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Introduction and Evaluation of Bacterial Virulence Factors

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Opinion Article

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ABOUT THE STUDY

The ability of a microbe to cause disease in its host is known as virulence. Food can include dangerous germs that can cause disease in people who eat it. Microorganisms have a variety of virulence mechanisms that allow them to bypass host defences, infiltrate host cells, and impair or lyse them. A multitude of components in the body, including mucosal immunity, safeguard the consumer of the meal. Virulence mechanisms are constantly evolving and being passed down between microbes *via* a process known as lateral or horizontal gene transfer.

Pathogens (bacteria, viruses, fungi, and protozoa) produce virulence factors, which allow them to colonise, evade, and inhibit immune responses, enter and exit cells, and receive nutrients from their hosts. The majority of virulence factors are schematically compared between Gram positive and Gram negative bacteria.

Understanding bacterial pathogenicity and interactions with the host requires the discovery of virulence factors, which may also serve as novel targets in medication and vaccine development. Traditional methods for discovering virulence factors have significant drawbacks. Identifying the genes that support the virulence phenotype, as well as

horizontal virulence gene transfer due to genetic exchange, are two examples. Alternatives to DNA microarrays for gene expression have begun to emerge since bacterial mRNA levels do not necessarily correlate with the amount of produced protein in the cells and because it has a short average life span.

Over the last few decades, the advent of post genomic methods such as genomes, transcriptomics, and proteomics has hastened the discovery of virulence factors. Not just in drug development, but also in the hunt for bacterial virulence proteins, functional proteomics is regarded as a prominent technology. Many of the networking proteins linked to the generation of virulence bacterial factors was discovered thanks to research into protein activities. It's difficult to picture a world without proteomics research because of the quantity of data that can be uncovered.

The technology compares the protein output of virulent bacterial cells (or mutants) with that of nonvirulent bacterial cells. *Edwardsiella tarda*, the causal agent of edwardsiellosis in freshwater and marine fish, is widely dispersed in aquatic habitats and has a wide host range among a number of animals, including humans, as an example of applying proteomics in virulence factor evaluation of pathologic bacteria. The identification of virulence factors between wild type and three mutant serotypes was done using proteomic methods (highly attenuated TnphoA mutants).

Protein extraction, quantification, 2-DE, and peptide mass fingerprinting were among the techniques used. It was determined that two putative secretion systems, TTSS (Type III Secretion System) and Evp (*E. tarda* virulence protein), exist and are essential for *E. tarda* pathogenicity using a combination of these techniques and additional DNA and RNA evaluation processes. Despite the development of numerous novel techniques, gel-based proteomics remains the most widely used method for studying harmful microorganisms. Two-Dimensional Gel Electrophoresis and Mass Spectrometry (2-DE-MS) have been widely employed to characterize and compare the proteomes of pathogenic bacteria (for more on the use of proteomic techniques in the discovery of bacterial virulence factors, see this article).