

# Bacteria Associated Molecules: Virulence Factors

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## Description

"Virulence factors are bacteria-connected molecules that are needed for a bacterium to cause disorder while infecting eukaryotic hosts such as humans. A surprisingly big number of virulence factors are encoded by prophage infecting bacterial pathogens, being cholera toxin, Shiga toxin, and diphtheria toxin. These three samples are a subgroup of virulence factors well known as exotoxins: soluble proteins that in some manner interfere with usual functioning of eukaryotic tissues (see 'Exotoxins'). Typically, it is hard to understand why these virulence factors would be prophage encoded instead of expressed from genes detected on the nonverbal portion of the bacterial chromosome. One possible explanation is that these virulence factors contribute to phage fitness. Clear way that this could occur if the host bacterium is more fit as a result of phage-encoded virulence factor utter, resulting in greater lysogen and consequently prophage fitness. In other words, maybe phage encoding of bacterial virulence factors is just other sample of lysogenic conversion. On the other hand, phage-encoded exotoxins could serve to modify environments in ways that are favourable to phage-like growth strategies, that is, impacting rates of virion circulation also densities of phage-susceptible bacteria, instead of affecting only bacteria-like population growth strategies.

Virulence factors are significant for microbial pathogenesis. A mutation of a virulence factor from a virulent pathogen will attenuate the pathogen strain. However, virulence factors may also be in attenuated and even avirulent strains. The attenuation of a virulent pathogen may be because to mutation of one virulence factor rather than all virulence factors.

## Branches of virulence factors

Discovering therapy options for pathogens is a continuous struggle, especially in the age of antibiotic resistance. It is becoming increasingly normal that virulence factors are recognized at the molecular and genetic measure, which opens up the chance of targeting virulence factors as a form of therapy against pathogens.

Many antibiotics kill both pathogenic and commensal, not injurious, bacteria, which can lead to adverse side effects. Since commensal

bacteria will not likely share a pathogenic bacteria's virulence factors, drugs choosing virulence factors can apparently prevent many of these deleterious effects. likewise, infections caused by or relevant to biofilms are not always treatable by antibiotics and could instead be handled by virulence factor-related drugs.

The fast evolution of the third-generation sequencing technologies (i.e. Pacific Biosciences and Oxford Nanopore) in late years enable the easy availability of complete/draft genomes of bacterial pathogens for the scientific community. However, it still a challenge for microbiologists or physicians with limited bioinformatics skills to productively define and extract biologically related information from volumes of genomic data. consequently, we recently developed an automatic and comprehensive platform for accurate bacterial VF recognition, named VFAnalyzer.

## Conclusion

The success of a pathogen to establish an infection in the host depends on its capability to counter the continuous onslaught mounted by the host to clear off the infection. The moderators of virulence in the bacterial system are often the moonlighting proteins, which are the main weapons for the host targeting and thus needs our sudden attention. Pathogens, whether intracellular or extracellular in nature, extensively use the secreted proteins to modulate the central pathways of host's signaling machinery. In this analysis, we have talk about some important virulence factors of two human pathogens, Mtb—the causative agent of the disorder tuberculosis and B. anthracis—the causative agent of the disease anthrax. Since, the secreted factors can be successfully targeted by therapeutic molecules or vaccines, an in-depth understanding of their part in virulence will assist in recognition of the 'right factors' which are most pivotal for the pathogen's survival.

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