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Opinion Article

# Proteomics in the Treatment of Infectious Pathogens

**Sangeetha Balashanmugam***

*Department of Medical Microbiology and Infectious Disease, Madras Medical College, Salem, Tamil Nadu, India*

## DESCRIPTION

With the rapid advancement of genomics technology, which is the study of an organism's genome and gene usage, a wealth of freely accessible genomic data is now available. The primary setting for the identification and characterization of proteins is the field of proteomics, which is the study of the entire range of proteins generated by an organism. Numerous environmental factors, particularly those brought on by infectious diseases, have an impact on the proteomic profiles of a given organism, tissue, or cell. Despite the fact that a variety of infectious agents have been the subject of proteome research such as HIV/AIDS, TB, malaria, measles, and hepatitis. A relatively limited number of infectious pathogens are accountable for the majority of infectious disease deaths. With the exception of HIV, the most of these pathogens have been responsible for significant human mortality rates for a very long time. The fact that these diseases continue to exist despite the enormous amount of scientific data generated by genomics suggests that further methodologies are required to better comprehend these conditions and develop cutting-edge methods for diagnosis and treatment.

One such approach that is increasingly being used as a tool to research various diseases conditions is proteomics. The goal of the study is to draw attention to the application of proteomics in research on infectious diseases, which are among the leading causes of death globally. Proteomics has the ability to identify functional protein networks that exist at the level of the cell, tissue, or entire organism. It is frequently used to identify expression patterns at a specific period in response to a specific stimulus. The search to precisely determine a protein's shapes and biological function is actively moving forward since proteins eventually regulate the vast majority of cellular processes. Proteomics has emerged as the top field for the identification and characterization of cellular gene products (proteins) that are present, absent, or altered in relative amounts under a specific environmental, physiological, and pathophysiological influence due to the abundance of genomic sequence data now available. For analyzing the current changes in gene expression profiles in response to a given circumstance, such as a disease state or the presence of a specific pathogen, proteomic analysis is frequently more suited than DNA microarray analysis. Serum samples associated with hepatitis have been investigated in numerous proteomic studies. Apolipoprotein A1 (ApoA1) isoform and the C-terminal portion of complement factor C3 were reported to exhibit consistently low levels in HBV-positive individuals with HCC compared to healthy participants, who showed greater mean values but also substantial variability. When compared to wild-type mice, the livers of HBV-mice had higher levels of fatty acid binding protein 5 and acyl-CoA binding protein.Immunoblotting on 2D-gels of proteins from cell culture lysates and liver tumours has been employed to identify serum autoantibodies that potentially serve as biomarkers for chronic hepatitis C or HCV-HCC. It has also been examined how HCV infection therapies affect serum protein levels. Proteins including cytoskeletal proteins, molecular chaperones (HSP70 family and HSP60), metabolic enzymes (Glutamine Synthetase (GS), enzymes involved in glycolysis, and urea cycle) have all shown significant alterations in patients. Proteomics has being utilised to identify novel biomarker which enhances the diagnosis of infection with Mycobacterium tuberculosis. Lower respiratory tract infections can be caused by a wide variety of bacteria and viruses, and studies of these pathogens' proteomes are just beginning. Proteomic investigations can aid in the identification of novel antigens for vaccine development and a deeper comprehension of pathophysiology. Examples include the identification of antigens as potential vaccine candidates in non-typable. Haemophilus influenzae, gram-negative bacteria that causes acute otitis media, sinusitis, and community-acquired pneumonia, using 2DE and two-dimensional semipreparative electrophoresis (2DPE) in conjunction with MS and tandem MS. Shotgun proteomics can now be applied to examine the proteome of different lifecycle stages by identifying peptide mass fingerprints. In one of the seminal proteomic investigations of malaria parasites, a shotgun strategy is used to examine the proteome of different Plasmodium falciparum lifecycle phases. To ascertain the protein makeup of sporozoites, merozoites, trophozoites, and gametocytes, MudPIT was used. Instead of using 2DE to separate proteins, MudPIT analysis uses 2-dimensional column chromatography. MS analysis is used to identify tryptic peptide fragments. The development of malaria prevention strategies and the study of pesticide resistance may be both benefit from a genomic and proteomic study of

**Correspondence to:** Sangeetha Balashanmugam, Department of Medical Microbiology and Infectious Diseases, Madras Medical College, Salem, Tamil Nadu, India, E-mail: sangeethabphotonics@gmail.com

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mosquito species. Recent reanalysis of genomic data and fresh proteomic data have led to a reconsideration of an early genome annotation. Proteomics is offering a fresh and potent way to examine the aetiology, diagnosis, treatment effectiveness, and disease mechanisms linked with infectious pathogens, as seen by the numerous examples given by recent studies. Pathogen proteome research has helped to identify possible targets for vaccines and medications. Proteomic technology still faces several difficulties, nevertheless. Proteomics is predicted to have an even bigger impact on solving the numerous unsolved mysteries related to infectious as well as chronic diseases as new approaches are developed and data management is made more automated.