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Original Research

Qualitative Comparison of Cultured Skin Microbiota From the Inguinal Region of Obese and Nonobese Patients Eligible for Hip Arthroplasty

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ABSTRACT

Background: With the rising prevalence of obesity, surgeons are frequently confronted with the problem of treating osteoarthritis of the hip via arthroplasty (total hip arthroplasty) in severely obese patients. To reduce the surgical impact, minimal-invasive approaches are often chosen. For this reason, the direct anterior approach has gained popularity but is suspected of leading to more wound complications in obese patients, especially by Gram-negative pathogens. Causative differences of the skin microbiome have been suspected but not yet proven.

Methods: Patients scheduled for total hip arthroplasty via direct anterior approach were screened for inclusion. The study group was defined as patients with a body mass index ≥35 and an abdominal pannus hanging over the incision site, whereas nonobese patients served as the control group. Samples of the microbiome were taken 2-3 cm distal and lateral to the superior anterior iliac spine using plates and swabs. Species identification was carried out by mass spectrometric analysis.

Results: The study group consisted of 28 patients, the control group of 36 patients. The most frequent potential pathogen on the skin was *Staphylococcus epidermidis* in both the groups. Microbiota found in obese patients showed significantly higher prevalence of Gram-negative bacteria from the order Enterobacterales. Wound complications were more frequent in the study group, but this was not statistically significant.

Conclusions: Obese patients with abdominal pannus present higher rates of colonization with Enterobacterales at the incision site of the direct anterior approach. Modifications of the antibiotic regime and the incision should be considered in this special patient population.

Introduction

Obesity is among the most frequent diseases worldwide. Within the last decades the prevalence of obesity has doubled and nearly one third of the world population is affected [1]. While contributing to many other disease conditions, obesity leads to a mechanical overload of joints and to altered metabolic and inflammatory pathways finally resulting in severe osteoarthritis making joint arthroplasty necessary in the end [2].

Generally, total joint arthroplasty of the hip and the knee is considered to be highly effective and the risk of severe complications is reported to be below 5% [3]. However, obesity leads to a significant rise in severe medical and surgical adverse events during and after total joint arthroplasty. Next to higher rates of thromboembolic events and renal insufficiency, for example, especially the risk of wound dehiscence and superficial and deep infections rises when transitioning to higher body mass index groups [4,5].

In total hip arthroplasty (THA), especially the direct anterior approach (DAA) has been reported to be associated with higher rates of wound complications and infections in obese patients [6-9]. Next to negative systemic medical effects of obesity such as malnutrition, diabetes mellitus, renal insufficiency and impaired immune status, the anatomic location of the skin incision during

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DAA has been discussed as a contributing factor. In particular, the proximity to the inguinal crease, frequently with overhanging abdominal pannus and critical hygiene, has been of concern [6,7]. These circumstances might furthermore lead to an unfavorable skin microbiome in this area being characterized by Gram-negative bacteria, possibly not addressed by the standard perioperative antibiotic therapy [9,10]. Nevertheless, clear evidence of this is lacking.

In order to close this gap of knowledge, this study was initiated. The hypothesis was that obese patients scheduled for THA via DAA would show a different type of microbiome in the area of the skin incision underneath the abdominal pannus compared to nonobese patients. Especially the presence of Gram-negative bacteria on the skin was of interest, as these lead to joint infections that are often more severe and are often not sufficiently addressed by the standard perioperative single-shot antibiotic therapy, mostly being cefazolin [11-13].

Materials and methods

Study design

After approval by the local ethics committee and registration in the German Clinical Trials Register, this prospective comparative noninterventional observation study was carried out from January 2022 to March 2023. All patients scheduled for THA at a high-volume academic medical center were screened for the following inclusion criteria:

- Primary osteoarthritis
- THA planned via the DAA
- Ability to give informed consent
- Age over 18 years
- Body mass index $\geq$35 kg/m^2 and abdominal pannus hanging over the incision site (study group)
- Body mass index $\leq$25 kg/m^2 and no abdominal pannus (control group)

The following criteria lead to exclusion from the study:

- Use of topical antibiotics or steroids in an area of 20 cm around the planned incision site within the last 7 days
- Use of systemic antibiotics, steroids, or immunosuppressants within the last 4 weeks
- Skin lesions and diseases within an area of 5 cm around the planed incision site
- Generalized skin diseases
- Body art (tattoos, piercings, and so on) in an area of 20 cm around the planned incision site
- Infectious diseases within the last 4 weeks
- Vaccination within the last 4 weeks

All patients received cefazolin as single-shot antibiotic prophylaxis within 1 hour prior to the intervention. When the body weight exceeded 120 kg, 3 g were given, otherwise 2 g.

The primary outcome was the bacterial spectrum in the incision area of the DAA and possible differences between the study and the control group. In order to detect clinically relevant bacteria, a culture-based approach was used.

The rate of wound complications within the first 3 months was defined as secondary outcome parameter. In case of wound complications, tissues samples were taken and the isolated pathogens were compared to the detected skin microbiome.

Due to missing estimates concerning the bacterial load and the composition of the microbiome in the incision area of the DAA, no *pre hoc* sample size analysis could be performed. Based on the sample sizes of other studies investigating the microbiome of the skin, it was planned to recruit approximately 30 patients for the study group and 30 patients for the control group [10,14,15].

Sampling

After informed consent, samples were taken by the study physician in the proximal area of the planned skin incision 2-3 cm distal and lateral to the superior anterior iliac spine using Replicate Organism Detection and Counting plates and bacteriologic swabs. The Replicate Organism Detection and Counting plates were pressed on to the skin and left there for 3 seconds. The swabs were moistened using sterile 0.9% NaCl and wiped on the skin. In cases of an abdominal pannus, the samples were taken underneath it. All samples were taken at least 1 day prior to the surgery to avoid interference with the perioperative antibiotic prophylaxis and the preoperative local skin decontamination which was performed by chlorhexidine lotions the evening before and the morning of surgery.

Bacteriologic analysis

Samples were transported to the microbiologic laboratory within 2 hours for bacteriologic analysis. For detection and quantification of aerobic microorganisms, Replicate Organism Detection and Counting plates containing Columbia sheep blood agar (bioMérieux, Marcy-l'Étoile, France) were incubated for 18-24 hours at 35 $\pm$ 2°C with 5% CO_2 atmosphere. For analysis of anaerobic bacteria, bacteriologic swabs in Amies medium (MASTASWAB, Mast Group Ltd., Reinfeld, Germany) were incubated in thioglycolate broth (Merck, Darmstadt, Germany) for 18-24 hours at 35 $\pm$ 2°C without CO_2. The thioglycolate broth was subsequently plated on viande levure agar and further incubated under anaerobic conditions at 35 $\pm$ 2°C for 48 hours.

Upon incubation, read out was carried out by trained personnel of the microbiologic institute. All distinguishable colony morphologies were registered and subsequently subcultured on Columbia sheep blood agar for aerobic or on viande levure agar for anaerobic growth. Species identification was carried out on subcultivated strains by mass spectrometric analysis using VITEK MS (bioMérieux, Marcy-l'Étoile, France).

Data analyses

All data were processed using Microsoft Excel, version 16.78.3 (Microsoft Corp., Redmond, WA, USA). Differences between categorical data were compared using 2-sided *Chi*-square or *Fisher's* exact test as appropriate. Statistical significance was assumed for $P < .05$.

Patient characteristics

A total of 64 patients were eligible for the study, 36 were assigned to the control group and 28 to the study group. The study group contained nearly 5 times more women than men. Table 1 summarizes the demographics.

Results

Description of the microbiota

The microbiologic analysis identified Gram-positive and Gram-negative aerobic and anaerobic bacteria that grew within 3 days of analysis (Table 2). All in all, 83 bacterial species of 36 genera from

the phyla Pseudomonadota, Bacillota, Bacteroidota, and Actinomycetota were differentiated. In addition, a yeast (*Candida parapsilosis*) was found in one case. The mean number of species that could be cultivated per patient was 6.03 (range, 2-11).

The species most frequently found was *Staphylococcus epidermidis*, which was present in 62 individuals. *Staphylococcus aureus* and *Streptococcus agalactiae* were present in 5 and 3 patients, respectively.

Gram-negative aerobic bacteria were isolated from 22 individuals. Among this bacterial group, the nonfermenters *Moraxella osloensis* and *Acinetobacter lwoffii* were the most frequent species and were each found in 5 patients. Eight patients were colonized by species of the order Enterobacterales. Among this group, *Escherichia coli* was the most common species.

Obligate anaerobes were found in 14 patients. Thereby, *Cutibacterium avidum* was the most common species and was detected in 5 patients.

Differences in microbiota between the study and the control groups

The number of detected bacterial species was comparable in both groups with a mean of 6.3 in the study group (range, 3 to 11) and 5.8 in the control group (range, 2 to 11), respectively. Enterobacterales were cultivated in significantly more patients ($P = .037$) from the study group (n = 6 [21.4%]) than the control group (n = 1 [2.8%]). The colonizing species included *E. coli*, *Klebsiella oxytoca*, *Klebsiella pneumoniae, Enterobacter cloacae* complex, and *Proteus mirabilis*. Table 3 provides an overview of the differences in microbiota between both groups.

Wound infections

Overall, 4 cases (6.5%) of surgical site infections leading to revision surgery occurred. Three of them happened within the study group (11.5%) and 1 in the control group (2.8%) ($P = .310$). Within the study group, surgeons decided in 12 cases (46%) to modify the incision using a curved incision to avoid lying under the pannus. All 3 wound infections occurred in the obese patients who had been operated via the standard incision leading to a wound complication rate of 21.4% in this subgroup ($P = .225$).

In 3 of the 4 wound infections, bacteria were cultivated from tissue samples taken during revision surgery. For the study group, these were *S. epidermidis* and *Pseudomonas aeruginosa*. The only infection in the control group was caused by *Streptococcus dysgalactiae*. In none of these cases was the same pathogen found before on the skin.

Table 1
Characteristics of patients included in the study.

Patient group (n)	Mean age (range)	Sex ratio (women/men)	Mean BMI (range)	ASA score n (%)
Control (36)	66 (48-83)	1.0	22.9 (19-25)	ASA 1: 3 (8) ASA 2: 31 (86) ASA 3: 2 (6) ASA 4: 0
Study (28)	66 (50-85)	4.6	37.8 (35-48)	ASA 1: 0 ASA 2: 21 (75) ASA 3: 6 (21) ASA 4: 1 (4)

ASA, American Society of Anesthesiologists; BMI, body mass index; n, Number.

Discussion

To our knowledge, this is the first study comparing the skin microbiome in the incision area of the DAA between obese and nonobese patients scheduled for THA. The most important finding was the significantly higher prevalence of Enterobacterales on the skin of obese patients with overhanging abdominal pannus. The order Enterobacterales consists of 7 families of Gram-negative bacteria [16]. Many known and frequently isolated pathogens of periprosthetic infections of the hip are members of these families, in particular *E. coli*, *Proteus mirabilis*, *K. pneumoniae,* and *E. cloacae*. It is these species that we found to be more frequently present in obese patients. Buchalter et al [9] presented significant higher rates of wound infections by Gram-negative pathogens in patients after THA through the DAA in contrast to non-DAA. The authors assumed the microbiome of the inguinal region to be responsible for this. Purcell et al [6] in 2016 presented his study showing higher rates of infections after THA via DAA in severely obese patients. Although not further discussed in their paper, the identified pathogens in the obese group were mostly Gram-negatives from the Enterobacterales order. Ilchmann et al [17] compared the infections rates after THA in 1104 cases between the lateral and the anterior approach. While there was no statistically significant higher infection risk in the DAA group, infections by Gram-negative bacteria were exclusively found in the DAA group. Therefore, our finding is not only consistent with results from these previous studies, but finally provides an explanation for their results.

While the higher prevalence of Enterobacterales in the groin region of obese patients might sufficiently be explained by the proximity to the urogenital region and possibly reduced local hygienic conditions in case of severe obesity with abdominal pannus, the clinical implications by this finding must be discussed further:

Our findings raise the question whether obese patients receiving THA via the DAA must be given an antibiotic prophylaxis that better addresses the Gram-negative microbiome of their skin. Cefazolin, which is commonly used as single shot antibiotic prophylaxis during THA, is not sufficiently effective against most species of the Enterobacterales order [18]. Generally, approximately 50% of Gram-negative bacteria causative for periprosthetic infections are known to be resistant to cefazolin [12]. This might additionally explain why these patients show higher rates of wound infections and why these are more often caused by Gram-negatives. Bosco et al [19] reported a reduction by nearly half when adding gentamicin or aztreonam to their perioperative antibiotic protocol. Though not discussed in their paper, it can be assumed that their patient population contained a high proportion of obese patients, as nearly 50 % of THA patients in the United States are obese or morbidly obese [20]. As usual, possible benefits by interventions must be weighed against potential risks. Adding gentamicin to the antibiotic protocol might lead to adverse events such as nephrotoxicity and the development of resistant bacteria. Nevertheless, periprosthetic joint infections are devastating complications, and the risk of their surgical and antibiotic treatment must be considered much higher than the risk of adding an additional antibiotic agent to the perioperative antibiotic protocol.

In our study, more cases of wound infections were found in obese patients than in the control group. Even though the sample size was not sufficient to reach statistical significance, this observation confirms previous reports about the higher risk of wound infections in obese patients [6-9]. In this context, it is also open to debate whether the standard skin incision during DAA is appropriate for obese patients with overhanging pannus. Many studies highlight the substantially elevated incidence of wound complications in obese patients undergoing THA via DAA with the standard incision [6-8,17,21]. As a possible solution, modifications of the

Table 2
Identified species of the microbiome and their distribution in the study and control groups.

Species	Control (total: 36)	Study (total: 28)	Phylum	Class	Order	Family
Acinetobacter johnsonii	0	1	Pseudomonadota	Gammaproteobacteria	Moraxellales	Moraxellaceae
Acinetobacter lwoffii	4	1	Pseudomonadota	Gammaproteobacteria	Moraxellales	Moraxellaceae
Acinetobacter radioresistens	0	1	Pseudomonadota	Gammaproteobacteria	Moraxellales	Moraxellaceae
Acinetobacter sp.	0	1	Pseudomonadota	Gammaproteobacteria	Moraxellales	Moraxellaceae
Acinetobacter ursingii	0	1	Pseudomonadota	Gammaproteobacteria	Moraxellales	Moraxellaceae
Aerococcus viridans	2	2	Bacillota	Bacilli	Lactobacillales	Aerococcaceae
Alloiococcus otitidis	1	0	Bacillota	Bacilli	Lactobacillales	Carnobacteriaceae
Bacillus altitudinis/pumilus	0	1	Bacillota	Bacilli	Bacillales	Bacillaceae
Bacillus cereus	6	7	Bacillota	Bacilli	Bacillales	Bacillaceae
Bacillus licheniformis	0	1	Bacillota	Bacilli	Bacillales	Bacillaceae
Bacteroides sp.	0	1	Bacteroidota	Bacteroidia	Bacteroidales	Bacteroidaceae
Bifidobacterium sp.	1	0	Actinomycetota	Actinomycetes	Bifidobacteriales	Bifidobacteriaceae
Candida parapsilosis	0	1	Ascomycota	Saccharomycetes	Saccharomycetales	Debaryomycetaceae
Citrobacter koseri	0	1	Pseudomonadota	Gammaproteobacteria	Enterobacterales	Enterobacteriaceae
Corynebacterium afermentans	1	1	Actinomycetota	Actinomycetes	Mycobacteriales	Corynebacteriaceae
Corynebacterium amycolatum	5	3	Actinomycetota	Actinomycetes	Mycobacteriales	Corynebacteriaceae
Corynebacterium aurimucosum	3	5	Actinomycetota	Actinomycetes	Mycobacteriales	Corynebacteriaceae
Corynebacterium coyleae	1	2	Actinomycetota	Actinomycetes	Mycobacteriales	Corynebacteriaceae
Corynebacterium durum	1	1	Actinomycetota	Actinomycetes	Mycobacteriales	Corynebacteriaceae
Corynebacterium glucuronolyticum	0	1	Actinomycetota	Actinomycetes	Mycobacteriales	Corynebacteriaceae
Corynebacterium jeikeium	0	1	Actinomycetota	Actinomycetes	Mycobacteriales	Corynebacteriaceae
Corynebacterium mucifaciens/ureicelerivorans	3	0	Actinomycetota	Actinomycetes	Mycobacteriales	Corynebacteriaceae
Corynebacterium propinquum	1	1	Actinomycetota	Actinomycetes	Mycobacteriales	Corynebacteriaceae
Corynebacterium simulans	1	2	Actinomycetota	Actinomycetes	Mycobacteriales	Corynebacteriaceae
Corynebacterium sp.	3	5	Actinomycetota	Actinomycetes	Mycobacteriales	Corynebacteriaceae
Corynebacterium striatum	0	1	Actinomycetota	Actinomycetes	Mycobacteriales	Corynebacteriaceae
Corynebacterium tuberculostearicum	9	12	Actinomycetota	Actinomycetes	Mycobacteriales	Corynebacteriaceae
Corynebacterium urealyticum	0	1	Actinomycetota	Actinomycetes	Mycobacteriales	Corynebacteriaceae
Cutibacterium acnes	1	1	Actinomycetota	Actinomycetes	Propionibacteriales	Propionibacteriaceae
Cutibacterium avidum	2	3	Actinomycetota	Actinomycetes	Propionibacteriales	Propionibacteriaceae
Dermabacter hominis	2	5	Actinomycetota	Actinomycetes	Micrococcales	Dermabacteraceae
Enterobacter cloacae/asburiae	0	1	Pseudomonadota	Gammaproteobacteria	Enterobacterales	Enterobacteriaceae
Enterococcus faecalis	4	6	Bacillota	Bacilli	Lactobacillales	Enterococcaceae
Enterococcus faecium	0	1	Bacillota	Bacilli	Lactobacillales	Enterococcaceae
Escherichia coli	1	3	Pseudomonadota	Gammaproteobacteria	Enterobacterales	Enterobacteriaceae
Facklamina hominis	1	0	Bacillota	Bacilli	Lactobacillales	Aerococcaceae
Globicatella sanguinis	1	0	Bacillota	Bacilli	Lactobacillales	Aerococcaceae
Klebsiella oxytoca	0	1	Pseudomonadota	Gammaproteobacteria	Enterobacterales	Enterobacteriaceae
Klebsiella pneumoniae	0	1	Pseudomonadota	Gammaproteobacteria	Enterobacterales	Enterobacteriaceae
Kocuria rhizophila	5	2	Actinomycetota	Actinomycetes	Micrococcales	Micrococcaceae
Kocuria rosea	1	0	Actinomycetota	Actinomycetes	Micrococcales	Micrococcaceae
Lacticaseibacillus casei/paracasei/rhamnosus	0	1	Bacillota	Bacilli	Lactobacillales	Lactobacillaceae
Leuconostoc mesenteroides	0	1	Bacillota	Bacilli	Lactobacillales	Lactobacillaceae
Lysinibacillus fusiformis	0	1	Bacillota	Bacilli	Bacillales	Bacillaceae
Mammaliicoccus sciuri	0	1	Bacillota	Bacilli	Bacillales	Staphylococcaceae
Micrococcus luteus	12	5	Actinomycetota	Actinomycetes	Micrococcales	Micrococcaceae
Micrococcus pneumoniae	0	1	Actinomycetota	Actinomycetes	Micrococcales	Micrococcaceae
Micrococcus terreus	1	0	Actinomycetota	Actinomycetes	Micrococcales	Micrococcaceae
Moraxella osloensis	5	3	Pseudomonadota	Gammaproteobacteria	Moraxellales	Moraxellaceae
Mycolicibacterium fortuitum	1	0	Actinomycetota	Actinomycetes	Mycobacteriales	Mycobacteriaceae
Paenibacillus lactis	1	0	Bacillota	Bacilli	Bacillales	Paenibacillaceae
Paracoccus yeei	2	0	Pseudomonadota	Alphaproteobacteria	Rhodobacterales	Paracoccaceae
Peribacillus simplex	2	0	Bacillota	Bacilli	Bacillales	Bacillaceae
Priestia megaterium	1	0	Bacillota	Bacilli	Bacillales	Bacillaceae
Proteus mirabilis	0	1	Pseudomonadota	Gammaproteobacteria	Enterobacterales	Morganellaceae
Pseudomonas oryzihabitans	1	0	Pseudomonadota	Gammaproteobacteria	Pseudomonadales	Pseudomonadaceae
Pseudomonas stutzeri	1	0	Pseudomonadota	Gammaproteobacteria	Pseudomonadales	Pseudomonadaceae
Schaalia odontolyticus	0	1	Actinomycetota	Actinomycetes	Actinomycetales	Actinomycetaceae
Schaalia turicensis	1	0	Actinomycetota	Actinomycetes	Actinomycetales	Actinomycetaceae
Sphingobacterium thalpophilum	1	0	Bacteroidota	Sphingobacteriia	Sphingobacteriales	Sphingobacteriaceae
Sphingomonas paucimobilis	1	0	Pseudomonadota	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae
Staphylococcus aureus	1	4	Bacillota	Bacilli	Bacillales	Staphylococcaceae
Staphylococcus auricularis	1	1	Bacillota	Bacilli	Bacillales	Staphylococcaceae
Staphylococcus capitis	10	14	Bacillota	Bacilli	Bacillales	Staphylococcaceae
Staphylococcus caprae	4	0	Bacillota	Bacilli	Bacillales	Staphylococcaceae
Staphylococcus cohnii	0	1	Bacillota	Bacilli	Bacillales	Staphylococcaceae
Staphylococcus epidermidis	38	24	Bacillota	Bacilli	Bacillales	Staphylococcaceae
Staphylococcus haemolyticus	12	7	Bacillota	Bacilli	Bacillales	Staphylococcaceae
Staphylococcus hominis	19	16	Bacillota	Bacilli	Bacillales	Staphylococcaceae
Staphylococcus lentus	1	0	Bacillota	Bacilli	Bacillales	Staphylococcaceae
Staphylococcus lugdunensis	7	3	Bacillota	Bacilli	Bacillales	Staphylococcaceae
Staphylococcus pasteuri	2	0	Bacillota	Bacilli	Bacillales	Staphylococcaceae
Staphylococcus pettenkoferi	2	0	Bacillota	Bacilli	Bacillales	Staphylococcaceae

Table 2 (*continued*)

Species	Control (total: 36)	Study (total: 28)	Phylum	Class	Order	Family
Staphylococcus saprophyticus	1	1	Bacillota	Bacilli	Bacillales	Staphylococcaceae
Staphylococcus simulans	2	2	Bacillota	Bacilli	Bacillales	Staphylococcaceae
Staphylococcus sp.	0	1	Bacillota	Bacilli	Bacillales	Staphylococcaceae
Staphylococcus succinus	0	1	Bacillota	Bacilli	Bacillales	Staphylococcaceae
Staphylococcus ureilyticus	1	0	Bacillota	Bacilli	Bacillales	Staphylococcaceae
Staphylococcus warneri	8	2	Bacillota	Bacilli	Bacillales	Staphylococcaceae
Streptococcus agalactiae	0	2	Bacillota	Bacilli	Lactobacillales	Streptococcaceae
Streptococcus cristatus	1	0	Bacillota	Bacilli	Lactobacillales	Streptococcaceae
Streptococcus mitis/oralis	2	0	Bacillota	Bacilli	Lactobacillales	Streptococcaceae
Streptococcus parasanguinis	1	0	Bacillota	Bacilli	Lactobacillales	Streptococcaceae
Winkia neuii	2	2	Actinomycetota	Actinomycetes	Actinomycetales	Actinomycetaceae

incision site have been proposed. Manrique et al [22] used a modified bikini incision and were able to reduce the rate of wound complications significantly in their cohort of obese patients. Butler et al [23] presented a systematic review of the literature in 2022 comparing the bikini incision vs the standard incision. While they concluded that the bikini incision is a safe alternative with favorable outcomes in terms of wound complications and cosmesis, a potential increase in injuries of the lateral femoral cutaneous nerve was found. Furthermore, limited options to extend the approach more distally in case of complications making access to the proximal femur necessary must be considered. At the authors' institution some surgeons perform a curved incision when carrying out THA via DAA in severely obese patients (Fig. 1). This modified incision is similar to the standard incision in the distal part but is curved posteriorly in the proximal part to avoid cutting in the inguinal crease under the abdominal pannus. In the study cohort, obese patients treated by this modified incision showed no cases of wound complications, whereas these occurred in 21.4 % of the obese patients with standard incision. As this study was clearly underpowered for this secondary outcome parameter, this difference was not statistically significant. Nevertheless, this trend is in line with the existing literature and emphasis the rule not to cut under the abdominal pannus in obese patients during THA via DAA.

Next to the significantly higher prevalence of Enterobacterales on the skin of obese patients with overhanging abdominal pannus, there was a tendency to more frequent colonization with *S. aureus* and *S. agalactiae* in the study group, both being among the most common pathogens for periprosthetic joint infections. Including more patients may have resulted in a statistically significant outcome. Further studies with larger patient numbers are needed to resolve this question.

When interpreting the presented results, the limitations of this study must be kept in mind. The number of included patients was rather small, but similar to comparable studies [10,14,15]. Including more patients in future studies might bring more pronounced differences in the microbiome to light. Next to the limited number of included patients, the sex asymmetry in the study group must be considered as potential confounder. As patients were recruited chronologically without respect to their sex, this difference might refer to the general higher laxity of soft tissues in females, possibly leading to an increased incidence of a hanging abdominal pannus in obese subjects [24]. While we are not aware of former studies comparing the microbiome of the groin area between men and women, there is evidence of sex-related differences of the microbiome of the face, for example [25]. Furthermore, this study was designed as a culture-based analysis of the microbiota to simulate the real-life situation of microbiologic diagnostics. For this reason, the prevalence of the skin microbiota was limited to culturable bacteria and a quantification of the bacterial load was not possible. In addition, the swabbing method for sampling is not optimal for the analysis of anaerobic bacteria. For example, Cutibacteria are increasingly recognized as difficult to detect causative organism of periprosthetic joint infections, not only in the shoulder [26]. Jacob et al found high rates of Cutibacteria in biopsies from the anterior thigh even after skin disinfection [27]. Böni et al [10] was able to show that *C. avidum* was significantly more often found in the groin than on the thigh and that obesity was associated with colonization of the groin. Future studies on the microbiome should therefore rely on more sensitive methods like molecular detection using 16 PCR to further specify differences between obese and nonobese patients.

In conclusion, this study for the first time proves higher rates of colonization with Gram-negative Enterobacterales on the skin of the incision sight of the DAA in severely obese patients with abdominal pannus in comparison to nonobese patients scheduled for THA. Orthopaedic surgeons must be aware of this potential source of PJI and should review their perioperative antibiotic regime and consider modifications to their skin incision when dealing with these complex patients.

Table 3
Differences in microbiota between the study and the control group.

Bacterial group	Study group n (%)	Control group n (%)	*P* value
Staphylocooccus aureus	4 (14.3)	1 (2.8)	.159
Streptococcus agalactiae	3 (10.7)	0	.083
Gram-negative aerobic bacteria	11 (39.3)	10 (27.8)	.109
Enterobacterales	6 (21.4)	1 (2.8)	**.037**
Non-fermenters	6 (21.4)	9 (25.0)	.775
Anaerobic bacteria	8 (28.6)	6 (16.7)	.362

n, Number.

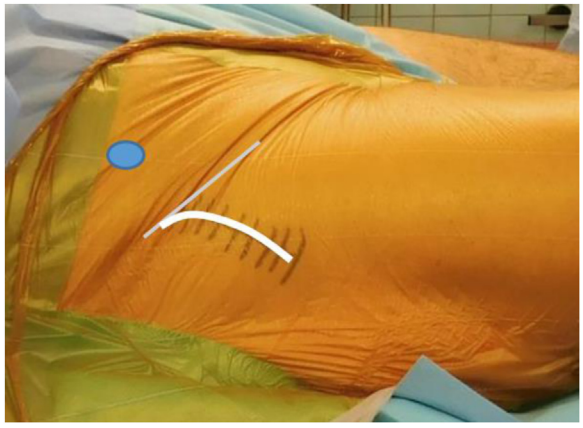

Figure 1. Curved incision for the direct anterior approach. The proximal part of the incision curves to the back to avoid cutting into the inguinal crease.

Conflicts of interest

The authors declare there are no conflicts of interest.

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CRediT authorship contribution statement

Philip Mark Anderson: Writing – review & editing, Writing – original draft, Methodology, Investigation, Formal analysis, Data curation, Conceptualization. **Thiemo Frank:** Investigation, Data curation. **Michaela Herz:** Writing – review & editing, Methodology, Investigation, Conceptualization. **Oliver Kurzai:** Writing – review & editing, Supervision, Project administration. **Maximilian Rudert:** Writing – review & editing, Supervision. **Tizian Heinz:** Writing – review & editing, Methodology. **Thiên-Trí Lâm:** Writing – review & editing, Supervision, Methodology, Formal analysis, Data curation, Conceptualization.

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