

Bacteria Associated Molecules and Virulence Factors

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Description

Viral factors are bacteria-binding molecules necessary for the bacteria to cause disorders while infecting eukaryotic hosts such as the humans. Surprisingly large number of virulence factors are encoded by the propellers that infect pathogenic bacteria, namely cholera toxin, shiga toxin, and diphtheria toxin. These three patterns form an alternative set of virulence factors also known as exotoxins, soluble proteins that interfere in one way or another with the normal functioning of eukaryotic tissues ("exotoxins"). Collectively, it is difficult to understand why these virulence factors are encoded by the prophage instead of being expressed by genes detected on the non-viral portion of the bacterial chromosome. One possible explanation is that these virulence factors contribute to phage abundance. This is clearly possible if the host bacterium is in better shape due to the virulence factor encoded by the phage, leading to a greater capacity to lysogen and, therefore, to prophage. In other words, it is possible that bacterial phage-encoding virulence factors are just another template of lysogenic conversion. On the other hand, exotoxins encoded by phages could serve to modify the environment in favour of phage-like developmental strategies, meaning that they would have an impact on the rate of circulation of the phage. virions as well as on the density of phage-sensitive bacteria rather than influencing the growth strategies of bacterial-like populations only.

Molecules and virulence factors

Microbial factors are very important for the pathogenesis of microorganisms. Mutation of a virulence factor of a virulent pathogen weakens the pathogenic strain. However, virulence factors can also be found in attenuated and even virulent strains of bacteria. The depletion of a virulent pathogen may result from the mutation of one virulence factor rather than all virulence factors.

The discovery of treatment options for pathogens is a constant struggle, especially in the age of antibiotic resistance. It is becoming increasingly common that virulence factors are recognised at the molecular and genetic levels, which opens the possibility of targeting virulence factors as a form of therapy against pathogens.

Many antibiotics kill both pathogenic and harmless commensal bacteria, which can lead to unwanted side effects. Since congeners do not have the ability to share virulence factors with pathogenic bacteria, drugs that select virulence factors can clearly prevent many of these deleterious effects. Similarly, infections caused by or involving biofilms are not always treatable with antibiotics and can instead be treated with drugs associated with virulence factors.

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 is 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 VF analyzer.

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 discussed about some important virulence factors of two human pathogens, Mtb—the causative agent of the disorder tuberculosis and bacterial. *B.anthraxis* is 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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