looking at 285 the individual result reports, we found that the overall trend was that NGS tended to detect a 286 polymicrobial profile, while the results demonstrated by cultures were mostly 287 monomicrobial. Gross et al. similarly identified that 25% of culture-positive infection also 288 showed polymicrobial growth.(5) Interestingly, while this has yet to be established in the 289 urologic literature, treatment of polymicrobial infections has been shown to have lower 290 success rates compared with monomicrobial infections in infected periprosthetic joints within the orthopedic literature.(31, 32) NGS may help to provide a better understanding of the 291 292 predominant organism (abundance data) on PP and help to established whether these profiles 293 are truly polymicrobial and require treatment, or rather an infection with a dominant species 294 with the other organisms acting in concert.(33)

295 Our study is not without limitations. Best techniques for sampling the microbiota of 296 PP and proper controls are still in development. Swabbing the implants may be not sufficient to dislodge microorganisms and may be an incomplete assessment of the microbial 297 298 microenvironment. Controls were not utilized at the time of surgery to ensure microbes on 299 the gauze were not contaminants from the field. Therefore, detected organisms may not 300 represent a clinically significant infection and may reflect a contamination during device 301 removal. Direct susceptibility testing was also not performed for NGS results and this made it 302 difficult to compare the rates of bacterial composition and antibiotic resistance in our study. 303 Samples were shipped overnight at ambient temperatures which may affect DNA integrity, 304 and factoring was not performed for varying biomass between specimens during molecular

305	testing. In addition, no clinical studies have yet been performed showing that treating
306	organisms identified in this study will have a positive clinical effect. A prospective,
307	randomized trial aimed at evaluating the clinical significance of NGS in patients with PP
308	infection and erosion is being performed. Despite these limitations, NGS was utilized to
309	further characterize the microbiome profiles of PP removed for infection, erosion, and
310	mechanical malfunction.
311	
312	CONCLUSIONS
313	NGS helped to further characterize distinct microbiomes of PP removed for infection,
314	erosion, and mechanical malfunction. The clinical potential of NGS is most useful in patients
315	with infected and eroded devices, compared to devices removed for mechanical malfunction.
316	PCR shows promise in rapidly detecting clinically significant organisms and resistance genes
317	in PP infections. A prospective, randomized trial aimed at evaluating the clinical significance

318 of NGS in patients with PP infection is being performed.

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442443 Figure 1. Histogram of species richness by surgical indication for penile prosthesis removal.



446 Figure 2. Bar chart of frequency of the most common species within each surgical indication

- 447 for penile prosthesis removal. For this illustration the top 10 most common species within
- 448 infection, erosion, and mechanical malfunction indications were identified, which resulted in
- 449 21 unique species.



452 Figure 3. Bar chart of mean relative abundances of the most common species within each

453 surgical indication for penile prosthesis removal. For this illustration the top 10 most

454 common species within infection, erosion, and mechanical malfunction indications were

455 identified, which resulted in 21 unique species.





Figure 4. Principal coordinates analysis based on Bray-Curtis Dissimilarities. Species that
had the strongest correlation with the first two axes are illustrated. The species evaluated for
plotting were those previously identified to be the most common in the study. The direction
and length of the arrow for each species represents increasing relative abundance of the

462 corresponding species for samples in that area of the plot.





464 Figure 5. Box and dot plots of relative abundances of species that were significant through
465 differential abundance testing comparing indication types. Each dot represents values for
466 individual samples. The boxes of the boxplots are defined by 25th and 75th quartiles, the

individual samples. The boxes of the boxplots are defined by 25th and 75th quartiles, thorizonal lines within boxes are medians, and whiskers calculated as 1.5 times the

468 interquartile range.

	Infected	Eroded		Mechanical Malfunction
	P. aeruginosa	S. epidermidis	C. jeikeium	E. coli
	Most abundant and frequent organism	Most frequent organism	Most abundant organism	Most abundant and frequent organism
Coverage of Common Antibiotic Coatings/Dips				
Minocycline/Rifampin		Х		Х
Gentamicin/Rifampin	Х	Х		Х
Gentamicin/Vancomycin	Х	х	х	Х
Gentamicin/Bacitracin	Х			Х
Rifampin/trimethoprim/sulfamethoxazole		Х		x