Virulence Factors, pathogenesis, and antibacterial resistance in pseudomonas areguinosa

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Abstract

Pseudomonas aeruginosa is a common bacterium, Gram-negative opportunistic pathogen capable of infecting humans with compromised natural defenses and causing severe pulmonary disease. It is one of the leading pathogen associated with nosocomial infections. It has a vast arsenal of pathogenicity factors that are used to interfere with host defenses. Pathogenesis in P. aeruginosa facilitates adhesion, modulate or disrupt host cell pathways, and target the extracellular matrix. The propensity of P. aeruginosa to form biofilms further protects it from antibiotics and the host immune system. P. aeruginosa is intrinsically resistant to a large number of antibiotics and can be acquired resistance to many others, making treatment difficult. ical for the development of effective therapeutic strategies to control the damage in the lung.

Introduction

P. aeruginosa is a motile, non-fermenting, Gram-negative organism belonging to the family Pseudomonadaceae. In 1850s, Sédillot observed that a blue-green discharge was frequently present and associated with infection in surgical wound dressings. The infectious organism has a rod-shaped and blue-green pigmented bacterium. By 1961, the ability of this organism to cause both severe acute and chronic infections was recognized. In 1960s, P. aeruginosa emerged as an important human pathogen. Despite anti-pseudomonas activity being one of the pharmaceutical drug discoveries for several decades. It remains one of the most recalcitrant and difficult to treat organisms. Accordingly, P. aeruginosa result has achieved Superbug status.

Pathogenesis and Virulence Factors

Pathogenesis in P. aeruginosa is mediated by multiple bacterial virulence factors that facilitate adhesion and/or disrupt host cell signaling pathways while targeting the extracellular matrix **(Figure 1)**. P. aeruginosa stands out as a unique and threating organism as it is capable of causing severe invasive disease and of evading immune defenses causing persisting infections that are nearly impossible to eradicate

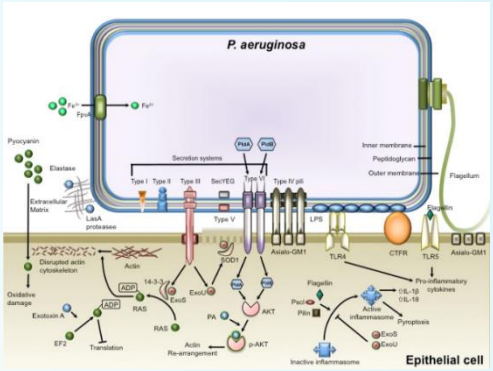

Figure (1)

Lipopolysaccharide

LPS is a predominant component of the outer membrane of P. aeruginosa. Bacterial LPS typically consist of a hydrophobic domain known as lipid A (or endotoxin), a non-repeating core oligosaccharide, and a distal polysaccharide (or O-antigen). LPS plays a prominent role in activation the host's innate and adaptive (or acquired) immune responses; and, eventually causes dysregulated inflammation responses that contribute to morbidity and mortality. Recognition of LPS occurs largely by TLR4–MD2–CD14 complex, which is present on many cell types including macrophages and dendritic cells. A number of LPS vaccines have been investigated for use in cystic fibrosis in phase II and III clinical trials; however, these have not been successful. The LPS based vaccines provided little immunity and did not appear to protect the patients from infection with P. aeruginosa.

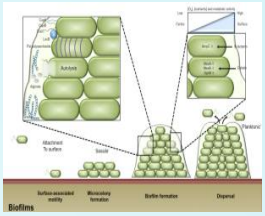

Figure (2)

Quorum Sensing

Quorum sensing is a mechanism of bacterial "cell-to-cell" communication via diffusible chemical compounds. A critical number of bacteria (the quorum) are required to produce a sufficient amount of a secreted signal molecule (termed an autoinducer) to trigger expression of a large regulon. Quorum sensing and biofilm development are two social phenomena exhibited by bacteria. The connection between quorum sensing and biofilms has been named sociomicrobiology.

Biofilm Formation

P. aeruginosa is capable of forming complex structures called biofilms. Resistance to antimicrobial agents is the most important features of biofilm infections. Biofilm development is a complex process and partly controlled by quorum sensing signals **(Figure 2)**. Furthermore, a variety of components play a role in the initial attachment of cells to the surface and development of biofilm matrix including extracellular DNA. It has been demonstrated that cells growing in a biofilm can be up to 1000 fold more resistant to antibiotics.

Antimicrobial Resistance

P. aeruginosa can be an especially challenging organism to treat once infection has been established as it is intrinsically resistant to many of the available antibiotics. The outer membrane of P. aeruginosa is restricted the penetration of antibiotics and the efficient removal of antibiotics molecules by efflux pumps before acting on their targets. P. aeruginosa has the genetic capacity to inactivate and modify of antibiotics. This bacterium can become resistant through mutational changes in antibiotic's targets.

Conclusion

In conclusion, it would be impossible to remove P. aeruginosa from the environment, even the internal environment of the hospital because it is so hardy and metabolically versatile. However, the last two decades have seen a remarkable addition to active medication and therapy to the regimen for treating CF lung infection. These therapies have enhanced the overall health of patients with CF and, they are apparently part of the reason that demanded survival has increased.

Reference: Alaa Alhazmi. Pseudomonas aeruginosa – Pathogenesis and Pathogenic Mechanisms. International Journal of Biology; Vol. 7, No. 2; 2015. doi:10.5539/ijb.v7n2p44