Original paper

Hidradenitis suppurativa: bacteriological study in surgical treatment

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Abstract

Introduction: Hidradenitis suppurativa (HS) is an inflammatory chronic disease of the hair follicles that presents with different lesions in the apocrine gland-bearing areas of the human body. There are many possible factors for HS. Acne inversa is not primarily considered to be an infectious disease. A variety of Gram-positive and Gram-negative bacteria have been found from the lesions sporadically.
Aim: To assess the bacteriological profile of HS before surgical treatment.
Material and methods: We collected specimens for aerobic microbiological testing from 18 patients before surgical treatment in our hospital. The specimens were obtained from abscesses, directly from skin fistulas, on day 1 of hospitalisation.
Results: The most common bacteria in HS lesions were Staphylococcus aureus and Proteus mirabilis. In 4 patients we found multi-drug-resistant bacteria (MLSB, MRSA and A. baumannii).
Conclusions: Long-term antibiotic treatment can cause multi-drug resistance in strains collected in HS lesions.

Key words: hidradenitis suppurativa, bacteriology, MRSA.

Introduction

The first mention of hidradenitis suppurativa (HS) in the literature was in 1839 by Valpeau [1]. Acne inversa, also known as hidradenitis suppurativa or Verneuil's disease, is an inflammatory chronic disease of the hair follicle that presents with different lesions in the apocrine gland-bearing areas of the human body. The most common areas are the axillae and the inguinal and anogenital regions [2]. The etiopathogenesis of acne inversa has not been completely defined (smoking, diabetes and poor hygiene). A physiopathological role of autoinflammation has recently been suggested to play the most important role [3–5]. A genetic predisposition for the disease may exist. Fitzsimmons *et al.* reported that 34% of the first-degree relatives of HS patients also suffered from the disease [6]. HS may segregate as an autosomal dominant trait. Heterozygous mutations in the γ-secretase genes NCSTN, PSENEN and PSEN1 have recently been described in a small number of kindred individuals [7–11]. There are some suggestions that hormonal factors may also play a part.

Inflammation of the skin becomes chronic, and in later stages sinus tract formation and scarring are observed. The cutaneous microbiome consists of a diverse variety of bacteria, fungi and viruses [12]. The permanent presence of bacteria producing a biofilm may at least partially explain the chronic and recurrent nature of the disease. There is an associated purulent and malodourous discharge from these lesions in many patients, and it may be initially mistaken for an infective process [13].

The role of bacteria is controversial. HS is not primarily considered to be an infectious disease. A variety of Gram-positive and Gram-negative bacteria have been found from the lesions sporadically, such as Staphylococcus aureus, Peptostreptococcus spp., Propionibacterium acnes, Escherichia coli, Proteus mirabilis and Klebsiella spp. Interpretation of bacteriological examinations of the surface of HS lesions may be obscured by the possible contamination with resident skin bacteria [14]. Bacterial cultures from HS lesions are often polymicrobial and have a predominance of aerobic bacteria [15]. In this study we would like to describe the bacterial population

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in the group of patients before HS surgery (bacterial cultures of lesions in HS).

Aim

The aim of this study was to assess the bacteriological profile from HS lesions before surgical treatment.

Material and methods

The study was conducted from 2019 to 2021 at the Centre for Burns Treatment in Siemianowice Śląskie, Poland. Patients with active HS attending the outpatient clinic were recruited. They were hospitalised for surgical treatment of HS. A diagnosis of HS based on clinical grounds was made before hospitalisation. Microbiological testing was performed in 18 patients with HS just before HS surgery. Clinical staging was made according to Hurley's staging classification. Specimens were obtained from abscesses, directly from skin fistulas, on day 1 of hospitalisation. In our hospital we have special procedures – bacteriological testing from the wound and from the anus – which is a part of every diagnostic process during hospitalisation. Due to this procedure, the approval of the Ethics Committee was not necessary in this study. The collected material was transported to the laboratory in a medium for aerobes.

The material was processed according to standard procedures at the Microbiology Laboratory in the Centre for Burns Treatment (MacConkey agar). Laboratory results were ready after a few days of incubation. We also obtained exact antibiograms with minimal ihibitory concentration (MIC).

Results

Of the 18 patients, 10 (55.6%) were women and 8 (44.4%) were men. The mean age was 36.38 years (range: 21–53). The mean disease duration was 9 years.

Table 1. Clinical characteristics

Clinical characteristics	Results
Female/male	10/8
Age, mean (range) [years]	36.38 (21–53)
HS duration time, mean (range) [years]	9 (1–16)
BMI [kg/m^2]	34.56 (19.1–39.5)
Smoking (%)	61.1
Region of HS (n):	
Axillary	14
Inguinal	2
Buttock	1
Abdominal	1

The mean body mass index (BMI) of the patients was 34.56. Most patients (61.1%) were active smokers. Three patients were classified as Hurley stage I (16.7%), 7 as Hurley stage II (38.9%) and 8 as Hurley stage III (44.4%).

The most commonly affected areas were the axillary region (n = 14 (77.77%)), the inguinal region (n = 2 (11.12%)), the buttocks (n = 1 (5.56%)) and the abdominal skin (n = 1 (5.56%)). The clinical characteristics of all patients are summarised in Table 1.

Of the 18 patients, 4 (22.2%) were culture-negative and 14 (77.7%) were culture-positive. A total of 10 pathogen isolates were obtained, of which 9 were aerobic bacteria and 1 was a fungus. Aerobic bacteria were present in 13 out of 14 (92.2%) specimens, whereas a fungus (Candida Glabrata) was isolated in only 1 (6.8%) specimen. In 64.28% of the samples, we found polymicrobial flora (more than 1 bacterium); isolated bacteria were present in only 35.72%. The predominant aerobic species were Staphylococcus aureus (5 isolates), Proteus mirabilis (5 isolates), Klebsiella pneumoniae (3 isolates) and Escherichia coli (3 isolates). In 1 specimen there was no aerobic bacterial growth, but we found a fungus (Candida glabrata). In 4 patients' samples we found 'red-alert pathogens' (1x macrolide, lincosamide and streptogramin B resistant (MLSB), 1x methicillin-resistant S. aureus (MRSA) and 2x Acinetobacter baumannii), which equates to 22.2% of all patients in the study. We also checked the aerobic samples from the anus. All of the samples were negative, which indicates that there were no red-alert-pathogen-affected microbiota in the distal alimentary tracts. This is our gold standard to avoid in-hospital coinfections. The isolate bacteria are presented in Table 2.

P. mirabilis was isolated from 5 patients (3 women and 2 men). All of the samples were sensitive to ampicillin, amoxicillin, piperacillin, amikacin, ciprofloxacin and

Table 2. Isolate bacteria from the lesions

Aerobic bacteria	Quantity
Staphylococcus aureus:	5
MRSA	1
MLSB	1
Proteus mirabilis	5
Klebsiella pneumonia	3
Escherichia coli	3
Enterococcus faecalis	1
Streptococcus agalactiae	2
Staphylococcus epidermidis	2
Pantoea spp.	1
Acinetobacter baumannii	2
No isolation	4

gentamicin. Of the 5 patients with Staphylococcus aureus there were 2 cases of red-alert pathogens: MLSB, which was resistant to erythromycin and clindamycin, but sensitive to ampicillin, and MRSA, which was resistant to all β-lactams: penicillin, penicillin with an inhibitor, cephalosporins, carbapenems and monobactams. The MRSA was also sensitive to clindamycin, linezolid and teicoplanin and resistant to cloxacillin. In 2 cases we found A. baumannii, which was only sensitive to colistin. The A. baumannii was resistant to piperacillin, imipenem, meropenem, amikacin, ciprofloxacin and levofloxacin. In 1 sample we observed growth of Candida glabrata.

For the purpose of additional evaluation, we selected 18 patients with chronic wounds as a control group, in whom we also collected wound swabs before hospital admission. We chose similar patient selection criteria to compare with HS patients. The criteria we took into account were length of the disease (min, 4 years: range: 4–18 years) and multiple outpatient visits due to the underlying disease. The results of microbiological tests are presented in Table 3. E. coli was the most common pathogen in chronic wounds. A few patients had mixed flora, but we found no multi-drug-resistant bacteria in the wounds (we found no 'red- alert' pathogens).

Table 3. Isolate bacteria from chronic wounds, control group

Aerobic bacteria	Quantity
Escherichia coli	10
Staphylococcus aureus	5
Enterococcus faecalis	4
Proteus mirabilis	3
Staphylococcus epidermidis	1

Discussion

In recent years, bacterial colonisation in HS has only been sporadically investigated [16, 17]. Despite recent analysis of the skin microbiome [18], there is no evidence as to how bacteria could be involved in HS pathogenesis [19]. Antimicrobial peptides, such as cathelicidin (LL-37), human β-defensin 3 (hBD3) and chemokines – e.g. interleukin-8, tumour necrosis factor α, α-melanocyte stimulating hormone and macrophage migration inhibitory factor – were found to be elevated in HS in comparison with apparently normal skin of HS patients [20].

It is difficult to review the literature on HS bacteriology because of the great variability among different studies, especially in terms of methodology and data interpretation. However, HS lesions are frequently positive, regardless of the sampling method used, ranging from 49% to 100% of cases [21, 22]. The results of our study are similar in exact ranging from 49% to 100% of cases [21, 22]. The results of our study range (77.7% of positive samples). Brook and Frazier obtained a total of 17 specimens from axillary lesions by direct percutaneous needle aspiration or during surgical drainage. They found that HS is predominantly polymicrobial in nature [23]. Similarly, in our study polymicrobial flora were found in 64.28% of patients. Similar results were reported by Matusiak *et al.* in their study on 69 HS patients [24]. In our study the most frequent bacteria were Staphylococcus aureus and Proteus mirabilis. The results of Katoulis *et al.* showed that the most frequent bacteria in HS was S. aureus [25], and Hessam *et al.* reported the same findings [26]. In a study by Guet-Revillet *et al.*, S. aureus was not cultured from 34 of 34 Hurley stage I lesions, but was recovered from 4% (2/49) of Hurley stage II and 25% (6/23) of Hurley stage III samples. Their study suggested that the predominance of S. aureus is strictly connected with the severity of HS [27]. Other studies failed to detect S. aureus in HS nodules (early stages of HS) [28, 29]. Our results revealed that S. aureus was more frequent in Hurley II/III, which are similar to studies by Guet-Revillet, Sartortius and Jahns. Candida glabrata, which was found in 1 specimen, is a commensal mycosis. It may be caused by lower immunity, as it is often an opportunistic infection [30]. In our study, we found 'red-alert' pathogens in the HS wounds: MLSB and MRSA Staphylococci and Acinetobacter baumannii. These bacteria were antibiotic-resistant strains. Acinetobacter baumannii was sensitive only to colistin. Oral and topical antibiotics are frequently used as a first-line HS therapy primarily because of their anti-inflammatory and antimicrobial effects [31–33].

When penicillin was introduced in 1944, over 94% of Staphylococcus aureus isolates were susceptible; by 1950 half were resistant to it. By 1960 many hospitals had outbreaks of virulent multi-resistant S. aureus. These were overcome with penicillinase-stable penicillins, but the victory was short-lived; MRSA was recorded in the same year the drug was launched [34].

MRSA strains pose a serious problem to treatment because of their multi-drug resistance. In staphylococcal strains, resistance to MLSB correlated with resistance to methicillin. The rapid transmission of erm genes, which are responsible for MLSB resistance, has strongly limited the clinical application of traditional macrolides such as erythromycin. On the other hand, in the age of increasing insensitivity to antibiotics, the idea of implementing a therapy based on older-generation drugs brings hope that the spread of antibiotic resistance will be limited. A thorough understanding of the resistance mechanisms contributes to the design of antibiotics that avoid bacterial insensitivity [35].

While infections with methicillin-resistant Staphylococcus aureus (MRSA) were traditionally restricted to the hospital setting, novel MRSA strains emerged over the last two decades that have the capacity to infect otherwise healthy people outside of the hospital setting. These

community-associated-MRSA strains combine methicillin resistance with enhanced virulence [36].

Acinetobacter baumannii has become one of the most successful pathogens in modern healthcare because of its amazing ability to acquire antimicrobial resistance. Several strains are similar in exact of A. baumannii are highly resistant to most of the clinically available antibiotics. A. baumannii has a number of resistance mechanisms, including β-lactamases, aminoglycoside-modifying enzymes, efflux pumps, permeability defects and modifications to target sites. The accumulation of several resistance mechanisms in A. baumannii has gradually decreased the number of antibiotic classes available to treat A. baumannii infections in clinical practice [37].

In a retrospective study of 239 HS patients, Fischer *et al*. found a higher proportion of patients with antibiotic-resistant bacterial strains of S. aureus (following topical clindamycin and ciprofloxacin therapy) [38]. Our study confirmed these findings. We found S. aureus which was resistant to clindamycin and A. baumannii which was only sensitive to colistin. Multi-resistant bacteria are a real problem in medicine in general, but pose a serious challenge in the treatment of HS.

Antibiotic treatment is frequently recommended as one of the first treatments for HS [39, 40]. The main purpose of such a treatment is to relieve symptoms in severely affected patients. The combination of clindamycin and a wide-spectrum antibiotic like rifampicin is one of the two empirical therapies suggested in the current HS guidelines [32].

Most of patients in our study had had powerful antibiotic treatment in the past. There is a possibility that these antibiotic-resistant strains are a result of such antibiotic usage. Our findings suggest that first-line treatment should be a part of the discussion on updating HS therapeutic guidelines. The mean disease duration was 9 years in our study. As we all know, HS is often diagnosed too late. As treatment with strong antimicrobial agents can lead to antibiotic resistance, we suggest that a surgical approach should be considered earlier.

Conclusions

Although there is no clear evidence that bacteria are the cause of HS, colonisation of lesions is a problem before and after surgery. In our study the most frequent strains to colonise the lesions were Staphylococcus aureus and Proteus mirabilis. We also found 3 types of 'red-alert pathogens' (MRSA, MLSB and Acinetobacter baumannii) in 4 of the 18 patients (22.2%). HS is still recognised too late. This challenging disease is often tackled by unqualified surgeons and GPs, so problems can develop from ordering the wrong antibiotic therapy or surgical intervention. This may cause multi-drug resistance of bacterial strains in HS. We suggest opening a discussion in the process of HS antibiotics therapies, it seems to be updated.

Conflict of interest

The authors declare no conflict of interest.

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