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MICROECOLOGY OF PYODERMIA PATHOGENS

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Abstract

Gram-positive cocci are usually considered the leading pathogens of pyoderma. However, understanding intermicrobial interactions, as well as identifying the leading pathogens and their associates, require a more detailed study of microbial contamination of the skin other than a simple statement of the taxonomic composition of the microbial community of the biofilm. The aim of this study is to determine the microecological indicators of pyoderma pathogens.

Material and methods. 97 patients with pyoderma were examined, material was taken during dressing and bacteriological examination was carried out no later than 2 hours later. A number of microecological indices were calculated (constancy index, Margalef species richness index, Whittaker species diversity index, Simpson and Berger-Parker species dominance indices, statistical processing – by the method of variation statistics.

Results. In total, 197 strains of conditionally pathogenic Gram-positive (89.85%) and Gram-negative (20-10.15%) bacteria were isolated and identified in the cohort of patients. Coagulase-positive S. aureus was the main one in the microbial group according to the constancy index, frequency of occurrence, Margalef species richness index, Simpson species diversity index and Berger-Parker species dominance. In 94 (96.91%) patients, associations consisting of two different taxa were detected, and in 3 (3.09%) associations consisting of 3 conditionally pathogenic taxa.

Conclusions. Pyodermas are polyetiological diseases caused by both Gram-positive and Gram-negative, facultative anaerobic and aerobic bacteria with a significant predominance of Gram-positive cocci, which are in association with other conditionally pathogenic microorganisms. According to the taxonomic composition and microecological indicators, the leading pathogens of pyodermas are S. aureus, P. aeruginosa, S. pyogenes and P. vulgaris, E. coli, E. coli Hly+ and E. Aerogenes.

Keywords. Pyodermas; pathogens; microflora; diagnostics; purulent inflammation; pathogenesis; etiology.

МІКРОЕКОЛОГІЯ ЗБУДНИКІВ ПІОДЕРМІЙ

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Резюме. Провідними збудниками піодермій зазвичай вважають Грампозитивні коки. Проте, розуміння міжмікробних взаємодій, а також визначення провідних збудників та їх асоціантів – вимагає більш детального дослідження мікробної контамінації шкіри, ніж проста констатація таксономічного складу мікробного угруповання біоплівки. Мета даного дослідження – визначити мікроекологічні показники збудників піодермії.

Матеріал і методи. Обстежено 97 хворих на піодермії, під час перев’язки відбирали матеріал і не пізніше 2-х годин здійснювали бактеріологічне дослідження. Розраховували ряд мікроекологічних індексів (індекс постійності, індекс видового багатства Margalef, Індекс видового розмаїття Whittaker, Індекси видового домінування Simpson та Berger-Parker, статистична обробка – методом варіаційної статистики.

Результати та обговорення. Загалом у когорті хворих виділено та ідентифіковано 197 штамів умовно патогенних Грампозитивних (89,85%) та

Грамнегативних (20-10,15%) бактерій. Коагулазопозитивний S. aureus за індексом постійності, частотою зустрічання, індексом видового багатства Margalef, індексом видового розмаїття Simpson та за видового домінування Berger-Parker виявився головним у мікробному угрупованні. У 94 (96,91%) хворих були виявлені асоціації, що складаються із двох різних таксонів, а у 3 (3,09%) асоціації складаються з 3-х умовно патогенних таксонів.

Висновки. Піодермії є поліетіологічними захворюваннями, які викликаються як Грампозитивними так і Грамнегативними, факультативно анаеробними та аеробними бактеріями із значною перевагою Грампозитивних коків, які знаходяться в асоціації з іншими умовно патогенними мікроорганізмами. За таксономічним складом, мікроекологічними показниками провідними збудниками піодермій виступають S. aureus, P. aeruginosa, S. pyogenes та P. vulgaris, E. coli, E coli Hly+ та E. Aerogenes.

Ключові слова. **Піодермії; збудники; мікрофлора; діагностика; гнійне запалення; патогенез; етіологія.**

Introduction. Pyodermas are any skin disease characterized by purulent inflammation. These include superficial bacterial infections such as impetigo, contagious impetigo, ecthyma, folliculitis, Bockhart's impetigo, furuncle, carbuncle, tropical ulcer, etc. [1-3]. Pyodermas affect over 111 million people worldwide annually, making them one of the three most common skin disorders in children, along with scabies and lichen planus. In the United States and Western Europe, up to 10% of all hospitalizations are due to such patients, and the annual economic loss is estimated at 9-10 billion dollars. [4-6].

In the pathogenesis of pyoderma, a significant role is played by comorbidities, diseases of various organs and systems, as well as impaired immune status, local skin resistance, pH changes, dishormonal disorders and virulence of microorganisms [7, 8].

Also, the synergism of the action of different taxa of microorganisms contributes to the creation of a biofilm on the infected surface and thus prevents the penetration of antimicrobial drugs into the environment of the purulent-inflammatory process or purulent wound [9-11]. The vast majority of researchers consider Gram-positive cocci to be the leading causative agents of pyoderma. At the same time, understanding intermicrobial interactions, as well as identifying the leading pathogens and their associates, requires a more detailed study of microbial contamination of the skin than a simple statement of the taxonomic composition of the microbial community of the biopellicle [12-15].

In connection with the above, it was considered appropriate to clarify the species composition and population levels of the microflora of the microflora in pyoderma. The data obtained may provide important information about the dominance of microorganisms of certain taxonomic groups in the future biotope of the wound surface and the creation of a biofilm, which will allow adjusting antibacterial therapy in such patients [10, 12, 16].

Purpose of the study. The purpose of this study is to determine the microecological indicators of pyoderma pathogens.

Material and methods. The study included 97 patients with pyoderma. In 50 (51.55%) patients, boils were diagnosed, in 47 (48.45%) chronic ulcers, hydradenitis, carbuncles, widespread furunculosis. When performing this study, we were guided by generally accepted international and domestic standards in accordance with GCP (1996), the Council of Europe Convention on Human Rights and Biomedicine (dated 04.04.1997), Declaration of Helsinki of the World Medical Association on the ethical principles of conducting scientific medical research with human participation (1964-2000), Order of the Ministry of Health of Ukraine No. 281 dated 01.11.2001 and Order of the Ministry of Health of Ukraine No. 616 dated 03.08.2012. All patients signed an informed consent to participate in the study. Intraoperatively, or during dressing, material was taken and bacteriological examination was carried out no later than 2 hours after. A number of microecological indices were calculated [2, 4], statistical processing was carried out by the method of variational statistics using the MS Excel 365 program. At a value of $p<0.05$, the difference in results between groups was considered significant.

Research results

In order to improve the presentation of the research results, it was considered appropriate to calculate microecological indicators for Gram-positive and Gram-negative microorganisms separately. The results of the study of the taxonomic composition and microecological indicators of Gram-positive conditionally pathogenic microorganisms - pathogens of the inflammatory process of the skin of patients with pyoderma are given in Table 1, and the corresponding results regarding Gram-negative microbial flora are given in Table 2.

In 97 samples of pathological material taken from patients with pyoderma, a total of 197 strains of conditionally pathogenic Gram-positive (89.85%) and Gram-negative (20-10.15%) bacteria were isolated and identified.

Table 1

Taxonomic composition of Gram-positive bacteria and microecological indicators of their microbial community in pyoderma

№	The taxa	Strains	Persistence index (%)	Frequency of occurrence	Species richness index Margalef	Species diversity index Whittaker	Species dominance index	
							Simpson	Berger-Parker
1	S.aureus	79	81,44	0,40	0,40	15,19	0,160	0,401
2	S. epidermidis	11	11,34	0,06	0,05	2,12	0,003	0,056
3	S. intermedius	28	28,87	0,14	0,14	5,38	0,020	0,142
4	S. capitis	22	22,68	0,11	0,11	4,23	0,012	0,112
5	S. haemolyticus	8	8,25	0,04	0,04	1,54	0,001	0,041
6.	S. warneri	4	4,12	0,02	0,02	0,77	-	0,020
7	S. hominis	4	4,12	0,02	0,02	0,77	-	0,020
8.	S. saprophyticus	6	6,19	0,03	0,03	1,15	0,001	0,030
9	S. sciuri	9	9,28	0,05	0,04	1,73	0,002	0,046
10	S. hyicus	1	1,03	0,01	-	0,19	-	0,005
11	S. pyogenes	5	5,15	0,03	0,03	1,96	0,001	0,025

Table 2

Taxonomic composition of Gram-negative bacteria and microecological indicators of their microbial community in pyoderma

№	The taxa	Strains	Persistence index (%)	Frequency of occurrence	Species richness index Margalef	Species diversity index Whittaker	Species dominance index	
							Simpson	Berger-Parker
1	E. coli	2	2,06	0,01	0,01	0,038	-	0,010
2	E. coli Hly+	1	1,03	0,01	-	0,19	-	0,005
3	Proteus vilgaris	6	6,19	0,03	0,03	1,15	0,001	0,030
4	Morganella morganii	2	2,06	0,01	0,01	0,38	-	0,010
5	Enterobacter aerogenes	3	3,09	0,02	0,01	0,58	-	0,015
6	Psedomonas aeruginosa	6	6,09	0,03	0,03	1,15	0,001	0,030

Among the isolated and identified pathogenic and conditionally pathogenic bacteria, the key one is coagulase-positive S. aureus, which is the main one in the microbial group according to the index of constancy, frequency of occurrence, Margalef species richness index, Simpson species diversity index, and Berger-Parker species dominance.

S. intermedius and S. capitis are often found, S. epidermidis, S. sciuri are rarely found, and S. haemolyticus is even more rarely found. Other taxa of Gram-positive and Gram-negative bacteria according to microecological indicators of the macroorganism-microbiome ecosystem are random microorganisms in the microbial community. In 94 (96.91%) patients, associations consisting of two different taxa were found, and in 3 (3.09%) associations consisting of 3 conditionally pathogenic taxa were found.

Conclusions

Pyodermas are polyetiological diseases caused by both Gram-positive and Gram-negative, facultative anaerobic and aerobic bacteria with a significant predominance of Gram-positive cocci, which are in association with other conditionally pathogenic microorganisms. According to the taxonomic composition and microecological indicators, the leading causative agents of pyodermas are S. aureus, P. aeruginosa, S. pyogenes and P. vulgaris, E. coli, E. coli Hly+ and E. Aerogenes.

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