Current application of proteomics in the veterinary field – a short summary and literature review

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Abstract

The biomedical research field's continuous search for innovative technologies has led to improved disease diagnosis, novel drug discovery, and therapeutic interventions, all aimed at enhancing animal and human health alike. In this context, proteomics has emerged as a critical new technology, focusing on detailed examinations of protein composition, abundance, structure, function, and interactions. Proteomics, the study of the entire set of proteins expressed by an organism, plays a crucial role in disease diagnosis, drug discovery, and therapeutic interventions in both human and animal health. Proteomics in veterinary medicine and animal health is an evolving field that holds significant promise for fundamental and applied discoveries related to the biology and pathology of domestic and companion species. It encompasses a broad spectrum of applications, including disease diagnosis, comparative medicine, pharmacology, nutrition, reproductive biology, livestock production, and pathology. By analysing protein profiles and interactions, proteomics contributes to enhancing animal health, welfare, and productivity across various fields of veterinary research and practice. Experimental proteomics in domestic animals offers advantages over the use of rodents, such as the ability to conduct multiple time-series samplings of biological samples for extensive analysis, allowing for the investigation of experimental and natural disease processes. This review highlights the current application of proteomics in veterinary medicine, focusing on its potential to advance diagnostics, research, and treatments in veterinary science. The current limitations of proteomics are also discussed.

Key words: *veterinary proteomics; biomarker; drug discovery; animal models; bioinformatics*

Introduction

The term "proteome" was coined by Marc Wilkins in 1995 to represent the complete set of proteins expressed by an organism (Sgrawal et al., 2013). The term can also be used to describe the assortment of proteins produced at a specific time in a particular cell or tissue. Proteomics involves studying the abundance, in-

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teractions, functions, compositions, and structures of proteins, as well as their cellular activities (Al-Amrani et al., 2021). It offers a deeper understanding of an organism's structure and function compared to genomics, the study of an organism's entire genetic material. Proteomics is more complex because protein abundance changes with time and environmental conditions. As an example, there are estimated to be nearly a million human proteins, many of which undergo modifications like post-translational modifications (PTMs), resulting in protein isoforms (Holman et al., 2013). These isoforms may have different biological activities, functions, cellular localisation, or stability compared to the canonical form of the protein, contributing to the complexity of proteomes and biological processes. In contrast, the human genome, the complete set of genetic material present in an organism, is estimated to encode about 26,000–31,000 proteins (Chandramouli et al., 2009). Additionally, identifying drug targets and characterising protein modifications are only possible through protein analysis (Graves et al., 2002). Therefore, studying genes alone cannot reveal various critical insights, such as the mechanisms behind disease development, aging, and the effects of environmental factors (Gobena et al., 2024).

Proteomics was long exclusively used in human clinical medicine (Ceciliani et al., 2014). However, in the last decade, there has been a growing interest in utilising proteomics to address different issues in the pathogenesis and diagnosis of diseases in veterinary medicine. Historically, serum protein analysis has been a crucial part of veterinary diagnostic investigations for disease pathogenesis, though this has been confined to measuring total protein, albumin, globulin, the albumin-to-globulin ratio, and conducting serum protein electrophoresis (SPE) on agarose (Eckersal, 2008). This method separates serum into about eight fractions, from albumin to the γ-globulin fraction, yet the protein bands seen on SPE conceal numerous proteins that, if identified and measured accurately, could provide a wealth of pathological and diagnostic biomarkers (Anderson, 2002) that could be used to assess biological processes, disease progression, or response to treatment.

Proteomic studies in veterinary medicine and animal health have recently increased (about 79,000 results in Google Scholar for keywords "veterinary medicine", "animal health" and "proteromics"), though they still represent a minor component of the extensive body of proteomics research. Studying the proteomes of tissues and biological fluids from animals can be applied to health and disease in veterinary medicine, paralleling research on human disease. In addition, comparative proteomics, a branch of proteomics that involves comparing the protein profiles of different biological samples to identify similarities and differences, offers additional scientific value by studying species such as cattle, dogs, poultry, cats, pigs, horses, and fish. In general, animal proteomics as a distinct field provides valuable insights into the biology and pathology of domestic species, enabling a fundamental understanding specific to each species. Comparative proteomics, by enabling the comparison of proteomes across different species in health and disease, provides insights into how species' proteomes have evolved, and the role of biomarkers in this context aids in identifying species-specific protein signatures associated with physiological changes and disease states. Proteomics can study both experimentally induced and naturally occurring disease processes in the same species, unlike human clinical studies, which rely only on patient samples from

naturally occurring disease. Experimental proteomics in domestic animals allows for greater use of multiple time-series samplings and access to non-invasive (milk, saliva, urine, stool) or minimally invasive (serum, plasma) samples in sufficient volumes for extensive analysis. Species other than rodents, such as pigs and dogs, often serve as better laboratory animal models for human physiology, especially for drug safety testing as new pharmaceuticals approach regulatory approval. Knowledge of population genetics in domestic animals, supported by decades of recorded breeding, provides invaluable insights into proteome-genome interactions (Bilić et al., 2018). Although proteomics adoption in veterinary medicine lags behind human medicine, recent activities have focused on farm animal health and disease (Doherty et al., 2008; Eckersall, 2008, 2011; Ceciliani et al., 2014).

Recent reviews highlight advances in animal proteomics over the last decade, aiming to encourage more research in this underexplored field (Ceciliani et al., 2014; Bilić et al. 2018). This review article addresses the technical challenges and showcases how comparative proteomics can tackle important issues. It also emphasises the current applications of proteomics methods in veterinary medicine, particularly in pathogenesis and diagnostics. The current limitations of proteomics are also discussed.

Proteomics: types and methods

Animal studies and preclinical research have been a crucial part of medical and basic biological and drug discovery research with research on a range of animals such as rats, mice, dogs, cats, rabbits, fish, birds, pigs, cows, and primates. Domestic animals provide significant advantages for proteomics research in terms of experimental design, sample selection, and sample preparation. They can adapt to different environments and offer a wide range of biological samples, including biofluids, cells and tissues (Bilić et al., 2018; Torres et al., 2018; Kuleš et al., 2023). The most common samples used so far in companion animals (specifically dogs) include serum and saliva (Bilić et al., 2018), though proteomic analysis have also been reported with the use of seminal plasma (Aquino-Cortez et al., 2017; De Souza et al, 2007), tear film (Winiarczyk et al., 2015), follicular fluid (Fahiminiya et al., 2010), bile (Plumb et al., 2009), cerebrospinal fluid (Nakamura, et al., 2012), synovial fluid (Kjelgaard-Hansen et al., 2007), bronchoalveolar lavage fluid (Lenz et al., 1990), liver (Lawrence et al., 2018), lymph nodes (Parachini-Winter et al., 2020) and myocardium (Yuan et al., 2006). Saliva, in particular, shows promise as an intriguing source of biomarkers, due to studies revealing a greater abundance of proteins compared to serum, the general safety for personnel and the patient during sampling, and reduced sampling stress. Further, saliva may reflect the overall physiological status of the organism, making it possible to use as a source for detection of biomarkers for early diagnosis or monitoring of disease progression (Franco-Martinez et al., 2020; González-Arostegui et al., 2022). Milk and dairy products can also be used as a source of proteins to be analysed via proteomics (Agregan et al., 2021).

Proteomics can be divided into expression proteomics, structural proteomics, and functional proteomics, each focusing on how proteins respond under stress conditions (Gobena et al., 2024). Expression (comparative) proteomics involves the qualitative and quantitative analysis of overall protein expression differences between samples affected by specific factors,

such as disease, drug treatment, or environmental conditions (Chandrasekhar et al., 2014). This approach allows for the comparison of protein expression across the entire proteome or subproteomes in normal and diseased cells. It can reveal novel proteins involved in signal transduction or identify disease-specific proteins (Al-Amrani et al., 2021; Gobena et al., 2024). Structural proteomics, also known as "cell mapping," aims to elucidate the 3D structure and intricate features of functional proteins within specific cellular organelles (Gobena et al., 2024). This field involves identifying and localising proteins within complex systems or organelles and determining potential protein-protein interactions (Chandrasekar et al., 2014). Functional proteomics investigates protein functions, molecular mechanisms within cells, and interactions among protein partners. Identifying an unknown protein that associates with partners in a specific protein complex involved in a particular mechanism can strongly indicate its biological function (Gavin et al., 2002).

In many proteomics-based approaches, abundant proteins (e.g., albumin, IgG, and transferrin) must be depleted to access low-abundance proteins. Until recently, a limitation in animal proteomics was that most depletion methods were designed for human, rat, or mouse proteins. However, the increased availability of species-specific antibodies, combinatorial peptide libraries, and library display technologies now facilitates the depletion of abundant proteins and the validation of candidate biomarkers in domestic animals (Soares et al., 2012)

Proteomics involves the resolution of complex protein mixtures into identifiable components, typically using mass spectrometry (MS) after initial fractionation. Mass spectrometry (MS) serves as a high-throughput analytical detection method capable of determining the molecular weights and chemical structures of peptides, proteins, carbohydrates, oligonucleotides, natural products, and drug metabolites (Biemann, 2014). The MS operation relies on the separation of molecules based on their mass-to-charge (m/z) ratio, achieved through high-energy electron ionisation that breaks molecules into smaller fragments (Ong and Mann, 2005). The process involves three steps: first, converting biomolecules from a liquid or solid phase into gas-phase ions; second, separating these ions based on their m/z values in a mass analyser using magnetic or electric fields; and finally, measuring and quantifying the separated ions for each specific m/z value (Yates, 2011). Other techniques used in proteomics include: one dimensional (1D) and two dimensional (2D) polyacrylamide gel electrophoresis, nuclear magnetic resonance spectroscopy, X-ray crystallography, protein microarray and Edman sequencing (Gobena et al., 2024).

Bioinformatics, using proteomic algorithms, is extensively used to manage the vast and varied data necessary for marker discovery (Domon and Abersold, 2006). These algorithms navigate the challenges of integrating data from various technologies. The primary challenge lies in extracting meaningful biological insights from large datasets (Vihinem, 2001). Databases like Reactome and Ingenuity pathway provide information on metabolism, signalling, and interactions, whilst protein pathways, internal cellular processes with distinct biological effects are documented in databases such as Kyoto Gene and Genome Encyclopedia, BioCarta, and the Pathway Knowledge Base (Croft et al., 2011; Gobena et al., 2024). Recent developments include signal transduction pathway databases such as GenMAPP and PANTHER (Mi et al., 2007).

Comparative aspects and application of proteomics in veterinary medicine

Comparative medicine is a field that studies the similarities and differences in biology among animal species, enhancing the understanding of disease mechanisms in both humans and animals. This discipline aids in translating basic scientific knowledge into clinical applications. As a component of the One Health initiative, comparative medicine represents the intersection of human and animal health, promoting a holistic approach to health issues, and underscores the importance of studying diseases shared between humans and animals, integrating human, animal, and environmental health (Macy and Horvath, 2017).

Rodents are the most economical laboratory model for comparative experimentation due to their availability and ease of management in the laboratory. However, larger animals such as dogs, sheep, goats, and pigs are more physiologically similar to humans, making them better models for certain studies. Despite this, research on companion and farm animals faces challenges such as time-consuming sample collection, high upkeep costs, and ongoing genome annotation. Proteomics can significantly impact this field by developing more accurate diagnostic tools for animal diseases, thus helping to reduce unnecessary antibiotic use (Bilić et al., 2018).

Most proteomic studies in domestic animals have focused on farm animals due to their economic impact. However, there is a growing interest in companion animal proteomics, particularly in dogs. Dogs and cats, sharing the same environment and frequently affected by diseases similar to those in humans, such as cancer, heart disease, kidney disease, and obesity, serve as valuable models for comparative proteomics research. Their anatomical and physiological similarities to humans, shared living environments, and relatively shorter lifespans render them ideal for investigating genetic diseases and response to therapies (Hayward et al., 2016; Bilić et al., 2018). Proteomics in dogs has predominantly analysed infectious diseases, including leishmaniasis, babesiosis, ehrlichiosis, dirofilariasis, and parvovirosis (Kuleš et al., 2016; Franco-Martinez et al., 2018, 2019; González-Arostegui et al., 2022). Inflammation-related proteins, haptoglobin and transferrin, were consistently detected across these diseases, indicating an inflammatory status. Apolipoprotein A-1 (Apo-A1) was commonly downregulated in cases of babesiosis, leishmaniasis, and parvovirosis, and found in the urine of dogs with *Dirofilaria immitis*. Apo-A1 is crucial for responding to oxidative damage and is also linked to obesity-related metabolic changes, showing an increase in overweight dogs. Proteomic studies suggest new biomarkers for diagnostics. For example, retinol-binding protein, elevated in urine and serum before azotemia develops could serve as an early (subclinical) indicator (biomarker) of renal damage and kidney disease (Nabity et al., 2011). These findings highlight the potential of proteomics to advance early disease diagnosis and improve understanding of canine health (González-Arostegui et al., 2022). In addition, dogs also develop tumours similar to humans, facilitating cancer research. For instance, immunoproteomics in dogs with breast cancer revealed autoantigens also present in human breast cancer (Zamani-Ahmadmahmudi et al., 2014). Other neoplasias such as hemangiosarcoma, multicentric lymphoma, squamous cell carcinoma, melanoma, osteosarcoma, mammary tumours and transitional cell carcinoma have also been studied using proteomics (González-Arostegui et al.,

2022). In cardiovascular research, dogs (and pigs) are commonly used due to their high degree of conservation in the heart proteome with humans. Studies have shown significant proteome similarities, aiding in the identification of biomarkers for diseases like idiopathic dilated cardiomyopathy in dogs, which could be relevant for humans. Veterinary proteomics contributes significantly to the identification of biomarkers for disease stratification in animals, enabling the categorisation of patients based on their distinct protein profiles. Other canine diseases studied using proteomics include congenital disease (like X-linked hereditary nephropathy), degenerative disease (chronic kidney disease, dilated cardiomyopathy, mitral valve disease and osteoarthritis), metabolic disease (obesity) and reproductive-tract disease (pyometra) (Nabity et al., 2011; Bilić et al., 2018, Ferelizza et al., 2020; González-Arostegui et al., 2022; Kuleš et al., 2023; Rešetar Maslov, 2023).

Proteomic analyses of biological fluids in healthy companion animals have created proteome catalogues, providing reference points for future studies. Notable efforts include CanisOme, a database of proteomics studies in dogs, aiding in disease research and health advancements (Fernandes et al., 2016). Biomarker identification in companion animals offers diagnostic tools and potential drug targets. For example, proteomic approaches have identified biomarkers for canine babesiosis and leishmaniosis, promising new diagnostic and treatment monitoring tools in veterinary practice (Bilić et al., 2018).

While canine models are applied in proteomic studies, feline models remain underutilised. Cats, clinically similar to humans in diseases like type 2 diabetes and muscular dystrophies, offer valuable research opportunities. For instance, feline hypertrophic cardiomyopathy (HCM) serves as a model for studying heart disease progression and treatment strategies (Liu et al., 2020). The feline urine proteome, global proteomic profiling of multiple organs during acute *Toxoplasma gondii* infections, and proteome profiles in cats with chronic enteropathies have been determined (Nie et al., 2022; Paßlak et al., 2022; Yu et al., 2023).

Farm animal proteomics primarily focuses on traits important for meat, milk, and other animal products, aiming to identify biomarkers for balancing productivity, quality, and welfare (Bilić et al., 2018). Recently, the field has expanded to include animal disease diagnostics, cancer biomarker research, and stress markers to monitor welfare under intensive farming practices. Most research has been on cattle, especially milk production and mastitis, revealing over 500 upregulated proteins in affected cows (Almeida et al., 2015; Thomas et al., 2016). Proteomic analysis of bovine nasal secretions also shows potential for studying pulmonary diseases. Proteomics has been applied to cattle adipose tissue, liver metabolism, and periparturient diseases like endometritis, lameness, and ketosis, offering new insights into dairy farming issues (Ametaj, 2017). Pigs are also significant in proteomics due to their similarity to humans and can serve as models of human disease. Research using miniature pigs has uncovered markers for acute liver failure, with potential clinical applications (Verma et al., 2011). Other farm animals, such as sheep and buffaloes, have been studied for various infections and milk production, with recent work on the buffalo plasma proteome and fibrin sealants (De Pontes et al., 2015). Proteomics also aims to discover stress markers, crucial as stress affects animal growth and meat quality. Quantitative proteomics in pigs has shown responses to Salmonella infection, offering a model for human in-

fection studies. Proteomics can be used as a mean of researching mastitis, respiratory and reproductive infections, milk production, and wool production and quality, emphasising the diverse applications of proteomics in improving animal and human health (Almeida et al., 2015; Bilić et al., 2018; Plowman et al., 2020; Thomas et al., 2016; Verma et al., 2011).

Advances in laboratory instrumentation and computational analysis in proteomics has also opened new doors for honeybee biological research at the molecular and biochemical levels, thus expanded the understanding of honeybee biology. Key signalling pathways and proteins that drive honeybee development and behavioural physiology have been identified and elucidated by means of proteomics (Altaye et al., 2019). Fisheries and aquaculture are rapidly growing industries vital to global food security, expected to meet the rising demand for animal protein as the population grows. However, aquaculture faces sustainability challenges. To address these, high-throughput omics technologies like genomics and proteomics are being increasingly applied in this field. Proteomics in fish biology research is improving our understanding of developmental biology, physiology, disease and stress responses, as well as species recognition (Jaiswal et al., 2023).

Limitations of proteomics

Studying proteins poses several challenges, primarily due to significant variations in protein expression based on cell type and environment (Gobena et al., 2024). Unlike genomics, proteomics lacks a polymerase chain reaction (PCR) equivalent, making it difficult to analyse low-abundance proteins, which often go undetected due to a typical loss of 30–40% during sample preparation (Ball and Roulhac, 2010). Additionally, maintaining native protein conformations is crucial for accurate protein interaction studies. Sample type and preparation methods significantly impact the data quality of proteomics data acquired by MS methods (Meric-Bernstam et al., 2014). Variability in experimental conditions and the absence of standardised protocols can undermine the reproducibility and comparability of proteomics findings. Processing MS-based proteomics data, particularly with extensive datasets, demands substantial time and expertise due to its complexity, necessitating advanced computational tools. Despite progress, proteomics methodologies may still exhibit limitations in comprehensively capturing the entire proteome, resulting in potential gaps in protein detection and quantification. These challenges underscore the ongoing need for refinement and standardisation within the field in order to enhance the reliability and utility of proteomics analyses.

Despite significant improvements in commercially available MS instrumentation, which offer high sensitivity, resolution, molecular specificity, and a wide dynamic range, major challenges remain in veterinary proteomics. These include incomplete characterisation of animal genome sequences, insufficient Gene Ontology annotations, and poorly mapped pathways, all of which complicate the study of non-model organisms (Bilić et al., 2018).

Whole genome sequencing of the most important animal species in veterinary sciences is a pre-requisite for application of MS in animal proteomics (Bay et al., 2012; Bilić et al., 2018). Furthermore, a notable limitation in the biostatistics of different domestic animal species is the comparatively low volume of data generated compared to more extensively researched species such as humans, mouse, or yeast.

As a consequence, domestic animal databases are significantly lagging behind in terms of information volume compared to human/mouse databases (Bilić et al., 2018).

A persistent issue in quantitative proteomics is the necessity to validate results before they can be fully accepted, often employing techniques and antibody-based methods such as Western blotting or enzyme-linked immunosorbent assays (ELISAs) to confirm protein measurements. In animal proteomics, the absence of species-specific antibodies limits these validation procedures. However, whenever available, antibodies should be used to validate results, ensuring their accuracy (Bilić et al., 2018).

Future considerations

Future directions in proteomics involve several key advancements. Technological improvements, such as the development of more sensitive and accurate MS techniques and enhanced MS data acquisition and analysis software, are essential. Achieving comprehensive proteome coverage requires refined methods to detect low-abundance proteins and effective integration of various data types. Standardising protocols and ensuring reproducibility across studies are crucial, as are advancements in detecting and quantifying post-translational modifications (PTMs). The field also focuses on enhancing quantitative proteomics, refining bioinformatics tools, and expanding applications in clinical and veterinary settings to improve disease diagnostics and personalised medicine. Additionally, addressing ethical and regulatory considerations is necessary to ensure the responsible use of proteomic technologies in both research and clinical applications.

The advancement of modern technology for monitoring and evaluating patient DNA, RNA, proteins, and metabolites has propelled the evolution of personalised health care in human medicine (Honda et al., 2012). Therapeutic decisions now rely on a few validated molecular diagnostics. However, to fully achieve the potential of personalised medicine, improvements are needed in robustness, cost-effectiveness, applicability, and regulatory compliance. Proteomics in personalised medicine identifies unique protein signatures, aiding in early diagnosis, prognosis, and treatment monitoring. By analysing individual-specific protein expression profiles, therapies can be tailored for each patient, optimising drug responses and treatment efficacy. Ultimately, proteomics enables precise and personalised healthcare interventions, improving patient outcomes in personalised medicine. A key challenge is managing the vast data from high-throughput techniques to enhance visualisation, analysis, and multi-omics integration. Despite their importance, computational tools for multidimensional data analysis remain scarce (Gobena et al., 2024).

Systems biology is a more holistic approach to describe and visualise interconnected cellular and systemic events, integrating biology and medicine with other scientific disciplines. It explains how molecular changes lead to altered cell behaviour under disease conditions, considering environmental impacts and network connectivity. This cross-disciplinary effort is essential for transforming multidimensional data into actionable information for categorising and stratifying disease states and identifying unique biomarkers for prognosis, diagnosis, and therapeutic response. A comprehensive understanding of regulated events using targeted medicines is necessary to avoid side effects and unsuccessful therapies. Systems bi-

ology can identify critical components in aberrant pathways and introduce novel clinical trial designs, targeting subpopulations where a targeted approach shows potential. This can accelerate the adoption of successful treatments and increase overall clinical success rates (Gobena et al., 2024). Systems biology leverages proteomics data to construct and analyse protein interaction networks, revealing how proteins interact and influence cellular functions. By identifying the roles of proteins in various biological pathways, proteomics enables systems biology to comprehend how these pathways interact and contribute to the behaviour of the entire system. Additionally, systems biology focuses on the dynamic changes within biological systems over time, and proteomics provides crucial temporal data on protein expression and modifications to facilitate this understanding. Detailed protein-level information from proteomics is also used to validate and refine systems biology models, ensuring they accurately depict biological processes. Integrating proteomics into systems biology enhances our grasp of biological complexity, leading to more precise models of cellular processes and advancing discoveries in health, disease, and therapeutics.

Conclusion

Proteomics is a fast, sensitive and growing technology that provides high proteome coverage and plays a crucial role in the area of biomedical sciences. Currently, it is applied drug and vaccine discovery, stem cell study, personalised medicine, and in the research and diagnosis of a plethora of diseases. Animal proteomics, despite being a neglected area of proteomics, is gaining more attention with novel studies contributing to our knowledge. This has encompassed the health and welfare of companion and farm animals alike, also benefiting human biomedicine field through the One Health Initiative.

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Aktualna primjena proteomike u veterinarskoj medicini – pregledni članak

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Stalna potraga za inovativnim tehnologijama u području biomedicinskih istraživanja dovela je do napretka u dijagnostici bolesti, otkrića novih lijekova i terapijskih intervencija, a sve s ciljem poboljšanja zdravlja životinja i ljudi. U tom kontekstu, proteomika se pojavljuje kao kritična nova tehnologija, usredotočena na detaljna ispitivanja sastava, obilja, strukture, funkcije i interakcija proteina. Proteomika, proučavanje cjelokupnog skupa proteina koje organizam eksprimira, ima ključnu ulogu u dijagnozi bolesti, otkrivanju lijekova i terapijskim intervencijama u zdravlju životinja i ljudi. Proteomika u veterinarskoj medicini i zdravlju životinja je polje u razvoju koje ima značajna obećanja za temeljna i primijenjena otkrića povezana s biologijom i patologijom domaćih životinja i kućnih ljubimaca. Obuhvaća širok spektar primjena, uključujući: dijagnostiku bolesti, komparativnu medicinu, farmakologiju, prehranu, reproduktivnu biologiju, stočarsku proizvodnju i patologiju. Analizirajući profile i interakcije proteina, proteomika pridonosi poboljšanju zdravlja, dobrobiti i produktivnosti životinja u raznim područjima veterinarskog istraživanja i prakse. Eksperimentalna proteomika u domaćih životinja nudi prednosti u odnosu na korištenje glodavaca, kao što je mogućnost provođenja višestrukih vremenskih serija uzorkovanja bioloških uzoraka za opsežnu analizu, što omogućuje istraživanje i eksperimentalnih i prirodnih procesa bolesti. Ovaj pregledni rad iscrtava trenutnu primjenu proteomike u veterinarskoj medicini, usredotočujući se na njezin potencijal za unapređenje dijagnostike, istraživanja i terapije u veterinarskoj znanosti, a raspravlja i o trenutnim ograničenjima proteomike.

Ključne riječi: *veterinarska proteomika, biološki biljeg, otkriće lijeka, životinjski modeli, bioinformatika*