

From Veterinary Medicine to
'Veterinomics'

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Editorial

Technologies that measure characteristics of large families of cellular molecules (e.g., genes, proteins, metabolites), have been collectively described by using the suffix '-omics' at the end of the name of the characteristic measured. Etymology of the suffix comes from the Latin suffix '-ome', derived from mass or many. Thanks to the omics approach, four major types of high-throughput measurements are commonly applied specifically genomics, transcriptomics, proteomics, and metabolomics. Further, over 200 '-omics' sub-disciplines have nowadays emerged, including (but not limited to) epigenomics, glycomics, interactomics, lipidomics, nutrigenomics and foodomics.

Veterinary science is concerned about the health of animals and deals with diagnosis and controls of diseases and disorders in animals, as well as with limiting spread of infectious diseases and zoonoses. The word 'Veterinomics' [1,2] to its essence and content has been coined to represent biotechnological and analytical approaches to high-throughput analysis and identification of various biomarkers for different, physiological or pathological, characteristics and conditions of animal species that are the responsibility of veterinary science (companion animals, farm animals, laboratory animals, wildlife), with the aim of improving health and welfare of animals ('welfareomics') and thus of public health.

Although the term 'Veterinomics' has not yet received wide citations, in reality, it is part of the vision for development of veterinary science in the future. In this context, Veterinomics would refer to proteins or metabolites expressed in animal cells, organs or tissues (including body fluids), which are considered to play a major role in various circumstances (normal situations or disease processes). Proteomics strategies employ a combination of efficient and high-throughput separation technologies, high resolution mass spectrometry and powerful bioinformatics tools to characterize and quantify proteins from various biological samples. Proteins that are qualitatively or quantitatively significantly altered in various diseases or pathological processes can be compared with a group of healthy ones; in this, they represent targets for new biomarkers, new diagnostic tests or new therapies.

Significant generalist examples of applying the technologies in veterinary science include the elucidation of many physiological processes occurring in the animal, the identification of differences between healthy and diseased animals and the detection of properties of bacteria involved at a disease process compared to those of the same organisms at *in vitro* conditions. Proteins and/or pathways that have been found to change during the above situations can be targets for future research. This approach can be helpful in studying host-pathogen interactions ('interactomics') for identification of animal or bacterial proteins of significance in disease processes and recovery, in organ development or in host response to stress, as well as to engineering networks and objects to understand and manipulate the regulatory mechanisms. Omics can also facilitate early and accurate diagnosis of diseases in a subclinical stage. Usually, a large array of proteins can be identified as biomarkers of respective phenotypic virulence characteristics. These should be later correlated to specific pathogenic effects in the host(s). Moreover, development of novel vaccines has also been advanced ('vaccinomics') [3]. In vaccine development, the functional genomics stage deals with experimental identification and selection of target proteins using proteomics techniques. In a proteomics approach in vaccine development, bacterial proteins (e.g., surface proteins - 'surfaceome') [4], are first resolved into their individual components, followed by digestion of each protein into its peptide fragments.

Another field of veterinary science that the methodology is increasingly used is within the food industry ('foodomics'). This includes analyses of food composition and quality, food authentication (traceability), safety assessment of genetically modified food and identification of food allergens or toxins ('chemicalomics', 'toxicomics').

Specific use of the various methods is defined by the frame of the approach employed each time. *In vitro* works include studies of microbial cells and interactions between cells or host analyses; these are advantageous in providing regulated conditions and may be used in identifying protein biomarkers associated with microbial virulence, but clarify only a limited spectrum of the microbial

proteome, as various genes are expressed and respective proteins can be identified only after their invasion to hosts. This can be partly rectified by using conditions simulating the *in vivo* circumstances, which provide relevant significant support. Further, proteomics application *in vivo* in infections contributes to elucidation of protein biomarkers in disease processes. However, in this approach, lack of fully sequenced genomes in many livestock species may prove to be a limiting factor of usage of the technologies, and hence searches of nucleotides or peptide sequences in tissue samples may fail to provide significant hits [5]. Lack of an amplification technique for proteins, which abound at tissue level during host invasion, can also be another limiting factor in those studies.

In the long term, development of 'Veterinomics' will support further progress of veterinary science in research and clinical level and, consequently, it will improve animal welfare and will enhance protection of public health.

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