Review of Contemporary Philosophy
ISSN: 1841-5261, e-ISSN: 2471-089X
Vol 22 (1), 2023
Pp 5776 - 5787

The Comprehensive Role of Proteomics in Elucidating the Molecular Mechanisms of Disease Pathogenesis and Diagnostics of Infectious Agents

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Abstract

Background: Proteomics, the comprehensive study of the proteome, has emerged as a critical tool in understanding disease pathogenesis. By characterizing protein functions and interactions, proteomics elucidates mechanisms underlying infectious diseases and aids in the identification of pathogen virulence factors.

Methods: This review synthesizes current proteomics technologies, including mass spectrometry and two-dimensional gel electrophoresis, that have facilitated advancements in pathogen identification and

characterization. We examine various methodologies employed for analyzing proteins derived from bacteria and viruses, highlighting their roles in diagnosing infections and developing therapeutic strategies.

Results: Recent studies reveal significant advancements in quantitative proteomics, enabling the identification of low-abundance proteins and enhancing the precision of pathogen detection. Techniques such as MALDI-TOF mass spectrometry have demonstrated high efficacy in identifying bacterial species from clinical samples, including urine and blood, while also facilitating the discovery of novel virulence factors. The integration of proteomics with bioinformatics tools has further enriched our understanding of pathogen biology and host-pathogen interactions.

Conclusion: Proteomics has revolutionized our ability to identify and characterize pathogens, providing essential insights into the molecular basis of infectious diseases. By elucidating the roles of specific proteins in disease onset and progression, proteomics offers promising avenues for improving diagnostics and therapeutic interventions. Continued advancements in proteomic methodologies will enhance our understanding of disease mechanisms and facilitate the development of innovative strategies for combating infectious diseases.

Keywords: Proteomics, Pathogenesis, Infectious Diseases, Mass Spectrometry, Virulence Factors.

Received: 05 October 2023 **Revised**: 19 November 2023 **Accepted**: 02 December 2023

1. Introduction

The whole protein composition of an organism is termed the proteome. The proteome, especially of prokaryotic organisms, encompasses many activities and pathogenic attributes, whereas proteomics pertains to the examination of these functions and traits (1). Proteomics has facilitated the identification of pathogen virulence factors and advanced the study of pathogen composition, pathogenesis, illness diagnostics, and vaccine development. Proteins derived from bacteria and viruses serve as pathogenic agents in the spread of illnesses in people and animals. Membrane proteins, cell surface proteins, and secreted proteins are crucial because to their significant involvement in pathogenicity and have been thoroughly investigated using proteomics methodologies. These proteins serve as enzymes, transport molecules, poisons, adhesins, invasive agents, evasive agents, and receptors, hence playing a vital role in the onset and progression of illness. Proteomics techniques have significantly advanced over the last decade, enabling the identification of essential proteins and the analysis of their structures, molecular activities, and involvement in illness.

Proteomics has been beneficial in identifying the bacteria responsible for different illnesses and their structural composition. Genomics can alone elucidate the pathophysiology of a disease, without the capacity to clarify the cellular state and pathogenic mechanisms of the molecules responsible for disease genesis. Proteins are acknowledged for indicating the condition of a disease by revealing the pathogenic elements that underlie the onset of sickness (9). Consequently, understanding the roles of these proteins is essential for elucidating the etiology, diagnosis, management, and treatment of infectious diseases. A multitude of proteomics technologies has been developed throughout time and has proven indispensable in the investigation of infections and the progression of diseases. Conventional proteomics methodologies, including chromatography and western blotting, have been used for an extended period. Gel-based methodologies, including 1-DE (1-Dimensional Gel Electrophoresis), 2-DE (2-Dimensional Gel Electrophoresis), and 2-DDGE (2-Dimensional Differential Gel Electrophoresis), facilitated protein separation and identification (10). Low-abundance proteins in the sample may be separated using isoelectric fractionators followed by two-dimensional gels. Isoelectric focusing (IEF) concentrates low-abundance proteins, enhancing the reliability of their identification and quantification. Commonly used fractionators are Rotofor (BioRad) and Zoom IEF fractionator (Invitrogen) (11).

The integration of Gel Electrophoresis with Mass Spectrometry (2-DE-MS) enhanced the precision of protein identification. Isotope-Coded Affinity Tag (ICAT), Stable Isotopic Labeling with Amino Acids (SILAC), and Isobaric Tag for Relative and Absolute Quantification (iTRAQ) are novel quantitative methodologies that have arisen from advancements in proteomics. Contemporary quantitative

methodologies include surface plasmon resonance (SPR) for protein-protein interactions and multidimensional protein identification technology (MudPIT), both of which are label-free instruments often used for protein identification (13, 14). Absolute quantification of proteins may be achieved using many methodologies, including protein epitope signature tags (PrEST), protein standard absolute quantification (PSAQ), and intensity-based absolute quantification (iBAQ) (15–17). Membrane-coated nanosponges, in conjunction with quantitative proteomics techniques, have recently been identified as a potent resource for the identification of virulence factors (18). The many proteomics approaches and their subdivisions are shown in Figure 1. Advancements in proteomics have enhanced our understanding of infectious illnesses, their causative agents, and diagnostic methods. This work aimed to clarify the role of several proteomics techniques in understanding the pathophysiology, diagnosis, and causative agents of infectious illnesses in people and animals. Furthermore, we examined the constraints of proteomics regarding the identification of pathogenic secreted proteins, along with its future potential.

2. The function of proteomics in pathogen identification

The first step in disease diagnosis is to ascertain the causative agent, since its accurate identification and verification facilitate the prevention of disease transmission and enhance understanding of its epidemiology. Biochemical characteristics, Gram staining, and carbohydrate metabolism are longstanding conventional techniques for bacterial identification. Proteomics methods, particularly Mass Spectrometry (MS), have lately gained prominence for the accurate identification and confirmation of bacterial infections (19, 20). Proteomic techniques are often used to elucidate pathogen architecture and other elements that enhance virulence. Proteomic techniques are used to elucidate the structures of bacterial and viral pathogens, aiming to discover both structural and non-structural proteins associated with virulence, as well as to examine metabolic and physiological aspects. The classification of unsequenced microorganisms has been facilitated by using capLC-MS/MS on an Orbitrap (21).

Proteomics has been used to detect bacterial infections responsible for numerous illnesses. Proteomics approaches have been used to detect bacterial populations in surface and soil samples. Samples were collected from children's literature in libraries throughout Texas and California, and the Orbitrap FusionTM TribridTM mass spectrometer detected several non-pathogenic and pathogenic bacterial species. S. Haemolyticus, S. Pneumoniae and A. Baumannii was the most often identified pathogenic species, responsible for skin infections and Multidrug-Resistant Tuberculosis (MDR) respectively (22). Streptomyces violaceoruber, Streptomyces albus, and Streptomyces badius were identified using MALDI-ToF-MS from soil samples obtained in the Sahara of Algeria (23).

Mass spectrometry's paramount and transformative function is in clinical microbiology, where it has shown to be an effective instrument for swiftly detecting infectious pathogens at the species level. Conventional techniques for pathogen identification are protracted, leading to a severe disease before treatment can begin (24). Antibiotic resistance arises from the use of broad-spectrum antibiotics before identifying the causal culprit, adversely affecting the patient's health (25). Forensic proteomics is an emerging technique for identifying bacterial species inside a sample. This technique relies on the identification of unique peptides and encounters many problems, including signature erosion (the loss of signature sequences resulting from the incorporation of new sequences from known species in the database), lack of statistical accuracy, and a restricted database (26). Body fluids, including urine, milk, and blood, are the most suitable specimens for microbial identification, and proteomics has effectively identified microbes from these samples, as well as from cerebrospinal fluid, joint cavity fluid, vitreous fluid, and pleural fluid.

3. Pathogen identification from urine specimens

Through the establishment of a specialized reference urine database named Urinf, 90% of 500 samples were precisely identified using MALDI-ToF (31). MALDI-ToF-MS effectively identified Corynebacterium rigelii, a pathogen responsible for urinary tract infections, in a case of urosepsis involving a 67-year-old female patient (32). The urine-short incubation MALDI-TOF (U-si-MALDI-ToF) technique was developed primarily for the identification of E. Escherichia coli, a bacterium responsible for urinary tract infections. This method targets 86% of Gram-negative bacteria implicated in urinary tract infections, including E.

Escherichia coli, Klebsiella pneumoniae, and Enterobacteriaceae were identified (33). Mass spectrometry has lately been integrated with other technologies to enhance identification precision. The Alfred 60 approach was used with MALDI-ToF-MS to identify bacteria responsible for urinary tract infections. The combined approach demonstrated greater reliability and accuracy in detecting uropathogens for the majority of positive samples (25).

The integration of mass spectrometry with other screening methods, such as flow cytometry, enhances identification quality and reduces time expenditure (34). Urine samples were first analyzed using a Sysmex (UF-1000i) flow cytometer prior to being sent for MALDI-ToF-MS analysis. This approach accurately identified 86.1% of Gram-negative bacteria without misidentifying any microorganisms (35). The integration of flow cytometry, namely the UF-5000i, with mass spectrometry decreases the duration required to identify the etiological agents of urinary tract infections from 24 hours to 1 hour (36). The combination of MALDI-ToF-MS with Urine Analysis improved sensitivity and specificity for detecting urinary pathogens in urine samples, achieving 93.4% and 96.3%, respectively, compared to 86.6% and 91.5% when MALDI-ToF-MS was used alone (37).

Leptospires responsible for leptospirosis were identified by mass spectrometry and whole cell protein spectrum analysis. MALDI-ToF-MS also detected intact leptospiral cells with peaks in urine samples (38). Researchers choose LC-MS-MS over MALDI-ToF-MS because of its superior sensitivity and specificity. A technique for detecting urinary tract infections using particular LC-MS-MS peptide signatures was developed. This targeted proteomics technology detected urinary tract infections in 97% of patients without requiring a culture and within less than 4 hours, demonstrating itself as the most quick and reliable method for pathogen detection in urinary tract infections (39). While mass spectrometry has emerged as an effective proteomics technique for detecting urinary tract infections, the culture-independent MALDI-ToF method is limited to identifying pathogens in individual microbial urine samples (40).

4. Pathogen identification from blood specimens

Similar to how mass spectrometry has streamlined and accelerated pathogen identification in blood, its integration with other technologies has significantly enhanced its efficacy in urine analysis. The microorganisms in blood culture samples were identified using comparative analysis. Compared to the SepsiTyper kit, which identified 99% (184/186) of isolates, MALDI-TOF-MS identified 90% (168/186). Consequently, it was concluded that MALDI-ToF-MS analysis is appropriate for bacterial identification in blood cultures owing to its rapidity and user-friendliness (41). MALDI-ToF-MS detected 93.43% (185/198) of Gram-negative bacteria and 78.43% (275/350) of Gram-positive bacteria from blood cultures, demonstrating specificity and sensitivity rates of 84.7% and 77.5%, respectively, in a separate study (42). Positive blood cultures were promptly cultivated on solid medium and then identified by MALDI-ToF-MS, which demonstrated reliability in bacterial identification. This method accurately identified bacteria at the species level with 64.1%, 85.0%, and 94.1% at 3, 5, and 24 hours, respectively. This is considered a feasible approach for the direct identification of microorganisms (43).

Bacteria in a blood sample were amplified using magnetite (Fe3O4) magnetic beads modified with human IgG (IgG@Fe3O4) and MALDI-ToF-MS, demonstrating superior sensitivity and reduced time compared to traditional culture-based approaches. Bacteria at a concentration of 10^5 CFU/100 μl in whole blood samples were rapidly detected (44). MALDI-ToF-MS was used to evaluate spiked blood culture samples, demonstrating an efficiency equivalent to SepsiTyper (94.4%). This method detected 82% of Gram-positive bacteria in blood samples and had a higher sensitivity (92.8%) for Gram-negative bacteria (45). The integration of MALDI-ToF-MS with immune-affinity has shown very consistent results for bacterial identification at low concentrations (500 cells/ml for blood serum and 8,000 cells/ml for whole blood samples). This combined approach successfully identified S. within around 4 hours *S. aureus* and *Escherichia coli* in clinical specimens (29).

5. Pathogen identification from milk samples

Milk is another vital bodily fluid for identifying pathogens that cause illnesses in people and animals. The only dependable source for diagnosing bacterial infections responsible for mastitis is milk. MALDI-ToF-MS detected 56 (53.3%) streptococcal isolates at the species level from a human milk sample. MALDI-ToF-MS was used to evaluate microbial diversity in 647 milk samples from women exhibiting clinical signs of mastitis. In milk samples, the predominant pathogens identified were *Staphylococcus epidermidis* (87.6%) and Staphylococcus aureus (22.1%), while *Streptococcus* (68.6%) ranked as the second most prevalent species (47). The colony culture of milk samples from cows with subclinical mastitis, followed by MALDI-ToF-MS, identified 106 out of 120 samples (88.3%) at the genus and species level (score 2.0), demonstrating more reliability than direct MALDI-ToF-MS after pre-incubation (48).

Mass spectrometry alone is inadequate for precise and fast pathogen identification; a combination methodology has shown greater reliability while conserving time. Thus, three methodologies for detecting bacteria in milk samples from calved cows or those with clinical mastitis were assessed for concordance: biochemical technique, MALDI-ToF-MS, and 16S rRNA partial genomic sequencing study. At the species level, *Escherichia coli* and *Staphylococcus aureus* was identified, while others were classified at the genus level. The positive agreement was found to be 94% across three techniques, and between 95% and 98% for each pair of methodologies (49). Over time, mass spectrometry has advanced, leading some labs to substitute biochemical methods with MALDI-ToF-MS for microbe identification in milk samples. The researchers used MALDI-ToF-MS to compare the bacterial isolates from the udder with other species in the database. Five hundred isolates were analyzed as bacterial colony material for this investigation, with 93.5% identified at the species level and 6.5% at the genus level.

Specimens that could not be identified at the species level were subjected to 16S rDNA sequencing. Streptococci, Staphylococci, Enterobacteriaceae, and Coryneform bacteria are the most prevalent (50). Wald et al. recently identified and differentiated S. Staphylococcus aureus and coagulase-negative Staphylococci were identified in 200 milk samples from animals exhibiting clinical and subclinical mastitis, as well as from cows with a somatic cell count of less than 100,000 cells/ml (51). MLADI-ToF-MS identified S. from milk samples of subclinical mastitis. Argenteus in seven isolates and S. Aureus in eight (52). In the comparison of MALDI-ToF-MS with PCR-RFLP for the detection of streptococci in milk samples, PCR-RFLP demonstrated superior efficiency and reproducibility (53). Alnakip et al. recently conducted a comparative analysis of MALDI-ToF-MS and 16S rRNA gene sequencing to identify streptococci implicated in bovine mastitis. MALDI-ToF-MS shown significant diversity in identifying streptococcus at both the species and sub-species levels. MALDI-ToF-MS is equally effective as 16S rRNA gene sequencing analysis, although it is more time-efficient and simpler to perform (54). Microbes may further be detected using mass spectrometry in many bodily fluids, including saliva, cerebrospinal fluid, and synovial fluid from both people and animals (55–57). The development of a unified MALDI-ToF-MS system is overdue, aiming to establish it as a standard and universal method for the precise identification of bacterial infections across various bodily fluids in clinical labs.

6. The use of proteomics in elucidating bacterial pathogenicity

Proteomics technologies are advancing throughout time to enhance the understanding of the genesis of almost all bacterial diseases. This strategy has revolutionized the discipline by offering a clear and varied approach to understanding etiology. Proteomic techniques are often used to examine virulence-associated factors, oxidative stress, and the function of proteins in host-pathogen interactions. Advancements in proteomics have enabled the exploration of the underlying processes of infections and the identification of the associated proteins. Pérez-Llarena and Bou (58), Katsafadou et al. (59), and Yang et al. (60) have authored many review papers in this domain. This section of the review will emphasize current progress in understanding bacterial pathogenesis.

7. Contemporary methodologies

Quantitative proteomics is increasingly favored for identifying a cohort of proteins associated with an illness, yielding favorable outcomes when the proteins are not pre-separated on a gel. The proteomes of persons with atopic dermatitis and healthy individuals were analyzed using the LC-MS-MS technique. Certain bacterial species, including *Aeromonas hydrophila*, *Staphylococcus aureus*, and *Shewanella* sp., have been identified as contributors to illness. Glyceraldehyde-3-phosphate, enolase, and chaperones such as DnaK and HtpG were identified as significant proteins in pathogenesis (61). Four acetyltransferases were identified and characterized by mass spectrometry in *Escherichia coli* (RimI, YiaC, YjaB, and PhnO). YiaC is a newly identified protein implicated in flagellar motility and bacterial pathogenicity (62). The phosphoproteome was constructed using LC-MS-MS to elucidate the process of protein phosphorylation associated with *S. aureus* was revealed. Compared to previously documented pathways, Ser/Thr kinase signaling demonstrated more efficacy in virulence (63).

A separate proteomic study examined the proteomes of ESBL and non-ESBL Klebsiella pneumoniae strains using nano LC-MS/MS. Stress proteins G and A, Lon proteases, and ElaB proteins were identified as common elements in the proteomes of the two strains. Additionally, virulence-associated proteins including lyase, oxidoreductase, catalase, and isochoristamase were identified in ESBL *K. pneumoniae*, indicating that it is a more virulent variant (64). The levels of pathogenic factors, including adenylate cyclase and O antigen, exhibited significant variation in the *Bordetella parapertussis* proteome when analyzed with nano LC-MS-MS under iron-limited conditions. The study was broadened to identify proteins that were absent or considered pseudogenes in *Bordetella pertussis*, aiming to differentiate between the two species responsible for whooping cough based on their virulence-associated proteins (65).

The proteomes of *Salmonella typhimurium* wild type and fnr null mutant were analyzed via label-free mass spectrometry. Among the 1,798 identified proteins, 153 exhibited high diversity, with each contributing to distinct metabolic functions. The fumarate nitrate reduction pathway in *Salmonella* modulates fis, a DNA-binding protein associated with virulence in Salmonella typhimurium, as shown by the results (66). The extracellular and cell-associated proteome profiles of mutant and wild-type strains of *Mycobacterium avium* hominissuis, implicated in human infections, were discovered using label-free analysis using an LTQ Orbitrap Velos mass spectrometer. The lysX gene in mutant strains was identified as important for metabolic activities, pathogenicity, and intracellular survival of the pathogen (67). Sputum and saliva from TB patients were subjected to quantitative proteomics using LTQ-Orbitrap technology to investigate the mechanisms occurring throughout the illness progression. Proteins associated with immune modulation, complement activation, and inflammation were identified in both samples. Samples from uninfected individuals included a variety of proteins associated with pathogen defense and the innate immune response (68).

Two proteins, PRRC2C and RAB14, were discovered using iTRAQ as exhibiting elevated levels among 606 proteins, whereas three bacterial taxa, *Streptococcus*, *Veillonella*, and *Haemophilus*, were shown to have a strong association with chronic rhinosinusitis. Proteins associated with these bacteria were scarce and fulfilled several functions pertaining to virulence and pathogenicity (61). In a separate study, iTRAQ was used to identify the differentially expressed proteins of *Lactobacillus acidophilus* at pH 7.4. A total of 207 proteins were identified as participating in carbohydrate and amino acid metabolism, in addition to peptidoglycan synthesis. At pH 7.5, the adhesion-related proteins fmtB and PrtP exhibited an increase, but the anti-adhesion protein pyruvate kinase was downregulated (69). In humans, *Acinetobacter baumannii* is recognized for causing nosocomial infections, including bacteremia, pneumonia, and meningitis, all of which exhibit considerable mortality and morbidity rates.

Differential proteins were identified using iTRAQ after the infection of pigs' intestines with enterotoxigenic *E. Coli* F4 (causing diarrhea in pigs) and pre-treating them with *Lactobacillus plantarum*. Cell division, differentiation, and cell cycle regulation were shown to be associated with differently expressed proteins between two bacterial species. The results demonstrated ETEC intestinal epithelial cell mechanisms and the protective role of *L. plantrum* (70). iTRAQ is the superior technique for quantitative proteome analysis,

offering more reliable and comprehensive results. Another experiment quantified the levels of Salmonella enteritidis proteins in LB medium enriched with egg white and whole egg. Protein abundance was seen to diminish when the quantity of egg white was decreased using iTRAQ. Several virulence-associated proteins were downregulated, while ABC transporters and co-factors were mostly upregulated (71).

The prevalence of ABC transporters and adhesion-related proteins in highly pathogenic bacteria was identified by LC-MS/MS and iTRAQ analysis. The sbp protein was shown to be involved in the disease's pathogenesis (90). iTRAQ combined with 2D LC-MS/MS was used to analyze the proteome of *A. baimannii* and tigecycline-resistant strain. A total of 3,639 proteins were identified, of which 961 exhibited differential expression. Functional study indicated that differential proteins were associated with cellular component organization, stress responses, protein synthesis, protein degradation, and related activities. Pathways associated with tigecycline resistance were also identified (72).

Nonetheless, recent applications of supplementary quantitative proteome approaches have emerged. The prevalence of outer membrane vesicles in coccoid was identified by a comparative proteomic analysis of coccoid and spiral-shaped *Helicobacter pylori* (gastric cancer) with the SILAC (stable isotopic labeling by amino acids in cell culture) proteomic methodology. Several proteins, including CagA, arginase RocF, and TNF-inducers, were identified as downregulated (73). Isotope dilution mass spectrometry is an alternative technique for identifying isotope-labeled proteins. An isotope-labeled 15N-Cysteine C protein in E. Coli was successfully identified via this approach (74). TMT (75,76) is a technique for measuring proteins and peptides using tissue, serum, plasma, or other bodily fluid samples from the damaged or diseased region. This approach has shown reliability in identifying proteins expressed throughout various illness stages, enabling researchers to monitor disease etiology and progression (77).

The previously stated technology has recently been replaced by membrane-coated nanosponges combined with quantitative proteomics technologies. This improved technique demonstrated significant efficacy in detecting bacterial toxins and/or pathogenic elements (18). Numerous mass spectrometry-based and isotopically labeled/label-free proteomics techniques have contributed to a deeper comprehension of the etiology of significant bacterial illnesses in humans and animals. Protein microarray is a contemporary sophisticated technology in proteomics. This include antibody microarrays, where proteins are tagged with captured antibodies; functional microarrays, which use pure proteins for diverse interactions; and reverse-phase protein microarrays, employed to investigate target proteins from cell lysates utilizing antibodies (1).

8. Identification of diagnostic biomarkers

Proteins serve as crucial indicators used for disease diagnosis, prognosis, staging, and monitoring. Hormones, carbohydrate epitopes, enzymes, genetic modifications, and receptors serve as examples of biomarkers (78). Pathogen proteins are implicated in virulence and infections, thereby serving as potential biomarkers for disease detection (79). Their significance as diagnostic indications have captivated scientists worldwide to use proteomics technology for identifying particular illness markers. Biomarkers, namely proteins and cytokines, have been identified in sheep suffering from pasteurellosis and pneumonia (80). Proteomics, including both conventional and contemporary approaches, is assuming a progressively significant role in diagnostics, delivering reliable and substantive outcomes. Over the last decade, mass spectrometry methods have progressed markedly and are becoming more valuable in the pursuit of potential diagnostic indicators. Recent advancements in quantitative proteomics and enhanced precision have facilitated the identification of efficient diagnostic markers for many illnesses (81). The LC-MS-MS technique is often used to identify conditions such as tuberculosis and periodontitis (82).

9. Conclusions

Proteomics has been essential in finding and differentiating bacterial infections, as well as in comprehending and diagnosing their pathogenesis. Employing a multifaceted approach, researchers successfully enhanced the detection of infections, and the identification and characterization of proteins implicated in pathogenicity. Proteomics facilitated the identification of the secretome of bacterial pathogens, including whole cell and membrane proteins, and provided a novel platform for preventative

medicine. Further advancements are necessary to validate and elucidate the secretory characteristics of proteins associated with bacterial pathogenicity.

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الدور الشامل للبروتيوميات في توضيح الآليات الجزيئية لمرض الإمراض وتشخيص العوامل المعدية

الملخص

الخلفية :برزت البروتيوميات، وهي الدراسة الشاملة للبروتيوم، كأداة أساسية في فهم إمراض الأمراض. من خلال توصيف وظائف البروتينات وتفاعلاتها، تسهم البروتيوميات في توضيح الآليات الكامنة وراء الأمراض المعدية وتساعد في تحديد عوامل الضراوة الممرضة.

الطرق :تستعرض هذه المراجعة تقنيات البروتيوميات الحالية، بما في ذلك مطياف الكتلة وتحليل الهلام ثنائي الأبعاد، التي أسهمت في تحقيق تقدم كبير في التعرف على الممرضات وتوصيفها. تم استعراض منهجيات مختلفة لتحليل البروتينات المستخلصة من البكتيريا والفيروسات، مع تسليط الضوء على أدوارها في تشخيص العدوى وتطوير استراتيجيات علاجية.

النتائج :كشفت الدراسات الحديثة عن تقدم كبير في البروتيوميات الكمية، مما أتاح التعرف على البروتينات منخفضة الوفرة وتحسين دقة اكتشاف الممرضات. أظهرت تقنيات مثل مطياف الكتلة MALDI-TOF كفاءة عالية في تحديد الأنواع البكتيرية من العينات السريرية، بما في ذلك البول والدم، كما ساهمت في اكتشاف عوامل ضراوة جديدة. علاوة على ذلك، أضاف تكامل البروتيوميات مع أدوات المعلوماتية الحيوية فهمًا عميقًا لبيولوجيا الممرضات وتفاعلات العائل والممرض.

الاستنتاج :أحدثت البروتيوميات ثورة في قدرتنا على تحديد الممرضات وتوصيفها، مما وفر رؤى أساسية حول الأسس الجزيئية للأمراض المعدية. من خلال توضيح أدوار البروتينات المحددة في ظهور الأمراض وتطورها، توفر البروتيوميات آفاقًا واعدة لتحسين التشخيص والتدخلات العلاجية. ستؤدي التطورات المستمرة في منهجيات البروتيوميات إلى تعزيز فهمنا لآليات الأمراض وتسهيل تطوير استراتيجيات مبتكرة لمكافحة الأمراض المعدية.

الكلمات المفتاحية :البروتيوميات، الإمراض، الأمراض المعدية، مطياف الكتلة، عوامل الضراوة.