Use of proteomics for diagnosis of subclinical mastitis in sheep and goats

A.I. Katsafadou and G.C. Fthenakis
University of Thessaly, Greece

Objective of the paper is to present use of proteomics in diagnosis of subclinical mastitis in sheep and goats. Traditionally, diagnosis is based on detection of infection (i.e., bacterial identification) and/or of inflammation (i.e., evidence of increased leucocyte numbers or of other biomarkers) in the mammary gland. Classical techniques include microbiological examination and evaluation of number of leukocytes ('somatic cells') in milk samples. Measurement of other biomarkers (e.g., N-acetyl-b-D-glucosaminidase, lactate dehydrogenase) in milk has also been described. However, the above techniques either offer a reduced diagnostic sensitivity or need a long time for diagnosis to be accomplished. Use of proteomics appears to be promising. By employing two-dimensional gel electrophoresis and mass spectroscopy, various proteins present in milk from animals with mastitis have been identified; these include the chaperonins (taking part in pathogen recognition) and various leucocyte-associated proteins (e.g., cathelicidin, peptidoglycan recognition protein, lymphocyte cytosolic protein 1, macrophage scavenger receptors). Moreover, in samples from animals with mastitis various whey-proteins (e.g., prostaglandin D synthase, serotransferrin, serum albumin) have been detected. Their detection can lead to rapid and accurate diagnosis of mastitis. Moreover, proteomics studies can provide specific information regarding protein expression patterns in studies of mastitis pathogenesis. Clinical application of those findings is a fruitful area of future research. Work in this presentation has received funding from the 'GOSHOMICS' program, which takes place within the SYNERGASIA 2009 action and is supported by the European Regional Development Fund and Greek national funds, project number 09SYN-23-990. The text represents the author's views.

Biography

A.I. Katsafadou has a DVM degree from University of Thessaly, Greece, and a MS from Agricultural University of Athens, Greece. Currently, she undertakes PhD studies at the University of Thessaly and the Biomedical Foundation of the Academy of Athens, where she is working in the field of application of 'omic' technologies in veterinary medicine.

agkatsaf@vet.uth.gr

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