

PROCEEDINGS

ANALYSIS OF DATA FROM THE AEROBIC MICROBIOLOGICAL LANDSCAPE IN ADULT PATIENTS OPERATED ON FOR ANORECTAL ABSCESES

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ABSTRACT

INTRODUCTION: Systematic analyses and studies on the microbiological spectrum of anorectal abscesses (ARAs) are currently lacking in modern proctology. Microorganisms from the colonic flora lead to retrograde infection of the anorectal glands with the subsequent appearance of ARA.

AIM: The aim of this article is to analyze the frequency, type, and structure of the aerobic microbiological landscape in adult patients operated on for ARA.

MATERIALS AND METHODS: A detailed analysis of the microbiological agents was performed in 254 operated adult patients, with a total of 274 isolates, which were divided as follows: 188 monocultures, 20 pairs of aerobic microbial associations, and 46 found sterile. Microbiological studies were performed by bacteriological examination of the purulent exudate taken during the operation.

RESULTS: A total of 17 types of microbial cultures were identified. The most common were as follows: *E. coli* (n=160, 58.4%), *Proteus spp.* (n=15, 5.5%), *Klebsiella spp.* (n=11, 4%), *Staphylococcus spp.* (n=12, 4.4%), *Enterococcus faecalis* (n=8, 2.9%), *Enterobacter cloacae* complex (n=6, 2.2%). Monocultures were found in 188 patients (74.0%) and mixed infection with microbial associations in 20 patients (7.9%). Of the isolates, Gram (-) predominated, accounting for 201 (73.3%) strains, and Gram (+) constituted 26 (9.5%).

CONCLUSION: So far, there have been only isolated reports on this issue in our country, without systematic studies. This determines the relevance and importance of our study on the aerobic microbiological landscape in operated adult patients with ARA. Routine microbiological screening should be an integral part of the diagnosis of ARA and of great help in the treatment.

Keywords: *anorectal abscess, microbiological culture*

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INTRODUCTION

Despite the great successes of modern proctology and purulent-septic surgery, there is currently an insufficient number of systematic analyses and studies on the microbiological landscape in anorectal abscesses (ARAs). The lack of sufficient information in the available literature requires research and establishment of the microbiological causes of purulent-



inflammatory changes in ARA and a study of the results of antibiograms with the prospect of applying effective and optimal antibacterial treatment. American coloproctologists from the American Society of Colon and Rectal Surgeons (ASCRS) recognize the role of cryptoglandular infection in the anal canal in 90% of cases of the occurrence of ARA, reporting in 30–50% of patients the presence of a persistent fistula tract to the internal opening of the abscess in the rectum (1). Importantly, due to the higher pressure in the lumen of the rectum, constant bacterial contamination occurs from it. Thus, microorganisms from the intestinal flora lead to retrograde infection of the anal glands, with the formation of a purulent retention cyst and subsequent formation of an initial intersphincteric abscess (2). Subsequently, secondary abscesses are formed in the intersphincter, subnodal, ischioanal, and supralelevator spaces, and accordingly, at a given location, they have different clinical symptoms. One of the features of the small pelvis is the presence of large tissue spaces immediately next to the rectum, which are easily infected by pathogenic microorganisms. The high frequency of anorectal inflammations is determined by this proximity to the lumen of the rectum, where more than 300 types of commensal bacteria have been found. This leads to monopathogenetic disease having a great variety of its clinical forms, according to the tissue spaces and the specificity of the topography in the anorectal region (3,4).

AIM

The present study aims to analyze the frequency, type, and structure of the aerobic microbiological landscape in adult patients operated on ARA.

MATERIALS AND METHODS

In all 254 operated adult patients, a detailed analysis of the microbiological studies was conducted to clarify the type of bacterial aerobic spectrum of the causative agents of ARA. For this purpose, a study of the results of the operated patients with a total of 274 isolates (188 monocultures + 20 pairs /20 x 2/ microbial associations + 46 sterile) from the microbiological analysis was conducted. A total of 228 isolates were found to be culture positive, of which 188 had a monoculture, and 20 (20x2=40) had microbial double associations. A total of 17 types of

microbial cultures were identified. Microbiological studies were carried out by bacteriological examination of the purulent exudate, taken during the operative intervention to clarify the spectrum of aerobic microorganisms in ARA, through culturing and identification of the etiological microbial agent. The purulent specimen was inoculated onto sheep blood and eosin-methylene blue agar and incubated at 36°C for 18–24 hours. The subsequent identification was performed by routine biochemical tests and/or automated identification systems (Vitek-2 Compact, Vitek MS, bioMerieux, France).

RESULTS AND DISCUSSION

According to the obtained data from the microbial cultures, we distinguish the following three main groups—microorganisms as monocultures, microbial associations such as mixed infection, and sterile (without microbial growth) (Table 1).

Table 1. Results of microbiological cultures in operated adult patients with ARA.

Examination of Cultures in Adult Patients	Frequency		Percentage
	n	%	
Monoculture	n	188	74.0%
	%		
Microbial associations	n	20	7.9%
	%		
Sterile	n	46	18.1%
	%		
Total	n	254	100%
	%		

Bacteriological studies of ARA in 254 patients revealed that microorganisms as a monoculture were present in 188 patients (74.0%), mixed infection with microbial associations in 20 patients (7.9%), and sterile cultures in 46 patients (18.1%). A predominance of aerobic bacteria was established mainly as monocultures in the microbial spectrum, while, in the past years, the opinion of a greater frequency of polymicrobial associations in ARA prevailed. In the statistical processing, it was found that monocultures occur more often compared to those of aerobic microbial associations ($p < 0.05$).

The etiological structure of aerobic microorganisms in adult patients with ARA is presented with great diversity as follows (Fig. 1).

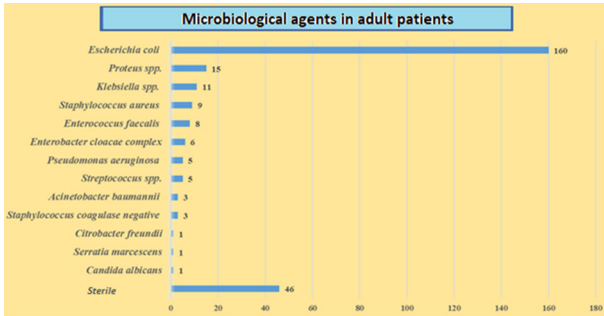


Fig. 1. Aerobic microbiological spectrum of etiological agents in adult patients with ARA.

In the analysis of the microbial spectrum in the operated adult patients with ARA, it was found that the most common bacterium is *E. coli*. This major isolate represented an intestinal nonpathogenic commensal, having the largest share in more than half of the patients (n=160, 58.4%). Among the microorganisms in the monoculture group, 142 *E. coli* were isolated.

The second most common isolates were *Proteus spp.* with 15 isolates (5.5%), followed by *Klebsiella spp.* (*K. pneumoniae complex* + *K. oxytoca* + *K. aerogenes*) with 11 isolates (4%). They were followed by *Staphylococcus spp.* with a total of 12 isolates (4.4%)—*S. aureus* in 9 and coagulase-negative staphylococci (CoNS)

in 3, *Enterococcus faecalis*—8 isolates (2.9%), and *Enterobacter cloacae complex*—6 isolates (2.2%)).

Based on our data, we identified 12 isolates of *Staphylococcus spp.* represented mainly by *S. aureus* (4.4%). According to various data, these bacteria are not often detected (2–9%), but in some cases, they are associated with clinically significantly more severe course.

The data on the species composition of the causative agents with microbial associations of ARA in adult patients are presented in Table 2.

Almost always, in the pairs of microbial associations with mixed aerobic infection, *E.coli* was involved, and the other types of bacteria were as follows: *Enterococcus faecalis* in 4 cases, *Proteus mirabilis* in 3 cases, *Klebsiella pneumoniae complex* also in 3 cases, *K.oxytoca* in 2 cases, *Staphylococcus aureus* in 2 cases, and another 4 cases with one microorganism. Of the total registered microbial associations, *E. coli* was involved in 18 cases (90%).

When summarizing all types of isolated microbial strains (monoculture + microbial associations) in the operated adult patients with ARA, the following isolated bacteria were found (Table 3).

With no surprise, it was found that the most common bacterium was *E. coli* in 160 cases (58.4%), of which as a monoculture in 142 isolates (88.75%) and as microbial associations in 18 isolates (11.25%). It is the leading pathogen in operated patients with ARA. The more frequent diagnosis and prevalence

Table 2. Results of established microbiological associations in adult patients operated on for ARA.

Types of Microbial Associations in Adults	Frequency	Percentage
<i>Escherichia coli</i> + <i>Enterococcus faecalis</i>	4	20%
<i>Escherichia coli</i> + <i>Proteus mirabilis</i>	3	15%
<i>Escherichia coli</i> + <i>Klebsiella pneumoniae complex</i>	3	15%
<i>Escherichia coli</i> + <i>Klebsiella oxytoca</i>	2	10%
<i>Escherichia coli</i> + <i>Staphylococcus aureus</i>	2	10%
<i>Escherichia coli</i> + <i>Enterobacter cloacae complex</i>	1	5%
<i>Escherichia coli</i> + <i>Acinetobacter baumannii</i>	1	5%
<i>Escherichia coli</i> + <i>Proteus vulgaris</i>	1	5%
<i>Escherichia coli</i> + <i>Streptococcus beta-haem. Group B</i>	1	5%
<i>Enterococcus faecalis</i> + <i>Klebsiella pneumoniae complex</i>	1	5%
<i>Proteus mirabilis</i> + <i>Enterobacter cloacae complex</i>	1	5%
Total	20	100%

Table 3. Cumulative aerobic microbiological spectrum in adult patients with ARA.

Structure of Isolates in Adult Patients	Frequency	Percentage
<i>Escherichia coli</i>	160	58.4%
<i>Proteus mirabilis</i>	13	4.7%
<i>Staphylococcus aureus</i>	9	3.3%
<i>Enterococcus faecalis</i>	8	2.9%
<i>Klebsiella pneumoniae complex</i>	6	2.2%
<i>Enterobacter cloacae complex</i>	6	2.2%
<i>Pseudomonas aeruginosa</i>	5	1.8%
<i>Acinetobacter baumannii</i>	3	1.1%
<i>Klebsiella oxytoca</i>	3	1.1%
<i>Staphylococcus coagulase negative</i>	3	1.1%
<i>Streptococcus beta-haem. Group B</i>	3	1.1%
<i>Klebsiella aerogenes</i>	2	0.7%
<i>Proteus vulgaris</i>	2	0.7%
<i>Streptococcus beta-haem. Group A</i>	2	0.7%
<i>Citobacter freundii</i>	1	0.4%
<i>Serratia marcescens</i>	1	0.4%
<i>Candida albicans</i>	1	0.4%
Sterile	46	16.8%
Total	274	100.0%

of *E. coli* compared to other microorganisms is statistically significant ($p < 0.05$). It should be noted that in recent years *E. coli* has had a markedly increasing trend in its occurrence.

The second most frequent microorganism in the aerobic etiological structure in the microbial landscape is also from enterobacteria - *Proteus mirabilis* ($n=13$, 4.7%), and it also shows a tendency to increase its prevalence.

Other causative agents found are *Staphylococcus aureus* in 3.3%, *Enterococcus faecalis* (2.9%), *Enterobacter cloacae complex* (2.2%), and bacteria of the genus *Klebsiella spp.* are found to be below 3%; *K. pneumoniae complex*—2.2%, *K. oxytoca*—1.1%, and *K. aerogenes*—0.7%.

The remaining bacterial causative agents occur in the order of 1.8% to 0.4%, followed by: *Pseudomonas aeruginosa*, *Acinetobacter baumannii*, *Staphylococcus coagulase negative*, *Streptococcus beta-haem. Group B* (*S. agalactiae*) and group A (*S. pyogenes*), *Proteus vulgaris*, etc.

The single isolate of *Candida albicans* ($n=1$; 0.4%) was recovered in a woman and was unlikely to be due to an exogenous infection, possibly of vaginal origin, evidence of immunosuppression, or previous inappropriate antimicrobial therapy.

The distribution of microbial isolates in adult patients with ARA is as follows (Table 4).

When comparing the results of Gram-negative to Gram-positive microorganisms in ARA, it was found that Gram (-) are much more often, with a ratio of 7.7:1.

Table 4. The distribution of microbial isolates in adult patients with ARA.

Adult Patients	Frequency	Percentage
Gram-negative bacteria	201	73.3%
Gram-positive bacteria	26	9.5%
Fungi	1	0.4%
Sterile	46	16.8%
Total	274	100.0%

Among the microbiological isolates, Gram (-) predominated accounting for 201 (73.3%) strains, and among them, most were from the *Enterobacteriales* order. Gram (+) made up 26 (9.5%) isolates, from which *Enterococcus spp.* were most often isolated.

Based on a large microbiological study with 274 isolates from 254 adult patients operated on for ARA, it was found that all bacteria from the normal intestinal flora can be the causative agents of purulent inflammation in perirectal tissues. In general, a diverse opportunistic flora exists in the lumen of the rectum, which, especially in immunocompromised patients, can quickly become highly virulent.

In the recent past, for one reason or another, routine microbiological screening in ARA was not systematically performed by operating surgeons. For a long time, there was no interest in it, which is why it is difficult to compare bacteriological data from the past and the present, with a view to establishing changes in the aerobic microbial landscape in the causative agents. Until the last 10–15 years, the investigation of microbial agents in perirectal abscesses was not performed regularly in many countries, and only now is it an integral part of the diagnostic process in ARA (5). Thus, the lack in the past years of a generally accepted methodological approach and standards for mandatory bacterial etiological research in ARA forms the presence of a significant gap in this area. In our country, it was only after the requirements of the National Health Insurance Fund (NHIF) from 2010 for the mandatory examination of microbiological culture in the treatment of this disease that the systematic collection of purulent material for microbiological analysis began. It was only after this requirement of the NHIF that mandatory bacteriological tests began in our country, through which the microbiological aerobic spectrum of the causative agents of ARA in adult patients could be systematically investigated. The initial bacteriological studies are mainly related to the severe clinical cases with complicated forms of ARA, in which manifestations of anorectal sepsis are present. Another group of microbiological studies is related to Fournier's gangrene, which is most often a consequence of necrotic fasciitis due to diffuse necrotic phlegmonous inflammation in deep ARA (6,7,8,9). S. J. Eykyn et al. (10), in 1986, studied 80 patients with *anorectal sepsis* over a three-year period. Predomi-

nantly intestinal aerobes, such as *E.coli*, were detected in 49 out of 53 patients with fistula (92.5%) and in 8 out of 27 patients without fistula (29.6%). They found that *S. aureus* was found in only 1 out of 53 fistula patients (1.9%). T. Yilmazlar et al. (6) studied 50 patients with a mean age of 58.5 years with *Fournier's gangrene* over a period of 6 years. The most frequently detected microorganism was *E. coli* in 72%, followed by *A. baumannii* and *K. pneumoniae* complex. The authors believe that the pathogenic agents in Fournier's gangrene are changing, requiring empiric antibiotic treatment in this disease to also change.

It is important to note that in some earlier serious studies in 2011, the authors even discussed the question of whether wound cultures were necessary and indicated in ARA, specifically noting that they were rarely done. These authors recommend microbiological cultures only in the presence of recurrence, long non-healing wounds, and in the possibility of the presence of atypical microbes (11,12).

Even one of the new studies by L. Lalou et al. (13) in 2020 also justifies the cases where the need for such bacteriological tests is not imperative. The authors refrain from routinely performing microbiological cultures on every drainage of perianal abscesses unless there is clinical evidence of recurrent perianal sepsis, immunocompromised status, or the occurrence of extensive soft tissue necrosis.

Studies show that these issues are still debatable, and even now supporters of regular microbiological monitoring in ARA are in the minority. Despite the successes of coloproctology, there appears to be a surprisingly small number of scientific studies on the composition of microbial spectrum in patients with ARA. These data indicate that there are still a number of coloproctologists who avoid performing routine microbiological evaluation in all cases with ARA. These authors consider the data of the aerobic microbial landscape in patients operated on for ARA to be necessary only in the case of deep, more severe, and septic abscesses. We consider such an opinion to be unfounded since undoubtedly an early bacteriological examination can greatly help in the timely clarification of the causes of the complicated and septic clinical course, especially in cases where more virulent microorganisms or multidrug-resistant strains are present.

CONCLUSION

In the medical literature, there is a small number of reports on the aerobic microbiological spectrum in patients operated on for ARA, and in our country, similar studies in larger groups of patients have not been performed. So far, there have been only isolated reports on this issue in our country, without systematic studies. This determines the relevance and importance of our study on the aerobic microbiological landscape in operated adult patients with ARA. The obtained results of the microbiological analysis for purulent diseases in coloproctology are an important factor for a complete clarification of the occurrence of the disease (14). The main way for the penetration of pyogenic bacteria is from the lumen of the rectum, from where the intestinal microbiota reaches the pararectal spaces. For these reasons, the main group of microbiological agents are the Gram-negative intestinal commensals, with the main causative pathogen of *E.coli*. Bacterial monocultures occur more often compared to those of aerobic microbial associations ($p < 0.05$). Our conducted study gives us reasons to consider that routine microbiological screening should be an integral part of the diagnosis of ARA and of great help in the treatment.

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