

Bacterial Infection of the Skin and Skin Microflora, Microbiome

Dr. Tabish Joshi*

Medical Center of Belgrade University of Vellore of Technology, India

Corresponding author: Dr. Tabish Joshi

✉ tabish.j@gmail.com

Medical Center of Belgrade University of Vellore of Technology, India

Citation: Joshi T (2022) Bacterial Infection of the Skin and Skin Microflora, Microbiome. Arch Clin Microbio, Vol. 13 No. 12: 220.

Abstract

Skin and soft tissue infections (SSTIs) involve microbial invasion of the skin and underlying soft tissues. They have variable presentations, etiologies and severities. The challenge of SSTIs is to efficiently differentiate those cases that require immediate attention and intervention, whether medical or surgical, from those that are less severe. Approximately 7% to 10% of hospitalized patients are affected by SSTIs, and they are very common in the emergency care setting. The skin has an extremely diverse ecology of organisms that may produce infection. The clinical manifestations of SSTIs are the culmination of a two-step process involving invasion and the interaction of bacteria with host defences. The cardinal signs of SSTIs involve the features of inflammatory response, with other manifestations such as fever, rapid progression of lesions and bullae. The diagnosis of SSTIs is difficult because they may commonly masquerade as other clinical syndromes. To improve the management of SSTIs, the development of a severity stratification approach to determine site of care and appropriate empirical treatment is advantageous. The selection of antimicrobial therapy is predicated on knowledge of the potential pathogens, the instrument of entry, disease severity and clinical complications.

The skin is the human body's largest organ, colonized by a diverse milieu of microorganisms, most of which are harmless or even beneficial to their host. Colonization is driven by the ecology of the skin surface, which is highly variable depending on topographical location, endogenous host factors and exogenous environmental factors. The cutaneous innate and adaptive immune responses can modulate the skin microbiota, but the microbiota also functions in educating the immune system. The development of molecular methods to identify microorganisms has led to an emerging view of the resident skin bacteria as highly diverse and variable. An enhanced understanding of the skin microbiome is necessary to gain insight into microbial involvement in human skin disorders and to enable novel promicrobial and antimicrobial therapeutic approaches for their treatment.

Keywords: Bacterial; Infections; Management; Skin

Received: 02-Dec-2022, Manuscript No. Ipacm-22-13322; **Editor assigned:** 05-Dec-2022, Pre-QC No. Ipacm-22-13322 (PQ); **Reviewed:** 12-Dec-2022, QC No. Ipacm-22-13322; **Revised:** 26-Dec-2022, Manuscript No. Ipacm-22-13322(R); **Published:** 30-Dec-2022, DOI: 10.36648/1989-8436X.22.13.12.220

Introduction

Skin diseases are caused by viruses, rickettsia, bacteria, fungi, and parasites. This chapter focuses on the common bacterial diseases of skin. Viral infections are also described, but of the cutaneous fungal diseases, only nail infections are included. The other fungal diseases are described in the Mycology section [1].

The skin is a milieu for controlled bacterial growth. Skin supports the growth of commensal bacteria, which protect the host from pathogenic bacteria. Environmental and local factors, host immunity, and organism adherence and virulence are intricately

related to cutaneous infection. Resident gram-positive bacteria include Staphylococcus, Micrococcus, and Corynebacterium sp. Staphylococcus aureus and Streptococcus pyogenes are notoriously pathogenic in the skin. In order for bacteria to be pathogenic, they must be able to adhere to, grow on, and invade the host [2]. Bacteria possess numerous virulence genes that allow for growth in these privileged niches. Epidermal infections caused by S. aureus and S. pyogenes include impetigo and ecthyma. Dermal infections consist of erysipelas, cellulitis, and necrotizing fasciitis. The pilosebaceous unit is involved in folliculitis, furunculosis, and carbunculosis. Moreover, S. aureus and S. pyogenes produce toxins that may elicit a superantigen

response, causing massive release of cytokines. Staphylococcal scalded skin syndrome, toxic shock syndrome, and scarlet fever are all superantigen-mediated. Gram-negative organisms such as *Pseudomonas aeruginosa*, *Pasteurella multocida*, *Capnocytophaga canimorsus*, *Bartonella* sp., *Klebsiella rhinoscleromatis*, and *Vibrio vulnificus* are not typical resident skin microflora but may cause cutaneous infection [3].

It is important to have a good understanding of the common clinical manifestations and pathogens involved in bacterial skin infections to be able to manage them appropriately. The type of skin infection depends on the depth and the skin compartment involved. Skin and soft tissue infections (SSTIs) are clinical entities of variable presentation, etiology and severity that involve microbial invasion of the layers of the skin and underlying soft tissues. SSTIs range from mild infections, such as pyoderma, to serious life-threatening infections, such as necrotizing fasciitis [4]. The minimum diagnostic criteria are erythema, edema, warmth, and pain or tenderness. The affected area may also become dysfunctional (eg, hands and legs) depending on the severity of the infection. A patient's comorbidities (eg, diabetes mellitus and AIDS) can easily transform a normally mild infection into a rapidly advancing threat to life. SSTIs present clinically diverse challenges requiring management strategies that efficiently and effectively identify those cases requiring immediate attention and intervention, whether medical or surgical, from those less severe cases. Your skin is the largest organ of your body [5]. Its function is to protect your body from infection. Sometimes the skin itself becomes infected. Skin infections are caused by a wide variety of germs, and symptoms can vary from mild to serious. Mild infections may be treatable with over-the-counter medications and home remedies, whereas other infections may require medical attention. Read on to learn more about skin infections and what to do if you have one.

The following are four different types of skin infections:

1. Bacterial skin infections
2. Viral skin infections
3. Fungal skin infections
4. Parasitic skin infection

Symptoms of Skin Infection

1. An irritated area of skin that tends to expand
2. Swelling
3. Tenderness
4. Pain
5. Warmth
6. Fever
7. Chills
8. Spots
9. Blisters
10. Skin dimpling

11. Pus
12. Blisters
13. Skin sloughing, breakdown
14. Dark, necrotic-appearing skin or skin that becomes discolored and painful

Bacterial Skin Infections involve microbial invasion of the skin with various causes and severities. Bacterial infections may be treated with antibiotics [6].

Cellulitis, Infection, skin, bacterial, Skin Infection, bacterial

Risk for Skin Infections

Have poor circulation, Have diabetes, Are older, Have an immune system disease, such as HIV/AIDS

Have a weakened immune system because of chemotherapy or other medicines that suppress your immune system.

Have to stay in one position for a long time, such as if you are sick and have to stay in bed for a long time or you are paralyzed, Are malnourished [7].

The Skin as a Milieu for Bacterial Growth

The skin is an intricate habitat for many bacteria. A sterile milieu prenatally, human skin soon becomes host to resident bacteria after birth. The type and density of bacteria are determined by anatomic location, local humidity, the amount of sebum and sweat production, and the host's hormonal status and age. Bacterial skin flora is commensal, symbiotic, or parasitic relative to the host; although alterations in host immune status are known to have a significant impact, the type of relationship established is often inherent to the bacteria. Persistent colonization is the result of the ability of bacteria to adhere to skin epithelium, grow in a relatively dry and acidic milieu, and rapidly re-adhere during the normal process of desquamation [8].

The skin is a milieu for controlled bacterial growth. Skin supports the growth of commensal bacteria, which protect the host from pathogenic bacteria. Environmental and local factors, host immunity, and organism adherence and virulence are intricately related to cutaneous infection. Resident gram-positive bacteria include *Staphylococcus*, *Micrococcus*, and *Corynebacterium* sp. *Staphylococcus aureus* and *Streptococcus pyogenes* are notoriously pathogenic in the skin. In order for bacteria to be pathogenic, they must be able to adhere to, grow on, and invade the host. Bacteria possess numerous virulence genes that allow for growth in these privileged niches. Epidermal infections caused by *S. aureus* and *S. pyogenes* include impetigo and erythema [9, 10].

Conclusion

Bacterial skin infections have a variety of presentations from localised, trivial infection to rapidly progressive infection with systemic toxicity and considerable mortality. It is important to be able to recognise and treat these infections in the community, and in cases of severe infection to refer the patient promptly

for specialist care. And the skin is an intricate habitat for many bacteria. A sterile milieu prenatally, human skin soon becomes host to resident bacteria after birth. The type and density of bacteria are determined by anatomic location, local humidity, the amount of sebum and sweat production, and the host's hormonal status and age.

Molecular approaches to characterizing microbial diversity have dramatically changed our view of the skin microbiome, subsequently raising many important questions about the host-microorganism relationship and its relevance to skin disease. Although it is now clear that several dominant organisms (that is, *Staphylococcus* and *Propionibacterium* spp.) constitute a large proportion of the skin microbiota, little is understood about the rare or transient organisms making up the balance. It is unclear what factors drive variation in these organisms, and how fluctuation is associated with skin disease. Metagenomic analysis to elucidate the full complement of microbial genes and their functions should provide insight into these questions. The US National Institutes of Health Common Fund Human Microbiome Project aims to characterize the human microbiota and its role in health by examining the microbial diversity of 250 healthy volunteers sampled at 18 skin sites, including two skin sites, nine oral cavity sites, the nares, the stool and five vaginal samples for women¹⁰¹. These results from healthy volunteers will be used to guide and examine the statistical power of clinical studies, including investigations into the skin disorders acne, AD and psoriasis.

References

- 1 Feng Siliang, Bao Linlin, Du Lanying, Liu Shuwen, Qin Chuan, et al. (2020) Inhibition of SARS-CoV-2 (previously 2019-nCoV) infection by a highly potent pan-coronavirus fusion inhibitor targeting its spike protein that harbors a high capacity to mediate membrane fusion. *Cell Res* 30: 343-355.
- 2 Outlaw Victor K, Bovier Francesca T, Mears Megan C, Cajimat Maria N, Lin Michelle J, et al. (2020) Inhibition of Coronavirus Entry In Vitro and Ex Vivo by a Lipid-Conjugated Peptide Derived from the SARS-CoV-2 Spike Glycoprotein HRC Domain. *mBio* 11.
- 3 Budker Tatiana, Subbotin Vladimir M, Wong So C, Hagstrom James E, Wolff Jon A, et al. (2006) Mechanism of plasmid delivery by hydrodynamic tail vein injection. I. Hepatocyte uptake of various molecules. *J Gene Med* 8: 852-873.
- 4 Lutz Carla, Erken Martina, Noorian Parisa Sun, Shuyang, McDougald Diane, et al. (2013) Environmental reservoirs and mechanisms of

Molecular approaches to characterizing microbial diversity have dramatically changed our view of the skin microbiome, subsequently raising many important questions about the host-microorganism relationship and its relevance to skin disease. Although it is now clear that several dominant organisms (that is, *Staphylococcus* and *Propionibacterium* spp.) constitute a large proportion of the skin microbiota, little is understood about the rare or transient organisms making up the balance. It is unclear what factors drive variation in these organisms, and how fluctuation is associated with skin disease. Metagenomic analysis to elucidate the full complement of microbial genes and their functions should provide insight into these questions. The US National Institutes of Health Common Fund Human Microbiome Project aims to characterize the human microbiota and its role in health by examining the microbial diversity of 250 healthy volunteers sampled at 18 skin sites, including two skin sites, nine oral cavity sites, the nares, the stool and five vaginal samples for women¹⁰¹. These results from healthy volunteers will be used to guide and examine the statistical power of clinical studies, including investigations into the skin disorders acne, AD and psoriasis.

Acknowledgement

None

Conflict of Interest

None

persistence of *Vibrio cholerae*. *Frontiers in Microbiology* 4: 375.

- 5 Harris Jason B, LaRocque Regina C, Qadri Firdausi, Ryan Edward T, Calderwood Stephen B, et al. (2012) Cholera. *Lancet* 379: 2466-2476.
- 6 Tognotti, Eugenia (2011) the dawn of medical microbiology: germ hunters and the discovery of the cause of cholera. *J Med Microbiol* 60: 555-558.
- 7 Lippi D, Gotuzzo E (2014) the greatest steps towards the discovery of *Vibrio cholerae*. *Clin Microbiol Infect* 20: 191-195.
- 8 Howard-Jones N (1984) Robert Koch and the cholera vibrio: a centenary. *British Medical Journal* 288: 379-381.
- 9 Pettersson E, Lundeberg J, Ahmadian A (2009) Generations of sequencing technologies. *Genomics* 93: 105-111.
- 10 Tang Tiffany, Bidon Miya, Jaimes Javier A, Whittaker Gary R, Daniel Susan, et al. (2020) Coronavirus membrane fusion mechanism offers a potential target for antiviral development. *Antiviral Research* 178: 104792.