Translational Biomedicine©
14 (4) 2023 : 001-002 • Review Article

# Bacterial pathogenesis: bacterial pathogens

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**AUTHORS' CONTRIBUTION: (A)** Study Design · **(B)** Data Collection . **(C)** Statistical Analysis · **(D)** Data Interpretation · **(E)** Manuscript Preparation · **(F)** Literature Search · **(G)** No Fund Collection

## ABSTRACT

Emerging pathogens are now considered to be a major microbiologic public health threat, and medical communities have been dealing with emerging and reemerging infectious diseases since the 1950s. This review focuses on bacterial emerging diseases and examines the factors that contributed to their emergence as well as potential obstacles in the future. We found 26 major bacterial-based emerging and recurrent infectious diseases; the majority of them came from either animals (known as zoonoses) or water sources. The following are significant contributors to the emergence of these bacterial infections: advancement of new demonstrative apparatuses, like enhancements in culture strategies, improvement of atomic procedures and execution of mass spectrometry in microbial science; increase in human bacterial pathogen exposure as a result of shifts in sociodemographics and the environment; and the emergence of more lethal bacterial strains as well as opportunistic infections, particularly affecting populations with compromised immune systems. It is difficult to precisely define their implications for human disease and necessitates the use of experimental models and the comprehensive integration of microbiological, clinical, and epidemiologic aspects. To better comprehend the clinical significance of these emerging waterborne and zoonotic diseases, it is urgent to allocate financial resources for their collection.

At least fifty new infectious agents have been identified in the last 40 years; about ten percent of them are bacteria. Similar to N. mikurensis, some of these have distinct clinical signs and necessitate specific antibiotic treatments and diagnostic tools. We discuss 26 significant new bacterial pathogens that have been discovered in the last fifty years. When it caused a clinical entity that was distinct from the other species in the genus, we decided to include only new genera and species that belonged to a previously characterized genus. As of now, the list is far from complete, and not all newly discovered pathogenic species are included. For instance, only two of the typhus and six of the spotted fever groups of Rickettsia were known to be human pathogens prior to 1984. At this time, at least 25 species of the spotted fever family are known to exist, the majority of which are either highly pathogenic to humans or strongly suspect of being so. In addition, new virulent strains of previously known species have been discovered, such as the enterohemorrhagic Escherichia coli, which in 2011 in Germany caused a large outbreak of haemolytic uremic syndrome and were linked to sprout consumption.

**Keywords:** Disease causation; emerging bacteria; emerging infectious diseases; intracellular bacteria; Koch postulates; zoonoses

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**Word count:** 1408 **Tables:** 00 **Figures:** 00 **References:** 10

**Received:** 3.07.2023, Manuscript No. ipacm-23-13561; **Editor assigned:** 5.07.2023, PreQC No. P-13561; **Reviewed:** 19.07.2023, QC No. Q-13561; **Revised** 24.07.2023, Manuscript No. R-13561; **Published:** 28.07.2023

## INTRODUCTION

It was thought that bacterial diseases could be easily controlled after Alexander Fleming discovered penicillin in 1928 and subsequent scientific advancements in the 20th century. However, physicians have been confronted with emerging and reemerging infectious diseases (EIDs) since the 1950s, posing significant problems for public health and financial resources [1]. For instance, in 2010, medical professionals were confronted with an enigmatic clinical picture that linked a severe inflammatory syndrome to vascular events like transient ischemic attacks or venous thromboembolisms. At least ten cases were reported, mostly in patients with autoimmune disorders or blood cancers [2]. A eubacterial 16S RNA PCR followed by genome sequencing revealed the presence of Neoehrlichia mikurensis, but no microbiologic agent was found, and no clinical improvement was observed on various antibiotic regimens. The Ehrlichia spp. is related to this strict intracellular bacterium, a tick-borne zoonotic pathogen is emerging as the agent of human ehrlichiosis. Following that, patients received doxycycline treatment, and their condition quickly improved [3].

EIDs are infections that have only recently been discovered in humans or that are rapidly spreading among humans in terms of incidence or distribution across different regions. EIDs are now considered to be a major microbiologic public health threat, despite the fact that they have been a problem for millennia [4]. However, the scientific community has recently shown an increased interest in the issue.

Microorganisms invade a host and then multiply in close proximity to the host's tissues, causing an infection [5]. Disease, a fatal condition that does not always involve infection, is distinct from infection. Numerous infections, ranging in severity from mild to severe, can be brought on by bacteria. A bacterium's relative pathogenicity is reflected in its disease-causing capacity [6]. Bacteria can be divided into three main categories on this basis. When secluded from a patient, straightforward or essential microbes are viewed as plausible specialists of infection. Pathogens that are isolated from patients whose host defenses have been compromised are known as opportunistic pathogens [7]. They might be the ones spreading disease. Last but not least, some bacteria, like Lactobacillus acidophilus, are regarded as non-pathogenic due to the fact that they rarely or never cause disease in humans. However, due to the adaptability of bacteria and the detrimental effects of modern radiation therapy, chemotherapy, and immunotherapy on resistance mechanisms, their classification as no pathogens may change. In fact, it is now known that some bacteria, which were once thought to be harmless, can cause disease.

Serratia marcescens, for instance, is a prevalent soil bacterium that in compromised hosts causes pneumonia, infections of the urinary tract, and bacteraemia [8]. A measure of an organism's pathogenicity is virulence. The organism's capacity to cause disease despite host resistance mechanisms is directly related to its degree of virulence; it is influenced by a number of factors, including the bacterium's virulence factors, entry route into the body, specific and nonspecific host defense mechanisms, and the number of infecting bacteria [9]. Virulence can be experimentally measured by determining the number of bacteria needed to kill, infect, or cause lesions in an animal within a predetermined time frame after the bacteria are administered through a predetermined route. As a result, when comparing the relative virulence of various bacteria, calculations of a lethal dose affecting 50% of a population of animals (LD50) or an effective dose causing a disease symptom in 50% of a population of animals (ED50) are useful [10].

## CONCLUSION

There are a vast number of prokaryote species in our environment, some of which may be harmful to humans. Zoonoses are the most recent emerging bacterial diseases that originate in animals. Zoonotic agents can be spread to humans through direct contact, bites or scratches, arthropod vectors, eating contaminated food, and coming into contact with dead animals or water or soil that has been contaminated with feces. Water sources, particularly water contaminated with amoebae, are an additional significant reservoir for prokaryotes. At last, numerous microorganisms with a potential pathogenic job are essential for the ordinary greenery in people. The dynamic equilibrium that exists between humans, prokaryotes, and their environment has been disrupted by major sociodemographic and environmental changes over the past century. This has increased human exposure to some environmental pathogenic species and person-to-person transmission of commensal bacteria.

Sociodemographic changes Fruitful rise of novel irresistible specialist by and large requires their quick scattering among human populaces. As a result, the spread of diseases like the plague in the 14th century or scrub typhus, which is caused by Orentia tsutsugamushi, among Allies during World War II is a direct result of an increase in population density. Healthcare-associated infections, such as Clostridium difficile infections, are now a significant public health challenge as a result of the rising population density, particularly in hospital settings, and the rising use of invasive procedures. Controlling new bacterial diseases will be difficult, if not impossible. New technologies like social networks and media, on the other hand, can be used to quickly identify the centers of potential epidemics and prevent their uncontrolled spread. The 2010 Haitian cholera outbreak mapping, which was based on reports from social media and the media, is a promising example. In addition, resources ought to be allocated for high-quality clinical studies in order to precisely define the clinical relevance of recently discovered bacteria, develop precise diagnostic tools, and evaluate the advantages of antibiotic treatments in order to avoid over-prescribing for antibiotics. Because of the increased spread of infectious diseases brought about by globalization, international collaborations are of the utmost importance. In addition, such collaborations will assist researchers in avoiding inconclusive, low-powered studies.

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