

Microbiological analysis of acute infections of the nail fold on the basis of bait thread test

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Adv Dermatol Allergol 2017; XXXIV (2): 110–115

DOI: <https://doi.org/10.5114/ada.2017.67072>

Abstract

Introduction: An acute infection of the nail fold, called paronychia, is a common clinical problem. The basis for the implementation of the treatment is the result of microbiological examination. Due to the rapid and painful course of infection, usually an empirical antimicrobial treatment prior to obtaining microbiological test results is introduced.

Aim: The microbial analysis of acute infections of the nail fold.

Material and methods: The study included 32 tests conducted on 31 patients of the Department of Dermatology. Microbiological analysis was performed with the use of the so-called bait thread test.

Results: In 73% of analyzed cases microbiological examination revealed mixed microbiological flora. Most cultured microorganisms were: *Enterococcus faecalis* (14%), *Staphylococcus aureus* (12%), *Candida albicans* (9%), *Enterobacter cloacae* (8%), and *Klebsiella pneumoniae* (7%). Most cultured bacteria belonged to the families or genera of *Enterobacteriaceae* (36%), other cultured bacteria were *staphylococci* (26%), *enterococci* (16%), *Candida species* (14%), and Gram-negative non-fermenting bacilli (8%).

Conclusions: The acute infection of the nail fold in the vast majority of cases is caused by mixed bacterial flora. A profile of isolated microorganisms suggests that the cause of the infection can be associated with neglect of hygiene. Fluoroquinolone and fusidic acid are recommended as the empirical therapy. Microbiological examination is the basis for the appropriate final treatment.

Key words: paronychia, nail fold, infection, *Enterobacteriaceae*, *staphylococci*, bait thread test.

Introduction

Acute infection of the nail fold, called paronychia, is a common clinical problem. From the dermatological point of view it is characterized by the presence of erythema, swelling and pain, which mostly are observed within the dominant hand, particularly the thumb or index finger. In most of cases it is caused by infection. This infection may result from minor injuries like nail biting, finger sucking or aggressive manicuring. Very important risk factors include diabetes mellitus and exposure to moisture conditions in a workplace. Therefore, cooks, laundresses, housekeepers and physical workers (mostly in rural areas) are specially predisposed to paronychia [1–6]. Table 1 summarizes the possible diseases/condi-

tions and occupations associated with an increased tendency to paronychia [7]. The basis for the implementation of the treatment is a result of microbiological examination of the swab obtained from the nail fold. However, it should be noted that not always purulent discharge from the nail plate is detected [2]. In such circumstances, the recommended examination is the use of a so-called bait thread test [7, 8]. Bait thread test was introduced by Alkiewicz (world famous Polish mycologist) to detect nail fold yeast infections. In this test the cotton sterile thread, which is soaked with Sabouraud broth, is placed underneath the nail fold for 24 h. After removing, thread is cultured [9, 10].

Due to the rapid and painful course of infection, usually prior to obtaining microbiological test results, an

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Received: 30.05.2015, **accepted:** 14.02.2016.

empirical antimicrobial treatment is introduced. What is more, this is desirable as the infection may continue to spread and involve the tendons or deep spaces of the hand, leading even to the amputation of the phalanx [11].

Aim

Therefore, the aim of this study was the analysis of microbial infections of the nail fold based on the so-called bait thread test in patients treated in the Department of Dermatology, Poznan University of Medical Sciences.

Material and methods

Microbiological analysis was performed with the use of the so-called bait thread test at the Central Laboratory of Microbiology in Święcicki University Hospital in Poznan in 2006–2011. This method was previously described in the literature by Alkiewicz and was based on the localization of the sterile thread soaked in Sabouraud broth underneath the nail fold for several hours [8–10, 12].

The study included 32 tests conducted on patients of the Department of Dermatology, University of Medical Sciences in whom, on the basis of the clinical picture, acute nail fold infection was suspected (Figure 1). In 2 cases (2 women), the results were negative – no growth of the pathogenic flora. The remaining 30 studies were taken from 29 patients (24 women, 5 men) and revealed

Table 1. The list of different diseases/conditions and occupations with a higher risk of paronychia (on the basis of [5, 7])

Diseases/conditions	Occupations
Celiac disease	Hairdressers
Chronic lymphocytic leukemia	Bartenders
Diabetes mellitus	Builders
Frostbite	Cooks
Histiocytosis X	Cosmetologists
Hypoparathyroidism	Dentists
Progressive systemic sclerosis	Farmers
Psoriasis	Fishermen
Raynaud's disease	Housewives
Retinoids	Meat/raw food handlers
Stevens-Johnson syndrome	Mechanics
Systemic lupus erythematosus	Pianists
Traumatic injury	Waitresses/waiters
Pemphigus	Masseurs

the presence of the pathogenic flora. From 1 patient (male) the material was collected twice.

Each thread obtained from the patient was then placed in the broth medium in a tube (BHI – brain-heart broth, bioMerieux) for initial proliferation. After 24 h of

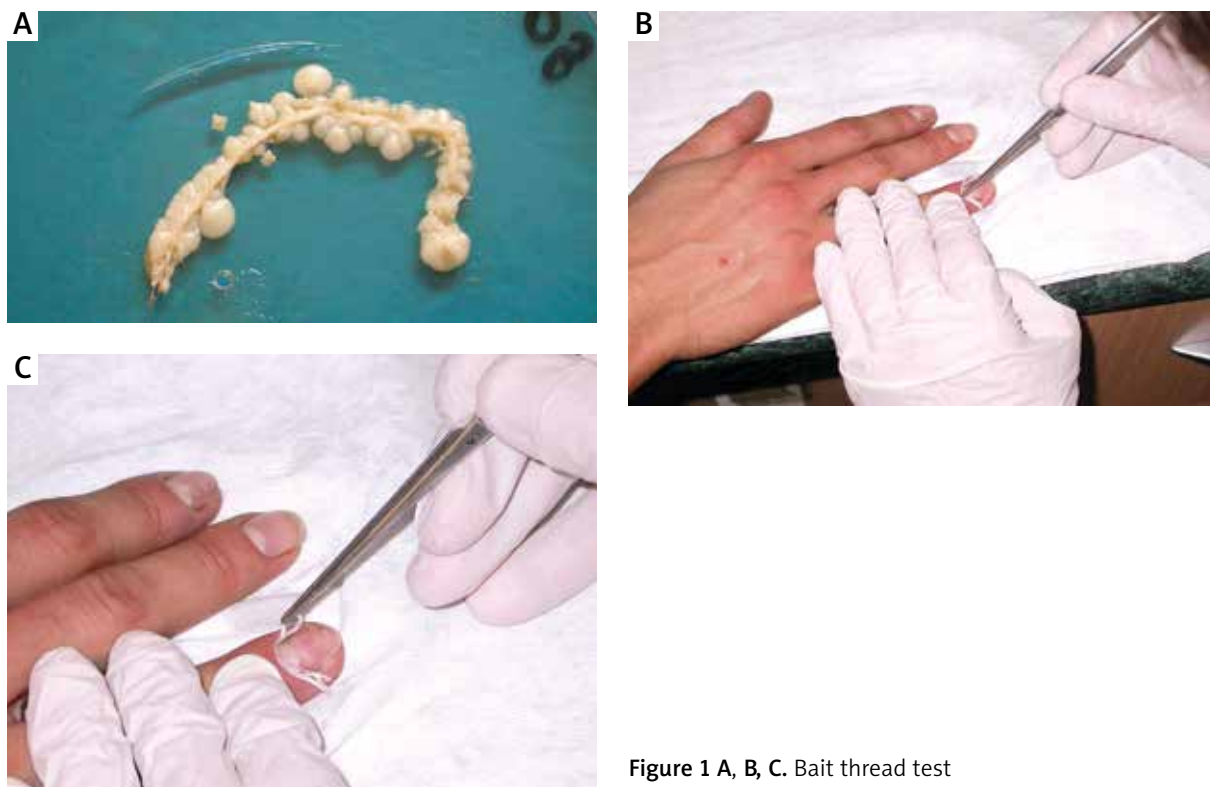


Figure 1 A, B, C. Bait thread test

incubation, broth was cultured on solid media (bioMerieux): Columbia agar with 5% blood, MacConkey's agar, Chapman Agar, D-coccosel Agar, Sabouraud agar with gentamicin and chloramphenicol. Cultured material was incubated under aerobic conditions in an incubator at 37°C for 24 h. Due to the absence of microbial growth on the first day after first culture, the cultivation time was extended to 48 h. After the period of incubation, 24 h for bacteria, 48 h for yeast, reading and further isolations were made. Finally the identification and assessment of the sensitivity to antibiotics or antifungal agents were performed. Identification of microorganisms was carried out using the bioMerieux VITEK system and bioMerieux ATB. Evaluation of sensitivity to antibiotics was performed in the automatic VITEK system. Organisms were also examined for the presence of resistance mechanisms.

Results

In the analyzed material 74 microorganisms were isolated. Pathogens were isolated from 30 tested threads. In 2 cases no microorganisms were cultured. The number of grown pathogens in 1 material ranged from 1 to 5 species, but only in 8 (27%) cases single microorganisms were isolated: *Staphylococcus (Staph.) aureus* (4 patients), *Enterococcus faecalis* (2 patients), *Klebsiella pneumonia* (1 patient), and *Escherichia coli* (1 patient). In the remaining tests mixed flora was found (Figure 2).

The most common cultured organisms were (in the following order): *Enterococcus faecalis* – 10× (14%), *Staph. aureus* – 9× (12%), *Candida albicans* – 7× (9%), *Enterobacter cloacae* – 6× (8%), *Klebsiella pneumonia* – 5× (7%), and *Staph. haemolyticus* – 4× (5%) (Figure 3).

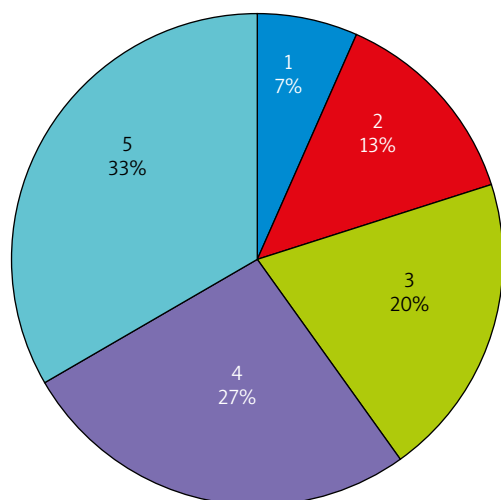


Figure 2. Number of pathogens isolated from one sample

Sorting cultured microorganisms according to their family or genera (in the following order), *Enterobacteriaceae* – 27× (36%), *staphylococci* – 19× (26%), *enterococci* – 12× (16%), *Candida species (spp.)* – 10× (14%), and Gram-negative non-fermenting bacilli – 6× (8%) were detected (Figure 4). Among the *Enterobacteriaceae* family the following species were isolated: *Enterobacter cloacae* – 6× (22%), *Klebsiella pneumoniae* – 5× (18%), *Escherichia coli* – 3× (11%), *Serratia marcescens* – 3× (11%), *Morganella morganii* – 2× (7%), *Citrobacter freundii* – 2× (7%), *Klebsiella oxytoca* – 2× (7%), *Proteus mirabilis* – 2× (7%), *Citrobacter braakii* – 1× (4%), *Providencia rettgeri* – 1× (4%) (Figure 5). Among *staphylococci*: *Staph. aureus* – 9× (47%), *Staph. haemolyticus* – 4× (21%), *Staph. warneri* – 3× (16%), *Staph. saprophyticus* – 1× (5%), *Staph. epidermidis* – 1× (5%), and *Staph. lugdunensis* – 1× (5%) (Figure 6). Among *enterococci*: *Enterococcus faecalis* – 10× (83%), *Enterococcus faecium* – 1× (8%), *Enterococcus avium* – 1× (8%). Among fungi: *Candida albicans* – 7× (70%) and *Candida parapsilosis* – 3× (30%). Among Gram-negative non-fermenting bacilli: *Pseudomonas aeruginosa* – 3× (50%), *Acinetobacter lwoffii* – 2× (33%), and *Acinetobacter baumannii* – 1× (17%).

Fungi of the genus *Candida* were isolated in 10 cases, representing 14% of the studies. These have always appeared together with 2–4 other pathogens, never as a single pathogen.

Among the strains of *Enterobacteriaceae* family all isolated strains were susceptible to most antibiotics (multisusceptible microorganisms), that were probably

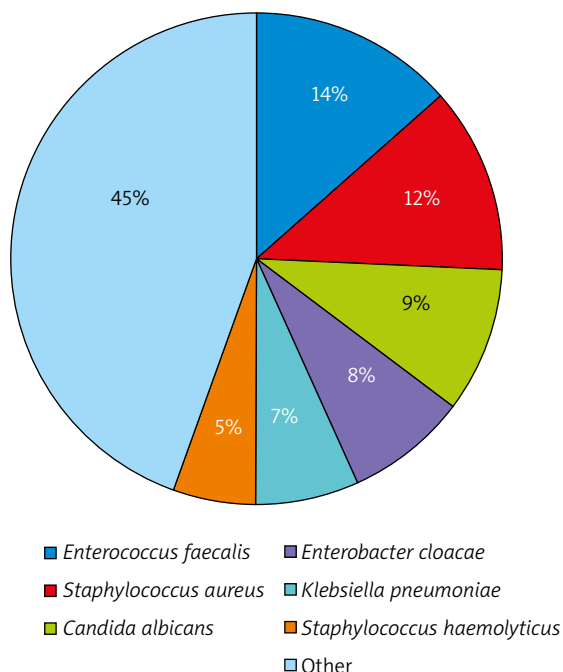


Figure 3. Most commonly isolated pathogens

own strains, the so-called wild. Twenty seven strains were cultured and analyzed. All analyzed strains were sensitive to amikacin, ciprofloxacin, second generation of cephalosporins – cefoxitin, third and fourth generation of cephalosporins (cefotaxime, ceftriaxone, cefepime), piperacillin/tazobactam, carbapenems (imipenem and meropenem), ticarcillin/clavulan acid. 96% were sensitive to gentamicin and trimethoprim/sulfamethoxazole, 63% to ampicillin/sulbactam or amoxicillin/clavulan acid, 40% to cephalothin (first-generation cephalosporin), 20% to cefazolin (first-generation cephalosporin) and 19% to ampicillin.

Among staphylococci, *Staph. aureus* revealed 100% sensitivity to fusidic acid, chloramphenicol, rifampicin, trimethoprim/sulfamethoxazole, gentamicin, vancomycin, teicoplanin, 88% to ofloxacin (representing quinolones), 77% to clindamycin and tetracycline, 62% to fosfomycin, and 44% to erythromycin. Coagulase-negative staphylococci (*Staph. haemolyticus*, *Staph. warneri*, *Staph. saprophyticus*, *Staph. epidermidis*) and *Staph. lugdunensis* demonstrated 100% sensitivity to rifampicin and vancomycin, 90% to trimethoprim/sulfamethoxazole, 88% to ofloxacin, 80% to lincomycin (clindamycin), 60% to tobramycin, 50% to erythromycin and fusidic acid and 30% to teicoplanin.

Susceptibility of *enterococci* was as follows: 100% sensitive to linezolid, moxifloxacin (representing quinolones), vancomycin, levofloxacin, 92% to penicillin, 75% to gentamycin, and 30% to tetracycline.

All cultured *Candida* were susceptible to amphotericin B and 5-fluorocytosine, 70% to fluconazole, and 60% to itraconazole and voriconazole.

All Gram-negative non-fermenting bacilli were sensitive to gentamicin, imipenem, meropenem, ceftazidime, cefepime, ciprofloxacin, 83% to ampicillin/sulbactam,

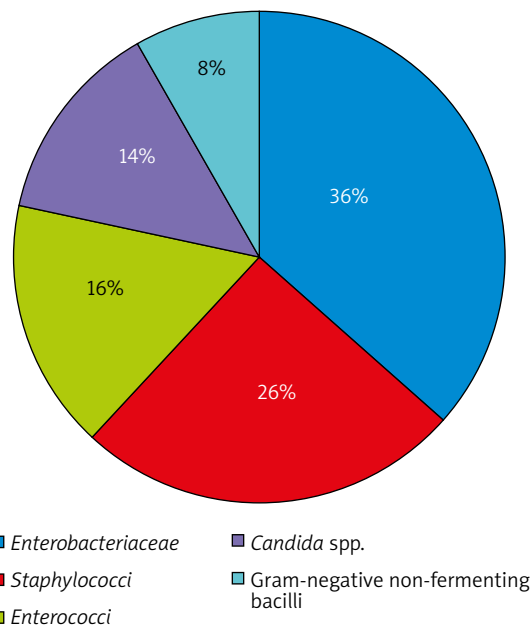


Figure 4. Most commonly isolated pathogens' families or genera

additionally all presented resistance to trimethoprim/sulfamethoxazole.

Discussion

Paronychia is one of the most frequently observed localized hand infections, which clinically can be divided into an acute and chronic form [3]. The acute type of infection usually arises spontaneously as a result of bacterial growth due to the different trauma. This form

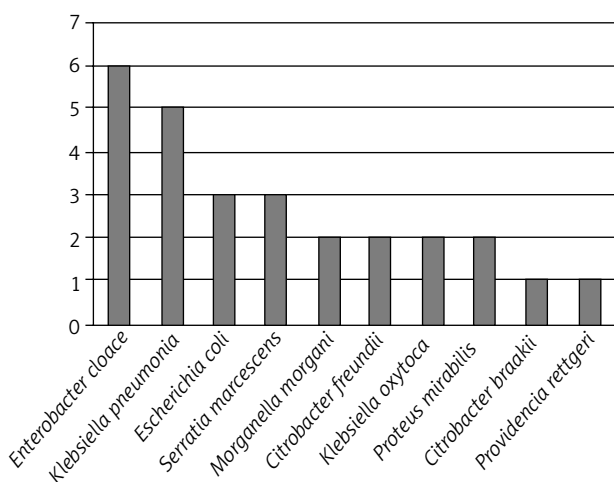


Figure 5. Most commonly isolated species from the Enterobacteriaceae family

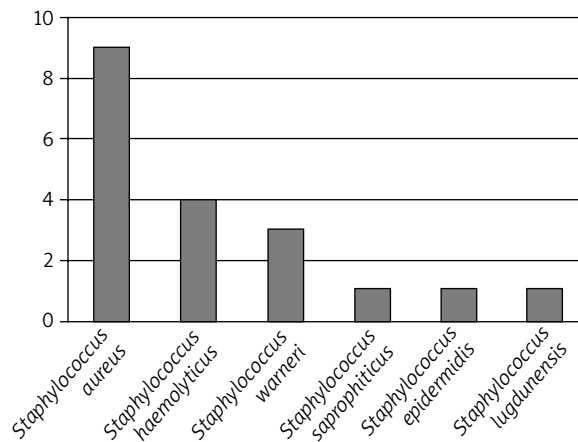


Figure 6. Most commonly isolated species from the Staphylococci genus

is associated with intense pain and tenderness of perionychium, provoked by collection of pus. On the other hand, the chronic type is more often detected among patients, who are continuously exposed to moist conditions, like bartenders, housekeepers, homemakers, dishwashers and swimmers (Table 1) [3, 7, 13–15]. Its cause is multi-factorial and includes *Candida*, low-grade bacterial infection, prolonged contact with contactants and irritants. From the clinical point of view, nail plates become thickened and discolored, the cuticle is reddened and pain is not so intense like in the acute form. It has to be underlined that in patients with recurrent infection, fungal infection should be always considered [3, 7].

In the presented material, nail fold infection was more frequently observed among women, which is confirmed in the literature [5, 12]. Usually mixed infections caused by 2 to 5 different pathogens were observed (73% of the samples), similarly to previous studies [1, 16]. In 27% (8 cases), the infection was caused by one pathogen. Then *Staph. aureus* (4 patients), *Enterococcus faecalis* (2 patients), *Klebsiella pneumonia* (1 patient), and *Escherichia coli* (1 patient) were isolated.

Among the most frequently isolated families or genera are the following: *Enterobacteriaceae* (representing 36%), *staphylococci* (26%), *enterococci* (16%), *Candida* sp. (14%), and Gram-negative non-fermenting bacilli (8%). In the literature, among the more commonly indicated pathogens are *enterococci*, *Enterobacteriaceae*, *Staphylococcus* and Gram-negative non-fermenting bacilli [2, 16]. The most common infectious pathogen is *Staph. aureus* [3, 4, 17]. Rarely cultured bacteria are anaerobic ones [11]. Among them Gram-positive cocci, *Bacteroides* spp. and *Fusobacterium* spp. are the most frequent [16]. It has to be stressed that in all study cases coagulase-negative *staphylococci* were isolated as a component of mixed flora. It is unclear whether they play a real role in paronychia or they are just contaminants. However methicillin-resistant strains should be considered as pathogenic. Moreover, coagulase-negative *staphylococci* can form biofilm and for example they can be responsible for catheter-related bloodstream infection [18]. The bacterial flora detected in our study is largely typical for the anogenital area. Similar results were observed by Iranian researchers [1].

Fungi of the genus *Candida* were isolated only in 14% of samples. Rare presence of yeast in nail fold infection was also noted by other authors [16]. In addition, it should be emphasized that none of our results suggested that fungi of the genus *Candida* are the single pathogen. In all cases they were a component of mixed fungobacterial infection. Additionally, the number of accompanied bacterial pathogens ranged from 2 to 4. Among fungal infections, the most frequently isolated fungi were *Candida albicans*, and then *Candida parapsilosis*, which was confirmed in previous reports [12]. In the literature there are also descriptions of other species of the genus *Can-*

didia, which may be occasionally a pathogenic factor in the nail fold infections, including *Candida guilliermondii*, *Candida glabrata*, *Candida tropicalis* and *Candida kefyr* [1, 12]. They were not isolated in this study.

Microbiological analysis of sensitivity to antibiotics indicates usefulness of fluoroquinolones (ciprofloxacin, ofloxacin, moxifloxacin, levofloxacin) in the treatment of paronychia because 100% of the isolated *Enterobacteriaceae* were *enterococci* and Gram-negative non-fermenting bacilli and 88% *staphylococci* were sensitive to them. However, the latter were in 100% sensitive to topical use of fusidic acid. This is an important issue in clinical practice, when a decision on empiric antibiotic therapy prior to obtaining a result of microbiological culture is made. The effectiveness of fluoroquinolones was also pointed by Eames *et al.* [19]. Importantly, the authors based their opinion on the microbiological analysis. These findings differ from the recommendations found in two papers of Rigopoulos *et al.* and Rockwell, who assumed that oral antibiotics should have primary antistaphylococcal action and suggested the use of amoxicillin with clavulanic acid, clindamycin and trimethoprim with sulfamethoxazole [3, 4]. Our analysis of susceptibility revealed that these drugs in empiric antibiotic therapy are not justified. On the other hand, among antifungal agents nystatin appears to be useful. This drug belongs to the same group as amphotericin B, which showed sensitivity of 100% of the tested strains. It should be noted that in this analysis, sensitivity of *Candida* spp. to fluconazole and itraconazole was only 70% and 60%, respectively. Due to the significant toxicity of these agents, one should therefore refrain from a decision on their inclusion until the result of the evaluation of their sensitivity is obtained.

To sum up, it should be emphasized that the acute infection of the nail fold in the vast majority of cases is a mixed flora infection. A profile of isolated microorganisms suggests that the cause of the infection in many cases can be associated with neglect of hygiene. Most frequently isolated bacteria belong to the *Enterobacteriaceae*, followed by *staphylococci*. For this reason, the preferred empirical treatment is a combination of fluoroquinolone and fusidic acid. The basis for the appropriate treatment is properly performed microbiological examination with the evaluation of susceptibility [20]. Due to the possibility of different etiological factors for infections with different resistance formula, there is a need to conduct periodic microbiological analyses on larger groups of subjects in a variety of environments.

Conclusions

Paronychia is an important clinical problem, which usually affects women. The bait thread test is a useful diagnostic tool to detect causative agents of paronychia. Mixed flora (including *Enterobacteriaceae* and *staphylococci*) is responsible for most cases of nail fold infections.

Proposed empirical treatment of paronychia should include a combination of fluoroquinolone and fusidic acid. Neglect of hygiene is a risk factor for paronychia.

Conflict of interest

The authors declare no conflict of interest.

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