

Epidemiological and antibiotic susceptibility pattern of bacterial paronychia infection

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Abstract

Objective: To identify the bacterial aetiology of paronychia, and assess the antibiotic resistance patterns of the isolated pathogens.

Method: The cross-sectional cohort study was conducted from December 1, 2021, to December 31, 2022, at the Department of Microbiology, Centre for Advanced Studies in Vaccinology and Biotechnology, Quetta, Pakistan, and comprised samples collected from Bolan Medical Complex Hospital, Quetta, and Sandeman Provisional Hospital, Quetta, of patients clinically diagnosed with paronychia. Organisms were isolated using selective and differential media, and they were categorised by using biochemical tests, antimicrobial susceptibility test and polymerase chain reaction. Data was analysed using SPSS 26.

Results: Of the 480 samples collected, 212(44.16%) were positive; 160(33.3%) females and 52(10.83%) males. The most affected age group was 20-30 years 70(14.56%). Among the positive samples, 90(18.75%) were identified as staphylococcus aureus, followed by staphylococcus. epidermidis 50(10.41%), *pseudomonas aeruginosa* 42(8.75%) and klebsiella pneumoniae 30(6.25%). Staphylococcus aureus and staphylococcus epidermidis were found resistant to ceftriaxone and amoxicillin, while *pseudomonas aeruginosa* was resistant against sulfamethoxazole and vancomycin, and klebsiella pneumoniae was resistant to doxycycline and vancomycin.

Conclusion: Staphylococcus aureus was the predominant pathogen in bacterial paronychia, with higher prevalence among females and young adults. Besides, high levels of antibiotic resistance was noted.

Key Words: Paronychia, Antibiotic resistance, Staphylococcus aureus, *Pseudomonas aeruginosa*, Epidemiology. (JPMA 76: 330; 2026) DOI: <https://doi.org/10.47391/JPMA.21641>

Introduction

Paronychia, characterised by swelling and redness around the nail, is a common nail infection that can progress to abscess formation if left untreated. It arises from a variety of infectious and non-infectious causes, with bacterial pathogens being the most frequent culprits. According to the American Academy of Dermatology, nail disorders affect nearly everyone at some point in their lives.¹ In the United States, paronychia accounts for approximately 35% of all nail infections, with a higher prevalence among women compared to men.² The condition is particularly common among individuals whose hands are frequently exposed to water or physical labour, such as housekeepers, chefs and manual labourers.³

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The infection typically develops following a break in the skin around the nail, often due to trauma, nail-biting or cuticle manipulation. While bacterial pathogens are the primary cause, other factors, such as contact dermatitis, fungal infections and herpes simplex virus, can also contribute.⁴ Chronic paronychia, which persists for six weeks or longer, is often associated with repeated exposure to moisture, chemical irritants, or underlying conditions, such as diabetes mellitus (DM).⁵ Additionally, certain medications, including epidermal growth factor receptor inhibitors, have been linked to the development of chronic paronychia.⁶ Paronychia can also develop due to injuries, such as biting or pulling on hangnails, or from trimming and pushing back the cuticle.⁷

Staphylococcus (S.) aureus is the most common bacterial pathogen implicated in paronychia, followed by *pseudomonas (P.) aeruginosa* and other gram-negative bacteria.⁸ In the United States, *S. aureus* infections, including those affecting nails and soft tissues, result in approximately 10 million outpatient visits and 500,000 hospital admissions annually.⁹

Certain medications, like epidermal growth factor receptor inhibitors, can potentially trigger chronic paronychia. The resistivity of paronychia infection

against antibiotics varies, depending on the geographic location and the specific bacteria involved. For example, a study in the United States found that methicillin-resistant *S. aureus* (MRSA) was the most common antibiotic-resistant bacteria isolated from patients with paronychia, accounting for 19% of the cases. A study in Europe found that vancomycin-resistant enterococci was the most common antibiotic-resistant bacteria isolated from patients with paronychia, accounting for 25% of the cases.¹⁰

There is limited data on the epidemiological and antibiotic resistance patterns of paronychia in low-resource settings. The current study was planned to address this gap in literature by identifying the bacterial aetiology of paronychia and evaluating antibiotic susceptibility patterns in a tertiary care setting.

Materials and Methods

The cross-sectional cohort study was conducted from December 1, 2021, to December 31, 2022, at the Department of Microbiology, Centre for Advanced Studies in Vaccinology and Biotechnology (CASVAB), University of Balochistan, Quetta, Pakistan, and comprised samples collected from Bolan Medical Complex Hospital, Quetta, and Sandeman Provisional Hospital, Quetta, of patients clinically diagnosed with paronychia. After approval from the ethics review board of the University of Balochistan, the sample size was calculated using the Cochran's formula.¹¹ Informed consent had been obtained from all the participants prior to sample collection.

Data was retrieved regarding patients regardless of gender and age who had paronychia whether acute or chronic. Data of patients having fungal infection or any other infection, such as eczema and psoriasis, and those who were on antibiotics, was excluded. The samples were collected using pre-sterilised cotton swabs. The samples were transported to the laboratory under cold chain conditions to maintain their integrity. Patient demographic details, including age, gender, ethnicity and socioeconomic status (SES), were recorded using a pre-designed checklist.

The samples were streaked onto selective media, including Mannitol Salt Agar, Eosin Methylene Blue Agar, and Cetrimide Agar, and incubated at 37°C for 24 hours. The isolates were sub cultured three times to obtain pure colonies for further analysis. Gram staining and biochemical tests, including catalase, coagulase, and sugar fermentation tests, were performed to identify bacterial species.

Antimicrobial susceptibility testing was done using the disc diffusion method, following the 2006 guidelines of the Clinical and Laboratory Standards Institute (CLSI).¹² A bacterial suspension equivalent to 0.5 McFarland standard was prepared and evenly spread on Mueller-Hinton agar plates. Antibiotic discs, including amoxicillin (25µg), ceftriaxone (30µg), doxycycline (30µg), sulfamethoxazole (25µg), furazolidone (15µg), vancomycin (30µg), fusidic acid (10µg), erythromycin (5µg), clindamycin (2µg) and ciprofloxacin (5µg), were placed on the agar surface. The plates were incubated at 37°C for 24 hours, and zones of inhibition were measured to determine susceptibility.

Deoxyribonucleic acid (DNA) was extracted from the bacterial isolates using a DNA purification kit (Thermo Scientific, Catalog No. K0512, Waltham, MA, USA) and stored at -20°C for further use. Polymerase chain reaction (PCR) was performed to amplify species-specific genes: the 16S ribosomal ribonucleic acid (rRNA) gene for *S. aureus* and *P. aeruginosa*, the amino acid permease (*aap*) gene for *S. epidermidis*, and the *rcaA* gene (regulator of capsule synthesis A gene) for *klebsiella* (*K.*) *pneumoniae*. The primers sequences were taken from peer-reviewed literature (Table 1), ensuring both specificity and sensitivity. The PCR reaction mixture (25µL) consisted of 11µL of master mix 2× AmpMaster™ Taq PCR Master Mix (GeneAll Biotechnology Co., Ltd., Seoul, South Korea), 1µL each of forward and reverse primers, 10µL of distilled water, and 2µL of DNA template. Amplification conditions included an initial denaturation at 94°C for 5 minutes, followed by 30 cycles of denaturation (94°C for 30 seconds), annealing (55-59.8°C for 60 seconds), and extension (72°C for 60 seconds), with a final extension at 72°C for 10 minutes. PCR products were visualised on a 2% agarose gel stained with ethidium bromide.

Data were analysed using SPSS 26. Data was subjected to descriptive statistics, such as frequencies and percentages. The chi-square test was applied to evaluate associations. $P < 0.05$ was considered statistically significant.¹³

Results

Of the 480 samples from patients having a mean age of 24.7±11.2 years, 260(54.2%) were collected from Bolan Medical Hospital, and 220(45.8%) from Sandeman Provisional Hospital. Overall, 212(44.16%) samples were positive for paronychia; 160(33.3%) females and 52(10.83%) males ($p < 0.05$). The most affected age group was 20-30 years 70(14.56%) ($p < 0.05$). The prevalence of *S. aureus* was 90(18.75%), followed by *S. epidermidis* 50(10.41%), *P. aeruginosa* 42(8.75%) and *K. pneumoniae*

Table -1: Primer sequences for *staphylococcus aureus*, *staphylococcus epidermidis*, *pseudomonas aeruginosa* and *klebsiella pneumonia*.

Organisms	Genes	Primer Sequences		References
		Sequences	Amplicon size (bp)	
<i>Staphylococcus aureus</i>	16s rRNA gene	F: ACGGTCTTGCTGCTCACTTATA R: TACACATATGTTCTCCCTAATAA	257 bp	Johnson et al., (2016) ²²
<i>Staphylococcus epidermidis</i>	aap gene	F: ATACAACGGTGCGAGATGGTT R: GTAGCCGTCGAAGTTTACCAG	399bp	Vandecasteele et al. ²³ , (2003)
<i>Pseudomonas aeruginosa</i>	16s rRNA gene	F: GGGGGATCTTCGGACCTCA R: TCCTTAGAGTGCCCAACCCG	956bp	Raheem & Mohammed ²⁴ , (2021)
<i>Klebsiella pneumonia</i>	rcaA gene	F: GGATATCTGACCAAGTCGG R: GGGTTTTGCGTAATGATCTG	176bp	Dong et al. ²⁵ , (2015)

RNA: Ribonucleic acid.

Table-2: Inferential analysis and epidemiological prevalence of paronychia infection.

		P value
Overall %		
Positive Sample	44.16%(n=212)	
Negative Sample	55.83%(n=268)	
Gender-wise%		
Female	33.33%(n=160)	<0.001
Male	10.83%(n=52)	
Age-wise %		
20-30 years	14.56% (n=70)	<0.001
10-20 years	11.04% (n=53)	
30-70 years	9.58% (n=46)	
1-10 years	8.95% (n=43)	
Ethnicity-wise %		
Pashtun	16.66% (n=80)	<0.001
Baloch	12.5% (n=60)	
Hazara	8.33% (n=40)	
Settlers	6.66% (n=32)	
Class-wise %		
Lower	22.91% (n=110)	0.048
Middle	12.5% (n=60)	
Higher	8.75% (n=42)	
Nail-wise %		
Fingernail	24.16% (n=116)	<0.001
Toenail	20% (n=96)	

30(6.25%). The most affected group was the one having Pashtun ethnicity 80(16.66%) ($p < 0.05$), and those having lower SES 110(22.91%) ($p < 0.05$). Additionally, paronychia infections were more common in fingernails 116(24.16%) than in toenails ($p < 0.050$ 9Table 2).

Gram staining, biochemical tests and sugar fermentation tests of *S. aureus*, *S. epidermidis*, *P. aeruginosa* and *K. pneumonia* isolates were noted in detail (Table 3).

The most resistant antibiotics against *S. aureus* and *S. epidermidis* were amoxicillin, ceftriaxone, and erythromycin, while *P. aeruginosa* was highly resistant against doxycycline, erythromycin, sulfamethazole, ceftriaxone, amoxicillin, vancomycin and clindamycin, and *K. pneumoniae* was most resistant to amoxicillin, vancomycin, clindamycin, sulfamethazole, doxycycline and erythromycin (Table4).

Isolates of *S. aureus* generated a specific 16S rRNA gene of 257-bp fragment, *S. epidermidis* produced aap gene of a 399-bp fragment. *P. aeruginosa* yielded 16S rRNA gene of a 956-bp fragment, and *K. pneumoniae* isolates generated rcaA gene of a 176-bp fragment (Figure).

Table-3: Biochemical characterisation of the isolated organisms from paronychia infection.

Growth on selective media				
<i>S.aureus</i>	Gram positive, yellow colony with yellow zones, cocci shape, size 0.5-1.5µm in diameter			
<i>S.epidermidis</i>	Gram positive, coccus, irregular clusters of cells blue to purple colored colonies, size 1-2µm in diameter			
<i>P.aeruginosae</i>	Gram negative, straight rod-shaped (bacilli) colonies, size 2-4µm in diameter			
<i>K.pneumoniae</i>	Gram-negative rod shaped (bacilli) bacterium which appear pink, singly or in pairs or in short chains, size 0.5-2µm in diameter			
Biochemical tests				
Biochemicals	<i>S.aureus</i>	<i>S.epidermidis</i>	<i>P.aeruginosae</i>	<i>K.pneumoniae</i>
Oxidase	-	-	+	-
Indole	-	-	-	-

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Motility	-	-	+	-
Citrate	+	-	+	+
MR	+	-	-	-
VP	+	-	-	+
Catalase	+	+	+	+
Urease	+	+	-	+
Sugar fermentation tests				
Sugars	<i>S.aureus</i>	<i>S.epidermidis</i>	<i>P.aeruginosae</i>	<i>K.pneumoniae</i>
Glucose	+	+	+	+
Lactose	+	+	-	+
Mannitol	+	-	+	+
Fructose	+	+	-	+
Sucrose	+	+	-	+
Raffinose	-	-	-	+
Mannose	+	+	-	+
Maltose	+	+	-	+

S.: *Staphylococcus*, *P.*: *Pseudomonas*, *K.*: *Klebsiella*.

Table-4: Antibiotic susceptibility pattern of the bacterial isolates.

Antibiotics	Abbreviation & potency	<i>S.a</i> n=20		<i>S.epi</i> n=20		<i>P.a</i> n=20		<i>K.p</i> n=20	
		S	R	S	R	S	R	S	R
Amoxicillin	AML 25	1(5%)	19(95%)	2(10%)	18(90%)	2(10%)	18(90%)	2(10%)	18(90%)
Ceftriaxone	CRO 30	3(15%)	17(85%)	2(10%)	18(90%)	3(15%)	17(85%)	17(85%)	3(15%)
Doxycycline	TE 30	17(85%)	3(15%)	17(85%)	3(15%)	1(5%)	19(95%)	2(10%)	18(90%)
Ciprofloxacin	CIP 5	18(90%)	2(10%)	18(90%)	2(10%)	18(90%)	2(10%)	17(85%)	3(15%)
Sulfamethoxazole	SXT 25	20(100%)	0(0%)	19(95%)	1(5%)	3(15%)	17(85%)	4(20%)	16(80%)
Vancomycin	VA 30	17(85%)	3(15%)	18(90%)	2(10%)	2(10%)	18(90%)	3(15%)	17(85%)
Clindamycin	DA 2	18(90%)	2(10%)	17(85%)	3(15%)	3(15%)	17(85%)	3(15%)	17(85%)
Erythromycin	E 5	2(10%)	18(90%)	3(15%)	17(85%)	1(5%)	19(95%)	2(10%)	18(90%)

S.a.: *Staphylococcus aureus*, *S.epi.*: *Staphylococcus epidermidis*, *P.a.*: *Pseudomonas aeruginosa*, *K.p.*: *Klebsiella pneumoniae*.

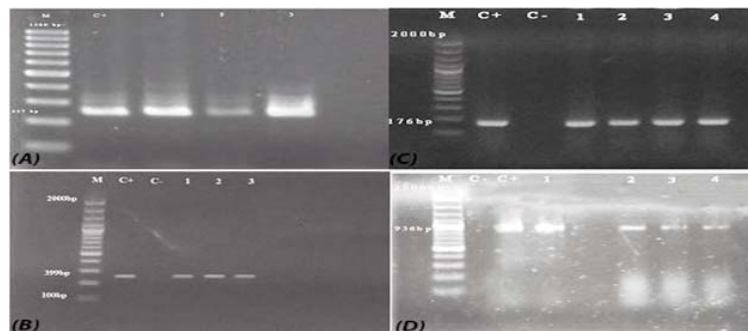


Figure: Identification based on polymerase chain reaction (PCR) of bacterial isolates from paronychia infected patients. (A) *S. aureus* produced specific size of 257-bp fragment of 16s rRNA gene; (B) *S. epidermidis* produced specific size of 399-bp fragment of aap gene; (C) *K. pneumoniae* produced specific size of 176-bp fragment of recA gene; and (D) *P. aeruginosa* produced specific size of 956-bp fragment of 16s rRNA gene.

S.: *Staphylococcus*, *P.*: *Pseudomonas*, *K.*: *Klebsiella*, rRNA: ribosomal ribonucleic acid.

Discussion

In the current study, 44.16% of the 480 infected nail samples collected were found to be positive for bacterial infection, while 55.83% were negative. *S. aureus* was detected in 90(18.75%) of the samples, followed by *S. epidermidis* 50(10.41%), *P. aeruginosa* 42(8.75%) and *K. pneumoniae* 30(6.25%). *S. aureus* was also reported to be the most common pathogen isolated in a similar study.¹⁴ *S. epidermidis* emerged as the second most prevalent pathogen, which matched earlier findings.¹⁵

Bacterial paronychia in the current study was found to be more prevalent in female patients than in male patients, which was consistent with the ratio reported earlier.¹⁶

Paronychia affects individuals across all age groups. In the current study, the highest rate of infection was found in patients aged 20-30 years (14.58%), and it was the least among those aged 1-10 years (8.95%). A 2020 study observed the highest incidence of paronychia in those aged 20-29 years.¹⁷

The current study showed that bacterial paronychia infections were common amongst patients having lower SES (22.91%). One study found that paronychia tends to affect persons whose jobs encompass regular water exposure and physical labour.¹⁸ Additionally, the current study showed that the infection rate was highest among those with Pashtun ethnicity (16.66%), and they were more prevalent in fingernails (24.16%). According to a 2020 study, the most frequently affected fingers were the right thumb (62%), followed by the right middle finger (52%), the left thumb (57.6%), and the left middle finger (51.5%).¹⁷

The current study carried out biochemical tests to validate the occurrence of *S. aureus*, *P. aeruginosa*, *K. pneumoniae* and *S. epidermidis*. The morphological and biochemical features of these organisms matched those described earlier.¹⁹ Treating paronychia infections has become increasingly challenging. Eight antibiotics, each from different generations and with varying mechanisms of action, were evaluated against the bacterial isolates in the current study, and the most resistant antibiotics against *S. aureus* and *S. epidermidis* were amoxicillin, ceftriaxone, and erythromycin, with resistance rates ranging from 85% to 95%. This was in line with earlier reports.²⁰ *P. aeruginosa* was found highly resistant to doxycycline, erythromycin, sulfamethazole, ceftriaxone, amoxicillin, vancomycin and clindamycin, with resistance rates ranging from 85% to 95%, which matched previous findings.²¹ The resistance rate of *K. pneumoniae* were 80% to 90% for amoxicillin, vancomycin, clindamycin, sulfamethazole, doxycycline and erythromycin. A 2021

study reported similar findings.²²

In the present research, PCR-based identification was utilised to check the presence of organisms. The findings of all the four types of isolates (Figure) were consistent with literature.²³⁻²⁶

The current study has several limitations. First, it was confined to tertiary care hospitals in Quetta, which may have limited the generalisability of the results to other regions or healthcare settings. The cross-sectional design provided only a snapshot of the bacterial aetiology and resistance patterns during the study period, without accounting for seasonal or temporal variations. Additionally, the study did not include fungal or viral pathogens, nor did it assess anaerobic or fastidious organisms, which may have led to an underestimation of the true spectrum of paronychia-causing agents. The panel of antibiotics tested was limited, potentially overlooking resistance to other important drugs.

Conclusion

S. aureus was the predominant pathogen in bacterial paronychia, with higher prevalence among females, young adults, and those having low SES. High levels of antibiotic resistance highlighted the need for culture-guided therapy and strengthened antimicrobial stewardship in clinical settings.

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